Supplemental Table 12. Gene ontology terms for modules in the vascular smooth muscle cell dataset.

category	over_represented_pvalue	under_represented_pvalue	numDEInCat	numInCat	term	ontology	p.adjust	GeneID	module	module_num
GO:0006695	9.172E-07	1.00	14	43	cholesterol biosynthetic process	BP	0.00462	INSIG1,FDFT1,SOD1,DHCR7,MVK,LSS,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,MVD,FDPS,IDI1	yellow	VSMC_M3
GO:1902653	9.172E-07	1.00	14	43	secondary alcohol biosynthetic process	BP	0.00462	INSIG1,FDFT1,SOD1,DHCR7,MVK,LSS,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,MVD,FDPS,IDI1	yellow	VSMC_M3
GO:1902652	2.158E-06	1.00	23	111	secondary alcohol metabolic process	BP	0.00815	SREBF2,SQLE,PPARD,FDXR,SNX17,INSIG1,IDH3B,SCARB1,FDFT1,SOD1,DHCR7,MVK,LSS,IDH1,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,MVD,GBA2,FDPS,IDI1	yellow	VSMC_M3
GO:0008203	6.583E-06	1.00	21	103	cholesterol metabolic process	BP	0.01988	SREBF2,SQLE,PPARD,FDXR,SNX17,INSIG1,SCARB1,FDFT1,SOD1,DHCR7,MVK,LSS,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,MVD,GBA2,FDPS,IDI1	yellow	VSMC_M3
GO:0016197	3.140E-05	1.00	30	209	endosomal transport	BP	0.07074	PQLC1,SQSTM1,SNX9,SCRIB,VPS28,TOM1,EIPR1,SNX3,EHD2,SNX17,LAMTOR1,DCTN1,RAB35,TRIM27,PLA2G3,PTPN23,VPS51,MVB12A,WASHC1,CCDC22,SNX8,SNF8,STX10,SNX18,DENND1C,AP3D1,PLA2G4E,AP5B1,ARFRP1,PHETA2	yellow	VSMC_M3
GO:0016125	3.279E-05	1.00	21	114	sterol metabolic process	BP	0.07074	SREBF2,SQLE,PPARD,FDXR,SNX17,INSIG1,SCARB1,FDFT1,SOD1,DHCR7,MVK,LSS,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,MVD,GBA2,FDPS,IDI1	yellow	VSMC_M3
GO:0009240	4.774E-05	1.00	4	4	isopentenyl diphosphate biosynthetic process	BP	0.08009	MVK,PMVK,MVD,IDI1	yellow	VSMC_M3
GO:0046490	4.774E-05	1.00	4	4	isopentenyl diphosphate metabolic process	BP	0.08009	MVK,PMVK,MVD,IDI1	yellow	VSMC_M3
GO:0032456	1.161E-04	1.00	14	70	endocytic recycling	BP	0.17528	SCRIB,EIPR1,SNX3,EHD2,SNX17,RAB35,PLA2G3,PTPN23,VPS51,WASHC1,CCDC22,SNF8,DENND1C,PLA2G4E	yellow	VSMC_M3
GO:1903725	1.861E-04	1.00	9	31	regulation of phospholipid metabolic process	BP	0.25544	SCARB1,CHP1,FABP3,PDGFA,IDH1,PHB2,CAPN2,MTMR4,TAZ	yellow	VSMC_M3
GO:0034660	2.410E-04	1.00	50	412	ncRNA metabolic process	BP	0.30327	NHP2,TRMT12,BOP1,SND1,RTCB,AARS2,ZC3H12A,KTI12,METTL3,PUS1,TARBP2,NAT10,RRS1,LSM6,GATB,NPM3,CARS,WDR4,RRP1B,MOCS3,NGDN,QARS,PSTK,RPS21,FTSJ3,BUD23,SART1,RELA,DDX52,TRMT112,NOP14,MRTO4,GTPBP3,ELP5,SEPSECS,INTS1,RRNAD1,TRMT1,FARSA,RPL7A,KHSRP,DUS3L,TBL3,TSR3,SARS,CTU2,RBFA,PIN4,TRIR,OSGEP	yellow	VSMC_M3
GO:0009451	2.882E-04	1.00	23	141	RNA modification	BP	0.33477	NHP2,TRMT12,AARS2,KTI12,METTL3,PUS1,NAT10,PCIF1,RBM15B,WDR4,MOCS3,FTSJ3,BUD23,TRMT2A,TRMT112,GTPBP3,ELP5,RRNAD1,TRMT1,DUS3L,TSR3,CTU2,OSGEP	yellow	VSMC_M3
GO:0006412	3.888E-04	1.00	62	548	translation	BP	0.38755	CDK4,EEF1D,RPL3,RPL8,MRPS18A,AARS2,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,RPL29,EIF4EBP1,TARBP2,NAT10,EIF4B,GATB,RPLP2,MRPL43,PCIF1,CARS,DCPS,APEH,NGDN,QARS,EIF3A,LSM14B,PSTK,RPS21,TACO1,MRPL49,IGFBP5,MPV17L2,C1QBP,AIMP2,SEPSECS,NANOS3,PER1,FARSA,TUFM,RPL37,RPL7A,EEF2K,MRPL4,EIF3G,C19orf66,AKT1,PAIP1,KHSRP,MRPL20,TRAP1,MKNK2,MRPL28,SARS,RBM8A,EEF1G,MRPL34,ZNF385A,MRPS16,ZAR1L	yellow	VSMC_M3
GO:0034641	4.107E-04	1.00	390	4878	cellular nitrogen compound metabolic process	BP	0.38755	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,HDAC10,NELFE,CERK,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,H2AFY,HNRNPA0,TRIM11,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,EEF1D,TSTA3,RPL3,MPST,BOP1,SLC52A2,RPL8,SND1,RTCB,DNPH1,MRPS18A,AARS2,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,FIGNL1,BLVRA,PNKP,CPT1C,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,MUTYH,DMAP1,CIC,GTF3C2,GALK1,UNK,BLVRB,OGG1,SERTAD1,TTC5,METTL3,CXXC5,FAAP100,DND1,FASN,SMOX,RPL29,EIF4EBP1,GNPDA1,PUS1,GSR,DEAF1,SMUG1,HOXC4,OGDHL,POLR1D,TARBP2,KMT2B,C12orf10,NAT10,HM13,ZNF740,PDE4D,EIF4B,RRS1,SWAP70,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,RBM15B,CARS,SRSF9,AK2,DCPS,IRX1,WDR4,GSTO1,RRP1B,TMTC1,MVK,BRD9,RBM6,ZCCHC17,PAPSS1,APEH,PABPN1,GPX1,AIP,MOCS3,CLCF1,NGDN,SRRD,TSHZ2,QARS,SLC19A1,IMPDH2,PIR,ANPEP,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,LSM14B,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,PPOX,SEC11A,BUD23,TACO1,GMEB2,CEP164,SART1,CCDC85B,PRPF6,PBX1,RNASEH2C,KAT5,RELA,ATP5MC3,ZNF511,DDX52,IDH1,LRWD1,ALKBH4,ARNT2,MRPL49,ZFPL1,LIMD1,SGPL1,SMARCB1,CHCHD10,SLC25A39,TRMT2A,PBX4,UBTF,GATAD2A,ATIC,THOC3,MEF2B,PHB2,TRMT112,NDP,IGFBP5,BAD,CTDSP1,MLF2,OTUB1,NOP14,EID1,SSBP4,METTL13,MPV17L2,ZNF394,LGALS3,	yellow	VSMC_M3
GO:0006694	5.508E-04	1.00	20	126	steroid biosynthetic process	BP	0.46207	SQLE,FDXR,INSIG1,SCARB1,FDFT1,SOD1,DHCR7,MVK,LSS,PBX1,HSD17B1,ACLY,ARMC5,PMVK,HMGCS1,DHCR24,NSDHL,MVD,FDPS,IDI1	yellow	VSMC_M3

GO:1901360	7.447E-04	1.00	364	4575	organic cyclic compound metabolic process	BP	0.59179	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,SQLE,H2AFY,HNRNPA0,TRIM11,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,TSTA3,BOP1,SLC52A2,SND1,RTCB,DNPH1,AARS2,PDGFRA,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,FIGNL1,BLVRA,PNKP,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,MUTYH,FDXR,DMAP1,CIC,GTF3C2,SNX17,GALK1,INSIG1,BLVRB,OGG1,SERTAD1,TTC5,METTL3,CXXC5,FAAP100,LAMTOR1,DND1,PYCR1,FASN,GNPDA1,PUS1,DEAF1,SMUG1,HOXC4,OGDHL,POLR1D,TARBP2,KMT2B,SCARB1,C12orf10,NAT10,ZNF740,PDE4D,RRS1,SWAP70,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,FDFT1,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,RBM15B,CARS,SRSF9,AK2,DCPS,IRX1,DHCR7,WDR4,GSTO1,RRP1B,TMTC1,MVK,BRD9,RBM6,ZCCHC17,PAPSS1,PABPN1,AIP,MOCS3,CLCF1,NGDN,SRRD,TSHZ2,QARS,SLC19A1,IMPDH2,LSS,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,PPOX,BUD23,GMEB2,THAP4,CEP164,SART1,CCDC85B,PRPF6,PBX1,RNASEH2C,KAT5,RELA,ATP5MC3,ZNF511,DDX52,LRWD1,ALKBH4,ARNT2,ZFPL1,LIMD1,SGPL1,SMARCB1,CHCHD10,SLC25A39,TRMT2A,PBX4,UBTF,GATAD2A,ATIC,THOC3,MEF2B,PHB2,TRMT112,NDP,BAD,CTDSP1,MLF2,OTUB1,NOP14,EID1,SSBP4,METTL13,HSD17B1,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,ASMTL,GTPBP3,BABAM1,TEAD4,C1QBP,CSTF2T,TAF6L,CHERP,ZBTB	yellow	VSMC_M3
GO:0043043	8.316E-04	1.00	62	566	peptide biosynthetic process	BP	0.60782	CDK4,EEF1D,RPL3,RPL8,MRPS18A,AARS2,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,RPL29,EIF4EBP1,TARBP2,NAT10,EIF4B,GATB,RPLP2,MRPL43,PCIF1,CARS,DCPS,APEH,NGDN,QARS,EIF3A,LSM14B,PSTK,RPS21,TACO1,MRPL49,IGFBP5,MPV17L2,C1QBP,AIMP2,SEPSECS,NANOS3,PER1,FARSA,TUFM,RPL37,RPL7A,EEF2K,MRPL4,EIF3G,C19orf66,AKT1,PAIP1,KHSRP,MRPL20,TRAP1,MKNK2,MRPL28,SARS,RBM8A,EEF1G,MRPL34,ZNF385A,MRPS16,ZAR1L	yellow	VSMC_M3
GO:0006396	8.454E-04	1.00	96	950	RNA processing	BP	0.60782	NHP2,DHX16,NELFE,TRMT12,HNRNPA0,BOP1,RTCB,AARS2,ZC3H12A,SNRNP70,KTI12,GEMIN7,METTL3,PUS1,TARBP2,NAT10,RRS1,RALY,ARL6IP4,LSM6,PRPF40B,CCAR2,NPM3,PCBP4,RBM15B,SRSF9,DCPS,WDR4,RRP1B,TMTC1,RBM6,PABPN1,MOCS3,NGDN,THOC5,SF3A1,RPS21,FTSJ3,BUD23,SART1,PRPF6,DDX52,TRMT2A,THOC3,TRMT112,NOP14,LGALS3,BUD31,MRTO4,GTPBP3,C1QBP,CSTF2T,CHERP,GPKOW,ELP5,INTS1,POLR2A,CWC25,SLTM,RRNAD1,CD2BP2,TRMT1,RPL7A,RAVER1,RBM22,ZNF830,KHSRP,DUS3L,SAFB,SAFB2,MAP2K2,CACTIN,CDK11B,SSU72,AURKAIP1,TBL3,TSR3,FAM50A,SARS,CTU2,SNORD24,SNORD3J,RBM8A,RBFA,PIN4,SNORD83B,SNORD56,SNORA61,SNORD17,SNORD32A,SNORD12,SNORA71D,SNORA50C,SNORD94,AKAP17A,OSGEP	yellow	VSMC_M3
GO:0008299	9.429E-04	1.00	7	23	isoprenoid biosynthetic process	BP	0.64713	MVK,LSS,PMVK,HMGCS1,MVD,FDPS,IDI1	yellow	VSMC_M3
GO:0006518	1.032E-03	1.00	72	688	peptide metabolic process	BP	0.67764	CDK4,EEF1D,RPL3,RPL8,MRPS18A,AARS2,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,RPL29,EIF4EBP1,GSR,TARBP2,NAT10,HM13,EIF4B,GATB,SOD1,RPLP2,MRPL43,PCIF1,CARS,DCPS,GSTO1,APEH,GPX1,NGDN,QARS,ANPEP,EIF3A,LSM14B,PSTK,RPS21,SEC11A,TACO1,RELA,IDH1,MRPL49,IGFBP5,MPV17L2,C1QBP,AIMP2,SEPSECS,NANOS3,PER1,FARSA,TUFM,RPL37,RPL7A,EEF2K,MRPL4,EIF3G,C19orf66,AKT1,PAIP1,KHSRP,MRPL20,TRAP1,CTNS,MKNK2,MRPL28,SARS,RBM8A,EEF1G,MRPL34,ZNF385A,MRPS16,ZAR1L	yellow	VSMC_M3
GO:0046596	1.235E-03	1.00	7	24	regulation of viral entry into host cell	BP	0.73793	TRIM11,LGALS1,SNX3,P4HB,TRIM27,TRIM25,MID2	yellow	VSMC_M3
GO:0046165	1.261E-03	1.00	17	108	alcohol biosynthetic process	BP	0.73793	INSIG1,FDFT1,SOD1,DHCR7,MVK,PCK2,LSS,ISYNA1,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,PGP,MVD,FDPS,IDI1	yellow	VSMC_M3
GO:0043414	1.271E-03	1.00	31	254	macromolecule methylation	BP	0.73793	NELFE,TRMT12,H2AFY,KMT2E,DMAP1,METTL3,KMT2B,SETD1B,PCIF1,KDM1B,RBM15B,WDR4,ETFBKMT,PRMT2,FTSJ3,BUD23,SMARCB1,TRMT2A,GATAD2A,TRMT112,GTPBP3,MTA2,MTHFR,RRNAD1,TRMT1,CARM1,COPRS,METTL22,EHMT1,MBD3,NTMT1	yellow	VSMC_M3
GO:0008202	1.349E-03	1.00	28	217	steroid metabolic process	BP	0.75439	SREBF2,SQLE,PPARD,PDGFRA,FDXR,SNX17,INSIG1,LAMTOR1,SCARB1,FDFT1,SOD1,DHCR7,MVK,LSS,PBX1,SGPL1,HSD17B1,ACLY,ARMC5,PMVK,HMGCS1,DHCR24,NSDHL,MVD,GBA2,FDPS,IDI1,STUB1	yellow	VSMC_M3
GO:0008654	1.422E-03	1.00	28	222	phospholipid biosynthetic process	BP	0.75981	PPARD,PIGO,SOCS5,TTC7A,INPPL1,PCYT2,PTDSS2,DGKZ,CHP1,CISH,MVK,FABP3,PDGFA,IDH1,ISYNA1,CAPN2,PIP4K2B,DPM3,PMVK,MTMR4,HMGCS1,TAZ,MVD,SLC44A3,VAC14,FADS1,FDPS,IDI1	yellow	VSMC_M3
GO:0019637	1.698E-03	1.00	74	743	organophosphate metabolic process	BP	0.85155	ENPP1,GUK1,NUDT3,PPARD,DNPH1,PIGO,SOCS5,TTC7A,GALK1,PLCD1,OGG1,INPPL1,PCYT2,FASN,PTDSS2,SMUG1,OGDHL,SCARB1,PDE4D,ACSL1,FDFT1,TKT,DGKZ,CHP1,CISH,AK2,MVK,FABP3,PAPSS1,PDGFA,MOCS3,IMPDH2,PLA2G3,ATP5MC3,IDH1,ATIC,PHB2,BAD,PLCB3,ISYNA1,ASMTL,UQCC3,CNP,ACLY,FOXK1,CAPN2,PIP4K2B,PGD,ACSF2,DPM3,FLAD1,PMVK,ATP5PD,MTMR4,HMGCS1,PGM1,GIT1,PGP,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,SLC44A3,VAC14,PLA2G4E,FADS1,NT5C,TALDO1,FDPS,IDI1,ITPA	yellow	VSMC_M3
GO:0032259	1.766E-03	1.00	34	290	methylation	BP	0.85155	NELFE,TRMT12,H2AFY,KMT2E,DMAP1,METTL3,KMT2B,SETD1B,PCIF1,KDM1B,RBM15B,WDR4,ETFBKMT,PRMT2,FTSJ3,BUD23,SMARCB1,TRMT2A,GATAD2A,TRMT112,METTL13,ASMTL,GTPBP3,COMTD1,MTA2,MTHFR,RRNAD1,TRMT1,CARM1,COPRS,METTL22,EHMT1,MBD3,NTMT1	yellow	VSMC_M3

GO:0009126	1.934E-03	1.00	9	39	purine nucleoside monophosphate metabolic process	BP	0.85155	GUK1,DNPH1,AK2,IMPDH2,ATIC,AMPD2,APRT,AK1,NT5C	yellow	VSMC_M3
GO:0006644	1.974E-03	1.00	36	314	phospholipid metabolic process	BP	0.85155	PPARD,PIGO,SOCS5,TTC7A,PLCD1,INPPL1,PCYT2,PTDSS2,SCARB1,FDFT1,DGKZ,CHP1,CISH,MVK,FABP3,PDGFA,PLA2G3,IDH1,PHB2,PLCB3,ISYNA1,CAPN2,PIP4K2B,DPM3,PMVK,MTMR4,HMGCS1,PGP,TAZ,MVD,SLC44A3,VAC14,PLA2G4E,FADS1,FDPS,IDI1	yellow	VSMC_M3
GO:0043603	2.054E-03	1.00	88	897	cellular amide metabolic process	BP	0.85381	CDK4,CERK,EEF1D,RPL3,RPL8,DNPH1,MRPS18A,AARS2,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,FASN,RPL29,EIF4EBP1,GNPDA1,GSR,TARBP2,NAT10,HM13,EIF4B,ACSL1,GATB,SOD1,RPLP2,MRPL43,PCIF1,CARS,DCPS,GSTO1,MVK,APEH,GPX1,NGDN,QARS,SLC19A1,ANPEP,EIF3A,LSM14B,PSTK,RPS21,SEC11A,TACO1,RELA,IDH1,MRPL49,SGPL1,IGFBP5,MPV17L2,C1QBP,AIMP2,ACLY,SEPSECS,NANOS3,PER1,ACSF2,FARSA,PMVK,TUFM,RPL37,RPL7A,EEF2K,MRPL4,EIF3G,C19orf66,AKT1,PAIP1,HMGCS1,KHSRP,MRPL20,TRAP1,CTNS,MKNK2,MRPL28,SARS,MVD,RBM8A,EEF1G,PLA2G4E,NT5C,MRPL34,ZNF385A,GBA2,MRPS16,ZAR1L	yellow	VSMC_M3
GO:0000478	2.149E-03	1.00	5	15	endonucleolytic cleavage involved in rRNA processing	BP	0.85381	BOP1,RRS1,RPS21,NOP14,TBL3	yellow	VSMC_M3
GO:0000479	2.149E-03	1.00	5	15	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	0.85381	BOP1,RRS1,RPS21,NOP14,TBL3	yellow	VSMC_M3
GO:0009303	2.233E-03	1.00	8	33	rRNA transcription	BP	0.86457	H2AFY,GTF3C2,NPM3,SMARCB1,SMARCA4,BRF1,GTF3C5,CAVIN1	yellow	VSMC_M3
GO:0006399	2.380E-03	1.00	23	162	tRNA metabolic process	BP	0.88731	TRMT12,RTCB,AARS2,KTI12,PUS1,NAT10,LSM6,GATB,CARS,WDR4,MOCS3,QARS,PSTK,TRMT112,GTPBP3,ELP5,SEPSECS,TRMT1,FARSA,DUS3L,SARS,CTU2,OSGEP	yellow	VSMC_M3
GO:0016071	2.409E-03	1.00	59	586	mRNA metabolic process	BP	0.88731	DHX16,NELFE,HNRNPA0,SND1,SECISBP2,CNOT3,ZC3H12A,SNRNP70,GEMIN7,METTL3,DND1,PUS1,RALY,ARL6IP4,LSM6,PRPF40B,CCAR2,PCIF1,PCBP4,RBM15B,SRSF9,DCPS,RRP1B,RBM6,PABPN1,ZNRD1,THOC5,SF3A1,SART1,PRPF6,THOC3,LGALS3,BUD31,MRTO4,C1QBP,CSTF2T,GPKOW,CWC25,SLTM,NANOS3,CD2BP2,RAVER1,RBM22,ZNF830,AKT1,PAIP1,KHSRP,SAFB,SAFB2,CARHSP1,CACTIN,CDK11B,SSU72,AURKAIP1,FAM50A,RBM8A,RNH1,TENT5B,AKAP17A	yellow	VSMC_M3
GO:0009058	2.699E-03	1.00	343	4393	biosynthetic process	BP	0.9358	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,SQLE,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,EEF1D,TSTA3,RPL3,MPST,RPL8,SND1,B4GALT1,MRPS18A,AARS2,PIGO,SECISBP2,PHF2,SOCS5,TTC7A,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,RCN3,CC2D1B,KTI12,MGLL,KMT2E,SIX5,ZNF282,ZNF296,RELB,SERP2,FDXR,EMILIN1,SEPHS1,DMAP1,CIC,GTF3C2,UNK,INSIG1,GALNT14,OGG1,SERTAD1,TTC5,METTL3,PHLDA1,CXXC5,INPPL1,PCYT2,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,GNPDA1,PTDSS2,DEAF1,HOXC4,POLR1D,TARBP2,KMT2B,AACS,SCARB1,NAT10,ZNF740,EIF4B,RALY,ACSL1,ZBTB38,SLC11A2,FDFT1,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,MCRS1,TKT,POLR2C,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,ACCS,RPLP2,CHP1,SCD,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,KDM1B,CHCHD2,SLC35C2,CARS,CISH,ST3GAL4,AK2,DCPS,IRX1,DHCR7,SELENOS,RRP1B,TMTC1,MVK,BRD9,FABP3,PAPSS1,PDGFA,APEH,AIP,MOCS3,NGDN,SRRD,TSHZ2,QARS,PCK2,IMPDH2,LSS,PIR,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,PSTK,RPS21,SMARCD2,EXTL1,BRMS1,PPOX,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,MGST3,ATP5MC3,ZNF511,IDH1,LRWD1,ARNT2,MRPL49,ZFPL1,LIMD1,MID1IP1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,SLC25A39,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,ISYNA1,SSBP4,METTL13,MPV17L2,HSD17B1,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FADS2,GLUD1,FOXK1,SDE2,ILVBL,KLF3,PKN1,CAPN2,S	yellow	VSMC_M3
GO:0046718	2.716E-03	1.00	15	100	viral entry into host cell	BP	0.9358	TRIM11,LGALS1,SLC52A2,SNX3,P4HB,SIGLEC1,SCARB1,ITGB7,TYRO3,NECTIN1,ANPEP,TRIM27,TRIM25,MID2,CLDN6	yellow	VSMC_M3
GO:1901576	2.727E-03	1.00	338	4324	organic substance biosynthetic process	BP	0.9358	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,SQLE,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,EEF1D,TSTA3,RPL3,RPL8,SND1,B4GALT1,MRPS18A,AARS2,PIGO,SECISBP2,PHF2,SOCS5,TTC7A,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,MGLL,KMT2E,SIX5,ZNF282,ZNF296,RELB,SERP2,FDXR,SEPHS1,DMAP1,CIC,GTF3C2,UNK,INSIG1,GALNT14,OGG1,SERTAD1,TTC5,METTL3,PHLDA1,CXXC5,INPPL1,PCYT2,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,GNPDA1,PTDSS2,DEAF1,HOXC4,POLR1D,TARBP2,KMT2B,AACS,SCARB1,NAT10,ZNF740,EIF4B,RALY,ACSL1,ZBTB38,SLC11A2,FDFT1,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,MCRS1,TKT,POLR2C,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,SCD,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,KDM1B,CHCHD2,SLC35C2,CARS,CISH,ST3GAL4,AK2,DCPS,IRX1,DHCR7,SELENOS,RRP1B,TMTC1,MVK,BRD9,FABP3,PAPSS1,PDGFA,APEH,AIP,MOCS3,NGDN,SRRD,TSHZ2,QARS,PCK2,IMPDH2,LSS,PIR,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,PSTK,RPS21,SMARCD2,EXTL1,BRMS1,PPOX,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,MGST3,ATP5MC3,ZNF511,IDH1,LRWD1,ARNT2,MRPL49,ZFPL1,LIMD1,MID1IP1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,SLC25A39,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,ISYNA1,SSBP4,METTL13,MPV17L2,HSD17B1,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FADS2,GLUD1,FOXK1,SDE2,ILVBL,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,MTHFR,PIP	yellow	VSMC_M3

GO:0006361	3.020E-03	1.00	4	11	transcription initiation from RNA polymerase I promoter	BP	0.95194	SMARCB1,UBTF,SMARCA4,CAVIN1	yellow	VSMC_M3
GO:0042303	3.086E-03	1.00	12	75	molting cycle	BP	0.95194	NUMA1,LRIG1,WNT10B,PDGFA,MPZL3,RELA,IGFBP5,TMEM79,PER1,NSDHL,TRADD,NOM1	yellow	VSMC_M3
GO:0042633	3.086E-03	1.00	12	75	hair cycle	BP	0.95194	NUMA1,LRIG1,WNT10B,PDGFA,MPZL3,RELA,IGFBP5,TMEM79,PER1,NSDHL,TRADD,NOM1	yellow	VSMC_M3
GO:0044539	3.089E-03	1.00	5	15	long-chain fatty acid import into cell	BP	0.95194	ACSL1,FABP3,SPX,AKT1,SLC27A4	yellow	VSMC_M3
GO:0140354	3.089E-03	1.00	5	15	lipid import into cell	BP	0.95194	ACSL1,FABP3,SPX,AKT1,SLC27A4	yellow	VSMC_M3
GO:0006397	3.266E-03	1.00	44	407	mRNA processing	BP	0.96947	DHX16,NELFE,HNRNPA0,SNRNP70,GEMIN7,METTL3,RALY,ARL6IP4,LSM6,PRPF40B,CCAR2,PCBP4,RBM15B,SRSF9,DCPS,RRP1B,RBM6,PABPN1,THOC5,SF3A1,SART1,PRPF6,THOC3,LGALS3,BUD31,C1QBP,CSTF2T,GPKOW,CWC25,SLTM,CD2BP2,RAVER1,RBM22,ZNF830,KHSRP,SAFB,SAFB2,CACTIN,CDK11B,SSU72,AURKAIP1,FAM50A,RBM8A,AKAP17A	yellow	VSMC_M3
GO:0046483	3.275E-03	1.00	343	4376	heterocycle metabolic process	BP	0.96947	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,H2AFY,HNRNPA0,TRIM11,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,TSTA3,BOP1,SLC52A2,SND1,RTCB,DNPH1,AARS2,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,FIGNL1,BLVRA,PNKP,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,MUTYH,DMAP1,CIC,GTF3C2,GALK1,BLVRB,OGG1,SERTAD1,TTC5,METTL3,CXXC5,FAAP100,DND1,PYCR1,FASN,GNPDA1,PUS1,DEAF1,SMUG1,HOXC4,OGDHL,POLR1D,TARBP2,KMT2B,C12orf10,NAT10,ZNF740,PDE4D,RRS1,SWAP70,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,RBM15B,CARS,SRSF9,AK2,DCPS,IRX1,WDR4,GSTO1,RRP1B,TMTC1,MVK,BRD9,RBM6,ZCCHC17,PAPSS1,PABPN1,AIP,MOCS3,CLCF1,NGDN,SRRD,TSHZ2,QARS,SLC19A1,IMPDH2,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,PPOX,BUD23,GMEB2,CEP164,SART1,CCDC85B,PRPF6,PBX1,RNASEH2C,KAT5,RELA,ATP5MC3,ZNF511,DDX52,LRWD1,ALKBH4,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,SLC25A39,TRMT2A,PBX4,UBTF,GATAD2A,ATIC,THOC3,MEF2B,PHB2,TRMT112,NDP,BAD,CTDSP1,MLF2,OTUB1,NOP14,EID1,SSBP4,METTL13,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,ASMTL,GTPBP3,BABAM1,TEAD4,C1QBP,CSTF2T,TAF6L,CHERP,ZBTB49,UQCC3,CNP,GPKOW,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,ELP5,KLF3,PKN1,SEPSECS,	yellow	VSMC_M3
GO:0071071	3.384E-03	1.00	5	15	regulation of phospholipid biosynthetic process	BP	0.98255	CHP1,FABP3,PDGFA,IDH1,CAPN2	yellow	VSMC_M3
GO:0045880	3.486E-03	1.00	7	31	positive regulation of smoothened signaling pathway	BP	0.98981	TXNDC15,EVC,TEDC1,RAB34,TEDC2,GAS8,NDST1	yellow	VSMC_M3
GO:0009150	3.591E-03	1.00	33	286	purine ribonucleotide metabolic process	BP	0.98981	ENPP1,GUK1,NUDT3,GALK1,FASN,OGDHL,PDE4D,ACSL1,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,UQCC3,ACLY,FOXK1,ACSF2,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0098876	3.671E-03	1.00	17	129	vesicle-mediated transport to the plasma membrane	BP	0.98981	SCRIB,EIPR1,SNX3,EHD2,SNX17,RAB35,PLA2G3,PTPN23,VPS51,WASHC1,CCDC22,SNF8,CSK,DENND1C,RAB34,PLA2G4E,ARFRP1	yellow	VSMC_M3
GO:0044403	3.671E-03	1.00	25	206	biological process involved in symbiotic interaction	BP	0.98981	TRIM11,LGALS1,SLC52A2,ZC3H12A,SNX3,P4HB,SIGLEC1,SCARB1,BCL2L1,ITGB7,TYRO3,RRP1B,GPX1,NECTIN1,ANPEP,TRIM27,THOC5,SMARCB1,THOC3,PHB2,TRIM25,SMARCA4,MID2,CLDN6,CARD9	yellow	VSMC_M3
GO:0008610	3.963E-03	1.00	55	544	lipid biosynthetic process	BP	1	CDK4,SQLE,PPARD,PIGO,SOCS5,TTC7A,MGLL,FDXR,INSIG1,INPPL1,PCYT2,FASN,PTDSS2,SCARB1,ACSL1,FDFT1,SOD1,DGKZ,CHP1,SCD,CISH,ST3GAL4,DHCR7,MVK,FABP3,PDGFA,PCK2,LSS,PLA2G3,PBX1,IDH1,MID1IP1,SGPL1,ISYNA1,HSD17B1,ACLY,FADS2,CAPN2,PIP4K2B,ARMC5,DPM3,PMVK,MTMR4,AKT1,HMGCS1,DHCR24,NSDHL,CSNK1G2,TAZ,MVD,SLC44A3,VAC14,FADS1,FDPS,IDI1	yellow	VSMC_M3
GO:0042407	4.038E-03	1.00	5	15	cristae formation	BP	1	SAMM50,CHCHD10,LETM1,UQCC3,TAZ	yellow	VSMC_M3
GO:0009167	4.171E-03	1.00	8	36	purine ribonucleoside monophosphate metabolic process	BP	1	GUK1,AK2,IMPDH2,ATIC,AMPD2,APRT,AK1,NT5C	yellow	VSMC_M3
GO:1903727	4.243E-03	1.00	4	10	positive regulation of phospholipid metabolic process	BP	1	CHP1,FABP3,CAPN2,TAZ	yellow	VSMC_M3
GO:0044249	4.387E-03	1.00	332	4271	cellular biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,EEF1D,TSTA3,RPL3,MPST,RPL8,SND1,B4GALT1,MRPS18A,AARS2,PIGO,SECISBP2,PHF2,SOCS5,TTC7A,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,MGLL,KMT2E,SIX5,ZNF282,ZNF296,RELB,SERP2,FDXR,SEPHS1,DMAP1,CIC,GTF3C2,UNK,INSIG1,GALNT14,OGG1,SERTAD1,TTC5,METTL3,PHLDA1,CXXC5,INPPL1,PCYT2,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,GNPDA1,PTDSS2,DEAF1,HOXC4,POLR1D,TARBP2,KMT2B,AACS,SCARB1,NAT10,ZNF740,EIF4B,RALY,ACSL1,ZBTB38,SLC11A2,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,MCRS1,TKT,POLR2C,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,SCD,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,KDM1B,CHCHD2,SLC35C2,CARS,CISH,ST3GAL4,AK2,DCPS,IRX1,SELENOS,RRP1B,TMTC1,MVK,BRD9,FABP3,PAPSS1,PDGFA,APEH,AIP,MOCS3,NGDN,SRRD,TSHZ2,QARS,PCK2,IMPDH2,LSS,PIR,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,PSTK,RPS21,SMARCD2,EXTL1,BRMS1,PPOX,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,MGST3,ATP5MC3,ZNF511,IDH1,LRWD1,ARNT2,MRPL49,ZFPL1,LIMD1,MID1IP1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,SLC25A39,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,ISYNA1,SSBP4,METTL13,MPV17L2,HSD17B1,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FADS2,GLUD1,FOXK1,SDE2,ILVBL,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,MTHFR,PIP4K2B,MAD2L2,	yellow	VSMC_M3

GO:0001101	4.449E-03	1.00	15	107	response to acid chemical	BP	1	PLEC,PDGFRA,KRT8,BAIAP2,LAMTOR1,BCL2L1,COL6A1,RELA,SIPA1,BAD,LAMTOR4,CD9,CAPN2,MTHFR,NSMF	yellow	VSMC_M3
GO:0006400	4.524E-03	1.00	14	85	tRNA modification	BP	1	TRMT12,AARS2,KTI12,PUS1,NAT10,WDR4,MOCS3,TRMT112,GTPBP3,ELP5,TRMT1,DUS3L,CTU2,OSGEP	yellow	VSMC_M3
GO:0044409	4.681E-03	1.00	15	106	entry into host	BP	1	TRIM11,LGALS1,SLC52A2,SNX3,P4HB,SIGLEC1,SCARB1,ITGB7,TYRO3,NECTIN1,ANPEP,TRIM27,TRIM25,MID2,CLDN6	yellow	VSMC_M3
GO:0034470	4.725E-03	1.00	39	345	ncRNA processing	BP	1	NHP2,TRMT12,BOP1,RTCB,AARS2,KTI12,METTL3,PUS1,TARBP2,NAT10,RRS1,LSM6,NPM3,WDR4,RRP1B,MOCS3,NGDN,RPS21,FTSJ3,BUD23,SART1,DDX52,TRMT112,NOP14,MRTO4,GTPBP3,ELP5,INTS1,RRNAD1,TRMT1,RPL7A,DUS3L,TBL3,TSR3,SARS,CTU2,RBFA,PIN4,OSGEP	yellow	VSMC_M3
GO:0006163	4.825E-03	1.00	34	302	purine nucleotide metabolic process	BP	1	ENPP1,GUK1,NUDT3,DNPH1,GALK1,FASN,OGDHL,PDE4D,ACSL1,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,UQCC3,ACLY,FOXK1,ACSF2,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0052372	4.916E-03	1.00	7	30	modulation by symbiont of entry into host	BP	1	TRIM11,LGALS1,SNX3,P4HB,TRIM27,TRIM25,MID2	yellow	VSMC_M3
GO:0030490	5.202E-03	1.00	9	46	maturation of SSU-rRNA	BP	1	NAT10,RRS1,LSM6,NGDN,RPS21,DDX52,NOP14,TBL3,TSR3	yellow	VSMC_M3
GO:0071704	5.233E-03	1.00	601	8083	organic substance metabolic process	BP	1	ENPP1,CD63,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,DHX16,ZNF608,LMF2,BAG6,SBF1,SNX9,HDAC10,NELFE,ACAT2,CERK,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,JADE2,TRMT12,SQLE,H2AFY,HNRNPA0,TRIM11,SGSM3,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,EEF1D,TSTA3,RPL3,SCRIB,PLEC,MPST,SHARPIN,BOP1,SLC52A2,VPS28,RPL8,SND1,CUL7,RTCB,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,IL1R1,SECISBP2,PHF2,GRHPR,SSC5D,HSPBP1,SOCS5,TTC7A,RPS9,CNOT3,KLF4,HOXA1,JOSD2,PTGR1,PSMB3,FHL3,SPRED2,EIPR1,MEAF6,ZC3H12A,FIGNL1,BLVRA,PNKP,CPT1C,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,MGLL,KMT2E,WDFY2,ACAD9,SIX5,ZNF282,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,FDXR,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,PAFAH1B3,CIC,GTF3C2,SNX17,GALK1,PPM1G,UNK,PLCD1,BCKDHA,INSIG1,GALNT14,BLVRB,OGG1,SERTAD1,TTC5,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,CXXC5,INPPL1,FAAP100,LAMTOR1,P4HB,PCYT2,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,DELE1,GNPDA1,CAVIN3,PUS1,GSR,PTDSS2,DEAF1,SMUG1,HOXC4,IDH3B,OGDHL,POLR1D,LDLRAD3,TARBP2,KMT2B,AACS,SCARB1,C12orf10,NAT10,HM13,ZNF740,PDE4D,TNS2,EIF4B,PCCB,RRS1,PEPD,SWAP70,LRP3,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,FDFT1,TNKS1BP1,MMP24,PINX1,GATB,SETD1B,GREM1,KDM2B,PDE3B,PRPF40B,MCRS1,TKT,POLR2C,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,ACCS,RPLP2,CHP1,TYRO3,SCD,MRPL43,YAF2,HTATIP2,PCIF1,PPM1M,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,TSPAN5,CISH,SRSF9,ST3GAL4,AK2,RNF19B,DCP	yellow	VSMC_M3
GO:0006725	5.331E-03	1.00	343	4410	cellular aromatic compound metabolic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,SQLE,H2AFY,HNRNPA0,TRIM11,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,TSTA3,BOP1,SND1,RTCB,DNPH1,AARS2,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,FIGNL1,BLVRA,PNKP,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,MUTYH,DMAP1,CIC,GTF3C2,GALK1,BLVRB,OGG1,SERTAD1,TTC5,METTL3,CXXC5,FAAP100,DND1,FASN,GNPDA1,PUS1,DEAF1,SMUG1,HOXC4,OGDHL,POLR1D,TARBP2,KMT2B,C12orf10,NAT10,ZNF740,PDE4D,RRS1,SWAP70,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,RBM15B,CARS,SRSF9,AK2,DCPS,IRX1,WDR4,RRP1B,TMTC1,MVK,BRD9,RBM6,ZCCHC17,PAPSS1,PABPN1,AIP,MOCS3,CLCF1,NGDN,SRRD,TSHZ2,QARS,SLC19A1,IMPDH2,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,PPOX,BUD23,GMEB2,THAP4,CEP164,SART1,CCDC85B,PRPF6,PBX1,RNASEH2C,KAT5,RELA,ATP5MC3,ZNF511,DDX52,LRWD1,ALKBH4,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,SLC25A39,TRMT2A,PBX4,UBTF,GATAD2A,ATIC,THOC3,MEF2B,PHB2,TRMT112,NDP,BAD,CTDSP1,MLF2,OTUB1,NOP14,EID1,SSBP4,METTL13,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,ASMTL,GTPBP3,BABAM1,TEAD4,C1QBP,CSTF2T,TAF6L,CHERP,ZBTB49,UQCC3,CNP,GPKOW,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,ELP5,KLF3,PKN1,SEPSECS,INTS1,POLR	yellow	VSMC_M3
GO:0006629	5.629E-03	1.00	90	982	lipid metabolic process	BP	1	CDK4,ACAT2,CERK,SREBF2,SQLE,H2AFY,PPARD,PIGO,PDGFRA,SOCS5,TTC7A,PTGR1,CPT1C,MGLL,ACAD9,FDXR,PAFAH1B3,SNX17,PLCD1,INSIG1,INPPL1,LAMTOR1,PCYT2,FASN,PTDSS2,AACS,SCARB1,PCCB,ACSL1,FDFT1,PDE3B,WNT10B,SOD1,DGKZ,CHP1,SCD,CISH,ST3GAL4,DHCR7,ETFBKMT,MVK,FABP3,PDGFA,GPX1,PCK2,LSS,PLA2G3,PBX1,MGST3,IDH1,MID1IP1,SGPL1,PHB2,PLCB3,ISYNA1,HSD17B1,TNFRSF1A,WASHC1,ACLY,CYP4F8,FADS2,ILVBL,CAPN2,PIP4K2B,MPDU1,CRABP2,ARMC5,ACSF2,DPM3,PMVK,SLC27A3,MTMR4,AKT1,HMGCS1,ALKBH7,DHCR24,NSDHL,PGP,CSNK1G2,TAZ,MVD,SLC27A4,SLC44A3,VAC14,PLA2G4E,FADS1,GBA2,FDPS,IDI1,STUB1	yellow	VSMC_M3
GO:0007249	5.641E-03	1.00	26	222	I-kappaB kinase/NF-kappaB signaling	BP	1	SQSTM1,EEF1D,LGALS1,SHARPIN,ZC3H12A,RELB,CXXC5,CX3CL1,TRIM27,RIPK3,RELA,RHOC,MAP3K14,TNFRSF1A,CCDC22,TBKBP1,PER1,TRIM25,S100A4,MID2,AKT1,CACTIN,IRAK1,JMJD8,CARD9,TRADD	yellow	VSMC_M3
GO:0045292	5.660E-03	1.00	6	24	mRNA cis splicing, via spliceosome	BP	1	PRPF40B,DCPS,SF3A1,SART1,RBM22,CACTIN	yellow	VSMC_M3

GO:0044238	5.666E-03	1.00	570	7641	primary metabolic process	BP	1	ENPP1,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,DHX16,ZNF608,LMF2,BAG6,SBF1,SNX9,HDAC10,NELFE,ACAT2,CERK,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,JADE2,TRMT12,SQLE,H2AFY,HNRNPA0,TRIM11,SGSM3,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,EEF1D,TSTA3,RPL3,PLEC,MPST,SHARPIN,BOP1,VPS28,RPL8,SND1,CUL7,RTCB,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,TTC7A,RPS9,CNOT3,KLF4,HOXA1,JOSD2,PTGR1,PSMB3,FHL3,SPRED2,EIPR1,MEAF6,ZC3H12A,FIGNL1,PNKP,CPT1C,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,MGLL,KMT2E,WDFY2,ACAD9,SIX5,ZNF282,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,FDXR,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,PAFAH1B3,CIC,GTF3C2,SNX17,GALK1,PPM1G,UNK,PLCD1,BCKDHA,INSIG1,GALNT14,OGG1,SERTAD1,TTC5,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,CXXC5,INPPL1,FAAP100,LAMTOR1,P4HB,PCYT2,DND1,PYCR1,FASN,RPL29,EIF4EBP1,DELE1,GNPDA1,PUS1,PTDSS2,DEAF1,SMUG1,HOXC4,IDH3B,OGDHL,POLR1D,LDLRAD3,TARBP2,KMT2B,AACS,SCARB1,C12orf10,NAT10,HM13,ZNF740,PDE4D,TNS2,EIF4B,PCCB,RRS1,PEPD,SWAP70,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,FDFT1,TNKS1BP1,MMP24,PINX1,GATB,SETD1B,GREM1,KDM2B,PDE3B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,ACCS,RPLP2,CHP1,TYRO3,SCD,MRPL43,YAF2,HTATIP2,PCIF1,PPM1M,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,TSPAN5,CISH,SRSF9,ST3GAL4,AK2,RNF19B,DCPS,IRX1,DHCR7,WDR4,SELENOS,GSTO1,RRP1B,ETFBKMT,MANBA,TMTC1,MVK,BRD9,RBM6,SD	yellow	VSMC_M3
GO:0031952	5.740E-03	1.00	7	37	regulation of protein autophosphorylation	BP	1	ENPP1,TNKS1BP1,GREM1,CHP1,PDGFA,MVP,EEF2K	yellow	VSMC_M3
GO:0009415	6.010E-03	1.00	4	13	response to water	BP	1	PLEC,KRT8,SIPA1,CD9	yellow	VSMC_M3
GO:0043436	6.089E-03	1.00	67	677	oxoacid metabolic process	BP	1	ENPP1,ACAT2,PPARD,MPST,AARS2,GRHPR,PTGR1,CPT1C,MGLL,ACAD9,SEPHS1,GALK1,BCKDHA,INSIG1,PYCR1,FASN,GNPDA1,IDH3B,OGDHL,AACS,PCCB,PEPD,ACSL1,GATB,ACCS,SCD,CARS,GSTO1,ETFBKMT,SDHA,FABP3,PAPSS1,GPX1,QARS,PCK2,SLC19A1,PLA2G3,THAP4,MGST3,IDH1,MID1IP1,SGPL1,ATIC,TNFRSF1A,ACLY,CYP4F8,FADS2,GLUD1,FOXK1,ILVBL,MTHFR,CRABP2,PGD,ACSF2,FARSA,SLC27A3,AKT1,PGM1,ALKBH7,GIT1,BLMH,CTNS,JMJD8,SARS,SLC27A4,FADS1,GBA2	yellow	VSMC_M3
GO:0008544	6.287E-03	1.00	23	201	epidermis development	BP	1	NAB2,H2AFY,PPARD,SCRIB,PLEC,SHARPIN,KLF4,WDPCP,SLC9A3R1,NUMA1,WNT10B,SOD1,PDGFA,RELA,IGFBP5,KRT10,CASP14,CRABP2,TMEM79,PPL,NSDHL,TRADD,NOM1	yellow	VSMC_M3
GO:0051701	6.300E-03	1.00	19	150	biological process involved in interaction with host	BP	1	TRIM11,LGALS1,SLC52A2,SNX3,P4HB,SIGLEC1,SCARB1,BCL2L1,ITGB7,TYRO3,NECTIN1,ANPEP,TRIM27,THOC5,THOC3,PHB2,TRIM25,MID2,CLDN6	yellow	VSMC_M3
GO:0071229	6.465E-03	1.00	10	65	cellular response to acid chemical	BP	1	PLEC,PDGFRA,BAIAP2,LAMTOR1,BCL2L1,COL6A1,SIPA1,LAMTOR4,CAPN2,NSMF	yellow	VSMC_M3
GO:0006139	6.488E-03	0.99	332	4274	nucleobase-containing compound metabolic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,H2AFY,HNRNPA0,TRIM11,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,TSTA3,BOP1,SND1,RTCB,DNPH1,AARS2,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,FIGNL1,PNKP,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,MUTYH,DMAP1,CIC,GTF3C2,GALK1,OGG1,SERTAD1,TTC5,METTL3,CXXC5,FAAP100,DND1,FASN,GNPDA1,PUS1,DEAF1,SMUG1,HOXC4,OGDHL,POLR1D,TARBP2,KMT2B,C12orf10,NAT10,ZNF740,PDE4D,RRS1,SWAP70,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,RBM15B,CARS,SRSF9,AK2,DCPS,IRX1,WDR4,RRP1B,TMTC1,MVK,BRD9,RBM6,ZCCHC17,PAPSS1,PABPN1,AIP,MOCS3,CLCF1,NGDN,TSHZ2,QARS,IMPDH2,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,BUD23,GMEB2,CEP164,SART1,CCDC85B,PRPF6,PBX1,RNASEH2C,KAT5,RELA,ATP5MC3,ZNF511,DDX52,LRWD1,ALKBH4,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,TRMT2A,PBX4,UBTF,GATAD2A,ATIC,THOC3,MEF2B,PHB2,TRMT112,NDP,BAD,CTDSP1,MLF2,OTUB1,NOP14,EID1,SSBP4,METTL13,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,ASMTL,GTPBP3,BABAM1,TEAD4,C1QBP,CSTF2T,TAF6L,CHERP,ZBTB49,UQCC3,CNP,GPKOW,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,ELP5,KLF3,PKN1,SEPSECS,INTS1,POLR2A,CWC25,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,RRNAD1,CRABP2,	yellow	VSMC_M3
GO:0001510	6.990E-03	1.00	12	73	RNA methylation	BP	1	TRMT12,METTL3,PCIF1,RBM15B,WDR4,FTSJ3,BUD23,TRMT2A,TRMT112,GTPBP3,RRNAD1,TRMT1	yellow	VSMC_M3
GO:0022404	7.156E-03	1.00	10	63	molting cycle process	BP	1	NUMA1,LRIG1,WNT10B,PDGFA,RELA,IGFBP5,TMEM79,NSDHL,TRADD,NOM1	yellow	VSMC_M3
GO:0022405	7.156E-03	1.00	10	63	hair cycle process	BP	1	NUMA1,LRIG1,WNT10B,PDGFA,RELA,IGFBP5,TMEM79,NSDHL,TRADD,NOM1	yellow	VSMC_M3
GO:0031424	7.215E-03	1.00	4	13	keratinization	BP	1	SHARPIN,CASP14,TMEM79,PPL	yellow	VSMC_M3
GO:0002098	7.266E-03	1.00	5	17	tRNA wobble uridine modification	BP	1	KTI12,MOCS3,GTPBP3,ELP5,CTU2	yellow	VSMC_M3
GO:0046597	7.285E-03	1.00	4	12	negative regulation of viral entry into host cell	BP	1	TRIM11,SNX3,TRIM25,MID2	yellow	VSMC_M3
GO:0019752	7.290E-03	1.00	65	659	carboxylic acid metabolic process	BP	1	ACAT2,PPARD,MPST,AARS2,GRHPR,PTGR1,CPT1C,MGLL,ACAD9,SEPHS1,GALK1,BCKDHA,INSIG1,PYCR1,FASN,GNPDA1,IDH3B,OGDHL,AACS,PCCB,PEPD,ACSL1,GATB,ACCS,SCD,CARS,GSTO1,ETFBKMT,SDHA,FABP3,GPX1,QARS,PCK2,SLC19A1,PLA2G3,THAP4,MGST3,IDH1,MID1IP1,SGPL1,ATIC,TNFRSF1A,ACLY,CYP4F8,FADS2,GLUD1,FOXK1,ILVBL,MTHFR,CRABP2,PGD,ACSF2,FARSA,SLC27A3,AKT1,PGM1,ALKBH7,GIT1,BLMH,CTNS,JMJD8,SARS,SLC27A4,FADS1,GBA2	yellow	VSMC_M3
GO:0008033	7.581E-03	1.00	17	117	tRNA processing	BP	1	TRMT12,RTCB,AARS2,KTI12,PUS1,NAT10,LSM6,WDR4,MOCS3,TRMT112,GTPBP3,ELP5,TRMT1,DUS3L,SARS,CTU2,OSGEP	yellow	VSMC_M3
GO:0007288	7.748E-03	1.00	5	18	sperm axoneme assembly	BP	1	CEP131,YIF1B,IQCG,PLA2G3,MEIG1	yellow	VSMC_M3

GO:0120316	7.748E-03	1.00	5	18	sperm flagellum assembly	BP	1	CEP131,YIF1B,IQCG,PLA2G3,MEIG1	yellow	VSMC_M3
GO:0000027	7.795E-03	1.00	5	18	ribosomal large subunit assembly	BP	1	RPL3,BOP1,RRS1,MRTO4,MRPL20	yellow	VSMC_M3
GO:0010467	7.983E-03	0.99	344	4455	gene expression	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,LMF2,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,H2AFY,HNRNPA0,TRIM11,TRAPPC9,PPARD,EEF1D,RPL3,SCRIB,PLEC,BOP1,RPL8,SND1,RTCB,MRPS18A,AARS2,PDGFRA,IL1R1,SECISBP2,PHF2,SSC5D,SOCS5,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,EMILIN1,DMAP1,CIC,GTF3C2,UNK,OGG1,SERTAD1,TTC5,METTL3,CXXC5,INPPL1,DND1,RPL29,EIF4EBP1,CAVIN3,PUS1,DEAF1,HOXC4,POLR1D,LDLRAD3,TARBP2,KMT2B,NAT10,HM13,ZNF740,PDE4D,EIF4B,RRS1,SWAP70,LRP3,RALY,ZBTB38,ARL6IP4,LSM6,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,TSPAN5,SRSF9,DCPS,IRX1,WDR4,SELENOS,RRP1B,TMTC1,BRD9,RBM6,ZCCHC17,MMP14,C14orf93,APEH,PABPN1,GPX1,AIP,MOCS3,CLCF1,NGDN,TSHZ2,QARS,PIR,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,SEC11A,BUD23,TACO1,PLA2G3,GMEB2,SART1,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,DDX52,ARNT2,MRPL49,ZFPL1,LIMD1,SMARCB1,CHCHD10,TRMT2A,PBX4,UBTF,GATAD2A,THOC3,MEF2B,PHB2,TRMT112,NDP,IGFBP5,BAD,CTDSP1,MLF2,NOP14,EID1,SSBP4,METTL13,MPV17L2,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,PLAU,TNFRSF1A,GTPBP3,TEAD4,C1QBP,NUP88,CSTF2T,AIMP2,TAF6L,CHERP,ZBTB49,GPKOW,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,ELP5,SDE2,KLF3,PKN1,CAPN2,SEPSECS,INTS1,PO	yellow	VSMC_M3
GO:0044255	8.503E-03	0.99	70	743	cellular lipid metabolic process	BP	1	ACAT2,CERK,PPARD,PIGO,SOCS5,TTC7A,PTGR1,CPT1C,MGLL,ACAD9,PLCD1,INSIG1,INPPL1,LAMTOR1,PCYT2,FASN,PTDSS2,AACS,SCARB1,PCCB,ACSL1,FDFT1,DGKZ,CHP1,SCD,CISH,ST3GAL4,ETFBKMT,MVK,FABP3,PDGFA,GPX1,PCK2,LSS,PLA2G3,IDH1,MID1IP1,SGPL1,PHB2,PLCB3,ISYNA1,TNFRSF1A,ACLY,CYP4F8,FADS2,ILVBL,CAPN2,PIP4K2B,MPDU1,CRABP2,ACSF2,DPM3,PMVK,SLC27A3,MTMR4,AKT1,HMGCS1,ALKBH7,PGP,CSNK1G2,TAZ,MVD,SLC27A4,SLC44A3,VAC14,PLA2G4E,FADS1,GBA2,FDPS,IDI1	yellow	VSMC_M3
GO:0009987	8.538E-03	0.99	829	11676	cellular process	BP	1	ENPP1,PQLC1,CD63,ESYT1,NAB2,DCTN2,NHP2,CDK4,CTDSP2,RUFY1,SQSTM1,GNL1,DHX16,CCHCR1,SPAG1,ZNF608,BAG6,NCAPH2,SBF1,SNX9,CTHRC1,HDAC10,NELFE,ACAT2,CERK,FNIP1,ATF6B,PBX2,PDLIM4,PRR5,SAMM50,TTLL12,RING1,SREBF2,JADE2,TRMT12,NDUFB9,SQLE,TXNDC15,H2AFY,ITPR3,HNRNPA0,TRIM11,SGSM3,GUK1,TRAPPC9,NUDT3,PACSIN1,DEF6,PPARD,FANCE,EEF1D,TSTA3,RPL3,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,BOP1,SLC52A2,VPS28,RPL8,SND1,TOM1,TBCC,CUL7,RTCB,PPP1R14B,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,IL1R1,SECISBP2,PHF2,GRHPR,COL15A1,EPN1,COL19A1,SSC5D,HSPBP1,SOCS5,TTC7A,RPS9,CNOT3,ASNA1,KLF4,DBNL,TPBG,HOXA1,JOSD2,PTGR1,PSMB3,PLEKHA8,WDPCP,CCM2,FHL3,SPRED2,EIPR1,RGS3,MEAF6,ZC3H12A,FIGNL1,PDIA4,BLVRA,PDIA6,PNKP,CPT1C,ZYX,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,PLEKHA4,EMP3,MGLL,EHD2,FAM120B,KMT2E,ANXA5,KRT8,WDFY2,ACAD9,SIX5,ZNF282,TMEM43,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,PLXND1,FDXR,EMILIN1,SLC16A5,SEPHS1,TMUB1,RNF220,DMAP1,SLC30A3,CIC,GTF3C2,SNX17,GALK1,H3F3B,PPM1G,UNK,PLCD1,DLEC1,CD79A,BCKDHA,INSIG1,MYRIP,SEC13,SEPT9,GALNT14,BLVRB,OGG1,SERTAD1,TTC5,PSMC4,KAT14,ARHGEF40,P4HA3,UCP2,SEL1L2,METTL3,PHLDA1,BAIAP2,CEP131,CXXC5,INPPL1,FAAP100,TSPAN10,LAMTOR1,NUMA1,P4HB,PCYT2,DND1,PYCR1,YIF1B,FASN,CCDC57,RAB20,SMOX,RPL29,EIF4EBP1,ARAP3,SIGLEC1,DELE1,GNPDA1,MORN2,CAVIN3,PUS1,RIC8A,GSR,PTDSS2,ARHGAP22,DEAF1,TBCB,SMUG1,HOXC4,IDH3B,SDHAF1,OGDHL,POLR1D,ARHGAP33,LDLRAD3,TARBP2,KMT2B,A	yellow	VSMC_M3
GO:0044237	8.597E-03	0.99	588	7918	cellular metabolic process	BP	1	ENPP1,CD63,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,DHX16,ZNF608,BAG6,SBF1,SNX9,HDAC10,NELFE,ACAT2,CERK,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,JADE2,TRMT12,NDUFB9,SQLE,H2AFY,HNRNPA0,TRIM11,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,EEF1D,TSTA3,RPL3,SCRIB,PLEC,MPST,SHARPIN,BOP1,SLC52A2,VPS28,RPL8,SND1,CUL7,RTCB,PPP1R14B,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,SECISBP2,PHF2,GRHPR,HSPBP1,SOCS5,TTC7A,RPS9,CNOT3,KLF4,HOXA1,JOSD2,PTGR1,PSMB3,FHL3,SPRED2,EIPR1,MEAF6,ZC3H12A,FIGNL1,BLVRA,PNKP,CPT1C,RCN3,SNRNP70,CC2D1B,KTI12,MICAL1,MGLL,KMT2E,WDFY2,ACAD9,SIX5,ZNF282,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,FDXR,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,CIC,GTF3C2,GALK1,PPM1G,UNK,PLCD1,BCKDHA,INSIG1,GALNT14,BLVRB,OGG1,SERTAD1,TTC5,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,CXXC5,INPPL1,FAAP100,LAMTOR1,P4HB,PCYT2,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,GNPDA1,CAVIN3,PUS1,GSR,PTDSS2,DEAF1,SMUG1,HOXC4,IDH3B,OGDHL,POLR1D,TARBP2,KMT2B,AACS,SCARB1,C12orf10,NAT10,HM13,ZNF740,PDE4D,TNS2,EIF4B,PCCB,RRS1,PEPD,SWAP70,RALY,PLEKHF1,UQCRFS1,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,FDFT1,TNKS1BP1,PINX1,GATB,SETD1B,GREM1,KDM2B,PRPF40B,MCRS1,TKT,POLR2C,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,ACCS,RPLP2,CHP1,TYRO3,SCD,MRPL43,YAF2,HTATIP2,PCIF1,PPM1M,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,CISH,SRSF9,ST3GAL4,AK2,RNF19B,DCPS,IRX1,WDR4,SELENOS,GSTO1,RRP1B,ETFBKMT,MANBA,TMTC	yellow	VSMC_M3

GO:0006082	8.637E-03	0.99	67	689	organic acid metabolic process	BP	1	ENPP1,ACAT2,PPARD,MPST,AARS2,GRHPR,PTGR1,CPT1C,MGLL,ACAD9,SEPHS1,GALK1,BCKDHA,INSIG1,PYCR1,FASN,GNPDA1,IDH3B,OGDHL,AACS,PCCB,PEPD,ACSL1,GATB,ACCS,SCD,CARS,GSTO1,ETFBKMT,SDHA,FABP3,PAPSS1,GPX1,QARS,PCK2,SLC19A1,PLA2G3,THAP4,MGST3,IDH1,MID1IP1,SGPL1,ATIC,TNFRSF1A,ACLY,CYP4F8,FADS2,GLUD1,FOXK1,ILVBL,MTHFR,CRABP2,PGD,ACSF2,FARSA,SLC27A3,AKT1,PGM1,ALKBH7,GIT1,BLMH,CTNS,JMJD8,SARS,SLC27A4,FADS1,GBA2	yellow	VSMC_M3
GO:0002093	8.767E-03	1.00	4	13	auditory receptor cell morphogenesis	BP	1	SCRIB,WDPCP,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:0009259	8.789E-03	0.99	33	302	ribonucleotide metabolic process	BP	1	ENPP1,GUK1,NUDT3,GALK1,FASN,OGDHL,PDE4D,ACSL1,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,UQCC3,ACLY,FOXK1,ACSF2,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0019693	8.807E-03	0.99	34	312	ribose phosphate metabolic process	BP	1	ENPP1,GUK1,NUDT3,GALK1,FASN,OGDHL,PDE4D,ACSL1,TKT,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,UQCC3,ACLY,FOXK1,ACSF2,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0000469	9.012E-03	1.00	6	26	cleavage involved in rRNA processing	BP	1	NHP2,BOP1,RRS1,RPS21,NOP14,TBL3	yellow	VSMC_M3
GO:0044281	9.298E-03	0.99	116	1301	small molecule metabolic process	BP	1	ENPP1,ACAT2,SREBF2,SQLE,GUK1,NUDT3,PPARD,TSTA3,MPST,SLC52A2,DNPH1,B4GALT1,AARS2,GRHPR,PTGR1,CPT1C,MGLL,ACAD9,FDXR,SEPHS1,SNX17,GALK1,BCKDHA,INSIG1,OGG1,INPPL1,PYCR1,FASN,GNPDA1,SMUG1,IDH3B,OGDHL,AACS,SCARB1,PDE4D,PCCB,PEPD,ACSL1,FDFT1,GATB,SOD1,ACCS,SCD,CARS,AK2,DHCR7,SELENOS,GSTO1,ETFBKMT,MVK,SDHA,FABP3,PAPSS1,GPX1,QARS,PCK2,SLC19A1,IMPDH2,LSS,PLA2G3,THAP4,MGST3,ATP5MC3,IDH1,MID1IP1,SGPL1,ATIC,BAD,ISYNA1,HSD17B1,TNFRSF1A,ASMTL,UQCC3,CNP,ACLY,CYP4F8,FADS2,GLUD1,FOXK1,ILVBL,MTHFR,CRABP2,PGD,COQ6,ACSF2,FARSA,FLAD1,PMVK,ATP5PD,SLC27A3,AKT1,HMGCS1,PGM1,ALKBH7,GIT1,DHCR24,BLMH,NSDHL,CTNS,PGP,MIDN,ATP5F1D,TAZ,JMJD8,AMPD2,SARS,APRT,MVD,SLC27A4,AK1,FADS1,NT5C,GBA2,FDPS,IDI1,ITPA	yellow	VSMC_M3
GO:0000154	9.652E-03	1.00	7	31	rRNA modification	BP	1	NHP2,NAT10,FTSJ3,BUD23,TRMT112,RRNAD1,TSR3	yellow	VSMC_M3
GO:0050728	0.01	1.00	13	91	negative regulation of inflammatory response	BP	1	PPARD,SHARPIN,SOCS5,KLF4,CX3CL1,SOD1,TYRO3,SELENOS,MVK,GPX1,PSMB4,TNFRSF1A,GIT1	yellow	VSMC_M3
GO:1903901	0.01	1.00	4	13	negative regulation of viral life cycle	BP	1	TRIM11,SNX3,TRIM25,MID2	yellow	VSMC_M3
GO:0072350	0.01	1.00	4	13	tricarboxylic acid metabolic process	BP	1	IDH3B,IDH1,ACLY,GLUD1	yellow	VSMC_M3
GO:0098781	0.01	1.00	9	53	ncRNA transcription	BP	1	H2AFY,GTF3C2,NPM3,SMARCB1,SMARCA4,BRF1,GTF3C5,CAVIN1,SNAPC2	yellow	VSMC_M3
GO:0072521	0.01	0.99	34	319	purine-containing compound metabolic process	BP	1	ENPP1,GUK1,NUDT3,DNPH1,GALK1,FASN,OGDHL,PDE4D,ACSL1,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,UQCC3,ACLY,FOXK1,ACSF2,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0019080	0.01	1.00	12	86	viral gene expression	BP	1	TRIM11,TARBP2,ST3GAL4,RRP1B,TRIM27,EIF3A,SMARCB1,SMARCA4,EIF3G,C19orf66,MID2,MAN1B1	yellow	VSMC_M3
GO:0042147	0.01	1.00	11	80	retrograde transport, endosome to Golgi	BP	1	PQLC1,EIPR1,SNX3,DCTN1,TRIM27,VPS51,WASHC1,SNX8,STX10,ARFRP1,PHETA2	yellow	VSMC_M3
GO:0090407	0.01	0.99	45	452	organophosphate biosynthetic process	BP	1	GUK1,PPARD,PIGO,SOCS5,TTC7A,INPPL1,PCYT2,PTDSS2,ACSL1,TKT,DGKZ,CHP1,CISH,AK2,MVK,FABP3,PAPSS1,PDGFA,MOCS3,IMPDH2,ATP5MC3,IDH1,ATIC,ISYNA1,UQCC3,ACLY,CAPN2,PIP4K2B,DPM3,FLAD1,PMVK,ATP5PD,MTMR4,HMGCS1,ATP5F1D,TAZ,AMPD2,APRT,MVD,AK1,SLC44A3,VAC14,FADS1,FDPS,IDI1	yellow	VSMC_M3
GO:0032008	0.01	1.00	7	38	positive regulation of TOR signaling	BP	1	FNIP1,SEC13,LAMTOR1,LAMTOR4,CTNS,TELO2,WDR24	yellow	VSMC_M3
GO:0007097	0.01	1.00	4	19	nuclear migration	BP	1	SLC9A3R1,DCTN1,SYNE3,TMEM201	yellow	VSMC_M3
GO:0019216	0.01	0.99	27	251	regulation of lipid metabolic process	BP	1	CDK4,H2AFY,PPARD,PDGFRA,INSIG1,LAMTOR1,SCARB1,PDE3B,SOD1,DGKZ,CHP1,DHCR7,ETFBKMT,FABP3,PDGFA,PLA2G3,IDH1,MID1IP1,PHB2,WASHC1,CAPN2,PIP4K2B,ARMC5,MTMR4,AKT1,TAZ,STUB1	yellow	VSMC_M3
GO:0006631	0.01	0.99	30	271	fatty acid metabolic process	BP	1	ACAT2,PPARD,PTGR1,CPT1C,MGLL,ACAD9,INSIG1,FASN,AACS,PCCB,ACSL1,SCD,ETFBKMT,FABP3,GPX1,PCK2,PLA2G3,MID1IP1,SGPL1,TNFRSF1A,ACLY,CYP4F8,FADS2,ILVBL,ACSF2,SLC27A3,AKT1,ALKBH7,SLC27A4,FADS1	yellow	VSMC_M3
GO:0006066	0.01	0.99	28	258	alcohol metabolic process	BP	1	SREBF2,SQLE,NUDT3,PPARD,FDXR,SNX17,GALK1,INSIG1,IDH3B,SCARB1,FDFT1,SOD1,DHCR7,MVK,PCK2,LSS,IDH1,ISYNA1,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,PGP,MVD,GBA2,FDPS,IDI1	yellow	VSMC_M3
GO:0042254	0.01	0.99	29	256	ribosome biogenesis	BP	1	NHP2,RPL3,BOP1,NAT10,RRS1,LSM6,NPM3,RRP1B,NGDN,RPS21,FTSJ3,BUD23,SART1,DDX52,TRMT112,NOP14,MPV17L2,MRTO4,C1QBP,NUP88,RRNAD1,RPL7A,AATF,MRPL20,TBL3,TSR3,RBFA,PIN4,NOM1	yellow	VSMC_M3
GO:0031348	0.01	0.99	18	149	negative regulation of defense response	BP	1	TTLL12,PPARD,SHARPIN,SOCS5,KLF4,METTL3,TARBP2,CX3CL1,SOD1,TYRO3,SELENOS,MVK,GPX1,PSMB4,TNFRSF1A,C1QBP,GIT1,CACTIN	yellow	VSMC_M3
GO:1903321	0.01	0.99	12	82	negative regulation of protein modification by small protein conjugation or removal	BP	1	SQSTM1,VPS28,PINX1,CHP1,LIMK1,RELA,OTUB1,UBXN1,MAD2L2,RPL37,AKT1,HMG20B	yellow	VSMC_M3
GO:0002097	0.02	1.00	5	20	tRNA wobble base modification	BP	1	KTI12,MOCS3,GTPBP3,ELP5,CTU2	yellow	VSMC_M3
GO:0006084	0.02	1.00	6	29	acetyl-CoA metabolic process	BP	1	FASN,MVK,ACLY,PMVK,HMGCS1,MVD	yellow	VSMC_M3
GO:0050775	0.02	1.00	6	35	positive regulation of dendrite morphogenesis	BP	1	CUL7,DBNL,BAIAP2,DBN1,EEF2K,ANAPC2	yellow	VSMC_M3
GO:0032787	0.02	0.99	41	404	monocarboxylic acid metabolic process	BP	1	ACAT2,PPARD,GRHPR,PTGR1,CPT1C,MGLL,ACAD9,GALK1,INSIG1,FASN,OGDHL,AACS,PCCB,ACSL1,SCD,ETFBKMT,FABP3,GPX1,PCK2,PLA2G3,IDH1,MID1IP1,SGPL1,TNFRSF1A,ACLY,CYP4F8,FADS2,FOXK1,ILVBL,CRABP2,PGD,ACSF2,SLC27A3,AKT1,PGM1,ALKBH7,GIT1,JMJD8,SLC27A4,FADS1,GBA2	yellow	VSMC_M3

GO:0043604	0.02	0.99	64	672	amide biosynthetic process	BP	1	CDK4,EEF1D,RPL3,RPL8,MRPS18A,AARS2,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,RPL29,EIF4EBP1,TARBP2,NAT10,EIF4B,ACSL1,GATB,RPLP2,MRPL43,PCIF1,CARS,DCPS,APEH,NGDN,QARS,EIF3A,LSM14B,PSTK,RPS21,TACO1,MRPL49,IGFBP5,MPV17L2,C1QBP,AIMP2,ACLY,SEPSECS,NANOS3,PER1,FARSA,TUFM,RPL37,RPL7A,EEF2K,MRPL4,EIF3G,C19orf66,AKT1,PAIP1,KHSRP,MRPL20,TRAP1,MKNK2,MRPL28,SARS,RBM8A,EEF1G,MRPL34,ZNF385A,MRPS16,ZAR1L	yellow	VSMC_M3
GO:0016070	0.02	0.99	269	3480	RNA metabolic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,H2AFY,HNRNPA0,TRIM11,TRAPPC9,NUDT3,PPARD,BOP1,SND1,RTCB,AARS2,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,PUS1,DEAF1,HOXC4,POLR1D,TARBP2,KMT2B,NAT10,ZNF740,RRS1,RALY,ZBTB38,ARL6IP4,LSM6,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,RBM15B,CARS,SRSF9,DCPS,IRX1,WDR4,RRP1B,TMTC1,BRD9,RBM6,ZCCHC17,PABPN1,AIP,MOCS3,NGDN,TSHZ2,QARS,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,BUD23,GMEB2,SART1,CCDC85B,PRPF6,PBX1,RNASEH2C,KAT5,RELA,ZNF511,DDX52,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,TRMT2A,PBX4,UBTF,GATAD2A,THOC3,MEF2B,PHB2,TRMT112,NDP,CTDSP1,MLF2,NOP14,EID1,SSBP4,METTL13,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,GTPBP3,TEAD4,C1QBP,CSTF2T,TAF6L,CHERP,ZBTB49,GPKOW,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,ELP5,KLF3,PKN1,SEPSECS,INTS1,POLR2A,CWC25,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,RRNAD1,CRABP2,SP2,ARHGEF2,SNF8,CD2BP2,PER1,NFIX,TRMT1,FARSA,IRF2BPL,TRIM25,SMARCA4,CARM1,RPL7A,RAVER1,AATF,MID2,RBM22,ZNF521,ZNF358,ZNF830,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,DUS3L,SAFB,SAFB2,CARHSP1,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72	yellow	VSMC_M3
GO:0043122	0.02	0.99	22	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	SQSTM1,EEF1D,LGALS1,SHARPIN,ZC3H12A,CXXC5,CX3CL1,TRIM27,RELA,RHOC,MAP3K14,TNFRSF1A,CCDC22,PER1,TRIM25,S100A4,MID2,CACTIN,IRAK1,JMJD8,CARD9,TRADD	yellow	VSMC_M3
GO:0001942	0.02	0.99	9	61	hair follicle development	BP	1	NUMA1,WNT10B,PDGFA,RELA,IGFBP5,TMEM79,NSDHL,TRADD,NOM1	yellow	VSMC_M3
GO:0009117	0.02	0.99	39	381	nucleotide metabolic process	BP	1	ENPP1,GUK1,NUDT3,DNPH1,GALK1,OGG1,FASN,SMUG1,OGDHL,PDE4D,ACSL1,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,ASMTL,UQCC3,CNP,ACLY,FOXK1,ACSF2,FLAD1,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0030833	0.02	0.99	17	145	regulation of actin filament polymerization	BP	1	SNX9,DBNL,BAIAP2,CAPG,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,DBN1,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0061003	0.02	1.00	4	19	positive regulation of dendritic spine morphogenesis	BP	1	DBNL,BAIAP2,DBN1,EEF2K	yellow	VSMC_M3
GO:0048814	0.02	0.99	8	57	regulation of dendrite morphogenesis	BP	1	CUL7,DBNL,BAIAP2,DBN1,EEF2K,ANAPC2,STK11,NSMF	yellow	VSMC_M3
GO:0007007	0.02	1.00	7	35	inner mitochondrial membrane organization	BP	1	SAMM50,CHCHD10,LETM1,UQCC3,MTX1,TAZ,TIMM22	yellow	VSMC_M3
GO:0008064	0.02	0.99	18	159	regulation of actin polymerization or depolymerization	BP	1	SNX9,DBNL,BAIAP2,SWAP70,CAPG,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,DBN1,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0046033	0.02	1.00	4	14	AMP metabolic process	BP	1	AK2,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:0030832	0.02	0.99	18	160	regulation of actin filament length	BP	1	SNX9,DBNL,BAIAP2,SWAP70,CAPG,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,DBN1,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0070542	0.02	0.99	8	49	response to fatty acid	BP	1	CDK4,ZC3H12A,UCP2,AACS,ACSL1,SCD,FABP3,BAD	yellow	VSMC_M3
GO:0043123	0.02	0.99	18	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	EEF1D,LGALS1,SHARPIN,CXXC5,CX3CL1,TRIM27,RELA,RHOC,MAP3K14,TNFRSF1A,CCDC22,TRIM25,S100A4,MID2,IRAK1,JMJD8,CARD9,TRADD	yellow	VSMC_M3
GO:0006897	0.02	0.99	40	444	endocytosis	BP	1	ENPP1,CD63,RUFY1,SNX9,PACSIN1,SCRIB,VPS28,TOM1,EPN1,SSC5D,DBNL,EHD2,SNX17,INPPL1,SIGLEC1,LDLRAD3,SCARB1,BCL2L1,LRP3,GREM1,PACSIN3,AP2A2,RIN3,AP1G2,TNK2,MRC2,SCARF2,LGALS3,CD9,FCHO1,CLTB,RABEP2,EEF2K,SNX18,DENND1C,RAB34,ANKRD13B,CSNK1G2,RABEPK,GSG1L	yellow	VSMC_M3
GO:0016570	0.02	0.99	37	399	histone modification	BP	1	HDAC10,NELFE,RING1,JADE2,H2AFY,PHF2,MEAF6,KMT2E,DMAP1,KAT14,KMT2B,SETD1B,KDM2B,MCRS1,KDM1B,PRMT2,BRMS1,KAT5,SMARCB1,TRMT112,OTUB1,EID1,TAF6L,MTA2,PKN1,MTHFR,CTBP1,FBXL19,PER1,SGF29,CARM1,COPRS,SIRT6,EHMT1,MBD3,NTMT1,THAP7	yellow	VSMC_M3
GO:0071404	0.02	1.00	4	16	cellular response to low-density lipoprotein particle stimulus	BP	1	SREBF2,SOCS5,CD9,HMGCS1	yellow	VSMC_M3
GO:0046627	0.02	1.00	5	25	negative regulation of insulin receptor signaling pathway	BP	1	ENPP1,TNS2,RELA,PIP4K2B,SLC27A4	yellow	VSMC_M3
GO:0070897	0.02	0.99	6	31	transcription preinitiation complex assembly	BP	1	WNT10B,SMARCB1,UBTF,TAF6L,SMARCA4,BRF1	yellow	VSMC_M3

GO:0048585	0.02	0.98	101	1229	negative regulation of response to stimulus	BP	1	ENPP1,CTHRC1,FNIP1,ATF6B,TTLL12,PPARD,SHARPIN,PDGFRA,SOCS5,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,SLC9A3R1,EMILIN1,INSIG1,OGG1,UCP2,METTL3,PYCR1,CAVIN3,TARBP2,BCL2L1,PDE4D,TNS2,GREM1,PDE3B,CX3CL1,SOD1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,CISH,SELENOS,ITPRIP,MVK,RIN3,PDGFA,MMP14,GPX1,CORO1B,QARS,TRIM27,EIF3A,SPX,THOC5,PSMB4,STMN3,RELA,LIMD1,PHB2,IGFBP5,IFI35,OTUB1,LGALS3,CD9,PLAU,TNFRSF1A,C1QBP,UBXN1,CCDC22,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,MTMR4,SMARCA4,AATF,CXorf57,CSK,AKT1,GIT1,CACTIN,VASN,HIC1,TRAP1,MNT,STK11,SLC27A4,TGFBR3,MIR214,RF00024,PTPRR,IGFBP6,JAGN1,ZNF385A,TXNDC12,CDC34,APCDD1L,RGS16,DUSP5,STUB1,RGS18	yellow	VSMC_M3
GO:0051647	0.02	1.00	4	21	nucleus localization	BP	1	SLC9A3R1,DCTN1,SYNE3,TMEM201	yellow	VSMC_M3
GO:0042274	0.02	0.99	10	64	ribosomal small subunit biogenesis	BP	1	NAT10,RRS1,LSM6,NGDN,RPS21,DDX52,NOP14,TBL3,TSR3,NOM1	yellow	VSMC_M3
GO:0006753	0.02	0.99	39	387	nucleoside phosphate metabolic process	BP	1	ENPP1,GUK1,NUDT3,DNPH1,GALK1,OGG1,FASN,SMUG1,OGDHL,PDE4D,ACSL1,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,ASMTL,UQCC3,CNP,ACLY,FOXK1,ACSF2,FLAD1,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0016032	0.02	0.99	32	325	viral process	BP	1	TRIM11,LGALS1,SLC52A2,VPS28,ZC3H12A,SNX3,P4HB,SIGLEC1,TARBP2,SCARB1,BCL2L1,ITGB7,TYRO3,ST3GAL4,RRP1B,NECTIN1,ANPEP,TRIM27,EIF3A,BANF1,SMARCB1,PHB2,MVB12A,CTBP1,SNF8,TRIM25,SMARCA4,EIF3G,C19orf66,MID2,CLDN6,MAN1B1	yellow	VSMC_M3
GO:0055094	0.02	1.00	5	24	response to lipoprotein particle	BP	1	SREBF2,SOCS5,CD9,AKT1,HMGCS1	yellow	VSMC_M3
GO:1901566	0.02	0.98	114	1317	organonitrogen compound biosynthetic process	BP	1	CDK4,GUK1,EEF1D,RPL3,RPL8,B4GALT1,MRPS18A,AARS2,PIGO,SECISBP2,RPS9,CNOT3,KLF4,ZC3H12A,SERP2,SEPHS1,UNK,GALNT14,METTL3,PHLDA1,DND1,PYCR1,SMOX,RPL29,EIF4EBP1,PTDSS2,TARBP2,NAT10,EIF4B,ACSL1,SLC11A2,GATB,RPLP2,CHP1,MRPL43,PCIF1,SLC35C2,CARS,ST3GAL4,AK2,DCPS,TMTC1,FABP3,PAPSS1,APEH,MOCS3,NGDN,SRRD,QARS,IMPDH2,EIF3A,LSM14B,PSTK,RPS21,EXTL1,PPOX,TACO1,ATP5MC3,MRPL49,ZDHHC3,SGPL1,SLC25A39,ATIC,IGFBP5,MPV17L2,C1QBP,AIMP2,UQCC3,ACLY,GLUD1,ILVBL,CAPN2,SEPSECS,MTHFR,NANOS3,MPDU1,PER1,DPM3,FARSA,FLAD1,TUFM,ATP5PD,RPL37,RPL7A,EEF2K,AATF,MRPL4,EIF3G,C19orf66,AKT1,PAIP1,KHSRP,MRPL20,TRAP1,MKNK2,CSNK1G2,MAN1B1,ATP5F1D,TAZ,MRPL28,AMPD2,SARS,APRT,POMT1,AK1,SLC44A3,B3GNT9,NDST1,RBM8A,EEF1G,MRPL34,ZNF385A,MRPS16,ZAR1L	yellow	VSMC_M3
GO:0006482	0.02	1.00	5	30	protein demethylation	BP	1	PHF2,KDM2B,KDM1B,ALKBH4,FBXL19	yellow	VSMC_M3
GO:0008214	0.02	1.00	5	30	protein dealkylation	BP	1	PHF2,KDM2B,KDM1B,ALKBH4,FBXL19	yellow	VSMC_M3
GO:0060117	0.02	1.00	4	17	auditory receptor cell development	BP	1	SCRIB,WDPCP,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:1902175	0.02	1.00	5	23	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	BP	1	P4HB,SOD1,GPX1,AKT1,TRAP1	yellow	VSMC_M3
GO:0008152	0.02	0.98	621	8467	metabolic process	BP	1	ENPP1,CD63,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,DHX16,ZNF608,LMF2,BAG6,SBF1,SNX9,HDAC10,NELFE,ACAT2,CERK,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,JADE2,TRMT12,NDUFB9,SQLE,H2AFY,HNRNPA0,TRIM11,SGSM3,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,EEF1D,TSTA3,RPL3,SCRIB,PLEC,MPST,SHARPIN,BOP1,SLC52A2,VPS28,RPL8,SND1,CUL7,RTCB,PPP1R14B,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,IL1R1,SECISBP2,PHF2,GRHPR,SSC5D,HSPBP1,SOCS5,TTC7A,RPS9,CNOT3,KLF4,HOXA1,JOSD2,PTGR1,PSMB3,FHL3,SPRED2,EIPR1,MEAF6,ZC3H12A,FIGNL1,BLVRA,PNKP,CPT1C,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,MGLL,KMT2E,WDFY2,ACAD9,SIX5,ZNF282,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,FDXR,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,PAFAH1B3,CIC,GTF3C2,SNX17,GALK1,PPM1G,UNK,PLCD1,BCKDHA,INSIG1,GALNT14,BLVRB,OGG1,SERTAD1,TTC5,PSMC4,KAT14,P4HA3,UCP2,SEL1L2,METTL3,PHLDA1,CXXC5,INPPL1,FAAP100,LAMTOR1,P4HB,PCYT2,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,DELE1,GNPDA1,CAVIN3,PUS1,GSR,PTDSS2,DEAF1,SMUG1,HOXC4,IDH3B,OGDHL,POLR1D,LDLRAD3,TARBP2,KMT2B,AACS,SCARB1,C12orf10,NAT10,HM13,ZNF740,PDE4D,TNS2,EIF4B,PCCB,RRS1,PEPD,SWAP70,LRP3,RALY,PLEKHF1,UQCRFS1,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,FDFT1,TNKS1BP1,MMP24,PINX1,GATB,SETD1B,GREM1,KDM2B,PDE3B,PRPF40B,MCRS1,TKT,POLR2C,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,ACCS,RPLP2,CHP1,TYRO3,SCD,MRPL43,YAF2,HTATIP2,PCIF1,PPM1M,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,TS	yellow	VSMC_M3
GO:0032271	0.02	0.99	21	199	regulation of protein polymerization	BP	1	SNX9,DBNL,BAIAP2,NUMA1,CAPG,DCTN1,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,DBN1,RANGRF,CORO1A,GIT1,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0008625	0.02	0.99	10	67	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	DELE1,BCL2L1,ITPRIP,GPX1,ZDHHC3,BAD,LGALS3,TNFRSF1A,ARHGEF2,TRADD	yellow	VSMC_M3
GO:0046040	0.02	1.00	4	16	IMP metabolic process	BP	1	ATIC,AMPD2,APRT,NT5C	yellow	VSMC_M3
GO:0052126	0.02	0.99	15	127	movement in host environment	BP	1	TRIM11,LGALS1,SLC52A2,SNX3,P4HB,SIGLEC1,SCARB1,ITGB7,TYRO3,NECTIN1,ANPEP,TRIM27,TRIM25,MID2,CLDN6	yellow	VSMC_M3
GO:0097320	0.02	1.00	4	18	plasma membrane tubulation	BP	1	SNX9,PACSIN1,EHD2,PACSIN3	yellow	VSMC_M3
GO:0032495	0.02	1.00	4	17	response to muramyl dipeptide	BP	1	RELA,ARHGEF2,LDOC1,CARD9	yellow	VSMC_M3
GO:0045684	0.02	0.99	5	25	positive regulation of epidermis development	BP	1	H2AFY,PPARD,NUMA1,KRT10,TMEM79	yellow	VSMC_M3
GO:0071498	0.02	1.00	4	18	cellular response to fluid shear stress	BP	1	SREBF2,PLEC,SOCS5,KLF4	yellow	VSMC_M3
GO:0006304	0.02	0.99	11	84	DNA modification	BP	1	KMT2E,MUTYH,DMAP1,OGG1,SMUG1,KDM1B,ALKBH4,GATAD2A,MTA2,EHMT1,MBD3	yellow	VSMC_M3
GO:2001135	0.02	1.00	4	18	regulation of endocytic recycling	BP	1	EIPR1,EHD2,PLA2G3,PLA2G4E	yellow	VSMC_M3

GO:1901362	0.02	0.98	230	3012	organic cyclic compound biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,SQLE,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,TSTA3,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,FDXR,DMAP1,CIC,GTF3C2,INSIG1,OGG1,SERTAD1,TTC5,CXXC5,PYCR1,GNPDA1,DEAF1,HOXC4,POLR1D,KMT2B,SCARB1,NAT10,ZNF740,RALY,ACSL1,ZBTB38,SLC11A2,FDFT1,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,NPM3,KDM1B,CHCHD2,AK2,IRX1,DHCR7,RRP1B,MVK,BRD9,PAPSS1,AIP,MOCS3,SRRD,TSHZ2,QARS,IMPDH2,LSS,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,PSTK,SMARCD2,BRMS1,PPOX,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ATP5MC3,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,SLC25A39,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,HSD17B1,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,ARMC5,SNF8,PER1,NFIX,FLAD1,IRF2BPL,PMVK,TRIM25,ATP5PD,USP43,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,HMGCS1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,DHCR24,MYDGF,HDGFL2,SIRT6,MAP2K2,NSDHL,CACTIN,CDK11B,SSU72,HIC1,MNT,CTNS,EHMT1,AP3D1,IRAK1,MBD3,ATP5F1D,TELO2,TAZ,MED16,CARD9,AMPD2,SARS,APRT,GTF3C5,MVD,AK1,TRADD,RF00024,ERBB4,JUND,PTMA,KLF13,FADS1,ZNF783,HOXC5,CAVIN1,IER5,AKAP17A,FDPS,ZNF	yellow	VSMC_M3
GO:0098773	0.02	0.99	9	65	skin epidermis development	BP	1	NUMA1,WNT10B,PDGFA,RELA,IGFBP5,TMEM79,NSDHL,TRADD,NOM1	yellow	VSMC_M3
GO:1901617	0.02	0.99	20	178	organic hydroxy compound biosynthetic process	BP	1	SQLE,INSIG1,FDFT1,SOD1,DHCR7,MVK,PCK2,LSS,ISYNA1,HSD17B1,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,CTNS,PGP,MVD,FDPS,IDI1	yellow	VSMC_M3
GO:0060119	0.02	0.99	6	35	inner ear receptor cell development	BP	1	CTHRC1,SCRIB,IFT27,WDPCP,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:0000466	0.02	0.99	5	24	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	1	BOP1,RRS1,RPS21,FTSJ3,NOP14	yellow	VSMC_M3
GO:0046782	0.02	1.00	4	17	regulation of viral transcription	BP	1	TRIM11,TARBP2,TRIM27,MID2	yellow	VSMC_M3
GO:0006091	0.02	0.98	40	392	generation of precursor metabolites and energy	BP	1	ENPP1,NDUFB9,PPARD,TSTA3,PLEC,FDXR,GALK1,GNPDA1,CAVIN3,GSR,IDH3B,OGDHL,AACS,UQCRFS1,TKT,CHCHD2,SELENOS,ETFBKMT,SDHA,NDUFV1,UQCRC1,TACO1,IDH1,CHCHD10,PHB2,UQCC3,FOXK1,PGD,ATP5PD,FDX2,AKT1,PGM1,GIT1,TRAP1,NDUFS7,ATP5F1D,TAZ,JMJD8,SURF1,TALDO1	yellow	VSMC_M3
GO:0034637	0.03	0.99	9	63	cellular carbohydrate biosynthetic process	BP	1	ENPP1,B4GALT1,SELENOS,PCK2,ISYNA1,AKT1,PGP,B3GNT9,NDST1	yellow	VSMC_M3
GO:0060122	0.03	0.99	5	26	inner ear receptor cell stereocilium organization	BP	1	CTHRC1,SCRIB,IFT27,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:0006414	0.03	0.99	8	50	translational elongation	BP	1	EEF1D,SECISBP2,RPLP2,SEPSECS,TUFM,EEF2K,C19orf66,EEF1G	yellow	VSMC_M3
GO:0008380	0.03	0.98	36	356	RNA splicing	BP	1	DHX16,RTCB,SNRNP70,GEMIN7,METTL3,RALY,ARL6IP4,LSM6,PRPF40B,CCAR2,PCBP4,RBM15B,SRSF9,DCPS,RRP1B,RBM6,THOC5,SF3A1,SART1,PRPF6,THOC3,LGALS3,BUD31,C1QBP,GPKOW,POLR2A,CWC25,CD2BP2,RAVER1,RBM22,ZNF830,KHSRP,CACTIN,FAM50A,RBM8A,AKAP17A	yellow	VSMC_M3
GO:1900077	0.03	0.99	5	27	negative regulation of cellular response to insulin stimulus	BP	1	ENPP1,TNS2,RELA,PIP4K2B,SLC27A4	yellow	VSMC_M3
GO:0045444	0.03	0.99	20	188	fat cell differentiation	BP	1	ENPP1,PPARD,PDGFRA,KLF4,ZC3H12A,FAM120B,WDFY2,INSIG1,AACS,LRP3,WNT10B,FABP3,GPX1,CCDC85B,TMEM120A,CTBP1,CARM1,AKT1,TRIB2,ZNF385A	yellow	VSMC_M3
GO:0022613	0.03	0.98	38	376	ribonucleoprotein complex biogenesis	BP	1	NHP2,RPL3,BOP1,GEMIN7,TARBP2,NAT10,EIF4B,RRS1,LSM6,NPM3,SRSF9,RRP1B,NGDN,EIF3A,SF3A1,RPS21,FTSJ3,BUD23,SART1,PRPF6,DDX52,TRMT112,NOP14,MPV17L2,MRTO4,C1QBP,NUP88,RRNAD1,CD2BP2,RPL7A,AATF,EIF3G,MRPL20,TBL3,TSR3,RBFA,PIN4,NOM1	yellow	VSMC_M3
GO:0046777	0.03	0.98	20	204	protein autophosphorylation	BP	1	ENPP1,PDGFRA,TNKS1BP1,GREM1,CHP1,TYRO3,HTATIP2,PDGFA,RIPK3,MEX3B,MVP,EEF2K,CSK,AKT1,MAP2K2,MKNK2,CSNK1G2,IRAK1,STK11,ERBB4	yellow	VSMC_M3
GO:1903311	0.03	0.98	25	247	regulation of mRNA metabolic process	BP	1	NELFE,HNRNPA0,SECISBP2,CNOT3,ZC3H12A,SNRNP70,METTL3,DND1,PCBP4,RBM15B,SRSF9,DCPS,C1QBP,SLTM,NANOS3,RAVER1,AKT1,PAIP1,KHSRP,SAFB,SAFB2,CARHSP1,CDK11B,RBM8A,TENT5B	yellow	VSMC_M3
GO:0071402	0.03	0.99	5	26	cellular response to lipoprotein particle stimulus	BP	1	SREBF2,SOCS5,CD9,AKT1,HMGCS1	yellow	VSMC_M3
GO:0010761	0.03	0.99	7	46	fibroblast migration	BP	1	PLEC,WDPCP,SGPL1,RCC2,MTA2,AKT1,TMEM201	yellow	VSMC_M3
GO:0016192	0.03	0.98	95	1192	vesicle-mediated transport	BP	1	ENPP1,PQLC1,CD63,RUFY1,SQSTM1,SNX9,SGSM3,PACSIN1,SCRIB,VPS28,TOM1,EPN1,SSC5D,DBNL,EIPR1,SNX3,MICAL1,EHD2,SNX17,INSIG1,SEC13,INPPL1,LAMTOR1,YIF1B,RAB20,ARAP3,SIGLEC1,LDLRAD3,SCARB1,BCL2L1,LRP3,GREM1,DCTN1,SOD1,PACSIN3,HPS1,CHP1,TYRO3,AP2A2,RAB35,EXOC3,RIN3,AP1G2,SYT12,TRIM27,LIMK1,TNK2,PLA2G3,PTPN23,MRC2,SCYL1,VPS51,ZFPL1,COPE,SCARF2,LGALS3,CD9,FCHO1,MVB12A,ANXA11,WASHC1,AP1M1,RAB3IL1,CCDC22,SNX8,LMAN2,PIP4K2B,CLTB,TMEM79,SNF8,RANGRF,STX10,CORO1A,RABEP2,TMED1,EEF2K,CSK,ATG3,SNX18,DENND1C,RAB34,GIT1,ANKRD13B,MAP2K2,AP3D1,CSNK1G2,RABEPK,TRAPPC5,PLA2G4E,AP5B1,JAGN1,UNC13A,ARFRP1,PHETA2,GSG1L	yellow	VSMC_M3
GO:0044270	0.03	0.98	35	361	cellular nitrogen compound catabolic process	BP	1	ENPP1,HNRNPA0,NUDT3,MPST,SND1,DNPH1,SECISBP2,CNOT3,ZC3H12A,BLVRA,BLVRB,OGG1,METTL3,DND1,SMUG1,PDE4D,LSM6,PCBP4,DCPS,ZCCHC17,RNASEH2C,MRTO4,CNP,NANOS3,DFFA,AKT1,PAIP1,KHSRP,CARHSP1,RBM8A,RNH1,NT5C,TENT5B,TRIR,ITPA	yellow	VSMC_M3
GO:1902903	0.03	0.98	30	327	regulation of supramolecular fiber organization	BP	1	SNX9,DBNL,EMILIN1,BAIAP2,NUMA1,SWAP70,CAPG,DCTN1,CX3CL1,GPX1,CORO1B,TRIM27,ARPIN,LIMK1,PFDN2,RHOC,MID1IP1,ARPC1B,WASHC1,DBN1,ARHGEF2,RANGRF,CORO1A,GIT1,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3

GO:0046034	0.03	0.98	25	219	ATP metabolic process	BP	1	ENPP1,NDUFB9,GUK1,FIGNL1,GALK1,OGDHL,CHCHD2,AK2,SDHA,NDUFV1,UQCRC1,ATP5MC3,CHCHD10,BAD,UQCC3,FOXK1,ATP5PD,PGM1,GIT1,CTNS,NDUFS7,ATP5F1D,TAZ,JMJD8,AK1	yellow	VSMC_M3
GO:0007080	0.03	0.99	7	43	mitotic metaphase plate congression	BP	1	DCTN2,RRS1,PINX1,NUDC,EML3,MAD1L1,MIS12	yellow	VSMC_M3
GO:0042634	0.03	0.99	4	20	regulation of hair cycle	BP	1	NUMA1,WNT10B,PER1,TRADD	yellow	VSMC_M3
GO:0019083	0.03	0.99	7	45	viral transcription	BP	1	TRIM11,TARBP2,RRP1B,TRIM27,SMARCB1,SMARCA4,MID2	yellow	VSMC_M3
GO:0045010	0.03	0.99	7	44	actin nucleation	BP	1	CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,CORO1A,ARPC5L	yellow	VSMC_M3
GO:0016072	0.03	0.98	23	206	rRNA metabolic process	BP	1	NHP2,BOP1,NAT10,RRS1,LSM6,NPM3,RRP1B,NGDN,RPS21,FTSJ3,BUD23,SART1,DDX52,TRMT112,NOP14,MRTO4,RRNAD1,RPL7A,TBL3,TSR3,RBFA,PIN4,TRIR	yellow	VSMC_M3
GO:0071230	0.03	0.99	8	59	cellular response to amino acid stimulus	BP	1	PDGFRA,BAIAP2,LAMTOR1,BCL2L1,COL6A1,LAMTOR4,CAPN2,NSMF	yellow	VSMC_M3
GO:0006807	0.03	0.97	535	7284	nitrogen compound metabolic process	BP	1	ENPP1,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,DHX16,ZNF608,LMF2,BAG6,SBF1,SNX9,HDAC10,NELFE,CERK,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,JADE2,TRMT12,H2AFY,HNRNPA0,TRIM11,SGSM3,GUK1,TRAPPC9,NUDT3,PPARD,FANCE,EEF1D,TSTA3,RPL3,PLEC,MPST,SHARPIN,BOP1,SLC52A2,VPS28,RPL8,SND1,CUL7,RTCB,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,JOSD2,PSMB3,FHL3,SPRED2,EIPR1,MEAF6,ZC3H12A,FIGNL1,BLVRA,PNKP,CPT1C,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,CIC,GTF3C2,GALK1,PPM1G,UNK,BCKDHA,GALNT14,BLVRB,OGG1,SERTAD1,TTC5,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,CXXC5,FAAP100,P4HB,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,DELE1,GNPDA1,PUS1,GSR,PTDSS2,DEAF1,SMUG1,HOXC4,OGDHL,POLR1D,LDLRAD3,TARBP2,KMT2B,SCARB1,C12orf10,NAT10,HM13,ZNF740,PDE4D,TNS2,EIF4B,RRS1,PEPD,SWAP70,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,SLC11A2,TNKS1BP1,MMP24,PINX1,GATB,SETD1B,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,ACCS,RPLP2,CHP1,TYRO3,MRPL43,YAF2,HTATIP2,PCIF1,PPM1M,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,TSPAN5,CISH,SRSF9,ST3GAL4,AK2,RNF19B,DCPS,IRX1,WDR4,SELENOS,GSTO1,RRP1B,ETFBKMT,MANBA,TMTC1,MVK,BRD9,RBM6,STK32C,FABP3,ZCCHC17,PAPSS1,PDGFA,MMP14,APEH,PABPN1,GPX1,AIP,HCCS,MOCS3,CLCF1,NGDN,SRRD,TSHZ2,QA	yellow	VSMC_M3
GO:0008154	0.03	0.98	19	183	actin polymerization or depolymerization	BP	1	SNX9,DBNL,MICAL1,BAIAP2,SWAP70,CAPG,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,DBN1,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0071353	0.03	0.99	5	26	cellular response to interleukin-4	BP	1	CDK4,RPL3,FASN,IMPDH2,CORO1A	yellow	VSMC_M3
GO:0006353	0.03	0.99	4	19	DNA-templated transcription, termination	BP	1	ZNRD1,POLR2A,SSU72,CAVIN1	yellow	VSMC_M3
GO:0090304	0.03	0.97	296	3916	nucleic acid metabolic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,DHX16,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,TRMT12,H2AFY,HNRNPA0,TRIM11,TRAPPC9,NUDT3,PPARD,FANCE,BOP1,SND1,RTCB,AARS2,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,FIGNL1,PNKP,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,GEMIN7,ZNF296,RELB,MUTYH,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,METTL3,CXXC5,FAAP100,DND1,PUS1,DEAF1,SMUG1,HOXC4,POLR1D,TARBP2,KMT2B,C12orf10,NAT10,ZNF740,RRS1,SWAP70,RALY,ZBTB38,ARL6IP4,LSM6,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,NPM3,PCBP4,KDM1B,CHCHD2,RBM15B,CARS,SRSF9,DCPS,IRX1,WDR4,RRP1B,TMTC1,BRD9,RBM6,ZCCHC17,PABPN1,AIP,MOCS3,CLCF1,NGDN,TSHZ2,QARS,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,SF3A1,ADRM1,PSTK,RPS21,SMARCD2,FTSJ3,BRMS1,BUD23,GMEB2,CEP164,SART1,CCDC85B,PRPF6,PBX1,RNASEH2C,KAT5,RELA,ZNF511,DDX52,LRWD1,ALKBH4,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,TRMT2A,PBX4,UBTF,GATAD2A,THOC3,MEF2B,PHB2,TRMT112,NDP,CTDSP1,MLF2,OTUB1,NOP14,EID1,SSBP4,METTL13,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,GTPBP3,BABAM1,TEAD4,C1QBP,CSTF2T,TAF6L,CHERP,ZBTB49,GPKOW,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,ELP5,KLF3,PKN1,SEPSECS,INTS1,POLR2A,CWC25,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,RRNAD1,CRABP2,DFFA,SP2,ARHGEF2,SNF8,CD2BP2,PER1,NFIX,TRMT1,PPP4C,FARSA,SLX1A,IRF2BPL,TRIM25,USP43,SMARCA4,CARM1,RPL7A,RAVER1,AATF,CXorf	yellow	VSMC_M3
GO:0031397	0.03	0.99	10	72	negative regulation of protein ubiquitination	BP	1	SQSTM1,VPS28,PINX1,CHP1,LIMK1,OTUB1,UBXN1,MAD2L2,RPL37,AKT1	yellow	VSMC_M3
GO:0046031	0.04	0.99	9	66	ADP metabolic process	BP	1	GALK1,OGDHL,AK2,BAD,FOXK1,PGM1,GIT1,JMJD8,AK1	yellow	VSMC_M3
GO:0051310	0.04	0.99	8	55	metaphase plate congression	BP	1	DCTN2,NUMA1,RRS1,PINX1,NUDC,EML3,MAD1L1,MIS12	yellow	VSMC_M3
GO:0018393	0.04	0.98	15	134	internal peptidyl-lysine acetylation	BP	1	BAG6,JADE2,MEAF6,DMAP1,KAT14,MCRS1,KAT5,SMARCB1,EID1,TAF6L,CTBP1,PER1,SGF29,MBD3,THAP7	yellow	VSMC_M3
GO:0001885	0.04	0.99	7	53	endothelial cell development	BP	1	COL15A1,CCM2,FASN,PDE4D,GPX1,TNFRSF1A,TJP3	yellow	VSMC_M3
GO:0009161	0.04	0.99	8	51	ribonucleoside monophosphate metabolic process	BP	1	GUK1,AK2,IMPDH2,ATIC,AMPD2,APRT,AK1,NT5C	yellow	VSMC_M3
GO:0006325	0.04	0.98	28	301	chromatin organization	BP	1	BAG6,HDAC10,H2AFY,PHF2,KMT2E,DMAP1,H3F3B,ACTR5,NPM3,BRD9,SMARCD2,BUD23,RELA,LRWD1,ALKBH4,ZNHIT1,SMARCB1,BABAM1,TAF6L,MTA2,H3F3A,SMARCA4,SAFB,UBN1,HMG20B,EHMT1,MBD3,FAM50A	yellow	VSMC_M3
GO:0019058	0.04	0.98	24	239	viral life cycle	BP	1	TRIM11,LGALS1,SLC52A2,VPS28,ZC3H12A,SNX3,P4HB,SIGLEC1,TARBP2,SCARB1,ITGB7,TYRO3,NECTIN1,ANPEP,TRIM27,BANF1,SMARCB1,MVB12A,CTBP1,SNF8,TRIM25,C19orf66,MID2,CLDN6	yellow	VSMC_M3

GO:0032102	0.04	0.98	26	266	negative regulation of response to external stimulus	BP	1	TTLL12,PPARD,SHARPIN,PDGFRA,SOCS5,KLF4,METTL3,TARBP2,GREM1,CX3CL1,SOD1,TYRO3,SELENOS,MVK,RIN3,PDGFA,GPX1,CORO1B,SPX,PSMB4,CD9,PLAU,TNFRSF1A,C1QBP,GIT1,CACTIN	yellow	VSMC_M3
GO:0006720	0.04	0.98	10	73	isoprenoid metabolic process	BP	1	PPARD,FDFT1,MVK,LSS,CRABP2,PMVK,HMGCS1,MVD,FDPS,IDI1	yellow	VSMC_M3
GO:0030041	0.04	0.98	17	160	actin filament polymerization	BP	1	SNX9,DBNL,BAIAP2,CAPG,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,DBN1,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0050773	0.04	0.98	10	87	regulation of dendrite development	BP	1	PACSIN1,CUL7,DBNL,BAIAP2,DBN1,CARM1,EEF2K,ANAPC2,STK11,NSMF	yellow	VSMC_M3
GO:0046700	0.04	0.97	34	357	heterocycle catabolic process	BP	1	ENPP1,HNRNPA0,NUDT3,SND1,DNPH1,SECISBP2,CNOT3,ZC3H12A,BLVRA,BLVRB,OGG1,METTL3,DND1,SMUG1,PDE4D,LSM6,PCBP4,DCPS,ZCCHC17,RNASEH2C,MRTO4,CNP,NANOS3,DFFA,AKT1,PAIP1,KHSRP,CARHSP1,RBM8A,RNH1,NT5C,TENT5B,TRIR,ITPA	yellow	VSMC_M3
GO:2001242	0.04	0.98	16	135	regulation of intrinsic apoptotic signaling pathway	BP	1	FIGNL1,SLC9A3R1,P4HB,BCL2L1,PLEKHF1,SOD1,CCAR2,SELENOS,GPX1,RIPK3,BAD,ARHGEF2,AKT1,TRAP1,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0016571	0.04	0.98	13	118	histone methylation	BP	1	NELFE,H2AFY,KMT2E,KMT2B,SETD1B,PRMT2,SMARCB1,TRMT112,MTHFR,CARM1,COPRS,EHMT1,NTMT1	yellow	VSMC_M3
GO:0070050	0.04	0.99	4	22	neuron cellular homeostasis	BP	1	DCTN1,CX3CL1,TYRO3,TSPOAP1	yellow	VSMC_M3
GO:0006364	0.04	0.98	22	198	rRNA processing	BP	1	NHP2,BOP1,NAT10,RRS1,LSM6,NPM3,RRP1B,NGDN,RPS21,FTSJ3,BUD23,SART1,DDX52,TRMT112,NOP14,MRTO4,RRNAD1,RPL7A,TBL3,TSR3,RBFA,PIN4	yellow	VSMC_M3
GO:0042472	0.04	0.98	9	73	inner ear morphogenesis	BP	1	CTHRC1,SCRIB,HOXA1,WDPCP,SLC9A3R1,INSIG1,LRIG1,SOD1,TTC39C	yellow	VSMC_M3
GO:0006749	0.04	0.99	7	42	glutathione metabolic process	BP	1	GSR,SOD1,GSTO1,GPX1,IDH1,CTNS,EEF1G	yellow	VSMC_M3
GO:0009168	0.04	0.99	4	18	purine ribonucleoside monophosphate biosynthetic process	BP	1	IMPDH2,ATIC,AMPD2,APRT	yellow	VSMC_M3
GO:0044271	0.04	0.97	260	3436	cellular nitrogen compound biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,EEF1D,TSTA3,RPL3,RPL8,SND1,MRPS18A,AARS2,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,GTF3C2,UNK,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,SMOX,RPL29,EIF4EBP1,GNPDA1,DEAF1,HOXC4,POLR1D,TARBP2,KMT2B,NAT10,ZNF740,EIF4B,RALY,ACSL1,ZBTB38,SLC11A2,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,KDM1B,CHCHD2,CARS,AK2,DCPS,IRX1,RRP1B,BRD9,PAPSS1,APEH,AIP,NGDN,SRRD,TSHZ2,QARS,IMPDH2,PIR,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,PSTK,RPS21,SMARCD2,BRMS1,PPOX,TACO1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ATP5MC3,ZNF511,ARNT2,MRPL49,ZFPL1,LIMD1,SMARCB1,CHCHD10,SLC25A39,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,FARSA,FLAD1,IRF2BPL,TUFM,TRIM25,ATP5PD,USP43,RPL37,SMARCA4,CARM1,RPL7A,EEF2K,AATF,MRPL4,EIF3G,C19orf66,MID2,ZNF521,ZNF358,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MRPL20,TRAP1,MNT,EHMT1,AP3D1,M	yellow	VSMC_M3
GO:0061001	0.04	0.99	6	42	regulation of dendritic spine morphogenesis	BP	1	DBNL,BAIAP2,ARHGAP33,NGEF,DBN1,EEF2K	yellow	VSMC_M3
GO:0006475	0.04	0.98	15	136	internal protein amino acid acetylation	BP	1	BAG6,JADE2,MEAF6,DMAP1,KAT14,MCRS1,KAT5,SMARCB1,EID1,TAF6L,CTBP1,PER1,SGF29,MBD3,THAP7	yellow	VSMC_M3
GO:0033559	0.04	0.98	9	64	unsaturated fatty acid metabolic process	BP	1	PTGR1,MGLL,SCD,GPX1,PLA2G3,TNFRSF1A,CYP4F8,FADS2,FADS1	yellow	VSMC_M3
GO:0009135	0.04	0.98	10	78	purine nucleoside diphosphate metabolic process	BP	1	GUK1,GALK1,OGDHL,AK2,BAD,FOXK1,PGM1,GIT1,JMJD8,AK1	yellow	VSMC_M3
GO:0009179	0.04	0.98	10	78	purine ribonucleoside diphosphate metabolic process	BP	1	GUK1,GALK1,OGDHL,AK2,BAD,FOXK1,PGM1,GIT1,JMJD8,AK1	yellow	VSMC_M3
GO:0007224	0.04	0.98	13	119	smoothened signaling pathway	BP	1	ENPP1,TXNDC15,IFT27,WDPCP,WNT10B,EVC,TEDC1,RAB34,NSDHL,TEDC2,SSNA1,GAS8,NDST1	yellow	VSMC_M3
GO:0034655	0.04	0.97	32	335	nucleobase-containing compound catabolic process	BP	1	ENPP1,HNRNPA0,NUDT3,SND1,DNPH1,SECISBP2,CNOT3,ZC3H12A,OGG1,METTL3,DND1,SMUG1,PDE4D,LSM6,PCBP4,DCPS,ZCCHC17,RNASEH2C,MRTO4,CNP,NANOS3,DFFA,AKT1,PAIP1,KHSRP,CARHSP1,RBM8A,RNH1,NT5C,TENT5B,TRIR,ITPA	yellow	VSMC_M3
GO:0034405	0.04	0.99	5	31	response to fluid shear stress	BP	1	SREBF2,PLEC,SOCS5,KLF4,AKT1	yellow	VSMC_M3
GO:0034622	0.04	0.97	72	830	cellular protein-containing complex assembly	BP	1	SPAG1,SNX9,SAMM50,NDUFB9,H2AFY,RPL3,BOP1,TBCC,DBNL,ACAD9,GEMIN7,H3F3B,BAIAP2,NUMA1,CCDC57,SDHAF1,TARBP2,EIF4B,RRS1,UQCRFS1,CAPG,GREM1,DCTN1,WNT10B,SRSF9,CORO1B,HCCS,TRIM27,ARPIN,EIF3A,SF3A1,ADRM1,TACO1,SART1,PRPF6,MID1IP1,SMARCB1,UBTF,ARPC1B,MRTO4,FCHO1,TAF6L,UQCC3,WASHC1,H3F3A,DBN1,CLTB,CD2BP2,RANGRF,CORO1A,SMARCA4,EIF3G,BRF1,GIT1,UBN1,MRPL20,NDUFS7,ATP5F1D,TAZ,TGFBR3,MIR214,TWF2,SURF1,MIS12,ELN,UNC13A,CDC42EP5,GBA2,TUBGCP2,STUB1,CCDC115,ARPC5L	yellow	VSMC_M3
GO:0042168	0.04	0.99	6	37	heme metabolic process	BP	1	BLVRA,BLVRB,SLC11A2,SRRD,PPOX,SLC25A39	yellow	VSMC_M3
GO:1902905	0.04	0.98	18	179	positive regulation of supramolecular fiber organization	BP	1	SNX9,BAIAP2,NUMA1,SWAP70,DCTN1,CX3CL1,GPX1,CORO1B,TRIM27,ARPIN,LIMK1,RHOC,ARPC1B,WASHC1,CORO1A,GIT1,CDC42EP5,ARPC5L	yellow	VSMC_M3
GO:0006898	0.04	0.98	19	192	receptor-mediated endocytosis	BP	1	CD63,SNX9,SCRIB,DBNL,SNX17,SIGLEC1,LDLRAD3,LRP3,GREM1,AP2A2,RIN3,AP1G2,TNK2,CD9,FCHO1,CLTB,ANKRD13B,RABEPK,GSG1L	yellow	VSMC_M3
GO:0043648	0.04	0.98	10	73	dicarboxylic acid metabolic process	BP	1	GRHPR,IDH3B,OGDHL,SDHA,PCK2,SLC19A1,IDH1,ATIC,ACLY,GLUD1	yellow	VSMC_M3

GO:0044782	0.04	0.97	27	288	cilium organization	BP	1	SPAG1,TXNDC15,IFT27,WDPCP,EHD2,SLC9A3R1,SEPT9,CEP131,YIF1B,CCDC57,DCTN1,CCDC32,CCDC28B,PCNT,IQCG,PLA2G3,CEP164,PTPN23,FAM161B,RABEP2,ATG3,TTC39C,RFX2,SSNA1,GAS8,WDR34,MEIG1	yellow	VSMC_M3
GO:0009913	0.04	0.98	13	120	epidermal cell differentiation	BP	1	H2AFY,SCRIB,PLEC,SHARPIN,KLF4,WDPCP,SLC9A3R1,NUMA1,SOD1,KRT10,CASP14,TMEM79,PPL	yellow	VSMC_M3
GO:0043588	0.04	0.98	17	171	skin development	BP	1	H2AFY,PLEC,SHARPIN,NUMA1,WNT10B,PDGFA,RELA,IGFBP5,KRT10,CASP14,TMEM79,DHCR24,PPL,NSDHL,SLC27A4,TRADD,NOM1	yellow	VSMC_M3
GO:0007020	0.04	0.99	5	32	microtubule nucleation	BP	1	CCDC57,DCTN1,RANGRF,GIT1,TUBGCP2	yellow	VSMC_M3
GO:0010586	0.04	0.99	4	23	miRNA metabolic process	BP	1	SND1,ZC3H12A,RELA,KHSRP	yellow	VSMC_M3
GO:0051258	0.04	0.97	24	250	protein polymerization	BP	1	SNX9,DBNL,BAIAP2,NUMA1,CCDC57,CAPG,DCTN1,CORO1B,TRIM27,ARPIN,MID1IP1,ARPC1B,WASHC1,DBN1,RANGRF,CORO1A,GIT1,MIR214,TWF2,ELN,CDC42EP5,GBA2,TUBGCP2,ARPC5L	yellow	VSMC_M3
GO:0015909	0.05	0.98	7	46	long-chain fatty acid transport	BP	1	ACSL1,FABP3,SPX,PLA2G3,SLC27A3,AKT1,SLC27A4	yellow	VSMC_M3
GO:0050994	0.05	0.99	6	39	regulation of lipid catabolic process	BP	1	CDK4,SCARB1,PDE3B,ETFBKMT,IDH1,AKT1	yellow	VSMC_M3
GO:0032273	0.05	0.98	13	116	positive regulation of protein polymerization	BP	1	SNX9,BAIAP2,NUMA1,DCTN1,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,CORO1A,GIT1,CDC42EP5,ARPC5L	yellow	VSMC_M3
GO:0070670	0.05	0.99	5	28	response to interleukin-4	BP	1	CDK4,RPL3,FASN,IMPDH2,CORO1A	yellow	VSMC_M3
GO:0043200	0.05	0.98	11	93	response to amino acid	BP	1	PDGFRA,BAIAP2,LAMTOR1,BCL2L1,COL6A1,RELA,BAD,LAMTOR4,CAPN2,MTHFR,NSMF	yellow	VSMC_M3
GO:0050772	0.05	0.98	8	68	positive regulation of axonogenesis	BP	1	DBNL,PLXND1,LIMK1,DBN1,CRABP2,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0010770	0.05	0.98	8	65	positive regulation of cell morphogenesis involved in differentiation	BP	1	CUL7,DBNL,BAIAP2,P4HB,C1QBP,DBN1,EEF2K,ANAPC2	yellow	VSMC_M3
GO:0018027	0.05	0.99	4	21	peptidyl-lysine dimethylation	BP	1	KMT2B,SETD1B,SMARCB1,EHMT1	yellow	VSMC_M3
GO:0001676	0.05	0.98	9	66	long-chain fatty acid metabolic process	BP	1	MGLL,ACAD9,ACSL1,GPX1,FADS2,ACSF2,SLC27A3,SLC27A4,FADS1	yellow	VSMC_M3
GO:0038061	0.05	0.98	12	99	NIK/NF-kappaB signaling	BP	1	ZC3H12A,RELB,GREM1,RIPK3,RELA,MAP3K14,PHB2,IFI35,PPP4C,AKT1,IRAK1,TRADD	yellow	VSMC_M3
GO:0009185	0.05	0.98	10	81	ribonucleoside diphosphate metabolic process	BP	1	GUK1,GALK1,OGDHL,AK2,BAD,FOXK1,PGM1,GIT1,JMJD8,AK1	yellow	VSMC_M3
GO:0002181	0.05	0.97	14	111	cytoplasmic translation	BP	1	RPL3,RPL8,RPS9,UNK,METTL3,RPL29,EIF4B,RPLP2,EIF3A,RPS21,RPL37,RPL7A,EIF3G,ZNF385A	yellow	VSMC_M3
GO:0032609	0.05	0.98	8	59	interferon-gamma production	BP	1	SCRIB,IL1R1,ZC3H12A,PDE4D,TRIM27,RIPK3,C1QBP,CD276	yellow	VSMC_M3
GO:0032649	0.05	0.98	8	59	regulation of interferon-gamma production	BP	1	SCRIB,IL1R1,ZC3H12A,PDE4D,TRIM27,RIPK3,C1QBP,CD276	yellow	VSMC_M3
GO:0010608	0.05	0.96	43	480	posttranscriptional regulation of gene expression	BP	1	CDK4,HNRNPA0,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,EIF4EBP1,TARBP2,NAT10,EIF4B,PCIF1,PCBP4,DCPS,ZCCHC17,NGDN,LSM14B,TACO1,LIMD1,IGFBP5,MPV17L2,C1QBP,SEPSECS,NANOS3,PER1,CDC37,C19orf66,AKT1,PAIP1,KHSRP,CARHSP1,MAP2K2,TRAP1,MKNK2,MIR214,MIR155,RBM8A,MIR374B,TENT5B,ZNF385A,ZAR1L	yellow	VSMC_M3
GO:0042255	0.05	0.98	7	45	ribosome assembly	BP	1	RPL3,BOP1,RRS1,MPV17L2,MRTO4,C1QBP,MRPL20	yellow	VSMC_M3
GO:0006305	0.05	0.98	7	53	DNA alkylation	BP	1	KMT2E,DMAP1,KDM1B,GATAD2A,MTA2,EHMT1,MBD3	yellow	VSMC_M3
GO:0006306	0.05	0.98	7	53	DNA methylation	BP	1	KMT2E,DMAP1,KDM1B,GATAD2A,MTA2,EHMT1,MBD3	yellow	VSMC_M3
GO:1903902	0.05	0.99	4	21	positive regulation of viral life cycle	BP	1	TRIM11,LGALS1,P4HB,TYRO3	yellow	VSMC_M3
GO:0051668	0.05	0.96	46	537	localization within membrane	BP	1	SQSTM1,BAG6,SAMM50,PACSIN1,SCRIB,TTC7A,ASNA1,TPBG,EIPR1,SNX3,EHD2,SLC9A3R1,SNX17,YIF1B,BCL2L1,ITGB7,PLEKHF1,RAPSN,CHP1,RAB35,TSPAN5,MMP14,PLA2G3,PTPN23,VPS51,PEX5,ZDHHC3,YJEFN3,LGALS3,TNFRSF1A,WASHC1,CCDC22,SNF8,RANGRF,SYNE3,CSK,ATG3,AKT1,PACS2,DENND1C,RAB34,AP3D1,SSNA1,PLA2G4E,ARFRP1,TIMM22	yellow	VSMC_M3
GO:0018394	0.05	0.97	15	143	peptidyl-lysine acetylation	BP	1	BAG6,JADE2,MEAF6,DMAP1,KAT14,MCRS1,KAT5,SMARCB1,EID1,TAF6L,CTBP1,PER1,SGF29,MBD3,THAP7	yellow	VSMC_M3
GO:1902600	0.05	0.97	14	115	proton transmembrane transport	BP	1	SLC9A3R1,UCP2,UQCRFS1,SLC11A2,CHP1,UQCRC1,TACO1,ATP5MC3,PHB2,ATP5PD,CTNS,NDUFS7,ATP5F1D,SURF1	yellow	VSMC_M3
GO:0002090	0.05	0.98	6	43	regulation of receptor internalization	BP	1	CD63,SCRIB,GREM1,RIN3,ANKRD13B,GSG1L	yellow	VSMC_M3
GO:1904994	0.05	0.99	4	21	regulation of leukocyte adhesion to vascular endothelial cell	BP	1	KLF4,ST3GAL4,RELA,IRAK1	yellow	VSMC_M3
GO:0043903	0.05	0.98	7	49	regulation of biological process involved in symbiotic interaction	BP	1	TRIM11,LGALS1,SNX3,P4HB,TRIM27,TRIM25,MID2	yellow	VSMC_M3
GO:0030838	0.06	0.98	10	82	positive regulation of actin filament polymerization	BP	1	SNX9,BAIAP2,CORO1B,TRIM27,ARPIN,ARPC1B,WASHC1,CORO1A,CDC42EP5,ARPC5L	yellow	VSMC_M3
GO:0006473	0.06	0.97	17	168	protein acetylation	BP	1	BAG6,JADE2,MEAF6,NAT9,DMAP1,KAT14,NAT10,MCRS1,KAT5,SMARCB1,EID1,TAF6L,CTBP1,PER1,SGF29,MBD3,THAP7	yellow	VSMC_M3
GO:0032715	0.06	0.98	5	30	negative regulation of interleukin-6 production	BP	1	SOCS5,ZC3H12A,CX3CL1,SELENOS,CSK	yellow	VSMC_M3
GO:0016573	0.06	0.97	14	131	histone acetylation	BP	1	JADE2,MEAF6,DMAP1,KAT14,MCRS1,KAT5,SMARCB1,EID1,TAF6L,CTBP1,PER1,SGF29,MBD3,THAP7	yellow	VSMC_M3
GO:0014037	0.06	0.98	5	35	Schwann cell differentiation	BP	1	NAB2,PLEC,SOD1,RELA,AKT1	yellow	VSMC_M3
GO:0045599	0.06	0.98	6	43	negative regulation of fat cell differentiation	BP	1	ENPP1,INSIG1,LRP3,WNT10B,CCDC85B,TRIB2	yellow	VSMC_M3
GO:0030307	0.06	0.97	14	134	positive regulation of cell growth	BP	1	DNPH1,DBNL,H3F3B,KDM2B,MMP14,LIMK1,H3F3A,DBN1,CRABP2,AKT1,HDGFL2,ANAPC2,TWF2,UNC13A	yellow	VSMC_M3
GO:0055086	0.06	0.96	41	439	nucleobase-containing small molecule metabolic process	BP	1	ENPP1,GUK1,NUDT3,TSTA3,DNPH1,GALK1,OGG1,FASN,GNPDA1,SMUG1,OGDHL,PDE4D,ACSL1,AK2,MVK,PAPSS1,IMPDH2,ATP5MC3,ATIC,BAD,ASMTL,UQCC3,CNP,ACLY,FOXK1,ACSF2,FLAD1,PMVK,ATP5PD,HMGCS1,PGM1,GIT1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,NT5C,ITPA	yellow	VSMC_M3
GO:0010155	0.06	0.99	4	19	regulation of proton transport	BP	1	SLC9A3R1,CHP1,TACO1,PHB2	yellow	VSMC_M3
GO:0042273	0.06	0.98	8	56	ribosomal large subunit biogenesis	BP	1	NHP2,RPL3,BOP1,RRS1,FTSJ3,MRTO4,RPL7A,MRPL20	yellow	VSMC_M3
GO:1902532	0.06	0.96	36	407	negative regulation of intracellular signal transduction	BP	1	FNIP1,KLF4,SPRED2,ZC3H12A,FIGNL1,SLC9A3R1,EMILIN1,CAVIN3,BCL2L1,PDE4D,PDE3B,CCAR2,CHP1,SELENOS,GPX1,QARS,EIF3A,THOC5,STMN3,RELA,LIMD1,IFI35,C1QBP,CCDC22,ARHGEF2,PER1,CSK,AKT1,CACTIN,TRAP1,STK11,PTPRR,ZNF385A,TXNDC12,CDC34,DUSP5	yellow	VSMC_M3

GO:0045598	0.06	0.97	12	109	regulation of fat cell differentiation	BP	1	ENPP1,PPARD,ZC3H12A,WDFY2,INSIG1,LRP3,WNT10B,CCDC85B,CARM1,AKT1,TRIB2,ZNF385A	yellow	VSMC_M3
GO:0009123	0.06	0.98	9	65	nucleoside monophosphate metabolic process	BP	1	GUK1,DNPH1,AK2,IMPDH2,ATIC,AMPD2,APRT,AK1,NT5C	yellow	VSMC_M3
GO:0009127	0.06	0.99	4	20	purine nucleoside monophosphate biosynthetic process	BP	1	IMPDH2,ATIC,AMPD2,APRT	yellow	VSMC_M3
GO:0018205	0.06	0.96	29	313	peptidyl-lysine modification	BP	1	BAG6,HDAC10,NELFE,JADE2,H2AFY,MEAF6,KMT2E,DMAP1,KAT14,KMT2B,SETD1B,MCRS1,ETFBKMT,TRIM27,KAT5,RELA,SMARCB1,TRMT112,EID1,TAF6L,CTBP1,PER1,SGF29,METTL22,HMG20B,EHMT1,MBD3,LOXL1,THAP7	yellow	VSMC_M3
GO:0016577	0.06	0.99	4	28	histone demethylation	BP	1	PHF2,KDM2B,KDM1B,FBXL19	yellow	VSMC_M3
GO:0032869	0.06	0.97	16	161	cellular response to insulin stimulus	BP	1	ENPP1,CDK4,INSIG1,UCP2,BAIAP2,TNS2,PDE3B,SELENOS,PCK2,CAPN10,RELA,PIP4K2B,EEF2K,AKT1,APRT,SLC27A4	yellow	VSMC_M3
GO:0016482	0.06	0.97	15	153	cytosolic transport	BP	1	PQLC1,EIPR1,SNX3,DCTN1,TRIM27,PTPN23,VPS51,WASHC1,SNX8,SNF8,STX10,CORO1A,MAP2K2,ARFRP1,PHETA2	yellow	VSMC_M3
GO:0043162	0.06	0.99	4	21	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	BP	1	VPS28,PTPN23,MVB12A,SNF8	yellow	VSMC_M3
GO:0010769	0.06	0.97	9	80	regulation of cell morphogenesis involved in differentiation	BP	1	CUL7,DBNL,BAIAP2,P4HB,C1QBP,RCC2,DBN1,EEF2K,ANAPC2	yellow	VSMC_M3
GO:1901564	0.06	0.95	356	4789	organonitrogen compound metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,LMF2,BAG6,SBF1,SNX9,HDAC10,NELFE,CERK,FNIP1,PRR5,TTLL12,RING1,JADE2,H2AFY,TRIM11,SGSM3,GUK1,NUDT3,PPARD,EEF1D,RPL3,PLEC,MPST,SHARPIN,SLC52A2,VPS28,RPL8,CUL7,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,JOSD2,PSMB3,SPRED2,EIPR1,MEAF6,ZC3H12A,BLVRA,PNKP,CPT1C,RCN3,SNRNP70,SNX3,MICAL1,KMT2E,WDFY2,SLC9A3R1,SERP2,NAT9,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,GALK1,PPM1G,UNK,BCKDHA,GALNT14,BLVRB,OGG1,SERTAD1,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,P4HB,DND1,PYCR1,FASN,SMOX,RPL29,EIF4EBP1,DELE1,GNPDA1,GSR,PTDSS2,SMUG1,OGDHL,LDLRAD3,TARBP2,KMT2B,SCARB1,NAT10,HM13,PDE4D,TNS2,EIF4B,PEPD,SWAP70,ACSL1,SLC11A2,TNKS1BP1,MMP24,PINX1,GATB,SETD1B,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,CCAR2,ACCS,RPLP2,CHP1,TYRO3,MRPL43,HTATIP2,PCIF1,PPM1M,KDM1B,SLC35C2,CARS,TSPAN5,CISH,ST3GAL4,AK2,RNF19B,DCPS,SELENOS,GSTO1,ETFBKMT,MANBA,TMTC1,MVK,STK32C,FABP3,PAPSS1,PDGFA,MMP14,APEH,GPX1,AIP,HCCS,MOCS3,CLCF1,NGDN,SRRD,QARS,SLC19A1,ASB9,IMPDH2,PSME2,ANPEP,TRIM27,EIF3A,LIMK1,RABGGTA,PRMT2,RIPK3,LSM14B,ADRM1,DPP3,PSTK,RPS21,CAPN10,PSMB4,EXTL1,PFDN2,BRMS1,PPOX,SEC11A,TNK2,TACO1,PLA2G3,THAP4,PTPN23,KAT5,RELA,ATP5MC3,SCYL1,IDH1,ALKBH4,MEX3B,MAP3K14,MRPL49,ZDHHC3,SGPL1,SMARCB1,SLC25A39,ATIC,PHB2,TRMT112,IGFBP5,BAD,FKBP2,CTDSP1,OTUB1,EID1,COPS6,MPV17L2,LGALS3,PLAU,TNFRSF1A,MVB12A,BABAM1,C1QBP,AIMP2,	yellow	VSMC_M3
GO:0046890	0.06	0.97	14	127	regulation of lipid biosynthetic process	BP	1	CDK4,INSIG1,SCARB1,SOD1,CHP1,DHCR7,FABP3,PDGFA,PLA2G3,IDH1,MID1IP1,CAPN2,ARMC5,AKT1	yellow	VSMC_M3
GO:1903312	0.06	0.97	9	74	negative regulation of mRNA metabolic process	BP	1	NELFE,HNRNPA0,SECISBP2,DND1,PCBP4,SRSF9,C1QBP,PAIP1,TENT5B	yellow	VSMC_M3
GO:0006778	0.06	0.98	6	40	porphyrin-containing compound metabolic process	BP	1	BLVRA,BLVRB,SLC11A2,SRRD,PPOX,SLC25A39	yellow	VSMC_M3
GO:0044728	0.06	0.97	8	67	DNA methylation or demethylation	BP	1	KMT2E,DMAP1,KDM1B,ALKBH4,GATAD2A,MTA2,EHMT1,MBD3	yellow	VSMC_M3
GO:0043550	0.06	0.98	7	58	regulation of lipid kinase activity	BP	1	PDGFRA,SOCS5,KLF4,DGKZ,CISH,WASHC1,PIP4K2B	yellow	VSMC_M3
GO:0090502	0.06	0.97	8	62	RNA phosphodiester bond hydrolysis, endonucleolytic	BP	1	BOP1,SND1,ZC3H12A,RRS1,KHNYN,RPS21,NOP14,TBL3	yellow	VSMC_M3
GO:0000423	0.06	0.98	4	24	mitophagy	BP	1	SQSTM1,PHB2,CDC37,TAZ	yellow	VSMC_M3
GO:0036314	0.06	0.98	4	25	response to sterol	BP	1	INSIG1,AACS,PMVK,HMGCS1	yellow	VSMC_M3
GO:0048015	0.06	0.97	13	133	phosphatidylinositol-mediated signaling	BP	1	PRR5,PPARD,PDGFRA,KLF4,SLC9A3R1,PLCD1,TYRO3,PDGFA,PLCB3,C1QBP,AKT1,MYDGF,ERBB4	yellow	VSMC_M3
GO:1901292	0.06	0.97	9	69	nucleoside phosphate catabolic process	BP	1	ENPP1,NUDT3,DNPH1,OGG1,SMUG1,PDE4D,CNP,NT5C,ITPA	yellow	VSMC_M3
GO:0071222	0.06	0.97	14	126	cellular response to lipopolysaccharide	BP	1	CDK4,PPARD,ZC3H12A,SCARB1,CX3CL1,SELENOS,PABPN1,RELA,CAPN2,AKT1,GIT1,LDOC1,CACTIN,IRAK1	yellow	VSMC_M3
GO:0060765	0.06	0.98	4	24	regulation of androgen receptor signaling pathway	BP	1	PRMT2,PKN1,SMARCA4,SAFB2	yellow	VSMC_M3
GO:1901361	0.07	0.95	36	395	organic cyclic compound catabolic process	BP	1	ENPP1,HNRNPA0,NUDT3,SND1,DNPH1,SECISBP2,CNOT3,ZC3H12A,BLVRA,SNX17,BLVRB,OGG1,METTL3,DND1,SMUG1,SCARB1,PDE4D,LSM6,PCBP4,DCPS,ZCCHC17,RNASEH2C,MRTO4,CNP,NANOS3,DFFA,AKT1,PAIP1,KHSRP,CARHSP1,RBM8A,RNH1,NT5C,TENT5B,TRIR,ITPA	yellow	VSMC_M3
GO:0006479	0.07	0.96	15	148	protein methylation	BP	1	NELFE,H2AFY,KMT2E,KMT2B,SETD1B,ETFBKMT,PRMT2,SMARCB1,TRMT112,MTHFR,CARM1,COPRS,METTL22,EHMT1,NTMT1	yellow	VSMC_M3
GO:0008213	0.07	0.96	15	148	protein alkylation	BP	1	NELFE,H2AFY,KMT2E,KMT2B,SETD1B,ETFBKMT,PRMT2,SMARCB1,TRMT112,MTHFR,CARM1,COPRS,METTL22,EHMT1,NTMT1	yellow	VSMC_M3
GO:0043039	0.07	0.98	6	40	tRNA aminoacylation	BP	1	AARS2,GATB,CARS,QARS,FARSA,SARS	yellow	VSMC_M3
GO:0046486	0.07	0.96	29	317	glycerolipid metabolic process	BP	1	PIGO,SOCS5,TTC7A,MGLL,PLCD1,INSIG1,INPPL1,PCYT2,PTDSS2,SCARB1,ACSL1,DGKZ,CISH,FABP3,PDGFA,GPX1,PCK2,PLA2G3,PHB2,PLCB3,CAPN2,PIP4K2B,DPM3,MTMR4,PGP,TAZ,SLC44A3,VAC14,PLA2G4E	yellow	VSMC_M3
GO:0046488	0.07	0.96	14	138	phosphatidylinositol metabolic process	BP	1	PIGO,SOCS5,TTC7A,PLCD1,INPPL1,CISH,PDGFA,PLA2G3,PLCB3,PIP4K2B,DPM3,MTMR4,VAC14,PLA2G4E	yellow	VSMC_M3
GO:0043966	0.07	0.97	7	54	histone H3 acetylation	BP	1	JADE2,MEAF6,KAT14,SMARCB1,TAF6L,PER1,SGF29	yellow	VSMC_M3
GO:0002064	0.07	0.96	16	173	epithelial cell development	BP	1	SCRIB,PLEC,B4GALT1,COL15A1,WDPCP,CCM2,SLC9A3R1,FASN,PDE4D,SOD1,GPX1,BAD,TNFRSF1A,TMEM79,AKT1,TJP3	yellow	VSMC_M3
GO:0031167	0.07	0.98	4	20	rRNA methylation	BP	1	FTSJ3,BUD23,TRMT112,RRNAD1	yellow	VSMC_M3

GO:0032438	0.07	0.98	4	23	melanosome organization	BP	1	HPS1,BLOC1S4,AP1M1,AP3D1	yellow	VSMC_M3
GO:0015908	0.07	0.97	8	60	fatty acid transport	BP	1	PPARD,ACSL1,FABP3,SPX,PLA2G3,SLC27A3,AKT1,SLC27A4	yellow	VSMC_M3
GO:0009152	0.07	0.96	15	137	purine ribonucleotide biosynthetic process	BP	1	GUK1,ACSL1,AK2,PAPSS1,IMPDH2,ATP5MC3,ATIC,UQCC3,ACLY,ATP5PD,ATP5F1D,TAZ,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:0033059	0.07	0.97	6	43	cellular pigmentation	BP	1	CD63,DCTN2,HPS1,BLOC1S4,AP1M1,AP3D1	yellow	VSMC_M3
GO:0046939	0.07	0.97	9	74	nucleotide phosphorylation	BP	1	GUK1,PNKP,GALK1,OGDHL,FOXK1,PGM1,GIT1,JMJD8,AK1	yellow	VSMC_M3
GO:0043038	0.07	0.97	6	41	amino acid activation	BP	1	AARS2,GATB,CARS,QARS,FARSA,SARS	yellow	VSMC_M3
GO:0007006	0.07	0.96	12	99	mitochondrial membrane organization	BP	1	SAMM50,BCL2L1,CHCHD10,BAD,LETM1,UQCC3,CNP,MTX1,ALKBH7,TAZ,SPG7,TIMM22	yellow	VSMC_M3
GO:0045773	0.07	0.98	5	37	positive regulation of axon extension	BP	1	DBNL,LIMK1,DBN1,ANAPC2,TWF2	yellow	VSMC_M3
GO:0019439	0.07	0.95	34	375	aromatic compound catabolic process	BP	1	ENPP1,HNRNPA0,NUDT3,SND1,DNPH1,SECISBP2,CNOT3,ZC3H12A,BLVRA,BLVRB,OGG1,METTL3,DND1,SMUG1,PDE4D,LSM6,PCBP4,DCPS,ZCCHC17,RNASEH2C,MRTO4,CNP,NANOS3,DFFA,AKT1,PAIP1,KHSRP,CARHSP1,RBM8A,RNH1,NT5C,TENT5B,TRIR,ITPA	yellow	VSMC_M3
GO:2000191	0.07	0.98	4	23	regulation of fatty acid transport	BP	1	ACSL1,FABP3,PLA2G3,AKT1	yellow	VSMC_M3
GO:0048753	0.07	0.98	4	24	pigment granule organization	BP	1	HPS1,BLOC1S4,AP1M1,AP3D1	yellow	VSMC_M3
GO:0006417	0.07	0.95	31	341	regulation of translation	BP	1	CDK4,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,EIF4EBP1,TARBP2,NAT10,EIF4B,PCIF1,DCPS,NGDN,LSM14B,TACO1,IGFBP5,MPV17L2,C1QBP,SEPSECS,NANOS3,PER1,C19orf66,AKT1,PAIP1,KHSRP,TRAP1,MKNK2,RBM8A,ZNF385A	yellow	VSMC_M3
GO:0031400	0.07	0.95	37	426	negative regulation of protein modification process	BP	1	ENPP1,CTDSP2,SQSTM1,H2AFY,PLEC,VPS28,SOCS5,SPRED2,ZC3H12A,PNKP,MICAL1,EMILIN1,TARBP2,PDE4D,SWAP70,PINX1,GREM1,CHP1,QARS,TRIM27,LIMK1,RELA,SMARCB1,CTDSP1,OTUB1,LGALS3,UBXN1,PKN1,MAD2L2,CTBP1,MVP,RPL37,AKT1,CACTIN,HMG20B,TRIB2,THAP7	yellow	VSMC_M3
GO:2001243	0.07	0.96	10	83	negative regulation of intrinsic apoptotic signaling pathway	BP	1	FIGNL1,BCL2L1,CCAR2,SELENOS,GPX1,ARHGEF2,AKT1,TRAP1,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:1902749	0.08	0.96	10	87	regulation of cell cycle G2/M phase transition	BP	1	CDK4,H2AFY,PINX1,WNT10B,PBX1,BABAM1,RCC2,MIP,ZNF830,NABP2	yellow	VSMC_M3
GO:0070373	0.08	0.97	7	53	negative regulation of ERK1 and ERK2 cascade	BP	1	KLF4,SPRED2,SLC9A3R1,EMILIN1,EIF3A,CSK,PTPRR	yellow	VSMC_M3
GO:0014912	0.08	0.98	4	24	negative regulation of smooth muscle cell migration	BP	1	PPARD,CORO1B,IGFBP5,MIR214	yellow	VSMC_M3
GO:0006401	0.08	0.95	22	237	RNA catabolic process	BP	1	HNRNPA0,SND1,SECISBP2,CNOT3,ZC3H12A,METTL3,DND1,LSM6,PCBP4,DCPS,ZCCHC17,RNASEH2C,MRTO4,NANOS3,AKT1,PAIP1,KHSRP,CARHSP1,RBM8A,RNH1,TENT5B,TRIR	yellow	VSMC_M3
GO:0006402	0.08	0.95	19	201	mRNA catabolic process	BP	1	HNRNPA0,SND1,SECISBP2,CNOT3,ZC3H12A,METTL3,DND1,LSM6,PCBP4,DCPS,MRTO4,NANOS3,AKT1,PAIP1,KHSRP,CARHSP1,RBM8A,RNH1,TENT5B	yellow	VSMC_M3
GO:0044283	0.08	0.95	38	414	small molecule biosynthetic process	BP	1	MGLL,FDXR,SEPHS1,INSIG1,PYCR1,FASN,AACS,FDFT1,SOD1,SCD,DHCR7,SELENOS,MVK,PCK2,LSS,PLA2G3,MGST3,MID1IP1,ISYNA1,HSD17B1,ACLY,FADS2,GLUD1,ILVBL,MTHFR,PGD,COQ6,PMVK,HMGCS1,PGM1,DHCR24,NSDHL,PGP,APRT,MVD,FADS1,FDPS,IDI1	yellow	VSMC_M3
GO:0010677	0.08	0.98	5	34	negative regulation of cellular carbohydrate metabolic process	BP	1	ENPP1,SELENOS,GIT1,PGP,MIDN	yellow	VSMC_M3
GO:0009166	0.08	0.97	8	61	nucleotide catabolic process	BP	1	NUDT3,DNPH1,OGG1,SMUG1,PDE4D,CNP,NT5C,ITPA	yellow	VSMC_M3
GO:0006650	0.08	0.95	24	257	glycerophospholipid metabolic process	BP	1	PIGO,SOCS5,TTC7A,PLCD1,INPPL1,PCYT2,PTDSS2,SCARB1,DGKZ,CISH,FABP3,PDGFA,PLA2G3,PHB2,PLCB3,CAPN2,PIP4K2B,DPM3,MTMR4,PGP,TAZ,SLC44A3,VAC14,PLA2G4E	yellow	VSMC_M3
GO:0048017	0.08	0.96	13	137	inositol lipid-mediated signaling	BP	1	PRR5,PPARD,PDGFRA,KLF4,SLC9A3R1,PLCD1,TYRO3,PDGFA,PLCB3,C1QBP,AKT1,MYDGF,ERBB4	yellow	VSMC_M3
GO:0014074	0.08	0.96	11	109	response to purine-containing compound	BP	1	AACS,WNT10B,SOD1,SLC26A6,RELA,IGFBP5,PER1,CARM1,EEF2K,HMGCS1,SLC6A4	yellow	VSMC_M3
GO:0034314	0.08	0.97	5	33	Arp2/3 complex-mediated actin nucleation	BP	1	CORO1B,TRIM27,ARPC1B,WASHC1,ARPC5L	yellow	VSMC_M3
GO:0006690	0.08	0.97	8	62	icosanoid metabolic process	BP	1	PTGR1,MGLL,GPX1,PLA2G3,MGST3,TNFRSF1A,CYP4F8,FADS1	yellow	VSMC_M3
GO:0061756	0.08	0.97	5	34	leukocyte adhesion to vascular endothelial cell	BP	1	KLF4,ITGB7,ST3GAL4,RELA,IRAK1	yellow	VSMC_M3
GO:0018208	0.08	0.97	7	48	peptidyl-proline modification	BP	1	P4HA3,P4HB,FKBP11,AIP,FKBP2,NTMT1,PIN4	yellow	VSMC_M3
GO:0008589	0.08	0.97	8	71	regulation of smoothened signaling pathway	BP	1	ENPP1,TXNDC15,EVC,TEDC1,RAB34,TEDC2,GAS8,NDST1	yellow	VSMC_M3
GO:0007520	0.08	0.98	4	25	myoblast fusion	BP	1	EHD2,PLEKHO1,CD9,CAPN2	yellow	VSMC_M3
GO:0042440	0.08	0.96	8	65	pigment metabolic process	BP	1	BLVRA,BLVRB,SLC11A2,SRRD,PPOX,SLC25A39,CTNS,APRT	yellow	VSMC_M3
GO:0046320	0.08	0.98	4	26	regulation of fatty acid oxidation	BP	1	PPARD,ETFBKMT,FABP3,AKT1	yellow	VSMC_M3
GO:0031057	0.08	0.97	5	37	negative regulation of histone modification	BP	1	H2AFY,SMARCB1,OTUB1,CTBP1,THAP7	yellow	VSMC_M3
GO:0051495	0.08	0.95	18	194	positive regulation of cytoskeleton organization	BP	1	SNX9,BAIAP2,NUMA1,SWAP70,DCTN1,CX3CL1,CORO1B,TRIM27,ARPIN,LIMK1,PFDN2,RHOC,ARPC1B,WASHC1,CORO1A,GIT1,CDC42EP5,ARPC5L	yellow	VSMC_M3
GO:0014065	0.08	0.96	11	111	phosphatidylinositol 3-kinase signaling	BP	1	PRR5,PPARD,PDGFRA,KLF4,SLC9A3R1,TYRO3,PDGFA,C1QBP,AKT1,MYDGF,ERBB4	yellow	VSMC_M3
GO:0007009	0.08	0.96	10	94	plasma membrane organization	BP	1	SNX9,PACSIN1,PLEC,EHD2,SLC9A3R1,BAIAP2,SOD1,PACSIN3,CD9,AKT1	yellow	VSMC_M3
GO:0032024	0.08	0.97	7	56	positive regulation of insulin secretion	BP	1	PPARD,MYRIP,AACS,PCK2,CAPN10,BAD,GLUD1	yellow	VSMC_M3
GO:0045454	0.08	0.97	5	32	cell redox homeostasis	BP	1	GSR,SELENOS,GPX1,TXNRD2,GIT1	yellow	VSMC_M3
GO:0032729	0.08	0.97	5	35	positive regulation of interferon-gamma production	BP	1	SCRIB,IL1R1,PDE4D,TRIM27,CD276	yellow	VSMC_M3
GO:0000470	0.08	0.98	4	23	maturation of LSU-rRNA	BP	1	NHP2,BOP1,FTSJ3,RPL7A	yellow	VSMC_M3
GO:0051235	0.08	0.95	22	248	maintenance of location	BP	1	ENPP1,SREBF2,SQLE,ITPR3,PPARD,ZC3H12A,SLC30A3,INSIG1,SCARB1,PDE4D,CX3CL1,GSTO1,CHCHD10,LETM1,CHERP,CCDC22,DBN1,CORO1A,AKT1,ALKBH7,AP3D1,TWF2	yellow	VSMC_M3
GO:0110053	0.09	0.95	21	237	regulation of actin filament organization	BP	1	SNX9,DBNL,BAIAP2,SWAP70,CAPG,CX3CL1,CORO1B,TRIM27,ARPIN,LIMK1,RHOC,ARPC1B,WASHC1,DBN1,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0048813	0.09	0.95	12	126	dendrite morphogenesis	BP	1	CUL7,DBNL,TPBG,BAIAP2,ARHGAP33,SLC11A2,NGEF,DBN1,EEF2K,ANAPC2,STK11,NSMF	yellow	VSMC_M3
GO:0090501	0.09	0.95	13	124	RNA phosphodiester bond hydrolysis	BP	1	NHP2,BOP1,SND1,ZC3H12A,RRS1,DCPS,ZNRD1,KHNYN,RPS21,NOP14,CSTF2T,TBL3,TRIR	yellow	VSMC_M3

GO:0043967	0.09	0.96	7	58	histone H4 acetylation	BP	1	JADE2,MEAF6,DMAP1,MCRS1,SMARCB1,CTBP1,PER1	yellow	VSMC_M3
GO:0060113	0.09	0.97	6	48	inner ear receptor cell differentiation	BP	1	CTHRC1,SCRIB,IFT27,WDPCP,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:0031122	0.09	0.97	6	52	cytoplasmic microtubule organization	BP	1	NUMA1,DCTN1,CHP1,CLIP2,STMN3,TUBGCP2	yellow	VSMC_M3
GO:0036503	0.09	0.96	11	99	ERAD pathway	BP	1	BAG6,RCN3,TMUB1,SEL1L2,HM13,SELENOS,UBXN1,TRIM25,MAN1B1,FBXO6,STUB1	yellow	VSMC_M3
GO:0099175	0.09	0.96	8	73	regulation of postsynapse organization	BP	1	DBNL,BAIAP2,ARHGAP22,ARHGAP33,NGEF,LRFN4,DBN1,EEF2K	yellow	VSMC_M3
GO:1902806	0.09	0.95	12	115	regulation of cell cycle G1/S phase transition	BP	1	CTDSP2,KLF4,KMT2E,CDK2AP2,PSME2,PRMT2,PHB2,CTDSP1,METTL13,SDE2,AKT1,MIR214	yellow	VSMC_M3
GO:0044458	0.09	0.97	5	33	motile cilium assembly	BP	1	CEP131,YIF1B,IQCG,PLA2G3,MEIG1	yellow	VSMC_M3
GO:1901798	0.09	0.97	4	24	positive regulation of signal transduction by p53 class mediator	BP	1	SPRED2,RPL37,HIC1,ZNF385A	yellow	VSMC_M3
GO:0031929	0.09	0.95	11	105	TOR signaling	BP	1	FNIP1,PRR5,SEC13,LAMTOR1,EIF4EBP1,LAMTOR4,AKT1,CTNS,STK11,TELO2,WDR24	yellow	VSMC_M3
GO:0070482	0.09	0.94	25	280	response to oxygen levels	BP	1	CDK4,PPARD,UCP2,P4HB,EIF4EBP1,SLC11A2,CHCHD2,MMP14,ARNT2,LIMD1,PHB2,BAD,PLAU,CAPN2,MTHFR,EEF2K,AKT1,SLC6A4,VASN,IRAK1,TGFBR3,MIR214,RF00024,STUB1,CCDC115	yellow	VSMC_M3
GO:0071219	0.09	0.95	14	133	cellular response to molecule of bacterial origin	BP	1	CDK4,PPARD,ZC3H12A,SCARB1,CX3CL1,SELENOS,PABPN1,RELA,CAPN2,AKT1,GIT1,LDOC1,CACTIN,IRAK1	yellow	VSMC_M3
GO:0000375	0.09	0.94	25	259	RNA splicing, via transesterification reactions	BP	1	DHX16,SNRNP70,GEMIN7,METTL3,RALY,LSM6,PRPF40B,PCBP4,RBM15B,SRSF9,DCPS,RBM6,SF3A1,SART1,PRPF6,BUD31,C1QBP,GPKOW,CWC25,CD2BP2,RAVER1,RBM22,KHSRP,CACTIN,RBM8A	yellow	VSMC_M3
GO:0035082	0.09	0.96	7	55	axoneme assembly	BP	1	SPAG1,CEP131,YIF1B,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:0032506	0.09	0.97	5	35	cytokinetic process	BP	1	SNX9,PLEC,ALKBH4,ANXA11,SNX18	yellow	VSMC_M3
GO:0022604	0.09	0.94	22	261	regulation of cell morphogenesis	BP	1	CUL7,DBNL,WDPCP,SLC9A3R1,PLXND1,BAIAP2,P4HB,CORO1B,PLEKHO1,ARPIN,RHOC,FMNL1,LIMD1,C1QBP,RCC2,DBN1,CORO1A,SYNE3,EEF2K,ANAPC2,UNC13A,CDC42EP5	yellow	VSMC_M3
GO:0009954	0.09	0.97	4	25	proximal/distal pattern formation	BP	1	PBX2,GREM1,IRX1,PBX1	yellow	VSMC_M3
GO:0036294	0.09	0.95	13	129	cellular response to decreased oxygen levels	BP	1	PPARD,P4HB,EIF4EBP1,CHCHD2,PHB2,BAD,EEF2K,AKT1,VASN,IRAK1,MIR214,RF00024,STUB1	yellow	VSMC_M3
GO:0030216	0.09	0.96	8	74	keratinocyte differentiation	BP	1	H2AFY,PLEC,SHARPIN,NUMA1,KRT10,CASP14,TMEM79,PPL	yellow	VSMC_M3
GO:0016050	0.09	0.94	23	255	vesicle organization	BP	1	SQSTM1,VPS28,SNX3,INSIG1,SEC13,LAMTOR1,RAB20,PLEKHF1,HPS1,CHP1,PLA2G3,BLOC1S4,MVB12A,AP1M1,PIP4K2B,SNF8,STX10,CORO1A,RFX2,RAB34,AP3D1,UNC13A,PHETA2	yellow	VSMC_M3
GO:0000462	0.09	0.97	5	34	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	1	RRS1,NGDN,RPS21,NOP14,TBL3	yellow	VSMC_M3
GO:1903900	0.10	0.95	11	104	regulation of viral life cycle	BP	1	TRIM11,LGALS1,SNX3,P4HB,TARBP2,TYRO3,TRIM27,BANF1,TRIM25,C19orf66,MID2	yellow	VSMC_M3
GO:0032088	0.10	0.96	8	67	negative regulation of NF-kappaB transcription factor activity	BP	1	KLF4,ZC3H12A,CHP1,PRMT2,BRMS1,CCDC22,CACTIN,IRAK1	yellow	VSMC_M3
GO:0000460	0.10	0.97	5	34	maturation of 5.8S rRNA	BP	1	BOP1,RRS1,RPS21,FTSJ3,NOP14	yellow	VSMC_M3
GO:0009968	0.10	0.92	76	973	negative regulation of signal transduction	BP	1	ENPP1,CTHRC1,FNIP1,ATF6B,TTLL12,SOCS5,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,SLC9A3R1,EMILIN1,INSIG1,METTL3,CAVIN3,BCL2L1,PDE4D,TNS2,GREM1,PDE3B,CX3CL1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,CISH,SELENOS,ITPRIP,MMP14,GPX1,QARS,EIF3A,THOC5,STMN3,RELA,LIMD1,PHB2,IGFBP5,IFI35,LGALS3,C1QBP,CCDC22,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,MTMR4,SMARCA4,AATF,CSK,AKT1,CACTIN,VASN,HIC1,TRAP1,MNT,STK11,SLC27A4,TGFBR3,PTPRR,IGFBP6,ZNF385A,TXNDC12,CDC34,APCDD1L,RGS16,DUSP5,STUB1,RGS18	yellow	VSMC_M3
GO:0050686	0.10	0.97	4	25	negative regulation of mRNA processing	BP	1	NELFE,PCBP4,SRSF9,C1QBP	yellow	VSMC_M3
GO:0070199	0.10	0.97	4	24	establishment of protein localization to chromosome	BP	1	H2AFY,LRWD1,SGF29,NABP2	yellow	VSMC_M3
GO:0001666	0.10	0.94	22	244	response to hypoxia	BP	1	PPARD,UCP2,P4HB,EIF4EBP1,SLC11A2,CHCHD2,MMP14,ARNT2,LIMD1,PHB2,BAD,PLAU,CAPN2,MTHFR,AKT1,SLC6A4,VASN,IRAK1,TGFBR3,MIR214,RF00024,STUB1	yellow	VSMC_M3
GO:0048701	0.10	0.97	5	40	embryonic cranial skeleton morphogenesis	BP	1	PDGFRA,HOXA1,MMP14,SLC39A1,NDST1	yellow	VSMC_M3
GO:0045017	0.10	0.94	20	214	glycerolipid biosynthetic process	BP	1	PIGO,SOCS5,TTC7A,INPPL1,PCYT2,PTDSS2,SCARB1,ACSL1,DGKZ,CISH,FABP3,PDGFA,PCK2,CAPN2,PIP4K2B,DPM3,MTMR4,TAZ,SLC44A3,VAC14	yellow	VSMC_M3
GO:1903649	0.10	0.97	4	28	regulation of cytoplasmic transport	BP	1	EIPR1,SNX3,PTPN23,MAP2K2	yellow	VSMC_M3
GO:0036293	0.10	0.94	23	258	response to decreased oxygen levels	BP	1	PPARD,UCP2,P4HB,EIF4EBP1,SLC11A2,CHCHD2,MMP14,ARNT2,LIMD1,PHB2,BAD,PLAU,CAPN2,MTHFR,EEF2K,AKT1,SLC6A4,VASN,IRAK1,TGFBR3,MIR214,RF00024,STUB1	yellow	VSMC_M3
GO:0071453	0.10	0.94	14	142	cellular response to oxygen levels	BP	1	PPARD,P4HB,EIF4EBP1,CHCHD2,PHB2,BAD,EEF2K,AKT1,VASN,IRAK1,MIR214,RF00024,STUB1,CCDC115	yellow	VSMC_M3
GO:0043467	0.10	0.95	11	104	regulation of generation of precursor metabolites and energy	BP	1	ENPP1,CAVIN3,CHCHD2,SELENOS,ETFBKMT,TACO1,PHB2,AKT1,GIT1,TRAP1,JMJD8	yellow	VSMC_M3
GO:0009144	0.10	0.95	8	63	purine nucleoside triphosphate metabolic process	BP	1	GUK1,IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ,ITPA	yellow	VSMC_M3

GO:0023051	0.10	0.91	182	2524	regulation of signaling	BP	1	ENPP1,CD63,CDK4,SQSTM1,CTHRC1,NELFE,FNIP1,ATF6B,PRR5,TTLL12,SREBF2,TXNDC15,ITPR3,SGSM3,DEF6,PPARD,EEF1D,SCRIB,LGALS1,SHARPIN,BOP1,PDGFRA,IL1R1,SOCS5,KLF4,TPBG,SPRED2,EIPR1,RGS3,ZC3H12A,FIGNL1,RCN3,SNX3,PLEKHA4,MGLL,SLC9A3R1,EMILIN1,RNF220,INSIG1,MYRIP,SEC13,ARHGEF40,UCP2,METTL3,BAIAP2,CXXC5,LAMTOR1,NUMA1,P4HB,CAVIN3,ARHGAP22,AACS,BCL2L1,PDE4D,TNS2,RRS1,SWAP70,PLEKHF1,GREM1,PDE3B,RAPSN,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,SLC35C2,TSPAN5,CISH,SELENOS,ITPRIP,PDGFA,MMP14,GPX1,AIP,NGEF,SYT12,QARS,PCK2,TRIM27,EIF3A,PRMT2,THOC5,RIPK3,CAPN10,PLA2G3,STMN3,PTPN23,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZDHHC3,SMARCB1,YJEFN3,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,LGALS3,BUD31,PLAU,TNFRSF1A,MVB12A,C1QBP,CHERP,EVC,CCDC22,GLUD1,PKN1,DBN1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,TRIM25,RPL37,MTMR4,S100A4,SMARCA4,CARM1,CDC37,AATF,CSK,MID2,AKT1,TEDC1,RAB34,SAFB2,GIT1,SLC6A4,MYDGF,MAP2K2,CACTIN,VASN,HIC1,TRAP1,NCLN,MNT,CTNS,TEDC2,CSNK1G2,IRAK1,ANAPC2,MIDN,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,SLC27A4,TGFBR3,TRADD,NDST1,TNFRSF12A,ERBB4,PTPRR,IGFBP6,JAGN1,UNC13A,ZNF385A,TXNDC12,NSMF,CDC34,APCDD1L,ARHGEF1,RGS16,DUSP5,GLIPR2,STUB1,RGS18,GSG1L	yellow	VSMC_M3
GO:0010971	0.10	0.97	4	25	positive regulation of G2/M transition of mitotic cell cycle	BP	1	CDK4,WNT10B,PBX1,RCC2	yellow	VSMC_M3
GO:0061013	0.10	0.94	14	144	regulation of mRNA catabolic process	BP	1	HNRNPA0,SECISBP2,CNOT3,ZC3H12A,METTL3,DND1,PCBP4,DCPS,NANOS3,AKT1,PAIP1,KHSRP,CARHSP1,TENT5B	yellow	VSMC_M3
GO:0002237	0.10	0.93	22	236	response to molecule of bacterial origin	BP	1	CDK4,HNRNPA0,PPARD,SSC5D,ZC3H12A,SCARB1,CX3CL1,SELENOS,PABPN1,PCK2,RELA,CNP,CAPN2,PALM3,AKT1,GIT1,LDOC1,CACTIN,IRAK1,CARD9,JUND,LOXL1	yellow	VSMC_M3
GO:0008150	0.10	0.92	854	12183	biological_process	BP	1	ENPP1,PQLC1,CD63,ESYT1,NAB2,DCTN2,NHP2,CDK4,CTDSP2,RUFY1,SQSTM1,GNL1,DHX16,CCHCR1,SPAG1,ZNF608,LMF2,BAG6,NCAPH2,SBF1,SNX9,CTHRC1,HDAC10,NELFE,ACAT2,CERK,FNIP1,ATF6B,PBX2,PDLIM4,PRR5,SAMM50,TTLL12,RING1,SREBF2,JADE2,TRMT12,NDUFB9,SQLE,TXNDC15,H2AFY,ITPR3,HNRNPA0,TRIM11,SGSM3,GUK1,TRAPPC9,NUDT3,PACSIN1,DEF6,PPARD,FANCE,EEF1D,TIGD5,TSTA3,RPL3,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,HGH1,BOP1,SLC52A2,VPS28,RPL8,SND1,TOM1,TBCC,CUL7,RTCB,PPP1R14B,DNPH1,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,IL1R1,SECISBP2,PHF2,GRHPR,COL15A1,EPN1,COL19A1,SSC5D,HSPBP1,SOCS5,TTC7A,RPS9,CNOT3,ASNA1,KLF4,DBNL,TPBG,HOXA1,JOSD2,PTGR1,PSMB3,PLEKHA8,WDPCP,CCM2,FHL3,SPRED2,EIPR1,RGS3,MEAF6,ZC3H12A,FIGNL1,PDIA4,BLVRA,PDIA6,PNKP,CPT1C,ZYX,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,PLEKHA4,EMP3,MGLL,EHD2,FAM120B,KMT2E,ANXA5,KRT8,WDFY2,ACAD9,SIX5,ZNF282,TMEM43,C17orf80,TTYH2,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,PLXND1,FDXR,EMILIN1,SLC16A5,SEPHS1,TMUB1,RNF220,DMAP1,SLC30A3,PAFAH1B3,CIC,GTF3C2,SNX17,GALK1,H3F3B,PPM1G,UNK,PLCD1,DLEC1,CD79A,BCKDHA,INSIG1,MYRIP,SEC13,MFSD11,SEPT9,GALNT14,BLVRB,OGG1,SERTAD1,TTC5,PSMC4,KAT14,ARHGEF40,P4HA3,UCP2,SEL1L2,METTL3,PHLDA1,BAIAP2,CEP131,CXXC5,INPPL1,FAAP100,TSPAN10,LAMTOR1,NUMA1,P4HB,PCYT2,DND1,PYCR1,YIF1B,FASN,CCDC57,RAB20,SMOX,RPL29,PXMP2,EIF4EBP1,ARAP3,SIGLEC1,DELE1,GNPDA1,MORN2,CAVIN3,PUS1,RIC8A,GSR,PTDSS2,ARHGAP22,DEAF1,TBCB,SMUG1,HOXC4,IDH3B,L	yellow	VSMC_M3
GO:0040029	0.10	0.95	9	86	regulation of gene expression, epigenetic	BP	1	H2AFY,PHF2,SERTAD1,METTL3,KDM1B,RBM15B,GPX1,TRIM27,MBD3	yellow	VSMC_M3
GO:0017004	0.10	0.96	5	31	cytochrome complex assembly	BP	1	UQCRFS1,HCCS,TACO1,UQCC3,SURF1	yellow	VSMC_M3
GO:0046390	0.10	0.94	16	156	ribose phosphate biosynthetic process	BP	1	GUK1,ACSL1,TKT,AK2,PAPSS1,IMPDH2,ATP5MC3,ATIC,UQCC3,ACLY,ATP5PD,ATP5F1D,TAZ,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:0006783	0.10	0.97	4	26	heme biosynthetic process	BP	1	SLC11A2,SRRD,PPOX,SLC25A39	yellow	VSMC_M3
GO:1901990	0.10	0.93	22	237	regulation of mitotic cell cycle phase transition	BP	1	CDK4,CTDSP2,KLF4,KMT2E,PINX1,WNT10B,CDK2AP2,PSME2,PRMT2,PBX1,PHB2,CTDSP1,BABAM1,RCC2,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,AKT1,MIR214,NABP2	yellow	VSMC_M3
GO:0007032	0.11	0.95	8	71	endosome organization	BP	1	SQSTM1,VPS28,SNX3,LAMTOR1,PLEKHF1,MVB12A,SNF8,PHETA2	yellow	VSMC_M3
GO:0031503	0.11	0.94	17	186	protein-containing complex localization	BP	1	SCRIB,IFT27,CEP131,RRS1,RBM15B,EXOC3,PABPN1,THOC5,ZDHHC3,THOC3,NUP88,RCC2,DBN1,AP3D1,SSNA1,WDR34,GSG1L	yellow	VSMC_M3
GO:0050684	0.11	0.94	12	118	regulation of mRNA processing	BP	1	NELFE,SNRNP70,PCBP4,RBM15B,SRSF9,C1QBP,SLTM,RAVER1,SAFB,SAFB2,CDK11B,RBM8A	yellow	VSMC_M3
GO:0050777	0.11	0.94	13	128	negative regulation of immune response	BP	1	TTLL12,SOCS5,ZC3H12A,METTL3,TARBP2,TYRO3,SELENOS,GPX1,TRIM27,PSMB4,LGALS3,C1QBP,CACTIN	yellow	VSMC_M3
GO:0051303	0.11	0.95	8	68	establishment of chromosome localization	BP	1	DCTN2,NUMA1,RRS1,PINX1,NUDC,EML3,MAD1L1,MIS12	yellow	VSMC_M3
GO:0042491	0.11	0.97	4	29	inner ear auditory receptor cell differentiation	BP	1	SCRIB,WDPCP,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:1905517	0.11	0.96	5	36	macrophage migration	BP	1	EMILIN1,CX3CL1,MMP14,LGALS3,CD9	yellow	VSMC_M3
GO:1902807	0.11	0.95	7	60	negative regulation of cell cycle G1/S phase transition	BP	1	CTDSP2,KLF4,CDK2AP2,PRMT2,CTDSP1,METTL13,SDE2	yellow	VSMC_M3
GO:0060997	0.11	0.96	6	54	dendritic spine morphogenesis	BP	1	DBNL,BAIAP2,ARHGAP33,NGEF,DBN1,EEF2K	yellow	VSMC_M3

GO:0010646	0.11	0.91	181	2513	regulation of cell communication	BP	1	ENPP1,CD63,CDK4,SQSTM1,CTHRC1,NELFE,FNIP1,ATF6B,PRR5,TTLL12,SREBF2,TXNDC15,ITPR3,SGSM3,DEF6,PPARD,EEF1D,LGALS1,SHARPIN,BOP1,PDGFRA,IL1R1,SOCS5,KLF4,TPBG,SPRED2,EIPR1,RGS3,ZC3H12A,FIGNL1,RCN3,SNX3,PLEKHA4,MGLL,SLC9A3R1,EMILIN1,RNF220,INSIG1,MYRIP,SEC13,ARHGEF40,UCP2,METTL3,BAIAP2,CXXC5,LAMTOR1,NUMA1,P4HB,CAVIN3,ARHGAP22,AACS,BCL2L1,PDE4D,TNS2,RRS1,SWAP70,PLEKHF1,GREM1,PDE3B,RAPSN,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,SLC35C2,TSPAN5,CISH,SELENOS,ITPRIP,PDGFA,MMP14,GPX1,AIP,NGEF,SYT12,QARS,PCK2,TRIM27,EIF3A,PRMT2,THOC5,RIPK3,CAPN10,PLA2G3,STMN3,PTPN23,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZDHHC3,SMARCB1,YJEFN3,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,LGALS3,BUD31,PLAU,TNFRSF1A,MVB12A,C1QBP,CHERP,EVC,CCDC22,GLUD1,PKN1,DBN1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,TRIM25,RPL37,MTMR4,S100A4,SMARCA4,CARM1,CDC37,AATF,CSK,MID2,AKT1,TEDC1,RAB34,SAFB2,GIT1,SLC6A4,MYDGF,MAP2K2,CACTIN,VASN,HIC1,TRAP1,NCLN,MNT,CTNS,TEDC2,CSNK1G2,IRAK1,ANAPC2,MIDN,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,SLC27A4,TGFBR3,TRADD,NDST1,TNFRSF12A,ERBB4,PTPRR,IGFBP6,JAGN1,UNC13A,ZNF385A,TXNDC12,NSMF,CDC34,APCDD1L,ARHGEF1,RGS16,DUSP5,GLIPR2,STUB1,RGS18,GSG1L	yellow	VSMC_M3
GO:0046626	0.11	0.96	6	50	regulation of insulin receptor signaling pathway	BP	1	ENPP1,CDK4,TNS2,RELA,PIP4K2B,SLC27A4	yellow	VSMC_M3
GO:0032543	0.11	0.95	9	72	mitochondrial translation	BP	1	MRPS18A,AARS2,GATB,MRPL43,TACO1,MPV17L2,C1QBP,TUFM,MRPS16	yellow	VSMC_M3
GO:0071456	0.11	0.94	12	119	cellular response to hypoxia	BP	1	PPARD,P4HB,EIF4EBP1,CHCHD2,PHB2,BAD,AKT1,VASN,IRAK1,MIR214,RF00024,STUB1	yellow	VSMC_M3
GO:0051092	0.11	0.94	12	119	positive regulation of NF-kappaB transcription factor activity	BP	1	TRAPPC9,GREM1,CX3CL1,TRIM27,RIPK3,RELA,ARHGEF2,TRIM25,MID2,IRAK1,CARD9,TRADD	yellow	VSMC_M3
GO:0045682	0.11	0.96	6	50	regulation of epidermis development	BP	1	NAB2,H2AFY,PPARD,NUMA1,KRT10,TMEM79	yellow	VSMC_M3
GO:0010389	0.11	0.95	9	82	regulation of G2/M transition of mitotic cell cycle	BP	1	CDK4,PINX1,WNT10B,PBX1,BABAM1,RCC2,MIIP,ZNF830,NABP2	yellow	VSMC_M3
GO:0098927	0.11	0.96	5	40	vesicle-mediated transport between endosomal compartments	BP	1	SNX3,PTPN23,SNF8,CORO1A,MAP2K2	yellow	VSMC_M3
GO:0009141	0.11	0.94	10	86	nucleoside triphosphate metabolic process	BP	1	ENPP1,GUK1,IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ,AK1,ITPA	yellow	VSMC_M3
GO:0050931	0.11	0.96	4	28	pigment cell differentiation	BP	1	ENPP1,CD63,AP1M1,AP3D1	yellow	VSMC_M3
GO:0043491	0.11	0.93	14	147	protein kinase B signaling	BP	1	KLF4,TPBG,RCN3,SLC9A3R1,CAVIN3,CX3CL1,TYRO3,PDGFA,GPX1,IGFBP5,C1QBP,AKT1,MYDGF,STK11	yellow	VSMC_M3
GO:0007346	0.11	0.92	31	360	regulation of mitotic cell cycle	BP	1	CDK4,CTDSP2,TTLL12,SCRIB,CUL7,KLF4,KMT2E,SLC9A3R1,CCDC57,EIF4EBP1,PINX1,WNT10B,CDK2AP2,PSME2,PRMT2,PBX1,PHB2,CTDSP1,BABAM1,RCC2,SDE2,MIIP,MAD1L1,MAD2L2,AATF,ZNF830,AKT1,CDK11B,AURKAIP1,MIR214,NABP2	yellow	VSMC_M3
GO:0010833	0.11	0.95	8	73	telomere maintenance via telomere lengthening	BP	1	NHP2,PNKP,NAT10,TNKS1BP1,PINX1,SLX1A,TELO2,RF00024	yellow	VSMC_M3
GO:0010243	0.12	0.91	62	793	response to organonitrogen compound	BP	1	ENPP1,CDK4,BAG6,SREBF2,PDGFRA,SOCS5,KLF4,RCN3,SLC9A3R1,TMUB1,INSIG1,OGG1,UCP2,SEL1L2,BAIAP2,INPPL1,LAMTOR1,AACS,HM13,BCL2L1,TNS2,PDE3B,WNT10B,SOD1,SRSF9,SELENOS,FABP3,PCK2,COL6A1,SLC26A6,UQCRC1,CAPN10,RELA,MGST3,IGFBP5,BAD,LAMTOR4,CD9,UBXN1,KLF3,CAPN2,MTHFR,PIP4K2B,ARHGEF2,PER1,TRIM25,CARM1,EEF2K,CSK,AKT1,HMGCS1,SLC6A4,LDOC1,MAN1B1,CARD9,APRT,SLC27A4,TGFBR3,JUND,NSMF,FBXO6,STUB1	yellow	VSMC_M3
GO:0045912	0.12	0.96	5	39	negative regulation of carbohydrate metabolic process	BP	1	ENPP1,SELENOS,GIT1,PGP,MIDN	yellow	VSMC_M3
GO:0006360	0.12	0.95	6	50	transcription by RNA polymerase I	BP	1	H2AFY,ZNRD1,SMARCB1,UBTF,SMARCA4,CAVIN1	yellow	VSMC_M3
GO:0042490	0.12	0.95	6	52	mechanoreceptor differentiation	BP	1	CTHRC1,SCRIB,IFT27,WDPCP,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:0001578	0.12	0.94	9	86	microtubule bundle formation	BP	1	SPAG1,CEP131,NUMA1,YIF1B,CHP1,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:1904888	0.12	0.95	6	54	cranial skeletal system development	BP	1	PDGFRA,HOXA1,INSIG1,MMP14,SLC39A1,NDST1	yellow	VSMC_M3
GO:0006352	0.12	0.94	11	105	DNA-templated transcription, initiation	BP	1	CDK4,WNT10B,SMARCB1,UBTF,TAF6L,SMARCA4,BRF1,GTF2F1,MED16,GTF3C5,CAVIN1	yellow	VSMC_M3
GO:0050792	0.12	0.94	12	119	regulation of viral process	BP	1	TRIM11,LGALS1,SNX3,P4HB,TARBP2,TYRO3,TRIM27,BANF1,SNF8,TRIM25,C19orf66,MID2	yellow	VSMC_M3
GO:0034340	0.12	0.95	6	47	response to type I interferon	BP	1	TTLL12,METTL3,CDC37,C19orf66,CACTIN,IRAK1	yellow	VSMC_M3
GO:0033143	0.12	0.95	7	63	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	PRMT2,PHB2,PKN1,PER1,SMARCA4,CARM1,SAFB2	yellow	VSMC_M3

GO:0034645	0.12	0.90	258	3533	cellular macromolecule biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,EEF1D,RPL3,RPL8,SND1,B4GALT1,MRPS18A,AARS2,PIGO,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,SERP2,DMAP1,CIC,GTF3C2,UNK,GALNT14,OGG1,SERTAD1,TTC5,METTL3,PHLDA1,CXXC5,DND1,RPL29,EIF4EBP1,DEAF1,HOXC4,POLR1D,TARBP2,KMT2B,NAT10,ZNF740,EIF4B,RALY,ZBTB38,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,KDM1B,CHCHD2,SLC35C2,CARS,ST3GAL4,DCPS,IRX1,SELENOS,RRP1B,TMTC1,BRD9,APEH,AIP,NGDN,TSHZ2,QARS,PIR,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,PSTK,RPS21,SMARCD2,EXTL1,BRMS1,TACO1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,LRWD1,ARNT2,MRPL49,ZFPL1,LIMD1,ZDHHC3,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,SDE2,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,MPDU1,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,DPM3,FARSA,IRF2BPL,TUFM,TRIM25,USP43,RPL37,SMARCA4,CARM1,RPL7A,EEF2K,AATF,MRPL4,EIF3G,C19orf66,MID2,ZNF521,ZNF358,ZNF830,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MRPL20,TRAP1,MNT,EHMT1,AP3D1,MKNK	yellow	VSMC_M3
GO:0031110	0.12	0.94	8	79	regulation of microtubule polymerization or depolymerization	BP	1	NUMA1,DCTN1,STMN3,MID1IP1,ARHGEF2,RANGRF,GIT1,GBA2	yellow	VSMC_M3
GO:0000377	0.12	0.92	24	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1	DHX16,SNRNP70,GEMIN7,METTL3,RALY,LSM6,PRPF40B,PCBP4,RBM15B,SRSF9,DCPS,RBM6,SF3A1,SART1,PRPF6,BUD31,C1QBP,GPKOW,CWC25,CD2BP2,RAVER1,RBM22,CACTIN,RBM8A	yellow	VSMC_M3
GO:0000398	0.12	0.92	24	255	mRNA splicing, via spliceosome	BP	1	DHX16,SNRNP70,GEMIN7,METTL3,RALY,LSM6,PRPF40B,PCBP4,RBM15B,SRSF9,DCPS,RBM6,SF3A1,SART1,PRPF6,BUD31,C1QBP,GPKOW,CWC25,CD2BP2,RAVER1,RBM22,CACTIN,RBM8A	yellow	VSMC_M3
GO:0048732	0.12	0.92	28	335	gland development	BP	1	SCRIB,MPST,PDGFRA,PHF2,SLC9A3R1,PLXND1,UCP2,FASN,DEAF1,AACS,SOD1,PDGFA,GPX1,PCK2,RIPK3,PBX1,RELA,PHB2,IGFBP5,MAD1L1,ARMC5,MTX1,AKT1,HMGCS1,STK11,APRT,TGFBR3,ERBB4	yellow	VSMC_M3
GO:0042471	0.12	0.94	9	89	ear morphogenesis	BP	1	CTHRC1,SCRIB,HOXA1,WDPCP,SLC9A3R1,INSIG1,LRIG1,SOD1,TTC39C	yellow	VSMC_M3
GO:2000045	0.12	0.94	10	97	regulation of G1/S transition of mitotic cell cycle	BP	1	CTDSP2,KLF4,KMT2E,CDK2AP2,PSME2,PRMT2,CTDSP1,SDE2,AKT1,MIR214	yellow	VSMC_M3
GO:0031334	0.12	0.92	18	199	positive regulation of protein-containing complex assembly	BP	1	SNX9,FNIP1,BAIAP2,NUMA1,DCTN1,WNT10B,CORO1B,TRIM27,ARPIN,RHOC,LGALS3,ARPC1B,WASHC1,CORO1A,GIT1,CDC42EP5,STUB1,ARPC5L	yellow	VSMC_M3
GO:0045834	0.12	0.93	11	109	positive regulation of lipid metabolic process	BP	1	PPARD,PDGFRA,SCARB1,DGKZ,CHP1,FABP3,PLA2G3,MID1IP1,CAPN2,AKT1,TAZ	yellow	VSMC_M3
GO:0050000	0.12	0.94	8	70	chromosome localization	BP	1	DCTN2,NUMA1,RRS1,PINX1,NUDC,EML3,MAD1L1,MIS12	yellow	VSMC_M3
GO:2000780	0.12	0.96	4	29	negative regulation of double-strand break repair	BP	1	OGG1,OTUB1,MAD2L2,CXorf57	yellow	VSMC_M3
GO:0009132	0.12	0.94	10	94	nucleoside diphosphate metabolic process	BP	1	GUK1,GALK1,OGDHL,AK2,BAD,FOXK1,PGM1,GIT1,JMJD8,AK1	yellow	VSMC_M3
GO:0006164	0.12	0.93	15	149	purine nucleotide biosynthetic process	BP	1	GUK1,ACSL1,AK2,PAPSS1,IMPDH2,ATP5MC3,ATIC,UQCC3,ACLY,ATP5PD,ATP5F1D,TAZ,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:1902751	0.12	0.96	4	27	positive regulation of cell cycle G2/M phase transition	BP	1	CDK4,WNT10B,PBX1,RCC2	yellow	VSMC_M3
GO:0002931	0.12	0.95	6	51	response to ischemia	BP	1	SQSTM1,EIF4EBP1,CX3CL1,EEF2K,AKT1,STUB1	yellow	VSMC_M3
GO:2001234	0.12	0.92	18	187	negative regulation of apoptotic signaling pathway	BP	1	FIGNL1,BCL2L1,CX3CL1,CCAR2,SELENOS,ITPRIP,GPX1,QARS,RELA,LGALS3,NANOS3,ARHGEF2,AATF,AKT1,TRAP1,MNT,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0009260	0.12	0.93	15	149	ribonucleotide biosynthetic process	BP	1	GUK1,ACSL1,AK2,PAPSS1,IMPDH2,ATP5MC3,ATIC,UQCC3,ACLY,ATP5PD,ATP5F1D,TAZ,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:0071470	0.12	0.95	5	40	cellular response to osmotic stress	BP	1	RELB,AQP5,BAD,LETM1,ARHGEF2	yellow	VSMC_M3
GO:1902042	0.12	0.96	4	26	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	1	BCL2L1,ITPRIP,GPX1,ARHGEF2	yellow	VSMC_M3
GO:0009966	0.12	0.89	162	2237	regulation of signal transduction	BP	1	ENPP1,CD63,CDK4,SQSTM1,CTHRC1,NELFE,FNIP1,ATF6B,PRR5,TTLL12,SREBF2,TXNDC15,SGSM3,DEF6,PPARD,EEF1D,LGALS1,SHARPIN,BOP1,PDGFRA,IL1R1,SOCS5,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,RCN3,SNX3,PLEKHA4,MGLL,SLC9A3R1,EMILIN1,RNF220,INSIG1,SEC13,ARHGEF40,METTL3,BAIAP2,CXXC5,LAMTOR1,NUMA1,P4HB,CAVIN3,ARHGAP22,BCL2L1,PDE4D,TNS2,RRS1,SWAP70,PLEKHF1,GREM1,PDE3B,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,SLC35C2,TSPAN5,CISH,SELENOS,ITPRIP,PDGFA,MMP14,GPX1,AIP,NGEF,QARS,TRIM27,EIF3A,PRMT2,THOC5,RIPK3,STMN3,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZDHHC3,SMARCB1,YJEFN3,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,LGALS3,BUD31,PLAU,TNFRSF1A,MVB12A,C1QBP,CHERP,EVC,CCDC22,PKN1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,TRIM25,RPL37,MTMR4,S100A4,SMARCA4,CARM1,CDC37,AATF,CSK,MID2,AKT1,TEDC1,RAB34,SAFB2,GIT1,MYDGF,MAP2K2,CACTIN,VASN,HIC1,TRAP1,NCLN,MNT,CTNS,TEDC2,CSNK1G2,IRAK1,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,SLC27A4,TGFBR3,TRADD,NDST1,TNFRSF12A,ERBB4,PTPRR,IGFBP6,ZNF385A,TXNDC12,CDC34,APCDD1L,ARHGEF1,RGS16,DUSP5,GLIPR2,STUB1,RGS18,GSG1L	yellow	VSMC_M3
GO:0007004	0.12	0.94	7	63	telomere maintenance via telomerase	BP	1	NHP2,PNKP,NAT10,TNKS1BP1,PINX1,TELO2,RF00024	yellow	VSMC_M3

GO:0010648	0.13	0.90	80	1047	negative regulation of cell communication	BP	1	ENPP1,CTHRC1,FNIP1,ATF6B,TTLL12,SOCS5,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,SLC9A3R1,EMILIN1,INSIG1,UCP2,METTL3,CAVIN3,BCL2L1,PDE4D,TNS2,GREM1,PDE3B,CX3CL1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,CISH,SELENOS,ITPRIP,MMP14,GPX1,QARS,EIF3A,THOC5,STMN3,RELA,LIMD1,PHB2,IGFBP5,IFI35,LGALS3,C1QBP,CCDC22,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,MTMR4,SMARCA4,AATF,CSK,AKT1,SLC6A4,CACTIN,VASN,HIC1,TRAP1,MNT,MIDN,STK11,SLC27A4,TGFBR3,PTPRR,IGFBP6,JAGN1,ZNF385A,TXNDC12,CDC34,APCDD1L,RGS16,DUSP5,STUB1,RGS18	yellow	VSMC_M3
GO:0045833	0.13	0.94	8	72	negative regulation of lipid metabolic process	BP	1	INSIG1,PDE3B,SOD1,ETFBKMT,PDGFA,WASHC1,PIP4K2B,AKT1	yellow	VSMC_M3
GO:0006418	0.13	0.95	5	37	tRNA aminoacylation for protein translation	BP	1	AARS2,CARS,QARS,FARSA,SARS	yellow	VSMC_M3
GO:0023057	0.13	0.90	80	1048	negative regulation of signaling	BP	1	ENPP1,CTHRC1,FNIP1,ATF6B,TTLL12,SOCS5,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,SLC9A3R1,EMILIN1,INSIG1,UCP2,METTL3,CAVIN3,BCL2L1,PDE4D,TNS2,GREM1,PDE3B,CX3CL1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,CISH,SELENOS,ITPRIP,MMP14,GPX1,QARS,EIF3A,THOC5,STMN3,RELA,LIMD1,PHB2,IGFBP5,IFI35,LGALS3,C1QBP,CCDC22,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,MTMR4,SMARCA4,AATF,CSK,AKT1,SLC6A4,CACTIN,VASN,HIC1,TRAP1,MNT,MIDN,STK11,SLC27A4,TGFBR3,PTPRR,IGFBP6,JAGN1,ZNF385A,TXNDC12,CDC34,APCDD1L,RGS16,DUSP5,STUB1,RGS18	yellow	VSMC_M3
GO:0051896	0.13	0.93	12	125	regulation of protein kinase B signaling	BP	1	KLF4,TPBG,RCN3,SLC9A3R1,CAVIN3,CX3CL1,PDGFA,GPX1,IGFBP5,C1QBP,MYDGF,STK11	yellow	VSMC_M3
GO:0048525	0.13	0.94	7	61	negative regulation of viral process	BP	1	TRIM11,SNX3,TRIM27,BANF1,TRIM25,C19orf66,MID2	yellow	VSMC_M3
GO:0010563	0.13	0.91	30	356	negative regulation of phosphorus metabolic process	BP	1	ENPP1,CTDSP2,H2AFY,PLEC,SOCS5,SPRED2,ZC3H12A,MICAL1,EMILIN1,TARBP2,PDE4D,SWAP70,GREM1,CHP1,PDGFA,QARS,TRIM27,PPP1R35,CTDSP1,LGALS3,WASHC1,PKN1,PIP4K2B,MVP,CSK,AKT1,GIT1,CACTIN,MIDN,TRIB2	yellow	VSMC_M3
GO:0045936	0.13	0.91	30	356	negative regulation of phosphate metabolic process	BP	1	ENPP1,CTDSP2,H2AFY,PLEC,SOCS5,SPRED2,ZC3H12A,MICAL1,EMILIN1,TARBP2,PDE4D,SWAP70,GREM1,CHP1,PDGFA,QARS,TRIM27,PPP1R35,CTDSP1,LGALS3,WASHC1,PKN1,PIP4K2B,MVP,CSK,AKT1,GIT1,CACTIN,MIDN,TRIB2	yellow	VSMC_M3
GO:0006278	0.13	0.94	7	64	RNA-dependent DNA biosynthetic process	BP	1	NHP2,PNKP,NAT10,TNKS1BP1,PINX1,TELO2,RF00024	yellow	VSMC_M3
GO:0043487	0.13	0.92	14	148	regulation of RNA stability	BP	1	HNRNPA0,CNOT3,ZC3H12A,METTL3,DND1,PCBP4,DCPS,ZCCHC17,NANOS3,AKT1,PAIP1,KHSRP,CARHSP1,TENT5B	yellow	VSMC_M3
GO:0033013	0.13	0.95	6	49	tetrapyrrole metabolic process	BP	1	BLVRA,BLVRB,SLC11A2,SRRD,PPOX,SLC25A39	yellow	VSMC_M3
GO:0006195	0.13	0.95	5	38	purine nucleotide catabolic process	BP	1	NUDT3,DNPH1,PDE4D,NT5C,ITPA	yellow	VSMC_M3
GO:0098869	0.13	0.94	8	67	cellular oxidant detoxification	BP	1	GSR,SOD1,SELENOS,GSTO1,GPX1,MGST3,TXNRD2,PRXL2A	yellow	VSMC_M3
GO:0043488	0.13	0.92	13	137	regulation of mRNA stability	BP	1	HNRNPA0,CNOT3,ZC3H12A,METTL3,DND1,PCBP4,DCPS,NANOS3,AKT1,PAIP1,KHSRP,CARHSP1,TENT5B	yellow	VSMC_M3
GO:1901987	0.13	0.91	27	311	regulation of cell cycle phase transition	BP	1	CDK4,CTDSP2,H2AFY,KLF4,KMT2E,PINX1,WNT10B,CCAR2,CDK2AP2,PSME2,PRMT2,THOC5,PBX1,PHB2,CTDSP1,METTL13,BABAM1,RCC2,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,AKT1,MIR214,NABP2,FBXO6	yellow	VSMC_M3
GO:0044267	0.13	0.88	272	3725	cellular protein metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,BAG6,SBF1,SNX9,HDAC10,NELFE,FNIP1,PRR5,TTLL12,RING1,JADE2,H2AFY,TRIM11,EEF1D,RPL3,PLEC,SHARPIN,VPS28,RPL8,CUL7,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,JOSD2,PSMB3,SPRED2,EIPR1,MEAF6,ZC3H12A,PNKP,RCN3,MICAL1,KMT2E,WDFY2,SLC9A3R1,SERP2,NAT9,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,PPM1G,UNK,GALNT14,SERTAD1,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,P4HB,DND1,RPL29,EIF4EBP1,TARBP2,KMT2B,NAT10,HM13,PDE4D,TNS2,EIF4B,SWAP70,ACSL1,TNKS1BP1,PINX1,GATB,SETD1B,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,CCAR2,RPLP2,CHP1,TYRO3,MRPL43,HTATIP2,PCIF1,PPM1M,KDM1B,SLC35C2,CARS,CISH,ST3GAL4,RNF19B,DCPS,SELENOS,ETFBKMT,MANBA,TMTC1,STK32C,PDGFA,MMP14,APEH,GPX1,AIP,HCCS,MOCS3,CLCF1,NGDN,QARS,ASB9,PSME2,TRIM27,EIF3A,LIMK1,RABGGTA,PRMT2,RIPK3,LSM14B,ADRM1,PSTK,RPS21,PSMB4,EXTL1,BRMS1,SEC11A,TNK2,TACO1,PTPN23,KAT5,RELA,SCYL1,ALKBH4,MEX3B,MAP3K14,MRPL49,ZDHHC3,SMARCB1,PHB2,TRMT112,IGFBP5,BAD,FKBP2,CTDSP1,OTUB1,EID1,COPS6,MPV17L2,LGALS3,TNFRSF1A,MVB12A,BABAM1,C1QBP,AIMP2,TAF6L,UBXN1,WASHC1,MTA2,MED11,CCDC22,USP27X,KRT10,SDE2,PKN1,CAPN2,SEPSECS,AMER1,MTHFR,MAD2L2,NANOS3,MPDU1,CTBP1,FBXL19,ARHGEF2,SNF8,RUSC1,MVP,PER1,DPM3,PPP4C,FARSA,SGF29,IRF2BPL,TUFM,TRIM25,USP43,RPL37,MTMR4,CARM1,SENP8,RPL7A,EEF2K,CDC37,MRPL4,EIF3G,C19orf66,CSK,MID2,ATG3,ANKRD9,AKT1,COPRS,PAIP1,KHSRP,SGK494,DHCR24,BLMH,MYDGF,METTL3,SIRT6,MAP3K3,CACTIN,UMPS,PPP1R35,CDK1AP1,ECH1	yellow	VSMC_M3
GO:0008593	0.13	0.94	8	76	regulation of Notch signaling pathway	BP	1	SREBF2,METTL3,DLL4,SLC35C2,TSPAN5,MMP14,YJEFN3,AKT1	yellow	VSMC_M3
GO:0051591	0.13	0.94	7	68	response to cAMP	BP	1	WNT10B,SLC26A6,RELA,IGFBP5,PER1,CARM1,EEF2K	yellow	VSMC_M3
GO:1905508	0.13	0.96	4	33	protein localization to microtubule organizing center	BP	1	DCTN2,CEP131,NUMA1,KIAA0753	yellow	VSMC_M3
GO:0006779	0.13	0.96	4	28	porphyrin-containing compound biosynthetic process	BP	1	SLC11A2,SRRD,PPOX,SLC25A39	yellow	VSMC_M3
GO:0033014	0.13	0.96	4	28	tetrapyrrole biosynthetic process	BP	1	SLC11A2,SRRD,PPOX,SLC25A39	yellow	VSMC_M3
GO:0009205	0.13	0.94	7	57	purine ribonucleoside triphosphate metabolic process	BP	1	IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ,ITPA	yellow	VSMC_M3
GO:0032868	0.14	0.91	18	206	response to insulin	BP	1	ENPP1,CDK4,INSIG1,UCP2,BAIAP2,INPPL1,TNS2,PDE3B,SELENOS,FABP3,PCK2,CAPN10,RELA,PIP4K2B,EEF2K,AKT1,APRT,SLC27A4	yellow	VSMC_M3

GO:0046474	0.14	0.91	17	185	glycerophospholipid biosynthetic process	BP	1	PIGO,SOCS5,TTC7A,INPPL1,PCYT2,PTDSS2,DGKZ,CISH,FABP3,PDGFA,CAPN2,PIP4K2B,DPM3,MTMR4,TAZ,SLC44A3,VAC14	yellow	VSMC_M3
GO:0018130	0.14	0.88	211	2900	heterocycle biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,TSTA3,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,CXXC5,PYCR1,GNPDA1,DEAF1,HOXC4,POLR1D,KMT2B,NAT10,ZNF740,RALY,ACSL1,ZBTB38,SLC11A2,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,NPM3,KDM1B,CHCHD2,AK2,IRX1,RRP1B,BRD9,PAPSS1,AIP,MOCS3,SRRD,TSHZ2,QARS,IMPDH2,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,PSTK,SMARCD2,BRMS1,PPOX,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ATP5MC3,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,SLC25A39,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,FLAD1,IRF2BPL,TRIM25,ATP5PD,USP43,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,ATP5F1D,TELO2,TAZ,MED16,CARD9,AMPD2,SARS,APRT,GTF3C5,AK1,TRADD,RF00024,ERBB4,JUND,PTMA,KLF13,FADS1,ZNF783,HOXC5,CAVIN1,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,SNAPC2,ZSCAN1	yellow	VSMC_M3
GO:0014812	0.14	0.93	8	79	muscle cell migration	BP	1	PPARD,PDGFA,CORO1B,PLEKHO1,IGFBP5,AAMP,PLAU,MIR214	yellow	VSMC_M3
GO:0043933	0.14	0.89	105	1370	protein-containing complex subunit organization	BP	1	SPAG1,SNX9,FNIP1,SAMM50,NDUFB9,H2AFY,RPL3,PLEC,BOP1,TBCC,DBNL,ZC3H12A,MICAL1,ACAD9,GEMIN7,SLC9A3R1,DMAP1,H3F3B,BAIAP2,NUMA1,CCDC57,EIF4EBP1,SDHAF1,TARBP2,SCARB1,EIF4B,RRS1,SWAP70,UQCRFS1,CAPG,GREM1,AQP5,DCTN1,CX3CL1,WNT10B,CHP1,SRSF9,LIX1L,APEH,CORO1B,HCCS,TRIM27,ARPIN,EIF3A,SF3A1,ADRM1,SMARCD2,TACO1,PLA2G3,STMN3,SART1,PRPF6,RHOC,TMEM120A,ZNHIT1,MID1IP1,PEX5,SMARCB1,CHCHD10,UBTF,BAD,LETM1,LGALS3,ARPC1B,MRTO4,FCHO1,AIMP2,TAF6L,UQCC3,WASHC1,KRT10,H3F3A,DBN1,CLTB,ARHGEF2,CD2BP2,RANGRF,FARSA,CORO1A,SMARCA4,EIF3G,C19orf66,BRF1,GIT1,UBN1,MRPL20,NCLN,NDUFS7,ATP5F1D,TAZ,CARD9,SPG7,TGFBR3,MIR214,TWF2,SURF1,MIS12,ELN,UNC13A,CDC42EP5,GBA2,TUBGCP2,STUB1,CCDC115,ARPC5L	yellow	VSMC_M3
GO:0019217	0.14	0.94	7	62	regulation of fatty acid metabolic process	BP	1	PPARD,INSIG1,ETFBKMT,FABP3,PLA2G3,MID1IP1,AKT1	yellow	VSMC_M3
GO:2001021	0.14	0.93	8	72	negative regulation of response to DNA damage stimulus	BP	1	OGG1,BCL2L1,CCAR2,THOC5,OTUB1,MAD2L2,CXorf57,ZNF385A	yellow	VSMC_M3
GO:0043543	0.14	0.91	18	202	protein acylation	BP	1	BAG6,JADE2,MEAF6,NAT9,DMAP1,KAT14,NAT10,MCRS1,KAT5,ZDHHC3,SMARCB1,EID1,TAF6L,CTBP1,PER1,SGF29,MBD3,THAP7	yellow	VSMC_M3
GO:0043484	0.14	0.92	12	126	regulation of RNA splicing	BP	1	SNRNP70,PCBP4,RBM15B,SRSF9,RRP1B,C1QBP,POLR2A,RAVER1,RBM22,FAM50A,RBM8A,AKAP17A	yellow	VSMC_M3
GO:0006739	0.14	0.95	4	27	NADP metabolic process	BP	1	TKT,IDH1,PGD,TALDO1	yellow	VSMC_M3
GO:1905521	0.14	0.95	4	29	regulation of macrophage migration	BP	1	EMILIN1,CX3CL1,MMP14,CD9	yellow	VSMC_M3
GO:0097435	0.14	0.89	47	622	supramolecular fiber organization	BP	1	SNX9,PACSIN1,PLEC,PDGFRA,DBNL,ZYX,MICAL1,KRT8,EMILIN1,BAIAP2,INPPL1,NUMA1,CCDC57,SWAP70,CAPG,GREM1,DCTN1,CX3CL1,CHP1,GPX1,CORO1B,CLIP2,TRIM27,ARPIN,LIMK1,RIPK3,PFDN2,STMN3,RHOC,MID1IP1,ARPC1B,WASHC1,DBN1,MAD2L2,ARHGEF2,RANGRF,CORO1A,MYO19,GIT1,MIR214,TWF2,LOXL1,ELN,CDC42EP5,GBA2,TUBGCP2,ARPC5L	yellow	VSMC_M3
GO:0060612	0.14	0.95	4	32	adipose tissue development	BP	1	CDK4,PPARD,AACS,AMER1	yellow	VSMC_M3
GO:0014909	0.14	0.93	7	67	smooth muscle cell migration	BP	1	PPARD,PDGFA,CORO1B,IGFBP5,AAMP,PLAU,MIR214	yellow	VSMC_M3
GO:0051091	0.14	0.91	18	204	positive regulation of DNA-binding transcription factor activity	BP	1	TRAPPC9,GREM1,CX3CL1,WNT10B,TRIM27,RIPK3,RELA,SMARCB1,PHB2,BUD31,ARHGEF2,TRIM25,SMARCA4,MID2,AKT1,IRAK1,CARD9,TRADD	yellow	VSMC_M3
GO:0016042	0.14	0.91	21	225	lipid catabolic process	BP	1	CDK4,ACAT2,PPARD,CPT1C,MGLL,PAFAH1B3,SNX17,PLCD1,SCARB1,PCCB,PDE3B,ETFBKMT,PCK2,IDH1,SGPL1,PLCB3,ILVBL,AKT1,SLC27A4,PLA2G4E,GBA2	yellow	VSMC_M3
GO:0009394	0.14	0.95	5	35	2'-deoxyribonucleotide metabolic process	BP	1	GUK1,DNPH1,OGG1,SMUG1,NT5C	yellow	VSMC_M3
GO:0045600	0.14	0.94	6	53	positive regulation of fat cell differentiation	BP	1	PPARD,ZC3H12A,WDFY2,CARM1,AKT1,ZNF385A	yellow	VSMC_M3

GO:0043412	0.14	0.88	219	3029	macromolecule modification	BP	1	ENPP1,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,BAG6,SBF1,SNX9,HDAC10,NELFE,FNIP1,PRR5,TTLL12,RING1,JADE2,TRMT12,H2AFY,TRIM11,PLEC,SHARPIN,VPS28,CUL7,B4GALT1,AARS2,PIGO,PDGFRA,PHF2,HSPBP1,SOCS5,JOSD2,SPRED2,EIPR1,MEAF6,ZC3H12A,PNKP,KTI12,MICAL1,KMT2E,WDFY2,SLC9A3R1,SERP2,NAT9,MUTYH,EMILIN1,SEPHS1,RNF220,DMAP1,PPM1G,GALNT14,OGG1,SERTAD1,KAT14,P4HA3,SEL1L2,METTL3,P4HB,PUS1,SMUG1,TARBP2,KMT2B,NAT10,PDE4D,TNS2,SWAP70,ACSL1,TNKS1BP1,PINX1,SETD1B,GREM1,KDM2B,MCRS1,CX3CL1,FKBP11,SOD1,CCAR2,CHP1,TYRO3,HTATIP2,PCIF1,PPM1M,KDM1B,SLC35C2,RBM15B,CISH,ST3GAL4,RNF19B,WDR4,ETFBKMT,MANBA,TMTC1,STK32C,PDGFA,GPX1,AIP,HCCS,MOCS3,CLCF1,QARS,ASB9,TRIM27,LIMK1,RABGGTA,PRMT2,RIPK3,EXTL1,FTSJ3,BRMS1,BUD23,TNK2,PTPN23,KAT5,RELA,SCYL1,ALKBH4,MEX3B,MAP3K14,ZDHHC3,SMARCB1,TRMT2A,GATAD2A,PHB2,TRMT112,FKBP2,CTDSP1,OTUB1,EID1,COPS6,LGALS3,TNFRSF1A,GTPBP3,BABAM1,AIMP2,TAF6L,UBXN1,WASHC1,MTA2,MED11,USP27X,KRT10,ELP5,SDE2,PKN1,AMER1,MTHFR,MAD2L2,MPDU1,CTBP1,FBXL19,RRNAD1,ARHGEF2,RUSC1,MVP,PER1,DPM3,TRMT1,PPP4C,SGF29,IRF2BPL,TRIM25,USP43,RPL37,MTMR4,CARM1,SENP8,EEF2K,CDC37,CSK,MID2,ATG3,ANKRD9,AKT1,COPRS,SGK494,DUS3L,BLMH,MYDGF,METTL22,SIRT6,MAP2K2,CACTIN,HMG20B,CDK11B,SSU72,EHMT1,PGP,MKNK2,CSNK1G2,IRAK1,ANAPC2,SPSB3,MBD3,MAN1B1,STK11,TELO2,TSR3,UBAC1,CTU2,POMT1,NTMT1,ZNRF1,TGFBR3,B3GNT9,NDST1,ERBB4,PTPRR,LOXL1,PIN4,TRIM7,TRIB2,NSMF,CDC34,FBXO6,DUSP5,THAP7,STUB1,NSMC	yellow	VSMC_M3
GO:0045931	0.14	0.92	10	97	positive regulation of mitotic cell cycle	BP	1	CDK4,KMT2E,CCDC57,EIF4EBP1,WNT10B,PBX1,PHB2,RCC2,AKT1,MIR214	yellow	VSMC_M3
GO:0097194	0.14	0.93	7	60	execution phase of apoptosis	BP	1	SHARPIN,ZC3H12A,BCL2L1,CAPN10,CASP14,DFFA,AKT1	yellow	VSMC_M3
GO:0046907	0.14	0.88	95	1261	intracellular transport	BP	1	PQLC1,CD63,SQSTM1,CCHCR1,SNX9,SAMM50,SREBF2,SGSM3,SCRIB,IFT27,VPS28,TOM1,ASNA1,PLEKHA8,EIPR1,ZC3H12A,SNX3,EHD2,SLC9A3R1,DMAP1,SNX17,INSIG1,MYRIP,SEC13,CEP131,LAMTOR1,NUMA1,YIF1B,RAB20,HM13,RRS1,DCTN1,SOD1,CHP1,AP2A2,HTATIP2,RAB35,RBM15B,SELENOS,FABP3,PABPN1,AIP,AP1G2,TRIM27,PCNT,THOC5,CAPN10,PLA2G3,PTPN23,VPS51,PEX5,ZDHHC3,THOC3,BLOC1S4,PHB2,COPE,MVB12A,NUP88,WASHC1,AP1M1,CCDC22,SNX8,LMAN2,RAB24,CLTB,ARHGEF2,SNF8,RANGRF,STX10,CORO1A,ATP5PD,TMED1,SYNE3,CDC37,MYO19,ATG3,RBM22,AKT1,SNX18,DENND1C,RANBP3,MAP2K2,AP3D1,SSNA1,ATP5F1D,STK11,TMEM201,SPG7,WDR34,TRAPPC5,PLA2G4E,AP5B1,ARFRP1,TIMM22,PHETA2	yellow	VSMC_M3
GO:0046889	0.14	0.93	7	61	positive regulation of lipid biosynthetic process	BP	1	SCARB1,CHP1,FABP3,PLA2G3,MID1IP1,CAPN2,AKT1	yellow	VSMC_M3
GO:1902750	0.14	0.94	6	52	negative regulation of cell cycle G2/M phase transition	BP	1	H2AFY,PINX1,BABAM1,MIIP,ZNF830,NABP2	yellow	VSMC_M3
GO:0046683	0.14	0.93	9	94	response to organophosphorus	BP	1	WNT10B,SOD1,SLC26A6,RELA,IGFBP5,PER1,CARM1,EEF2K,SLC6A4	yellow	VSMC_M3
GO:0006099	0.14	0.95	4	27	tricarboxylic acid cycle	BP	1	IDH3B,OGDHL,SDHA,IDH1	yellow	VSMC_M3
GO:0031324	0.14	0.88	140	1896	negative regulation of cellular metabolic process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,ZNF608,BAG6,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,PPARD,PLEC,VPS28,SECISBP2,SOCS5,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,SNRNP70,CC2D1B,MICAL1,SIX5,ZNF282,ZNF296,RELB,EMILIN1,DMAP1,CIC,UNK,INSIG1,OGG1,METTL3,CXXC5,DND1,EIF4EBP1,CAVIN3,DEAF1,TARBP2,NAT10,PDE4D,SWAP70,ZBTB38,PINX1,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,CHP1,YAF2,PCIF1,PCBP4,KDM1B,SRSF9,DCPS,IRX1,SELENOS,ETFBKMT,RIN3,ZCCHC17,PDGFA,GPX1,QARS,TRIM27,LIMK1,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,SMARCB1,GATAD2A,PHB2,PPP1R35,IGFBP5,CTDSP1,OTUB1,EID1,METTL13,LGALS3,C11orf95,C1QBP,ZBTB49,UBXN1,WASHC1,MTA2,FOXK1,KLF3,PKN1,PIP4K2B,MAD2L2,NANOS3,CTBP1,DFFA,SP2,MVP,PER1,NFIX,SLX1A,IRF2BPL,RPL37,SMARCA4,AATF,CXorf57,C19orf66,CSK,ZNF830,AKT1,PAIP1,KHSRP,GIT1,ANKRD13B,DHCR24,SIRT6,CACTIN,HMG20B,HIC1,TRAP1,MNT,CTNS,EHMT1,PGP,MBD3,MIDN,SARS,TENT5B,TRIB2,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0043403	0.14	0.95	4	28	skeletal muscle tissue regeneration	BP	1	PPARD,WNT10B,GPX1,CD9	yellow	VSMC_M3
GO:1901135	0.14	0.89	64	791	carbohydrate derivative metabolic process	BP	1	ENPP1,CERK,GUK1,NUDT3,PPARD,TSTA3,DNPH1,B4GALT1,PIGO,SERP2,GALK1,GALNT14,OGG1,PHLDA1,FASN,GNPDA1,SMUG1,OGDHL,PDE4D,ACSL1,TKT,CHP1,SLC35C2,ST3GAL4,AK2,MANBA,TMTC1,MVK,PAPSS1,IMPDH2,EXTL1,ATP5MC3,ATIC,BAD,UQCC3,ACLY,FOXK1,MPDU1,PGD,ACSF2,DPM3,PMVK,ATP5PD,AATF,AKT1,HMGCS1,PGM1,GIT1,MAN1B1,ATP5F1D,TAZ,JMJD8,AMPD2,APRT,MVD,POMT1,AK1,B3GNT9,NDST1,NT5C,TALDO1,FBXO6,GBA2,ITPA	yellow	VSMC_M3
GO:1903573	0.14	0.94	5	39	negative regulation of response to endoplasmic reticulum stress	BP	1	ATF6B,BCL2L1,SELENOS,UBXN1,TXNDC12	yellow	VSMC_M3
GO:0008631	0.14	0.94	5	39	intrinsic apoptotic signaling pathway in response to oxidative stress	BP	1	P4HB,SOD1,GPX1,AKT1,TRAP1	yellow	VSMC_M3
GO:2000779	0.14	0.93	8	76	regulation of double-strand break repair	BP	1	FIGNL1,PNKP,OGG1,OTUB1,MAD2L2,PPP4C,CXorf57,SIRT6	yellow	VSMC_M3

GO:0045934	0.14	0.88	84	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,PPARD,SECISBP2,KLF4,ZC3H12A,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,OGG1,CXXC5,DND1,DEAF1,NAT10,ZBTB38,PINX1,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,PCBP4,KDM1B,SRSF9,IRX1,ZCCHC17,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,OTUB1,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,CTBP1,DFFA,SP2,PER1,NFIX,SLX1A,IRF2BPL,SMARCA4,CXorf57,PAIP1,GIT1,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,TENT5B,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0009890	0.15	0.88	92	1222	negative regulation of biosynthetic process	BP	1	ENPP1,NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,TRIM11,PPARD,CNOT3,KLF4,ZC3H12A,CC2D1B,SIX5,ZNF282,ZNF296,RELB,EMILIN1,DMAP1,CIC,UNK,INSIG1,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,NAT10,ZBTB38,PINX1,GREM1,KDM2B,WNT10B,SOD1,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,PCIF1,KDM1B,DCPS,IRX1,SELENOS,PDGFA,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,IGFBP5,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,NANOS3,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,AATF,C19orf66,ZNF830,KHSRP,SIRT6,HIC1,TRAP1,MNT,CTNS,EHMT1,PGP,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0009264	0.15	0.95	4	26	deoxyribonucleotide catabolic process	BP	1	DNPH1,OGG1,SMUG1,NT5C	yellow	VSMC_M3
GO:0043551	0.15	0.94	5	47	regulation of phosphatidylinositol 3-kinase activity	BP	1	PDGFRA,SOCS5,KLF4,CISH,WASHC1	yellow	VSMC_M3
GO:0009892	0.15	0.87	165	2254	negative regulation of metabolic process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,ZNF608,BAG6,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,PPARD,PLEC,VPS28,SND1,SECISBP2,PHF2,SSC5D,SOCS5,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,SNRNP70,CC2D1B,SNX3,MICAL1,SIX5,ZNF282,ZNF296,RELB,EMILIN1,DMAP1,CIC,UNK,INSIG1,OGG1,METTL3,CXXC5,INPPL1,DND1,EIF4EBP1,CAVIN3,DEAF1,TARBP2,NAT10,PDE4D,SWAP70,LRP3,ZBTB38,LSM6,PINX1,GREM1,KDM2B,PDE3B,CX3CL1,WNT10B,SOD1,ANKRD2,CCAR2,DNAJC17,DLL4,CHP1,YAF2,PCIF1,PCBP4,KDM1B,SLC35C2,SRSF9,DCPS,IRX1,SELENOS,ETFBKMT,RIN3,ZCCHC17,PDGFA,GPX1,QARS,TRIM27,LIMK1,PRMT2,TWIST2,PFDN2,BRMS1,PLA2G3,CCDC85B,KAT5,RELA,LIMD1,SMARCB1,GATAD2A,PHB2,PPP1R35,IGFBP5,CTDSP1,OTUB1,EID1,METTL13,LGALS3,C11orf95,MRTO4,C1QBP,ZBTB49,UBXN1,WASHC1,MTA2,FOXK1,KLF3,PKN1,PIP4K2B,MAD2L2,NANOS3,CTBP1,DFFA,SP2,MVP,PER1,NFIX,SLX1A,IRF2BPL,RPL37,SMARCA4,AATF,CXorf57,C19orf66,CSK,ZNF830,AKT1,PAIP1,KHSRP,GIT1,ANKRD13B,DHCR24,CARHSP1,SIRT6,MAP2K2,CACTIN,HMG20B,HIC1,TRAP1,MNT,CTNS,EHMT1,PGP,ANAPC2,MBD3,MIDN,STK11,SARS,SLC27A4,MIR214,MIR155,RBM8A,RNH1,MIR374B,TENT5B,TRIB2,THAP7,NSMCE3,ERF,ZAR1L	yellow	VSMC_M3
GO:0006692	0.15	0.95	4	29	prostanoid metabolic process	BP	1	PTGR1,PLA2G3,TNFRSF1A,CYP4F8	yellow	VSMC_M3
GO:0006693	0.15	0.95	4	29	prostaglandin metabolic process	BP	1	PTGR1,PLA2G3,TNFRSF1A,CYP4F8	yellow	VSMC_M3
GO:1903131	0.15	0.90	25	297	mononuclear cell differentiation	BP	1	NCAPH2,FNIP1,LGALS1,SOCS5,ZC3H12A,RELB,CD79A,METTL3,FASN,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,PIR,THOC5,RIPK3,SART1,PBX1,BAD,ARMC5,DOCK11,AP3D1,STK11	yellow	VSMC_M3
GO:0006383	0.15	0.94	5	39	transcription by RNA polymerase III	BP	1	NAB2,GTF3C2,BRF1,GTF3C5,SNAPC2	yellow	VSMC_M3
GO:0030866	0.15	0.95	4	35	cortical actin cytoskeleton organization	BP	1	PLEC,EHD2,CAVIN3,FMNL1	yellow	VSMC_M3
GO:0045806	0.15	0.94	5	41	negative regulation of endocytosis	BP	1	PACSIN1,PACSIN3,RIN3,LGALS3,ANKRD13B	yellow	VSMC_M3
GO:1901224	0.15	0.93	6	51	positive regulation of NIK/NF-kappaB signaling	BP	1	GREM1,RELA,PHB2,IFI35,IRAK1,TRADD	yellow	VSMC_M3
GO:0009206	0.15	0.93	6	46	purine ribonucleoside triphosphate biosynthetic process	BP	1	IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ	yellow	VSMC_M3
GO:0045927	0.15	0.90	17	199	positive regulation of growth	BP	1	PPARD,DNPH1,DBNL,H3F3B,KDM2B,MMP14,LIMK1,H3F3A,DBN1,CRABP2,AKT1,HDGFL2,ANAPC2,TGFBR3,ERBB4,TWF2,UNC13A	yellow	VSMC_M3
GO:0010883	0.15	0.94	5	41	regulation of lipid storage	BP	1	SREBF2,PPARD,ZC3H12A,SCARB1,ALKBH7	yellow	VSMC_M3
GO:0045738	0.15	0.95	4	31	negative regulation of DNA repair	BP	1	OGG1,OTUB1,MAD2L2,CXorf57	yellow	VSMC_M3
GO:1901575	0.15	0.87	124	1628	organic substance catabolic process	BP	1	ENPP1,CDK4,SQSTM1,BAG6,SNX9,ACAT2,HNRNPA0,SGSM3,NUDT3,PPARD,MPST,SHARPIN,VPS28,SND1,CUL7,DNPH1,SECISBP2,HSPBP1,SOCS5,CNOT3,PSMB3,ZC3H12A,BLVRA,CPT1C,RCN3,SNRNP70,SNX3,MGLL,TMUB1,PAFAH1B3,SNX17,GALK1,PLCD1,BCKDHA,BLVRB,OGG1,PSMC4,SEL1L2,METTL3,DND1,SMOX,GNPDA1,SMUG1,OGDHL,SCARB1,HM13,PDE4D,PCCB,LSM6,PDE3B,WNT10B,PACSIN3,CCAR2,PCBP4,RNF19B,DCPS,SELENOS,ETFBKMT,MANBA,ZCCHC17,GPX1,PCK2,ASB9,PSME2,ANPEP,ADRM1,PSMB4,PTPN23,RNASEH2C,KAT5,RELA,IDH1,SGPL1,BAD,PLCB3,MRTO4,MVB12A,UBXN1,CNP,CCDC22,USP27X,GLUD1,FOXK1,ILVBL,CAPN2,AMER1,MAD2L2,NANOS3,FBXL19,DFFA,PGD,SNF8,TRIM25,USP43,ANKRD9,AKT1,PAIP1,KHSRP,PGM1,GIT1,CARHSP1,BLMH,SIRT6,ANAPC2,SPSB3,MAN1B1,JMJD8,SLC27A4,ZNRF1,PSMB10,CTRL,RBM8A,RNH1,PLA2G4E,NT5C,TENT5B,TRIB2,CDC34,FBXO6,GBA2,TRIR,STUB1,ITPA,CCDC115	yellow	VSMC_M3
GO:1901992	0.15	0.92	8	73	positive regulation of mitotic cell cycle phase transition	BP	1	CDK4,KMT2E,WNT10B,PBX1,PHB2,RCC2,AKT1,MIR214	yellow	VSMC_M3
GO:0140053	0.15	0.91	11	101	mitochondrial gene expression	BP	1	MRPS18A,AARS2,PUS1,GATB,MRPL43,TACO1,CHCHD10,MPV17L2,C1QBP,TUFM,MRPS16	yellow	VSMC_M3
GO:0097191	0.15	0.90	16	173	extrinsic apoptotic signaling pathway	BP	1	KRT8,DELE1,BCL2L1,CX3CL1,ITPRIP,GPX1,RELA,ZDHHC3,BAD,LGALS3,TNFRSF1A,ARHGEF2,AKT1,MKNK2,TRADD,TNFRSF12A	yellow	VSMC_M3
GO:0050819	0.15	0.94	5	38	negative regulation of coagulation	BP	1	PDGFRA,ANXA5,PDGFA,CD9,PLAU	yellow	VSMC_M3
GO:0061180	0.15	0.93	6	58	mammary gland epithelium development	BP	1	SCRIB,DEAF1,GPX1,PHB2,AKT1,ERBB4	yellow	VSMC_M3
GO:0062125	0.15	0.95	4	27	regulation of mitochondrial gene expression	BP	1	TACO1,CHCHD10,MPV17L2,C1QBP	yellow	VSMC_M3

GO:0019915	0.15	0.93	7	65	lipid storage	BP	1	ENPP1,SREBF2,SQLE,PPARD,ZC3H12A,SCARB1,ALKBH7	yellow	VSMC_M3
GO:0030574	0.15	0.95	4	31	collagen catabolic process	BP	1	PEPD,MMP24,MMP14,MRC2	yellow	VSMC_M3
GO:0042326	0.15	0.89	26	311	negative regulation of phosphorylation	BP	1	ENPP1,CTDSP2,H2AFY,PLEC,SOCS5,SPRED2,ZC3H12A,MICAL1,EMILIN1,TARBP2,PDE4D,GREM1,CHP1,QARS,TRIM27,CTDSP1,WASHC1,PKN1,PIP4K2B,MVP,CSK,AKT1,GIT1,CACTIN,MIDN,TRIB2	yellow	VSMC_M3
GO:1901988	0.15	0.90	18	201	negative regulation of cell cycle phase transition	BP	1	CTDSP2,H2AFY,KLF4,PINX1,CCAR2,CDK2AP2,PRMT2,THOC5,CTDSP1,METTL13,BABAM1,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,NABP2,FBXO6	yellow	VSMC_M3
GO:0031109	0.15	0.92	10	109	microtubule polymerization or depolymerization	BP	1	NUMA1,CCDC57,DCTN1,STMN3,MID1IP1,ARHGEF2,RANGRF,GIT1,GBA2,TUBGCP2	yellow	VSMC_M3
GO:0030098	0.15	0.90	22	259	lymphocyte differentiation	BP	1	NCAPH2,FNIP1,LGALS1,SOCS5,ZC3H12A,RELB,CD79A,METTL3,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,RIPK3,SART1,PBX1,BAD,ARMC5,DOCK11,AP3D1,STK11	yellow	VSMC_M3
GO:0072583	0.15	0.94	5	46	clathrin-dependent endocytosis	BP	1	SIGLEC1,AP2A2,TNK2,FCHO1,CLTB	yellow	VSMC_M3
GO:0072659	0.15	0.90	20	239	protein localization to plasma membrane	BP	1	SQSTM1,PACSIN1,SCRIB,TTC7A,TPBG,EHD2,SLC9A3R1,BCL2L1,PLEKHF1,TSPAN5,MMP14,ZDHHC3,LGALS3,TNFRSF1A,RANGRF,CSK,AKT1,PACS2,RAB34,ARFRP1	yellow	VSMC_M3
GO:0019438	0.15	0.86	210	2902	aromatic compound biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,TSTA3,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,CXXC5,GNPDA1,DEAF1,HOXC4,POLR1D,KMT2B,NAT10,ZNF740,RALY,ACSL1,ZBTB38,SLC11A2,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,NPM3,KDM1B,CHCHD2,AK2,IRX1,RRP1B,BRD9,PAPSS1,AIP,SRRD,TSHZ2,QARS,IMPDH2,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,PSTK,SMARCD2,BRMS1,PPOX,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ATP5MC3,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,SLC25A39,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,FLAD1,IRF2BPL,TRIM25,ATP5PD,USP43,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,CTNS,EHMT1,AP3D1,IRAK1,MBD3,ATP5F1D,TELO2,TAZ,MED16,CARD9,AMPD2,SARS,APRT,GTF3C5,AK1,TRADD,RF00024,ERBB4,JUND,PTMA,KLF13,FADS1,ZNF783,HOXC5,CAVIN1,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,SNAPC2,ZSCAN1	yellow	VSMC_M3
GO:1902533	0.16	0.88	57	731	positive regulation of intracellular signal transduction	BP	1	NELFE,FNIP1,PRR5,PPARD,EEF1D,LGALS1,SHARPIN,PDGFRA,TPBG,SPRED2,ZC3H12A,SLC9A3R1,SEC13,CXXC5,LAMTOR1,CAVIN3,PLEKHF1,GREM1,CX3CL1,SOD1,CCAR2,PDGFA,GPX1,TRIM27,RIPK3,RELA,RHOC,MAP3K14,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,TNFRSF1A,C1QBP,CHERP,CCDC22,TRIM25,RPL37,S100A4,CSK,MID2,MYDGF,MAP2K2,HIC1,CTNS,IRAK1,TELO2,WDR24,JMJD8,CARD9,TRADD,NDST1,ERBB4,IGFBP6,ZNF385A,GLIPR2	yellow	VSMC_M3
GO:0046148	0.16	0.93	6	52	pigment biosynthetic process	BP	1	SLC11A2,SRRD,PPOX,SLC25A39,CTNS,APRT	yellow	VSMC_M3
GO:0035904	0.16	0.94	5	50	aorta development	BP	1	PLXND1,SNX17,DLL4,NDST1,LOXL1	yellow	VSMC_M3
GO:0032535	0.16	0.89	26	325	regulation of cellular component size	BP	1	CDK4,SNX9,DBNL,SLC9A3R1,BAIAP2,SWAP70,CAPG,RIN3,CORO1B,TRIM27,ARPIN,LIMK1,LAMTOR4,ARPC1B,WASHC1,DBN1,CRABP2,CORO1A,AKT1,ANAPC2,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0046386	0.16	0.94	4	27	deoxyribose phosphate catabolic process	BP	1	DNPH1,OGG1,SMUG1,NT5C	yellow	VSMC_M3
GO:0060966	0.16	0.94	5	42	regulation of gene silencing by RNA	BP	1	ZC3H12A,DND1,TARBP2,LIMD1,MAP2K2	yellow	VSMC_M3
GO:0090277	0.16	0.92	7	65	positive regulation of peptide hormone secretion	BP	1	PPARD,MYRIP,AACS,PCK2,CAPN10,BAD,GLUD1	yellow	VSMC_M3
GO:0006356	0.16	0.94	4	31	regulation of transcription by RNA polymerase I	BP	1	H2AFY,SMARCB1,UBTF,SMARCA4	yellow	VSMC_M3
GO:0009059	0.16	0.86	258	3569	macromolecule biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,EEF1D,RPL3,RPL8,SND1,B4GALT1,MRPS18A,AARS2,PIGO,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,SERP2,DMAP1,CIC,GTF3C2,UNK,GALNT14,OGG1,SERTAD1,TTC5,METTL3,PHLDA1,CXXC5,DND1,RPL29,EIF4EBP1,DEAF1,HOXC4,POLR1D,TARBP2,KMT2B,NAT10,ZNF740,EIF4B,RALY,ZBTB38,TNKS1BP1,PINX1,GATB,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,MRPL43,YAF2,HTATIP2,PCIF1,NPM3,KDM1B,CHCHD2,SLC35C2,CARS,ST3GAL4,DCPS,IRX1,SELENOS,RRP1B,TMTC1,BRD9,APEH,AIP,NGDN,TSHZ2,QARS,PIR,TRIM27,EIF3A,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,PSTK,RPS21,SMARCD2,EXTL1,BRMS1,TACO1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,LRWD1,ARNT2,MRPL49,ZFPL1,LIMD1,ZDHHC3,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,SDE2,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,MPDU1,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,DPM3,FARSA,IRF2BPL,TUFM,TRIM25,USP43,RPL37,SMARCA4,CARM1,RPL7A,EEF2K,AATF,MRPL4,EIF3G,C19orf66,MID2,ZNF521,ZNF358,ZNF830,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MRPL20,TRAP1,MNT,EHMT1,AP3D1,MKNK	yellow	VSMC_M3
GO:0007281	0.16	0.90	16	177	germ cell development	BP	1	SBF1,SIX5,METTL3,CEP131,DND1,YIF1B,DEAF1,BCL2L1,SLC26A6,IQCG,PLA2G3,NANOS3,ZNF830,AKT1,RFX2,MEIG1	yellow	VSMC_M3

GO:0009145	0.16	0.93	6	47	purine nucleoside triphosphate biosynthetic process	BP	1	IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ	yellow	VSMC_M3
GO:0003176	0.16	0.94	4	34	aortic valve development	BP	1	EMILIN1,DLL4,TNFRSF1A,ELN	yellow	VSMC_M3
GO:0006790	0.16	0.89	24	270	sulfur compound metabolic process	BP	1	ENPP1,MPST,MICAL1,FASN,GSR,ACSL1,SOD1,ST3GAL4,GSTO1,MVK,PAPSS1,GPX1,IDH1,ACLY,MTHFR,ACSF2,PMVK,HMGCS1,BLMH,CTNS,NUBP2,MVD,NDST1,EEF1G	yellow	VSMC_M3
GO:0032496	0.16	0.89	20	225	response to lipopolysaccharide	BP	1	CDK4,HNRNPA0,PPARD,ZC3H12A,SCARB1,CX3CL1,SELENOS,PABPN1,PCK2,RELA,CNP,CAPN2,PALM3,AKT1,GIT1,LDOC1,CACTIN,IRAK1,JUND,LOXL1	yellow	VSMC_M3
GO:0033108	0.16	0.91	10	83	mitochondrial respiratory chain complex assembly	BP	1	SAMM50,NDUFB9,ACAD9,SDHAF1,UQCRFS1,TACO1,UQCC3,NDUFS7,TAZ,SURF1	yellow	VSMC_M3
GO:0071320	0.16	0.94	4	37	cellular response to cAMP	BP	1	WNT10B,SLC26A6,IGFBP5,EEF2K	yellow	VSMC_M3
GO:1903320	0.16	0.89	19	211	regulation of protein modification by small protein conjugation or removal	BP	1	SQSTM1,VPS28,HSPBP1,ZC3H12A,PINX1,CHP1,LIMK1,RELA,OTUB1,AIMP2,UBXN1,WASHC1,AMER1,MAD2L2,RPL37,AKT1,HMG20B,STUB1,NSMCE3	yellow	VSMC_M3
GO:0051090	0.16	0.88	27	328	regulation of DNA-binding transcription factor activity	BP	1	ENPP1,TRAPPC9,KLF4,ZC3H12A,GREM1,CX3CL1,WNT10B,CHP1,TRIM27,PRMT2,RIPK3,BRMS1,RELA,SMARCB1,PHB2,BUD31,CCDC22,MAD2L2,ARHGEF2,TRIM25,SMARCA4,MID2,AKT1,CACTIN,IRAK1,CARD9,TRADD	yellow	VSMC_M3
GO:0019692	0.16	0.93	5	37	deoxyribose phosphate metabolic process	BP	1	GUK1,DNPH1,OGG1,SMUG1,NT5C	yellow	VSMC_M3
GO:0018022	0.16	0.91	10	108	peptidyl-lysine methylation	BP	1	NELFE,H2AFY,KMT2E,KMT2B,SETD1B,ETFBKMT,SMARCB1,TRMT112,METTL22,EHMT1	yellow	VSMC_M3
GO:0090305	0.16	0.89	19	213	nucleic acid phosphodiester bond hydrolysis	BP	1	ENPP1,NHP2,BOP1,SND1,ZC3H12A,PNKP,OGG1,C12orf10,RRS1,DCPS,ZNRD1,KHNYN,RPS21,NOP14,CSTF2T,DFFA,SLX1A,TBL3,TRIR	yellow	VSMC_M3
GO:0060337	0.16	0.93	5	41	type I interferon signaling pathway	BP	1	TTLL12,METTL3,CDC37,CACTIN,IRAK1	yellow	VSMC_M3
GO:0032720	0.16	0.93	5	41	negative regulation of tumor necrosis factor production	BP	1	ZC3H12A,CX3CL1,SELENOS,TRIM27,CACTIN	yellow	VSMC_M3
GO:0051651	0.16	0.90	14	163	maintenance of location in cell	BP	1	ITPR3,SLC30A3,INSIG1,PDE4D,CX3CL1,GSTO1,CHCHD10,LETM1,CHERP,DBN1,CORO1A,AKT1,AP3D1,TWF2	yellow	VSMC_M3
GO:0034654	0.16	0.86	205	2841	nucleobase-containing compound biosynthetic process	BP	1	ENPP1,NAB2,NHP2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,GUK1,TRAPPC9,PPARD,TSTA3,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,CXXC5,GNPDA1,DEAF1,HOXC4,POLR1D,KMT2B,NAT10,ZNF740,RALY,ACSL1,ZBTB38,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,NPM3,KDM1B,CHCHD2,AK2,IRX1,RRP1B,BRD9,PAPSS1,AIP,TSHZ2,QARS,IMPDH2,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,PSTK,SMARCD2,BRMS1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ATP5MC3,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,ATIC,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,UQCC3,MTA2,ZNF316,ACLY,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,FLAD1,IRF2BPL,TRIM25,ATP5PD,USP43,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,ATP5F1D,TELO2,TAZ,MED16,CARD9,AMPD2,SARS,APRT,GTF3C5,AK1,TRADD,RF00024,ERBB4,JUND,PTMA,KLF13,FADS1,ZNF783,HOXC5,CAVIN1,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,SNAPC2,ZSCAN1	yellow	VSMC_M3
GO:1902893	0.17	0.93	5	47	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SREBF2,PPARD,KLF4,RELA,SMARCA4	yellow	VSMC_M3
GO:0060271	0.17	0.89	22	266	cilium assembly	BP	1	SPAG1,TXNDC15,WDPCP,EHD2,SEPT9,CEP131,YIF1B,CCDC57,DCTN1,CCDC28B,PCNT,IQCG,PLA2G3,CEP164,PTPN23,RABEP2,ATG3,TTC39C,RFX2,GAS8,WDR34,MEIG1	yellow	VSMC_M3
GO:0072329	0.17	0.91	10	95	monocarboxylic acid catabolic process	BP	1	ACAT2,PPARD,CPT1C,PCCB,ETFBKMT,PCK2,ILVBL,PGD,AKT1,SLC27A4	yellow	VSMC_M3
GO:0046902	0.17	0.92	6	50	regulation of mitochondrial membrane permeability	BP	1	BCL2L1,CHCHD10,BAD,CNP,ALKBH7,SPG7	yellow	VSMC_M3
GO:0032963	0.17	0.91	8	78	collagen metabolic process	BP	1	PPARD,RCN3,EMILIN1,TNS2,PEPD,MMP24,MMP14,MRC2	yellow	VSMC_M3
GO:0070227	0.17	0.92	6	52	lymphocyte apoptotic process	BP	1	FNIP1,RIPK3,LGALS3,PKN1,DFFA,AKT1	yellow	VSMC_M3
GO:0007015	0.17	0.88	29	373	actin filament organization	BP	1	SNX9,PACSIN1,PLEC,DBNL,ZYX,MICAL1,BAIAP2,INPPL1,SWAP70,CAPG,CX3CL1,CORO1B,TRIM27,ARPIN,LIMK1,RHOC,ARPC1B,WASHC1,DBN1,MAD2L2,ARHGEF2,CORO1A,MYO19,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0035315	0.17	0.94	4	34	hair cell differentiation	BP	1	SCRIB,WDPCP,SLC9A3R1,SOD1	yellow	VSMC_M3
GO:0010569	0.17	0.93	5	43	regulation of double-strand break repair via homologous recombination	BP	1	FIGNL1,MAD2L2,PPP4C,CXorf57,SIRT6	yellow	VSMC_M3
GO:0000768	0.17	0.94	4	34	syncytium formation by plasma membrane fusion	BP	1	EHD2,PLEKHO1,CD9,CAPN2	yellow	VSMC_M3
GO:0140253	0.17	0.94	4	34	cell-cell fusion	BP	1	EHD2,PLEKHO1,CD9,CAPN2	yellow	VSMC_M3
GO:0002183	0.17	0.94	4	30	cytoplasmic translational initiation	BP	1	METTL3,EIF4B,EIF3A,EIF3G	yellow	VSMC_M3
GO:0042073	0.17	0.94	4	34	intraciliary transport	BP	1	IFT27,CEP131,SSNA1,WDR34	yellow	VSMC_M3
GO:2001237	0.17	0.91	8	79	negative regulation of extrinsic apoptotic signaling pathway	BP	1	BCL2L1,CX3CL1,ITPRIP,GPX1,RELA,LGALS3,ARHGEF2,AKT1	yellow	VSMC_M3

GO:0023056	0.17	0.86	93	1258	positive regulation of signaling	BP	1	CD63,SQSTM1,NELFE,FNIP1,PRR5,TXNDC15,ITPR3,PPARD,EEF1D,SCRIB,LGALS1,SHARPIN,PDGFRA,IL1R1,TPBG,SPRED2,ZC3H12A,PLEKHA4,SLC9A3R1,RNF220,MYRIP,SEC13,BAIAP2,CXXC5,LAMTOR1,NUMA1,CAVIN3,AACS,PLEKHF1,GREM1,RAPSN,CX3CL1,WNT10B,SOD1,CCAR2,DLL4,SLC35C2,TSPAN5,PDGFA,GPX1,SYT12,PCK2,TRIM27,RIPK3,CAPN10,PLA2G3,PTPN23,RELA,RHOC,MAP3K14,ZDHHC3,SMARCB1,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,TNFRSF1A,C1QBP,CHERP,EVC,CCDC22,GLUD1,AMER1,TRIM25,RPL37,S100A4,SMARCA4,CSK,MID2,TEDC1,RAB34,MYDGF,MAP2K2,HIC1,CTNS,TEDC2,CSNK1G2,IRAK1,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,TGFBR3,TRADD,NDST1,TNFRSF12A,ERBB4,IGFBP6,ZNF385A,GLIPR2	yellow	VSMC_M3
GO:0072522	0.17	0.89	15	157	purine-containing compound biosynthetic process	BP	1	GUK1,ACSL1,AK2,PAPSS1,IMPDH2,ATP5MC3,ATIC,UQCC3,ACLY,ATP5PD,ATP5F1D,TAZ,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:0002793	0.17	0.92	7	66	positive regulation of peptide secretion	BP	1	PPARD,MYRIP,AACS,PCK2,CAPN10,BAD,GLUD1	yellow	VSMC_M3
GO:0045333	0.17	0.89	19	191	cellular respiration	BP	1	NDUFB9,PLEC,IDH3B,OGDHL,UQCRFS1,CHCHD2,SDHA,NDUFV1,UQCRC1,IDH1,CHCHD10,UQCC3,ATP5PD,AKT1,TRAP1,NDUFS7,ATP5F1D,TAZ,SURF1	yellow	VSMC_M3
GO:0014066	0.17	0.91	8	86	regulation of phosphatidylinositol 3-kinase signaling	BP	1	PRR5,PPARD,PDGFRA,KLF4,SLC9A3R1,PDGFA,MYDGF,ERBB4	yellow	VSMC_M3
GO:0030488	0.17	0.93	5	39	tRNA methylation	BP	1	TRMT12,WDR4,TRMT112,GTPBP3,TRMT1	yellow	VSMC_M3
GO:2000134	0.17	0.92	6	56	negative regulation of G1/S transition of mitotic cell cycle	BP	1	CTDSP2,KLF4,CDK2AP2,PRMT2,CTDSP1,SDE2	yellow	VSMC_M3
GO:0009262	0.17	0.93	5	38	deoxyribonucleotide metabolic process	BP	1	GUK1,DNPH1,OGG1,SMUG1,NT5C	yellow	VSMC_M3
GO:0022412	0.17	0.88	21	247	cellular process involved in reproduction in multicellular organism	BP	1	NCAPH2,SBF1,FIGNL1,SIX5,METTL3,CEP131,DND1,YIF1B,DEAF1,BCL2L1,KDM1B,SLC26A6,IQCG,PLA2G3,CD9,NANOS3,ZNF830,AKT1,RFX2,TAZ,MEIG1	yellow	VSMC_M3
GO:0051817	0.17	0.91	7	67	modulation of process of other organism involved in symbiotic interaction	BP	1	ZC3H12A,BCL2L1,RRP1B,SMARCB1,PHB2,SMARCA4,CARD9	yellow	VSMC_M3
GO:0009636	0.17	0.89	16	174	response to toxic substance	BP	1	CDK4,MPST,GSR,ARHGAP33,SOD1,SRSF9,SELENOS,GSTO1,GPX1,MGST3,TXNRD2,CNP,PRXL2A,SLC6A4,BLMH,EHMT1	yellow	VSMC_M3
GO:0030433	0.17	0.91	8	78	ubiquitin-dependent ERAD pathway	BP	1	BAG6,TMUB1,SEL1L2,SELENOS,TRIM25,MAN1B1,FBXO6,STUB1	yellow	VSMC_M3
GO:0051348	0.17	0.88	19	219	negative regulation of transferase activity	BP	1	H2AFY,PLEC,SOCS5,TARBP2,PINX1,CHP1,QARS,TRIM27,LIMK1,WASHC1,PKN1,PIP4K2B,MAD2L2,MVP,RPL37,CSK,AKT1,MIDN,TRIB2	yellow	VSMC_M3
GO:0032200	0.17	0.90	12	130	telomere organization	BP	1	NHP2,PNKP,H3F3B,NAT10,TNKS1BP1,PINX1,H3F3A,SLX1A,SIRT6,TELO2,RF00024,NABP2	yellow	VSMC_M3
GO:0060976	0.18	0.93	4	39	coronary vasculature development	BP	1	PLXND1,SNX17,TGFBR3,NDST1	yellow	VSMC_M3
GO:2000113	0.18	0.85	85	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	ENPP1,NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,TRIM11,PPARD,CNOT3,KLF4,ZC3H12A,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,UNK,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,NAT10,ZBTB38,PINX1,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,PCIF1,KDM1B,DCPS,IRX1,SELENOS,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,IGFBP5,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,NANOS3,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,AATF,C19orf66,ZNF830,KHSRP,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0061028	0.18	0.93	4	38	establishment of endothelial barrier	BP	1	FASN,PDE4D,TNFRSF1A,TJP3	yellow	VSMC_M3
GO:0071357	0.18	0.92	5	42	cellular response to type I interferon	BP	1	TTLL12,METTL3,CDC37,CACTIN,IRAK1	yellow	VSMC_M3
GO:0048066	0.18	0.93	4	32	developmental pigmentation	BP	1	ENPP1,CD63,AP1M1,AP3D1	yellow	VSMC_M3
GO:0061614	0.18	0.92	5	48	pri-miRNA transcription by RNA polymerase II	BP	1	SREBF2,PPARD,KLF4,RELA,SMARCA4	yellow	VSMC_M3
GO:0043254	0.18	0.87	29	361	regulation of protein-containing complex assembly	BP	1	SNX9,FNIP1,DBNL,BAIAP2,NUMA1,EIF4EBP1,CAPG,DCTN1,WNT10B,CORO1B,TRIM27,ARPIN,RHOC,PEX5,LGALS3,ARPC1B,WASHC1,DBN1,RANGRF,CORO1A,GIT1,NCLN,MIR214,TWF2,ELN,CDC42EP5,GBA2,STUB1,ARPC5L	yellow	VSMC_M3
GO:0031327	0.18	0.85	89	1198	negative regulation of cellular biosynthetic process	BP	1	ENPP1,NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,TRIM11,PPARD,CNOT3,KLF4,ZC3H12A,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,UNK,INSIG1,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,NAT10,ZBTB38,PINX1,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,PCIF1,KDM1B,DCPS,IRX1,SELENOS,PDGFA,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,IGFBP5,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,NANOS3,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,AATF,C19orf66,ZNF830,KHSRP,SIRT6,HIC1,MNT,CTNS,EHMT1,PGP,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0032527	0.18	0.92	5	43	protein exit from endoplasmic reticulum	BP	1	INSIG1,SEC13,HM13,SELENOS,RANGRF	yellow	VSMC_M3
GO:0006805	0.18	0.92	5	41	xenobiotic metabolic process	BP	1	GUK1,SMOX,ACSL1,GSTO1,AIP	yellow	VSMC_M3
GO:1901991	0.18	0.89	13	142	negative regulation of mitotic cell cycle phase transition	BP	1	CTDSP2,KLF4,PINX1,CDK2AP2,PRMT2,CTDSP1,BABAM1,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,NABP2	yellow	VSMC_M3
GO:0046434	0.18	0.89	12	126	organophosphate catabolic process	BP	1	ENPP1,NUDT3,DNPH1,OGG1,SMUG1,SCARB1,PDE4D,IDH1,CNP,PLA2G4E,NT5C,ITPA	yellow	VSMC_M3
GO:0006754	0.18	0.92	5	39	ATP biosynthetic process	BP	1	ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ	yellow	VSMC_M3
GO:1902895	0.18	0.93	4	37	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SREBF2,KLF4,RELA,SMARCA4	yellow	VSMC_M3
GO:1902041	0.18	0.92	5	42	regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	1	BCL2L1,ITPRIP,GPX1,LGALS3,ARHGEF2	yellow	VSMC_M3
GO:0009062	0.18	0.90	9	86	fatty acid catabolic process	BP	1	ACAT2,PPARD,CPT1C,PCCB,ETFBKMT,PCK2,ILVBL,AKT1,SLC27A4	yellow	VSMC_M3
GO:1903432	0.18	0.93	4	32	regulation of TORC1 signaling	BP	1	SEC13,CTNS,STK11,TELO2	yellow	VSMC_M3
GO:0060999	0.19	0.93	4	38	positive regulation of dendritic spine development	BP	1	DBNL,BAIAP2,DBN1,EEF2K	yellow	VSMC_M3
GO:0006949	0.19	0.93	4	35	syncytium formation	BP	1	EHD2,PLEKHO1,CD9,CAPN2	yellow	VSMC_M3
GO:0014910	0.19	0.91	6	60	regulation of smooth muscle cell migration	BP	1	PPARD,PDGFA,CORO1B,IGFBP5,PLAU,MIR214	yellow	VSMC_M3

GO:0010647	0.19	0.84	92	1251	positive regulation of cell communication	BP	1	CD63,SQSTM1,NELFE,FNIP1,PRR5,TXNDC15,ITPR3,PPARD,EEF1D,LGALS1,SHARPIN,PDGFRA,IL1R1,TPBG,SPRED2,ZC3H12A,PLEKHA4,SLC9A3R1,RNF220,MYRIP,SEC13,BAIAP2,CXXC5,LAMTOR1,NUMA1,CAVIN3,AACS,PLEKHF1,GREM1,RAPSN,CX3CL1,WNT10B,SOD1,CCAR2,DLL4,SLC35C2,TSPAN5,PDGFA,GPX1,SYT12,PCK2,TRIM27,RIPK3,CAPN10,PLA2G3,PTPN23,RELA,RHOC,MAP3K14,ZDHHC3,SMARCB1,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,TNFRSF1A,C1QBP,CHERP,EVC,CCDC22,GLUD1,AMER1,TRIM25,RPL37,S100A4,SMARCA4,CSK,MID2,TEDC1,RAB34,MYDGF,MAP2K2,HIC1,CTNS,TEDC2,CSNK1G2,IRAK1,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,TGFBR3,TRADD,NDST1,TNFRSF12A,ERBB4,IGFBP6,ZNF385A,GLIPR2	yellow	VSMC_M3
GO:0097193	0.19	0.87	21	242	intrinsic apoptotic signaling pathway	BP	1	BAG6,FIGNL1,SLC9A3R1,P4HB,BCL2L1,PLEKHF1,SOD1,CCAR2,SELENOS,GPX1,RIPK3,ZNF385B,BAD,TNFRSF1A,ARHGEF2,AKT1,HIC1,TRAP1,STK11,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0044419	0.19	0.84	73	948	biological process involved in interspecies interaction between organisms	BP	1	CDK4,TTLL12,HNRNPA0,TRIM11,PPARD,LGALS1,SLC52A2,PPP1R14B,SSC5D,ZC3H12A,ZYX,SNX3,KRT8,RELB,METTL3,BAIAP2,P4HB,RAB20,SIGLEC1,TARBP2,SCARB1,BCL2L1,ITGB7,CX3CL1,TYRO3,RNF19B,SELENOS,RRP1B,PABPN1,GPX1,PCK2,NECTIN1,ANPEP,TRIM27,SLC26A6,THOC5,RIPK3,TNK2,BANF1,RELA,MAP3K14,SMARCB1,THOC3,PHB2,IFI35,LGALS3,TNFRSF1A,C1QBP,CNP,CAPN2,PALM3,TBKBP1,ARHGEF2,ARMC5,CORO1A,TRIM25,SMARCA4,CDC37,C19orf66,MID2,AKT1,GTF2F1,GIT1,LDOC1,CACTIN,CLDN6,IRAK1,C8G,CARD9,JUND,LOXL1,EEF1G,JAGN1	yellow	VSMC_M3
GO:0080164	0.19	0.92	5	45	regulation of nitric oxide metabolic process	BP	1	KLF4,ZC3H12A,SELENOS,AKT1,KHSRP	yellow	VSMC_M3
GO:0001558	0.19	0.86	27	339	regulation of cell growth	BP	1	ENPP1,PPARD,DNPH1,DBNL,H3F3B,LAMTOR1,GREM1,KDM2B,CCAR2,CISH,MMP14,LIMK1,CCDC85B,SIPA1,IGFBP5,H3F3A,DBN1,MAD2L2,CRABP2,SMARCA4,AKT1,HDGFL2,CDK11B,ANAPC2,STK11,TWF2,UNC13A	yellow	VSMC_M3
GO:0070988	0.19	0.92	5	52	demethylation	BP	1	PHF2,KDM2B,KDM1B,ALKBH4,FBXL19	yellow	VSMC_M3
GO:0007162	0.19	0.87	18	215	negative regulation of cell adhesion	BP	1	SCRIB,LGALS1,SOCS5,KLF4,ZC3H12A,PLXND1,METTL3,SWAP70,PDE3B,CX3CL1,MMP14,SIPA1,LGALS3,CD9,RCC2,MAD1L1,MAD2L2,AKT1	yellow	VSMC_M3
GO:0031113	0.19	0.92	5	49	regulation of microtubule polymerization	BP	1	NUMA1,DCTN1,RANGRF,GIT1,GBA2	yellow	VSMC_M3
GO:0010558	0.19	0.84	85	1150	negative regulation of macromolecule biosynthetic process	BP	1	ENPP1,NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,TRIM11,PPARD,CNOT3,KLF4,ZC3H12A,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,UNK,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,NAT10,ZBTB38,PINX1,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,PCIF1,KDM1B,DCPS,IRX1,SELENOS,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,IGFBP5,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,NANOS3,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,AATF,C19orf66,ZNF830,KHSRP,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0030031	0.19	0.86	34	443	cell projection assembly	BP	1	SPAG1,TXNDC15,DBNL,WDPCP,EMP3,EHD2,SLC9A3R1,SEPT9,CEP131,INPPL1,YIF1B,CCDC57,CAPG,DCTN1,CCDC28B,PDGFA,PCNT,IQCG,PLA2G3,CEP164,PTPN23,WASHC1,RCC2,RABEP2,ATG3,TTC39C,DOCK11,RFX2,GAS8,WDR34,MIR214,TWF2,CDC42EP5,MEIG1	yellow	VSMC_M3
GO:0006996	0.19	0.83	209	2943	organelle organization	BP	1	ESYT1,DCTN2,NHP2,SQSTM1,SPAG1,BAG6,NCAPH2,SNX9,HDAC10,PDLIM4,SAMM50,SREBF2,NDUFB9,SQLE,TXNDC15,H2AFY,PACSIN1,RPL3,PLEC,IFT27,SHARPIN,BOP1,VPS28,CUL7,PDGFRA,PHF2,ASNA1,DBNL,WDPCP,FHL3,FIGNL1,PNKP,ZYX,SNX3,MICAL1,EHD2,KMT2E,KRT8,ACAD9,TMEM43,SLC9A3R1,DMAP1,H3F3B,INSIG1,SEC13,SEPT9,BAIAP2,CEP131,INPPL1,LAMTOR1,NUMA1,YIF1B,CCDC57,RAB20,ARAP3,CAVIN3,SDHAF1,NAT10,BCL2L1,SPRYD3,RRS1,SWAP70,PLEKHF1,UQCRFS1,CAPG,TNKS1BP1,PINX1,DCTN1,CX3CL1,SOD1,PACSIN3,ACTR5,CCDC32,CCAR2,HPS1,CHP1,NPM3,CHCHD2,CCDC28B,BRD9,PDGFA,CDK2AP2,GPX1,AIP,CORO1B,LRFN4,CLIP2,TRIM27,ARPIN,PCNT,LIMK1,NUDC,CAPN10,SMARCD2,IQCG,PFDN2,BUD23,TACO1,PLA2G3,STMN3,CEP164,BANF1,PTPN23,RELA,SIPA1,RHOC,LRWD1,ALKBH4,ZNHIT1,FMNL1,VPS51,SAC3D1,LIMD1,MID1IP1,PEX5,SMARCB1,CHCHD10,BLOC1S4,PHB2,NDP,BAD,MPV17L2,LETM1,ARPC1B,MRTO4,MVB12A,KIAA0753,BABAM1,C1QBP,TAF6L,UQCC3,WASHC1,CNP,AP1M1,EML3,MTA2,H3F3A,DBN1,CAPN2,LMAN2,MAD1L1,PIP4K2B,MAD2L2,FAM161B,ARHGEF2,SNF8,MTX1,RANGRF,STX10,CORO1A,SLX1A,RABEP2,SMARCA4,TMED1,SYNE3,CDC37,MYO19,EML1,ATG3,TTC39C,INF2,ZNF830,AKT1,PACS2,ALKBH7,RFX2,RAB34,SAFB,GIT1,SIRT6,PPL,MAP2K2,UBN1,HMG20B,MRPL20,AURKAIP1,EHMT1,AP3D1,SSNA1,MBD3,NDUFS7,ATP5F1D,TELO2,TAZ,FAM50A,GAS8,SPG7,NTMT1,WDR34,MIR214,RF00024,NABP2,ERBB4,TWF2,SURF1,MAP7D1,JAGN1,MIS12,ELN,UNC13A,CDC42EP5,GBA2,TUBGCP2,MEIG1,TIMM22,ITPA,PHETA2,CCDC115,ARPC5L	yellow	VSMC_M3
GO:0043124	0.19	0.93	4	34	negative regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	ZC3H12A,CCDC22,PER1,CACTIN	yellow	VSMC_M3
GO:0051493	0.19	0.86	34	457	regulation of cytoskeleton organization	BP	1	SNX9,PDGFRA,DBNL,BAIAP2,NUMA1,SWAP70,CAPG,DCTN1,CX3CL1,PDGFA,CDK2AP2,CORO1B,TRIM27,ARPIN,LIMK1,PFDN2,STMN3,RHOC,MID1IP1,ARPC1B,WASHC1,EML3,DBN1,CAPN2,ARHGEF2,RANGRF,CORO1A,GIT1,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:1905314	0.19	0.93	4	37	semi-lunar valve development	BP	1	EMILIN1,DLL4,TNFRSF1A,ELN	yellow	VSMC_M3

GO:0006793	0.19	0.83	157	2169	phosphorus metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,SBF1,SNX9,CERK,FNIP1,PRR5,H2AFY,GUK1,NUDT3,PPARD,TSTA3,PLEC,PPP1R14B,DNPH1,PIGO,PDGFRA,SOCS5,TTC7A,KLF4,SPRED2,ZC3H12A,PNKP,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SEPHS1,GALK1,PPM1G,PLCD1,OGG1,SERTAD1,INPPL1,PCYT2,FASN,GNPDA1,PTDSS2,SMUG1,OGDHL,TARBP2,SCARB1,PDE4D,TNS2,SWAP70,ACSL1,FDFT1,TNKS1BP1,GREM1,TKT,CX3CL1,SOD1,DGKZ,CHP1,TYRO3,HTATIP2,PPM1M,CISH,AK2,MVK,STK32C,FABP3,PAPSS1,PDGFA,MOCS3,CLCF1,QARS,IMPDH2,TRIM27,LIMK1,RIPK3,PSTK,TNK2,PLA2G3,PTPN23,ATP5MC3,SCYL1,IDH1,MEX3B,MAP3K14,LIMD1,ATIC,PHB2,PPP1R35,BAD,PLCB3,CTDSP1,ISYNA1,LGALS3,TNFRSF1A,ASMTL,UQCC3,WASHC1,CNP,ACLY,FOXK1,PKN1,CAPN2,PIP4K2B,MAD2L2,CTBP1,PGD,ARHGEF2,MVP,ACSF2,DPM3,PPP4C,FLAD1,PMVK,ATP5PD,MTMR4,HDHD2,EEF2K,CDC37,CSK,AKT1,HMGCS1,PGM1,SGK494,GIT1,MYDGF,MAP2K2,CACTIN,CDK11B,SSU72,PGP,MKNK2,CSNK1G2,IRAK1,MIDN,ATP5F1D,STK11,TELO2,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,SLC44A3,VAC14,TGFBR3,ERBB4,PTPRR,PLA2G4E,FADS1,NT5C,TRIB2,NSMF,TALDO1,DUSP5,FDPS,IDI1,ITPA	yellow	VSMC_M3
GO:0071887	0.19	0.90	8	79	leukocyte apoptotic process	BP	1	FNIP1,SELENOS,RIPK3,LGALS3,PKN1,DFFA,PLEKHO2,AKT1	yellow	VSMC_M3
GO:0009156	0.19	0.93	4	30	ribonucleoside monophosphate biosynthetic process	BP	1	IMPDH2,ATIC,AMPD2,APRT	yellow	VSMC_M3
GO:0046785	0.19	0.90	7	74	microtubule polymerization	BP	1	NUMA1,CCDC57,DCTN1,RANGRF,GIT1,GBA2,TUBGCP2	yellow	VSMC_M3
GO:1903556	0.19	0.92	5	43	negative regulation of tumor necrosis factor superfamily cytokine production	BP	1	ZC3H12A,CX3CL1,SELENOS,TRIM27,CACTIN	yellow	VSMC_M3
GO:0022407	0.19	0.86	24	293	regulation of cell-cell adhesion	BP	1	SCRIB,LGALS1,SOCS5,KLF4,ZC3H12A,METTL3,SWAP70,CX3CL1,EGR3,ST3GAL4,SART1,PTPN23,RELA,BAD,LGALS3,CD9,MAD1L1,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1,IRAK1	yellow	VSMC_M3
GO:0106027	0.19	0.90	7	78	neuron projection organization	BP	1	DBNL,BAIAP2,ARHGAP33,DCTN1,NGEF,DBN1,EEF2K	yellow	VSMC_M3
GO:0014902	0.19	0.90	8	86	myotube differentiation	BP	1	PLEC,EHD2,WNT10B,MMP14,GPX1,PLEKHO1,CD9,CAPN2	yellow	VSMC_M3
GO:0008585	0.19	0.90	7	72	female gonad development	BP	1	PDGFRA,BCL2L1,SOD1,MMP14,IDH1,SGPL1,ZNF830	yellow	VSMC_M3
GO:0072523	0.19	0.91	5	43	purine-containing compound catabolic process	BP	1	NUDT3,DNPH1,PDE4D,NT5C,ITPA	yellow	VSMC_M3
GO:0030855	0.20	0.85	33	430	epithelial cell differentiation	BP	1	H2AFY,SCRIB,PLEC,SHARPIN,DNPH1,B4GALT1,COL15A1,KLF4,WDPCP,CCM2,SPRED2,SLC9A3R1,NUMA1,FASN,PDE4D,GREM1,WNT10B,SOD1,GPX1,TAGLN2,PCK2,BAD,LGALS3,TNFRSF1A,AIMP2,KRT10,CASP14,TMEM79,AKT1,SAFB2,PPL,TJP3,ERBB4	yellow	VSMC_M3
GO:0030879	0.20	0.89	10	114	mammary gland development	BP	1	SCRIB,FASN,DEAF1,GPX1,PHB2,IGFBP5,MTX1,AKT1,APRT,ERBB4	yellow	VSMC_M3
GO:0050764	0.20	0.90	6	59	regulation of phagocytosis	BP	1	SNX3,SCARB1,SOD1,LMAN2,CSK,ATG3	yellow	VSMC_M3
GO:0007517	0.20	0.86	21	259	muscle organ development	BP	1	PLEC,COL19A1,FHL3,WNT10B,ANKRD2,EGR3,DLL4,GPX1,MEF2B,TEAD4,EVC,FOXK1,PRR14,COPRS,SIRT6,HMG20B,TAZ,GTF3C5,TGFBR3,IGSF8,ELN	yellow	VSMC_M3
GO:0010762	0.20	0.92	4	35	regulation of fibroblast migration	BP	1	WDPCP,RCC2,MTA2,AKT1	yellow	VSMC_M3
GO:1903201	0.20	0.90	6	56	regulation of oxidative stress-induced cell death	BP	1	P4HB,PYCR1,SOD1,GPX1,AKT1,TRAP1	yellow	VSMC_M3
GO:0009894	0.20	0.84	61	806	regulation of catabolic process	BP	1	CDK4,BAG6,SNX9,SREBF2,HNRNPA0,SGSM3,VPS28,SECISBP2,HSPBP1,SOCS5,CNOT3,ZC3H12A,SNRNP70,SNX3,PSMC4,METTL3,DND1,SCARB1,PLEKHF1,PDE3B,WNT10B,PACSIN3,CCAR2,PCBP4,RNF19B,DCPS,ETFBKMT,ZCCHC17,GPX1,ASB9,PSME2,TRIM27,KAT5,RELA,IDH1,PHB2,BAD,UBXN1,WASHC1,CCDC22,FOXK1,AMER1,PIP4K2B,MAD2L2,NANOS3,DFFA,SNF8,MTMR4,MID2,AKT1,PAIP1,KHSRP,GIT1,CARHSP1,SIRT6,STK11,WDR24,JMJD8,TENT5B,TRIB2,STUB1	yellow	VSMC_M3
GO:0006721	0.20	0.90	6	56	terpenoid metabolic process	BP	1	PPARD,FDFT1,LSS,CRABP2,HMGCS1,FDPS	yellow	VSMC_M3
GO:0033865	0.20	0.88	10	102	nucleoside bisphosphate metabolic process	BP	1	ENPP1,FASN,ACSL1,MVK,PAPSS1,ACLY,ACSF2,PMVK,HMGCS1,MVD	yellow	VSMC_M3
GO:0033875	0.20	0.88	10	102	ribonucleoside bisphosphate metabolic process	BP	1	ENPP1,FASN,ACSL1,MVK,PAPSS1,ACLY,ACSF2,PMVK,HMGCS1,MVD	yellow	VSMC_M3
GO:0034032	0.20	0.88	10	102	purine nucleoside bisphosphate metabolic process	BP	1	ENPP1,FASN,ACSL1,MVK,PAPSS1,ACLY,ACSF2,PMVK,HMGCS1,MVD	yellow	VSMC_M3
GO:0032006	0.20	0.89	8	84	regulation of TOR signaling	BP	1	FNIP1,SEC13,LAMTOR1,LAMTOR4,CTNS,STK11,TELO2,WDR24	yellow	VSMC_M3
GO:0072698	0.20	0.91	5	52	protein localization to microtubule cytoskeleton	BP	1	DCTN2,CEP131,NUMA1,KIAA0753,MID2	yellow	VSMC_M3
GO:0060968	0.20	0.90	6	59	regulation of gene silencing	BP	1	PHF2,ZC3H12A,DND1,TARBP2,LIMD1,MAP2K2	yellow	VSMC_M3
GO:0031396	0.20	0.87	16	180	regulation of protein ubiquitination	BP	1	SQSTM1,VPS28,HSPBP1,PINX1,CHP1,LIMK1,OTUB1,AIMP2,UBXN1,WASHC1,AMER1,MAD2L2,RPL37,AKT1,STUB1,NSMCE3	yellow	VSMC_M3
GO:1901989	0.20	0.89	9	91	positive regulation of cell cycle phase transition	BP	1	CDK4,KMT2E,WNT10B,THOC5,PBX1,PHB2,RCC2,AKT1,MIR214	yellow	VSMC_M3

GO:0009056	0.20	0.82	148	2000	catabolic process	BP	1	ENPP1,CDK4,SQSTM1,BAG6,SNX9,HDAC10,ACAT2,SREBF2,HNRNPA0,SGSM3,NUDT3,PPARD,MPST,SHARPIN,VPS28,SND1,CUL7,DNPH1,SECISBP2,HSPBP1,SOCS5,CNOT3,PSMB3,ZC3H12A,BLVRA,CPT1C,RCN3,SNRNP70,SNX3,MGLL,TMUB1,PAFAH1B3,SNX17,GALK1,PLCD1,BCKDHA,BLVRB,OGG1,PSMC4,SEL1L2,METTL3,DND1,SMOX,GNPDA1,SMUG1,OGDHL,SCARB1,HM13,PDE4D,PCCB,PEPD,PLEKHF1,ACSL1,LSM6,MMP24,PDE3B,WNT10B,PACSIN3,CCAR2,PCBP4,RNF19B,DCPS,SELENOS,GSTO1,ETFBKMT,MANBA,ZCCHC17,MMP14,LIX1L,GPX1,PCK2,ASB9,PSME2,ANPEP,TRIM27,ADRM1,PSMB4,PTPN23,MRC2,RNASEH2C,KAT5,RELA,IDH1,VPS51,SGPL1,PHB2,BAD,PLCB3,MRTO4,MVB12A,UBXN1,WASHC1,CNP,CCDC22,USP27X,GLUD1,FOXK1,ILVBL,CAPN2,RAB24,AMER1,PIP4K2B,MAD2L2,NANOS3,FBXL19,DFFA,PGD,SNF8,TRIM25,USP43,MTMR4,CDC37,MID2,ATG3,ANKRD9,AKT1,PACS2,PAIP1,KHSRP,PGM1,GIT1,CARHSP1,BLMH,SIRT6,ANAPC2,SPSB3,MAN1B1,STK11,TAZ,WDR24,JMJD8,SLC27A4,ZNRF1,PSMB10,CTRL,RBM8A,RNH1,PLA2G4E,NT5C,TENT5B,TRIB2,CDC34,FBXO6,GBA2,TRIR,STUB1,ITPA,CCDC115	yellow	VSMC_M3
GO:0019219	0.20	0.82	203	2852	regulation of nucleobase-containing compound metabolic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,TRAPPC9,PPARD,SND1,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,FIGNL1,PNKP,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,DEAF1,HOXC4,TARBP2,KMT2B,NAT10,ZNF740,RALY,ZBTB38,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCBP4,KDM1B,CHCHD2,RBM15B,SRSF9,DCPS,IRX1,RRP1B,BRD9,ZCCHC17,AIP,CLCF1,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,SMARCD2,BRMS1,BUD23,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,NDP,CTDSP1,MLF2,OTUB1,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,BABAM1,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,DFFA,SP2,ARHGEF2,SNF8,PER1,NFIX,PPP4C,SLX1A,IRF2BPL,TRIM25,SMARCA4,CARM1,RAVER1,AATF,CXorf57,MID2,RBM22,ZNF521,ZNF358,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,GIT1,CARHSP1,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,TAZ,FAM50A,JMJD8,MED16,CARD9,SARS,TRADD,NABP2,RBM8A,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,TENT5B,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0044242	0.20	0.87	15	164	cellular lipid catabolic process	BP	1	ACAT2,PPARD,CPT1C,MGLL,SCARB1,PCCB,ETFBKMT,PCK2,IDH1,SGPL1,ILVBL,AKT1,SLC27A4,PLA2G4E,GBA2	yellow	VSMC_M3
GO:0006637	0.20	0.89	8	78	acyl-CoA metabolic process	BP	1	FASN,ACSL1,MVK,ACLY,ACSF2,PMVK,HMGCS1,MVD	yellow	VSMC_M3
GO:0035383	0.20	0.89	8	78	thioester metabolic process	BP	1	FASN,ACSL1,MVK,ACLY,ACSF2,PMVK,HMGCS1,MVD	yellow	VSMC_M3
GO:0031663	0.20	0.91	5	44	lipopolysaccharide-mediated signaling pathway	BP	1	SCARB1,CX3CL1,AKT1,CACTIN,IRAK1	yellow	VSMC_M3
GO:0009199	0.20	0.89	7	64	ribonucleoside triphosphate metabolic process	BP	1	IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ,ITPA	yellow	VSMC_M3
GO:0071331	0.20	0.88	10	112	cellular response to hexose stimulus	BP	1	PPARD,LGALS1,UCP2,AACS,PCK2,SLC26A6,SMARCB1,BAD,SMARCA4,JAGN1	yellow	VSMC_M3
GO:0045746	0.20	0.92	4	33	negative regulation of Notch signaling pathway	BP	1	METTL3,DLL4,MMP14,AKT1	yellow	VSMC_M3
GO:0001667	0.20	0.85	28	360	ameboidal-type cell migration	BP	1	PPARD,TSTA3,PLEC,KLF4,TPBG,WDPCP,ZC3H12A,PLXND1,RIC8A,SCARB1,ITGB7,GREM1,EGR3,DLL4,GPX1,CORO1B,PTPN23,SGPL1,AAMP,C1QBP,RCC2,MTA2,PKN1,AKT1,TMEM201,ERBB4,PTPRR,GLIPR2	yellow	VSMC_M3
GO:0007010	0.21	0.83	83	1177	cytoskeleton organization	BP	1	DCTN2,SPAG1,SNX9,PDLIM4,PACSIN1,PLEC,CUL7,PDGFRA,DBNL,WDPCP,FHL3,FIGNL1,ZYX,MICAL1,EHD2,KRT8,SLC9A3R1,BAIAP2,CEP131,INPPL1,NUMA1,YIF1B,CCDC57,ARAP3,CAVIN3,NAT10,SPRYD3,SWAP70,CAPG,DCTN1,CX3CL1,SOD1,PACSIN3,CHP1,PDGFA,CDK2AP2,CORO1B,CLIP2,TRIM27,ARPIN,PCNT,LIMK1,NUDC,CAPN10,IQCG,PFDN2,PLA2G3,STMN3,SIPA1,RHOC,ALKBH4,FMNL1,SAC3D1,LIMD1,MID1IP1,ARPC1B,KIAA0753,WASHC1,CNP,EML3,DBN1,CAPN2,MAD2L2,ARHGEF2,RANGRF,CORO1A,SYNE3,MYO19,EML1,INF2,GIT1,PPL,GAS8,NTMT1,MIR214,TWF2,MAP7D1,ELN,CDC42EP5,GBA2,TUBGCP2,MEIG1,ARPC5L	yellow	VSMC_M3
GO:0035924	0.21	0.90	6	62	cellular response to vascular endothelial growth factor stimulus	BP	1	CD63,PDGFRA,EGR3,DLL4,RELA,AKT1	yellow	VSMC_M3
GO:0060998	0.21	0.91	5	54	regulation of dendritic spine development	BP	1	DBNL,BAIAP2,NGEF,DBN1,EEF2K	yellow	VSMC_M3
GO:0065003	0.21	0.83	92	1210	protein-containing complex assembly	BP	1	SPAG1,SNX9,FNIP1,SAMM50,NDUFB9,H2AFY,RPL3,BOP1,TBCC,DBNL,ZC3H12A,ACAD9,GEMIN7,SLC9A3R1,H3F3B,BAIAP2,NUMA1,CCDC57,EIF4EBP1,SDHAF1,TARBP2,EIF4B,RRS1,UQCRFS1,CAPG,GREM1,AQP5,DCTN1,CX3CL1,WNT10B,CHP1,SRSF9,CORO1B,HCCS,TRIM27,ARPIN,EIF3A,SF3A1,ADRM1,TACO1,SART1,PRPF6,RHOC,TMEM120A,MID1IP1,PEX5,SMARCB1,CHCHD10,UBTF,BAD,LETM1,LGALS3,ARPC1B,MRTO4,FCHO1,AIMP2,TAF6L,UQCC3,WASHC1,KRT10,H3F3A,DBN1,CLTB,CD2BP2,RANGRF,FARSA,CORO1A,SMARCA4,EIF3G,BRF1,GIT1,UBN1,MRPL20,NCLN,NDUFS7,ATP5F1D,TAZ,CARD9,SPG7,TGFBR3,MIR214,TWF2,SURF1,MIS12,ELN,UNC13A,CDC42EP5,GBA2,TUBGCP2,STUB1,CCDC115,ARPC5L	yellow	VSMC_M3
GO:1903037	0.21	0.86	18	206	regulation of leukocyte cell-cell adhesion	BP	1	SCRIB,LGALS1,SOCS5,KLF4,ZC3H12A,EGR3,ST3GAL4,SART1,RELA,BAD,LGALS3,MAD1L1,CORO1A,CD276,CSK,AKT1,AP3D1,IRAK1	yellow	VSMC_M3

GO:0034248	0.21	0.84	32	395	regulation of cellular amide metabolic process	BP	1	CDK4,SECISBP2,RPS9,CNOT3,ZC3H12A,UNK,METTL3,DND1,EIF4EBP1,TARBP2,NAT10,EIF4B,PCIF1,DCPS,NGDN,LSM14B,TACO1,RELA,IGFBP5,MPV17L2,C1QBP,SEPSECS,NANOS3,PER1,C19orf66,AKT1,PAIP1,KHSRP,TRAP1,MKNK2,RBM8A,ZNF385A	yellow	VSMC_M3
GO:0009311	0.21	0.91	5	44	oligosaccharide metabolic process	BP	1	B4GALT1,ST3GAL4,MANBA,MPDU1,MAN1B1	yellow	VSMC_M3
GO:0006796	0.21	0.82	155	2150	phosphate-containing compound metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,SBF1,SNX9,CERK,FNIP1,PRR5,H2AFY,GUK1,NUDT3,PPARD,PLEC,PPP1R14B,DNPH1,PIGO,PDGFRA,SOCS5,TTC7A,KLF4,SPRED2,ZC3H12A,PNKP,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SEPHS1,GALK1,PPM1G,PLCD1,OGG1,SERTAD1,INPPL1,PCYT2,FASN,PTDSS2,SMUG1,OGDHL,TARBP2,SCARB1,PDE4D,TNS2,SWAP70,ACSL1,FDFT1,TNKS1BP1,GREM1,TKT,CX3CL1,SOD1,DGKZ,CHP1,TYRO3,HTATIP2,PPM1M,CISH,AK2,MVK,STK32C,FABP3,PAPSS1,PDGFA,MOCS3,CLCF1,QARS,IMPDH2,TRIM27,LIMK1,RIPK3,PSTK,TNK2,PLA2G3,PTPN23,ATP5MC3,SCYL1,IDH1,MEX3B,MAP3K14,LIMD1,ATIC,PHB2,PPP1R35,BAD,PLCB3,CTDSP1,ISYNA1,LGALS3,TNFRSF1A,ASMTL,UQCC3,WASHC1,CNP,ACLY,FOXK1,PKN1,CAPN2,PIP4K2B,MAD2L2,CTBP1,PGD,ARHGEF2,MVP,ACSF2,DPM3,PPP4C,FLAD1,PMVK,ATP5PD,MTMR4,HDHD2,EEF2K,CDC37,CSK,AKT1,HMGCS1,PGM1,SGK494,GIT1,MYDGF,MAP2K2,CACTIN,CDK11B,SSU72,PGP,MKNK2,CSNK1G2,IRAK1,MIDN,ATP5F1D,STK11,TELO2,TAZ,JMJD8,AMPD2,APRT,MVD,AK1,SLC44A3,VAC14,TGFBR3,ERBB4,PTPRR,PLA2G4E,FADS1,NT5C,TRIB2,NSMF,TALDO1,DUSP5,FDPS,IDI1,ITPA	yellow	VSMC_M3
GO:0009142	0.21	0.89	7	62	nucleoside triphosphate biosynthetic process	BP	1	IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ,AK1	yellow	VSMC_M3
GO:0051568	0.21	0.91	5	51	histone H3-K4 methylation	BP	1	NELFE,H2AFY,KMT2E,KMT2B,SETD1B	yellow	VSMC_M3
GO:0045930	0.21	0.86	16	186	negative regulation of mitotic cell cycle	BP	1	CTDSP2,SCRIB,KLF4,SLC9A3R1,PINX1,CDK2AP2,PRMT2,CTDSP1,BABAM1,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,AURKAIP1,NABP2	yellow	VSMC_M3
GO:1903039	0.21	0.87	13	143	positive regulation of leukocyte cell-cell adhesion	BP	1	LGALS1,SOCS5,EGR3,ST3GAL4,SART1,RELA,BAD,CORO1A,CD276,CSK,AKT1,AP3D1,IRAK1	yellow	VSMC_M3
GO:0030512	0.21	0.90	6	64	negative regulation of transforming growth factor beta receptor signaling pathway	BP	1	SPRED2,EMILIN1,MTMR4,VASN,TGFBR3,STUB1	yellow	VSMC_M3
GO:0050818	0.21	0.90	6	54	regulation of coagulation	BP	1	PDGFRA,ANXA5,ST3GAL4,PDGFA,CD9,PLAU	yellow	VSMC_M3
GO:0071326	0.21	0.87	10	113	cellular response to monosaccharide stimulus	BP	1	PPARD,LGALS1,UCP2,AACS,PCK2,SLC26A6,SMARCB1,BAD,SMARCA4,JAGN1	yellow	VSMC_M3
GO:1901615	0.21	0.84	31	382	organic hydroxy compound metabolic process	BP	1	SREBF2,SQLE,NUDT3,PPARD,PTGR1,FDXR,SNX17,GALK1,INSIG1,IDH3B,SCARB1,FDFT1,SOD1,DHCR7,MVK,PCK2,LSS,IDH1,ISYNA1,HSD17B1,ACLY,PMVK,HMGCS1,DHCR24,NSDHL,CTNS,PGP,MVD,GBA2,FDPS,IDI1	yellow	VSMC_M3
GO:0043154	0.21	0.90	6	55	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	FNIP1,KLF4,MICAL1,GPX1,AKT1,DHCR24	yellow	VSMC_M3
GO:1901698	0.21	0.83	63	845	response to nitrogen compound	BP	1	ENPP1,CDK4,BAG6,SREBF2,PDGFRA,SOCS5,KLF4,RCN3,SLC9A3R1,TMUB1,INSIG1,OGG1,UCP2,SEL1L2,BAIAP2,INPPL1,LAMTOR1,AACS,HM13,BCL2L1,TNS2,PDE3B,WNT10B,SOD1,SRSF9,SELENOS,FABP3,PCK2,COL6A1,SLC26A6,UQCRC1,CAPN10,RELA,MGST3,IGFBP5,BAD,LAMTOR4,CD9,UBXN1,KLF3,CAPN2,MTHFR,PIP4K2B,ARHGEF2,PER1,TRIM25,CARM1,EEF2K,CSK,AKT1,HMGCS1,SLC6A4,LDOC1,MAN1B1,CARD9,APRT,SLC27A4,TGFBR3,JUND,NSMF,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0002686	0.21	0.91	4	33	negative regulation of leukocyte migration	BP	1	EMILIN1,GREM1,RIN3,AKT1	yellow	VSMC_M3
GO:0071216	0.21	0.86	14	157	cellular response to biotic stimulus	BP	1	CDK4,PPARD,ZC3H12A,SCARB1,CX3CL1,SELENOS,PABPN1,RELA,CAPN2,AKT1,GIT1,LDOC1,CACTIN,IRAK1	yellow	VSMC_M3
GO:0030521	0.21	0.91	4	37	androgen receptor signaling pathway	BP	1	PRMT2,PKN1,SMARCA4,SAFB2	yellow	VSMC_M3
GO:0046649	0.22	0.83	37	470	lymphocyte activation	BP	1	BAG6,NCAPH2,FNIP1,SCRIB,LGALS1,SOCS5,ZC3H12A,RELB,CD79A,METTL3,SWAP70,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,IMPDH2,RIPK3,SART1,PBX1,PHB2,BAD,LGALS3,PKN1,MAD1L1,MAD2L2,ARMC5,CORO1A,CD276,CSK,DOCK11,AKT1,AP3D1,STK11,PSMB10,AKAP17A	yellow	VSMC_M3
GO:0006096	0.22	0.89	6	60	glycolytic process	BP	1	GALK1,OGDHL,FOXK1,PGM1,GIT1,JMJD8	yellow	VSMC_M3
GO:0006757	0.22	0.89	6	60	ATP generation from ADP	BP	1	GALK1,OGDHL,FOXK1,PGM1,GIT1,JMJD8	yellow	VSMC_M3
GO:0030317	0.22	0.89	6	58	flagellated sperm motility	BP	1	CEP131,YIF1B,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:0097722	0.22	0.89	6	58	sperm motility	BP	1	CEP131,YIF1B,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:0000910	0.22	0.86	12	141	cytokinesis	BP	1	SNX9,PLEC,CUL7,SEPT9,BCL2L1,RAB35,RHOC,ALKBH4,ANXA11,MYO19,SNX18,GIT1	yellow	VSMC_M3
GO:0051276	0.22	0.83	51	682	chromosome organization	BP	1	DCTN2,NHP2,BAG6,NCAPH2,HDAC10,H2AFY,PHF2,PNKP,KMT2E,DMAP1,H3F3B,NUMA1,NAT10,RRS1,TNKS1BP1,PINX1,ACTR5,NPM3,BRD9,NUDC,SMARCD2,BUD23,BANF1,RELA,LRWD1,ALKBH4,ZNHIT1,SMARCB1,PHB2,BABAM1,TAF6L,EML3,MTA2,H3F3A,MAD1L1,MAD2L2,SLX1A,SMARCA4,ZNF830,SAFB,SIRT6,UBN1,HMG20B,EHMT1,MBD3,TELO2,FAM50A,RF00024,NABP2,MIS12,ITPA	yellow	VSMC_M3
GO:0022900	0.22	0.86	15	149	electron transport chain	BP	1	NDUFB9,TSTA3,PLEC,GSR,IDH3B,UQCRFS1,CHCHD2,SDHA,NDUFV1,UQCRC1,UQCC3,FDX2,NDUFS7,TAZ,SURF1	yellow	VSMC_M3
GO:0022618	0.22	0.86	15	163	ribonucleoprotein complex assembly	BP	1	RPL3,BOP1,GEMIN7,TARBP2,EIF4B,RRS1,SRSF9,EIF3A,SF3A1,SART1,PRPF6,MRTO4,CD2BP2,EIF3G,MRPL20	yellow	VSMC_M3
GO:1901136	0.22	0.86	12	126	carbohydrate derivative catabolic process	BP	1	NUDT3,DNPH1,OGG1,GNPDA1,SMUG1,PDE4D,MANBA,MAN1B1,NT5C,FBXO6,GBA2,ITPA	yellow	VSMC_M3
GO:0006476	0.22	0.88	8	88	protein deacetylation	BP	1	HDAC10,SPRED2,CCAR2,BRMS1,MTA2,CTBP1,PER1,SIRT6	yellow	VSMC_M3
GO:0019933	0.22	0.91	4	40	cAMP-mediated signaling	BP	1	SLC9A3R1,PDE4D,PDE3B,CDC34	yellow	VSMC_M3
GO:0048639	0.22	0.87	11	134	positive regulation of developmental growth	BP	1	PPARD,DBNL,LIMK1,DBN1,CRABP2,AKT1,ANAPC2,TGFBR3,ERBB4,TWF2,UNC13A	yellow	VSMC_M3
GO:0006575	0.22	0.86	13	136	cellular modified amino acid metabolic process	BP	1	CPT1C,GSR,PTDSS2,SOD1,GSTO1,GPX1,SLC19A1,PLA2G3,IDH1,ATIC,MTHFR,CTNS,EEF1G	yellow	VSMC_M3
GO:0045022	0.22	0.91	4	37	early endosome to late endosome transport	BP	1	SNX3,PTPN23,SNF8,MAP2K2	yellow	VSMC_M3

GO:1902369	0.22	0.89	6	60	negative regulation of RNA catabolic process	BP	1	HNRNPA0,SECISBP2,DND1,ZCCHC17,PAIP1,TENT5B	yellow	VSMC_M3
GO:2001233	0.22	0.84	25	292	regulation of apoptotic signaling pathway	BP	1	FIGNL1,SLC9A3R1,P4HB,BCL2L1,PLEKHF1,CX3CL1,SOD1,CCAR2,SELENOS,ITPRIP,GPX1,QARS,RIPK3,RELA,BAD,LGALS3,NANOS3,ARHGEF2,AATF,AKT1,TRAP1,MNT,TNFRSF12A,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0046660	0.22	0.88	8	88	female sex differentiation	BP	1	PDGFRA,BCL2L1,SOD1,TYRO3,MMP14,IDH1,SGPL1,ZNF830	yellow	VSMC_M3
GO:0009201	0.22	0.89	6	52	ribonucleoside triphosphate biosynthetic process	BP	1	IMPDH2,ATP5MC3,UQCC3,ATP5PD,ATP5F1D,TAZ	yellow	VSMC_M3
GO:0097190	0.22	0.83	38	471	apoptotic signaling pathway	BP	1	BAG6,PPARD,FIGNL1,KRT8,SLC9A3R1,P4HB,DELE1,BCL2L1,PLEKHF1,CX3CL1,SOD1,CCAR2,SELENOS,ITPRIP,GPX1,QARS,RIPK3,RELA,ZDHHC3,SGPL1,CHCHD10,ZNF385B,BAD,LGALS3,TNFRSF1A,NANOS3,ARHGEF2,AATF,AKT1,HIC1,TRAP1,MNT,MKNK2,STK11,TRADD,TNFRSF12A,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0044260	0.22	0.80	418	5916	cellular macromolecule metabolic process	BP	1	ENPP1,CD63,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,ZNF608,BAG6,SBF1,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,JADE2,TRMT12,H2AFY,HNRNPA0,TRIM11,TRAPPC9,PPARD,FANCE,EEF1D,RPL3,SCRIB,PLEC,SHARPIN,VPS28,RPL8,SND1,CUL7,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,JOSD2,PSMB3,FHL3,SPRED2,EIPR1,MEAF6,ZC3H12A,FIGNL1,PNKP,RCN3,CC2D1B,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,CIC,GTF3C2,PPM1G,UNK,GALNT14,OGG1,SERTAD1,TTC5,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,CXXC5,FAAP100,LAMTOR1,P4HB,DND1,RPL29,EIF4EBP1,DEAF1,SMUG1,HOXC4,POLR1D,TARBP2,KMT2B,NAT10,HM13,ZNF740,PDE4D,TNS2,EIF4B,SWAP70,RALY,ACSL1,ZBTB38,LSM6,TNKS1BP1,PINX1,GATB,SETD1B,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,TYRO3,MRPL43,YAF2,HTATIP2,PCIF1,PPM1M,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,CISH,ST3GAL4,RNF19B,DCPS,IRX1,WDR4,SELENOS,RRP1B,ETFBKMT,MANBA,TMTC1,BRD9,RIN3,STK32C,ZCCHC17,PDGFA,MMP14,APEH,GPX1,AIP,HCCS,MOCS3,CLCF1,NGDN,TSHZ2,QARS,ASB9,PSME2,PIR,TRIM27,EIF3A,LIMK1,ZNRD1,RABGGTA,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,PSTK,RPS21,PSMB4,SMARCD2,EXTL1,FTSJ3,BRMS1,SEC11A,BUD23,TNK2,TACO1,GMEB2,CEP164,CCDC85B,PRPF6,PTPN23,PBX1,RNASEH2C,KAT5,RELA,ZNF511,SCYL1,LRWD1,ALKBH4,MEX3B,MAP3K14,ARNT2,MRPL49,ZFPL	yellow	VSMC_M3
GO:0051253	0.22	0.82	76	1032	negative regulation of RNA metabolic process	BP	1	NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,PPARD,SECISBP2,KLF4,ZC3H12A,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,CXXC5,DND1,DEAF1,ZBTB38,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,PCBP4,KDM1B,SRSF9,IRX1,ZCCHC17,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,PAIP1,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,TENT5B,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0007159	0.22	0.85	20	234	leukocyte cell-cell adhesion	BP	1	TSTA3,SCRIB,LGALS1,SOCS5,KLF4,ZC3H12A,ITGB7,EGR3,ST3GAL4,SART1,RELA,BAD,LGALS3,MAD1L1,CORO1A,CD276,CSK,AKT1,AP3D1,IRAK1	yellow	VSMC_M3
GO:1990778	0.22	0.84	22	279	protein localization to cell periphery	BP	1	SQSTM1,PACSIN1,SCRIB,TTC7A,TPBG,EHD2,SLC9A3R1,NUMA1,BCL2L1,PLEKHF1,RAPSN,TSPAN5,MMP14,ZDHHC3,LGALS3,TNFRSF1A,RANGRF,CSK,AKT1,PACS2,RAB34,ARFRP1	yellow	VSMC_M3
GO:0045732	0.22	0.85	17	203	positive regulation of protein catabolic process	BP	1	BAG6,SNX9,SGSM3,VPS28,HSPBP1,SOCS5,PSMC4,PACSIN3,RNF19B,ASB9,CCDC22,AMER1,SNF8,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0050807	0.22	0.86	13	165	regulation of synapse organization	BP	1	DBNL,TPBG,BAIAP2,ARHGAP22,ARHGAP33,DCTN1,NGEF,IGSF9,LRFN4,NECTIN1,DBN1,EEF2K,ANAPC2	yellow	VSMC_M3
GO:0014068	0.22	0.89	6	66	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	PRR5,PPARD,PDGFRA,PDGFA,MYDGF,ERBB4	yellow	VSMC_M3
GO:0051252	0.22	0.80	188	2654	regulation of RNA metabolic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,TRAPPC9,PPARD,SND1,SECISBP2,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,DEAF1,HOXC4,TARBP2,KMT2B,ZNF740,RALY,ZBTB38,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCBP4,KDM1B,CHCHD2,RBM15B,SRSF9,DCPS,IRX1,RRP1B,BRD9,ZCCHC17,AIP,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,SMARCD2,BRMS1,BUD23,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,RAVER1,AATF,MID2,RBM22,ZNF521,ZNF358,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,CARHSP1,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,FAM50A,MED16,CARD9,SARS,TRADD,RBM8A,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,TENT5B,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0034728	0.22	0.87	9	97	nucleosome organization	BP	1	H2AFY,DMAP1,H3F3B,SMARCD2,ZNHIT1,SMARCB1,H3F3A,SMARCA4,UBN1	yellow	VSMC_M3
GO:1902373	0.22	0.90	5	49	negative regulation of mRNA catabolic process	BP	1	HNRNPA0,SECISBP2,DND1,PAIP1,TENT5B	yellow	VSMC_M3

GO:0046545	0.22	0.88	7	75	development of primary female sexual characteristics	BP	1	PDGFRA,BCL2L1,SOD1,MMP14,IDH1,SGPL1,ZNF830	yellow	VSMC_M3
GO:0031060	0.23	0.89	5	52	regulation of histone methylation	BP	1	NELFE,H2AFY,KMT2E,SMARCB1,MTHFR	yellow	VSMC_M3
GO:0010605	0.23	0.80	150	2090	negative regulation of macromolecule metabolic process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,ZNF608,BAG6,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,PPARD,PLEC,VPS28,SND1,SECISBP2,PHF2,SSC5D,SOCS5,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,SNRNP70,CC2D1B,SNX3,MICAL1,SIX5,ZNF282,ZNF296,RELB,EMILIN1,DMAP1,CIC,UNK,OGG1,METTL3,CXXC5,INPPL1,DND1,EIF4EBP1,DEAF1,TARBP2,NAT10,PDE4D,SWAP70,LRP3,ZBTB38,LSM6,PINX1,GREM1,KDM2B,CX3CL1,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,CHP1,YAF2,PCIF1,PCBP4,KDM1B,SLC35C2,SRSF9,DCPS,IRX1,SELENOS,RIN3,ZCCHC17,GPX1,QARS,TRIM27,LIMK1,PRMT2,TWIST2,PFDN2,BRMS1,PLA2G3,CCDC85B,KAT5,RELA,LIMD1,SMARCB1,GATAD2A,PHB2,IGFBP5,CTDSP1,OTUB1,EID1,METTL13,LGALS3,C11orf95,MRTO4,C1QBP,ZBTB49,UBXN1,MTA2,FOXK1,KLF3,PKN1,MAD2L2,NANOS3,CTBP1,DFFA,SP2,MVP,PER1,NFIX,SLX1A,IRF2BPL,RPL37,SMARCA4,AATF,CXorf57,C19orf66,CSK,ZNF830,AKT1,PAIP1,KHSRP,GIT1,ANKRD13B,DHCR24,CARHSP1,SIRT6,MAP2K2,CACTIN,HMG20B,HIC1,MNT,EHMT1,ANAPC2,MBD3,SARS,MIR214,MIR155,RBM8A,RNH1,MIR374B,TENT5B,TRIB2,THAP7,NSMCE3,ERF,ZAR1L	yellow	VSMC_M3
GO:0061383	0.23	0.90	4	40	trabecula morphogenesis	BP	1	GREM1,WNT10B,DLL4,TGFBR3	yellow	VSMC_M3
GO:0006661	0.23	0.86	10	115	phosphatidylinositol biosynthetic process	BP	1	PIGO,SOCS5,TTC7A,INPPL1,CISH,PDGFA,PIP4K2B,DPM3,MTMR4,VAC14	yellow	VSMC_M3
GO:0022409	0.23	0.85	15	176	positive regulation of cell-cell adhesion	BP	1	LGALS1,SOCS5,CX3CL1,EGR3,ST3GAL4,SART1,PTPN23,RELA,BAD,CORO1A,CD276,CSK,AKT1,AP3D1,IRAK1	yellow	VSMC_M3
GO:0060338	0.23	0.90	4	34	regulation of type I interferon-mediated signaling pathway	BP	1	TTLL12,METTL3,CDC37,CACTIN	yellow	VSMC_M3
GO:0061640	0.23	0.87	8	87	cytoskeleton-dependent cytokinesis	BP	1	SNX9,PLEC,CUL7,SEPT9,RAB35,RHOC,ALKBH4,SNX18	yellow	VSMC_M3
GO:0044380	0.23	0.89	5	55	protein localization to cytoskeleton	BP	1	DCTN2,CEP131,NUMA1,KIAA0753,MID2	yellow	VSMC_M3
GO:1902531	0.23	0.80	94	1309	regulation of intracellular signal transduction	BP	1	SQSTM1,NELFE,FNIP1,PRR5,SGSM3,DEF6,PPARD,EEF1D,LGALS1,SHARPIN,BOP1,PDGFRA,KLF4,TPBG,SPRED2,ZC3H12A,FIGNL1,RCN3,SLC9A3R1,EMILIN1,SEC13,ARHGEF40,CXXC5,LAMTOR1,P4HB,CAVIN3,ARHGAP22,BCL2L1,PDE4D,RRS1,SWAP70,PLEKHF1,GREM1,PDE3B,CX3CL1,SOD1,CCAR2,CHP1,SELENOS,PDGFA,GPX1,AIP,NGEF,QARS,TRIM27,EIF3A,THOC5,RIPK3,STMN3,RELA,SIPA1,RHOC,MAP3K14,LIMD1,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,TNFRSF1A,C1QBP,CHERP,CCDC22,ARHGEF2,PER1,TRIM25,RPL37,S100A4,CSK,MID2,AKT1,MYDGF,MAP2K2,CACTIN,HIC1,TRAP1,CTNS,IRAK1,STK11,TELO2,WDR24,JMJD8,CARD9,TRADD,NDST1,ERBB4,PTPRR,IGFBP6,ZNF385A,TXNDC12,CDC34,ARHGEF1,DUSP5,GLIPR2	yellow	VSMC_M3
GO:0009154	0.23	0.90	4	35	purine ribonucleotide catabolic process	BP	1	NUDT3,PDE4D,NT5C,ITPA	yellow	VSMC_M3
GO:0097300	0.23	0.90	4	35	programmed necrotic cell death	BP	1	RIPK3,ARHGEF2,ALKBH7,MIR214	yellow	VSMC_M3
GO:0006165	0.23	0.88	7	72	nucleoside diphosphate phosphorylation	BP	1	GALK1,OGDHL,FOXK1,PGM1,GIT1,JMJD8,AK1	yellow	VSMC_M3
GO:1901796	0.23	0.87	8	83	regulation of signal transduction by p53 class mediator	BP	1	BOP1,SPRED2,RRS1,RPL37,AKT1,HIC1,STK11,ZNF385A	yellow	VSMC_M3
GO:0060627	0.23	0.82	31	403	regulation of vesicle-mediated transport	BP	1	CD63,RUFY1,PACSIN1,SCRIB,VPS28,EIPR1,SNX3,MICAL1,EHD2,SNX17,SCARB1,GREM1,SOD1,PACSIN3,RIN3,SYT12,TNK2,PLA2G3,PTPN23,LGALS3,LMAN2,SNF8,CORO1A,EEF2K,CSK,ATG3,GIT1,ANKRD13B,MAP2K2,PLA2G4E,GSG1L	yellow	VSMC_M3
GO:0050727	0.23	0.84	20	239	regulation of inflammatory response	BP	1	PPARD,SHARPIN,IL1R1,SOCS5,KLF4,ZYX,MGLL,CX3CL1,SOD1,TYRO3,SELENOS,MVK,GPX1,PSMB4,PLA2G3,RELA,IFI35,TNFRSF1A,GIT1,TRADD	yellow	VSMC_M3
GO:0043473	0.23	0.87	7	75	pigmentation	BP	1	ENPP1,CD63,DCTN2,HPS1,BLOC1S4,AP1M1,AP3D1	yellow	VSMC_M3
GO:0008286	0.23	0.87	8	93	insulin receptor signaling pathway	BP	1	ENPP1,CDK4,BAIAP2,TNS2,RELA,PIP4K2B,AKT1,SLC27A4	yellow	VSMC_M3
GO:0031529	0.23	0.89	5	49	ruffle organization	BP	1	DBNL,WDPCP,INPPL1,CORO1B,RCC2	yellow	VSMC_M3
GO:0071300	0.23	0.89	5	52	cellular response to retinoic acid	BP	1	KLF4,WNT10B,PHB2,SLC6A4,TWF2	yellow	VSMC_M3
GO:0009060	0.23	0.84	16	161	aerobic respiration	BP	1	NDUFB9,IDH3B,OGDHL,CHCHD2,SDHA,NDUFV1,UQCRC1,IDH1,CHCHD10,UQCC3,ATP5PD,AKT1,NDUFS7,ATP5F1D,TAZ,SURF1	yellow	VSMC_M3
GO:0032434	0.23	0.85	11	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,WNT10B,CCAR2,RNF19B,UBXN1,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0051881	0.23	0.87	7	66	regulation of mitochondrial membrane potential	BP	1	UCP2,PYCR1,BCL2L1,SOD1,BAD,AKT1,CTNS	yellow	VSMC_M3
GO:0050796	0.24	0.85	11	127	regulation of insulin secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:1900076	0.24	0.89	5	51	regulation of cellular response to insulin stimulus	BP	1	ENPP1,TNS2,RELA,PIP4K2B,SLC27A4	yellow	VSMC_M3
GO:0040008	0.24	0.81	39	518	regulation of growth	BP	1	ENPP1,CDK4,PPARD,DNPH1,SOCS5,DBNL,DMAP1,H3F3B,LAMTOR1,BCL2L1,GREM1,KDM2B,TKT,SOD1,CCAR2,CISH,MMP14,LIMK1,CCDC85B,KAT5,SIPA1,SGPL1,IGFBP5,H3F3A,DBN1,MAD2L2,CRABP2,SMARCA4,AKT1,SLC6A4,HDGFL2,CDK11B,ANAPC2,STK11,TGFBR3,ERBB4,TWF2,UNC13A,NSMCE3	yellow	VSMC_M3
GO:0006081	0.24	0.89	5	46	cellular aldehyde metabolic process	BP	1	GRHPR,TKT,RELA,IDH1,TALDO1	yellow	VSMC_M3
GO:0007040	0.24	0.88	6	61	lysosome organization	BP	1	LAMTOR1,RAB20,HPS1,CORO1A,RAB34,CCDC115	yellow	VSMC_M3
GO:0080171	0.24	0.88	6	61	lytic vacuole organization	BP	1	LAMTOR1,RAB20,HPS1,CORO1A,RAB34,CCDC115	yellow	VSMC_M3
GO:0022406	0.24	0.87	7	76	membrane docking	BP	1	ESYT1,SNX3,CHP1,STX10,PACS2,RABEPK,UNC13A	yellow	VSMC_M3
GO:0051209	0.24	0.87	7	82	release of sequestered calcium ion into cytosol	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A	yellow	VSMC_M3
GO:2001057	0.24	0.88	6	61	reactive nitrogen species metabolic process	BP	1	KLF4,ZC3H12A,SELENOS,THAP4,AKT1,KHSRP	yellow	VSMC_M3
GO:0032956	0.24	0.82	23	304	regulation of actin cytoskeleton organization	BP	1	SNX9,PDGFRA,DBNL,BAIAP2,SWAP70,CAPG,CX3CL1,PDGFA,CORO1B,TRIM27,ARPIN,LIMK1,RHOC,ARPC1B,WASHC1,DBN1,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0008360	0.24	0.85	11	134	regulation of cell shape	BP	1	WDPCP,SLC9A3R1,PLXND1,BAIAP2,PLEKHO1,RHOC,FMNL1,LIMD1,CORO1A,SYNE3,CDC42EP5	yellow	VSMC_M3
GO:0044843	0.24	0.84	15	180	cell cycle G1/S phase transition	BP	1	CDK4,CTDSP2,KLF4,KMT2E,EIF4EBP1,CDK2AP2,PSME2,PRMT2,PHB2,CTDSP1,METTL13,SDE2,AKT1,MIR214,CDC34	yellow	VSMC_M3

GO:0051702	0.24	0.87	6	61	biological process involved in interaction with symbiont	BP	1	ZC3H12A,RRP1B,GPX1,SMARCB1,SMARCA4,CARD9	yellow	VSMC_M3
GO:0071824	0.24	0.84	14	163	protein-DNA complex subunit organization	BP	1	H2AFY,DMAP1,H3F3B,WNT10B,SMARCD2,ZNHIT1,SMARCB1,UBTF,TAF6L,H3F3A,SMARCA4,BRF1,UBN1,MIS12	yellow	VSMC_M3
GO:0071396	0.24	0.81	32	422	cellular response to lipid	BP	1	CDK4,PPARD,KLF4,ZC3H12A,INSIG1,AACS,SCARB1,CX3CL1,WNT10B,SELENOS,PABPN1,PCK2,PRMT2,KAT5,RELA,PHB2,BAD,PKN1,CAPN2,PER1,SMARCA4,CARM1,AKT1,HMGCS1,SAFB,SAFB2,GIT1,SLC6A4,LDOC1,CACTIN,IRAK1,TWF2	yellow	VSMC_M3
GO:0046887	0.25	0.86	8	86	positive regulation of hormone secretion	BP	1	PPARD,MYRIP,AACS,PCK2,CAPN10,PLA2G3,BAD,GLUD1	yellow	VSMC_M3
GO:0050852	0.25	0.86	8	85	T cell receptor signaling pathway	BP	1	ZC3H12A,PDE4D,DGKZ,RELA,LGALS3,CD276,CSK,STK11	yellow	VSMC_M3
GO:0007566	0.25	0.89	4	36	embryo implantation	BP	1	PPARD,RPL29,SOD1,C1QBP	yellow	VSMC_M3
GO:0032388	0.25	0.84	14	173	positive regulation of intracellular transport	BP	1	SREBF2,EIPR1,ZC3H12A,EHD2,DMAP1,CEP131,NUMA1,CHP1,PCNT,CAPN10,PTPN23,RBM22,STK11,PLA2G4E	yellow	VSMC_M3
GO:0033273	0.25	0.86	7	75	response to vitamin	BP	1	PPARD,OGG1,DCPS,RELA,MTHFR,TRIM25,HMGCS1	yellow	VSMC_M3
GO:0018023	0.25	0.89	4	39	peptidyl-lysine trimethylation	BP	1	KMT2E,SETD1B,ETFBKMT,SMARCB1	yellow	VSMC_M3
GO:0046323	0.25	0.88	5	54	glucose import	BP	1	ENPP1,SELENOS,CAPN10,AKT1,SLC27A4	yellow	VSMC_M3
GO:0046916	0.25	0.86	8	86	cellular transition metal ion homeostasis	BP	1	TTC7A,SLC30A3,SLC11A2,SOD1,CCDC22,ANKRD9,AP3D1,CCDC115	yellow	VSMC_M3
GO:0048538	0.25	0.89	4	38	thymus development	BP	1	SOD1,RIPK3,PBX1,MAD1L1	yellow	VSMC_M3
GO:0032970	0.25	0.81	25	337	regulation of actin filament-based process	BP	1	SNX9,PDGFRA,DBNL,BAIAP2,PDE4D,SWAP70,CAPG,CX3CL1,PDGFA,CORO1B,TRIM27,ARPIN,LIMK1,RHOC,ARPC1B,WASHC1,DBN1,RANGRF,CORO1A,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:1990748	0.25	0.86	8	79	cellular detoxification	BP	1	GSR,SOD1,SELENOS,GSTO1,GPX1,MGST3,TXNRD2,PRXL2A	yellow	VSMC_M3
GO:0048568	0.25	0.81	26	341	embryonic organ development	BP	1	CTHRC1,PBX2,SCRIB,PDGFRA,EPN1,HOXA1,WDPCP,KRT8,SLC9A3R1,INSIG1,HOXC4,LRIG1,KDM2B,SOD1,PDGFA,MMP14,THOC5,PBX1,PBX4,TEAD4,SLC39A1,TTC39C,AKT1,NSDHL,MBD3,NDST1	yellow	VSMC_M3
GO:0062014	0.25	0.86	7	73	negative regulation of small molecule metabolic process	BP	1	INSIG1,SOD1,ETFBKMT,AKT1,GIT1,PGP,SLC27A4	yellow	VSMC_M3
GO:0050769	0.25	0.83	14	181	positive regulation of neurogenesis	BP	1	CUL7,DBNL,PLXND1,BAIAP2,CX3CL1,CLCF1,LIMK1,RELA,DBN1,CRABP2,EEF2K,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0000413	0.25	0.89	4	32	protein peptidyl-prolyl isomerization	BP	1	FKBP11,AIP,FKBP2,PIN4	yellow	VSMC_M3
GO:0051283	0.25	0.86	7	83	negative regulation of sequestering of calcium ion	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A	yellow	VSMC_M3
GO:0001706	0.25	0.89	4	43	endoderm formation	BP	1	H2AFY,MMP14,COL6A1,DUSP5	yellow	VSMC_M3
GO:0097061	0.25	0.87	6	70	dendritic spine organization	BP	1	DBNL,BAIAP2,ARHGAP33,NGEF,DBN1,EEF2K	yellow	VSMC_M3
GO:0097178	0.25	0.89	4	38	ruffle assembly	BP	1	DBNL,WDPCP,INPPL1,RCC2	yellow	VSMC_M3
GO:0032774	0.25	0.77	179	2534	RNA biosynthetic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,POLR1D,KMT2B,ZNF740,RALY,ZBTB38,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,NPM3,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,AIP,TSHZ2,QARS,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,PSTK,SMARCD2,BRMS1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,MED16,CARD9,SARS,GTF3C5,TRADD,ERBB4,JUND,PTMA,KLF13,FADS1,ZNF783,HOXC5,CAVIN1,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,SNAPC2,ZSCAN1	yellow	VSMC_M3
GO:0050803	0.25	0.83	13	170	regulation of synapse structure or activity	BP	1	DBNL,TPBG,BAIAP2,ARHGAP22,ARHGAP33,DCTN1,NGEF,IGSF9,LRFN4,NECTIN1,DBN1,EEF2K,ANAPC2	yellow	VSMC_M3
GO:0010256	0.26	0.80	32	422	endomembrane system organization	BP	1	ESYT1,SQSTM1,BAG6,SNX9,PACSIN1,PLEC,VPS28,CUL7,ASNA1,SNX3,EHD2,TMEM43,SLC9A3R1,BAIAP2,LAMTOR1,PLEKHF1,DCTN1,SOD1,PACSIN3,PLA2G3,VPS51,CD9,MVB12A,LMAN2,SNF8,TMED1,AKT1,RFX2,MAP2K2,AP3D1,JAGN1,PHETA2	yellow	VSMC_M3
GO:0002250	0.26	0.81	20	244	adaptive immune response	BP	1	GNL1,IL1R1,SOCS5,DBNL,ZC3H12A,RELB,CD79A,SWAP70,RNF19B,CLCF1,TRIM27,RIPK3,SIPA1,OTUB1,C1QBP,PKN1,MAD2L2,CSK,C8G,CARD9	yellow	VSMC_M3
GO:1900182	0.26	0.86	7	76	positive regulation of protein localization to nucleus	BP	1	ZC3H12A,DMAP1,PINX1,MCRS1,RBM22,AKT1,STK11	yellow	VSMC_M3
GO:0009895	0.26	0.81	20	254	negative regulation of catabolic process	BP	1	BAG6,HNRNPA0,SECISBP2,SNRNP70,SNX3,DND1,PDE3B,CCAR2,ETFBKMT,ZCCHC17,RELA,UBXN1,WASHC1,FOXK1,MAD2L2,DFFA,AKT1,PAIP1,GIT1,TENT5B	yellow	VSMC_M3
GO:0035821	0.26	0.86	7	75	modulation of process of other organism	BP	1	ZC3H12A,BCL2L1,RRP1B,SMARCB1,PHB2,SMARCA4,CARD9	yellow	VSMC_M3
GO:0001701	0.26	0.81	24	314	in utero embryonic development	BP	1	PDGFRA,EPN1,CNOT3,KLF4,CCM2,KRT8,UNK,PSMC4,RIC8A,HM13,BCL2L1,STMN3,ARNT2,SMARCB1,DBN1,CAPN2,ARMC5,SLC39A1,ZNF830,AKT1,NSDHL,SLC35E2B,MBD3,PTPRR	yellow	VSMC_M3

GO:0009628	0.26	0.78	66	891	response to abiotic stimulus	BP	1	CDK4,PPARD,EEF1D,PLEC,HOXA1,FIGNL1,PNKP,KRT8,RELB,OGG1,UCP2,METTL3,P4HB,EIF4EBP1,RIC8A,BCL2L1,SLC11A2,TNKS1BP1,MMP24,AQP5,SOD1,ACTR5,CCAR2,CHP1,CHCHD2,MMP14,GPX1,KAT5,RELA,SIPA1,TMEM120A,MAP3K14,ARNT2,LIMD1,PHB2,BAD,LETM1,CD9,PLAU,TNFRSF1A,BABAM1,SDE2,PKN1,CAPN2,MTHFR,ARHGEF2,PER1,EEF2K,AKT1,HMGCS1,SLC6A4,PPL,VASN,CTNS,IRAK1,STK11,TGFBR3,MIR214,RF00024,NABP2,JUND,NSMF,IER5,STUB1,NSMCE3,CCDC115	yellow	VSMC_M3
GO:0050866	0.26	0.83	12	136	negative regulation of cell activation	BP	1	SCRIB,PDGFRA,SOCS5,ZC3H12A,EMILIN1,CX3CL1,TYRO3,PDGFA,LGALS3,CD9,PKN1,MAD1L1	yellow	VSMC_M3
GO:0045123	0.26	0.87	5	50	cellular extravasation	BP	1	IL1R1,ITGB7,CX3CL1,ST3GAL4,RIPK3	yellow	VSMC_M3
GO:0030195	0.26	0.89	4	35	negative regulation of blood coagulation	BP	1	PDGFRA,PDGFA,CD9,PLAU	yellow	VSMC_M3
GO:0090311	0.26	0.88	4	42	regulation of protein deacetylation	BP	1	SPRED2,CCAR2,BRMS1,CTBP1	yellow	VSMC_M3
GO:1901653	0.26	0.81	21	270	cellular response to peptide	BP	1	ENPP1,CDK4,KLF4,INSIG1,UCP2,BAIAP2,TNS2,PDE3B,SELENOS,PCK2,CAPN10,RELA,KLF3,PIP4K2B,ARHGEF2,EEF2K,CSK,AKT1,LDOC1,APRT,SLC27A4	yellow	VSMC_M3
GO:0030100	0.26	0.82	14	174	regulation of endocytosis	BP	1	CD63,RUFY1,PACSIN1,SCRIB,VPS28,SNX17,GREM1,PACSIN3,RIN3,TNK2,LGALS3,EEF2K,ANKRD13B,GSG1L	yellow	VSMC_M3
GO:0071347	0.26	0.85	7	75	cellular response to interleukin-1	BP	1	IL1R1,ZC3H12A,CX3CL1,RELA,OTUB1,CACTIN,IRAK1	yellow	VSMC_M3
GO:0007422	0.26	0.86	6	69	peripheral nervous system development	BP	1	NAB2,PLEC,SOD1,EGR3,RELA,AKT1	yellow	VSMC_M3
GO:1902904	0.26	0.83	11	139	negative regulation of supramolecular fiber organization	BP	1	EMILIN1,SWAP70,CAPG,CORO1B,ARPIN,PFDN2,MID1IP1,ARHGEF2,CORO1A,MIR214,TWF2	yellow	VSMC_M3
GO:0033692	0.26	0.87	5	52	cellular polysaccharide biosynthetic process	BP	1	ENPP1,SELENOS,AKT1,B3GNT9,NDST1	yellow	VSMC_M3
GO:0097305	0.26	0.82	14	174	response to alcohol	BP	1	CDK4,KLF4,DMAP1,OGG1,EIF4EBP1,AACS,BCL2L1,SOD1,BAD,PMVK,TUFM,AKT1,HMGCS1,TGFBR3	yellow	VSMC_M3
GO:0006636	0.26	0.88	4	36	unsaturated fatty acid biosynthetic process	BP	1	SCD,PLA2G3,FADS2,FADS1	yellow	VSMC_M3
GO:0002028	0.26	0.86	6	66	regulation of sodium ion transport	BP	1	SLC9A3R1,CHP1,NKAIN1,PER1,RANGRF,AKT1	yellow	VSMC_M3
GO:0010972	0.26	0.87	5	51	negative regulation of G2/M transition of mitotic cell cycle	BP	1	PINX1,BABAM1,MIIP,ZNF830,NABP2	yellow	VSMC_M3
GO:0071826	0.26	0.82	15	170	ribonucleoprotein complex subunit organization	BP	1	RPL3,BOP1,GEMIN7,TARBP2,EIF4B,RRS1,SRSF9,EIF3A,SF3A1,SART1,PRPF6,MRTO4,CD2BP2,EIF3G,MRPL20	yellow	VSMC_M3
GO:0006338	0.26	0.82	14	175	chromatin remodeling	BP	1	H2AFY,DMAP1,H3F3B,ACTR5,NPM3,SMARCD2,ZNHIT1,SMARCB1,TAF6L,MTA2,H3F3A,SMARCA4,UBN1,MBD3	yellow	VSMC_M3
GO:0051282	0.26	0.85	7	84	regulation of sequestering of calcium ion	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A	yellow	VSMC_M3
GO:0090559	0.26	0.86	6	59	regulation of membrane permeability	BP	1	BCL2L1,CHCHD10,BAD,CNP,ALKBH7,SPG7	yellow	VSMC_M3
GO:0006090	0.27	0.85	7	76	pyruvate metabolic process	BP	1	GALK1,OGDHL,PCK2,FOXK1,PGM1,GIT1,JMJD8	yellow	VSMC_M3
GO:0071417	0.27	0.79	34	466	cellular response to organonitrogen compound	BP	1	ENPP1,CDK4,PDGFRA,KLF4,SLC9A3R1,INSIG1,UCP2,BAIAP2,LAMTOR1,BCL2L1,TNS2,PDE3B,WNT10B,SOD1,SELENOS,PCK2,COL6A1,SLC26A6,CAPN10,RELA,IGFBP5,LAMTOR4,KLF3,CAPN2,PIP4K2B,ARHGEF2,EEF2K,CSK,AKT1,SLC6A4,LDOC1,APRT,SLC27A4,NSMF	yellow	VSMC_M3
GO:0007286	0.27	0.84	9	100	spermatid development	BP	1	SBF1,SIX5,CEP131,YIF1B,SLC26A6,IQCG,PLA2G3,RFX2,MEIG1	yellow	VSMC_M3
GO:0016458	0.27	0.82	14	169	gene silencing	BP	1	SND1,PHF2,CNOT3,ZC3H12A,METTL3,DND1,TARBP2,LIMD1,MAP2K2,MBD3,MIR214,MIR155,MIR374B,ZAR1L	yellow	VSMC_M3
GO:0010508	0.27	0.84	9	105	positive regulation of autophagy	BP	1	ZC3H12A,PLEKHF1,TRIM27,KAT5,PHB2,BAD,PIP4K2B,MID2,STK11	yellow	VSMC_M3
GO:0009889	0.27	0.76	212	3010	regulation of biosynthetic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,EMILIN1,DMAP1,CIC,UNK,INSIG1,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,HOXC4,TARBP2,KMT2B,SCARB1,NAT10,ZNF740,EIF4B,RALY,ZBTB38,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,DCPS,IRX1,DHCR7,SELENOS,RRP1B,BRD9,FABP3,PDGFA,AIP,NGDN,SRRD,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,SMARCD2,BRMS1,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,IDH1,ARNT2,ZFPL1,LIMD1,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,ARMC5,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,C19orf66,MID2,ZNF521,ZNF358,ZNF830,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,TRAP1,MNT,CTNS,EHMT1,PGP,AP3D1,MKNK2,IRAK1,MBD3,TAZ,MED16,CARD9,SARS,POMT1,TRADD,RBM8A,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,ZNF385A,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0009896	0.27	0.79	32	420	positive regulation of catabolic process	BP	1	BAG6,SNX9,SGSM3,VPS28,HSPBP1,SOCS5,CNOT3,ZC3H12A,PSMC4,METTL3,DND1,PLEKHF1,PACSIN3,RNF19B,DCPS,ASB9,TRIM27,KAT5,PHB2,BAD,CCDC22,AMER1,PIP4K2B,NANOS3,SNF8,MID2,AKT1,KHSRP,SIRT6,STK11,TRIB2,STUB1	yellow	VSMC_M3
GO:0038034	0.27	0.87	5	49	signal transduction in absence of ligand	BP	1	BCL2L1,CX3CL1,BAD,AKT1,MKNK2	yellow	VSMC_M3
GO:0097192	0.27	0.87	5	49	extrinsic apoptotic signaling pathway in absence of ligand	BP	1	BCL2L1,CX3CL1,BAD,AKT1,MKNK2	yellow	VSMC_M3
GO:0042632	0.27	0.86	6	62	cholesterol homeostasis	BP	1	SREBF2,INSIG1,LAMTOR1,SCARB1,RALY,FABP3	yellow	VSMC_M3
GO:0051851	0.27	0.87	5	51	modulation by host of symbiont process	BP	1	ZC3H12A,RRP1B,SMARCB1,SMARCA4,CARD9	yellow	VSMC_M3
GO:0043409	0.27	0.83	11	131	negative regulation of MAPK cascade	BP	1	KLF4,SPRED2,SLC9A3R1,EMILIN1,QARS,EIF3A,PER1,CSK,AKT1,PTPRR,DUSP5	yellow	VSMC_M3

GO:0120031	0.27	0.79	32	435	plasma membrane bounded cell projection assembly	BP	1	SPAG1,TXNDC15,DBNL,WDPCP,EMP3,EHD2,SLC9A3R1,SEPT9,CEP131,INPPL1,YIF1B,CCDC57,DCTN1,CCDC28B,PCNT,IQCG,PLA2G3,CEP164,PTPN23,WASHC1,RCC2,RABEP2,ATG3,TTC39C,DOCK11,RFX2,GAS8,WDR34,MIR214,TWF2,CDC42EP5,MEIG1	yellow	VSMC_M3
GO:0030518	0.27	0.84	8	96	intracellular steroid hormone receptor signaling pathway	BP	1	PRMT2,PHB2,PKN1,PER1,SMARCA4,CARM1,SAFB,SAFB2	yellow	VSMC_M3
GO:0001824	0.27	0.84	8	86	blastocyst development	BP	1	CNOT3,KLF4,PSMC4,STMN3,SMARCB1,CAPN2,ZNF830,SLC35E2B	yellow	VSMC_M3
GO:0000723	0.27	0.83	10	118	telomere maintenance	BP	1	NHP2,PNKP,NAT10,TNKS1BP1,PINX1,SLX1A,SIRT6,TELO2,RF00024,NABP2	yellow	VSMC_M3
GO:2000378	0.27	0.88	4	37	negative regulation of reactive oxygen species metabolic process	BP	1	AATF,AKT1,TRAP1,CTNS	yellow	VSMC_M3
GO:0043489	0.27	0.87	5	52	RNA stabilization	BP	1	HNRNPA0,DND1,ZCCHC17,PAIP1,TENT5B	yellow	VSMC_M3
GO:0070231	0.27	0.88	4	36	T cell apoptotic process	BP	1	RIPK3,LGALS3,DFFA,AKT1	yellow	VSMC_M3
GO:1902882	0.27	0.85	7	74	regulation of response to oxidative stress	BP	1	H2AFY,P4HB,PYCR1,SOD1,GPX1,AKT1,TRAP1	yellow	VSMC_M3
GO:0031326	0.27	0.75	208	2955	regulation of cellular biosynthetic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,UNK,INSIG1,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,HOXC4,TARBP2,KMT2B,SCARB1,NAT10,ZNF740,EIF4B,RALY,ZBTB38,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,DCPS,IRX1,SELENOS,RRP1B,BRD9,FABP3,PDGFA,AIP,NGDN,SRRD,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,SMARCD2,BRMS1,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,IDH1,ARNT2,ZFPL1,LIMD1,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,C19orf66,MID2,ZNF521,ZNF358,ZNF830,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,TRAP1,MNT,CTNS,EHMT1,PGP,AP3D1,MKNK2,IRAK1,MBD3,TAZ,MED16,CARD9,SARS,POMT1,TRADD,RBM8A,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,ZNF385A,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0001541	0.27	0.88	4	39	ovarian follicle development	BP	1	BCL2L1,SOD1,MMP14,ZNF830	yellow	VSMC_M3
GO:0071375	0.27	0.81	17	219	cellular response to peptide hormone stimulus	BP	1	ENPP1,CDK4,INSIG1,UCP2,BAIAP2,TNS2,PDE3B,SELENOS,PCK2,CAPN10,RELA,PIP4K2B,EEF2K,CSK,AKT1,APRT,SLC27A4	yellow	VSMC_M3
GO:0030865	0.27	0.86	5	55	cortical cytoskeleton organization	BP	1	PLEC,EHD2,CAVIN3,RHOC,FMNL1	yellow	VSMC_M3
GO:0016358	0.27	0.81	15	204	dendrite development	BP	1	PACSIN1,CUL7,DBNL,TPBG,BAIAP2,ARHGAP33,SLC11A2,NGEF,IGSF9,DBN1,CARM1,EEF2K,ANAPC2,STK11,NSMF	yellow	VSMC_M3
GO:2000117	0.27	0.85	6	60	negative regulation of cysteine-type endopeptidase activity	BP	1	FNIP1,KLF4,MICAL1,GPX1,AKT1,DHCR24	yellow	VSMC_M3
GO:0071840	0.27	0.75	333	4827	cellular component organization or biogenesis	BP	1	ENPP1,PQLC1,CD63,ESYT1,DCTN2,NHP2,CDK4,RUFY1,SQSTM1,SPAG1,BAG6,NCAPH2,SNX9,CTHRC1,HDAC10,FNIP1,PDLIM4,SAMM50,SREBF2,NDUFB9,SQLE,TXNDC15,H2AFY,PACSIN1,PPARD,RPL3,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,BOP1,VPS28,TBCC,CUL7,DNPH1,B4GALT1,PDGFRA,PHF2,COL15A1,COL19A1,ASNA1,KLF4,DBNL,TPBG,PLEKHA8,WDPCP,CCM2,FHL3,ZC3H12A,FIGNL1,PNKP,ZYX,SNX3,MICAL1,EMP3,EHD2,KMT2E,KRT8,ACAD9,TMEM43,GEMIN7,SLC9A3R1,PLXND1,EMILIN1,DMAP1,SNX17,H3F3B,INSIG1,SEC13,SEPT9,BAIAP2,CEP131,INPPL1,LAMTOR1,NUMA1,YIF1B,CCDC57,RAB20,EIF4EBP1,ARAP3,CAVIN3,RIC8A,ARHGAP22,SDHAF1,ARHGAP33,TARBP2,SCARB1,NAT10,BCL2L1,SPRYD3,EIF4B,RRS1,SWAP70,PLEKHF1,UQCRFS1,LSM6,CAPG,SLC11A2,TNKS1BP1,MMP24,PINX1,GREM1,KDM2B,AQP5,DCTN1,RAPSN,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,CCDC32,CCAR2,HPS1,CHP1,NPM3,RAB35,CHCHD2,CISH,SRSF9,RRP1B,CCDC28B,BRD9,RIN3,PDGFA,MMP14,CDK2AP2,LIX1L,APEH,GPX1,AIP,CORO1B,NGEF,HCCS,NGDN,PLEKHO1,IGSF9,LRFN4,CLIP2,NECTIN1,TRIM27,ARPIN,PCNT,EIF3A,LIMK1,NUDC,RIPK3,SF3A1,ADRM1,RPS21,CAPN10,SMARCD2,IQCG,PFDN2,FTSJ3,MPZL3,BUD23,TNK2,TACO1,PLA2G3,STMN3,CEP164,BANF1,SART1,CCDC85B,PRPF6,PTPN23,RELA,SIPA1,RHOC,TMEM120A,DDX52,LRWD1,ALKBH4,ZNHIT1,FMNL1,VPSS1,SAC3D1,LIMD1,MID1IP1,PEX5,SMARCB1,CHCHD10,YJEFN3,UBTF,BLOC1S4,PHB2,TRMT112,NDP,IGFBP5,C12orf57,BAD,LAMTOR4,NOP14,MPV17L2,LETM1,LGALS3,ARPC1B,CD9,MRTO4,TNFRSF1A,FCHO1,MVB12A,KIAA0753,BABAM1,C1QBP,NUP88,AIMP2,TAF6L,UQCC3,WASHC1,RCC2,CNP,A	yellow	VSMC_M3
GO:0006942	0.28	0.85	6	68	regulation of striated muscle contraction	BP	1	ZC3H12A,PDE4D,GSTO1,SCN4A,C12orf57,RANGRF	yellow	VSMC_M3
GO:1900047	0.28	0.88	4	36	negative regulation of hemostasis	BP	1	PDGFRA,PDGFA,CD9,PLAU	yellow	VSMC_M3
GO:0090087	0.28	0.82	12	144	regulation of peptide transport	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,SLC26A6,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0034968	0.28	0.84	8	98	histone lysine methylation	BP	1	NELFE,H2AFY,KMT2E,KMT2B,SETD1B,SMARCB1,TRMT112,EHMT1	yellow	VSMC_M3
GO:0010948	0.28	0.80	19	237	negative regulation of cell cycle process	BP	1	CTDSP2,H2AFY,KLF4,PINX1,CCAR2,CDK2AP2,PRMT2,THOC5,CTDSP1,METTL13,BABAM1,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,AURKAIP1,NABP2,FBXO6	yellow	VSMC_M3
GO:0035305	0.28	0.87	4	40	negative regulation of dephosphorylation	BP	1	SWAP70,CHP1,PPP1R35,LGALS3	yellow	VSMC_M3
GO:0048839	0.28	0.82	11	139	inner ear development	BP	1	CTHRC1,SCRIB,IFT27,HOXA1,WDPCP,CCM2,SLC9A3R1,INSIG1,LRIG1,SOD1,TTC39C	yellow	VSMC_M3

GO:0071214	0.28	0.80	21	267	cellular response to abiotic stimulus	BP	1	EEF1D,PLEC,FIGNL1,RELB,METTL3,BCL2L1,TNKS1BP1,AQP5,ACTR5,CHP1,SIPA1,MAP3K14,BAD,LETM1,TNFRSF1A,SDE2,ARHGEF2,AKT1,STK11,NSMF,NSMCE3	yellow	VSMC_M3
GO:0104004	0.28	0.80	21	267	cellular response to environmental stimulus	BP	1	EEF1D,PLEC,FIGNL1,RELB,METTL3,BCL2L1,TNKS1BP1,AQP5,ACTR5,CHP1,SIPA1,MAP3K14,BAD,LETM1,TNFRSF1A,SDE2,ARHGEF2,AKT1,STK11,NSMF,NSMCE3	yellow	VSMC_M3
GO:1905952	0.28	0.82	10	118	regulation of lipid localization	BP	1	SREBF2,PPARD,ZC3H12A,LAMTOR1,SCARB1,ACSL1,FABP3,PLA2G3,YJEFN3,AKT1	yellow	VSMC_M3
GO:0071322	0.28	0.82	10	121	cellular response to carbohydrate stimulus	BP	1	PPARD,LGALS1,UCP2,AACS,PCK2,SLC26A6,SMARCB1,BAD,SMARCA4,JAGN1	yellow	VSMC_M3
GO:0060964	0.28	0.87	4	39	regulation of gene silencing by miRNA	BP	1	ZC3H12A,DND1,LIMD1,MAP2K2	yellow	VSMC_M3
GO:0038202	0.28	0.87	4	40	TORC1 signaling	BP	1	SEC13,CTNS,STK11,TELO2	yellow	VSMC_M3
GO:0051053	0.28	0.83	8	94	negative regulation of DNA metabolic process	BP	1	OGG1,NAT10,PINX1,OTUB1,MAD2L2,DFFA,SLX1A,CXorf57	yellow	VSMC_M3
GO:2001244	0.28	0.86	5	46	positive regulation of intrinsic apoptotic signaling pathway	BP	1	SLC9A3R1,PLEKHF1,SOD1,RIPK3,BAD	yellow	VSMC_M3
GO:0016051	0.28	0.81	13	155	carbohydrate biosynthetic process	BP	1	ENPP1,B4GALT1,ST3GAL4,SELENOS,PCK2,ISYNA1,MPDU1,PGD,AKT1,PGM1,PGP,B3GNT9,NDST1	yellow	VSMC_M3
GO:0002260	0.28	0.86	5	50	lymphocyte homeostasis	BP	1	RIPK3,PKN1,CORO1A,DOCK11,AKT1	yellow	VSMC_M3
GO:0006457	0.28	0.81	15	166	protein folding	BP	1	TBCC,HSPBP1,PDIA4,PDIA6,SNRNP70,P4HB,FKBP11,AIP,NUDC,PFDN2,FKBP2,MPDU1,DFFA,CDC37,TRAP1	yellow	VSMC_M3
GO:0044085	0.28	0.75	174	2454	cellular component biogenesis	BP	1	NHP2,SPAG1,BAG6,SNX9,FNIP1,SAMM50,NDUFB9,SQLE,TXNDC15,H2AFY,RPL3,PLEC,BOP1,VPS28,TBCC,PDGFRA,PHF2,DBNL,TPBG,WDPCP,ZC3H12A,ZYX,MICAL1,EMP3,EHD2,KRT8,ACAD9,GEMIN7,SLC9A3R1,PLXND1,EMILIN1,H3F3B,SEPT9,BAIAP2,CEP131,INPPL1,NUMA1,YIF1B,CCDC57,RAB20,EIF4EBP1,SDHAF1,TARBP2,NAT10,EIF4B,RRS1,SWAP70,UQCRFS1,LSM6,CAPG,GREM1,AQP5,DCTN1,CX3CL1,WNT10B,HPS1,CHP1,NPM3,SRSF9,RRP1B,CCDC28B,PDGFA,MMP14,CORO1B,HCCS,NGDN,LRFN4,NECTIN1,TRIM27,ARPIN,PCNT,EIF3A,LIMK1,SF3A1,ADRM1,RPS21,IQCG,FTSJ3,BUD23,TACO1,PLA2G3,CEP164,SART1,PRPF6,PTPN23,RHOC,TMEM120A,DDX52,SAC3D1,LIMD1,MID1IP1,PEX5,SMARCB1,CHCHD10,UBTF,TRMT112,BAD,NOP14,MPV17L2,LETM1,LGALS3,ARPC1B,CD9,MRTO4,FCHO1,MVB12A,KIAA0753,C1QBP,NUP88,AIMP2,TAF6L,UQCC3,WASHC1,RCC2,EML3,KRT10,H3F3A,DBN1,PIP4K2B,CLTB,RRNAD1,SNF8,CD2BP2,RANGRF,FARSA,CORO1A,SLX1A,RABEP2,SMARCA4,RPL7A,EEF2K,AATF,EIF3G,ATG3,TTC39C,DOCK11,BRF1,PACS2,RFX2,RAB34,GIT1,UBN1,MRPL20,NCLN,CLDN6,TBL3,NUBP2,NDUFS7,ATP5F1D,TAZ,TSR3,CARD9,GAS8,SPG7,WDR34,TGFBR3,MIR214,ERBB4,TWF2,SURF1,RBFA,PIN4,MIS12,ELN,UNC13A,CDC42EP5,CDC34,NOM1,GBA2,TUBGCP2,MEIG1,STUB1,CCDC115,ARPC5L	yellow	VSMC_M3
GO:1901880	0.28	0.86	5	62	negative regulation of protein depolymerization	BP	1	SWAP70,CAPG,MID1IP1,ARHGEF2,TWF2	yellow	VSMC_M3
GO:0055092	0.28	0.85	6	63	sterol homeostasis	BP	1	SREBF2,INSIG1,LAMTOR1,SCARB1,RALY,FABP3	yellow	VSMC_M3
GO:0006351	0.28	0.74	177	2521	transcription, DNA-templated	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,POLR1D,KMT2B,ZNF740,RALY,ZBTB38,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,NPM3,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,AIP,TSHZ2,QARS,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,SMARCD2,BRMS1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,MED16,CARD9,SARS,GTF3C5,TRADD,ERBB4,JUND,PTMA,KLF13,FADS1,ZNF783,HOXC5,CAVIN1,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,SNAPC2,ZSCAN1	yellow	VSMC_M3
GO:0045668	0.28	0.87	4	41	negative regulation of osteoblast differentiation	BP	1	GREM1,TWIST2,LIMD1,IGFBP5	yellow	VSMC_M3
GO:0051726	0.28	0.76	61	827	regulation of cell cycle	BP	1	CDK4,CTDSP2,TTLL12,H2AFY,SCRIB,BOP1,SND1,CUL7,KLF4,FIGNL1,KMT2E,SLC9A3R1,PPM1G,SERTAD1,METTL3,CEP131,NUMA1,CCDC57,EIF4EBP1,NAT10,BCL2L1,PINX1,DCTN1,WNT10B,CCAR2,CDK2AP2,PSME2,PRMT2,THOC5,PBX1,SIPA1,PHB2,CTDSP1,METTL13,BABAM1,ZBTB49,RCC2,EML3,SDE2,MIIP,MAD1L1,MAD2L2,NANOS3,CTBP1,CDC37,MYO19,AATF,ZNF830,AKT1,GIT1,SLC6A4,DHCR24,CDK11B,AURKAIP1,MNT,STK11,MIR214,NABP2,JUND,FBXO6,AC093323.1	yellow	VSMC_M3
GO:0043401	0.29	0.82	9	111	steroid hormone mediated signaling pathway	BP	1	PPARD,PRMT2,PHB2,PKN1,PER1,SMARCA4,CARM1,SAFB,SAFB2	yellow	VSMC_M3
GO:1901222	0.29	0.84	7	75	regulation of NIK/NF-kappaB signaling	BP	1	ZC3H12A,GREM1,RELA,PHB2,IFI35,IRAK1,TRADD	yellow	VSMC_M3
GO:0031331	0.29	0.78	28	366	positive regulation of cellular catabolic process	BP	1	BAG6,SNX9,HSPBP1,SOCS5,CNOT3,ZC3H12A,PSMC4,METTL3,DND1,PLEKHF1,PACSIN3,RNF19B,DCPS,TRIM27,KAT5,PHB2,BAD,CCDC22,AMER1,PIP4K2B,NANOS3,MID2,AKT1,KHSRP,SIRT6,STK11,TRIB2,STUB1	yellow	VSMC_M3

GO:0097659	0.29	0.74	177	2522	nucleic acid-templated transcription	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,GTF3C2,OGG1,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,POLR1D,KMT2B,ZNF740,RALY,ZBTB38,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,NPM3,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,AIP,TSHZ2,QARS,PIR,TRIM27,ZNRD1,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,SMARCD2,BRMS1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,MED16,CARD9,SARS,GTF3C5,TRADD,ERBB4,JUND,PTMA,KLF13,FADS1,ZNF783,HOXC5,CAVIN1,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,SNAPC2,ZSCAN1	yellow	VSMC_M3
GO:0019538	0.29	0.74	292	4113	protein metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,LMF2,BAG6,SBF1,SNX9,HDAC10,NELFE,FNIP1,PRR5,TTLL12,RING1,JADE2,H2AFY,TRIM11,SGSM3,PPARD,EEF1D,RPL3,PLEC,SHARPIN,VPS28,RPL8,CUL7,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,JOSD2,PSMB3,SPRED2,EIPR1,MEAF6,ZC3H12A,PNKP,RCN3,SNRNP70,SNX3,MICAL1,KMT2E,WDFY2,SLC9A3R1,SERP2,NAT9,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,PPM1G,UNK,GALNT14,SERTAD1,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,P4HB,DND1,RPL29,EIF4EBP1,DELE1,LDLRAD3,TARBP2,KMT2B,NAT10,HM13,PDE4D,TNS2,EIF4B,PEPD,SWAP70,ACSL1,TNKS1BP1,MMP24,PINX1,GATB,SETD1B,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,CCAR2,RPLP2,CHP1,TYRO3,MRPL43,HTATIP2,PCIF1,PPM1M,KDM1B,SLC35C2,CARS,TSPAN5,CISH,ST3GAL4,RNF19B,DCPS,SELENOS,ETFBKMT,MANBA,TMTC1,STK32C,PDGFA,MMP14,APEH,GPX1,AIP,HCCS,MOCS3,CLCF1,NGDN,QARS,ASB9,PSME2,ANPEP,TRIM27,EIF3A,LIMK1,RABGGTA,PRMT2,RIPK3,LSM14B,ADRM1,DPP3,PSTK,RPS21,CAPN10,PSMB4,EXTL1,PFDN2,BRMS1,SEC11A,TNK2,TACO1,PTPN23,KAT5,RELA,SCYL1,ALKBH4,MEX3B,MAP3K14,MRPL49,ZDHHC3,SMARCB1,PHB2,TRMT112,IGFBP5,BAD,FKBP2,CTDSP1,OTUB1,EID1,COPS6,MPV17L2,LGALS3,PLAU,TNFRSF1A,MVB12A,BABAM1,C1QBP,AIMP2,TAF6L,UBXN1,WASHC1,MTA2,MED11,CCDC22,USP27X,KRT10,SDE2,CASP14,PKN1,CAPN2,SEPSECS,AMER1,MTHFR,MAD2L2,NANOS3,MPDU1,CTBP1,FBXL19,ARHGEF2,SNF8,RUSC1,MVP,PER1,DPM3,PPP4C,FARSA,SGF29,IRF2BPL,TUFM,TRIM25,USP43,RPL37,MTMR4,CARM1,SENP8,R	yellow	VSMC_M3
GO:0070925	0.29	0.76	51	705	organelle assembly	BP	1	SPAG1,SQLE,TXNDC15,RPL3,PLEC,BOP1,VPS28,PDGFRA,DBNL,WDPCP,EHD2,KRT8,SEPT9,CEP131,NUMA1,YIF1B,CCDC57,RAB20,RRS1,DCTN1,HPS1,CCDC28B,LRFN4,PCNT,IQCG,PLA2G3,CEP164,PTPN23,SAC3D1,LIMD1,MPV17L2,MRTO4,MVB12A,KIAA0753,C1QBP,EML3,PIP4K2B,SNF8,CORO1A,RABEP2,ATG3,TTC39C,PACS2,RFX2,RAB34,MRPL20,GAS8,WDR34,MIS12,TUBGCP2,MEIG1	yellow	VSMC_M3
GO:0061136	0.29	0.80	14	166	regulation of proteasomal protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,PSMC4,WNT10B,CCAR2,RNF19B,GPX1,PSME2,UBXN1,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0022408	0.29	0.81	11	130	negative regulation of cell-cell adhesion	BP	1	SCRIB,SOCS5,KLF4,ZC3H12A,METTL3,SWAP70,LGALS3,CD9,MAD1L1,MAD2L2,AKT1	yellow	VSMC_M3
GO:0022904	0.29	0.82	10	99	respiratory electron transport chain	BP	1	NDUFB9,PLEC,UQCRFS1,CHCHD2,SDHA,NDUFV1,UQCRC1,UQCC3,NDUFS7,TAZ	yellow	VSMC_M3
GO:0050863	0.29	0.79	17	206	regulation of T cell activation	BP	1	SCRIB,LGALS1,SOCS5,ZC3H12A,METTL3,SOD1,EGR3,RIPK3,SART1,BAD,LGALS3,MAD1L1,CORO1A,CD276,CSK,AKT1,AP3D1	yellow	VSMC_M3
GO:0001678	0.29	0.81	10	124	cellular glucose homeostasis	BP	1	PPARD,LGALS1,UCP2,AACS,PCK2,SMARCB1,BAD,FOXK1,SMARCA4,JAGN1	yellow	VSMC_M3
GO:1903202	0.29	0.87	4	38	negative regulation of oxidative stress-induced cell death	BP	1	PYCR1,GPX1,AKT1,TRAP1	yellow	VSMC_M3
GO:0051172	0.29	0.74	126	1770	negative regulation of nitrogen compound metabolic process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,ZNF608,BAG6,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,PPARD,PLEC,VPS28,SECISBP2,SOCS5,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,SNRNP70,CC2D1B,SNX3,MICAL1,SIX5,ZNF282,ZNF296,RELB,EMILIN1,DMAP1,CIC,UNK,OGG1,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,TARBP2,NAT10,PDE4D,SWAP70,ZBTB38,PINX1,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,CHP1,YAF2,PCIF1,PCBP4,KDM1B,SRSF9,DCPS,IRX1,ZCCHC17,GPX1,QARS,TRIM27,LIMK1,PRMT2,TWIST2,PFDN2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,SMARCB1,GATAD2A,PHB2,IGFBP5,CTDSP1,OTUB1,EID1,METTL13,LGALS3,C11orf95,C1QBP,ZBTB49,UBXN1,MTA2,FOXK1,KLF3,PKN1,MAD2L2,NANOS3,CTBP1,DFFA,SP2,MVP,PER1,NFIX,SLX1A,IRF2BPL,RPL37,SMARCA4,AATF,CXorf57,C19orf66,AKT1,PAIP1,KHSRP,GIT1,DHCR24,SIRT6,CACTIN,HMG20B,HIC1,MNT,EHMT1,MBD3,SARS,TENT5B,TRIB2,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0048232	0.29	0.77	29	371	male gamete generation	BP	1	BAG6,SBF1,IFT27,FIGNL1,SIX5,ZNF296,PAFAH1B3,DLEC1,METTL3,CEP131,DND1,YIF1B,MORN2,BCL2L1,KDM2B,SOD1,TYRO3,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,BAD,NANOS3,RFX2,STK11,TAZ,FAM50A,MEIG1	yellow	VSMC_M3

GO:0043624	0.29	0.82	9	119	cellular protein complex disassembly	BP	1	MICAL1,SWAP70,CAPG,APEH,STMN3,MID1IP1,ARHGEF2,C19orf66,TWF2	yellow	VSMC_M3
GO:0061157	0.29	0.83	7	79	mRNA destabilization	BP	1	CNOT3,ZC3H12A,METTL3,DND1,DCPS,NANOS3,KHSRP	yellow	VSMC_M3
GO:0051208	0.29	0.83	7	87	sequestering of calcium ion	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A	yellow	VSMC_M3
GO:0045445	0.29	0.84	6	67	myoblast differentiation	BP	1	PPARD,PLEC,LGALS1,GREM1,WNT10B,ANKRD2	yellow	VSMC_M3
GO:0031047	0.29	0.81	11	129	gene silencing by RNA	BP	1	SND1,CNOT3,ZC3H12A,METTL3,DND1,TARBP2,LIMD1,MAP2K2,MIR214,MIR155,MIR374B	yellow	VSMC_M3
GO:0010629	0.29	0.75	56	766	negative regulation of gene expression	BP	1	H2AFY,HNRNPA0,SND1,SECISBP2,PHF2,SSC5D,SOCS5,CNOT3,KLF4,ZC3H12A,RELB,EMILIN1,UNK,METTL3,INPPL1,DND1,EIF4EBP1,TARBP2,LRP3,LSM6,CX3CL1,DLL4,PCIF1,PCBP4,SLC35C2,SRSF9,DCPS,SELENOS,TRIM27,PLA2G3,KAT5,LIMD1,IGFBP5,MRTO4,C1QBP,NANOS3,C19orf66,CSK,AKT1,PAIP1,KHSRP,GIT1,CARHSP1,MAP2K2,CACTIN,ANAPC2,MBD3,SARS,MIR214,MIR155,RBM8A,RNH1,MIR374B,TENT5B,TRIB2,ZAR1L	yellow	VSMC_M3
GO:0051926	0.29	0.86	4	39	negative regulation of calcium ion transport	BP	1	PACSIN3,GSTO1,TRIM27,AKT1	yellow	VSMC_M3
GO:0010035	0.30	0.77	33	435	response to inorganic substance	BP	1	CDK4,ITPR3,PLEC,KLF4,ZC3H12A,KRT8,SLC30A3,OGG1,UCP2,PYCR1,SLC11A2,SOD1,GPX1,SYT12,RIPK3,RELA,SIPA1,ATIC,TXNRD2,BAD,HSD17B1,CD9,ANXA11,CAPN2,S100A16,EEF2K,AKT1,HMGCS1,TRAP1,ATP5F1D,JUND,OSER1,NSMCE3	yellow	VSMC_M3
GO:0007283	0.30	0.77	28	357	spermatogenesis	BP	1	BAG6,SBF1,IFT27,SIX5,ZNF296,PAFAH1B3,DLEC1,METTL3,CEP131,DND1,YIF1B,MORN2,BCL2L1,KDM2B,SOD1,TYRO3,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,BAD,NANOS3,RFX2,STK11,TAZ,FAM50A,MEIG1	yellow	VSMC_M3
GO:2000058	0.30	0.80	12	143	regulation of ubiquitin-dependent protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,WNT10B,CCAR2,RNF19B,UBXN1,CCDC22,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0002685	0.30	0.80	13	152	regulation of leukocyte migration	BP	1	IL1R1,EMILIN1,SWAP70,GREM1,CX3CL1,ST3GAL4,RIN3,MMP14,RIPK3,LGALS3,CD9,C1QBP,AKT1	yellow	VSMC_M3
GO:0000082	0.30	0.80	13	160	G1/S transition of mitotic cell cycle	BP	1	CDK4,CTDSP2,KLF4,KMT2E,EIF4EBP1,CDK2AP2,PSME2,PRMT2,CTDSP1,SDE2,AKT1,MIR214,CDC34	yellow	VSMC_M3
GO:0008347	0.30	0.86	4	40	glial cell migration	BP	1	SCRIB,CX3CL1,MMP14,CD9	yellow	VSMC_M3
GO:0070372	0.30	0.79	17	211	regulation of ERK1 and ERK2 cascade	BP	1	NELFE,PDGFRA,KLF4,TPBG,SPRED2,SLC9A3R1,EMILIN1,CAVIN3,CX3CL1,PDGFA,EIF3A,PHB2,CSK,CARD9,ERBB4,PTPRR,GLIPR2	yellow	VSMC_M3
GO:0016441	0.30	0.81	10	115	posttranscriptional gene silencing	BP	1	ZC3H12A,METTL3,DND1,TARBP2,LIMD1,MAP2K2,MIR214,MIR155,MIR374B,ZAR1L	yellow	VSMC_M3
GO:0009790	0.30	0.75	59	841	embryo development	BP	1	BAG6,CTHRC1,PBX2,H2AFY,SCRIB,PDGFRA,EPN1,CNOT3,KLF4,HOXA1,WDPCP,CCM2,KRT8,SLC9A3R1,RNF220,UNK,INSIG1,PSMC4,RIC8A,DEAF1,HOXC4,LRIG1,HM13,BCL2L1,GREM1,KDM2B,SOD1,DLL4,IRX1,PDGFA,MMP14,COL6A1,THOC5,STMN3,PBX1,ARNT2,SMARCB1,PBX4,TEAD4,DBN1,CAPN2,MTHFR,CRABP2,ARMC5,SLC39A1,AATF,TTC39C,ZNF358,ZNF830,AKT1,NSDHL,SLC35E2B,EHMT1,MBD3,NDST1,ERBB4,PTPRR,ARFRP1,DUSP5	yellow	VSMC_M3
GO:0033993	0.30	0.75	48	657	response to lipid	BP	1	CDK4,HNRNPA0,PPARD,KLF4,ZC3H12A,INSIG1,OGG1,UCP2,AACS,SCARB1,ACSL1,CX3CL1,WNT10B,SCD,SELENOS,FABP3,PABPN1,PCK2,PRMT2,KAT5,RELA,IDH1,ARNT2,PHB2,BAD,ARPC1B,CNP,PKN1,CAPN2,PALM3,PER1,PMVK,TRIM25,SMARCA4,CARM1,AKT1,HMGCS1,SAFB,SAFB2,GIT1,SLC6A4,LDOC1,CACTIN,IRAK1,MBD3,TWF2,JUND,LOXL1	yellow	VSMC_M3
GO:0046324	0.30	0.86	4	44	regulation of glucose import	BP	1	ENPP1,SELENOS,CAPN10,AKT1	yellow	VSMC_M3
GO:0001818	0.30	0.79	16	195	negative regulation of cytokine production	BP	1	SSC5D,SOCS5,KLF4,ZC3H12A,RELB,CX3CL1,SELENOS,TRIM27,KAT5,C1QBP,CSK,GIT1,CACTIN,SARS,MIR155,TRIB2	yellow	VSMC_M3
GO:0002534	0.30	0.86	4	40	cytokine production involved in inflammatory response	BP	1	ZC3H12A,PLA2G3,PER1,CARD9	yellow	VSMC_M3
GO:1900015	0.30	0.86	4	40	regulation of cytokine production involved in inflammatory response	BP	1	ZC3H12A,PLA2G3,PER1,CARD9	yellow	VSMC_M3
GO:0071333	0.30	0.81	9	110	cellular response to glucose stimulus	BP	1	PPARD,LGALS1,UCP2,AACS,PCK2,SMARCB1,BAD,SMARCA4,JAGN1	yellow	VSMC_M3
GO:0006282	0.30	0.81	10	118	regulation of DNA repair	BP	1	HDAC10,FIGNL1,PNKP,OGG1,OTUB1,BABAM1,MAD2L2,PPP4C,CXorf57,SIRT6	yellow	VSMC_M3
GO:0045814	0.30	0.86	4	43	negative regulation of gene expression, epigenetic	BP	1	H2AFY,PHF2,TRIM27,MBD3	yellow	VSMC_M3
GO:0006333	0.30	0.81	9	106	chromatin assembly or disassembly	BP	1	H2AFY,PHF2,H3F3B,SMARCD2,SMARCB1,MTA2,H3F3A,SMARCA4,UBN1	yellow	VSMC_M3
GO:0006284	0.30	0.86	4	39	base-excision repair	BP	1	PNKP,MUTYH,OGG1,SMUG1	yellow	VSMC_M3
GO:0015980	0.30	0.77	22	259	energy derivation by oxidation of organic compounds	BP	1	ENPP1,NDUFB9,PLEC,CAVIN3,IDH3B,OGDHL,UQCRFS1,CHCHD2,SELENOS,SDHA,NDUFV1,UQCRC1,IDH1,CHCHD10,UQCC3,ATP5PD,AKT1,TRAP1,NDUFS7,ATP5F1D,TAZ,SURF1	yellow	VSMC_M3
GO:0080134	0.30	0.74	71	970	regulation of response to stress	BP	1	BAG6,HDAC10,ATF6B,TTLL12,H2AFY,PPARD,SHARPIN,PDGFRA,IL1R1,SOCS5,KLF4,SPRED2,ZC3H12A,FIGNL1,PNKP,ZYX,MGLL,INSIG1,OGG1,METTL3,P4HB,PYCR1,TARBP2,BCL2L1,CX3CL1,SOD1,CCAR2,TYRO3,CHCHD2,ST3GAL4,SELENOS,MVK,PDGFA,GPX1,QARS,THOC5,PSMB4,PLA2G3,RELA,BAD,IFI35,OTUB1,LETM1,CD9,PLAU,TNFRSF1A,BABAM1,C1QBP,UBXN1,MAD2L2,ARHGEF2,PER1,PPP4C,CDC37,CXorf57,AKT1,GIT1,SIRT6,MAP2K2,CACTIN,HIC1,TRAP1,CARD9,TRADD,MIR214,RF00024,TNFRSF12A,IGFBP6,ZNF385A,TXNDC12,IER5	yellow	VSMC_M3
GO:0032507	0.30	0.84	5	55	maintenance of protein location in cell	BP	1	INSIG1,CHCHD10,DBN1,AKT1,TWF2	yellow	VSMC_M3

GO:0010468	0.30	0.72	239	3428	regulation of gene expression	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,TRAPPC9,PPARD,SCRIB,SND1,PDGFRA,IL1R1,SECISBP2,PHF2,SSC5D,SOCS5,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,SNRNP70,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,EMILIN1,DMAP1,CIC,UNK,OGG1,SERTAD1,TTC5,METTL3,CXXC5,INPPL1,DND1,EIF4EBP1,CAVIN3,DEAF1,HOXC4,LDLRAD3,TARBP2,KMT2B,NAT10,ZNF740,PDE4D,EIF4B,LRP3,RALY,ZBTB38,LSM6,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,SRSF9,DCPS,IRX1,SELENOS,RRP1B,BRD9,ZCCHC17,MMP14,C14orf93,GPX1,AIP,CLCF1,NGDN,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,SMARCD2,BRMS1,BUD23,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,MRTO4,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,CDC37,CD276,RAVER1,AATF,C19orf66,CSK,MID2,RBM22,ZNF521,ZNF358,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,GIT1,SLC6A4,CARHSP1,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,HMG20B,CDK11B,SSU72,HIC1,TRAP1,MNT,EHMT1,AP3D1,MKNK2,IRAK1,ANAPC2,MBD3,FAM50A,MED16,CARD9,SARS,TRADD,MIR214,MI	yellow	VSMC_M3
GO:0048259	0.30	0.82	7	85	regulation of receptor-mediated endocytosis	BP	1	CD63,SCRIB,GREM1,RIN3,TNK2,ANKRD13B,GSG1L	yellow	VSMC_M3
GO:0015718	0.30	0.83	6	66	monocarboxylic acid transport	BP	1	SLC9A3R1,SLC16A5,SLC16A14,SLC26A6,PLA2G3,SLC27A4	yellow	VSMC_M3
GO:0060147	0.30	0.86	4	41	regulation of posttranscriptional gene silencing	BP	1	ZC3H12A,DND1,LIMD1,MAP2K2	yellow	VSMC_M3
GO:0051649	0.30	0.73	118	1679	establishment of localization in cell	BP	1	PQLC1,CD63,DCTN2,SQSTM1,CCHCR1,SNX9,SAMM50,SREBF2,ITPR3,SGSM3,PACSIN1,PPARD,SCRIB,IFT27,VPS28,TOM1,ASNA1,PLEKHA8,EIPR1,ZC3H12A,SNX3,EHD2,SLC9A3R1,DMAP1,SNX17,INSIG1,MYRIP,SEC13,UCP2,CEP131,LAMTOR1,NUMA1,YIF1B,RAB20,HM13,PDE4D,RRS1,SLC11A2,PINX1,DCTN1,CX3CL1,SOD1,CHP1,AP2A2,HTATIP2,RAB35,RBM15B,SELENOS,GSTO1,FABP3,PABPN1,AIP,AP1G2,SYT12,TRIM27,PCNT,NUDC,THOC5,CAPN10,PLA2G3,PTPN23,VPS51,PEX5,ZDHHC3,THOC3,BLOC1S4,PHB2,BAD,COPE,LETM1,MVB12A,NUP88,CHERP,WASHC1,AP1M1,EML3,CCDC22,SNX8,LMAN2,RAB24,MAD1L1,CLTB,ARHGEF2,SNF8,RANGRF,STX10,CORO1A,ATP5PD,TMED1,SYNE3,CDC37,MYO19,ATG3,RBM22,AKT1,SNX18,DENND1C,RANBP3,GIT1,SLC6A4,MAP2K2,AP3D1,SSNA1,ATP5F1D,STK11,TMEM201,SPG7,WDR34,TRAPPC5,PLA2G4E,AP5B1,JAGN1,MIS12,UNC13A,ARFRP1,TIMM22,PHETA2,GSG1L	yellow	VSMC_M3
GO:0062197	0.31	0.77	22	282	cellular response to chemical stress	BP	1	PLEC,PDGFRA,KLF4,ZC3H12A,RELB,P4HB,PYCR1,GSR,AQP5,SOD1,ANKRD2,CHCHD2,SELENOS,GPX1,RIPK3,RELA,BAD,LETM1,ARHGEF2,AKT1,TRAP1,OSER1	yellow	VSMC_M3
GO:0070371	0.31	0.78	18	227	ERK1 and ERK2 cascade	BP	1	NELFE,PDGFRA,KLF4,TPBG,SPRED2,SLC9A3R1,EMILIN1,CAVIN3,CX3CL1,PDGFA,EIF3A,PHB2,CSK,MAP2K2,CARD9,ERBB4,PTPRR,GLIPR2	yellow	VSMC_M3
GO:0010720	0.31	0.78	17	231	positive regulation of cell development	BP	1	CUL7,DBNL,PLXND1,BAIAP2,P4HB,CX3CL1,CLCF1,LIMK1,RELA,BAD,C1QBP,DBN1,CRABP2,EEF2K,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0010564	0.31	0.75	38	515	regulation of cell cycle process	BP	1	CDK4,CTDSP2,H2AFY,SND1,CUL7,KLF4,KMT2E,CEP131,NUMA1,NAT10,BCL2L1,PINX1,DCTN1,WNT10B,CCAR2,CDK2AP2,PSME2,PRMT2,THOC5,PBX1,PHB2,CTDSP1,METTL13,BABAM1,RCC2,EML3,SDE2,MIIP,MAD1L1,MAD2L2,MYO19,ZNF830,AKT1,GIT1,AURKAIP1,MIR214,NABP2,FBXO6	yellow	VSMC_M3
GO:0016525	0.31	0.82	7	82	negative regulation of angiogenesis	BP	1	EPN1,KLF4,EMILIN1,PDE3B,YJEFN3,SARS,MIR214	yellow	VSMC_M3
GO:0051128	0.31	0.72	129	1877	regulation of cellular component organization	BP	1	ENPP1,CD63,RUFY1,SQSTM1,SNX9,FNIP1,SREBF2,H2AFY,PACSIN1,PPARD,SCRIB,LGALS1,VPS28,CUL7,DNPH1,PDGFRA,PHF2,KLF4,DBNL,TPBG,WDPCP,PNKP,SNX3,EHD2,PLXND1,EMILIN1,SNX17,H3F3B,SEPT9,BAIAP2,CEP131,LAMTOR1,NUMA1,EIF4EBP1,ARHGAP22,ARHGAP33,NAT10,BCL2L1,SWAP70,CAPG,PINX1,GREM1,KDM2B,DCTN1,RAPSN,CX3CL1,WNT10B,PACSIN3,CCAR2,CISH,RIN3,PDGFA,MMP14,CDK2AP2,GPX1,CORO1B,NGEF,PLEKHO1,IGSF9,LRFN4,NECTIN1,TRIM27,ARPIN,LIMK1,PFDN2,TNK2,PLA2G3,STMN3,CCDC85B,PTPN23,SIPA1,RHOC,ALKBH4,MID1IP1,PEX5,CHCHD10,IGFBP5,BAD,LGALS3,ARPC1B,TNFRSF1A,WASHC1,RCC2,EML3,H3F3A,DBN1,CAPN2,MAD1L1,PIP4K2B,MAD2L2,CRABP2,ARHGEF2,RANGRF,CORO1A,SLX1A,RABEP2,SMARCA4,CARM1,EEF2K,MYO19,C19orf66,ATG3,DOCK11,INF2,AKT1,GIT1,ANKRD13B,HDGFL2,SIRT6,MAP2K2,CDK11B,AURKAIP1,NCLN,ACAP3,ANAPC2,STK11,NEGR1,MIR214,NABP2,TWF2,ELN,UNC13A,CDC42EP5,NSMF,CDC34,GBA2,STUB1,ARPC5L,GSG1L	yellow	VSMC_M3
GO:1901607	0.31	0.84	5	49	alpha-amino acid biosynthetic process	BP	1	SEPHS1,PYCR1,GLUD1,ILVBL,MTHFR	yellow	VSMC_M3

GO:1901700	0.31	0.73	88	1234	response to oxygen-containing compound	BP	1	ENPP1,CDK4,HNRNPA0,PPARD,PLEC,LGALS1,PDGFRA,KLF4,ZC3H12A,KRT8,SLC9A3R1,DMAP1,INSIG1,OGG1,UCP2,BAIAP2,INPPL1,LAMTOR1,PYCR1,EIF4EBP1,AACS,SCARB1,BCL2L1,TNS2,ACSL1,PDE3B,CX3CL1,WNT10B,SOD1,SCD,DCPS,SELENOS,FABP3,PABPN1,GPX1,PCK2,COL6A1,SLC26A6,RIPK3,CAPN10,KAT5,RELA,SIPA1,ARNT2,SMARCB1,TXNRD2,PHB2,IGFBP5,BAD,LAMTOR4,ARPC1B,CD9,CNP,KLF3,CAPN2,PALM3,MTHFR,PIP4K2B,ARHGEF2,PER1,PMVK,TUFM,TRIM25,SMARCA4,CARM1,EEF2K,CSK,AKT1,HMGCS1,GIT1,SLC6A4,LDOC1,CACTIN,TRAP1,IRAK1,MBD3,MAN1B1,CARD9,APRT,SLC27A4,TGFBR3,TWF2,JUND,LOXL1,JAGN1,COL6A2,NSMF,OSER1	yellow	VSMC_M3
GO:0048524	0.31	0.84	5	55	positive regulation of viral process	BP	1	TRIM11,LGALS1,P4HB,TARBP2,TYRO3	yellow	VSMC_M3
GO:0009261	0.31	0.85	4	40	ribonucleotide catabolic process	BP	1	NUDT3,PDE4D,NT5C,ITPA	yellow	VSMC_M3
GO:0033673	0.31	0.78	15	191	negative regulation of kinase activity	BP	1	H2AFY,PLEC,SOCS5,TARBP2,CHP1,QARS,TRIM27,WASHC1,PKN1,PIP4K2B,MVP,CSK,AKT1,MIDN,TRIB2	yellow	VSMC_M3
GO:0030193	0.31	0.84	5	50	regulation of blood coagulation	BP	1	PDGFRA,ST3GAL4,PDGFA,CD9,PLAU	yellow	VSMC_M3
GO:0002042	0.31	0.84	5	55	cell migration involved in sprouting angiogenesis	BP	1	KLF4,GREM1,EGR3,DLL4,AKT1	yellow	VSMC_M3
GO:0048146	0.31	0.85	4	41	positive regulation of fibroblast proliferation	BP	1	CDK4,PDGFRA,PDGFA,S100A6	yellow	VSMC_M3
GO:0044265	0.31	0.73	69	947	cellular macromolecule catabolic process	BP	1	SQSTM1,BAG6,HNRNPA0,SHARPIN,VPS28,SND1,CUL7,SECISBP2,HSPBP1,SOCS5,CNOT3,PSMB3,ZC3H12A,RCN3,TMUB1,PSMC4,SEL1L2,METTL3,DND1,HM13,LSM6,WNT10B,CCAR2,PCBP4,RNF19B,DCPS,SELENOS,MANBA,ZCCHC17,GPX1,PSME2,ADRM1,PSMB4,PTPN23,RNASEH2C,KAT5,MRTO4,MVB12A,UBXN1,CCDC22,USP27X,CAPN2,AMER1,NANOS3,FBXL19,DFFA,SNF8,TRIM25,USP43,ANKRD9,AKT1,PAIP1,KHSRP,CARHSP1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,PSMB10,RBM8A,RNH1,TENT5B,TRIB2,CDC34,FBXO6,TRIR,STUB1,CCDC115	yellow	VSMC_M3
GO:0016049	0.31	0.75	29	399	cell growth	BP	1	ENPP1,PPARD,DNPH1,DBNL,H3F3B,LAMTOR1,GREM1,KDM2B,CCAR2,CISH,MMP14,LIMK1,PRMT2,CCDC85B,SIPA1,IGFBP5,H3F3A,DBN1,MAD2L2,CRABP2,SMARCA4,AKT1,HDGFL2,SIRT6,CDK11B,ANAPC2,STK11,TWF2,UNC13A	yellow	VSMC_M3
GO:0009124	0.31	0.85	4	37	nucleoside monophosphate biosynthetic process	BP	1	IMPDH2,ATIC,AMPD2,APRT	yellow	VSMC_M3
GO:0048255	0.31	0.85	4	43	mRNA stabilization	BP	1	HNRNPA0,DND1,PAIP1,TENT5B	yellow	VSMC_M3
GO:0097237	0.31	0.81	8	85	cellular response to toxic substance	BP	1	GSR,SOD1,SELENOS,GSTO1,GPX1,MGST3,TXNRD2,PRXL2A	yellow	VSMC_M3
GO:0030217	0.31	0.78	14	179	T cell differentiation	BP	1	NCAPH2,SOCS5,ZC3H12A,RELB,METTL3,SOD1,EGR3,DLL4,RIPK3,SART1,BAD,ARMC5,AP3D1,STK11	yellow	VSMC_M3
GO:2001020	0.31	0.77	16	200	regulation of response to DNA damage stimulus	BP	1	HDAC10,SPRED2,FIGNL1,PNKP,OGG1,BCL2L1,CCAR2,THOC5,OTUB1,BABAM1,MAD2L2,PPP4C,CXorf57,SIRT6,HIC1,ZNF385A	yellow	VSMC_M3
GO:0080090	0.32	0.71	293	4206	regulation of primary metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,ZNF608,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,SGSM3,TRAPPC9,PPARD,PLEC,VPS28,SND1,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,FHL3,SPRED2,ZC3H12A,FIGNL1,PNKP,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,EMILIN1,DMAP1,CIC,UNK,INSIG1,OGG1,SERTAD1,TTC5,PSMC4,METTL3,CXXC5,LAMTOR1,DND1,EIF4EBP1,DELE1,DEAF1,HOXC4,LDLRAD3,TARBP2,KMT2B,SCARB1,NAT10,ZNF740,PDE4D,EIF4B,SWAP70,RALY,ACSL1,ZBTB38,TNKS1BP1,PINX1,GREM1,KDM2B,PDE3B,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,CHCHD2,RBM15B,SRSF9,RNF19B,DCPS,IRX1,DHCR7,SELENOS,RRP1B,ETFBKMT,BRD9,FABP3,ZCCHC17,PDGFA,MMP14,GPX1,AIP,CLCF1,NGDN,TSHZ2,QARS,ASB9,PSME2,PIR,TRIM27,LIMK1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,SMARCD2,PFDN2,BRMS1,BUD23,TNK2,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,IDH1,ARNT2,ZFPL1,LIMD1,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,NDP,IGFBP5,BAD,CTDSP1,MLF2,OTUB1,EID1,SSBP4,METTL13,MPV17L2,ZNF394,LGALS3,C11orf95,BUD31,TNFRSF1A,BABAM1,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UBXN1,WASHC1,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,AMER1,MTHFR,PIP4K2B,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,DFFA,SP2,ARHGEF2,ARMC5,SNF8,MVP,PER1,NFIX,PPP4C,SLX1A,IRF2BPL,TRIM25,	yellow	VSMC_M3
GO:0045446	0.32	0.81	7	91	endothelial cell differentiation	BP	1	COL15A1,CCM2,FASN,PDE4D,GPX1,TNFRSF1A,TJP3	yellow	VSMC_M3
GO:0071426	0.32	0.82	6	66	ribonucleoprotein complex export from nucleus	BP	1	RRS1,RBM15B,PABPN1,THOC5,THOC3,NUP88	yellow	VSMC_M3
GO:0000387	0.32	0.85	4	38	spliceosomal snRNP assembly	BP	1	GEMIN7,SART1,PRPF6,CD2BP2	yellow	VSMC_M3
GO:1901800	0.32	0.80	9	104	positive regulation of proteasomal protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,PSMC4,RNF19B,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0062012	0.32	0.76	19	243	regulation of small molecule metabolic process	BP	1	ENPP1,PPARD,INSIG1,SOD1,DHCR7,SELENOS,ETFBKMT,FABP3,PLA2G3,MID1IP1,BAD,FOXK1,AKT1,GIT1,PGP,MIDN,TAZ,JMJD8,SLC27A4	yellow	VSMC_M3
GO:0006406	0.32	0.83	5	53	mRNA export from nucleus	BP	1	RBM15B,PABPN1,THOC5,THOC3,NUP88	yellow	VSMC_M3
GO:0071427	0.32	0.83	5	53	mRNA-containing ribonucleoprotein complex export from nucleus	BP	1	RBM15B,PABPN1,THOC5,THOC3,NUP88	yellow	VSMC_M3
GO:1903052	0.32	0.79	10	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,PSMC4,RNF19B,CCDC22,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0042698	0.32	0.84	4	46	ovulation cycle	BP	1	PDGFRA,TYRO3,SGPL1,ZNF830	yellow	VSMC_M3
GO:0061014	0.32	0.81	7	82	positive regulation of mRNA catabolic process	BP	1	CNOT3,ZC3H12A,METTL3,DND1,DCPS,NANOS3,KHSRP	yellow	VSMC_M3

GO:0043207	0.32	0.73	61	820	response to external biotic stimulus	BP	1	CDK4,TTLL12,HNRNPA0,TRIM11,PPARD,PPP1R14B,SSC5D,ZC3H12A,ZYX,SNX3,KRT8,RELB,METTL3,BAIAP2,RAB20,TARBP2,SCARB1,BCL2L1,CX3CL1,TYRO3,RNF19B,SELENOS,RRP1B,PABPN1,GPX1,PCK2,TRIM27,SLC26A6,RIPK3,TNK2,BANF1,RELA,MAP3K14,PHB2,IFI35,LGALS3,TNFRSF1A,C1QBP,CNP,CAPN2,PALM3,TBKBP1,ARHGEF2,ARMC5,CORO1A,TRIM25,CDC37,C19orf66,MID2,AKT1,GTF2F1,GIT1,LDOC1,CACTIN,IRAK1,C8G,CARD9,JUND,LOXL1,EEF1G,JAGN1	yellow	VSMC_M3
GO:0051707	0.32	0.73	61	820	response to other organism	BP	1	CDK4,TTLL12,HNRNPA0,TRIM11,PPARD,PPP1R14B,SSC5D,ZC3H12A,ZYX,SNX3,KRT8,RELB,METTL3,BAIAP2,RAB20,TARBP2,SCARB1,BCL2L1,CX3CL1,TYRO3,RNF19B,SELENOS,RRP1B,PABPN1,GPX1,PCK2,TRIM27,SLC26A6,RIPK3,TNK2,BANF1,RELA,MAP3K14,PHB2,IFI35,LGALS3,TNFRSF1A,C1QBP,CNP,CAPN2,PALM3,TBKBP1,ARHGEF2,ARMC5,CORO1A,TRIM25,CDC37,C19orf66,MID2,AKT1,GTF2F1,GIT1,LDOC1,CACTIN,IRAK1,C8G,CARD9,JUND,LOXL1,EEF1G,JAGN1	yellow	VSMC_M3
GO:0008637	0.32	0.80	8	87	apoptotic mitochondrial changes	BP	1	BCL2L1,CCAR2,GPX1,CHCHD10,BAD,ATG3,AKT1,ERBB4	yellow	VSMC_M3
GO:0001933	0.32	0.76	21	276	negative regulation of protein phosphorylation	BP	1	ENPP1,CTDSP2,H2AFY,PLEC,SOCS5,SPRED2,ZC3H12A,MICAL1,EMILIN1,TARBP2,PDE4D,GREM1,CHP1,QARS,TRIM27,CTDSP1,PKN1,MVP,AKT1,CACTIN,TRIB2	yellow	VSMC_M3
GO:1900407	0.32	0.82	6	66	regulation of cellular response to oxidative stress	BP	1	P4HB,PYCR1,SOD1,GPX1,AKT1,TRAP1	yellow	VSMC_M3
GO:0009967	0.32	0.72	80	1127	positive regulation of signal transduction	BP	1	CD63,NELFE,FNIP1,PRR5,TXNDC15,PPARD,EEF1D,LGALS1,SHARPIN,PDGFRA,IL1R1,TPBG,SPRED2,ZC3H12A,PLEKHA4,SLC9A3R1,RNF220,SEC13,BAIAP2,CXXC5,LAMTOR1,NUMA1,CAVIN3,PLEKHF1,GREM1,CX3CL1,WNT10B,SOD1,CCAR2,DLL4,SLC35C2,TSPAN5,PDGFA,GPX1,TRIM27,RIPK3,RELA,RHOC,MAP3K14,SMARCB1,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,TNFRSF1A,C1QBP,CHERP,EVC,CCDC22,AMER1,TRIM25,RPL37,S100A4,SMARCA4,CSK,MID2,TEDC1,RAB34,MYDGF,MAP2K2,HIC1,CTNS,TEDC2,CSNK1G2,IRAK1,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,TGFBR3,TRADD,NDST1,TNFRSF12A,ERBB4,IGFBP6,ZNF385A,GLIPR2	yellow	VSMC_M3
GO:1990090	0.32	0.84	4	46	cellular response to nerve growth factor stimulus	BP	1	RAB35,CORO1A,EEF2K,AKT1	yellow	VSMC_M3
GO:0060688	0.32	0.84	4	42	regulation of morphogenesis of a branching structure	BP	1	GREM1,PDGFA,PHB2,SIRT6	yellow	VSMC_M3
GO:0044839	0.32	0.78	11	132	cell cycle G2/M phase transition	BP	1	CDK4,H2AFY,CCDC57,PINX1,WNT10B,PBX1,BABAM1,RCC2,MIIP,ZNF830,NABP2	yellow	VSMC_M3
GO:0031329	0.32	0.73	50	689	regulation of cellular catabolic process	BP	1	BAG6,SNX9,SREBF2,HNRNPA0,SECISBP2,HSPBP1,SOCS5,CNOT3,ZC3H12A,SNRNP70,PSMC4,METTL3,DND1,SCARB1,PLEKHF1,WNT10B,PACSIN3,CCAR2,PCBP4,RNF19B,DCPS,ETFBKMT,ZCCHC17,GPX1,PSME2,TRIM27,KAT5,IDH1,PHB2,BAD,UBXN1,WASHC1,CCDC22,FOXK1,AMER1,PIP4K2B,NANOS3,DFFA,MTMR4,MID2,AKT1,PAIP1,KHSRP,CARHSP1,SIRT6,STK11,WDR24,TENT5B,TRIB2,STUB1	yellow	VSMC_M3
GO:2000181	0.32	0.81	7	83	negative regulation of blood vessel morphogenesis	BP	1	EPN1,KLF4,EMILIN1,PDE3B,YJEFN3,SARS,MIR214	yellow	VSMC_M3
GO:0098609	0.32	0.73	41	592	cell-cell adhesion	BP	1	TSTA3,SCRIB,LGALS1,PDGFRA,COL19A1,SOCS5,KLF4,ZC3H12A,METTL3,BAIAP2,SIGLEC1,RIC8A,ITGB7,SWAP70,MMP24,CX3CL1,EGR3,TYRO3,ST3GAL4,IGSF9,LRFN4,NECTIN1,SART1,PTPN23,RELA,BLOC1S4,BAD,SCARF2,LGALS3,CD9,MAD1L1,MAD2L2,CORO1A,CD276,CSK,AKT1,TJP3,CLDN6,AP3D1,IRAK1,NEGR1	yellow	VSMC_M3
GO:0050779	0.32	0.81	7	82	RNA destabilization	BP	1	CNOT3,ZC3H12A,METTL3,DND1,DCPS,NANOS3,KHSRP	yellow	VSMC_M3
GO:1904377	0.32	0.83	5	58	positive regulation of protein localization to cell periphery	BP	1	SQSTM1,NUMA1,LGALS3,RANGRF,AKT1	yellow	VSMC_M3
GO:0006970	0.33	0.81	6	71	response to osmotic stress	BP	1	RELB,AQP5,BAD,LETM1,PKN1,ARHGEF2	yellow	VSMC_M3
GO:0051341	0.33	0.81	7	79	regulation of oxidoreductase activity	BP	1	SCARB1,HM13,ETFBKMT,RIPK3,TACO1,PHB2,AKT1	yellow	VSMC_M3
GO:0080135	0.33	0.73	41	553	regulation of cellular response to stress	BP	1	BAG6,HDAC10,ATF6B,KLF4,SPRED2,ZC3H12A,FIGNL1,PNKP,INSIG1,OGG1,P4HB,PYCR1,BCL2L1,SOD1,CCAR2,CHCHD2,SELENOS,GPX1,QARS,THOC5,BAD,OTUB1,LETM1,BABAM1,UBXN1,MAD2L2,ARHGEF2,PER1,PPP4C,CXorf57,AKT1,SIRT6,MAP2K2,HIC1,TRAP1,CARD9,RF00024,IGFBP6,ZNF385A,TXNDC12,IER5	yellow	VSMC_M3
GO:0048515	0.33	0.79	9	106	spermatid differentiation	BP	1	SBF1,SIX5,CEP131,YIF1B,SLC26A6,IQCG,PLA2G3,RFX2,MEIG1	yellow	VSMC_M3
GO:0090066	0.33	0.74	30	418	regulation of anatomical structure size	BP	1	CDK4,SNX9,PPARD,DBNL,SLC9A3R1,BAIAP2,SWAP70,CAPG,SOD1,RIN3,GPX1,CORO1B,TRIM27,ARPIN,LIMK1,LAMTOR4,ARPC1B,WASHC1,DBN1,CRABP2,CORO1A,AKT1,SLC6A4,ANAPC2,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:1900046	0.33	0.83	5	51	regulation of hemostasis	BP	1	PDGFRA,ST3GAL4,PDGFA,CD9,PLAU	yellow	VSMC_M3
GO:0042176	0.33	0.74	26	342	regulation of protein catabolic process	BP	1	BAG6,SNX9,SGSM3,VPS28,HSPBP1,SOCS5,SNRNP70,SNX3,PSMC4,WNT10B,PACSIN3,CCAR2,RNF19B,GPX1,ASB9,PSME2,RELA,UBXN1,CCDC22,AMER1,MAD2L2,SNF8,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:2001022	0.33	0.80	8	95	positive regulation of response to DNA damage stimulus	BP	1	HDAC10,SPRED2,PNKP,CCAR2,BABAM1,MAD2L2,HIC1,ZNF385A	yellow	VSMC_M3
GO:0070507	0.33	0.78	10	135	regulation of microtubule cytoskeleton organization	BP	1	NUMA1,DCTN1,CDK2AP2,STMN3,MID1IP1,EML3,ARHGEF2,RANGRF,GIT1,GBA2	yellow	VSMC_M3
GO:0000422	0.33	0.81	6	71	autophagy of mitochondrion	BP	1	SQSTM1,SREBF2,PHB2,CDC37,ATG3,TAZ	yellow	VSMC_M3
GO:0061726	0.33	0.81	6	71	mitochondrion disassembly	BP	1	SQSTM1,SREBF2,PHB2,CDC37,ATG3,TAZ	yellow	VSMC_M3
GO:0051271	0.33	0.76	18	241	negative regulation of cellular component movement	BP	1	PPARD,KLF4,SLC9A3R1,EMILIN1,GREM1,CX3CL1,DLL4,RIN3,CORO1B,ARPIN,PTPN23,IGFBP5,CD9,MIIP,AKT1,TGFBR3,MIR214,PTPRR	yellow	VSMC_M3
GO:1902808	0.33	0.84	4	41	positive regulation of cell cycle G1/S phase transition	BP	1	KMT2E,PHB2,AKT1,MIR214	yellow	VSMC_M3
GO:0030258	0.33	0.77	14	171	lipid modification	BP	1	ACAT2,CERK,PPARD,CPT1C,INPPL1,LAMTOR1,DGKZ,ST3GAL4,ETFBKMT,FABP3,ILVBL,MTMR4,AKT1,GBA2	yellow	VSMC_M3

GO:0000122	0.33	0.72	50	694	negative regulation of transcription by RNA polymerase II	BP	1	SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,SREBF2,H2AFY,PPARD,KLF4,CC2D1B,ZNF282,ZNF296,DMAP1,CXXC5,DEAF1,KDM2B,WNT10B,ANKRD2,DNAJC17,DLL4,KDM1B,IRX1,TRIM27,BRMS1,KAT5,RELA,GATAD2A,EID1,METTL13,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0008089	0.33	0.84	4	44	anterograde axonal transport	BP	1	SOD1,BLOC1S4,AP3D1,SPG7	yellow	VSMC_M3
GO:0044089	0.33	0.74	31	441	positive regulation of cellular component biogenesis	BP	1	SNX9,FNIP1,TPBG,EMILIN1,SEPT9,BAIAP2,NUMA1,SWAP70,DCTN1,CX3CL1,WNT10B,CORO1B,TRIM27,ARPIN,LIMK1,RHOC,LGALS3,ARPC1B,WASHC1,PIP4K2B,SNF8,CORO1A,SLX1A,EEF2K,DOCK11,GIT1,TWF2,CDC42EP5,CDC34,STUB1,ARPC5L	yellow	VSMC_M3
GO:0000271	0.33	0.82	5	58	polysaccharide biosynthetic process	BP	1	ENPP1,SELENOS,AKT1,B3GNT9,NDST1	yellow	VSMC_M3
GO:0006470	0.33	0.76	17	228	protein dephosphorylation	BP	1	CTDSP2,SBF1,PPM1G,TNS2,SWAP70,PPM1M,PTPN23,CTDSP1,LGALS3,PPP4C,MTMR4,SSU72,PGP,STK11,PTPRR,NSMF,DUSP5	yellow	VSMC_M3
GO:0045428	0.33	0.84	4	43	regulation of nitric oxide biosynthetic process	BP	1	KLF4,ZC3H12A,AKT1,KHSRP	yellow	VSMC_M3
GO:0030036	0.33	0.73	41	600	actin cytoskeleton organization	BP	1	SNX9,PDLIM4,PACSIN1,PLEC,PDGFRA,DBNL,FHL3,ZYX,MICAL1,EHD2,KRT8,SLC9A3R1,BAIAP2,INPPL1,CAVIN3,SWAP70,CAPG,CX3CL1,PDGFA,CORO1B,TRIM27,ARPIN,LIMK1,CAPN10,RHOC,ALKBH4,FMNL1,ARPC1B,WASHC1,DBN1,MAD2L2,ARHGEF2,CORO1A,MYO19,INF2,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0050714	0.33	0.79	8	100	positive regulation of protein secretion	BP	1	PPARD,MYRIP,AACS,PCK2,CAPN10,PTPN23,BAD,GLUD1	yellow	VSMC_M3
GO:0061024	0.33	0.72	44	599	membrane organization	BP	1	PQLC1,BAG6,SNX9,SAMM50,PACSIN1,PLEC,ASNA1,PLEKHA8,SNX3,EHD2,TMEM43,SLC9A3R1,INSIG1,SEC13,BAIAP2,RAB20,BCL2L1,DCTN1,RAPSN,SOD1,PACSIN3,CHP1,ALKBH4,CHCHD10,YJEFN3,BAD,LETM1,CD9,UQCC3,CNP,PIP4K2B,MTX1,STX10,CORO1A,AKT1,SNX18,ALKBH7,RAB34,DHCR24,AP3D1,TAZ,SPG7,GBA2,TIMM22	yellow	VSMC_M3
GO:0065004	0.33	0.78	11	132	protein-DNA complex assembly	BP	1	H2AFY,H3F3B,WNT10B,SMARCB1,UBTF,TAF6L,H3F3A,SMARCA4,BRF1,UBN1,MIS12	yellow	VSMC_M3
GO:0071166	0.33	0.81	6	67	ribonucleoprotein complex localization	BP	1	RRS1,RBM15B,PABPN1,THOC5,THOC3,NUP88	yellow	VSMC_M3
GO:0090630	0.33	0.80	7	93	activation of GTPase activity	BP	1	SGSM3,SCRIB,ARHGAP22,NGEF,SIPA1,RCC2,SLC27A4	yellow	VSMC_M3
GO:0007423	0.33	0.73	29	415	sensory organ development	BP	1	CDK4,CTHRC1,PBX2,RING1,SCRIB,IFT27,PDGFRA,KLF4,HOXA1,WDPCP,CCM2,SPRED2,SIX5,SLC9A3R1,INSIG1,LRIG1,KDM2B,AQP5,WNT10B,SOD1,DLL4,IMPDH2,NECTIN1,PBX1,PBX4,C12orf57,SMARCA4,TTC39C,CTNS	yellow	VSMC_M3
GO:1901343	0.34	0.80	7	84	negative regulation of vasculature development	BP	1	EPN1,KLF4,EMILIN1,PDE3B,YJEFN3,SARS,MIR214	yellow	VSMC_M3
GO:0035601	0.34	0.79	8	99	protein deacylation	BP	1	HDAC10,SPRED2,CCAR2,BRMS1,MTA2,CTBP1,PER1,SIRT6	yellow	VSMC_M3
GO:0007005	0.34	0.73	35	436	mitochondrion organization	BP	1	SQSTM1,SAMM50,SREBF2,NDUFB9,PLEC,SHARPIN,ACAD9,SDHAF1,BCL2L1,UQCRFS1,CCAR2,CHCHD2,GPX1,AIP,TACO1,CHCHD10,PHB2,BAD,LETM1,UQCC3,CNP,MTX1,CDC37,MYO19,ATG3,INF2,AKT1,ALKBH7,NDUFS7,ATP5F1D,TAZ,SPG7,ERBB4,SURF1,TIMM22	yellow	VSMC_M3
GO:1902743	0.34	0.83	4	45	regulation of lamellipodium organization	BP	1	CORO1B,ARPIN,MIR214,TWF2	yellow	VSMC_M3
GO:0045892	0.34	0.71	67	943	negative regulation of transcription, DNA-templated	BP	1	NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,TRIM11,PPARD,KLF4,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,CXXC5,DEAF1,ZBTB38,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,KDM1B,IRX1,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0031346	0.34	0.74	21	302	positive regulation of cell projection organization	BP	1	PACSIN1,CUL7,DBNL,SNX3,PLXND1,SEPT9,BAIAP2,CX3CL1,CORO1B,LIMK1,PLA2G3,WASHC1,DBN1,CRABP2,EEF2K,DOCK11,ANAPC2,STK11,NEGR1,TWF2,CDC42EP5	yellow	VSMC_M3
GO:0016575	0.34	0.80	6	71	histone deacetylation	BP	1	HDAC10,BRMS1,MTA2,CTBP1,PER1,SIRT6	yellow	VSMC_M3
GO:2000060	0.34	0.79	8	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	HSPBP1,SOCS5,RNF19B,CCDC22,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:2000112	0.34	0.69	196	2822	regulation of cellular macromolecule biosynthetic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,UNK,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,HOXC4,TARBP2,KMT2B,NAT10,ZNF740,EIF4B,RALY,ZBTB38,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,DCPS,IRX1,SELENOS,RRP1B,BRD9,AIP,NGDN,TSH2Z2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,SMARCD2,BRMS1,TACO1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,C19orf66,MID2,ZNF521,ZNF358,ZNF830,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,TRAP1,MNT,EHMT1,AP3D1,MKNK2,IRAK1,MBD3,MED16,CARD9,SARS,POMT1,TRADD,RBM8A,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,ZNF385A,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3

GO:0044248	0.34	0.70	126	1755	cellular catabolic process	BP	1	ENPP1,SQSTM1,BAG6,SNX9,HDAC10,ACAT2,SREBF2,HNRNPA0,NUDT3,PPARD,MPST,SHARPIN,VPS28,SND1,CUL7,DNPH1,SECISBP2,HSPBP1,SOCS5,CNOT3,PSMB3,ZC3H12A,BLVRA,CPT1C,RCN3,SNRNP70,MGLL,TMUB1,BCKDHA,BLVRB,OGG1,PSMC4,SEL1L2,METTL3,DND1,GNPDA1,SMUG1,SCARB1,HM13,PDE4D,PCCB,PLEKHF1,ACSL1,LSM6,WNT10B,PACSIN3,CCAR2,PCBP4,RNF19B,DCPS,SELENOS,GSTO1,ETFBKMT,MANBA,ZCCHC17,LIX1L,GPX1,PCK2,PSME2,ANPEP,TRIM27,ADRM1,PSMB4,PTPN23,RNASEH2C,KAT5,IDH1,VPS51,SGPL1,PHB2,BAD,MRTO4,MVB12A,UBXN1,WASHC1,CNP,CCDC22,USP27X,GLUD1,FOXK1,ILVBL,CAPN2,RAB24,AMER1,PIP4K2B,NANOS3,FBXL19,DFFA,PGD,SNF8,TRIM25,USP43,MTMR4,CDC37,MID2,ATG3,ANKRD9,AKT1,PACS2,PAIP1,KHSRP,CARHSP1,BLMH,SIRT6,ANAPC2,SPSB3,MAN1B1,STK11,TAZ,WDR24,SLC27A4,ZNRF1,PSMB10,RBM8A,RNH1,PLA2G4E,NT5C,TENT5B,TRIB2,CDC34,FBXO6,GBA2,TRIR,STUB1,ITPA,CCDC115	yellow	VSMC_M3
GO:0048583	0.34	0.69	196	2834	regulation of response to stimulus	BP	1	ENPP1,CD63,CDK4,SQSTM1,BAG6,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PRR5,TTLL12,SREBF2,TXNDC15,H2AFY,SGSM3,DEF6,PPARD,EEF1D,LGALS1,SHARPIN,BOP1,PDGFRA,IL1R1,SOCS5,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,PNKP,ZYX,RCN3,SNX3,PLEKHA4,MGLL,SLC9A3R1,EMILIN1,RNF220,CD79A,INSIG1,SEC13,OGG1,ARHGEF40,UCP2,METTL3,BAIAP2,CXXC5,LAMTOR1,NUMA1,P4HB,PYCR1,CAVIN3,ARHGAP22,TARBP2,BCL2L1,PDE4D,TNS2,RRS1,SWAP70,PLEKHF1,GREM1,PDE3B,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,CHCHD2,SLC35C2,TSPAN5,CISH,ST3GAL4,SELENOS,ITPRIP,MVK,RIN3,PDGFA,MMP14,GPX1,AIP,CORO1B,NGEF,CLCF1,QARS,TRIM27,EIF3A,LIMK1,PRMT2,SPX,THOC5,RIPK3,PSMB4,PLA2G3,STMN3,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZDHHC3,SMARCB1,YJEFN3,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,OTUB1,LETM1,LGALS3,BUD31,CD9,PLAU,TNFRSF1A,MVB12A,BABAM1,C1QBP,CHERP,UBXN1,EVC,CCDC22,PKN1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,ARHGEF2,MVP,PER1,PPP4C,TRIM25,RPL37,MTMR4,S100A4,SMARCA4,CARM1,CDC37,CD276,AATF,CXorf57,CSK,MID2,AKT1,TEDC1,RAB34,SAFB2,GIT1,MYDGF,SIRT6,MAP2K2,CACTIN,VASN,HIC1,TRAP1,NCLN,MNT,CTNS,TEDC2,CSNK1G2,IRAK1,C8G,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,SLC27A4,TGFBR3,TRADD,MIR214,RF00024,NDST1,TNFRSF12A,ERBB4,PTPRR,IGFBP6,JAGN1,ZNF385A,TXNDC12,CDC34,IER5,APCDD1L,ARHGEF1,RGS16,DUSP5,GLIPR2,STUB1,RGS18,GSG1L	yellow	VSMC_M3
GO:0031623	0.34	0.79	7	85	receptor internalization	BP	1	CD63,SCRIB,GREM1,RIN3,CD9,ANKRD13B,GSG1L	yellow	VSMC_M3
GO:0033344	0.34	0.83	4	42	cholesterol efflux	BP	1	SREBF2,LAMTOR1,SCARB1,YJEFN3	yellow	VSMC_M3
GO:0060294	0.34	0.80	6	68	cilium movement involved in cell motility	BP	1	CEP131,YIF1B,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:0032635	0.34	0.79	8	96	interleukin-6 production	BP	1	SOCS5,ZC3H12A,CX3CL1,SELENOS,CAPN2,ARHGEF2,CSK,CARD9	yellow	VSMC_M3
GO:0032675	0.34	0.79	8	96	regulation of interleukin-6 production	BP	1	SOCS5,ZC3H12A,CX3CL1,SELENOS,CAPN2,ARHGEF2,CSK,CARD9	yellow	VSMC_M3
GO:0031638	0.34	0.83	4	38	zymogen activation	BP	1	MMP14,BAD,PLAU,DHCR24	yellow	VSMC_M3
GO:0090090	0.34	0.78	9	113	negative regulation of canonical Wnt signaling pathway	BP	1	CTHRC1,TPBG,SLC9A3R1,GREM1,LIMD1,AMER1,MAD2L2,STK11,IGFBP6	yellow	VSMC_M3
GO:1990089	0.34	0.83	4	47	response to nerve growth factor	BP	1	RAB35,CORO1A,EEF2K,AKT1	yellow	VSMC_M3
GO:0009607	0.34	0.71	63	856	response to biotic stimulus	BP	1	CDK4,TTLL12,HNRNPA0,TRIM11,PPARD,PPP1R14B,SSC5D,KLF4,ZC3H12A,ZYX,SNX3,KRT8,RELB,DLEC1,METTL3,BAIAP2,RAB20,TARBP2,SCARB1,BCL2L1,CX3CL1,TYRO3,RNF19B,SELENOS,RRP1B,PABPN1,GPX1,PCK2,TRIM27,SLC26A6,RIPK3,TNK2,BANF1,RELA,MAP3K14,PHB2,IFI35,LGALS3,TNFRSF1A,C1QBP,CNP,CAPN2,PALM3,TBKBP1,ARHGEF2,ARMC5,CORO1A,TRIM25,CDC37,C19orf66,MID2,AKT1,GTF2F1,GIT1,LDOC1,CACTIN,IRAK1,C8G,CARD9,JUND,LOXL1,EEF1G,JAGN1	yellow	VSMC_M3
GO:0006641	0.34	0.80	6	70	triglyceride metabolic process	BP	1	MGLL,INSIG1,SCARB1,ACSL1,GPX1,PCK2	yellow	VSMC_M3
GO:0007584	0.34	0.77	11	137	response to nutrient	BP	1	PPARD,OGG1,AACS,ACSL1,DCPS,RELA,MTHFR,TRIM25,HMGCS1,SLC6A4,SLC27A4	yellow	VSMC_M3
GO:0051028	0.34	0.78	9	109	mRNA transport	BP	1	SEC13,RBM15B,PABPN1,THOC5,THOC3,NUP88,MVP,KHSRP,RBM8A	yellow	VSMC_M3
GO:0031050	0.35	0.83	4	46	dsRNA processing	BP	1	ZC3H12A,METTL3,TARBP2,MAP2K2	yellow	VSMC_M3
GO:0035196	0.35	0.83	4	46	production of miRNAs involved in gene silencing by miRNA	BP	1	ZC3H12A,METTL3,TARBP2,MAP2K2	yellow	VSMC_M3
GO:0070918	0.35	0.83	4	46	production of small RNA involved in gene silencing by RNA	BP	1	ZC3H12A,METTL3,TARBP2,MAP2K2	yellow	VSMC_M3
GO:1903507	0.35	0.70	67	945	negative regulation of nucleic acid-templated transcription	BP	1	NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,TRIM11,PPARD,KLF4,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,CXXC5,DEAF1,ZBTB38,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,KDM1B,IRX1,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0042246	0.35	0.81	5	53	tissue regeneration	BP	1	PPARD,WNT10B,GPX1,CD9,ERBB4	yellow	VSMC_M3
GO:0002285	0.35	0.77	10	127	lymphocyte activation involved in immune response	BP	1	LGALS1,SOCS5,ZC3H12A,RELB,SWAP70,CLCF1,LGALS3,MAD2L2,CORO1A,DOCK11	yellow	VSMC_M3
GO:0006633	0.35	0.77	9	107	fatty acid biosynthetic process	BP	1	MGLL,INSIG1,FASN,SCD,PLA2G3,MID1IP1,ACLY,FADS2,FADS1	yellow	VSMC_M3

GO:0006355	0.35	0.69	167	2411	regulation of transcription, DNA-templated	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,OGG1,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,KMT2B,ZNF740,RALY,ZBTB38,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,AIP,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,SMARCD2,BRMS1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,MED16,CARD9,SARS,TRADD,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0043170	0.35	0.68	494	7034	macromolecule metabolic process	BP	1	ENPP1,CD63,NAB2,NHP2,CDK4,CTDSP2,SQSTM1,DHX16,ZNF608,LMF2,BAG6,SBF1,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,JADE2,TRMT12,H2AFY,HNRNPA0,TRIM11,SGSM3,TRAPPC9,NUDT3,PPARD,FANCE,EEF1D,RPL3,SCRIB,PLEC,SHARPIN,BOP1,VPS28,RPL8,SND1,CUL7,RTCB,B4GALT1,MRPS18A,AARS2,PIGO,PDGFRA,IL1R1,SECISBP2,PHF2,SSC5D,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,JOSD2,PSMB3,FHL3,SPRED2,EIPR1,MEAF6,ZC3H12A,FIGNL1,PNKP,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,GEMIN7,ZNF296,RELB,SLC9A3R1,SERP2,NAT9,MUTYH,EMILIN1,SEPHS1,TMUB1,RNF220,DMAP1,CIC,GTF3C2,PPM1G,UNK,GALNT14,OGG1,SERTAD1,TTC5,PSMC4,KAT14,P4HA3,SEL1L2,METTL3,PHLDA1,CXXC5,INPPL1,FAAP100,LAMTOR1,P4HB,DND1,RPL29,EIF4EBP1,DELE1,CAVIN3,PUS1,DEAF1,SMUG1,HOXC4,POLR1D,LDLRAD3,TARBP2,KMT2B,C12orf10,NAT10,HM13,ZNF740,PDE4D,TNS2,EIF4B,RRS1,PEPD,SWAP70,LRP3,RALY,ACSL1,ZBTB38,ARL6IP4,LSM6,TNKS1BP1,MMP24,PINX1,GATB,SETD1B,GREM1,KDM2B,PRPF40B,MCRS1,POLR2C,CX3CL1,WNT10B,FKBP11,SOD1,PACSIN3,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,RPLP2,CHP1,TYRO3,MRPL43,YAF2,HTATIP2,PCIF1,PPM1M,NPM3,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CARS,TSPAN5,CISH,SRSF9,ST3GAL4,RNF19B,DCPS,IRX1,WDR4,SELENOS,RRP1B,ETFBKMT,MANBA,TMTC1,BRD9,RBM6,RIN3,STK32C,ZCCHC17,PDGFA,MMP14,C14orf93,APEH,PABPN1,GPX1,AIP,HCCS,MOCS3,CLCF1,NGDN,TSHZ2,QARS,ASB9,PSME2,PIR,ANPEP,TRIM27,EIF3A,LIMK1,ZNRD1,RABGGTA,PRMT2,THOC5,RIPK3,KHNYN,TWIST2,LSM14B,SF3A1,	yellow	VSMC_M3
GO:0051897	0.35	0.79	7	88	positive regulation of protein kinase B signaling	BP	1	TPBG,CX3CL1,PDGFA,GPX1,IGFBP5,C1QBP,MYDGF	yellow	VSMC_M3
GO:0006984	0.35	0.82	4	44	ER-nucleus signaling pathway	BP	1	ATF6B,SREBF2,INSIG1,SELENOS	yellow	VSMC_M3
GO:0042542	0.35	0.77	10	118	response to hydrogen peroxide	BP	1	KLF4,PYCR1,SOD1,GPX1,RIPK3,RELA,BAD,CAPN2,TRAP1,OSER1	yellow	VSMC_M3
GO:0090276	0.35	0.76	11	140	regulation of peptide hormone secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:1903506	0.35	0.68	167	2412	regulation of nucleic acid-templated transcription	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,OGG1,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,KMT2B,ZNF740,RALY,ZBTB38,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,AIP,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,SMARCD2,BRMS1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,MED16,CARD9,SARS,TRADD,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0060840	0.35	0.79	6	81	artery development	BP	1	HOXA1,PLXND1,SNX17,DLL4,NDST1,LOXL1	yellow	VSMC_M3
GO:1902679	0.35	0.70	67	946	negative regulation of RNA biosynthetic process	BP	1	NAB2,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,RING1,SREBF2,H2AFY,TRIM11,PPARD,KLF4,CC2D1B,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,CXXC5,DEAF1,ZBTB38,GREM1,KDM2B,WNT10B,ANKRD2,CCAR2,DNAJC17,DLL4,YAF2,KDM1B,IRX1,QARS,TRIM27,PRMT2,TWIST2,BRMS1,CCDC85B,KAT5,RELA,LIMD1,GATAD2A,PHB2,EID1,METTL13,C11orf95,C1QBP,ZBTB49,MTA2,FOXK1,KLF3,MAD2L2,CTBP1,SP2,PER1,NFIX,IRF2BPL,SMARCA4,SIRT6,HIC1,MNT,EHMT1,MBD3,SARS,THAP7,NSMCE3,ERF	yellow	VSMC_M3
GO:0035195	0.35	0.77	9	107	gene silencing by miRNA	BP	1	ZC3H12A,METTL3,DND1,TARBP2,LIMD1,MAP2K2,MIR214,MIR155,MIR374B	yellow	VSMC_M3
GO:0051972	0.35	0.82	4	42	regulation of telomerase activity	BP	1	KLF4,PNKP,PINX1,GREM1	yellow	VSMC_M3
GO:0003158	0.35	0.77	8	107	endothelium development	BP	1	COL15A1,CCM2,FASN,PDE4D,DLL4,GPX1,TNFRSF1A,TJP3	yellow	VSMC_M3
GO:0030178	0.35	0.76	11	142	negative regulation of Wnt signaling pathway	BP	1	CTHRC1,TPBG,SLC9A3R1,GREM1,LIMD1,AMER1,MAD2L2,HIC1,STK11,IGFBP6,APCDD1L	yellow	VSMC_M3

GO:0072331	0.36	0.76	11	139	signal transduction by p53 class mediator	BP	1	BAG6,BOP1,SPRED2,RRS1,KAT5,ZNF385B,RPL37,AKT1,HIC1,STK11,ZNF385A	yellow	VSMC_M3
GO:0032204	0.36	0.79	6	74	regulation of telomere maintenance	BP	1	PNKP,NAT10,PINX1,SLX1A,SIRT6,NABP2	yellow	VSMC_M3
GO:1905954	0.36	0.79	6	73	positive regulation of lipid localization	BP	1	SREBF2,ZC3H12A,SCARB1,ACSL1,FABP3,PLA2G3	yellow	VSMC_M3
GO:0043112	0.36	0.76	10	131	receptor metabolic process	BP	1	CD63,SCRIB,LAMTOR1,GREM1,RIN3,CD9,MVB12A,ANKRD13B,PHETA2,GSG1L	yellow	VSMC_M3
GO:0002521	0.36	0.71	28	383	leukocyte differentiation	BP	1	NCAPH2,FNIP1,LGALS1,SOCS5,ZC3H12A,RELB,CD79A,METTL3,FASN,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,PIR,THOC5,RIPK3,PLA2G3,SART1,PBX1,BAD,PRXL2A,ARMC5,DOCK11,AP3D1,STK11,JAGN1	yellow	VSMC_M3
GO:2001141	0.36	0.67	167	2416	regulation of RNA biosynthetic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,PHF2,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,OGG1,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,KMT2B,ZNF740,RALY,ZBTB38,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,AIP,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,SMARCD2,BRMS1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,CTDSP1,MLF2,EID1,SSBP4,METTL13,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,ZNF358,AKT1,BRF1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,MNT,EHMT1,AP3D1,IRAK1,MBD3,MED16,CARD9,SARS,TRADD,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0051298	0.36	0.80	5	64	centrosome duplication	BP	1	CEP131,CCDC57,NAT10,SAC3D1,KIAA0753	yellow	VSMC_M3
GO:2001252	0.36	0.79	6	72	positive regulation of chromosome organization	BP	1	H2AFY,PNKP,NUMA1,SLX1A,SIRT6,NABP2	yellow	VSMC_M3
GO:0045580	0.36	0.77	8	98	regulation of T cell differentiation	BP	1	SOCS5,ZC3H12A,METTL3,SOD1,EGR3,SART1,BAD,AP3D1	yellow	VSMC_M3
GO:0051641	0.36	0.67	158	2295	cellular localization	BP	1	PQLC1,CD63,ESYT1,DCTN2,SQSTM1,CCHCR1,BAG6,SNX9,SAMM50,SREBF2,H2AFY,ITPR3,SGSM3,PACSIN1,PPARD,SCRIB,PLEC,IFT27,VPS28,TOM1,TTC7A,ASNA1,TPBG,PLEKHA8,EIPR1,ZC3H12A,SNX3,EHD2,SLC9A3R1,DMAP1,SLC30A3,SNX17,INSIG1,MYRIP,SEC13,SEPT9,UCP2,CEP131,TSPAN10,LAMTOR1,NUMA1,YIF1B,RAB20,HM13,BCL2L1,ITGB7,PDE4D,RRS1,PLEKHF1,SLC11A2,PINX1,MCRS1,DCTN1,RAPSN,CX3CL1,SOD1,CHP1,AP2A2,HTATIP2,RAB35,RBM15B,TSPAN5,SELENOS,GSTO1,EXOC3,FABP3,MMP14,PABPN1,AIP,AP1G2,CORO1B,SYT12,TRIM27,PCNT,NUDC,THOC5,CAPN10,PLA2G3,PTPN23,SCYL1,LRWD1,VPS51,PEX5,ZDHHC3,CHCHD10,YJEFN3,THOC3,BLOC1S4,PHB2,BAD,COPE,LAMTOR4,LETM1,LGALS3,TNFRSF1A,MVB12A,KIAA0753,NUP88,CHERP,WASHC1,RCC2,AP1M1,EML3,CCDC22,DBN1,SNX8,LMAN2,RAB24,MAD1L1,CLTB,ARHGEF2,SNF8,RANGRF,STX10,CORO1A,SGF29,ATP5PD,TMED1,SYNE3,CDC37,MYO19,CSK,MID2,ATG3,RBM22,AKT1,SNX18,PACS2,DENND1C,RANBP3,RAB34,GIT1,SLC6A4,MAP2K2,AP3D1,SSNA1,ATP5F1D,STK11,TMEM201,GAS8,SPG7,WDR34,RABEPK,NABP2,ERBB4,TWF2,TRAPPC5,PLA2G4E,AP5B1,JAGN1,MIS12,UNC13A,ZNF385A,ARFRP1,MEIG1,TIMM22,PHETA2,GSG1L	yellow	VSMC_M3
GO:0030101	0.36	0.81	4	43	natural killer cell activation	BP	1	BAG6,TYRO3,PBX1,CORO1A	yellow	VSMC_M3
GO:0008630	0.36	0.77	7	84	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	BAG6,BCL2L1,CCAR2,BAD,TNFRSF1A,HIC1,ZNF385A	yellow	VSMC_M3
GO:1903364	0.37	0.75	11	137	positive regulation of cellular protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,PSMC4,RNF19B,CCDC22,AMER1,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0070555	0.37	0.76	8	98	response to interleukin-1	BP	1	IL1R1,ZC3H12A,CX3CL1,RELA,OTUB1,MTHFR,CACTIN,IRAK1	yellow	VSMC_M3
GO:0097553	0.37	0.77	7	95	calcium ion transmembrane import into cytosol	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A	yellow	VSMC_M3
GO:0090199	0.37	0.81	4	39	regulation of release of cytochrome c from mitochondria	BP	1	BCL2L1,GPX1,BAD,AKT1	yellow	VSMC_M3
GO:0030042	0.37	0.81	4	51	actin filament depolymerization	BP	1	MICAL1,SWAP70,CAPG,TWF2	yellow	VSMC_M3
GO:0002683	0.37	0.71	22	290	negative regulation of immune system process	BP	1	TTLL12,SCRIB,SOCS5,ZC3H12A,EMILIN1,METTL3,TARBP2,GREM1,CX3CL1,DGKZ,TYRO3,SELENOS,RIN3,GPX1,TRIM27,PSMB4,LGALS3,C1QBP,PKN1,MAD1L1,AKT1,CACTIN	yellow	VSMC_M3
GO:0098754	0.37	0.76	8	90	detoxification	BP	1	GSR,SOD1,SELENOS,GSTO1,GPX1,MGST3,TXNRD2,PRXL2A	yellow	VSMC_M3
GO:0050865	0.37	0.70	29	385	regulation of cell activation	BP	1	SCRIB,LGALS1,PDGFRA,SOCS5,ZC3H12A,EMILIN1,METTL3,CX3CL1,SOD1,EGR3,TYRO3,PDGFA,MMP14,CLCF1,RIPK3,PLA2G3,SART1,BAD,LGALS3,CD9,PKN1,MAD1L1,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1,JUND	yellow	VSMC_M3
GO:0043433	0.37	0.75	10	126	negative regulation of DNA-binding transcription factor activity	BP	1	KLF4,ZC3H12A,CHP1,PRMT2,BRMS1,PHB2,CCDC22,MAD2L2,CACTIN,IRAK1	yellow	VSMC_M3
GO:0048008	0.37	0.81	4	48	platelet-derived growth factor receptor signaling pathway	BP	1	PDGFRA,SLC9A3R1,PDGFA,SGPL1	yellow	VSMC_M3
GO:0017148	0.37	0.74	12	158	negative regulation of translation	BP	1	CNOT3,ZC3H12A,UNK,METTL3,DND1,EIF4EBP1,PCIF1,DCPS,IGFBP5,NANOS3,C19orf66,KHSRP	yellow	VSMC_M3
GO:0046470	0.37	0.79	5	55	phosphatidylcholine metabolic process	BP	1	SCARB1,FABP3,PLA2G3,CAPN2,SLC44A3	yellow	VSMC_M3
GO:0032436	0.37	0.77	7	83	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	HSPBP1,SOCS5,RNF19B,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0034502	0.37	0.77	7	86	protein localization to chromosome	BP	1	H2AFY,PINX1,LRWD1,RCC2,SGF29,NABP2,MIS12	yellow	VSMC_M3
GO:0048024	0.37	0.77	7	85	regulation of mRNA splicing, via spliceosome	BP	1	SNRNP70,PCBP4,RBM15B,SRSF9,C1QBP,RAVER1,RBM8A	yellow	VSMC_M3
GO:0043242	0.37	0.79	5	70	negative regulation of protein-containing complex disassembly	BP	1	SWAP70,CAPG,MID1IP1,ARHGEF2,TWF2	yellow	VSMC_M3

GO:0051261	0.37	0.77	7	99	protein depolymerization	BP	1	MICAL1,SWAP70,CAPG,STMN3,MID1IP1,ARHGEF2,TWF2	yellow	VSMC_M3
GO:0051249	0.37	0.71	22	287	regulation of lymphocyte activation	BP	1	SCRIB,LGALS1,SOCS5,ZC3H12A,METTL3,SOD1,EGR3,TYRO3,MMP14,CLCF1,RIPK3,SART1,BAD,LGALS3,PKN1,MAD1L1,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1	yellow	VSMC_M3
GO:0030858	0.37	0.81	4	45	positive regulation of epithelial cell differentiation	BP	1	H2AFY,NUMA1,WNT10B,BAD	yellow	VSMC_M3
GO:0002791	0.37	0.74	11	142	regulation of peptide secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0009165	0.37	0.72	16	198	nucleotide biosynthetic process	BP	1	GUK1,ACSL1,AK2,PAPSS1,IMPDH2,ATP5MC3,ATIC,UQCC3,ACLY,FLAD1,ATP5PD,ATP5F1D,TAZ,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:1901655	0.37	0.78	6	77	cellular response to ketone	BP	1	CDK4,KLF4,AACS,DCPS,PCK2,AKT1	yellow	VSMC_M3
GO:0000086	0.37	0.75	10	124	G2/M transition of mitotic cell cycle	BP	1	CDK4,CCDC57,PINX1,WNT10B,PBX1,BABAM1,RCC2,MIIP,ZNF830,NABP2	yellow	VSMC_M3
GO:0008104	0.37	0.66	140	2028	protein localization	BP	1	CD63,DCTN2,RUFY1,SQSTM1,CCHCR1,BAG6,SNX9,SAMM50,SREBF2,H2AFY,SGSM3,GUK1,PACSIN1,PPARD,SCRIB,PLEC,IFT27,VPS28,TOM1,TTC7A,ASNA1,TPBG,PLEKHA8,WDPCP,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,EHD2,SLC9A3R1,SERP2,DMAP1,SNX17,INSIG1,MYRIP,SEC13,SEPT9,UCP2,BAIAP2,CEP131,TSPAN10,LAMTOR1,NUMA1,YIF1B,RAB20,ARHGAP33,AACS,HM13,BCL2L1,ITGB7,RRS1,SWAP70,PLEKHF1,PINX1,MCRS1,RAPSN,CHP1,AP2A2,SNX21,RAB35,TSPAN5,APBA2,SELENOS,EXOC3,MMP14,AIP,AP1G2,CORO1B,PCK2,NECTIN1,TRIM27,PCNT,CAPN10,PTPN23,SCYL1,LRWD1,VPS51,PEX5,ZDHHC3,CHCHD10,PHB2,BAD,COPE,LAMTOR4,LGALS3,TNFRSF1A,MVB12A,KIAA0753,NUP88,WASHC1,RCC2,AP1M1,RAB3IL1,CCDC22,GLUD1,DBN1,SNX8,LMAN2,RAB24,CLTB,ARHGEF2,SNF8,MVP,MTX1,RANGRF,STX10,SGF29,RABEP2,TRIM25,TMED1,SYNE3,CDC37,CSK,MID2,ATG3,RBM22,AKT1,SNX18,PACS2,RANBP3,RAB34,DHCR24,TJP3,CTNS,AP3D1,SSNA1,MIDN,STK11,GAS8,NABP2,ERBB4,TWF2,AP5B1,JAGN1,CAVIN1,MIS12,ARFRP1,MEIG1,TIMM22	yellow	VSMC_M3
GO:0035335	0.37	0.78	6	77	peptidyl-tyrosine dephosphorylation	BP	1	TNS2,PTPN23,MTMR4,PGP,PTPRR,DUSP5	yellow	VSMC_M3
GO:0016043	0.37	0.65	316	4652	cellular component organization	BP	1	ENPP1,PQLC1,CD63,ESYT1,DCTN2,NHP2,CDK4,RUFY1,SQSTM1,SPAG1,BAG6,NCAPH2,SNX9,CTHRC1,HDAC10,FNIP1,PDLIM4,SAMM50,SREBF2,NDUFB9,SQLE,TXNDC15,H2AFY,PACSIN1,PPARD,RPL3,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,BOP1,VPS28,TBCC,CUL7,DNPH1,B4GALT1,PDGFRA,PHF2,COL15A1,COL19A1,ASNA1,KLF4,DBNL,TPBG,PLEKHA8,WDPCP,CCM2,FHL3,ZC3H12A,FIGNL1,PNKP,ZYX,SNX3,MICAL1,EMP3,EHD2,KMT2E,KRT8,ACAD9,TMEM43,GEMIN7,SLC9A3R1,PLXND1,EMILIN1,DMAP1,SNX17,H3F3B,INSIG1,SEC13,SEPT9,BAIAP2,CEP131,INPPL1,LAMTOR1,NUMA1,YIF1B,CCDC57,RAB20,EIF4EBP1,ARAP3,CAVIN3,RIC8A,ARHGAP22,SDHAF1,ARHGAP33,TARBP2,SCARB1,NAT10,BCL2L1,SPRYD3,EIF4B,RRS1,SWAP70,PLEKHF1,UQCRFS1,CAPG,SLC11A2,TNKS1BP1,MMP24,PINX1,GREM1,KDM2B,AQP5,DCTN1,RAPSN,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,CCDC32,CCAR2,HPS1,CHP1,NPM3,RAB35,CHCHD2,CISH,SRSF9,CCDC28B,BRD9,RIN3,PDGFA,MMP14,CDK2AP2,LIX1L,APEH,GPX1,AIP,CORO1B,NGEF,HCCS,PLEKHO1,IGSF9,LRFN4,CLIP2,NECTIN1,TRIM27,ARPIN,PCNT,EIF3A,LIMK1,NUDC,RIPK3,SF3A1,ADRM1,CAPN10,SMARCD2,IQCG,PFDN2,MPZL3,BUD23,TNK2,TACO1,PLA2G3,STMN3,CEP164,BANF1,SART1,CCDC85B,PRPF6,PTPN23,RELA,SIPA1,RHOC,TMEM120A,LRWD1,ALKBH4,ZNHIT1,FMNL1,VPS51,SAC3D1,LIMD1,MID1IP1,PEX5,SMARCB1,CHCHD10,YJEFN3,UBTF,BLOC1S4,PHB2,NDP,IGFBP5,C12orf57,BAD,LAMTOR4,MPV17L2,LETM1,LGALS3,ARPC1B,CD9,MRTO4,TNFRSF1A,FCHO1,MVB12A,KIAA0753,BABAM1,C1QBP,AIMP2,TAF6L,UQCC3,WASHC1,RCC2,CNP,AP1M1,EML3,MTA2,KRT10,H3F3A,DBN1,CAPN2,LMAN2,MAD1L1,	yellow	VSMC_M3
GO:0098732	0.37	0.76	8	102	macromolecule deacylation	BP	1	HDAC10,SPRED2,CCAR2,BRMS1,MTA2,CTBP1,PER1,SIRT6	yellow	VSMC_M3
GO:0051962	0.38	0.72	15	216	positive regulation of nervous system development	BP	1	CUL7,DBNL,TPBG,PLXND1,BAIAP2,CX3CL1,CLCF1,LIMK1,RELA,DBN1,CRABP2,EEF2K,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0098742	0.38	0.74	10	152	cell-cell adhesion via plasma-membrane adhesion molecules	BP	1	KLF4,RIC8A,MMP24,CX3CL1,IGSF9,LRFN4,NECTIN1,PTPN23,SCARF2,CLDN6	yellow	VSMC_M3
GO:0090596	0.38	0.72	14	198	sensory organ morphogenesis	BP	1	CTHRC1,RING1,SCRIB,HOXA1,WDPCP,SLC9A3R1,INSIG1,LRIG1,KDM2B,AQP5,SOD1,NECTIN1,C12orf57,TTC39C	yellow	VSMC_M3
GO:0032623	0.38	0.80	4	43	interleukin-2 production	BP	1	PDE4D,TRIM27,KAT5,CARD9	yellow	VSMC_M3
GO:0032663	0.38	0.80	4	43	regulation of interleukin-2 production	BP	1	PDE4D,TRIM27,KAT5,CARD9	yellow	VSMC_M3
GO:1901652	0.38	0.70	27	375	response to peptide	BP	1	ENPP1,CDK4,KLF4,INSIG1,UCP2,BAIAP2,INPPL1,TNS2,PDE3B,SELENOS,FABP3,PCK2,CAPN10,RELA,IGFBP5,KLF3,PIP4K2B,ARHGEF2,EEF2K,CSK,AKT1,LDOC1,CARD9,APRT,SLC27A4,TGFBR3,JUND	yellow	VSMC_M3
GO:0045471	0.38	0.76	7	87	response to ethanol	BP	1	DMAP1,OGG1,EIF4EBP1,AACS,SOD1,BAD,TUFM	yellow	VSMC_M3
GO:1901293	0.38	0.72	16	199	nucleoside phosphate biosynthetic process	BP	1	GUK1,ACSL1,AK2,PAPSS1,IMPDH2,ATP5MC3,ATIC,UQCC3,ACLY,FLAD1,ATP5PD,ATP5F1D,TAZ,AMPD2,APRT,AK1	yellow	VSMC_M3
GO:0002819	0.38	0.74	9	111	regulation of adaptive immune response	BP	1	IL1R1,SOCS5,ZC3H12A,CLCF1,TRIM27,RIPK3,PKN1,MAD2L2,CARD9	yellow	VSMC_M3
GO:0051438	0.38	0.80	4	43	regulation of ubiquitin-protein transferase activity	BP	1	LIMK1,MAD2L2,RPL37,STUB1	yellow	VSMC_M3
GO:0043086	0.38	0.68	41	555	negative regulation of catalytic activity	BP	1	FNIP1,H2AFY,PLEC,PPP1R14B,HSPBP1,SOCS5,KLF4,SPRED2,MICAL1,ANXA5,TARBP2,PINX1,CCAR2,CHP1,ITPRIP,RRP1B,ETFBKMT,GPX1,AIP,QARS,TRIM27,LIMK1,TNK2,PPP1R35,LGALS3,UBXN1,WASHC1,RCC2,PKN1,PIP4K2B,MAD2L2,DFFA,MVP,RPL37,CSK,AKT1,DHCR24,MIDN,SLC27A4,RNH1,TRIB2	yellow	VSMC_M3
GO:0042110	0.38	0.70	23	310	T cell activation	BP	1	NCAPH2,SCRIB,LGALS1,SOCS5,ZC3H12A,RELB,METTL3,SOD1,EGR3,DLL4,RIPK3,SART1,BAD,LGALS3,MAD1L1,ARMC5,CORO1A,CD276,CSK,AKT1,AP3D1,STK11,PSMB10	yellow	VSMC_M3

GO:1903050	0.38	0.72	15	192	regulation of proteolysis involved in cellular protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,PSMC4,WNT10B,CCAR2,RNF19B,GPX1,PSME2,UBXN1,CCDC22,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0000070	0.38	0.73	11	143	mitotic sister chromatid segregation	BP	1	DCTN2,NCAPH2,H2AFY,NUMA1,RRS1,PINX1,NUDC,EML3,MAD1L1,MAD2L2,MIS12	yellow	VSMC_M3
GO:1905897	0.38	0.77	6	70	regulation of response to endoplasmic reticulum stress	BP	1	BAG6,ATF6B,BCL2L1,SELENOS,UBXN1,TXNDC12	yellow	VSMC_M3
GO:0035065	0.38	0.80	4	45	regulation of histone acetylation	BP	1	SMARCB1,EID1,CTBP1,THAP7	yellow	VSMC_M3
GO:0060429	0.38	0.67	55	810	epithelium development	BP	1	CTHRC1,H2AFY,SCRIB,PLEC,SHARPIN,DNPH1,B4GALT1,COL15A1,KLF4,WDPCP,CCM2,SPRED2,RCN3,PLEKHA4,SLC9A3R1,PLXND1,RNF220,NUMA1,FASN,DEAF1,PDE4D,GREM1,KDM2B,WNT10B,SOD1,DLL4,IRX1,PDGFA,MMP14,GPX1,TAGLN2,PCK2,PBX1,RELA,RHOC,PHB2,IGFBP5,BAD,LGALS3,TNFRSF1A,AIMP2,KRT10,CASP14,MTHFR,TMEM79,ZNF358,AKT1,SAFB2,SIRT6,PPL,NSDHL,TJP3,TRADD,ERBB4,NOM1	yellow	VSMC_M3
GO:0045621	0.38	0.77	6	72	positive regulation of lymphocyte differentiation	BP	1	SOCS5,EGR3,MMP14,SART1,BAD,AP3D1	yellow	VSMC_M3
GO:0016052	0.39	0.74	9	113	carbohydrate catabolic process	BP	1	GALK1,OGDHL,MANBA,BAD,FOXK1,PGD,PGM1,GIT1,JMJD8	yellow	VSMC_M3
GO:0016579	0.39	0.75	8	108	protein deubiquitination	BP	1	JOSD2,ZC3H12A,OTUB1,BABAM1,UBXN1,USP27X,USP43,SENP8	yellow	VSMC_M3
GO:0070647	0.39	0.66	57	806	protein modification by small protein conjugation or removal	BP	1	SQSTM1,RING1,JADE2,TRIM11,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,JOSD2,EIPR1,ZC3H12A,RNF220,SEL1L2,PINX1,KDM2B,CHP1,CISH,RNF19B,MOCS3,ASB9,TRIM27,LIMK1,RELA,OTUB1,COPS6,BABAM1,AIMP2,UBXN1,WASHC1,MED11,USP27X,SDE2,AMER1,MAD2L2,RUSC1,IRF2BPL,TRIM25,USP43,RPL37,SENP8,MIDD2,ATG3,ANKRD9,AKT1,BLMH,HMG20B,ANAPC2,SPSB3,UBAC1,CTU2,ZNRF1,TRIM7,CDC34,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0030336	0.39	0.71	16	223	negative regulation of cell migration	BP	1	PPARD,KLF4,SLC9A3R1,EMILIN1,GREM1,CX3CL1,DLL4,RIN3,CORO1B,ARPIN,PTPN23,IGFBP5,MIIP,AKT1,MIR214,PTPRR	yellow	VSMC_M3
GO:0009057	0.39	0.66	78	1102	macromolecule catabolic process	BP	1	SQSTM1,BAG6,SNX9,HNRNPA0,SGSM3,SHARPIN,VPS28,SND1,CUL7,SECISBP2,HSPBP1,SOCS5,CNOT3,PSMB3,ZC3H12A,RCN3,SNRNP70,SNX3,TMUB1,PSMC4,SEL1L2,METTL3,DND1,HM13,LSM6,WNT10B,PACSIN3,CCAR2,PCBP4,RNF19B,DCPS,SELENOS,MANBA,ZCCHC17,GPX1,ASB9,PSME2,ADRM1,PSMB4,PTPN23,RNASEH2C,KAT5,RELA,MRTO4,MVB12A,UBXN1,CCDC22,USP27X,CAPN2,AMER1,MAD2L2,NANOS3,FBXL19,DFFA,SNF8,TRIM25,USP43,ANKRD9,AKT1,PAIP1,KHSRP,CARHSP1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,PSMB10,CTRL,RBM8A,RNH1,TENT5B,TRIB2,CDC34,FBXO6,TRIR,STUB1,CCDC115	yellow	VSMC_M3
GO:0010556	0.39	0.64	196	2846	regulation of macromolecule biosynthetic process	BP	1	ENPP1,NAB2,CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,RING1,SREBF2,H2AFY,TRIM11,TRAPPC9,PPARD,SND1,SECISBP2,PHF2,RPS9,CNOT3,KLF4,HOXA1,FHL3,ZC3H12A,PNKP,CC2D1B,KTI12,KMT2E,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,UNK,OGG1,SERTAD1,TTC5,METTL3,CXXC5,DND1,EIF4EBP1,DEAF1,HOXC4,TARBP2,KMT2B,NAT10,ZNF740,EIF4B,RALY,ZBTB38,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,DCPS,IRX1,SELENOS,RRP1B,BRD9,AIP,NGDN,TSHZ2,QARS,PIR,TRIM27,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,SMARCD2,BRMS1,TACO1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,NDP,IGFBP5,CTDSP1,MLF2,EID1,SSBP4,METTL13,MPV17L2,ZNF394,C11orf95,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,SEPSECS,POLR2A,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,C19orf66,MID2,ZNF521,ZNF358,ZNF830,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,MAP2K2,CACTIN,CDK11B,SSU72,HIC1,TRAP1,MNT,EHMT1,AP3D1,MKNK2,IRAK1,MBD3,MED16,CARD9,SARS,POMT1,TRADD,RBM8A,ERBB4,JUND,KLF13,FADS1,ZNF783,HOXC5,ZNF385A,IER5,AKAP17A,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:0010498	0.39	0.68	32	434	proteasomal protein catabolic process	BP	1	BAG6,SHARPIN,HSPBP1,SOCS5,PSMB3,RCN3,TMUB1,PSMC4,SEL1L2,HM13,WNT10B,CCAR2,RNF19B,SELENOS,GPX1,PSME2,PSMB4,KAT5,UBXN1,FBXL19,TRIM25,ANKRD9,AKT1,SIRT6,SPSB3,MAN1B1,ZNRF1,PSMB10,TRIB2,CDC34,FBXO6,STUB1	yellow	VSMC_M3
GO:0001649	0.39	0.71	14	190	osteoblast differentiation	BP	1	CTHRC1,SND1,FIGNL1,FASN,LRP3,GREM1,WNT10B,COL6A1,TWIST2,MRC2,LIMD1,IGFBP5,AKT1,JUND	yellow	VSMC_M3

GO:0033036	0.39	0.64	162	2356	macromolecule localization	BP	1	ENPP1,PQLC1,CD63,ESYT1,DCTN2,NHP2,RUFY1,SQSTM1,CCHCR1,BAG6,SNX9,SAMM50,SREBF2,SQLE,H2AFY,SGSM3,GUK1,PACSIN1,PPARD,SCRIB,PLEC,IFT27,VPS28,TOM1,TTC7A,ASNA1,TPBG,PLEKHA8,WDPCP,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,EHD2,SLC9A3R1,SERP2,DMAP1,SNX17,INSIG1,MYRIP,SEC13,SEPT9,UCP2,BAIAP2,CEP131,TSPAN10,LAMTOR1,NUMA1,YIF1B,RAB20,ARHGAP33,AACS,SCARB1,HM13,BCL2L1,ITGB7,RRS1,SWAP70,PLEKHF1,ACSL1,PINX1,MCRS1,RAPSN,CHP1,AP2A2,SNX21,RAB35,RBM15B,TSPAN5,APBA2,SELENOS,EXOC3,FABP3,MMP14,PABPN1,AIP,AP1G2,CORO1B,PCK2,NECTIN1,TRIM27,PCNT,SPX,THOC5,CAPN10,PLA2G3,PRPF6,PTPN23,SCYL1,LRWD1,VPS51,PEX5,ZDHHC3,CHCHD10,YJEFN3,THOC3,PHB2,BAD,COPE,LAMTOR4,LGALS3,TNFRSF1A,MVB12A,KIAA0753,NUP88,WASHC1,RCC2,AP1M1,RAB3IL1,CCDC22,GLUD1,DBN1,SNX8,LMAN2,RAB24,CLTB,ARHGEF2,SNF8,MVP,MTX1,RANGRF,STX10,SGF29,RABEP2,TRIM25,SLC27A3,TMED1,SYNE3,CDC37,CSK,MID2,ATG3,RBM22,AKT1,SNX18,PACS2,KHSRP,ALKBH7,RANBP3,RAB34,DHCR24,TJP3,CTNS,AP3D1,SSNA1,MIDN,STK11,GAS8,SLC27A4,NABP2,RBM8A,ERBB4,TWF2,AP5B1,JAGN1,CAVIN1,MIS12,ZNF385A,ARFRP1,MEIG1,TIMM22	yellow	VSMC_M3
GO:0009746	0.39	0.72	12	159	response to hexose	BP	1	PPARD,LGALS1,UCP2,AACS,SELENOS,PCK2,SLC26A6,SMARCB1,BAD,SMARCA4,JAGN1,COL6A2	yellow	VSMC_M3
GO:1903076	0.39	0.75	7	90	regulation of protein localization to plasma membrane	BP	1	SQSTM1,BCL2L1,MMP14,LGALS3,RANGRF,CSK,AKT1	yellow	VSMC_M3
GO:0032502	0.39	0.63	309	4589	developmental process	BP	1	ENPP1,CD63,NAB2,CDK4,SQSTM1,CCHCR1,BAG6,NCAPH2,SBF1,CTHRC1,HDAC10,FNIP1,PBX2,PDLIM4,RING1,H2AFY,TRIM11,TRAPPC9,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,SND1,TBCC,CUL7,DNPH1,B4GALT1,PDGFRA,SECISBP2,PHF2,COL15A1,EPN1,COL19A1,SOCS5,TTC7A,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,ZC3H12A,FIGNL1,RCN3,SNX3,PLEKHA4,EHD2,FAM120B,KMT2E,KRT8,WDFY2,SIX5,ZNF296,RELB,SLC9A3R1,PLXND1,EMILIN1,RNF220,PAFAH1B3,CIC,SNX17,UNK,DLEC1,CD79A,INSIG1,OGG1,PSMC4,UCP2,METTL3,BAIAP2,CEP131,INPPL1,NUMA1,P4HB,DND1,YIF1B,FASN,RPL29,EIF4EBP1,MORN2,RIC8A,ARHGAP22,DEAF1,TBCB,HOXC4,LRIG1,ARHGAP33,AACS,HM13,BCL2L1,ITGB7,PDE4D,TNS2,SWAP70,LRP3,CAPG,SLC11A2,MMP24,GREM1,KDM2B,AQP5,PDE3B,DCTN1,CX3CL1,WNT10B,SOD1,CCDC32,ANKRD2,EGR3,DLL4,TYRO3,HTATIP2,RAB35,APBA2,IRX1,SDHA,FABP3,PAPSS1,PDGFA,MMP14,C14orf93,GPX1,CORO1B,NGEF,HCCS,CLCF1,PLEKHO1,TAGLN2,IGSF9,QARS,LRFN4,PCK2,COL6A1,IMPDH2,PIR,NECTIN1,ANPEP,TRIM27,ARPIN,LIMK1,SLC26A6,PRMT2,THOC5,RIPK3,TWIST2,EXTL1,IQCG,TNK2,PLA2G3,STMN3,SART1,CCDC85B,MRC2,PBX1,KAT5,RELA,RHOC,TMEM120A,SCYL1,IDH1,FMNL1,ARNT2,VPS51,LIMD1,SGPL1,SMARCB1,PBX4,YJEFN3,ATIC,BLOC1S4,MEF2B,PHB2,NDP,IGFBP5,C12orf57,BAD,AAMP,CTDSP1,EID1,HSD17B1,LGALS3,CD9,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,CHERP,EVC,RCC2,CNP,AP1M1,PRXL2A,KRT10,GLUD1,FOXK1,CASP14,KLF3,PKN1,DBN1,CAPN2,MAD1L1,AMER1,MTHFR,MAD2L2,NANOS3,PRR14,CTBP1,CRABP2,SP2,TMEM79,ARHGEF2,ARMC5,MTX1,	yellow	VSMC_M3
GO:0046209	0.40	0.77	5	60	nitric oxide metabolic process	BP	1	KLF4,ZC3H12A,SELENOS,AKT1,KHSRP	yellow	VSMC_M3
GO:1904659	0.40	0.76	6	80	glucose transmembrane transport	BP	1	ENPP1,PPARD,SELENOS,CAPN10,AKT1,SLC27A4	yellow	VSMC_M3
GO:0034976	0.40	0.70	17	222	response to endoplasmic reticulum stress	BP	1	BAG6,ATF6B,PDIA4,RCN3,SERP2,TMUB1,SEL1L2,P4HB,HM13,BCL2L1,SELENOS,UBXN1,TRIM25,MAN1B1,TXNDC12,FBXO6,STUB1	yellow	VSMC_M3
GO:0032446	0.40	0.66	50	703	protein modification by small protein conjugation	BP	1	SQSTM1,RING1,JADE2,TRIM11,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,EIPR1,RNF220,SEL1L2,PINX1,KDM2B,CHP1,CISH,RNF19B,MOCS3,ASB9,TRIM27,LIMK1,RELA,OTUB1,AIMP2,UBXN1,WASHC1,MED11,SDE2,AMER1,MAD2L2,RUSC1,IRF2BPL,TRIM25,RPL37,MID2,ATG3,ANKRD9,AKT1,BLMH,HMG20B,ANAPC2,SPSB3,UBAC1,CTU2,ZNRF1,TRIM7,CDC34,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0006493	0.40	0.76	6	74	protein O-linked glycosylation	BP	1	GALNT14,SLC35C2,ST3GAL4,TMTC1,DPM3,POMT1	yellow	VSMC_M3
GO:0035194	0.40	0.73	9	112	post-transcriptional gene silencing by RNA	BP	1	ZC3H12A,METTL3,DND1,TARBP2,LIMD1,MAP2K2,MIR214,MIR155,MIR374B	yellow	VSMC_M3
GO:0010976	0.40	0.72	10	140	positive regulation of neuron projection development	BP	1	PACSIN1,DBNL,SNX3,BAIAP2,CX3CL1,PLA2G3,DBN1,EEF2K,NEGR1,TWF2	yellow	VSMC_M3
GO:0022411	0.40	0.68	26	375	cellular component disassembly	BP	1	SQSTM1,SREBF2,SHARPIN,MICAL1,SWAP70,CAPG,DCTN1,CX3CL1,MMP14,LIX1L,APEH,CAPN10,SMARCD2,STMN3,MID1IP1,SMARCB1,PHB2,WASHC1,DFFA,ARHGEF2,SMARCA4,CDC37,C19orf66,ATG3,TAZ,TWF2	yellow	VSMC_M3
GO:0045582	0.40	0.77	5	60	positive regulation of T cell differentiation	BP	1	SOCS5,EGR3,SART1,BAD,AP3D1	yellow	VSMC_M3
GO:1901699	0.40	0.67	35	508	cellular response to nitrogen compound	BP	1	ENPP1,CDK4,PDGFRA,KLF4,SLC9A3R1,INSIG1,UCP2,BAIAP2,LAMTOR1,BCL2L1,TNS2,PDE3B,WNT10B,SOD1,SELENOS,PCK2,COL6A1,SLC26A6,CAPN10,RELA,IGFBP5,LAMTOR4,KLF3,CAPN2,PIP4K2B,ARHGEF2,EEF2K,CSK,AKT1,SLC6A4,LDOC1,APRT,SLC27A4,NSMF,NSMCE3	yellow	VSMC_M3
GO:0019218	0.40	0.75	6	73	regulation of steroid metabolic process	BP	1	INSIG1,LAMTOR1,SOD1,DHCR7,ARMC5,STUB1	yellow	VSMC_M3
GO:0002088	0.40	0.77	5	63	lens development in camera-type eye	BP	1	CDK4,SPRED2,SIX5,NECTIN1,CTNS	yellow	VSMC_M3
GO:0000302	0.40	0.70	14	177	response to reactive oxygen species	BP	1	PDGFRA,KLF4,UCP2,PYCR1,SOD1,GPX1,RIPK3,RELA,TXNRD2,BAD,CAPN2,AKT1,TRAP1,OSER1	yellow	VSMC_M3
GO:0051170	0.40	0.72	10	132	import into nucleus	BP	1	ZC3H12A,DMAP1,SEC13,CHP1,HTATIP2,PHB2,NUP88,RANGRF,RBM22,AKT1	yellow	VSMC_M3
GO:0061077	0.40	0.77	5	55	chaperone-mediated protein folding	BP	1	PDIA4,FKBP11,FKBP2,DFFA,TRAP1	yellow	VSMC_M3

GO:0051248	0.40	0.65	58	813	negative regulation of protein metabolic process	BP	1	ENPP1,CTDSP2,SQSTM1,BAG6,FNIP1,H2AFY,PLEC,VPS28,SOCS5,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,SNRNP70,SNX3,MICAL1,EMILIN1,UNK,METTL3,DND1,EIF4EBP1,TARBP2,PDE4D,SWAP70,PINX1,GREM1,CCAR2,CHP1,PCIF1,DCPS,GPX1,QARS,TRIM27,LIMK1,PFDN2,RELA,SMARCB1,IGFBP5,CTDSP1,OTUB1,LGALS3,UBXN1,PKN1,MAD2L2,NANOS3,CTBP1,MVP,RPL37,AATF,C19orf66,AKT1,KHSRP,DHCR24,CACTIN,HMG20B,TRIB2,THAP7	yellow	VSMC_M3
GO:0000281	0.40	0.76	5	63	mitotic cytokinesis	BP	1	SNX9,CUL7,RAB35,RHOC,SNX18	yellow	VSMC_M3
GO:0010970	0.40	0.72	10	139	transport along microtubule	BP	1	IFT27,CEP131,SOD1,BLOC1S4,AP3D1,SSNA1,STK11,TMEM201,SPG7,WDR34	yellow	VSMC_M3
GO:0006909	0.40	0.71	12	163	phagocytosis	BP	1	SNX3,RAB20,SCARB1,SOD1,TYRO3,LIMK1,ANXA11,LMAN2,CORO1A,CSK,ATG3,RAB34	yellow	VSMC_M3
GO:0042773	0.40	0.73	8	83	ATP synthesis coupled electron transport	BP	1	NDUFB9,CHCHD2,SDHA,NDUFV1,UQCRC1,UQCC3,NDUFS7,TAZ	yellow	VSMC_M3
GO:0042775	0.40	0.73	8	83	mitochondrial ATP synthesis coupled electron transport	BP	1	NDUFB9,CHCHD2,SDHA,NDUFV1,UQCRC1,UQCC3,NDUFS7,TAZ	yellow	VSMC_M3
GO:0006464	0.40	0.63	196	2859	cellular protein modification process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,BAG6,SBF1,SNX9,HDAC10,NELFE,FNIP1,PRR5,TTLL12,RING1,JADE2,H2AFY,TRIM11,PLEC,SHARPIN,VPS28,CUL7,B4GALT1,PIGO,PDGFRA,PHF2,HSPBP1,SOCS5,JOSD2,SPRED2,EIPR1,MEAF6,ZC3H12A,PNKP,MICAL1,KMT2E,WDFY2,SLC9A3R1,SERP2,NAT9,EMILIN1,SEPHS1,RNF220,DMAP1,PPM1G,GALNT14,SERTAD1,KAT14,P4HA3,SEL1L2,P4HB,TARBP2,KMT2B,NAT10,PDE4D,TNS2,SWAP70,ACSL1,TNKS1BP1,PINX1,SETD1B,GREM1,KDM2B,MCRS1,CX3CL1,FKBP11,SOD1,CCAR2,CHP1,TYRO3,HTATIP2,PPM1M,KDM1B,SLC35C2,CISH,ST3GAL4,RNF19B,ETFBKMT,MANBA,TMTC1,STK32C,PDGFA,GPX1,AIP,HCCS,MOCS3,CLCF1,QARS,ASB9,TRIM27,LIMK1,RABGGTA,PRMT2,RIPK3,EXTL1,BRMS1,TNK2,PTPN23,KAT5,RELA,SCYL1,ALKBH4,MEX3B,MAP3K14,ZDHHC3,SMARCB1,PHB2,TRMT112,FKBP2,CTDSP1,OTUB1,EID1,COPS6,LGALS3,TNFRSF1A,BABAM1,AIMP2,TAF6L,UBXN1,WASHC1,MTA2,MED11,USP27X,KRT10,SDE2,PKN1,AMER1,MTHFR,MAD2L2,MPDU1,CTBP1,FBXL19,ARHGEF2,RUSC1,MVP,PER1,DPM3,PPP4C,SGF29,IRF2BPL,TRIM25,USP43,RPL37,MTMR4,CARM1,SENP8,EEF2K,CDC37,CSK,MID2,ATG3,ANKRD9,AKT1,COPRS,SGK494,BLMH,MYDGF,METTL22,SIRT6,MAP2K2,CACTIN,HMG20B,CDK11B,SSU72,EHMT1,PGP,MKNK2,CSNK1G2,IRAK1,ANAPC2,SPSB3,MBD3,MAN1B1,STK11,TELO2,UBAC1,CTU2,POMT1,NTMT1,ZNRF1,TGFBR3,B3GNT9,NDST1,ERBB4,PTPRR,LOXL1,PIN4,TRIM7,TRIB2,NSMF,CDC34,FBXO6,DUSP5,THAP7,STUB1,NSMCE3,RCE1	yellow	VSMC_M3
GO:0036211	0.40	0.63	196	2859	protein modification process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,BAG6,SBF1,SNX9,HDAC10,NELFE,FNIP1,PRR5,TTLL12,RING1,JADE2,H2AFY,TRIM11,PLEC,SHARPIN,VPS28,CUL7,B4GALT1,PIGO,PDGFRA,PHF2,HSPBP1,SOCS5,JOSD2,SPRED2,EIPR1,MEAF6,ZC3H12A,PNKP,MICAL1,KMT2E,WDFY2,SLC9A3R1,SERP2,NAT9,EMILIN1,SEPHS1,RNF220,DMAP1,PPM1G,GALNT14,SERTAD1,KAT14,P4HA3,SEL1L2,P4HB,TARBP2,KMT2B,NAT10,PDE4D,TNS2,SWAP70,ACSL1,TNKS1BP1,PINX1,SETD1B,GREM1,KDM2B,MCRS1,CX3CL1,FKBP11,SOD1,CCAR2,CHP1,TYRO3,HTATIP2,PPM1M,KDM1B,SLC35C2,CISH,ST3GAL4,RNF19B,ETFBKMT,MANBA,TMTC1,STK32C,PDGFA,GPX1,AIP,HCCS,MOCS3,CLCF1,QARS,ASB9,TRIM27,LIMK1,RABGGTA,PRMT2,RIPK3,EXTL1,BRMS1,TNK2,PTPN23,KAT5,RELA,SCYL1,ALKBH4,MEX3B,MAP3K14,ZDHHC3,SMARCB1,PHB2,TRMT112,FKBP2,CTDSP1,OTUB1,EID1,COPS6,LGALS3,TNFRSF1A,BABAM1,AIMP2,TAF6L,UBXN1,WASHC1,MTA2,MED11,USP27X,KRT10,SDE2,PKN1,AMER1,MTHFR,MAD2L2,MPDU1,CTBP1,FBXL19,ARHGEF2,RUSC1,MVP,PER1,DPM3,PPP4C,SGF29,IRF2BPL,TRIM25,USP43,RPL37,MTMR4,CARM1,SENP8,EEF2K,CDC37,CSK,MID2,ATG3,ANKRD9,AKT1,COPRS,SGK494,BLMH,MYDGF,METTL22,SIRT6,MAP2K2,CACTIN,HMG20B,CDK11B,SSU72,EHMT1,PGP,MKNK2,CSNK1G2,IRAK1,ANAPC2,SPSB3,MBD3,MAN1B1,STK11,TELO2,UBAC1,CTU2,POMT1,NTMT1,ZNRF1,TGFBR3,B3GNT9,NDST1,ERBB4,PTPRR,LOXL1,PIN4,TRIM7,TRIB2,NSMF,CDC34,FBXO6,DUSP5,THAP7,STUB1,NSMCE3,RCE1	yellow	VSMC_M3
GO:0043434	0.40	0.68	22	308	response to peptide hormone	BP	1	ENPP1,CDK4,INSIG1,UCP2,BAIAP2,INPPL1,TNS2,PDE3B,SELENOS,FABP3,PCK2,CAPN10,RELA,IGFBP5,PIP4K2B,EEF2K,CSK,AKT1,APRT,SLC27A4,TGFBR3,JUND	yellow	VSMC_M3
GO:0006119	0.40	0.71	11	119	oxidative phosphorylation	BP	1	NDUFB9,CHCHD2,SDHA,NDUFV1,UQCRC1,CHCHD10,UQCC3,ATP5PD,NDUFS7,ATP5F1D,TAZ	yellow	VSMC_M3
GO:0033077	0.41	0.76	5	61	T cell differentiation in thymus	BP	1	NCAPH2,SOD1,EGR3,RIPK3,STK11	yellow	VSMC_M3
GO:0008652	0.41	0.76	5	56	cellular amino acid biosynthetic process	BP	1	SEPHS1,PYCR1,GLUD1,ILVBL,MTHFR	yellow	VSMC_M3
GO:0007276	0.41	0.66	34	469	gamete generation	BP	1	BAG6,NCAPH2,SBF1,IFT27,FIGNL1,SIX5,ZNF296,PAFAH1B3,DLEC1,METTL3,CEP131,DND1,YIF1B,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,BAD,NANOS3,ZNF830,AKT1,RFX2,STK11,TAZ,FAM50A,MEIG1	yellow	VSMC_M3
GO:0032890	0.41	0.78	4	47	regulation of organic acid transport	BP	1	ACSL1,FABP3,PLA2G3,AKT1	yellow	VSMC_M3
GO:0005996	0.41	0.69	15	199	monosaccharide metabolic process	BP	1	ENPP1,PPARD,B4GALT1,GALK1,INPPL1,SELENOS,GSTO1,PCK2,BAD,FOXK1,PGD,AKT1,PGM1,PGP,MIDN	yellow	VSMC_M3
GO:0048662	0.41	0.78	4	44	negative regulation of smooth muscle cell proliferation	BP	1	PPARD,KLF4,IGFBP5,MIR214	yellow	VSMC_M3
GO:0048706	0.41	0.73	8	105	embryonic skeletal system development	BP	1	PDGFRA,HOXA1,DEAF1,HOXC4,MMP14,PBX1,SLC39A1,NDST1	yellow	VSMC_M3
GO:0032870	0.41	0.66	31	450	cellular response to hormone stimulus	BP	1	ENPP1,CDK4,PPARD,INSIG1,UCP2,BAIAP2,TNS2,ACSL1,PDE3B,WNT10B,SELENOS,PCK2,PRMT2,CAPN10,RELA,PHB2,PELP1,PKN1,PIP4K2B,PER1,SMARCA4,CARM1,EEF2K,CSK,AKT1,HMGCS1,SAFB,SAFB2,APRT,SLC27A4,NSMF	yellow	VSMC_M3

GO:0031330	0.41	0.69	15	207	negative regulation of cellular catabolic process	BP	1	BAG6,HNRNPA0,SECISBP2,SNRNP70,DND1,CCAR2,ETFBKMT,ZCCHC17,UBXN1,WASHC1,FOXK1,DFFA,AKT1,PAIP1,TENT5B	yellow	VSMC_M3
GO:0051168	0.41	0.71	10	131	nuclear export	BP	1	CCHCR1,RRS1,CHP1,RBM15B,PABPN1,THOC5,THOC3,NUP88,RBM22,RANBP3	yellow	VSMC_M3
GO:0006520	0.41	0.68	18	224	cellular amino acid metabolic process	BP	1	MPST,AARS2,SEPHS1,BCKDHA,PYCR1,PEPD,GATB,ACCS,CARS,QARS,THAP4,GLUD1,ILVBL,MTHFR,FARSA,BLMH,CTNS,SARS	yellow	VSMC_M3
GO:0120035	0.41	0.66	35	524	regulation of plasma membrane bounded cell projection organization	BP	1	PACSIN1,LGALS1,CUL7,KLF4,DBNL,WDPCP,SNX3,PLXND1,SEPT9,BAIAP2,ARHGAP33,CX3CL1,CORO1B,NGEF,ARPIN,LIMK1,PLA2G3,WASHC1,RCC2,DBN1,CRABP2,RABEP2,CARM1,EEF2K,ATG3,DOCK11,AKT1,ACAP3,ANAPC2,STK11,NEGR1,MIR214,TWF2,CDC42EP5,NSMF	yellow	VSMC_M3
GO:0032269	0.41	0.64	54	760	negative regulation of cellular protein metabolic process	BP	1	ENPP1,CTDSP2,SQSTM1,BAG6,FNIP1,H2AFY,PLEC,VPS28,SOCS5,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,MICAL1,EMILIN1,UNK,METTL3,DND1,EIF4EBP1,TARBP2,PDE4D,SWAP70,PINX1,GREM1,CCAR2,CHP1,PCIF1,DCPS,GPX1,QARS,TRIM27,LIMK1,RELA,SMARCB1,IGFBP5,CTDSP1,OTUB1,LGALS3,UBXN1,PKN1,MAD2L2,NANOS3,CTBP1,MVP,RPL37,C19orf66,AKT1,KHSRP,DHCR24,CACTIN,HMG20B,TRIB2,THAP7	yellow	VSMC_M3
GO:1901983	0.41	0.76	5	63	regulation of protein acetylation	BP	1	KAT5,SMARCB1,EID1,CTBP1,THAP7	yellow	VSMC_M3
GO:0043009	0.42	0.65	36	522	chordate embryonic development	BP	1	CTHRC1,SCRIB,PDGFRA,EPN1,CNOT3,KLF4,HOXA1,CCM2,KRT8,RNF220,UNK,PSMC4,RIC8A,DEAF1,HOXC4,HM13,BCL2L1,KDM2B,MMP14,STMN3,PBX1,ARNT2,SMARCB1,DBN1,CAPN2,MTHFR,ARMC5,SLC39A1,ZNF358,ZNF830,AKT1,NSDHL,SLC35E2B,MBD3,NDST1,PTPRR	yellow	VSMC_M3
GO:0050918	0.42	0.77	4	47	positive chemotaxis	BP	1	SCRIB,CX3CL1,LGALS3,CORO1A	yellow	VSMC_M3
GO:0072657	0.42	0.65	33	466	protein localization to membrane	BP	1	SQSTM1,BAG6,SAMM50,PACSIN1,SCRIB,TTC7A,ASNA1,TPBG,EHD2,SLC9A3R1,YIF1B,BCL2L1,ITGB7,PLEKHF1,RAPSN,CHP1,TSPAN5,MMP14,PEX5,ZDHHC3,LGALS3,TNFRSF1A,RANGRF,SYNE3,CSK,ATG3,AKT1,PACS2,RAB34,AP3D1,SSNA1,ARFRP1,TIMM22	yellow	VSMC_M3
GO:0048522	0.42	0.61	287	4212	positive regulation of cellular process	BP	1	CD63,NAB2,CDK4,SQSTM1,BAG6,SNX9,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,SREBF2,TXNDC15,H2AFY,ITPR3,PACSIN1,PPARD,EEF1D,TSTA3,SCRIB,LGALS1,SHARPIN,VPS28,CUL7,DNPH1,B4GALT1,PDGFRA,IL1R1,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,DBNL,TPBG,HOXA1,SPRED2,EIPR1,ZC3H12A,PNKP,RCN3,SNRNP70,SNX3,PLEKHA4,EHD2,KMT2E,WDFY2,SIX5,ZNF296,SLC9A3R1,PLXND1,EMILIN1,RNF220,DMAP1,H3F3B,MYRIP,SEC13,SEPT9,SERTAD1,TTC5,PSMC4,UCP2,METTL3,PHLDA1,BAIAP2,CEP131,CXXC5,LAMTOR1,NUMA1,P4HB,DND1,CCDC57,EIF4EBP1,CAVIN3,DEAF1,HOXC4,KMT2B,AACS,SCARB1,NAT10,BCL2L1,SWAP70,LRP3,PLEKHF1,ACSL1,ZBTB38,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,DCTN1,RAPSN,CX3CL1,WNT10B,SOD1,PACSIN3,DGKZ,EGR3,CCAR2,DLL4,CHP1,TYRO3,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,SLC35C2,TSPAN5,ST3GAL4,RNF19B,DCPS,GSTO1,RRP1B,FABP3,PDGFA,MMP14,GPX1,AIP,CORO1B,CLCF1,SYT12,PCK2,PSME2,TRIM27,ARPIN,PCNT,LIMK1,SLC26A6,PRMT2,THOC5,RIPK3,TWIST2,ADRM1,CAPN10,SMARCD2,PFDN2,BRMS1,BUD23,TNK2,PLA2G3,GMEB2,SART1,PRPF6,PTPN23,PBX1,KAT5,RELA,RHOC,MAP3K14,ARNT2,MID1IP1,ZDHHC3,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,PHB2,TRMT112,NDP,IGFBP5,BAD,LAMTOR4,IFI35,AAMP,SSBP4,MPV17L2,LGALS3,BUD31,ARPC1B,PLAU,TNFRSF1A,BABAM1,C1QBP,AIMP2,TAF6L,CHERP,ZBTB49,WASHC1,EVC,RCC2,MTA2,PELP1,CCDC22,USP27X,GLUD1,FOXK1,ELP5,H3F3A,PKN1,DBN1,CAPN2,LMAN2,POLR2A,AMER1,PIP4K2B,MAD2L2,NANOS3,CTBP1,CRABP2,DFFA,ARHGEF2,SNF8,PER1,NFIX,RANGRF,CORO1A,SLX1A,IRF2BPL,TRIM25,RPL37,S1	yellow	VSMC_M3
GO:0070265	0.42	0.77	4	45	necrotic cell death	BP	1	RIPK3,ARHGEF2,ALKBH7,MIR214	yellow	VSMC_M3
GO:0045619	0.42	0.71	9	117	regulation of lymphocyte differentiation	BP	1	SOCS5,ZC3H12A,METTL3,SOD1,EGR3,MMP14,SART1,BAD,AP3D1	yellow	VSMC_M3
GO:0016567	0.42	0.64	46	656	protein ubiquitination	BP	1	SQSTM1,RING1,JADE2,TRIM11,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,EIPR1,RNF220,SEL1L2,PINX1,KDM2B,CHP1,CISH,RNF19B,ASB9,TRIM27,LIMK1,OTUB1,AIMP2,UBXN1,WASHC1,MED11,SDE2,AMER1,MAD2L2,RUSC1,IRF2BPL,TRIM25,RPL37,MID2,ATG3,ANKRD9,AKT1,BLMH,ANAPC2,SPSB3,UBAC1,ZNRF1,TRIM7,CDC34,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0010812	0.42	0.77	4	53	negative regulation of cell-substrate adhesion	BP	1	LGALS1,CX3CL1,MMP14,RCC2	yellow	VSMC_M3
GO:0006639	0.42	0.73	7	92	acylglycerol metabolic process	BP	1	MGLL,INSIG1,SCARB1,ACSL1,DGKZ,GPX1,PCK2	yellow	VSMC_M3
GO:0031667	0.42	0.66	26	362	response to nutrient levels	BP	1	FNIP1,SREBF2,PPARD,PLEC,ZC3H12A,OGG1,UCP2,EIF4EBP1,AACS,ACSL1,SOD1,DCPS,PCK2,SPX,RELA,FOXK1,MTHFR,TRIM25,AKT1,HMGCS1,SLC6A4,SIRT6,MBD3,WDR24,SLC27A4,FADS1	yellow	VSMC_M3
GO:0051051	0.42	0.66	23	314	negative regulation of transport	BP	1	ENPP1,SREBF2,PACSIN1,SNX3,SLC9A3R1,INSIG1,UCP2,PACSIN3,CHP1,SELENOS,GSTO1,RIN3,TRIM27,SPX,LGALS3,TNFRSF1A,CORO1A,CSK,ATG3,AKT1,ANKRD13B,MIDN,JAGN1	yellow	VSMC_M3

GO:0022607	0.42	0.61	153	2230	cellular component assembly	BP	1	SPAG1,BAG6,SNX9,FNIP1,SAMM50,NDUFB9,SQLE,TXNDC15,H2AFY,RPL3,PLEC,BOP1,VPS28,TBCC,PDGFRA,PHF2,DBNL,TPBG,WDPCP,ZC3H12A,ZYX,MICAL1,EMP3,EHD2,KRT8,ACAD9,GEMIN7,SLC9A3R1,PLXND1,EMILIN1,H3F3B,SEPT9,BAIAP2,CEP131,INPPL1,NUMA1,YIF1B,CCDC57,RAB20,EIF4EBP1,SDHAF1,TARBP2,EIF4B,RRS1,SWAP70,UQCRFS1,CAPG,GREM1,AQP5,DCTN1,CX3CL1,WNT10B,HPS1,CHP1,SRSF9,CCDC28B,PDGFA,MMP14,CORO1B,HCCS,LRFN4,NECTIN1,TRIM27,ARPIN,PCNT,EIF3A,LIMK1,SF3A1,ADRM1,IQCG,TACO1,PLA2G3,CEP164,SART1,PRPF6,PTPN23,RHOC,TMEM120A,SAC3D1,LIMD1,MID1IP1,PEX5,SMARCB1,CHCHD10,UBTF,BAD,MPV17L2,LETM1,LGALS3,ARPC1B,CD9,MRTO4,FCHO1,MVB12A,KIAA0753,C1QBP,AIMP2,TAF6L,UQCC3,WASHC1,RCC2,EML3,KRT10,H3F3A,DBN1,PIP4K2B,CLTB,SNF8,CD2BP2,RANGRF,FARSA,CORO1A,SLX1A,RABEP2,SMARCA4,EEF2K,EIF3G,ATG3,TTC39C,DOCK11,BRF1,PACS2,RFX2,RAB34,GIT1,UBN1,MRPL20,NCLN,CLDN6,NUBP2,NDUFS7,ATP5F1D,TAZ,CARD9,GAS8,SPG7,WDR34,TGFBR3,MIR214,ERBB4,TWF2,SURF1,MIS12,ELN,UNC13A,CDC42EP5,CDC34,GBA2,TUBGCP2,MEIG1,STUB1,CCDC115,ARPC5L	yellow	VSMC_M3
GO:0010927	0.43	0.73	6	87	cellular component assembly involved in morphogenesis	BP	1	PLEC,PDGFRA,KRT8,PLA2G3,CD9,RFX2	yellow	VSMC_M3
GO:0030073	0.43	0.69	11	149	insulin secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0045185	0.43	0.73	6	80	maintenance of protein location	BP	1	INSIG1,CHCHD10,CCDC22,DBN1,AKT1,TWF2	yellow	VSMC_M3
GO:0097306	0.43	0.74	5	71	cellular response to alcohol	BP	1	CDK4,KLF4,AACS,AKT1,HMGCS1	yellow	VSMC_M3
GO:0031056	0.43	0.70	9	124	regulation of histone modification	BP	1	NELFE,H2AFY,KMT2E,SMARCB1,OTUB1,EID1,MTHFR,CTBP1,THAP7	yellow	VSMC_M3
GO:0044706	0.43	0.69	12	159	multi-multicellular organism process	BP	1	PPARD,B4GALT1,EPN1,UCP2,RPL29,SOD1,SLC19A1,IGFBP5,C1QBP,CAPN2,AKT1,SLC6A4	yellow	VSMC_M3
GO:0016054	0.43	0.67	15	186	organic acid catabolic process	BP	1	ACAT2,PPARD,MPST,CPT1C,BCKDHA,GNPDA1,PCCB,ETFBKMT,PCK2,GLUD1,ILVBL,PGD,AKT1,BLMH,SLC27A4	yellow	VSMC_M3
GO:0007586	0.43	0.74	5	63	digestion	BP	1	SCARB1,AQP5,PIR,SLC26A6,ZNF830	yellow	VSMC_M3
GO:0007519	0.43	0.70	9	122	skeletal muscle tissue development	BP	1	PLEC,COL19A1,WNT10B,GPX1,HMG20B,TAZ,GTF3C5,IGSF8,ELN	yellow	VSMC_M3
GO:0070527	0.43	0.76	4	51	platelet aggregation	BP	1	PDGFRA,TYRO3,BLOC1S4,CD9	yellow	VSMC_M3
GO:0045321	0.43	0.63	42	586	leukocyte activation	BP	1	BAG6,NCAPH2,FNIP1,SCRIB,LGALS1,SOCS5,ZC3H12A,KMT2E,RELB,CD79A,METTL3,SWAP70,CX3CL1,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,IMPDH2,RIPK3,PLA2G3,SART1,PBX1,PHB2,BAD,IFI35,LGALS3,PKN1,MAD1L1,MAD2L2,ARMC5,CORO1A,CD276,CSK,DOCK11,AKT1,AP3D1,STK11,PSMB10,JUND,AKAP17A	yellow	VSMC_M3
GO:0097529	0.43	0.69	11	142	myeloid leukocyte migration	BP	1	IL1R1,EMILIN1,SWAP70,GREM1,CX3CL1,RIN3,MMP14,LGALS3,CD9,C1QBP,JAGN1	yellow	VSMC_M3
GO:1904375	0.43	0.71	8	107	regulation of protein localization to cell periphery	BP	1	SQSTM1,NUMA1,BCL2L1,MMP14,LGALS3,RANGRF,CSK,AKT1	yellow	VSMC_M3
GO:0034284	0.43	0.68	12	164	response to monosaccharide	BP	1	PPARD,LGALS1,UCP2,AACS,SELENOS,PCK2,SLC26A6,SMARCB1,BAD,SMARCA4,JAGN1,COL6A2	yellow	VSMC_M3
GO:0050851	0.43	0.70	9	117	antigen receptor-mediated signaling pathway	BP	1	ZC3H12A,CD79A,PDE4D,DGKZ,RELA,LGALS3,CD276,CSK,STK11	yellow	VSMC_M3
GO:0070646	0.43	0.70	9	125	protein modification by small protein removal	BP	1	JOSD2,ZC3H12A,OTUB1,COPS6,BABAM1,UBXN1,USP27X,USP43,SENP8	yellow	VSMC_M3
GO:1903038	0.43	0.72	7	87	negative regulation of leukocyte cell-cell adhesion	BP	1	SCRIB,SOCS5,KLF4,ZC3H12A,LGALS3,MAD1L1,AKT1	yellow	VSMC_M3
GO:0046854	0.43	0.76	4	54	phosphatidylinositol phosphate biosynthetic process	BP	1	SOCS5,TTC7A,CISH,PIP4K2B	yellow	VSMC_M3
GO:0022603	0.43	0.63	50	761	regulation of anatomical structure morphogenesis	BP	1	CTHRC1,CUL7,EPN1,KLF4,DBNL,WDPCP,ZC3H12A,PLEKHA4,SLC9A3R1,PLXND1,EMILIN1,BAIAP2,P4HB,ARHGAP33,GREM1,PDE3B,HTATIP2,PDGFA,CORO1B,NGEF,PLEKHO1,ARPIN,LIMK1,RHOC,FMNL1,LIMD1,YJEFN3,PHB2,C1QBP,RCC2,PKN1,DBN1,CRABP2,CORO1A,SYNE3,EEF2K,MYO19,INF2,MYDGF,SIRT6,ANAPC2,STK11,JMJD8,SARS,MIR214,TWF2,RNH1,UNC13A,CDC42EP5,NSMF	yellow	VSMC_M3
GO:0035556	0.43	0.60	139	2063	intracellular signal transduction	BP	1	RUFY1,SQSTM1,BAG6,NELFE,FNIP1,PRR5,ITPR3,SGSM3,DEF6,PPARD,EEF1D,LGALS1,SHARPIN,BOP1,PDGFRA,SOCS5,KLF4,DBNL,TPBG,CCM2,SPRED2,ZC3H12A,FIGNL1,RCN3,RELB,SLC9A3R1,EMILIN1,PLCD1,SEC13,ARHGEF40,CXXC5,LAMTOR1,P4HB,EIF4EBP1,CAVIN3,ARHGAP22,ARHGAP33,BCL2L1,PDE4D,TNS2,RRS1,SWAP70,PLEKHF1,GREM1,DOK1,PDE3B,CX3CL1,SOD1,DGKZ,CCAR2,CHP1,TYRO3,RAB35,CISH,SELENOS,GSTO1,STK32C,PDGFA,PABPN1,GPX1,AIP,NGEF,QARS,ASB9,TRIM27,EIF3A,LIMK1,THOC5,RIPK3,TNK2,STMN3,KAT5,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZNF385B,PHB2,IGFBP5,BAD,PLCB3,LAMTOR4,IFI35,TNFRSF1A,BABAM1,TEAD4,C1QBP,CHERP,CCDC22,SDE2,PKN1,MAD1L1,MAD2L2,TBKBP1,ARHGEF2,PER1,RANGRF,PPP4C,TRIM25,RPL37,S100A4,CSK,MID2,DOCK11,ZNF830,AKT1,DHCR24,CARHSP1,MYDGF,MAP2K2,CACTIN,HIC1,TRAP1,CTNS,MKNK2,IRAK1,STK11,TELO2,WDR24,JMJD8,CARD9,TGFBR3,TRADD,NDST1,NABP2,ERBB4,PTPRR,IGFBP6,UNC13A,ZNF385A,TXNDC12,CDC42EP5,CDC34,FBXO6,ARHGEF1,DUSP5,GLIPR2,RCE1	yellow	VSMC_M3
GO:0002822	0.43	0.71	8	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	IL1R1,SOCS5,ZC3H12A,CLCF1,RIPK3,PKN1,MAD2L2,CARD9	yellow	VSMC_M3
GO:0006767	0.43	0.76	4	47	water-soluble vitamin metabolic process	BP	1	SLC52A2,GSTO1,SLC19A1,FLAD1	yellow	VSMC_M3
GO:0008645	0.43	0.72	6	83	hexose transmembrane transport	BP	1	ENPP1,PPARD,SELENOS,CAPN10,AKT1,SLC27A4	yellow	VSMC_M3
GO:0032206	0.44	0.76	4	48	positive regulation of telomere maintenance	BP	1	PNKP,SLX1A,SIRT6,NABP2	yellow	VSMC_M3
GO:0006638	0.44	0.71	7	93	neutral lipid metabolic process	BP	1	MGLL,INSIG1,SCARB1,ACSL1,DGKZ,GPX1,PCK2	yellow	VSMC_M3

GO:0048514	0.44	0.63	34	508	blood vessel morphogenesis	BP	1	CUL7,B4GALT1,PDGFRA,COL15A1,EPN1,KLF4,HOXA1,CCM2,ZC3H12A,PLXND1,EMILIN1,ARHGAP22,GREM1,PDE3B,CX3CL1,EGR3,DLL4,HTATIP2,PDGFA,MMP14,GPX1,ANPEP,SGPL1,YJEFN3,AAMP,AKT1,MYDGF,SIRT6,JMJD8,SARS,TGFBR3,MIR214,TNFRSF12A,RNH1	yellow	VSMC_M3
GO:0050900	0.44	0.66	18	245	leukocyte migration	BP	1	PLEC,B4GALT1,IL1R1,EMILIN1,ITGB7,SWAP70,GREM1,CX3CL1,ST3GAL4,RIN3,MMP14,RIPK3,LGALS3,CD9,C1QBP,CORO1A,AKT1,JAGN1	yellow	VSMC_M3
GO:0060996	0.44	0.72	6	87	dendritic spine development	BP	1	DBNL,BAIAP2,ARHGAP33,NGEF,DBN1,EEF2K	yellow	VSMC_M3
GO:0030029	0.44	0.62	43	662	actin filament-based process	BP	1	SNX9,PDLIM4,PACSIN1,PLEC,PDGFRA,DBNL,FHL3,ZYX,MICAL1,EHD2,KRT8,SLC9A3R1,BAIAP2,INPPL1,CAVIN3,PDE4D,SWAP70,CAPG,CX3CL1,PDGFA,CORO1B,TRIM27,ARPIN,LIMK1,CAPN10,RHOC,ALKBH4,FMNL1,ARPC1B,WASHC1,DBN1,MAD2L2,ARHGEF2,RANGRF,CORO1A,MYO19,INF2,MIR214,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:1901879	0.44	0.73	5	75	regulation of protein depolymerization	BP	1	SWAP70,CAPG,MID1IP1,ARHGEF2,TWF2	yellow	VSMC_M3
GO:0019395	0.44	0.71	7	87	fatty acid oxidation	BP	1	ACAT2,PPARD,CPT1C,ETFBKMT,FABP3,ILVBL,AKT1	yellow	VSMC_M3
GO:0120162	0.44	0.72	6	78	positive regulation of cold-induced thermogenesis	BP	1	CNOT3,UCP2,ACSL1,SCD,SIRT6,EHMT1	yellow	VSMC_M3
GO:0045824	0.44	0.75	4	47	negative regulation of innate immune response	BP	1	TTLL12,METTL3,TYRO3,CACTIN	yellow	VSMC_M3
GO:0001525	0.44	0.64	29	428	angiogenesis	BP	1	B4GALT1,PDGFRA,COL15A1,EPN1,KLF4,ZC3H12A,PLXND1,EMILIN1,ARHGAP22,GREM1,PDE3B,CX3CL1,EGR3,DLL4,HTATIP2,PDGFA,MMP14,GPX1,ANPEP,YJEFN3,AAMP,AKT1,MYDGF,SIRT6,JMJD8,SARS,MIR214,TNFRSF12A,RNH1	yellow	VSMC_M3
GO:1903078	0.44	0.75	4	52	positive regulation of protein localization to plasma membrane	BP	1	SQSTM1,LGALS3,RANGRF,AKT1	yellow	VSMC_M3
GO:0061178	0.44	0.75	4	50	regulation of insulin secretion involved in cellular response to glucose stimulus	BP	1	PPARD,UCP2,BAD,JAGN1	yellow	VSMC_M3
GO:0015749	0.44	0.72	6	84	monosaccharide transmembrane transport	BP	1	ENPP1,PPARD,SELENOS,CAPN10,AKT1,SLC27A4	yellow	VSMC_M3
GO:0045184	0.44	0.60	97	1395	establishment of protein localization	BP	1	CD63,RUFY1,CCHCR1,BAG6,SNX9,SAMM50,SREBF2,H2AFY,SGSM3,GUK1,PPARD,SCRIB,IFT27,VPS28,TOM1,ASNA1,PLEKHA8,WDPCP,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,SERP2,DMAP1,SNX17,INSIG1,MYRIP,SEC13,UCP2,CEP131,TSPAN10,YIF1B,RAB20,ARHGAP33,AACS,HM13,RAPSN,CHP1,AP2A2,SNX21,RAB35,APBA2,SELENOS,EXOC3,AIP,AP1G2,PCK2,PCNT,CAPN10,PTPN23,LRWD1,VPS51,PEX5,ZDHHC3,PHB2,BAD,COPE,MVB12A,NUP88,WASHC1,RCC2,AP1M1,RAB3IL1,CCDC22,GLUD1,SNX8,LMAN2,RAB24,CLTB,ARHGEF2,SNF8,MVP,MTX1,RANGRF,STX10,SGF29,RABEP2,TMED1,SYNE3,CDC37,CSK,ATG3,RBM22,AKT1,SNX18,RANBP3,RAB34,CTNS,AP3D1,MIDN,NABP2,AP5B1,JAGN1,CAVIN1,ARFRP1,TIMM22	yellow	VSMC_M3
GO:1903035	0.44	0.73	5	64	negative regulation of response to wounding	BP	1	PDGFRA,PDGFA,CD9,PLAU,GIT1	yellow	VSMC_M3
GO:0009755	0.44	0.68	10	142	hormone-mediated signaling pathway	BP	1	PPARD,ACSL1,PRMT2,PHB2,PKN1,PER1,SMARCA4,CARM1,SAFB,SAFB2	yellow	VSMC_M3
GO:0002460	0.44	0.67	13	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	GNL1,IL1R1,SOCS5,ZC3H12A,RELB,SWAP70,CLCF1,RIPK3,C1QBP,PKN1,MAD2L2,C8G,CARD9	yellow	VSMC_M3
GO:0032784	0.44	0.75	4	49	regulation of DNA-templated transcription, elongation	BP	1	NELFE,CCAR2,THOC5,GTF2F1	yellow	VSMC_M3
GO:0042593	0.44	0.67	13	183	glucose homeostasis	BP	1	PPARD,LGALS1,UCP2,AACS,PCK2,SMARCB1,IGFBP5,BAD,FOXK1,SMARCA4,AKT1,STK11,JAGN1	yellow	VSMC_M3
GO:0045667	0.44	0.70	8	109	regulation of osteoblast differentiation	BP	1	CTHRC1,LRP3,GREM1,WNT10B,TWIST2,LIMD1,IGFBP5,JUND	yellow	VSMC_M3
GO:0014855	0.44	0.75	4	56	striated muscle cell proliferation	BP	1	PPARD,SIX5,TGFBR3,ERBB4	yellow	VSMC_M3
GO:0032984	0.44	0.67	13	195	protein-containing complex disassembly	BP	1	MICAL1,SWAP70,CAPG,LIX1L,APEH,SMARCD2,STMN3,MID1IP1,SMARCB1,ARHGEF2,SMARCA4,C19orf66,TWF2	yellow	VSMC_M3
GO:0045786	0.45	0.64	22	306	negative regulation of cell cycle	BP	1	CTDSP2,H2AFY,SCRIB,KLF4,SLC9A3R1,PINX1,CCAR2,CDK2AP2,PRMT2,THOC5,SIPA1,CTDSP1,METTL13,BABAM1,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,AURKAIP1,NABP2,FBXO6	yellow	VSMC_M3
GO:0036473	0.45	0.72	6	76	cell death in response to oxidative stress	BP	1	P4HB,PYCR1,SOD1,GPX1,AKT1,TRAP1	yellow	VSMC_M3
GO:0006888	0.45	0.69	8	106	endoplasmic reticulum to Golgi vesicle-mediated transport	BP	1	INSIG1,SEC13,YIF1B,COPE,LMAN2,RANGRF,TMED1,TRAPPC5	yellow	VSMC_M3
GO:0016311	0.45	0.64	24	342	dephosphorylation	BP	1	CTDSP2,SBF1,PNKP,PPM1G,INPPL1,TNS2,SWAP70,CHP1,PPM1M,RIPK3,PTPN23,PPP1R35,CTDSP1,LGALS3,PPP4C,MTMR4,HDHD2,SSU72,PGP,STK11,PTPRR,NT5C,NSMF,DUSP5	yellow	VSMC_M3
GO:0002312	0.45	0.73	5	64	B cell activation involved in immune response	BP	1	LGALS1,SWAP70,CLCF1,MAD2L2,DOCK11	yellow	VSMC_M3
GO:0050810	0.45	0.75	4	50	regulation of steroid biosynthetic process	BP	1	INSIG1,SOD1,DHCR7,ARMC5	yellow	VSMC_M3
GO:0006611	0.45	0.75	4	49	protein export from nucleus	BP	1	CCHCR1,CHP1,RBM22,RANBP3	yellow	VSMC_M3
GO:0033500	0.45	0.66	13	184	carbohydrate homeostasis	BP	1	PPARD,LGALS1,UCP2,AACS,PCK2,SMARCB1,IGFBP5,BAD,FOXK1,SMARCA4,AKT1,STK11,JAGN1	yellow	VSMC_M3
GO:1903313	0.45	0.69	8	105	positive regulation of mRNA metabolic process	BP	1	CNOT3,ZC3H12A,SNRNP70,METTL3,DND1,DCPS,NANOS3,KHSRP	yellow	VSMC_M3
GO:0002429	0.45	0.67	11	148	immune response-activating cell surface receptor signaling pathway	BP	1	BAG6,ZC3H12A,CD79A,PDE4D,DGKZ,LIMK1,RELA,LGALS3,CD276,CSK,STK11	yellow	VSMC_M3
GO:0002757	0.45	0.67	11	148	immune response-activating signal transduction	BP	1	BAG6,ZC3H12A,CD79A,PDE4D,DGKZ,LIMK1,RELA,LGALS3,CD276,CSK,STK11	yellow	VSMC_M3
GO:0008285	0.45	0.62	39	548	negative regulation of cell population proliferation	BP	1	PPARD,SCRIB,B4GALT1,KLF4,TPBG,SIX5,SLC9A3R1,DLEC1,INPPL1,TNS2,PINX1,GREM1,KDM2B,WNT10B,DLL4,FABP3,SMARCB1,PHB2,IGFBP5,IFI35,CD9,AIMP2,CHERP,ZBTB49,PKN1,MAD1L1,CTBP1,CSK,SLC6A4,DHCR24,LDOC1,MNT,STK11,GAS8,TGFBR3,MIR214,ERBB4,KLF13,IGFBP6	yellow	VSMC_M3

GO:0019220	0.45	0.60	73	1074	regulation of phosphate metabolic process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,SNX9,FNIP1,PRR5,H2AFY,PLEC,PPP1R14B,PDGFRA,SOCS5,KLF4,SPRED2,ZC3H12A,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SERTAD1,TARBP2,SCARB1,PDE4D,SWAP70,ACSL1,TNKS1BP1,GREM1,CX3CL1,SOD1,DGKZ,CHP1,TYRO3,CISH,FABP3,PDGFA,CLCF1,QARS,TRIM27,RIPK3,TNK2,IDH1,PHB2,PPP1R35,BAD,CTDSP1,LGALS3,TNFRSF1A,WASHC1,PKN1,CAPN2,PIP4K2B,MAD2L2,ARHGEF2,MVP,MTMR4,EEF2K,CDC37,CSK,AKT1,GIT1,MYDGF,MAP2K2,CACTIN,IRAK1,MIDN,STK11,TELO2,TAZ,JMJD8,VAC14,ERBB4,TRIB2,NSMF	yellow	VSMC_M3
GO:0051174	0.45	0.60	73	1074	regulation of phosphorus metabolic process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,SNX9,FNIP1,PRR5,H2AFY,PLEC,PPP1R14B,PDGFRA,SOCS5,KLF4,SPRED2,ZC3H12A,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SERTAD1,TARBP2,SCARB1,PDE4D,SWAP70,ACSL1,TNKS1BP1,GREM1,CX3CL1,SOD1,DGKZ,CHP1,TYRO3,CISH,FABP3,PDGFA,CLCF1,QARS,TRIM27,RIPK3,TNK2,IDH1,PHB2,PPP1R35,BAD,CTDSP1,LGALS3,TNFRSF1A,WASHC1,PKN1,CAPN2,PIP4K2B,MAD2L2,ARHGEF2,MVP,MTMR4,EEF2K,CDC37,CSK,AKT1,GIT1,MYDGF,MAP2K2,CACTIN,IRAK1,MIDN,STK11,TELO2,TAZ,JMJD8,VAC14,ERBB4,TRIB2,NSMF	yellow	VSMC_M3
GO:0090101	0.45	0.70	7	101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SPRED2,EMILIN1,GREM1,MTMR4,VASN,TGFBR3,STUB1	yellow	VSMC_M3
GO:0017015	0.45	0.70	7	102	regulation of transforming growth factor beta receptor signaling pathway	BP	1	SPRED2,EMILIN1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0021510	0.45	0.72	5	70	spinal cord development	BP	1	MPST,DCTN1,DLL4,SCYL1,AKT1	yellow	VSMC_M3
GO:0040007	0.45	0.60	50	742	growth	BP	1	ENPP1,CDK4,PPARD,PLEC,DNPH1,SOCS5,DBNL,CCM2,DMAP1,H3F3B,LAMTOR1,BCL2L1,TNS2,GREM1,KDM2B,TKT,WNT10B,SOD1,CCAR2,CISH,MMP14,GPX1,LIMK1,PRMT2,CCDC85B,KAT5,SIPA1,SGPL1,IGFBP5,CD9,EVC,H3F3A,DBN1,MAD2L2,CRABP2,SP2,SMARCA4,ZNF830,AKT1,SLC6A4,HDGFL2,SIRT6,CDK11B,ANAPC2,STK11,TGFBR3,ERBB4,TWF2,UNC13A,NSMCE3	yellow	VSMC_M3
GO:0001539	0.46	0.71	6	79	cilium or flagellum-dependent cell motility	BP	1	CEP131,YIF1B,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:0060285	0.46	0.71	6	79	cilium-dependent cell motility	BP	1	CEP131,YIF1B,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:0002832	0.46	0.71	6	77	negative regulation of response to biotic stimulus	BP	1	TTLL12,METTL3,TARBP2,TYRO3,C1QBP,CACTIN	yellow	VSMC_M3
GO:0050870	0.46	0.67	10	130	positive regulation of T cell activation	BP	1	LGALS1,SOCS5,EGR3,SART1,BAD,CORO1A,CD276,CSK,AKT1,AP3D1	yellow	VSMC_M3
GO:0001568	0.46	0.61	38	576	blood vessel development	BP	1	CUL7,B4GALT1,PDGFRA,COL15A1,EPN1,KLF4,HOXA1,CCM2,ZC3H12A,PLXND1,EMILIN1,SNX17,ARHGAP22,GREM1,PDE3B,CX3CL1,EGR3,DLL4,HTATIP2,PDGFA,MMP14,GPX1,ANPEP,SGPL1,YJEFN3,AAMP,AKT1,MYDGF,SIRT6,NSDHL,JMJD8,SARS,TGFBR3,MIR214,NDST1,TNFRSF12A,LOXL1,RNH1	yellow	VSMC_M3
GO:0001944	0.46	0.61	40	607	vasculature development	BP	1	CUL7,B4GALT1,PDGFRA,COL15A1,EPN1,KLF4,HOXA1,CCM2,ZC3H12A,PLXND1,EMILIN1,SNX17,RIC8A,ARHGAP22,GREM1,PDE3B,CX3CL1,EGR3,DLL4,HTATIP2,PDGFA,MMP14,GPX1,ANPEP,SGPL1,YJEFN3,AAMP,AKT1,MYDGF,SIRT6,NSDHL,STK11,JMJD8,SARS,TGFBR3,MIR214,NDST1,TNFRSF12A,LOXL1,RNH1	yellow	VSMC_M3
GO:0019953	0.46	0.61	40	565	sexual reproduction	BP	1	SPAG1,BAG6,NCAPH2,SBF1,IFT27,B4GALT1,FIGNL1,SIX5,ZNF296,PAFAH1B3,DLEC1,METTL3,CEP131,DND1,YIF1B,GNPDA1,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,BAD,CD9,NANOS3,ZNF830,AKT1,RFX2,SLC6A4,STK11,TAZ,FAM50A,IGSF8,MEIG1	yellow	VSMC_M3
GO:0009749	0.46	0.66	11	153	response to glucose	BP	1	PPARD,LGALS1,UCP2,AACS,SELENOS,PCK2,SMARCB1,BAD,SMARCA4,JAGN1,COL6A2	yellow	VSMC_M3
GO:0048511	0.46	0.64	15	223	rhythmic process	BP	1	CDK4,PDGFRA,RELB,METTL3,CAVIN3,EGR3,CCAR2,TYRO3,SRRD,IMPDH2,SGPL1,PER1,ZNF830,SLC6A4,JUND	yellow	VSMC_M3
GO:0048193	0.46	0.64	18	259	Golgi vesicle transport	BP	1	SNX3,INSIG1,SEC13,YIF1B,AP1G2,SCYL1,VPS51,COPE,CCDC22,SNX8,LMAN2,RANGRF,TMED1,CSK,RAB34,AP3D1,TRAPPC5,ARFRP1	yellow	VSMC_M3
GO:0060761	0.46	0.72	5	61	negative regulation of response to cytokine stimulus	BP	1	TTLL12,KLF4,METTL3,PALM3,CACTIN	yellow	VSMC_M3
GO:0010324	0.46	0.73	4	54	membrane invagination	BP	1	SNX9,SNX3,ALKBH4,SNX18	yellow	VSMC_M3
GO:0010631	0.46	0.63	18	261	epithelial cell migration	BP	1	PPARD,TSTA3,KLF4,WDPCP,ZC3H12A,PLXND1,SCARB1,GREM1,EGR3,DLL4,GPX1,CORO1B,PTPN23,AAMP,PKN1,AKT1,PTPRR,GLIPR2	yellow	VSMC_M3
GO:0007492	0.46	0.73	4	59	endoderm development	BP	1	H2AFY,MMP14,COL6A1,DUSP5	yellow	VSMC_M3
GO:0140056	0.46	0.71	5	67	organelle localization by membrane tethering	BP	1	ESYT1,STX10,PACS2,RABEPK,UNC13A	yellow	VSMC_M3
GO:0042886	0.46	0.64	15	210	amide transport	BP	1	PPARD,PLEKHA8,EIPR1,SLC9A3R1,MYRIP,UCP2,AACS,PCK2,SLC19A1,SLC26A6,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0048598	0.46	0.61	31	469	embryonic morphogenesis	BP	1	CTHRC1,PBX2,H2AFY,SCRIB,PDGFRA,KLF4,HOXA1,WDPCP,SLC9A3R1,INSIG1,RIC8A,DEAF1,HOXC4,LRIG1,GREM1,KDM2B,SOD1,DLL4,IRX1,MMP14,COL6A1,PBX1,MTHFR,CRABP2,ARMC5,SLC39A1,TTC39C,ZNF358,NDST1,ARFRP1,DUSP5	yellow	VSMC_M3
GO:0000819	0.47	0.65	12	168	sister chromatid segregation	BP	1	DCTN2,NCAPH2,H2AFY,NUMA1,RRS1,PINX1,NUDC,PHB2,EML3,MAD1L1,MAD2L2,MIS12	yellow	VSMC_M3

GO:0031323	0.47	0.56	300	4391	regulation of cellular metabolic process	BP	1	ENPP1,CD63,NAB2,CDK4,CTDSP2,SQSTM1,ZNF608,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,TRAPPC9,PPARD,SCRIB,PLEC,VPS28,SND1,PPP1R14B,PDGFRA,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,FHL3,SPRED2,ZC3H12A,FIGNL1,PNKP,RCN3,SNRNP70,CC2D1B,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,EMILIN1,DMAP1,CIC,UNK,INSIG1,OGG1,SERTAD1,TTC5,PSMC4,METTL3,CXXC5,LAMTOR1,DND1,EIF4EBP1,CAVIN3,DEAF1,HOXC4,TARBP2,KMT2B,SCARB1,NAT10,ZNF740,PDE4D,EIF4B,SWAP70,RALY,PLEKHF1,ACSL1,ZBTB38,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,CHP1,TYRO3,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,CHCHD2,RBM15B,CISH,SRSF9,RNF19B,DCPS,IRX1,SELENOS,RRP1B,ETFBKMT,BRD9,RIN3,FABP3,ZCCHC17,PDGFA,MMP14,GPX1,AIP,CLCF1,NGDN,SRRD,TSHZ2,QARS,PSME2,PIR,TRIM27,LIMK1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,SMARCD2,BRMS1,BUD23,TNK2,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,IDH1,ARNT2,ZFPL1,LIMD1,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,PPP1R35,NDP,IGFBP5,BAD,CTDSP1,MLF2,OTUB1,EID1,SSBP4,METTL13,MPV17L2,ZNF394,LGALS3,C11orf95,BUD31,TNFRSF1A,BABAM1,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UBXN1,WASHC1,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,AMER1,MTHFR,PIP4K2B,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,DFFA,SP2,ARHGEF2,SNF8,MVP,PER1,NFIX,PPP4C,SLX1A,IRF2BPL,	yellow	VSMC_M3
GO:0034219	0.47	0.70	6	86	carbohydrate transmembrane transport	BP	1	ENPP1,PPARD,SELENOS,CAPN10,AKT1,SLC27A4	yellow	VSMC_M3
GO:0032368	0.47	0.68	7	95	regulation of lipid transport	BP	1	SREBF2,LAMTOR1,ACSL1,FABP3,PLA2G3,YJEFN3,AKT1	yellow	VSMC_M3
GO:0090132	0.47	0.63	18	262	epithelium migration	BP	1	PPARD,TSTA3,KLF4,WDPCP,ZC3H12A,PLXND1,SCARB1,GREM1,EGR3,DLL4,GPX1,CORO1B,PTPN23,AAMP,PKN1,AKT1,PTPRR,GLIPR2	yellow	VSMC_M3
GO:0002637	0.47	0.73	4	48	regulation of immunoglobulin production	BP	1	CLCF1,PHB2,PKN1,MAD2L2	yellow	VSMC_M3
GO:2001236	0.47	0.67	9	121	regulation of extrinsic apoptotic signaling pathway	BP	1	BCL2L1,CX3CL1,ITPRIP,GPX1,RELA,LGALS3,ARHGEF2,AKT1,TNFRSF12A	yellow	VSMC_M3
GO:0051052	0.47	0.62	21	297	regulation of DNA metabolic process	BP	1	HDAC10,KLF4,FIGNL1,PNKP,OGG1,NAT10,PINX1,GREM1,KDM1B,CLCF1,OTUB1,BABAM1,MAD2L2,DFFA,PPP4C,SLX1A,CXorf57,AKT1,SIRT6,MBD3,NABP2	yellow	VSMC_M3
GO:0030183	0.47	0.68	7	96	B cell differentiation	BP	1	FNIP1,LGALS1,CD79A,MMP14,CLCF1,BAD,DOCK11	yellow	VSMC_M3
GO:0009991	0.47	0.61	27	385	response to extracellular stimulus	BP	1	FNIP1,SREBF2,PPARD,PLEC,ZC3H12A,OGG1,UCP2,EIF4EBP1,AACS,ACSL1,SOD1,DCPS,PCK2,SPX,RELA,SIPA1,FOXK1,MTHFR,TRIM25,AKT1,HMGCS1,SLC6A4,SIRT6,MBD3,WDR24,SLC27A4,FADS1	yellow	VSMC_M3
GO:0032233	0.47	0.72	4	56	positive regulation of actin filament bundle assembly	BP	1	SWAP70,CX3CL1,LIMK1,RHOC	yellow	VSMC_M3
GO:0048856	0.47	0.56	278	4193	anatomical structure development	BP	1	ENPP1,NAB2,CDK4,BAG6,NCAPH2,SBF1,CTHRC1,HDAC10,FNIP1,PBX2,PDLIM4,RING1,H2AFY,TRIM11,TRAPPC9,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,TBCC,CUL7,DNPH1,B4GALT1,PDGFRA,SECISBP2,PHF2,COL15A1,EPN1,COL19A1,SOCS5,TTC7A,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,ZC3H12A,RCN3,SNX3,PLEKHA4,EHD2,KMT2E,KRT8,SIX5,RELB,SLC9A3R1,PLXND1,EMILIN1,RNF220,PAFAH1B3,CIC,SNX17,UNK,CD79A,INSIG1,PSMC4,UCP2,METTL3,BAIAP2,CEP131,INPPL1,NUMA1,P4HB,DND1,YIF1B,FASN,RPL29,EIF4EBP1,RIC8A,ARHGAP22,DEAF1,TBCB,HOXC4,LRIG1,ARHGAP33,AACS,HM13,BCL2L1,ITGB7,PDE4D,TNS2,SWAP70,CAPG,SLC11A2,MMP24,GREM1,KDM2B,AQP5,PDE3B,DCTN1,CX3CL1,WNT10B,SOD1,CCDC32,ANKRD2,EGR3,DLL4,TYRO3,HTATIP2,RAB35,APBA2,IRX1,SDHA,PAPSS1,PDGFA,MMP14,C14orf93,GPX1,CORO1B,NGEF,HCCS,CLCF1,PLEKHO1,TAGLN2,IGSF9,QARS,LRFN4,PCK2,COL6A1,IMPDH2,PIR,NECTIN1,ANPEP,ARPIN,LIMK1,SLC26A6,PRMT2,THOC5,RIPK3,EXTL1,IQCG,PLA2G3,STMN3,SART1,PBX1,RELA,RHOC,SCYL1,IDH1,FMNL1,ARNT2,VPS51,LIMD1,SGPL1,SMARCB1,PBX4,YJEFN3,ATIC,BLOC1S4,MEF2B,PHB2,NDP,IGFBP5,C12orf57,BAD,AAMP,CTDSP1,HSD17B1,LGALS3,CD9,TNFRSF1A,TEAD4,C1QBP,AIMP2,CHERP,EVC,RCC2,CNP,PRXL2A,KRT10,GLUD1,FOXK1,CASP14,KLF3,PKN1,DBN1,CAPN2,MAD1L1,AMER1,MTHFR,MAD2L2,NANOS3,PRR14,CRABP2,TMEM79,ARHGEF2,ARMC5,MTX1,CORO1A,IRF2BPL,SLC39A1,S100A4,S100A6,SMARCA4,CARM1,SYNE3,EEF2K,MYO19,EML1,AATF,CSK,ZNF521,TTC39C,ZNF358,DOCK11,INF2,ZNF830,AKT1,COPRS,HMGCS1,RFX2,SAFB2,GIT1	yellow	VSMC_M3

GO:0051171	0.47	0.56	279	4082	regulation of nitrogen compound metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,ZNF608,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,SGSM3,TRAPPC9,PPARD,PLEC,VPS28,SND1,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,FHL3,SPRED2,ZC3H12A,FIGNL1,PNKP,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,EMILIN1,DMAP1,CIC,UNK,OGG1,SERTAD1,TTC5,PSMC4,METTL3,CXXC5,DND1,EIF4EBP1,DELE1,DEAF1,HOXC4,LDLRAD3,TARBP2,KMT2B,SCARB1,NAT10,ZNF740,PDE4D,EIF4B,SWAP70,RALY,ACSL1,ZBTB38,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,CHCHD2,RBM15B,SRSF9,RNF19B,DCPS,IRX1,SELENOS,RRP1B,BRD9,FABP3,ZCCHC17,PDGFA,MMP14,GPX1,AIP,CLCF1,NGDN,SRRD,TSHZ2,QARS,ASB9,PSME2,PIR,TRIM27,LIMK1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,SMARCD2,PFDN2,BRMS1,BUD23,TNK2,TACO1,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,NDP,IGFBP5,BAD,CTDSP1,MLF2,OTUB1,EID1,SSBP4,METTL13,MPV17L2,ZNF394,LGALS3,C11orf95,BUD31,TNFRSF1A,BABAM1,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UBXN1,WASHC1,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,AMER1,MTHFR,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,DFFA,SP2,ARHGEF2,SNF8,MVP,PER1,NFIX,PPP4C,SLX1A,IRF2BPL,TRIM25,RPL37,SMARCA4,CARM1,EEF2K,CDC37,RAVER1,AATF,CXorf57,C19orf66,CSK,MID2,RB	yellow	VSMC_M3
GO:0031344	0.47	0.60	35	538	regulation of cell projection organization	BP	1	PACSIN1,LGALS1,CUL7,KLF4,DBNL,WDPCP,SNX3,PLXND1,SEPT9,BAIAP2,ARHGAP33,CX3CL1,CORO1B,NGEF,ARPIN,LIMK1,PLA2G3,WASHC1,RCC2,DBN1,CRABP2,RABEP2,CARM1,EEF2K,ATG3,DOCK11,AKT1,ACAP3,ANAPC2,STK11,NEGR1,MIR214,TWF2,CDC42EP5,NSMF	yellow	VSMC_M3
GO:0043583	0.47	0.65	11	162	ear development	BP	1	CTHRC1,SCRIB,IFT27,HOXA1,WDPCP,CCM2,SLC9A3R1,INSIG1,LRIG1,SOD1,TTC39C	yellow	VSMC_M3
GO:0010906	0.47	0.68	7	96	regulation of glucose metabolic process	BP	1	ENPP1,SELENOS,BAD,FOXK1,AKT1,PGP,MIDN	yellow	VSMC_M3
GO:0003170	0.47	0.72	4	58	heart valve development	BP	1	EMILIN1,DLL4,TNFRSF1A,ELN	yellow	VSMC_M3
GO:0044772	0.48	0.61	25	350	mitotic cell cycle phase transition	BP	1	CDK4,CTDSP2,KLF4,KMT2E,CCDC57,EIF4EBP1,PINX1,WNT10B,CDK2AP2,PSME2,PRMT2,PBX1,PHB2,CTDSP1,BABAM1,RCC2,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,AKT1,MIR214,NABP2,CDC34	yellow	VSMC_M3
GO:0002040	0.48	0.67	8	114	sprouting angiogenesis	BP	1	EPN1,KLF4,GREM1,EGR3,DLL4,YJEFN3,AKT1,JMJD8	yellow	VSMC_M3
GO:0043161	0.48	0.61	26	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	BAG6,SHARPIN,HSPBP1,SOCS5,PSMB3,TMUB1,PSMC4,SEL1L2,WNT10B,CCAR2,RNF19B,SELENOS,KAT5,UBXN1,FBXL19,TRIM25,ANKRD9,AKT1,SIRT6,SPSB3,MAN1B1,ZNRF1,TRIB2,CDC34,FBXO6,STUB1	yellow	VSMC_M3
GO:0060021	0.48	0.70	5	71	roof of mouth development	BP	1	PDGFRA,WDPCP,INSIG1,SGPL1,TGFBR3	yellow	VSMC_M3
GO:0051205	0.48	0.72	4	44	protein insertion into membrane	BP	1	BAG6,SAMM50,ASNA1,TIMM22	yellow	VSMC_M3
GO:0034440	0.48	0.67	7	90	lipid oxidation	BP	1	ACAT2,PPARD,CPT1C,ETFBKMT,FABP3,ILVBL,AKT1	yellow	VSMC_M3
GO:0019935	0.48	0.72	4	57	cyclic-nucleotide-mediated signaling	BP	1	SLC9A3R1,PDE4D,PDE3B,CDC34	yellow	VSMC_M3
GO:0009617	0.48	0.60	26	362	response to bacterium	BP	1	CDK4,HNRNPA0,PPARD,SSC5D,ZC3H12A,SNX3,BAIAP2,SCARB1,CX3CL1,SELENOS,PABPN1,GPX1,PCK2,RELA,TNFRSF1A,CNP,CAPN2,PALM3,AKT1,GIT1,LDOC1,CACTIN,IRAK1,CARD9,JUND,LOXL1	yellow	VSMC_M3
GO:0070059	0.48	0.72	4	50	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP	1	BAG6,BCL2L1,SELENOS,TXNDC12	yellow	VSMC_M3
GO:1903844	0.48	0.67	7	104	regulation of cellular response to transforming growth factor beta stimulus	BP	1	SPRED2,EMILIN1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0030155	0.48	0.59	36	541	regulation of cell adhesion	BP	1	TSTA3,SCRIB,LGALS1,SOCS5,KLF4,WDPCP,ZC3H12A,PLXND1,EMILIN1,METTL3,P4HB,SWAP70,GREM1,PDE3B,CX3CL1,EGR3,ST3GAL4,MMP14,SART1,PTPN23,RELA,SIPA1,BAD,LGALS3,CD9,PLAU,C1QBP,RCC2,MAD1L1,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1,IRAK1	yellow	VSMC_M3
GO:2000146	0.48	0.62	16	234	negative regulation of cell motility	BP	1	PPARD,KLF4,SLC9A3R1,EMILIN1,GREM1,CX3CL1,DLL4,RIN3,CORO1B,ARPIN,PTPN23,IGFBP5,MIIP,AKT1,MIR214,PTPRR	yellow	VSMC_M3
GO:0030030	0.48	0.57	79	1226	cell projection organization	BP	1	SPAG1,CTHRC1,TXNDC15,PACSIN1,SCRIB,LGALS1,IFT27,CUL7,KLF4,DBNL,TPBG,WDPCP,SNX3,EMP3,EHD2,SLC9A3R1,PLXND1,SEPT9,BAIAP2,CEP131,INPPL1,YIF1B,CCDC57,ARHGAP33,CAPG,SLC11A2,DCTN1,CX3CL1,SOD1,CCDC32,RAB35,CCDC28B,PDGFA,CORO1B,NGEF,PLEKHO1,IGSF9,NECTIN1,ARPIN,PCNT,LIMK1,IQCG,PLA2G3,STMN3,CEP164,PTPN23,BLOC1S4,C12orf57,WASHC1,RCC2,CNP,DBN1,CRABP2,FAM161B,CORO1A,RABEP2,S100A6,CARM1,EEF2K,ATG3,TTC39C,DOCK11,AKT1,RFX2,RAB34,ACAP3,SSNA1,ANAPC2,NUBP2,STK11,GAS8,WDR34,NEGR1,MIR214,TWF2,UNC13A,CDC42EP5,NSMF,MEIG1	yellow	VSMC_M3
GO:0051494	0.48	0.66	9	138	negative regulation of cytoskeleton organization	BP	1	SWAP70,CAPG,CORO1B,ARPIN,MID1IP1,ARHGEF2,CORO1A,MIR214,TWF2	yellow	VSMC_M3
GO:0099173	0.48	0.66	9	137	postsynapse organization	BP	1	DBNL,BAIAP2,ARHGAP22,ARHGAP33,RAPSN,NGEF,LRFN4,DBN1,EEF2K	yellow	VSMC_M3
GO:0006979	0.48	0.60	26	357	response to oxidative stress	BP	1	H2AFY,PDGFRA,KLF4,ZC3H12A,PNKP,OGG1,UCP2,P4HB,PYCR1,GSR,SOD1,ANKRD2,CHCHD2,SELENOS,MMP14,GPX1,RIPK3,RELA,IDH1,TXNRD2,BAD,CAPN2,AKT1,DHCR24,TRAP1,OSER1	yellow	VSMC_M3

GO:0048518	0.48	0.55	307	4533	positive regulation of biological process	BP	1	CD63,NAB2,NHP2,CDK4,SQSTM1,BAG6,SNX9,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,SREBF2,TXNDC15,H2AFY,ITPR3,HNRNPA0,TRIM11,SGSM3,PACSIN1,PPARD,EEF1D,TSTA3,SCRIB,LGALS1,SHARPIN,VPS28,CUL7,DNPH1,B4GALT1,PDGFRA,IL1R1,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,DBNL,TPBG,HOXA1,SPRED2,EIPR1,ZC3H12A,PNKP,RCN3,SNRNP70,SNX3,PLEKHA4,EHD2,KMT2E,WDFY2,SIX5,ZNF296,RELB,SLC9A3R1,PLXND1,EMILIN1,RNF220,DMAP1,SLC30A3,H3F3B,CD79A,MYRIP,SEC13,SEPT9,SERTAD1,TTC5,PSMC4,UCP2,METTL3,PHLDA1,BAIAP2,CEP131,CXXC5,LAMTOR1,NUMA1,P4HB,DND1,CCDC57,EIF4EBP1,CAVIN3,DEAF1,HOXC4,TARBP2,KMT2B,AACS,SCARB1,NAT10,BCL2L1,PDE4D,SWAP70,LRP3,PLEKHF1,ACSL1,ZBTB38,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,DCTN1,RAPSN,CX3CL1,WNT10B,SOD1,PACSIN3,DGKZ,EGR3,CCAR2,DLL4,CHP1,TYRO3,SCD,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,SLC35C2,TSPAN5,ST3GAL4,RNF19B,DCPS,GSTO1,RRP1B,FABP3,PDGFA,MMP14,C14orf93,GPX1,AIP,CORO1B,CLCF1,SYT12,PCK2,ASB9,PSME2,TRIM27,ARPIN,PCNT,LIMK1,SLC26A6,PRMT2,SPX,THOC5,RIPK3,TWIST2,ADRM1,CAPN10,SMARCD2,PFDN2,BRMS1,BUD23,TNK2,PLA2G3,GMEB2,SART1,PRPF6,PTPN23,PBX1,KAT5,RELA,RHOC,MAP3K14,ARNT2,LIMD1,MID1IP1,ZDHHC3,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,PHB2,TRMT112,NDP,IGFBP5,BAD,LAMTOR4,IFI35,AAMP,SSBP4,MPV17L2,LGALS3,BUD31,ARPC1B,PLAU,TNFRSF1A,BABAM1,C1QBP,AIMP2,TAF6L,CHERP,ZBTB49,WASHC1,EVC,RCC2,MTA2,PELP1,CCDC22,USP27X,KRT10,GLUD1,FOXK1,ELP5,H3F3A,PKN1,DBN1,CAPN2,LMAN2,POLR2A,AMER1,PIP4K2B,MA	yellow	VSMC_M3
GO:0044770	0.48	0.59	30	426	cell cycle phase transition	BP	1	CDK4,CTDSP2,H2AFY,KLF4,KMT2E,CCDC57,EIF4EBP1,PINX1,WNT10B,CCAR2,CDK2AP2,PSME2,PRMT2,THOC5,PBX1,PHB2,CTDSP1,METTL13,BABAM1,RCC2,SDE2,MIIP,MAD1L1,MAD2L2,ZNF830,AKT1,MIR214,NABP2,CDC34,FBXO6	yellow	VSMC_M3
GO:0009792	0.48	0.59	36	537	embryo development ending in birth or egg hatching	BP	1	CTHRC1,SCRIB,PDGFRA,EPN1,CNOT3,KLF4,HOXA1,CCM2,KRT8,RNF220,UNK,PSMC4,RIC8A,DEAF1,HOXC4,HM13,BCL2L1,KDM2B,MMP14,STMN3,PBX1,ARNT2,SMARCB1,DBN1,CAPN2,MTHFR,ARMC5,SLC39A1,ZNF358,ZNF830,AKT1,NSDHL,SLC35E2B,MBD3,NDST1,PTPRR	yellow	VSMC_M3
GO:0007623	0.48	0.64	11	160	circadian rhythm	BP	1	CDK4,RELB,METTL3,CAVIN3,EGR3,CCAR2,SRRD,IMPDH2,PER1,SLC6A4,JUND	yellow	VSMC_M3
GO:0043087	0.48	0.61	18	285	regulation of GTPase activity	BP	1	SBF1,SNX9,SGSM3,SCRIB,PLXND1,ARAP3,ARHGAP22,CX3CL1,SOD1,RRP1B,NGEF,STMN3,SIPA1,RCC2,DOCK11,SNX18,SLC27A4,RGS16	yellow	VSMC_M3
GO:0061061	0.49	0.59	34	504	muscle structure development	BP	1	PDLIM4,PPARD,PLEC,LGALS1,PDGFRA,COL19A1,FHL3,EHD2,KRT8,GREM1,WNT10B,ANKRD2,EGR3,DLL4,MMP14,GPX1,PLEKHO1,MEF2B,IGFBP5,CD9,TEAD4,EVC,FOXK1,CAPN2,PRR14,AKT1,COPRS,SIRT6,HMG20B,TAZ,GTF3C5,TGFBR3,IGSF8,ELN	yellow	VSMC_M3
GO:0061045	0.49	0.71	4	52	negative regulation of wound healing	BP	1	PDGFRA,PDGFA,CD9,PLAU	yellow	VSMC_M3
GO:0006893	0.49	0.71	4	56	Golgi to plasma membrane transport	BP	1	CCDC22,CSK,RAB34,ARFRP1	yellow	VSMC_M3
GO:1901264	0.49	0.69	5	61	carbohydrate derivative transport	BP	1	GUK1,PLEKHA8,SCARB1,SLC35C2,SLC19A1	yellow	VSMC_M3
GO:0010565	0.49	0.67	7	95	regulation of cellular ketone metabolic process	BP	1	PPARD,INSIG1,ETFBKMT,FABP3,PLA2G3,MID1IP1,AKT1	yellow	VSMC_M3
GO:0010001	0.49	0.63	12	173	glial cell differentiation	BP	1	NAB2,HDAC10,PLEC,METTL3,MMP24,SOD1,CLCF1,RELA,CD9,CNP,CSK,AKT1	yellow	VSMC_M3
GO:0006006	0.49	0.64	11	155	glucose metabolic process	BP	1	ENPP1,PPARD,INPPL1,SELENOS,PCK2,BAD,FOXK1,AKT1,PGM1,PGP,MIDN	yellow	VSMC_M3
GO:2000756	0.49	0.71	4	53	regulation of peptidyl-lysine acetylation	BP	1	SMARCB1,EID1,CTBP1,THAP7	yellow	VSMC_M3
GO:1903362	0.49	0.61	16	222	regulation of cellular protein catabolic process	BP	1	BAG6,HSPBP1,SOCS5,PSMC4,WNT10B,CCAR2,RNF19B,GPX1,PSME2,UBXN1,CCDC22,AMER1,AKT1,SIRT6,TRIB2,STUB1	yellow	VSMC_M3
GO:0031347	0.49	0.59	28	397	regulation of defense response	BP	1	TTLL12,PPARD,SHARPIN,IL1R1,SOCS5,KLF4,ZC3H12A,ZYX,MGLL,METTL3,TARBP2,CX3CL1,SOD1,TYRO3,SELENOS,MVK,GPX1,PSMB4,PLA2G3,RELA,IFI35,TNFRSF1A,C1QBP,CDC37,GIT1,CACTIN,CARD9,TRADD	yellow	VSMC_M3
GO:0001952	0.49	0.66	7	105	regulation of cell-matrix adhesion	BP	1	TSTA3,WDPCP,GREM1,CX3CL1,MMP14,PLAU,RCC2	yellow	VSMC_M3
GO:0006354	0.49	0.67	6	80	DNA-templated transcription, elongation	BP	1	NELFE,SERTAD1,CCAR2,THOC5,ADRM1,GTF2F1	yellow	VSMC_M3
GO:0043547	0.49	0.62	13	202	positive regulation of GTPase activity	BP	1	SNX9,SGSM3,SCRIB,ARAP3,ARHGAP22,CX3CL1,NGEF,SIPA1,RCC2,DOCK11,SNX18,SLC27A4,RGS16	yellow	VSMC_M3
GO:1903047	0.49	0.57	42	608	mitotic cell cycle process	BP	1	DCTN2,CDK4,CTDSP2,NCAPH2,SNX9,H2AFY,CUL7,KLF4,KMT2E,NUMA1,CCDC57,EIF4EBP1,RRS1,PINX1,DCTN1,WNT10B,RAB35,CDK2AP2,PSME2,PCNT,NUDC,PRMT2,PBX1,RHOC,PHB2,CTDSP1,BABAM1,RCC2,EML3,SDE2,MIIP,MAD1L1,MAD2L2,EML1,ZNF830,AKT1,SNX18,AURKAIP1,MIR214,NABP2,MIS12,CDC34	yellow	VSMC_M3
GO:0055076	0.49	0.65	8	107	transition metal ion homeostasis	BP	1	TTC7A,SLC30A3,SLC11A2,SOD1,CCDC22,ANKRD9,AP3D1,CCDC115	yellow	VSMC_M3
GO:0051893	0.49	0.71	4	60	regulation of focal adhesion assembly	BP	1	WDPCP,GREM1,MMP14,RCC2	yellow	VSMC_M3
GO:0090109	0.49	0.71	4	60	regulation of cell-substrate junction assembly	BP	1	WDPCP,GREM1,MMP14,RCC2	yellow	VSMC_M3
GO:0001775	0.49	0.57	48	692	cell activation	BP	1	BAG6,NCAPH2,FNIP1,SCRIB,LGALS1,PDGFRA,SOCS5,ZC3H12A,KMT2E,RELB,EMILIN1,CD79A,METTL3,SWAP70,CX3CL1,SOD1,DGKZ,EGR3,DLL4,TYRO3,PDGFA,MMP14,CLCF1,IMPDH2,RIPK3,PLA2G3,SART1,PBX1,BLOC1S4,PHB2,BAD,IFI35,LGALS3,CD9,PKN1,MAD1L1,MAD2L2,ARMC5,CORO1A,CD276,CSK,DOCK11,AKT1,AP3D1,STK11,PSMB10,JUND,AKAP17A	yellow	VSMC_M3
GO:0043068	0.49	0.58	30	422	positive regulation of programmed cell death	BP	1	CDK4,SQSTM1,FNIP1,SCRIB,B4GALT1,ZC3H12A,SLC9A3R1,PHLDA1,PLEKHF1,RAPSN,WNT10B,SOD1,CCAR2,HTATIP2,RRP1B,PRMT2,RIPK3,CAPN10,BRMS1,BAD,TNFRSF1A,C1QBP,USP27X,CAPN2,DFFA,AKT1,SLC27A4,TRADD,TNFRSF12A,CDC34	yellow	VSMC_M3
GO:0034109	0.49	0.69	5	71	homotypic cell-cell adhesion	BP	1	LGALS1,PDGFRA,TYRO3,BLOC1S4,CD9	yellow	VSMC_M3
GO:0070085	0.49	0.62	14	194	glycosylation	BP	1	B4GALT1,SERP2,GALNT14,CHP1,SLC35C2,ST3GAL4,TMTC1,EXTL1,MPDU1,DPM3,MAN1B1,POMT1,B3GNT9,GBA2	yellow	VSMC_M3

GO:0030097	0.49	0.57	42	618	hemopoiesis	BP	1	NCAPH2,FNIP1,LGALS1,PDGFRA,SOCS5,TTC7A,KLF4,ZC3H12A,KMT2E,RELB,CD79A,METTL3,FASN,SLC11A2,WNT10B,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,PIR,THOC5,RIPK3,PLA2G3,SART1,PBX1,SGPL1,YJEFN3,BAD,PRXL2A,ARMC5,EML1,DOCK11,AP3D1,MKNK2,STK11,TAZ,TGFBR3,KLF13,JAGN1,ZNF385A	yellow	VSMC_M3
GO:0001654	0.50	0.60	18	280	eye development	BP	1	CDK4,PBX2,RING1,PDGFRA,KLF4,WDPCP,SPRED2,SIX5,KDM2B,AQP5,DLL4,IMPDH2,NECTIN1,PBX1,PBX4,C12orf57,SMARCA4,CTNS	yellow	VSMC_M3
GO:0090130	0.50	0.60	18	266	tissue migration	BP	1	PPARD,TSTA3,KLF4,WDPCP,ZC3H12A,PLXND1,SCARB1,GREM1,EGR3,DLL4,GPX1,CORO1B,PTPN23,AAMP,PKN1,AKT1,PTPRR,GLIPR2	yellow	VSMC_M3
GO:0019827	0.50	0.66	7	106	stem cell population maintenance	BP	1	CNOT3,KLF4,METTL3,MMP24,KDM2B,TAF6L,ZNF358	yellow	VSMC_M3
GO:0044703	0.50	0.56	48	688	multi-organism reproductive process	BP	1	SPAG1,BAG6,NCAPH2,SBF1,PPARD,IFT27,B4GALT1,EPN1,FIGNL1,SIX5,ZNF296,PAFAH1B3,DLEC1,UCP2,METTL3,CEP131,DND1,YIF1B,RPL29,GNPDA1,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,SLC19A1,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,IGFBP5,BAD,CD9,C1QBP,CAPN2,NANOS3,ZNF830,AKT1,RFX2,SLC6A4,STK11,TAZ,FAM50A,IGSF8,MEIG1	yellow	VSMC_M3
GO:1901565	0.50	0.55	75	1069	organonitrogen compound catabolic process	BP	1	SQSTM1,BAG6,SNX9,SGSM3,NUDT3,MPST,SHARPIN,VPS28,CUL7,DNPH1,HSPBP1,SOCS5,PSMB3,BLVRA,RCN3,SNRNP70,SNX3,TMUB1,BCKDHA,BLVRB,OGG1,PSMC4,SEL1L2,SMOX,GNPDA1,SMUG1,SCARB1,HM13,PDE4D,WNT10B,PACSIN3,CCAR2,RNF19B,SELENOS,MANBA,GPX1,ASB9,PSME2,ANPEP,ADRM1,PSMB4,PTPN23,KAT5,RELA,SGPL1,MVB12A,UBXN1,CCDC22,USP27X,GLUD1,CAPN2,AMER1,MAD2L2,FBXL19,SNF8,TRIM25,USP43,ANKRD9,AKT1,BLMH,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,PSMB10,CTRL,NT5C,TRIB2,CDC34,FBXO6,GBA2,STUB1,ITPA,CCDC115	yellow	VSMC_M3
GO:0042306	0.50	0.70	4	52	regulation of protein import into nucleus	BP	1	ZC3H12A,DMAP1,CHP1,RBM22	yellow	VSMC_M3
GO:0007565	0.50	0.63	10	139	female pregnancy	BP	1	PPARD,EPN1,UCP2,RPL29,SOD1,SLC19A1,IGFBP5,C1QBP,CAPN2,AKT1	yellow	VSMC_M3
GO:0048704	0.50	0.67	6	83	embryonic skeletal system morphogenesis	BP	1	PDGFRA,HOXA1,HOXC4,MMP14,SLC39A1,NDST1	yellow	VSMC_M3
GO:0046364	0.50	0.68	5	65	monosaccharide biosynthetic process	BP	1	SELENOS,PCK2,PGD,PGM1,PGP	yellow	VSMC_M3
GO:0048534	0.50	0.56	44	649	hematopoietic or lymphoid organ development	BP	1	NCAPH2,FNIP1,LGALS1,PDGFRA,SOCS5,TTC7A,KLF4,ZC3H12A,KMT2E,RELB,CD79A,METTL3,FASN,SLC11A2,WNT10B,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,PIR,THOC5,RIPK3,PLA2G3,SART1,PBX1,SGPL1,YJEFN3,BAD,PRXL2A,PKN1,MAD1L1,ARMC5,EML1,DOCK11,AP3D1,MKNK2,STK11,TAZ,TGFBR3,KLF13,JAGN1,ZNF385A	yellow	VSMC_M3
GO:0042770	0.50	0.62	11	155	signal transduction in response to DNA damage	BP	1	SPRED2,CCAR2,THOC5,KAT5,BABAM1,SDE2,MAD2L2,ZNF830,HIC1,ZNF385A,FBXO6	yellow	VSMC_M3
GO:0002252	0.50	0.58	25	360	immune effector process	BP	1	GNL1,PLEC,LGALS1,IL1R1,SOCS5,ZC3H12A,KMT2E,RELB,SWAP70,RNF19B,CLCF1,LIMK1,RIPK3,PLA2G3,PHB2,IFI35,LGALS3,C1QBP,PKN1,MAD2L2,CORO1A,DOCK11,C8G,CARD9,JAGN1	yellow	VSMC_M3
GO:0015833	0.50	0.61	13	186	peptide transport	BP	1	PPARD,EIPR1,SLC9A3R1,MYRIP,UCP2,AACS,PCK2,SLC26A6,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0000956	0.50	0.65	7	102	nuclear-transcribed mRNA catabolic process	BP	1	SECISBP2,CNOT3,ZC3H12A,DCPS,MRTO4,NANOS3,RBM8A	yellow	VSMC_M3
GO:0010975	0.50	0.58	24	376	regulation of neuron projection development	BP	1	PACSIN1,LGALS1,CUL7,KLF4,DBNL,SNX3,PLXND1,BAIAP2,ARHGAP33,CX3CL1,NGEF,LIMK1,PLA2G3,DBN1,CRABP2,CARM1,EEF2K,AKT1,ACAP3,ANAPC2,STK11,NEGR1,TWF2,NSMF	yellow	VSMC_M3
GO:0006635	0.50	0.68	5	64	fatty acid beta-oxidation	BP	1	ACAT2,PPARD,CPT1C,ETFBKMT,AKT1	yellow	VSMC_M3
GO:0046395	0.50	0.61	14	182	carboxylic acid catabolic process	BP	1	ACAT2,PPARD,CPT1C,BCKDHA,GNPDA1,PCCB,ETFBKMT,PCK2,GLUD1,ILVBL,PGD,AKT1,BLMH,SLC27A4	yellow	VSMC_M3
GO:0061951	0.50	0.70	4	55	establishment of protein localization to plasma membrane	BP	1	SCRIB,CSK,RAB34,ARFRP1	yellow	VSMC_M3
GO:0044262	0.50	0.60	16	229	cellular carbohydrate metabolic process	BP	1	ENPP1,B4GALT1,GALK1,SELENOS,PCK2,IDH1,BAD,ISYNA1,FOXK1,PGD,AKT1,GIT1,PGP,MIDN,B3GNT9,NDST1	yellow	VSMC_M3
GO:0060402	0.50	0.65	7	107	calcium ion transport into cytosol	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A	yellow	VSMC_M3
GO:0042116	0.50	0.68	5	69	macrophage activation	BP	1	ZC3H12A,CX3CL1,PLA2G3,IFI35,JUND	yellow	VSMC_M3
GO:0043367	0.50	0.70	4	56	CD4-positive, alpha-beta T cell differentiation	BP	1	SOCS5,ZC3H12A,RELB,ARMC5	yellow	VSMC_M3
GO:0150063	0.51	0.59	18	282	visual system development	BP	1	CDK4,PBX2,RING1,PDGFRA,KLF4,WDPCP,SPRED2,SIX5,KDM2B,AQP5,DLL4,IMPDH2,NECTIN1,PBX1,PBX4,C12orf57,SMARCA4,CTNS	yellow	VSMC_M3
GO:0006367	0.51	0.68	5	65	transcription initiation from RNA polymerase II promoter	BP	1	CDK4,WNT10B,TAF6L,GTF2F1,MED16	yellow	VSMC_M3
GO:0006606	0.51	0.63	9	129	protein import into nucleus	BP	1	ZC3H12A,DMAP1,SEC13,CHP1,PHB2,NUP88,RANGRF,RBM22,AKT1	yellow	VSMC_M3
GO:0070301	0.51	0.66	6	79	cellular response to hydrogen peroxide	BP	1	KLF4,PYCR1,RIPK3,RELA,TRAP1,OSER1	yellow	VSMC_M3
GO:0043065	0.51	0.57	29	410	positive regulation of apoptotic process	BP	1	CDK4,SQSTM1,FNIP1,SCRIB,B4GALT1,ZC3H12A,SLC9A3R1,PHLDA1,PLEKHF1,RAPSN,WNT10B,SOD1,CCAR2,RRP1B,PRMT2,RIPK3,CAPN10,BRMS1,BAD,TNFRSF1A,C1QBP,USP27X,CAPN2,DFFA,AKT1,SLC27A4,TRADD,TNFRSF12A,CDC34	yellow	VSMC_M3
GO:0010827	0.51	0.69	4	58	regulation of glucose transmembrane transport	BP	1	ENPP1,SELENOS,CAPN10,AKT1	yellow	VSMC_M3
GO:1903829	0.51	0.60	16	241	positive regulation of cellular protein localization	BP	1	SQSTM1,SREBF2,VPS28,ZC3H12A,DMAP1,NUMA1,PINX1,MCRS1,CHP1,LGALS3,RANGRF,RBM22,AKT1,STK11,GAS8,ERBB4	yellow	VSMC_M3
GO:0043524	0.51	0.64	8	115	negative regulation of neuron apoptotic process	BP	1	BCL2L1,KDM2B,CX3CL1,SOD1,TYRO3,CLCF1,PLA2G3,CORO1A	yellow	VSMC_M3
GO:0070664	0.51	0.69	4	53	negative regulation of leukocyte proliferation	BP	1	SCRIB,GREM1,PKN1,MAD1L1	yellow	VSMC_M3
GO:0000018	0.51	0.66	6	83	regulation of DNA recombination	BP	1	FIGNL1,CLCF1,MAD2L2,PPP4C,CXorf57,SIRT6	yellow	VSMC_M3
GO:0098930	0.51	0.69	4	58	axonal transport	BP	1	SOD1,BLOC1S4,AP3D1,SPG7	yellow	VSMC_M3
GO:0071345	0.51	0.56	40	574	cellular response to cytokine stimulus	BP	1	CDK4,TTLL12,RPL3,SHARPIN,IL1R1,SOCS5,KLF4,ZC3H12A,ZYX,KRT8,METTL3,P4HB,FASN,RAB20,ACSL1,DOK1,CX3CL1,LSP1,CLCF1,PCK2,IMPDH2,SLC26A6,RELA,ATIC,BAD,OTUB1,TNFRSF1A,CAPN2,PALM3,ARHGEF2,CORO1A,TRIM25,CDC37,AKT1,KHSRP,CACTIN,IRAK1,TRADD,JAGN1,CDC34	yellow	VSMC_M3

GO:0006486	0.51	0.60	13	182	protein glycosylation	BP	1	B4GALT1,SERP2,GALNT14,CHP1,SLC35C2,ST3GAL4,TMTC1,EXTL1,MPDU1,DPM3,MAN1B1,POMT1,B3GNT9	yellow	VSMC_M3
GO:0043413	0.51	0.60	13	182	macromolecule glycosylation	BP	1	B4GALT1,SERP2,GALNT14,CHP1,SLC35C2,ST3GAL4,TMTC1,EXTL1,MPDU1,DPM3,MAN1B1,POMT1,B3GNT9	yellow	VSMC_M3
GO:0010821	0.51	0.63	9	124	regulation of mitochondrion organization	BP	1	SQSTM1,SREBF2,BCL2L1,GPX1,CHCHD10,BAD,MYO19,INF2,AKT1	yellow	VSMC_M3
GO:0048562	0.51	0.60	15	225	embryonic organ morphogenesis	BP	1	CTHRC1,SCRIB,PDGFRA,HOXA1,WDPCP,SLC9A3R1,INSIG1,HOXC4,LRIG1,KDM2B,SOD1,MMP14,SLC39A1,TTC39C,NDST1	yellow	VSMC_M3
GO:0006511	0.51	0.56	37	542	ubiquitin-dependent protein catabolic process	BP	1	SQSTM1,BAG6,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,PSMB3,TMUB1,PSMC4,SEL1L2,WNT10B,CCAR2,RNF19B,SELENOS,ADRM1,PTPN23,KAT5,MVB12A,UBXN1,CCDC22,USP27X,FBXL19,SNF8,TRIM25,USP43,ANKRD9,AKT1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,TRIB2,CDC34,FBXO6,STUB1	yellow	VSMC_M3
GO:0002694	0.51	0.57	25	352	regulation of leukocyte activation	BP	1	SCRIB,LGALS1,SOCS5,ZC3H12A,METTL3,CX3CL1,SOD1,EGR3,TYRO3,MMP14,CLCF1,RIPK3,PLA2G3,SART1,BAD,LGALS3,PKN1,MAD1L1,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1,JUND	yellow	VSMC_M3
GO:0019318	0.51	0.60	13	185	hexose metabolic process	BP	1	ENPP1,PPARD,B4GALT1,GALK1,INPPL1,SELENOS,PCK2,BAD,FOXK1,AKT1,PGM1,PGP,MIDN	yellow	VSMC_M3
GO:0006900	0.51	0.69	4	55	vesicle budding from membrane	BP	1	SNX3,INSIG1,SEC13,AP3D1	yellow	VSMC_M3
GO:1901137	0.51	0.56	35	494	carbohydrate derivative biosynthetic process	BP	1	GUK1,TSTA3,B4GALT1,PIGO,SERP2,GALNT14,PHLDA1,GNPDA1,ACSL1,TKT,CHP1,SLC35C2,ST3GAL4,AK2,TMTC1,PAPSS1,IMPDH2,EXTL1,ATP5MC3,ATIC,UQCC3,ACLY,MPDU1,DPM3,ATP5PD,AATF,MAN1B1,ATP5F1D,TAZ,AMPD2,APRT,POMT1,AK1,B3GNT9,NDST1	yellow	VSMC_M3
GO:0099111	0.51	0.61	11	165	microtubule-based transport	BP	1	IFT27,SLC9A3R1,CEP131,SOD1,BLOC1S4,AP3D1,SSNA1,STK11,TMEM201,SPG7,WDR34	yellow	VSMC_M3
GO:0006839	0.51	0.59	16	210	mitochondrial transport	BP	1	SAMM50,SREBF2,UCP2,BCL2L1,SFXN5,AIP,CHCHD10,BAD,LETM1,CNP,ATP5PD,AKT1,ALKBH7,ATP5F1D,SPG7,TIMM22	yellow	VSMC_M3
GO:0030163	0.52	0.54	56	815	protein catabolic process	BP	1	SQSTM1,BAG6,SNX9,SGSM3,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,PSMB3,RCN3,SNRNP70,SNX3,TMUB1,PSMC4,SEL1L2,HM13,WNT10B,PACSIN3,CCAR2,RNF19B,SELENOS,MANBA,GPX1,ASB9,PSME2,ADRM1,PSMB4,PTPN23,KAT5,RELA,MVB12A,UBXN1,CCDC22,USP27X,CAPN2,AMER1,MAD2L2,FBXL19,SNF8,TRIM25,USP43,ANKRD9,AKT1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,PSMB10,CTRL,TRIB2,CDC34,FBXO6,STUB1,CCDC115	yellow	VSMC_M3
GO:0060828	0.52	0.59	14	210	regulation of canonical Wnt signaling pathway	BP	1	CTHRC1,TPBG,PLEKHA4,SLC9A3R1,RNF220,GREM1,WNT10B,CCAR2,LIMD1,AMER1,MAD2L2,CSNK1G2,STK11,IGFBP6	yellow	VSMC_M3
GO:0009411	0.52	0.62	9	127	response to UV	BP	1	METTL3,ACTR5,CCAR2,GPX1,RELA,SDE2,AKT1,STK11,NSMCE3	yellow	VSMC_M3
GO:0010675	0.52	0.63	8	114	regulation of cellular carbohydrate metabolic process	BP	1	ENPP1,SELENOS,BAD,FOXK1,AKT1,GIT1,PGP,MIDN	yellow	VSMC_M3
GO:0006405	0.52	0.66	5	69	RNA export from nucleus	BP	1	RBM15B,PABPN1,THOC5,THOC3,NUP88	yellow	VSMC_M3
GO:0051224	0.52	0.64	7	96	negative regulation of protein transport	BP	1	SNX3,INSIG1,UCP2,CHP1,CSK,MIDN,JAGN1	yellow	VSMC_M3
GO:0001704	0.52	0.65	6	93	formation of primary germ layer	BP	1	H2AFY,KLF4,MMP14,COL6A1,ARMC5,DUSP5	yellow	VSMC_M3
GO:0032886	0.52	0.59	13	202	regulation of microtubule-based process	BP	1	CEP131,NUMA1,NAT10,DCTN1,CDK2AP2,STMN3,MID1IP1,EML3,ARHGEF2,RANGRF,GIT1,STK11,GBA2	yellow	VSMC_M3
GO:0001836	0.52	0.68	4	48	release of cytochrome c from mitochondria	BP	1	BCL2L1,GPX1,BAD,AKT1	yellow	VSMC_M3
GO:0000902	0.52	0.54	49	799	cell morphogenesis	BP	1	PACSIN1,SCRIB,PLEC,TBCC,CUL7,COL15A1,DBNL,TPBG,WDPCP,SLC9A3R1,PLXND1,UNK,METTL3,BAIAP2,P4HB,ARHGAP33,ITGB7,SLC11A2,GREM1,SOD1,TYRO3,CORO1B,NGEF,PLEKHO1,IGSF9,NECTIN1,ARPIN,LIMK1,RHOC,FMNL1,LIMD1,C12orf57,C1QBP,RCC2,CNP,DBN1,CRABP2,ARHGEF2,CORO1A,S100A6,SYNE3,EEF2K,ANAPC2,STK11,PSMB10,TWF2,UNC13A,CDC42EP5,NSMF	yellow	VSMC_M3
GO:0006809	0.52	0.68	4	55	nitric oxide biosynthetic process	BP	1	KLF4,ZC3H12A,AKT1,KHSRP	yellow	VSMC_M3
GO:0035303	0.52	0.63	7	106	regulation of dephosphorylation	BP	1	SWAP70,CHP1,RIPK3,PPP1R35,LGALS3,MTMR4,NSMF	yellow	VSMC_M3
GO:0051603	0.52	0.54	44	639	proteolysis involved in cellular protein catabolic process	BP	1	SQSTM1,BAG6,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,PSMB3,RCN3,TMUB1,PSMC4,SEL1L2,HM13,WNT10B,CCAR2,RNF19B,SELENOS,GPX1,PSME2,ADRM1,PSMB4,PTPN23,KAT5,MVB12A,UBXN1,CCDC22,USP27X,CAPN2,FBXL19,SNF8,TRIM25,USP43,ANKRD9,AKT1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,PSMB10,TRIB2,CDC34,FBXO6,STUB1	yellow	VSMC_M3
GO:0098727	0.52	0.63	7	108	maintenance of cell number	BP	1	CNOT3,KLF4,METTL3,MMP24,KDM2B,TAF6L,ZNF358	yellow	VSMC_M3
GO:0007160	0.52	0.60	12	192	cell-matrix adhesion	BP	1	CD63,TSTA3,WDPCP,ZYX,EMILIN1,SIGLEC1,ITGB7,GREM1,CX3CL1,MMP14,PLAU,RCC2	yellow	VSMC_M3
GO:0051704	0.52	0.54	49	709	multi-organism process	BP	1	SPAG1,BAG6,NCAPH2,SBF1,PPARD,IFT27,B4GALT1,EPN1,FIGNL1,SIX5,ZNF296,PAFAH1B3,DLEC1,UCP2,METTL3,CEP131,DND1,YIF1B,RPL29,SIGLEC1,GNPDA1,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,SLC19A1,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,IGFBP5,BAD,CD9,C1QBP,CAPN2,NANOS3,ZNF830,AKT1,RFX2,SLC6A4,STK11,TAZ,FAM50A,IGSF8,MEIG1	yellow	VSMC_M3
GO:0051017	0.53	0.61	9	139	actin filament bundle assembly	BP	1	ZYX,MICAL1,BAIAP2,SWAP70,CX3CL1,CORO1B,LIMK1,RHOC,ELN	yellow	VSMC_M3
GO:0071260	0.53	0.66	5	69	cellular response to mechanical stimulus	BP	1	PLEC,MAP3K14,BAD,TNFRSF1A,AKT1	yellow	VSMC_M3
GO:0045727	0.53	0.62	8	109	positive regulation of translation	BP	1	CDK4,RPS9,METTL3,NAT10,PCIF1,MPV17L2,C1QBP,PAIP1	yellow	VSMC_M3
GO:0051279	0.53	0.68	4	58	regulation of release of sequestered calcium ion into cytosol	BP	1	PDE4D,CX3CL1,GSTO1,CORO1A	yellow	VSMC_M3
GO:0002768	0.53	0.60	11	158	immune response-regulating cell surface receptor signaling pathway	BP	1	BAG6,ZC3H12A,CD79A,PDE4D,DGKZ,LIMK1,RELA,LGALS3,CD276,CSK,STK11	yellow	VSMC_M3
GO:0045669	0.53	0.67	4	56	positive regulation of osteoblast differentiation	BP	1	CTHRC1,LRP3,WNT10B,JUND	yellow	VSMC_M3
GO:1904356	0.53	0.67	4	57	regulation of telomere maintenance via telomere lengthening	BP	1	PNKP,NAT10,PINX1,SLX1A	yellow	VSMC_M3

GO:0006357	0.53	0.51	119	1784	regulation of transcription by RNA polymerase II	BP	1	CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,SREBF2,H2AFY,PPARD,PHF2,KLF4,HOXA1,ZC3H12A,CC2D1B,KTI12,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,ZNF740,ZBTB38,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,ANKRD2,EGR3,DNAJC17,DLL4,HTATIP2,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,TSH2Z,TRIM27,TWIST2,SMARCD2,BRMS1,GMEB2,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,SMARCB1,PBX4,GATAD2A,MEF2B,CTDSP1,EID1,SSBP4,METTL13,ZNF394,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,FOXK1,KLF3,PKN1,MAD2L2,SLTM,CTBP1,FBXL19,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,SMARCA4,AATF,ZNF521,ZNF358,AKT1,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,SSU72,HIC1,MNT,EHMT1,AP3D1,MBD3,MED16,SARS,JUND,KLF13,ZNF783,HOXC5,IER5,ZNF250,THAP7,NSMCE3,ERF,ZSCAN1	yellow	VSMC_M3
GO:1901701	0.53	0.53	59	887	cellular response to oxygen-containing compound	BP	1	ENPP1,CDK4,PPARD,PLEC,LGALS1,PDGFRA,KLF4,ZC3H12A,SLC9A3R1,INSIG1,UCP2,BAIAP2,LAMTOR1,PYCR1,AACS,SCARB1,BCL2L1,TNS2,PDE3B,CX3CL1,WNT10B,SOD1,DCPS,SELENOS,PABPN1,PCK2,COL6A1,SLC26A6,RIPK3,CAPN10,KAT5,RELA,SIPA1,SMARCB1,PHB2,IGFBP5,BAD,LAMTOR4,KLF3,CAPN2,PIP4K2B,ARHGEF2,SMARCA4,EEF2K,CSK,AKT1,HMGCS1,GIT1,SLC6A4,LDOC1,CACTIN,TRAP1,IRAK1,APRT,SLC27A4,TWF2,JAGN1,NSMF,OSER1	yellow	VSMC_M3
GO:0022600	0.53	0.67	4	56	digestive system process	BP	1	SCARB1,AQP5,SLC26A6,ZNF830	yellow	VSMC_M3
GO:0055117	0.53	0.67	4	58	regulation of cardiac muscle contraction	BP	1	ZC3H12A,PDE4D,GSTO1,RANGRF	yellow	VSMC_M3
GO:0046883	0.53	0.59	12	174	regulation of hormone secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,PLA2G3,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0048880	0.53	0.57	18	286	sensory system development	BP	1	CDK4,PBX2,RING1,PDGFRA,KLF4,WDPCP,SPRED2,SIX5,KDM2B,AQP5,DLL4,IMPDH2,NECTIN1,PBX1,PBX4,C12orf57,SMARCA4,CTNS	yellow	VSMC_M3
GO:0001776	0.53	0.65	5	70	leukocyte homeostasis	BP	1	RIPK3,PKN1,CORO1A,DOCK11,AKT1	yellow	VSMC_M3
GO:1901214	0.53	0.57	17	251	regulation of neuron death	BP	1	BCL2L1,KDM2B,RAPSN,CX3CL1,SOD1,CHP1,TYRO3,CLCF1,PLA2G3,BAD,AIMP2,CAPN2,CORO1A,AKT1,DHCR24,NSMF,CDC34	yellow	VSMC_M3
GO:0005975	0.53	0.54	32	458	carbohydrate metabolic process	BP	1	ENPP1,PPARD,B4GALT1,GALK1,INPPL1,GNPDA1,OGDHL,ST3GAL4,SELENOS,GSTO1,MANBA,PCK2,TPD52L2,IDH1,BAD,ISYNA1,FOXK1,MPDU1,PGD,DPM3,AKT1,PGM1,GIT1,PGP,MAN1B1,MIDN,JMJD8,POMT1,B3GNT9,NDST1,TALDO1,GBA2	yellow	VSMC_M3
GO:0030705	0.53	0.59	11	173	cytoskeleton-dependent intracellular transport	BP	1	IFT27,CEP131,SOD1,BLOC1S4,MYO19,AP3D1,SSNA1,STK11,TMEM201,SPG7,WDR34	yellow	VSMC_M3
GO:0090150	0.53	0.57	15	210	establishment of protein localization to membrane	BP	1	BAG6,SAMM50,SCRIB,ASNA1,YIF1B,RAPSN,CHP1,PEX5,ZDHHC3,SYNE3,CSK,ATG3,RAB34,ARFRP1,TIMM22	yellow	VSMC_M3
GO:0034614	0.53	0.60	9	124	cellular response to reactive oxygen species	BP	1	PDGFRA,KLF4,PYCR1,SOD1,RIPK3,RELA,AKT1,TRAP1,OSER1	yellow	VSMC_M3
GO:0051222	0.53	0.57	16	241	positive regulation of protein transport	BP	1	SREBF2,PPARD,VPS28,ZC3H12A,DMAP1,MYRIP,CEP131,AACS,CHP1,PCK2,PCNT,CAPN10,PTPN23,BAD,GLUD1,RBM22	yellow	VSMC_M3
GO:0050770	0.54	0.61	8	132	regulation of axonogenesis	BP	1	DBNL,PLXND1,LIMK1,DBN1,CRABP2,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0008361	0.54	0.59	10	157	regulation of cell size	BP	1	CDK4,DBNL,SLC9A3R1,LIMK1,LAMTOR4,DBN1,CRABP2,AKT1,ANAPC2,TWF2	yellow	VSMC_M3
GO:0060538	0.54	0.60	9	132	skeletal muscle organ development	BP	1	PLEC,COL19A1,WNT10B,GPX1,HMG20B,TAZ,GTF3C5,IGSF8,ELN	yellow	VSMC_M3
GO:0044282	0.54	0.55	21	284	small molecule catabolic process	BP	1	ACAT2,NUDT3,PPARD,MPST,CPT1C,SNX17,GALK1,BCKDHA,GNPDA1,SCARB1,PCCB,ETFBKMT,PCK2,BAD,GLUD1,FOXK1,ILVBL,PGD,AKT1,BLMH,SLC27A4	yellow	VSMC_M3
GO:0061387	0.54	0.63	6	95	regulation of extent of cell growth	BP	1	DBNL,LIMK1,DBN1,CRABP2,ANAPC2,TWF2	yellow	VSMC_M3
GO:0090257	0.54	0.58	12	179	regulation of muscle system process	BP	1	KLF4,ZC3H12A,PDE4D,SOD1,GSTO1,SCN4A,SPX,IGFBP5,C12orf57,TNFRSF1A,RANGRF,MIR214	yellow	VSMC_M3
GO:0048519	0.54	0.49	266	3961	negative regulation of biological process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,ZNF608,BAG6,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,TTLL12,RING1,SREBF2,H2AFY,ITPR3,HNRNPA0,TRIM11,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,SHARPIN,VPS28,SND1,B4GALT1,PDGFRA,SECISBP2,PHF2,EPN1,SSC5D,SOCS5,CNOT3,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,PNKP,SNRNP70,CC2D1B,SNX3,MICAL1,ANXA5,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,PLXND1,EMILIN1,DMAP1,CIC,UNK,DLEC1,INSIG1,OGG1,UCP2,METTL3,CXXC5,INPPL1,DND1,PYCR1,EIF4EBP1,CAVIN3,DEAF1,TARBP2,NAT10,BCL2L1,PDE4D,TNS2,SWAP70,LRP3,ZBTB38,LSM6,CAPG,PINX1,GREM1,KDM2B,PDE3B,CX3CL1,WNT10B,SOD1,PACSIN3,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,CHP1,TYRO3,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,SLC35C2,CISH,SRSF9,DCPS,IRX1,SELENOS,GSTO1,ITPRIP,RRP1B,ETFBKMT,MVK,RIN3,FABP3,ZCCHC17,PDGFA,MMP14,CDK2AP2,GPX1,CORO1B,NGEF,CLCF1,QARS,TRIM27,ARPIN,EIF3A,LIMK1,PRMT2,SPX,THOC5,TWIST2,PSMB4,PFDN2,BRMS1,PLA2G3,STMN3,BANF1,CCDC85B,PTPN23,PBX1,KAT5,RELA,SIPA1,ARNT2,LIMD1,MID1IP1,PEX5,SMARCB1,YJEFN3,GATAD2A,PHB2,PPP1R35,IGFBP5,IFI35,CTDSP1,OTUB1,EID1,METTL13,LETM1,LGALS3,C11orf95,CD9,MRTO4,PLAU,TNFRSF1A,BABAM1,C1QBP,AIMP2,CHERP,ZBTB49,UBXN1,WASHC1,RCC2,MTA2,CCDC22,FOXK1,SDE2,KLF3,PKN1,MIIP,MAD1L1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,CTBP1,DFFA,SP2,ARHGEF2,MVP,PER1,NFIX,CORO1A,SLX1A,IRF2BPL,TRIM25,RPL37,MTMR4,SMARCA4,CARM1,EEF2K,AATF,CXorf57,C19orf66,CSK,MID2,ATG3,ZNF830,AKT1,PAIP1,KHSRP,GIT1,ANKRD13B,SLC6A4,DHCR24,CARHSP1,MYDGF,LDOC1,SIRT6,MAP2K2,CACTIN,HMGCR,HSPA1A,TRAP1,ANPEP,MNT	yellow	VSMC_M3
GO:0061572	0.54	0.60	9	141	actin filament bundle organization	BP	1	ZYX,MICAL1,BAIAP2,SWAP70,CX3CL1,CORO1B,LIMK1,RHOC,ELN	yellow	VSMC_M3
GO:0033627	0.54	0.66	4	60	cell adhesion mediated by integrin	BP	1	ITGB7,SWAP70,PDE3B,PLAU	yellow	VSMC_M3
GO:0001838	0.54	0.61	7	107	embryonic epithelial tube formation	BP	1	CTHRC1,SCRIB,DEAF1,GREM1,KDM2B,IRX1,MTHFR	yellow	VSMC_M3
GO:0006403	0.54	0.58	12	171	RNA localization	BP	1	NHP2,SEC13,RBM15B,PABPN1,THOC5,PRPF6,THOC3,NUP88,MVP,KHSRP,RBM8A,ZNF385A	yellow	VSMC_M3

GO:0043069	0.54	0.52	47	681	negative regulation of programmed cell death	BP	1	BAG6,FNIP1,PPARD,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,OGG1,UCP2,BCL2L1,GREM1,KDM2B,CX3CL1,SOD1,EGR3,CCAR2,TYRO3,HTATIP2,DCPS,SELENOS,ITPRIP,GPX1,CLCF1,QARS,TWIST2,PLA2G3,RELA,ARNT2,PHB2,LGALS3,NANOS3,DFFA,ARHGEF2,CORO1A,EEF2K,AATF,ZNF830,AKT1,DHCR24,MYDGF,TRAP1,MNT,MIR214,PTMA,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0051453	0.54	0.66	4	58	regulation of intracellular pH	BP	1	RAB20,CHP1,SLC26A6,CCDC115	yellow	VSMC_M3
GO:0032504	0.54	0.52	39	571	multicellular organism reproduction	BP	1	BAG6,NCAPH2,SBF1,PPARD,IFT27,B4GALT1,PDGFRA,FIGNL1,SIX5,ZNF296,PAFAH1B3,DLEC1,METTL3,CEP131,DND1,YIF1B,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,BAD,CD9,NANOS3,ZNF830,AKT1,RFX2,SLC6A4,STK11,TAZ,FAM50A,MEIG1	yellow	VSMC_M3
GO:1900180	0.54	0.60	8	116	regulation of protein localization to nucleus	BP	1	ZC3H12A,DMAP1,PINX1,MCRS1,CHP1,RBM22,AKT1,STK11	yellow	VSMC_M3
GO:0001889	0.54	0.60	8	116	liver development	BP	1	MPST,PHF2,UCP2,AACS,PCK2,RELA,HMGCS1,TGFBR3	yellow	VSMC_M3
GO:1904589	0.55	0.66	4	55	regulation of protein import	BP	1	ZC3H12A,DMAP1,CHP1,RBM22	yellow	VSMC_M3
GO:0010810	0.55	0.58	11	175	regulation of cell-substrate adhesion	BP	1	TSTA3,LGALS1,WDPCP,EMILIN1,P4HB,GREM1,CX3CL1,MMP14,PLAU,C1QBP,RCC2	yellow	VSMC_M3
GO:0090263	0.55	0.62	6	92	positive regulation of canonical Wnt signaling pathway	BP	1	PLEKHA4,RNF220,WNT10B,CCAR2,AMER1,CSNK1G2	yellow	VSMC_M3
GO:1905330	0.55	0.66	4	56	regulation of morphogenesis of an epithelium	BP	1	GREM1,PDGFA,PHB2,SIRT6	yellow	VSMC_M3
GO:0046632	0.55	0.64	5	74	alpha-beta T cell differentiation	BP	1	SOCS5,ZC3H12A,RELB,ARMC5,AP3D1	yellow	VSMC_M3
GO:0051254	0.55	0.50	90	1357	positive regulation of RNA metabolic process	BP	1	SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,CNOT3,KLF4,HOXA1,ZC3H12A,SNRNP70,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,METTL3,DND1,DEAF1,HOXC4,KMT2B,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,YAF2,HTATIP2,KDM1B,CHCHD2,DCPS,RRP1B,AIP,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,BUD23,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,TRMT112,NDP,SSBP4,BUD31,TNFRSF1A,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,POLR2A,MAD2L2,NANOS3,ARHGEF2,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,RBM22,ZNF521,AKT1,BRF1,KHSRP,GTF2F1,MYDGF,MAP2K2,AP3D1,MED16,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3
GO:0061351	0.55	0.61	7	111	neural precursor cell proliferation	BP	1	KDM2B,CX3CL1,DLL4,DBN1,ARHGEF2,EML1,SLC6A4	yellow	VSMC_M3
GO:0006366	0.55	0.49	124	1862	transcription by RNA polymerase II	BP	1	CDK4,SQSTM1,ZNF608,HDAC10,NELFE,FNIP1,ATF6B,PBX2,SREBF2,H2AFY,PPARD,PHF2,KLF4,HOXA1,ZC3H12A,CC2D1B,KTI12,SIX5,ZNF282,ZNF296,RELB,DMAP1,CIC,SERTAD1,TTC5,CXXC5,DEAF1,HOXC4,ZNF740,ZBTB38,GREM1,KDM2B,MCRS1,POLR2C,CX3CL1,WNT10B,ANKRD2,EGR3,DNAJC17,DLL4,HTATIP2,KDM1B,CHCHD2,IRX1,RRP1B,BRD9,TSHZ2,PIR,TRIM27,TWIST2,ADRM1,SMARCD2,BRMS1,GMEB2,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,SMARCB1,PBX4,GATAD2A,MEF2B,CTDSP1,EID1,SSBP4,METTL13,ZNF394,BUD31,TNFRSF1A,TEAD4,C1QBP,TAF6L,ZBTB49,MTA2,ZNF316,MED11,PELP1,FOXK1,KLF3,PKN1,POLR2A,MAD2L2,SLTM,CTBP1,FBXL19,SP2,ARHGEF2,SNF8,PER1,NFIX,IRF2BPL,SMARCA4,AATF,ZNF521,ZNF358,AKT1,GTF2F1,RFX2,SAFB,SAFB2,MYDGF,HDGFL2,SIRT6,SSU72,HIC1,MNT,EHMT1,AP3D1,MBD3,MED16,SARS,JUND,KLF13,ZNF783,HOXC5,IER5,ZNF250,THAP7,NSMCE3,ERF,SNAPC2,ZSCAN1	yellow	VSMC_M3
GO:0060401	0.55	0.60	8	126	cytosolic calcium ion transport	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A,AKT1	yellow	VSMC_M3
GO:0044264	0.55	0.63	5	75	cellular polysaccharide metabolic process	BP	1	ENPP1,SELENOS,AKT1,B3GNT9,NDST1	yellow	VSMC_M3
GO:0022610	0.55	0.50	66	1050	biological adhesion	BP	1	CD63,PPARD,TSTA3,SCRIB,LGALS1,B4GALT1,PDGFRA,COL15A1,COL19A1,SOCS5,KLF4,TPBG,WDPCP,ZC3H12A,ZYX,PLXND1,EMILIN1,METTL3,BAIAP2,INPPL1,P4HB,SIGLEC1,RIC8A,SCARB1,ITGB7,SWAP70,MMP24,GREM1,PDE3B,CX3CL1,EGR3,TYRO3,ST3GAL4,MMP14,IGSF9,LRFN4,COL6A1,NECTIN1,MPZL3,SART1,PTPN23,RELA,SIPA1,BLOC1S4,BAD,SCARF2,LGALS3,CD9,PLAU,C1QBP,RCC2,MAD1L1,MAD2L2,CORO1A,CD276,AATF,CSK,AKT1,CD99L2,TJP3,CLDN6,AP3D1,IRAK1,NEGR1,TNFRSF12A,COL6A2	yellow	VSMC_M3
GO:0097006	0.55	0.65	4	53	regulation of plasma lipoprotein particle levels	BP	1	SCARB1,PLA2G3,CSK,KHSRP	yellow	VSMC_M3
GO:0032268	0.55	0.49	124	1819	regulation of cellular protein metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,BAG6,SNX9,NELFE,FNIP1,PRR5,H2AFY,PLEC,VPS28,SECISBP2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,RCN3,MICAL1,KMT2E,WDFY2,SLC9A3R1,EMILIN1,UNK,SERTAD1,PSMC4,METTL3,DND1,EIF4EBP1,TARBP2,NAT10,PDE4D,EIF4B,SWAP70,ACSL1,TNKS1BP1,PINX1,GREM1,CX3CL1,WNT10B,SOD1,PACSIN3,CCAR2,CHP1,PCIF1,RNF19B,DCPS,PDGFA,MMP14,GPX1,CLCF1,NGDN,QARS,PSME2,TRIM27,LIMK1,RIPK3,LSM14B,ADRM1,BRMS1,TNK2,TACO1,KAT5,RELA,SMARCB1,PHB2,IGFBP5,BAD,CTDSP1,OTUB1,EID1,MPV17L2,LGALS3,TNFRSF1A,C1QBP,AIMP2,UBXN1,WASHC1,CCDC22,PKN1,SEPSECS,AMER1,MTHFR,MAD2L2,NANOS3,CTBP1,ARHGEF2,MVP,PER1,RPL37,EEF2K,CDC37,C19orf66,CSK,AKT1,PAIP1,KHSRP,DHCR24,MYDGF,SIRT6,MAP2K2,CACTIN,HMG20B,TRAP1,AURKAIP1,MKNK2,IRAK1,STK11,TELO2,CARD9,POMT1,RBM8A,ERBB4,TRIB2,ZNF385A,NSMF,THAP7,STUB1,NSMCE3	yellow	VSMC_M3
GO:0045765	0.55	0.56	15	229	regulation of angiogenesis	BP	1	EPN1,KLF4,ZC3H12A,PLXND1,EMILIN1,GREM1,PDE3B,HTATIP2,YJEFN3,MYDGF,SIRT6,JMJD8,SARS,MIR214,RNH1	yellow	VSMC_M3
GO:0035264	0.55	0.60	7	108	multicellular organism growth	BP	1	CDK4,PLEC,CCM2,TNS2,SOD1,SGPL1,SP2	yellow	VSMC_M3

GO:0031399	0.55	0.50	79	1182	regulation of protein modification process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,SNX9,NELFE,FNIP1,PRR5,H2AFY,PLEC,VPS28,HSPBP1,SOCS5,SPRED2,ZC3H12A,PNKP,MICAL1,KMT2E,WDFY2,SLC9A3R1,EMILIN1,SERTAD1,TARBP2,PDE4D,SWAP70,ACSL1,TNKS1BP1,PINX1,GREM1,CX3CL1,SOD1,CCAR2,CHP1,PDGFA,CLCF1,QARS,TRIM27,LIMK1,RIPK3,BRMS1,TNK2,KAT5,RELA,SMARCB1,PHB2,CTDSP1,OTUB1,EID1,LGALS3,TNFRSF1A,AIMP2,UBXN1,WASHC1,PKN1,AMER1,MTHFR,MAD2L2,CTBP1,ARHGEF2,MVP,RPL37,EEF2K,CDC37,CSK,AKT1,MYDGF,MAP2K2,CACTIN,HMG20B,IRAK1,STK11,TELO2,POMT1,ERBB4,TRIB2,NSMF,THAP7,STUB1,NSMCE3	yellow	VSMC_M3
GO:0051607	0.55	0.57	12	174	defense response to virus	BP	1	TRIM11,ZC3H12A,TARBP2,BCL2L1,RIPK3,RELA,MAP3K14,PHB2,C1QBP,ARMC5,C19orf66,CARD9	yellow	VSMC_M3
GO:0140546	0.55	0.57	12	174	defense response to symbiont	BP	1	TRIM11,ZC3H12A,TARBP2,BCL2L1,RIPK3,RELA,MAP3K14,PHB2,C1QBP,ARMC5,C19orf66,CARD9	yellow	VSMC_M3
GO:0019725	0.55	0.51	42	638	cellular homeostasis	BP	1	ENPP1,ITPR3,PPARD,LGALS1,PDGFRA,TTC7A,SLC9A3R1,SLC30A3,UCP2,RAB20,GSR,AACS,PDE4D,TNS2,SWAP70,SLC11A2,DCTN1,CX3CL1,SOD1,CHP1,TYRO3,SELENOS,GSTO1,GPX1,PCK2,SLC26A6,SMARCB1,TXNRD2,BAD,LETM1,CHERP,CCDC22,FOXK1,CORO1A,TSPOAP1,SMARCA4,ANKRD9,PACS2,GIT1,AP3D1,JAGN1,CCDC115	yellow	VSMC_M3
GO:0019941	0.55	0.52	37	550	modification-dependent protein catabolic process	BP	1	SQSTM1,BAG6,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,PSMB3,TMUB1,PSMC4,SEL1L2,WNT10B,CCAR2,RNF19B,SELENOS,ADRM1,PTPN23,KAT5,MVB12A,UBXN1,CCDC22,USP27X,FBXL19,SNF8,TRIM25,USP43,ANKRD9,AKT1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,TRIB2,CDC34,FBXO6,STUB1	yellow	VSMC_M3
GO:0071897	0.55	0.58	10	150	DNA biosynthetic process	BP	1	NHP2,KLF4,PNKP,NAT10,TNKS1BP1,PINX1,GREM1,USP43,TELO2,RF00024	yellow	VSMC_M3
GO:0120036	0.55	0.50	75	1193	plasma membrane bounded cell projection organization	BP	1	SPAG1,CTHRC1,TXNDC15,PACSIN1,SCRIB,LGALS1,IFT27,CUL7,KLF4,DBNL,TPBG,WDPCP,SNX3,EMP3,EHD2,SLC9A3R1,PLXND1,SEPT9,BAIAP2,CEP131,INPPL1,YIF1B,CCDC57,ARHGAP33,SLC11A2,DCTN1,CX3CL1,SOD1,CCDC32,RAB35,CCDC28B,CORO1B,NGEF,PLEKHO1,IGSF9,NECTIN1,ARPIN,PCNT,LIMK1,IQCG,PLA2G3,STMN3,CEP164,PTPN23,BLOC1S4,C12orf57,WASHC1,RCC2,CNP,DBN1,CRABP2,FAM161B,CORO1A,RABEP2,S100A6,CARM1,EEF2K,ATG3,TTC39C,DOCK11,AKT1,RFX2,ACAP3,SSNA1,ANAPC2,STK11,GAS8,WDR34,NEGR1,MIR214,TWF2,UNC13A,CDC42EP5,NSMF,MEIG1	yellow	VSMC_M3
GO:0042177	0.55	0.60	7	101	negative regulation of protein catabolic process	BP	1	BAG6,SNRNP70,SNX3,CCAR2,RELA,UBXN1,MAD2L2	yellow	VSMC_M3
GO:0140694	0.55	0.54	20	305	non-membrane-bounded organelle assembly	BP	1	SQLE,RPL3,PLEC,BOP1,PDGFRA,DBNL,KRT8,NUMA1,CCDC57,RRS1,SAC3D1,LIMD1,MPV17L2,MRTO4,KIAA0753,C1QBP,EML3,MRPL20,MIS12,TUBGCP2	yellow	VSMC_M3
GO:0150116	0.55	0.65	4	65	regulation of cell-substrate junction organization	BP	1	WDPCP,GREM1,MMP14,RCC2	yellow	VSMC_M3
GO:0006879	0.56	0.65	4	56	cellular iron ion homeostasis	BP	1	TTC7A,SLC11A2,SOD1,CCDC115	yellow	VSMC_M3
GO:0045216	0.56	0.58	9	146	cell-cell junction organization	BP	1	PLEC,CCM2,NECTIN1,PTPN23,RHOC,CD9,CSK,TJP3,CLDN6	yellow	VSMC_M3
GO:1904950	0.56	0.60	7	100	negative regulation of establishment of protein localization	BP	1	SNX3,INSIG1,UCP2,CHP1,CSK,MIDN,JAGN1	yellow	VSMC_M3
GO:0051251	0.56	0.56	13	186	positive regulation of lymphocyte activation	BP	1	LGALS1,SOCS5,EGR3,MMP14,CLCF1,SART1,BAD,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1	yellow	VSMC_M3
GO:0031589	0.56	0.54	18	294	cell-substrate adhesion	BP	1	CD63,PPARD,TSTA3,LGALS1,WDPCP,ZYX,EMILIN1,P4HB,SIGLEC1,ITGB7,GREM1,CX3CL1,TYRO3,MMP14,PLAU,C1QBP,RCC2,CORO1A	yellow	VSMC_M3
GO:0000278	0.56	0.50	49	729	mitotic cell cycle	BP	1	DCTN2,CDK4,CTDSP2,NCAPH2,SNX9,TTLL12,H2AFY,SCRIB,CUL7,KLF4,KMT2E,SLC9A3R1,NUMA1,CCDC57,EIF4EBP1,RRS1,PINX1,DCTN1,WNT10B,RAB35,CDK2AP2,PSME2,PCNT,NUDC,PRMT2,PBX1,RHOC,PHB2,CTDSP1,BABAM1,NUP88,RCC2,EML3,SDE2,MIIP,MAD1L1,MAD2L2,EML1,AATF,ZNF830,AKT1,SNX18,CDK11B,AURKAIP1,MIR214,NABP2,MIS12,CDC34,TUBGCP2	yellow	VSMC_M3
GO:0060759	0.56	0.58	9	128	regulation of response to cytokine stimulus	BP	1	TTLL12,SHARPIN,IL1R1,KLF4,METTL3,PALM3,CDC37,CACTIN,IRAK1	yellow	VSMC_M3
GO:0010633	0.56	0.64	4	59	negative regulation of epithelial cell migration	BP	1	KLF4,DLL4,PTPN23,PTPRR	yellow	VSMC_M3
GO:0070661	0.56	0.55	14	201	leukocyte proliferation	BP	1	SCRIB,CD79A,GREM1,CX3CL1,CLCF1,IMPDH2,RIPK3,LGALS3,PKN1,MAD1L1,ARMC5,CORO1A,CD276,PSMB10	yellow	VSMC_M3
GO:0051250	0.56	0.59	7	99	negative regulation of lymphocyte activation	BP	1	SCRIB,SOCS5,ZC3H12A,TYRO3,LGALS3,PKN1,MAD1L1	yellow	VSMC_M3
GO:0030326	0.56	0.60	6	96	embryonic limb morphogenesis	BP	1	PBX2,WDPCP,GREM1,PBX1,CRABP2,ZNF358	yellow	VSMC_M3
GO:0035113	0.56	0.60	6	96	embryonic appendage morphogenesis	BP	1	PBX2,WDPCP,GREM1,PBX1,CRABP2,ZNF358	yellow	VSMC_M3
GO:0099518	0.56	0.64	4	65	vesicle cytoskeletal trafficking	BP	1	BLOC1S4,MYO19,AP3D1,STK11	yellow	VSMC_M3
GO:0035773	0.56	0.64	4	58	insulin secretion involved in cellular response to glucose stimulus	BP	1	PPARD,UCP2,BAD,JAGN1	yellow	VSMC_M3
GO:0006368	0.56	0.64	4	58	transcription elongation from RNA polymerase II promoter	BP	1	NELFE,SERTAD1,ADRM1,GTF2F1	yellow	VSMC_M3
GO:0072665	0.56	0.64	4	60	protein localization to vacuole	BP	1	VPS28,LAMTOR4,SNF8,AP3D1	yellow	VSMC_M3

GO:0051246	0.56	0.47	133	1953	regulation of protein metabolic process	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,BAG6,SNX9,NELFE,FNIP1,PRR5,H2AFY,SGSM3,PLEC,VPS28,SECISBP2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,SPRED2,ZC3H12A,PNKP,RCN3,SNRNP70,SNX3,MICAL1,KMT2E,WDFY2,SLC9A3R1,EMILIN1,UNK,SERTAD1,PSMC4,METTL3,DND1,EIF4EBP1,DELE1,LDLRAD3,TARBP2,NAT10,PDE4D,EIF4B,SWAP70,ACSL1,TNKS1BP1,PINX1,GREM1,CX3CL1,WNT10B,SOD1,PACSIN3,CCAR2,CHP1,PCIF1,RNF19B,DCPS,PDGFA,MMP14,GPX1,CLCF1,NGDN,QARS,ASB9,PSME2,TRIM27,LIMK1,RIPK3,LSM14B,ADRM1,PFDN2,BRMS1,TNK2,TACO1,KAT5,RELA,SMARCB1,PHB2,IGFBP5,BAD,CTDSP1,OTUB1,EID1,MPV17L2,LGALS3,TNFRSF1A,C1QBP,AIMP2,UBXN1,WASHC1,CCDC22,PKN1,SEPSECS,AMER1,MTHFR,MAD2L2,NANOS3,CTBP1,ARHGEF2,SNF8,MVP,PER1,RPL37,EEF2K,CDC37,AATF,C19orf66,CSK,AKT1,PAIP1,KHSRP,DHCR24,MYDGF,SIRT6,MAP2K2,CACTIN,HMG20B,TRAP1,AURKAIP1,MKNK2,IRAK1,STK11,TELO2,CARD9,POMT1,RBM8A,ERBB4,TRIB2,ZNF385A,NSMF,THAP7,STUB1,NSMCE3	yellow	VSMC_M3
GO:0006766	0.57	0.62	5	71	vitamin metabolic process	BP	1	PPARD,SLC52A2,GSTO1,SLC19A1,FLAD1	yellow	VSMC_M3
GO:1901654	0.57	0.56	10	151	response to ketone	BP	1	CDK4,KLF4,AACS,BCL2L1,DCPS,PCK2,RELA,BAD,AKT1,TGFBR3	yellow	VSMC_M3
GO:0002520	0.57	0.50	46	694	immune system development	BP	1	NCAPH2,FNIP1,LGALS1,PDGFRA,SOCS5,TTC7A,KLF4,ZC3H12A,KMT2E,RELB,CD79A,METTL3,FASN,SWAP70,SLC11A2,WNT10B,SOD1,EGR3,DLL4,TYRO3,MMP14,CLCF1,PIR,THOC5,RIPK3,PLA2G3,SART1,PBX1,SGPL1,YJEFN3,BAD,PRXL2A,PKN1,MAD1L1,MAD2L2,ARMC5,EML1,DOCK11,AP3D1,MKNK2,STK11,TAZ,TGFBR3,KLF13,JAGN1,ZNF385A	yellow	VSMC_M3
GO:2000177	0.57	0.64	4	62	regulation of neural precursor cell proliferation	BP	1	KDM2B,CX3CL1,DLL4,SLC6A4	yellow	VSMC_M3
GO:0097581	0.57	0.61	5	78	lamellipodium organization	BP	1	CORO1B,PLEKHO1,ARPIN,MIR214,TWF2	yellow	VSMC_M3
GO:0048869	0.57	0.47	198	3033	cellular developmental process	BP	1	ENPP1,CD63,NAB2,SQSTM1,CCHCR1,BAG6,NCAPH2,SBF1,CTHRC1,HDAC10,FNIP1,PBX2,H2AFY,TRIM11,TRAPPC9,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,SND1,CUL7,DNPH1,B4GALT1,PDGFRA,SECISBP2,COL15A1,COL19A1,SOCS5,CNOT3,KLF4,DBNL,TPBG,WDPCP,CCM2,SPRED2,ZC3H12A,FIGNL1,SNX3,EHD2,FAM120B,KMT2E,KRT8,WDFY2,SIX5,RELB,SLC9A3R1,PLXND1,UNK,DLEC1,CD79A,INSIG1,METTL3,BAIAP2,CEP131,NUMA1,P4HB,DND1,YIF1B,FASN,MORN2,ARHGAP22,DEAF1,TBCB,ARHGAP33,AACS,BCL2L1,ITGB7,PDE4D,LRP3,SLC11A2,MMP24,GREM1,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,TYRO3,HTATIP2,RAB35,IRX1,FABP3,MMP14,C14orf93,GPX1,CORO1B,NGEF,CLCF1,PLEKHO1,TAGLN2,IGSF9,PCK2,COL6A1,PIR,NECTIN1,ANPEP,ARPIN,LIMK1,SLC26A6,PRMT2,THOC5,RIPK3,TWIST2,IQCG,TNK2,PLA2G3,STMN3,SART1,CCDC85B,MRC2,PBX1,KAT5,RELA,TMEM120A,SCYL1,LIMD1,SGPL1,SMARCB1,PBX4,BLOC1S4,MEF2B,IGFBP5,C12orf57,BAD,AAMP,CTDSP1,EID1,LGALS3,CD9,TNFRSF1A,C1QBP,AIMP2,RCC2,CNP,AP1M1,PRXL2A,KRT10,FOXK1,CASP14,DBN1,CAPN2,AMER1,MAD2L2,NANOS3,CTBP1,CRABP2,TMEM79,ARHGEF2,ARMC5,S100A4,S100A6,CARM1,EEF2K,EML1,CSK,ZNF521,DOCK11,ZNF830,AKT1,RFX2,SAFB2,GIT1,SLC6A4,SIRT6,PPL,TJP3,HMG20B,VASN,ACAP3,MNT,AP3D1,ANAPC2,STK11,GTF3C5,TGFBR3,NEGR1,MIR214,RF00024,TNFRSF12A,ERBB4,TWF2,JUND,KLF13,FADS1,JAGN1,UNC13A,TRIB2,ZNF385A,NSMF,GBA2,GLIPR2,TUBGCP2,MEIG1,ERF	yellow	VSMC_M3
GO:0043010	0.57	0.54	15	242	camera-type eye development	BP	1	CDK4,RING1,PDGFRA,KLF4,WDPCP,SPRED2,SIX5,KDM2B,AQP5,DLL4,IMPDH2,NECTIN1,C12orf57,SMARCA4,CTNS	yellow	VSMC_M3
GO:0043627	0.57	0.63	4	57	response to estrogen	BP	1	MMP14,ARPC1B,PELP1,TRIM25	yellow	VSMC_M3
GO:0030111	0.57	0.53	18	277	regulation of Wnt signaling pathway	BP	1	CTHRC1,TPBG,SNX3,PLEKHA4,SLC9A3R1,RNF220,GREM1,WNT10B,CCAR2,LIMD1,AMER1,MAD2L2,SMARCA4,HIC1,CSNK1G2,STK11,IGFBP6,APCDD1L	yellow	VSMC_M3
GO:0048609	0.57	0.50	38	563	multicellular organismal reproductive process	BP	1	BAG6,NCAPH2,SBF1,PPARD,IFT27,B4GALT1,PDGFRA,FIGNL1,SIX5,ZNF296,PAFAH1B3,DLEC1,METTL3,CEP131,DND1,YIF1B,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,TRIM27,SLC26A6,IQCG,PLA2G3,SGPL1,BAD,NANOS3,ZNF830,AKT1,RFX2,SLC6A4,STK11,TAZ,FAM50A,MEIG1	yellow	VSMC_M3
GO:0034599	0.57	0.53	16	234	cellular response to oxidative stress	BP	1	PDGFRA,KLF4,ZC3H12A,P4HB,PYCR1,GSR,SOD1,ANKRD2,CHCHD2,SELENOS,GPX1,RIPK3,RELA,AKT1,TRAP1,OSER1	yellow	VSMC_M3
GO:0061008	0.57	0.57	8	119	hepaticobiliary system development	BP	1	MPST,PHF2,UCP2,AACS,PCK2,RELA,HMGCS1,TGFBR3	yellow	VSMC_M3
GO:0072676	0.57	0.61	5	72	lymphocyte migration	BP	1	PLEC,ITGB7,CX3CL1,RIPK3,AKT1	yellow	VSMC_M3
GO:0007272	0.57	0.58	7	110	ensheathment of neurons	BP	1	NAB2,PPARD,PLEC,SOD1,CD9,AKT1,MARVELD1	yellow	VSMC_M3
GO:0008366	0.57	0.58	7	110	axon ensheathment	BP	1	NAB2,PPARD,PLEC,SOD1,CD9,AKT1,MARVELD1	yellow	VSMC_M3
GO:0048705	0.57	0.55	12	186	skeletal system morphogenesis	BP	1	NAB2,PDGFRA,HOXA1,INSIG1,INPPL1,HOXC4,GREM1,WNT10B,MMP14,SGPL1,SLC39A1,NDST1	yellow	VSMC_M3
GO:0009416	0.57	0.53	16	239	response to light stimulus	BP	1	HOXA1,OGG1,METTL3,RIC8A,ACTR5,CCAR2,GPX1,RELA,SDE2,PER1,AKT1,HMGCS1,CTNS,STK11,JUND,NSMCE3	yellow	VSMC_M3
GO:0006937	0.57	0.57	8	121	regulation of muscle contraction	BP	1	ZC3H12A,PDE4D,SOD1,GSTO1,SCN4A,SPX,C12orf57,RANGRF	yellow	VSMC_M3
GO:1901342	0.58	0.53	15	232	regulation of vasculature development	BP	1	EPN1,KLF4,ZC3H12A,PLXND1,EMILIN1,GREM1,PDE3B,HTATIP2,YJEFN3,MYDGF,SIRT6,JMJD8,SARS,MIR214,RNH1	yellow	VSMC_M3
GO:0042063	0.58	0.53	15	230	gliogenesis	BP	1	NAB2,HDAC10,SCRIB,PLEC,METTL3,MMP24,CX3CL1,SOD1,MMP14,CLCF1,RELA,CD9,CNP,CSK,AKT1	yellow	VSMC_M3
GO:0002366	0.58	0.54	12	181	leukocyte activation involved in immune response	BP	1	LGALS1,SOCS5,ZC3H12A,RELB,SWAP70,CLCF1,PLA2G3,IFI35,LGALS3,MAD2L2,CORO1A,DOCK11	yellow	VSMC_M3
GO:0032677	0.58	0.63	4	56	regulation of interleukin-8 production	BP	1	SSC5D,KLF4,RELA,CACTIN	yellow	VSMC_M3
GO:0002449	0.58	0.55	11	159	lymphocyte mediated immunity	BP	1	GNL1,IL1R1,SWAP70,RNF19B,CLCF1,RIPK3,C1QBP,MAD2L2,CORO1A,C8G,CARD9	yellow	VSMC_M3
GO:0071356	0.58	0.55	11	163	cellular response to tumor necrosis factor	BP	1	SHARPIN,ZC3H12A,KRT8,CX3CL1,PCK2,RELA,TNFRSF1A,ARHGEF2,AKT1,CACTIN,TRADD	yellow	VSMC_M3

GO:2001251	0.58	0.60	5	77	negative regulation of chromosome organization	BP	1	NAT10,PINX1,MAD1L1,MAD2L2,SLX1A	yellow	VSMC_M3
GO:0007155	0.58	0.47	65	1044	cell adhesion	BP	1	CD63,PPARD,TSTA3,SCRIB,LGALS1,B4GALT1,PDGFRA,COL15A1,COL19A1,SOCS5,KLF4,TPBG,WDPCP,ZC3H12A,ZYX,PLXND1,EMILIN1,METTL3,BAIAP2,INPPL1,P4HB,SIGLEC1,RIC8A,ITGB7,SWAP70,MMP24,GREM1,PDE3B,CX3CL1,EGR3,TYRO3,ST3GAL4,MMP14,IGSF9,LRFN4,COL6A1,NECTIN1,MPZL3,SART1,PTPN23,RELA,SIPA1,BLOC1S4,BAD,SCARF2,LGALS3,CD9,PLAU,C1QBP,RCC2,MAD1L1,MAD2L2,CORO1A,CD276,AATF,CSK,AKT1,CD99L2,TJP3,CLDN6,AP3D1,IRAK1,NEGR1,TNFRSF12A,COL6A2	yellow	VSMC_M3
GO:0061912	0.58	0.62	4	63	selective autophagy	BP	1	SQSTM1,PHB2,CDC37,TAZ	yellow	VSMC_M3
GO:0009314	0.58	0.50	24	359	response to radiation	BP	1	EEF1D,HOXA1,FIGNL1,PNKP,OGG1,METTL3,RIC8A,BCL2L1,TNKS1BP1,ACTR5,CCAR2,GPX1,KAT5,RELA,BABAM1,SDE2,PER1,AKT1,HMGCS1,CTNS,STK11,NABP2,JUND,NSMCE3	yellow	VSMC_M3
GO:0046394	0.58	0.53	15	213	carboxylic acid biosynthetic process	BP	1	MGLL,SEPHS1,INSIG1,PYCR1,FASN,SCD,PLA2G3,MGST3,MID1IP1,ACLY,FADS2,GLUD1,ILVBL,MTHFR,FADS1	yellow	VSMC_M3
GO:0007049	0.58	0.46	94	1405	cell cycle	BP	1	DCTN2,CDK4,CTDSP2,BAG6,NCAPH2,SNX9,PRR5,TTL12,H2AFY,SGSM3,SCRIB,PLEC,BOP1,SND1,CUL7,KLF4,FIGNL1,KMT2E,SLC9A3R1,PPM1G,SEPT9,SERTAD1,METTL3,CEP131,NUMA1,CCDC57,EIF4EBP1,NAT10,BCL2L1,PDCD2L,RRS1,PINX1,DCTN1,WNT10B,CCAR2,RAB35,CDK2AP2,PSME2,PCNT,NUDC,PRMT2,THOC5,CEP164,PBX1,SIPA1,RHOC,ALKBH4,SAC3D1,SMARCB1,PHB2,CTDSP1,EID1,METTL13,KIAA0753,BABAM1,NUP88,ZBTB49,ANXA11,RCC2,EML3,SDE2,MIIP,MAD1L1,MAD2L2,NANOS3,CTBP1,ARHGEF2,GADD45GIP1,CDC37,MYO19,EML1,AATF,ZNF830,AKT1,SNX18,GIT1,SLC6A4,DHCR24,HMG20B,CDK11B,AURKAIP1,MNT,ANAPC2,STK11,NTMT1,MIR214,NABP2,JUND,MIS12,CDC34,FBXO6,TUBGCP2,MARVELD1,AC093323.1	yellow	VSMC_M3
GO:0044087	0.58	0.48	51	801	regulation of cellular component biogenesis	BP	1	SNX9,FNIP1,PHF2,DBNL,TPBG,WDPCP,EMILIN1,SEPT9,BAIAP2,NUMA1,EIF4EBP1,SWAP70,CAPG,GREM1,DCTN1,CX3CL1,WNT10B,MMP14,CORO1B,LRFN4,NECTIN1,TRIM27,ARPIN,LIMK1,RHOC,PEX5,LGALS3,ARPC1B,WASHC1,RCC2,EML3,DBN1,PIP4K2B,SNF8,RANGRF,CORO1A,SLX1A,RABEP2,EEF2K,ATG3,DOCK11,GIT1,NCLN,MIR214,TWF2,ELN,CDC42EP5,CDC34,GBA2,STUB1,ARPC5L	yellow	VSMC_M3
GO:0048870	0.58	0.47	79	1234	cell motility	BP	1	CD63,CTHRC1,PPARD,TSTA3,SCRIB,PLEC,B4GALT1,PDGFRA,IL1R1,KLF4,TPBG,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,UNK,CEP131,YIF1B,RIC8A,SCARB1,ITGB7,SWAP70,GREM1,CX3CL1,DGKZ,EGR3,DLL4,TYRO3,ST3GAL4,RIN3,PDGFA,MMP14,GPX1,CORO1B,PLEKHO1,ARPIN,RIPK3,TWIST2,IQCG,PLA2G3,PTPN23,RHOC,FMNL1,LIMD1,SGPL1,PHB2,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,CORO1A,AKT1,ACAP3,TMEM201,GAS8,TGFBR3,TRADD,MIR214,ERBB4,PTPRR,IGFBP6,JAGN1,CAVIN1,IGSF8,NSMF,GLIPR2,TUBGCP2,MEIG1,ARPC5L	yellow	VSMC_M3
GO:0051674	0.58	0.47	79	1234	localization of cell	BP	1	CD63,CTHRC1,PPARD,TSTA3,SCRIB,PLEC,B4GALT1,PDGFRA,IL1R1,KLF4,TPBG,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,UNK,CEP131,YIF1B,RIC8A,SCARB1,ITGB7,SWAP70,GREM1,CX3CL1,DGKZ,EGR3,DLL4,TYRO3,ST3GAL4,RIN3,PDGFA,MMP14,GPX1,CORO1B,PLEKHO1,ARPIN,RIPK3,TWIST2,IQCG,PLA2G3,PTPN23,RHOC,FMNL1,LIMD1,SGPL1,PHB2,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,CORO1A,AKT1,ACAP3,TMEM201,GAS8,TGFBR3,TRADD,MIR214,ERBB4,PTPRR,IGFBP6,JAGN1,CAVIN1,IGSF8,NSMF,GLIPR2,TUBGCP2,MEIG1,ARPC5L	yellow	VSMC_M3
GO:0070374	0.58	0.55	10	145	positive regulation of ERK1 and ERK2 cascade	BP	1	NELFE,PDGFRA,TPBG,CAVIN3,CX3CL1,PDGFA,PHB2,CARD9,ERBB4,GLIPR2	yellow	VSMC_M3
GO:0002253	0.58	0.53	13	191	activation of immune response	BP	1	BAG6,ZC3H12A,CD79A,PDE4D,DGKZ,LIMK1,RELA,LGALS3,C1QBP,CD276,CSK,C8G,STK11	yellow	VSMC_M3
GO:0070727	0.58	0.46	97	1462	cellular macromolecule localization	BP	1	CD63,DCTN2,SQSTM1,CCHCR1,BAG6,SNX9,SAMM50,SREBF2,H2AFY,SGSM3,PACSIN1,SCRIB,PLEC,IFT27,VPS28,TTC7A,ASNA1,TPBG,ZC3H12A,EHD2,SLC9A3R1,DMAP1,SNX17,INSIG1,MYRIP,SEC13,SEPT9,CEP131,TSPAN10,LAMTOR1,NUMA1,YIF1B,RAB20,HM13,BCL2L1,ITGB7,RRS1,PLEKHF1,PINX1,MCRS1,RAPSN,CHP1,AP2A2,RAB35,TSPAN5,SELENOS,EXOC3,MMP14,AIP,AP1G2,CORO1B,PCNT,SCYL1,LRWD1,PEX5,ZDHHC3,CHCHD10,PHB2,LAMTOR4,LGALS3,TNFRSF1A,KIAA0753,NUP88,RCC2,AP1M1,DBN1,SNX8,RAB24,CLTB,ARHGEF2,SNF8,RANGRF,STX10,SGF29,TMED1,SYNE3,CDC37,CSK,MID2,ATG3,RBM22,AKT1,PACS2,RANBP3,RAB34,AP3D1,SSNA1,STK11,GAS8,NABP2,ERBB4,TWF2,MIS12,ZNF385A,ARFRP1,MEIG1,TIMM22	yellow	VSMC_M3
GO:0001738	0.58	0.60	5	84	morphogenesis of a polarized epithelium	BP	1	CTHRC1,SCRIB,PLEKHA4,SLC9A3R1,ERBB4	yellow	VSMC_M3
GO:0034249	0.58	0.54	12	183	negative regulation of cellular amide metabolic process	BP	1	CNOT3,ZC3H12A,UNK,METTL3,DND1,EIF4EBP1,PCIF1,DCPS,IGFBP5,NANOS3,C19orf66,KHSRP	yellow	VSMC_M3
GO:0007044	0.58	0.60	5	89	cell-substrate junction assembly	BP	1	PLEC,WDPCP,GREM1,MMP14,RCC2	yellow	VSMC_M3

GO:0060255	0.58	0.44	301	4468	regulation of macromolecule metabolic process	BP	1	ENPP1,CD63,NAB2,CDK4,CTDSP2,SQSTM1,ZNF608,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,SGSM3,TRAPPC9,PPARD,SCRIB,PLEC,VPS28,SND1,PDGFRA,IL1R1,SECISBP2,PHF2,SSC5D,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,FHL3,SPRED2,ZC3H12A,FIGNL1,PNKP,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,EMILIN1,DMAP1,CIC,UNK,OGG1,SERTAD1,TTC5,PSMC4,METTL3,CXXC5,INPPL1,LAMTOR1,DND1,EIF4EBP1,DELE1,CAVIN3,DEAF1,HOXC4,LDLRAD3,TARBP2,KMT2B,NAT10,ZNF740,PDE4D,EIF4B,SWAP70,LRP3,RALY,ACSL1,ZBTB38,LSM6,TNKS1BP1,PINX1,GREM1,KDM2B,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,EGR3,CCAR2,DNAJC17,DLL4,CHP1,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,SRSF9,RNF19B,DCPS,IRX1,SELENOS,RRP1B,BRD9,RIN3,ZCCHC17,PDGFA,MMP14,C14orf93,GPX1,AIP,CLCF1,NGDN,TSHZ2,QARS,ASB9,PSME2,PIR,TRIM27,LIMK1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,SMARCD2,PFDN2,BRMS1,BUD23,TNK2,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,ARNT2,ZFPL1,LIMD1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,NDP,IGFBP5,BAD,CTDSP1,MLF2,OTUB1,EID1,SSBP4,METTL13,MPV17L2,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,BABAM1,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UBXN1,WASHC1,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,AMER1,MTHFR,MAD2L2,SLTM,NANOS3,CTBP1,FBXL19,CRABP2,DFFA,SP2,ARHGEF2,SNF8,MVP,PER1,NFIX,PPP4C,SLX1A,IRF2BPL,TRIM25,	yellow	VSMC_M3
GO:0006974	0.58	0.48	47	699	cellular response to DNA damage stimulus	BP	1	GNL1,BAG6,HDAC10,FANCE,SPRED2,ZC3H12A,FIGNL1,PNKP,MUTYH,DMAP1,OGG1,TTC5,METTL3,FAAP100,SMUG1,BCL2L1,ZBTB38,TNKS1BP1,MCRS1,ACTR5,CCAR2,WDR4,THOC5,CEP164,KAT5,BAD,OTUB1,TNFRSF1A,BABAM1,SDE2,MAD2L2,PPP4C,SLX1A,USP43,AATF,CXorf57,ZNF830,AKT1,ALKBH7,SIRT6,HIC1,STK11,NABP2,ZNF385A,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0002696	0.58	0.52	15	218	positive regulation of leukocyte activation	BP	1	LGALS1,SOCS5,EGR3,MMP14,CLCF1,PLA2G3,SART1,BAD,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1,JUND	yellow	VSMC_M3
GO:0007219	0.59	0.55	9	138	Notch signaling pathway	BP	1	SREBF2,EPN1,METTL3,DLL4,SLC35C2,TSPAN5,MMP14,YJEFN3,AKT1	yellow	VSMC_M3
GO:0044257	0.59	0.48	46	685	cellular protein catabolic process	BP	1	SQSTM1,BAG6,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,PSMB3,RCN3,TMUB1,PSMC4,SEL1L2,HM13,WNT10B,CCAR2,RNF19B,SELENOS,GPX1,PSME2,ADRM1,PSMB4,PTPN23,KAT5,MVB12A,UBXN1,CCDC22,USP27X,CAPN2,AMER1,FBXL19,SNF8,TRIM25,USP43,ANKRD9,AKT1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,PSMB10,TRIB2,CDC34,FBXO6,STUB1,CCDC115	yellow	VSMC_M3
GO:0032637	0.59	0.62	4	57	interleukin-8 production	BP	1	SSC5D,KLF4,RELA,CACTIN	yellow	VSMC_M3
GO:0106106	0.59	0.56	8	123	cold-induced thermogenesis	BP	1	CNOT3,UCP2,ACSL1,WNT10B,SCD,SIRT6,EHMT1,STK11	yellow	VSMC_M3
GO:0120161	0.59	0.56	8	123	regulation of cold-induced thermogenesis	BP	1	CNOT3,UCP2,ACSL1,WNT10B,SCD,SIRT6,EHMT1,STK11	yellow	VSMC_M3
GO:0032355	0.59	0.57	7	105	response to estradiol	BP	1	OGG1,KAT5,ARNT2,BAD,ARPC1B,SLC6A4,MBD3	yellow	VSMC_M3
GO:0043066	0.59	0.47	45	662	negative regulation of apoptotic process	BP	1	BAG6,FNIP1,PPARD,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,OGG1,UCP2,BCL2L1,GREM1,KDM2B,CX3CL1,SOD1,EGR3,CCAR2,TYRO3,HTATIP2,SELENOS,ITPRIP,GPX1,CLCF1,QARS,TWIST2,PLA2G3,RELA,ARNT2,PHB2,LGALS3,NANOS3,DFFA,ARHGEF2,CORO1A,EEF2K,AATF,ZNF830,AKT1,DHCR24,MYDGF,TRAP1,MNT,PTMA,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0043534	0.59	0.57	7	108	blood vessel endothelial cell migration	BP	1	KLF4,SCARB1,GREM1,EGR3,DLL4,GPX1,AKT1	yellow	VSMC_M3
GO:0022612	0.59	0.58	6	95	gland morphogenesis	BP	1	SCRIB,SLC9A3R1,PLXND1,PDGFA,PHB2,IGFBP5	yellow	VSMC_M3
GO:2000106	0.59	0.61	4	59	regulation of leukocyte apoptotic process	BP	1	FNIP1,SELENOS,RIPK3,LGALS3	yellow	VSMC_M3
GO:0016064	0.59	0.58	6	85	immunoglobulin mediated immune response	BP	1	SWAP70,CLCF1,C1QBP,MAD2L2,C8G,CARD9	yellow	VSMC_M3
GO:0006109	0.59	0.55	9	139	regulation of carbohydrate metabolic process	BP	1	ENPP1,SELENOS,BAD,FOXK1,AKT1,GIT1,PGP,MIDN,JMJD8	yellow	VSMC_M3
GO:0031100	0.59	0.61	4	58	animal organ regeneration	BP	1	CDK4,UCP2,ATIC,TGFBR3	yellow	VSMC_M3
GO:0019221	0.59	0.50	21	306	cytokine-mediated signaling pathway	BP	1	TTLL12,SHARPIN,IL1R1,SOCS5,KRT8,METTL3,P4HB,ACSL1,DOK1,CX3CL1,CLCF1,RELA,BAD,TNFRSF1A,PALM3,CDC37,AKT1,CACTIN,IRAK1,TRADD,JAGN1	yellow	VSMC_M3
GO:0010212	0.59	0.55	9	137	response to ionizing radiation	BP	1	EEF1D,FIGNL1,BCL2L1,TNKS1BP1,GPX1,KAT5,BABAM1,STK11,NABP2	yellow	VSMC_M3
GO:0042325	0.59	0.46	63	967	regulation of phosphorylation	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,SNX9,FNIP1,PRR5,H2AFY,PLEC,PPP1R14B,PDGFRA,SOCS5,KLF4,SPRED2,ZC3H12A,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SERTAD1,TARBP2,PDE4D,ACSL1,TNKS1BP1,GREM1,CX3CL1,SOD1,DGKZ,CHP1,TYRO3,CISH,PDGFA,CLCF1,QARS,TRIM27,RIPK3,TNK2,PHB2,BAD,CTDSP1,TNFRSF1A,WASHC1,PKN1,PIP4K2B,MAD2L2,ARHGEF2,MVP,EEF2K,CDC37,CSK,AKT1,GIT1,MYDGF,MAP2K2,CACTIN,IRAK1,MIDN,STK11,TELO2,JMJD8,VAC14,ERBB4,TRIB2	yellow	VSMC_M3
GO:0030072	0.59	0.53	11	168	peptide hormone secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0030516	0.59	0.59	5	83	regulation of axon extension	BP	1	DBNL,LIMK1,DBN1,ANAPC2,TWF2	yellow	VSMC_M3

GO:0019222	0.59	0.43	328	4858	regulation of metabolic process	BP	1	ENPP1,CD63,NAB2,CDK4,CTDSP2,SQSTM1,ZNF608,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,RING1,SREBF2,H2AFY,HNRNPA0,TRIM11,SGSM3,TRAPPC9,PPARD,SCRIB,PLEC,VPS28,SND1,PPP1R14B,PDGFRA,IL1R1,SECISBP2,PHF2,SSC5D,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,FHL3,SPRED2,ZC3H12A,FIGNL1,PNKP,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,KMT2E,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,EMILIN1,DMAP1,CIC,UNK,INSIG1,OGG1,SERTAD1,TTC5,PSMC4,UCP2,METTL3,CXXC5,INPPL1,LAMTOR1,DND1,EIF4EBP1,DELE1,CAVIN3,DEAF1,HOXC4,LDLRAD3,TARBP2,KMT2B,SCARB1,NAT10,ZNF740,PDE4D,EIF4B,SWAP70,LRP3,RALY,PLEKHF1,ACSL1,ZBTB38,LSM6,TNKS1BP1,PINX1,GREM1,KDM2B,PDE3B,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,CHP1,TYRO3,SCD,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,CHCHD2,SLC35C2,RBM15B,CISH,SRSF9,RNF19B,DCPS,IRX1,DHCR7,SELENOS,RRP1B,ETFBKMT,BRD9,RIN3,FABP3,ZCCHC17,PDGFA,MMP14,C14orf93,GPX1,AIP,CLCF1,NGDN,SRRD,TSHZ2,QARS,ASB9,PSME2,PIR,TRIM27,LIMK1,PRMT2,THOC5,RIPK3,TWIST2,LSM14B,ADRM1,SMARCD2,PFDN2,BRMS1,BUD23,TNK2,TACO1,PLA2G3,GMEB2,CCDC85B,PRPF6,PBX1,KAT5,RELA,ZNF511,IDH1,ARNT2,ZFPL1,LIMD1,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,GATAD2A,MEF2B,PHB2,TRMT112,PPP1R35,NDP,IGFBP5,BAD,CTDSP1,MLF2,OTUB1,EID1,SSBP4,METTL13,MPV17L2,ZNF394,LGALS3,C11orf95,BUD31,MRTO4,TNFRSF1A,BABAM1,TEAD4,C1QBP,AIMP2,TAF6L,ZBTB49,UBXN1,WASHC1,MTA2,ZNF316,MED11,PELP1,CCDC22,FOXK1,KLF3,PKN1,CAPN2,SEPSECS,POLR2A,AMER1,	yellow	VSMC_M3
GO:0016477	0.59	0.46	71	1120	cell migration	BP	1	CD63,CTHRC1,PPARD,TSTA3,SCRIB,PLEC,B4GALT1,PDGFRA,IL1R1,KLF4,TPBG,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,UNK,RIC8A,SCARB1,ITGB7,SWAP70,GREM1,CX3CL1,DGKZ,EGR3,DLL4,TYRO3,ST3GAL4,RIN3,PDGFA,MMP14,GPX1,CORO1B,PLEKHO1,ARPIN,RIPK3,TWIST2,PTPN23,RHOC,FMNL1,LIMD1,SGPL1,PHB2,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,CORO1A,AKT1,ACAP3,TMEM201,TGFBR3,TRADD,MIR214,ERBB4,PTPRR,IGFBP6,JAGN1,NSMF,GLIPR2,TUBGCP2,ARPC5L	yellow	VSMC_M3
GO:1902414	0.59	0.59	5	82	protein localization to cell junction	BP	1	SCRIB,BAIAP2,RAPSN,NECTIN1,TJP3	yellow	VSMC_M3
GO:0034613	0.59	0.45	96	1451	cellular protein localization	BP	1	CD63,DCTN2,SQSTM1,CCHCR1,BAG6,SNX9,SAMM50,SREBF2,H2AFY,SGSM3,PACSIN1,SCRIB,PLEC,IFT27,VPS28,TTC7A,ASNA1,TPBG,ZC3H12A,EHD2,SLC9A3R1,DMAP1,SNX17,INSIG1,MYRIP,SEC13,SEPT9,CEP131,TSPAN10,LAMTOR1,NUMA1,YIF1B,RAB20,HM13,BCL2L1,ITGB7,RRS1,PLEKHF1,PINX1,MCRS1,RAPSN,CHP1,AP2A2,RAB35,TSPAN5,SELENOS,EXOC3,MMP14,AIP,AP1G2,CORO1B,PCNT,SCYL1,LRWD1,PEX5,ZDHHC3,CHCHD10,PHB2,LAMTOR4,LGALS3,TNFRSF1A,KIAA0753,NUP88,RCC2,AP1M1,DBN1,SNX8,RAB24,CLTB,ARHGEF2,SNF8,RANGRF,STX10,SGF29,TMED1,SYNE3,CDC37,CSK,MID2,ATG3,RBM22,AKT1,PACS2,RANBP3,RAB34,AP3D1,SSNA1,STK11,GAS8,NABP2,ERBB4,TWF2,MIS12,ARFRP1,MEIG1,TIMM22	yellow	VSMC_M3
GO:0003341	0.60	0.56	7	103	cilium movement	BP	1	SLC9A3R1,CEP131,YIF1B,IQCG,PLA2G3,GAS8,MEIG1	yellow	VSMC_M3
GO:0043523	0.60	0.53	11	169	regulation of neuron apoptotic process	BP	1	BCL2L1,KDM2B,RAPSN,CX3CL1,SOD1,TYRO3,CLCF1,PLA2G3,CORO1A,NSMF,CDC34	yellow	VSMC_M3
GO:0006094	0.60	0.61	4	58	gluconeogenesis	BP	1	SELENOS,PCK2,PGM1,PGP	yellow	VSMC_M3
GO:0034250	0.60	0.54	9	130	positive regulation of cellular amide metabolic process	BP	1	CDK4,RPS9,METTL3,NAT10,PCIF1,RELA,MPV17L2,C1QBP,PAIP1	yellow	VSMC_M3
GO:0001822	0.60	0.51	15	248	kidney development	BP	1	BAG6,MPST,IFT27,PDGFRA,WDPCP,PLXND1,SNX17,TNS2,GREM1,IRX1,PDGFA,PBX1,SGPL1,AMER1,ERBB4	yellow	VSMC_M3
GO:0043244	0.60	0.57	6	107	regulation of protein-containing complex disassembly	BP	1	SWAP70,CAPG,MID1IP1,ARHGEF2,C19orf66,TWF2	yellow	VSMC_M3
GO:0120032	0.60	0.53	10	158	regulation of plasma membrane bounded cell projection assembly	BP	1	WDPCP,SEPT9,WASHC1,RCC2,RABEP2,ATG3,DOCK11,MIR214,TWF2,CDC42EP5	yellow	VSMC_M3
GO:0035148	0.60	0.55	8	129	tube formation	BP	1	CTHRC1,SCRIB,HOXA1,DEAF1,GREM1,KDM2B,IRX1,MTHFR	yellow	VSMC_M3
GO:0016053	0.60	0.51	15	215	organic acid biosynthetic process	BP	1	MGLL,SEPHS1,INSIG1,PYCR1,FASN,SCD,PLA2G3,MGST3,MID1IP1,ACLY,FADS2,GLUD1,ILVBL,MTHFR,FADS1	yellow	VSMC_M3
GO:0072594	0.60	0.49	24	355	establishment of protein localization to organelle	BP	1	SAMM50,SREBF2,H2AFY,SCRIB,VPS28,ASNA1,ZC3H12A,DMAP1,SEC13,TSPAN10,CHP1,AIP,LRWD1,PEX5,PHB2,NUP88,SNF8,RANGRF,SGF29,RBM22,AKT1,AP3D1,NABP2,TIMM22	yellow	VSMC_M3
GO:0030168	0.60	0.57	6	96	platelet activation	BP	1	PDGFRA,DGKZ,TYRO3,PDGFA,BLOC1S4,CD9	yellow	VSMC_M3
GO:0010942	0.60	0.47	32	470	positive regulation of cell death	BP	1	CDK4,SQSTM1,FNIP1,SCRIB,B4GALT1,ZC3H12A,SLC9A3R1,UCP2,PHLDA1,PLEKHF1,RAPSN,WNT10B,SOD1,CCAR2,HTATIP2,RRP1B,PRMT2,RIPK3,CAPN10,BRMS1,BAD,TNFRSF1A,C1QBP,AIMP2,USP27X,CAPN2,DFFA,AKT1,SLC27A4,TRADD,TNFRSF12A,CDC34	yellow	VSMC_M3
GO:0045935	0.60	0.44	98	1489	positive regulation of nucleobase-containing compound metabolic process	BP	1	SQSTM1,HDAC10,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,CNOT3,KLF4,HOXA1,ZC3H12A,PNKP,SNRNP70,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,METTL3,DND1,DEAF1,HOXC4,KMT2B,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,YAF2,HTATIP2,KDM1B,CHCHD2,DCPS,RRP1B,AIP,CLCF1,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,BUD23,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,TRMT112,NDP,SSBP4,BUD31,TNFRSF1A,BABAM1,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,POLR2A,MAD2L2,NANOS3,ARHGEF2,PER1,NFIX,SLX1A,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,RBM22,ZNF521,AKT1,BRF1,KHSRP,GTF2F1,MYDGF,SIRT6,MAP2K2,AP3D1,TAZ,MED16,NABP2,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3

GO:0002376	0.60	0.44	112	1656	immune system process	BP	1	ENPP1,SQSTM1,GNL1,BAG6,NCAPH2,FNIP1,TTLL12,TRIM11,SCRIB,PLEC,LGALS1,PPP1R14B,B4GALT1,PDGFRA,IL1R1,SSC5D,SOCS5,TTC7A,KLF4,DBNL,ZC3H12A,ZYX,KMT2E,RELB,EMILIN1,CD79A,METTL3,INPPL1,FASN,RAB20,TARBP2,BCL2L1,ITGB7,PDE4D,SWAP70,SLC11A2,GREM1,CX3CL1,WNT10B,SOD1,DGKZ,EGR3,DLL4,TYRO3,RAB35,ST3GAL4,RNF19B,SELENOS,RIN3,MMP14,GPX1,CLCF1,IMPDH2,PIR,NECTIN1,TRIM27,LIMK1,SLC26A6,THOC5,RIPK3,PSMB4,TNK2,PLA2G3,SART1,PBX1,RELA,SIPA1,MAP3K14,SGPL1,YJEFN3,PHB2,BAD,IFI35,OTUB1,LGALS3,CD9,TNFRSF1A,C1QBP,PRXL2A,PKN1,MAD1L1,MAD2L2,TBKBP1,SP2,ARHGEF2,ARMC5,CORO1A,TRIM25,CDC37,CD276,EML1,C19orf66,CSK,MID2,DOCK11,AKT1,RAB34,CACTIN,AP3D1,MKNK2,IRAK1,C8G,STK11,TAZ,CARD9,TGFBR3,PSMB10,JUND,KLF13,JAGN1,ZNF385A,AKAP17A	yellow	VSMC_M3
GO:0050657	0.60	0.53	9	135	nucleic acid transport	BP	1	SEC13,RBM15B,PABPN1,THOC5,THOC3,NUP88,MVP,KHSRP,RBM8A	yellow	VSMC_M3
GO:0050658	0.60	0.53	9	135	RNA transport	BP	1	SEC13,RBM15B,PABPN1,THOC5,THOC3,NUP88,MVP,KHSRP,RBM8A	yellow	VSMC_M3
GO:0060491	0.60	0.53	10	159	regulation of cell projection assembly	BP	1	WDPCP,SEPT9,WASHC1,RCC2,RABEP2,ATG3,DOCK11,MIR214,TWF2,CDC42EP5	yellow	VSMC_M3
GO:0006892	0.60	0.56	6	99	post-Golgi vesicle-mediated transport	BP	1	AP1G2,CCDC22,CSK,RAB34,AP3D1,ARFRP1	yellow	VSMC_M3
GO:0006913	0.60	0.49	17	257	nucleocytoplasmic transport	BP	1	CCHCR1,ZC3H12A,DMAP1,SEC13,RRS1,CHP1,HTATIP2,RBM15B,PABPN1,THOC5,THOC3,PHB2,NUP88,RANGRF,RBM22,AKT1,RANBP3	yellow	VSMC_M3
GO:0051169	0.60	0.49	17	257	nuclear transport	BP	1	CCHCR1,ZC3H12A,DMAP1,SEC13,RRS1,CHP1,HTATIP2,RBM15B,PABPN1,THOC5,THOC3,PHB2,NUP88,RANGRF,RBM22,AKT1,RANBP3	yellow	VSMC_M3
GO:0046651	0.60	0.51	12	177	lymphocyte proliferation	BP	1	SCRIB,CD79A,CLCF1,IMPDH2,RIPK3,LGALS3,PKN1,MAD1L1,ARMC5,CORO1A,CD276,PSMB10	yellow	VSMC_M3
GO:0010717	0.60	0.58	5	80	regulation of epithelial to mesenchymal transition	BP	1	SPRED2,GREM1,MAD2L2,VASN,GLIPR2	yellow	VSMC_M3
GO:0043632	0.60	0.46	37	561	modification-dependent macromolecule catabolic process	BP	1	SQSTM1,BAG6,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,PSMB3,TMUB1,PSMC4,SEL1L2,WNT10B,CCAR2,RNF19B,SELENOS,ADRM1,PTPN23,KAT5,MVB12A,UBXN1,CCDC22,USP27X,FBXL19,SNF8,TRIM25,USP43,ANKRD9,AKT1,SIRT6,ANAPC2,SPSB3,MAN1B1,ZNRF1,TRIB2,CDC34,FBXO6,STUB1	yellow	VSMC_M3
GO:0001659	0.61	0.53	9	141	temperature homeostasis	BP	1	CNOT3,UCP2,ACSL1,WNT10B,SCD,GPX1,SIRT6,EHMT1,STK11	yellow	VSMC_M3
GO:0002263	0.61	0.51	12	185	cell activation involved in immune response	BP	1	LGALS1,SOCS5,ZC3H12A,RELB,SWAP70,CLCF1,PLA2G3,IFI35,LGALS3,MAD2L2,CORO1A,DOCK11	yellow	VSMC_M3
GO:0031099	0.61	0.52	10	150	regeneration	BP	1	CDK4,PPARD,KLF4,UCP2,WNT10B,GPX1,ATIC,CD9,TGFBR3,ERBB4	yellow	VSMC_M3
GO:0051130	0.61	0.45	55	870	positive regulation of cellular component organization	BP	1	CD63,SNX9,FNIP1,H2AFY,PACSIN1,VPS28,CUL7,DBNL,TPBG,PNKP,SNX3,EHD2,PLXND1,EMILIN1,SEPT9,BAIAP2,NUMA1,SWAP70,GREM1,DCTN1,CX3CL1,WNT10B,GPX1,CORO1B,TRIM27,ARPIN,LIMK1,PFDN2,PLA2G3,PTPN23,RHOC,CHCHD10,BAD,LGALS3,ARPC1B,WASHC1,DBN1,CAPN2,PIP4K2B,CRABP2,CORO1A,SLX1A,EEF2K,DOCK11,GIT1,SIRT6,ANAPC2,STK11,NEGR1,NABP2,TWF2,CDC42EP5,CDC34,STUB1,ARPC5L	yellow	VSMC_M3
GO:0010876	0.61	0.48	20	311	lipid localization	BP	1	ENPP1,PQLC1,ESYT1,SREBF2,SQLE,PPARD,PLEKHA8,ZC3H12A,LAMTOR1,SCARB1,ACSL1,FABP3,SPX,PLA2G3,VPS51,YJEFN3,SLC27A3,AKT1,ALKBH7,SLC27A4	yellow	VSMC_M3
GO:0015031	0.61	0.44	87	1301	protein transport	BP	1	CD63,RUFY1,CCHCR1,SNX9,SAMM50,SREBF2,SGSM3,GUK1,PPARD,SCRIB,IFT27,VPS28,TOM1,ASNA1,PLEKHA8,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,SERP2,DMAP1,SNX17,INSIG1,MYRIP,SEC13,UCP2,CEP131,YIF1B,RAB20,ARHGAP33,AACS,HM13,CHP1,AP2A2,SNX21,RAB35,APBA2,SELENOS,EXOC3,AIP,AP1G2,PCK2,PCNT,CAPN10,PTPN23,VPS51,PEX5,ZDHHC3,PHB2,BAD,COPE,MVB12A,NUP88,WASHC1,AP1M1,RAB3IL1,CCDC22,GLUD1,SNX8,LMAN2,RAB24,CLTB,ARHGEF2,SNF8,MVP,MTX1,RANGRF,STX10,RABEP2,TMED1,CDC37,CSK,ATG3,RBM22,AKT1,SNX18,RANBP3,RAB34,CTNS,AP3D1,MIDN,AP5B1,JAGN1,CAVIN1,ARFRP1,TIMM22	yellow	VSMC_M3
GO:0048667	0.61	0.47	26	446	cell morphogenesis involved in neuron differentiation	BP	1	SCRIB,CUL7,DBNL,TPBG,WDPCP,SLC9A3R1,PLXND1,UNK,BAIAP2,ARHGAP33,SLC11A2,SOD1,NGEF,IGSF9,NECTIN1,LIMK1,C12orf57,CNP,DBN1,CRABP2,S100A6,EEF2K,ANAPC2,STK11,TWF2,NSMF	yellow	VSMC_M3
GO:0001843	0.61	0.57	5	82	neural tube closure	BP	1	CTHRC1,SCRIB,DEAF1,KDM2B,MTHFR	yellow	VSMC_M3
GO:0009743	0.61	0.51	12	186	response to carbohydrate	BP	1	PPARD,LGALS1,UCP2,AACS,SELENOS,PCK2,SLC26A6,SMARCB1,BAD,SMARCA4,JAGN1,COL6A2	yellow	VSMC_M3
GO:0046620	0.61	0.57	5	78	regulation of organ growth	BP	1	SOD1,AKT1,SLC6A4,TGFBR3,ERBB4	yellow	VSMC_M3
GO:0006906	0.61	0.55	6	90	vesicle fusion	BP	1	RAB20,CHP1,PIP4K2B,STX10,CORO1A,RAB34	yellow	VSMC_M3
GO:0072028	0.61	0.59	4	65	nephron morphogenesis	BP	1	GREM1,IRX1,PBX1,ERBB4	yellow	VSMC_M3

GO:0030154	0.61	0.42	192	2966	cell differentiation	BP	1	ENPP1,CD63,NAB2,SQSTM1,CCHCR1,BAG6,NCAPH2,SBF1,CTHRC1,HDAC10,FNIP1,PBX2,H2AFY,TRIM11,TRAPPC9,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,SND1,CUL7,DNPH1,B4GALT1,PDGFRA,SECISBP2,COL15A1,COL19A1,SOCS5,CNOT3,KLF4,DBNL,TPBG,WDPCP,CCM2,SPRED2,ZC3H12A,FIGNL1,SNX3,EHD2,FAM120B,KMT2E,KRT8,WDFY2,SIX5,RELB,SLC9A3R1,PLXND1,UNK,DLEC1,CD79A,INSIG1,METTL3,BAIAP2,CEP131,NUMA1,P4HB,DND1,YIF1B,FASN,MORN2,ARHGAP22,DEAF1,TBCB,ARHGAP33,AACS,BCL2L1,ITGB7,PDE4D,LRP3,SLC11A2,MMP24,GREM1,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,TYRO3,HTATIP2,RAB35,IRX1,FABP3,MMP14,C14orf93,GPX1,NGEF,CLCF1,PLEKHO1,TAGLN2,IGSF9,PCK2,COL6A1,PIR,NECTIN1,ANPEP,LIMK1,SLC26A6,PRMT2,THOC5,RIPK3,TWIST2,IQCG,TNK2,PLA2G3,STMN3,SART1,CCDC85B,MRC2,PBX1,RELA,TMEM120A,SCYL1,LIMD1,SGPL1,SMARCB1,PBX4,BLOC1S4,MEF2B,IGFBP5,C12orf57,BAD,AAMP,CTDSP1,EID1,LGALS3,CD9,TNFRSF1A,C1QBP,AIMP2,RCC2,CNP,AP1M1,PRXL2A,KRT10,FOXK1,CASP14,DBN1,CAPN2,AMER1,MAD2L2,NANOS3,CTBP1,CRABP2,TMEM79,ARHGEF2,ARMC5,S100A4,S100A6,CARM1,EEF2K,EML1,CSK,ZNF521,DOCK11,ZNF830,AKT1,RFX2,SAFB2,GIT1,SLC6A4,SIRT6,PPL,TJP3,HMG20B,VASN,ACAP3,AP3D1,ANAPC2,STK11,GTF3C5,TGFBR3,NEGR1,TNFRSF12A,ERBB4,TWF2,JUND,KLF13,FADS1,JAGN1,UNC13A,TRIB2,ZNF385A,NSMF,GBA2,GLIPR2,TUBGCP2,MEIG1,ERF	yellow	VSMC_M3
GO:0009101	0.61	0.49	16	245	glycoprotein biosynthetic process	BP	1	B4GALT1,SERP2,GALNT14,PHLDA1,CHP1,SLC35C2,ST3GAL4,TMTC1,EXTL1,MPDU1,DPM3,AATF,MAN1B1,POMT1,B3GNT9,NDST1	yellow	VSMC_M3
GO:0050905	0.61	0.55	6	103	neuromuscular process	BP	1	HOXA1,DCTN1,GSTO1,SCN4A,BLOC1S4,C12orf57	yellow	VSMC_M3
GO:0019724	0.62	0.55	6	87	B cell mediated immunity	BP	1	SWAP70,CLCF1,C1QBP,MAD2L2,C8G,CARD9	yellow	VSMC_M3
GO:0051338	0.62	0.44	46	706	regulation of transferase activity	BP	1	NAB2,SNX9,H2AFY,PLEC,PDGFRA,SOCS5,KLF4,PNKP,SLC9A3R1,SERTAD1,TARBP2,ACSL1,PINX1,GREM1,SOD1,DGKZ,CHP1,TYRO3,CISH,PDGFA,PABPN1,QARS,TRIM27,LIMK1,RIPK3,PHB2,BAD,WASHC1,PKN1,PIP4K2B,MAD2L2,MVP,RPL37,CDC37,CSK,AKT1,MAP2K2,IRAK1,MIDN,STK11,TELO2,JMJD8,VAC14,ERBB4,TRIB2,STUB1	yellow	VSMC_M3
GO:0001960	0.62	0.59	4	58	negative regulation of cytokine-mediated signaling pathway	BP	1	TTLL12,METTL3,PALM3,CACTIN	yellow	VSMC_M3
GO:0000904	0.62	0.45	33	562	cell morphogenesis involved in differentiation	BP	1	SCRIB,CUL7,COL15A1,DBNL,TPBG,WDPCP,SLC9A3R1,PLXND1,UNK,METTL3,BAIAP2,P4HB,ARHGAP33,ITGB7,SLC11A2,SOD1,TYRO3,NGEF,IGSF9,NECTIN1,LIMK1,C12orf57,C1QBP,RCC2,CNP,DBN1,CRABP2,S100A6,EEF2K,ANAPC2,STK11,TWF2,NSMF	yellow	VSMC_M3
GO:0019646	0.62	0.55	6	75	aerobic electron transport chain	BP	1	NDUFB9,SDHA,NDUFV1,UQCRC1,UQCC3,NDUFS7	yellow	VSMC_M3
GO:0002695	0.62	0.53	8	118	negative regulation of leukocyte activation	BP	1	SCRIB,SOCS5,ZC3H12A,CX3CL1,TYRO3,LGALS3,PKN1,MAD1L1	yellow	VSMC_M3
GO:0007052	0.62	0.54	7	109	mitotic spindle organization	BP	1	DCTN2,NUMA1,DCTN1,PCNT,NUDC,EML3,EML1	yellow	VSMC_M3
GO:0032640	0.62	0.53	7	111	tumor necrosis factor production	BP	1	ZC3H12A,CX3CL1,SELENOS,TRIM27,ARHGEF2,CACTIN,CARD9	yellow	VSMC_M3
GO:0032680	0.62	0.53	7	111	regulation of tumor necrosis factor production	BP	1	ZC3H12A,CX3CL1,SELENOS,TRIM27,ARHGEF2,CACTIN,CARD9	yellow	VSMC_M3
GO:0072175	0.62	0.53	7	116	epithelial tube formation	BP	1	CTHRC1,SCRIB,DEAF1,GREM1,KDM2B,IRX1,MTHFR	yellow	VSMC_M3
GO:0030641	0.62	0.58	4	64	regulation of cellular pH	BP	1	RAB20,CHP1,SLC26A6,CCDC115	yellow	VSMC_M3
GO:0009725	0.62	0.44	42	652	response to hormone	BP	1	ENPP1,CDK4,PPARD,INSIG1,UCP2,BAIAP2,INPPL1,TNS2,ACSL1,PDE3B,WNT10B,SELENOS,FABP3,MMP14,PCK2,PRMT2,CAPN10,RELA,IDH1,PHB2,IGFBP5,BAD,ARPC1B,PELP1,PKN1,PIP4K2B,PER1,TRIM25,SMARCA4,CARM1,EEF2K,CSK,AKT1,HMGCS1,SAFB,SAFB2,DHCR24,APRT,SLC27A4,TGFBR3,JUND,NSMF	yellow	VSMC_M3
GO:0002532	0.62	0.58	4	59	production of molecular mediator involved in inflammatory response	BP	1	ZC3H12A,PLA2G3,PER1,CARD9	yellow	VSMC_M3
GO:0007612	0.62	0.55	6	104	learning	BP	1	TPBG,CIC,RIC8A,TACO1,GIT1,CTNS	yellow	VSMC_M3
GO:0032943	0.62	0.50	12	179	mononuclear cell proliferation	BP	1	SCRIB,CD79A,CLCF1,IMPDH2,RIPK3,LGALS3,PKN1,MAD1L1,ARMC5,CORO1A,CD276,PSMB10	yellow	VSMC_M3
GO:0051236	0.62	0.52	9	138	establishment of RNA localization	BP	1	SEC13,RBM15B,PABPN1,THOC5,THOC3,NUP88,MVP,KHSRP,RBM8A	yellow	VSMC_M3
GO:0006914	0.62	0.46	29	450	autophagy	BP	1	SQSTM1,HDAC10,SREBF2,VPS28,ZC3H12A,SNRNP70,PLEKHF1,LIX1L,TRIM27,KAT5,VPS51,PHB2,BAD,MVB12A,WASHC1,FOXK1,RAB24,PIP4K2B,SNF8,MTMR4,CDC37,MID2,ATG3,AKT1,PACS2,STK11,TAZ,WDR24,STUB1	yellow	VSMC_M3
GO:0061919	0.62	0.46	29	450	process utilizing autophagic mechanism	BP	1	SQSTM1,HDAC10,SREBF2,VPS28,ZC3H12A,SNRNP70,PLEKHF1,LIX1L,TRIM27,KAT5,VPS51,PHB2,BAD,MVB12A,WASHC1,FOXK1,RAB24,PIP4K2B,SNF8,MTMR4,CDC37,MID2,ATG3,AKT1,PACS2,STK11,TAZ,WDR24,STUB1	yellow	VSMC_M3
GO:0045862	0.62	0.47	20	297	positive regulation of proteolysis	BP	1	BAG6,SNX9,HSPBP1,SOCS5,ZC3H12A,RCN3,PSMC4,PACSIN3,RNF19B,MMP14,PSME2,ADRM1,BAD,CCDC22,AKT1,SIRT6,AURKAIP1,CARD9,TRIB2,STUB1	yellow	VSMC_M3
GO:0009791	0.62	0.58	4	68	post-embryonic development	BP	1	KLF4,INPPL1,SGPL1,C12orf57	yellow	VSMC_M3
GO:0008643	0.62	0.53	7	112	carbohydrate transport	BP	1	ENPP1,PPARD,SELENOS,SLC26A6,CAPN10,AKT1,SLC27A4	yellow	VSMC_M3
GO:0001837	0.62	0.52	8	131	epithelial to mesenchymal transition	BP	1	CUL7,SPRED2,GREM1,MAD2L2,S100A4,VASN,TGFBR3,GLIPR2	yellow	VSMC_M3
GO:0050808	0.62	0.47	19	329	synapse organization	BP	1	DBNL,TPBG,PLXND1,BAIAP2,ARHGAP22,ARHGAP33,DCTN1,RAPSN,CX3CL1,NGEF,IGSF9,LRFN4,NECTIN1,CHCHD10,DBN1,EEF2K,ANAPC2,ERBB4,UNC13A	yellow	VSMC_M3

GO:0048584	0.62	0.42	99	1488	positive regulation of response to stimulus	BP	1	CD63,BAG6,HDAC10,NELFE,FNIP1,PRR5,TXNDC15,PPARD,EEF1D,LGALS1,SHARPIN,PDGFRA,IL1R1,SOCS5,TPBG,SPRED2,ZC3H12A,PNKP,PLEKHA4,SLC9A3R1,RNF220,CD79A,SEC13,BAIAP2,CXXC5,LAMTOR1,NUMA1,CAVIN3,PDE4D,SWAP70,PLEKHF1,GREM1,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,DLL4,SLC35C2,TSPAN5,ST3GAL4,PDGFA,GPX1,CLCF1,TRIM27,LIMK1,RIPK3,PLA2G3,RELA,RHOC,MAP3K14,SMARCB1,PHB2,IGFBP5,BAD,LAMTOR4,IFI35,LGALS3,TNFRSF1A,BABAM1,C1QBP,CHERP,EVC,CCDC22,AMER1,MAD2L2,TRIM25,RPL37,S100A4,SMARCA4,CD276,CSK,MID2,TEDC1,RAB34,MYDGF,MAP2K2,HIC1,CTNS,TEDC2,CSNK1G2,IRAK1,C8G,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,TGFBR3,TRADD,MIR214,NDST1,TNFRSF12A,ERBB4,IGFBP6,ZNF385A,IER5,GLIPR2	yellow	VSMC_M3
GO:0001959	0.62	0.52	8	119	regulation of cytokine-mediated signaling pathway	BP	1	TTLL12,SHARPIN,IL1R1,METTL3,PALM3,CDC37,CACTIN,IRAK1	yellow	VSMC_M3
GO:1903034	0.62	0.52	8	123	regulation of response to wounding	BP	1	PDGFRA,KLF4,ST3GAL4,PDGFA,CD9,PLAU,GIT1,TNFRSF12A	yellow	VSMC_M3
GO:0048661	0.62	0.56	5	78	positive regulation of smooth muscle cell proliferation	BP	1	CX3CL1,IGFBP5,AKT1,IRAK1,MIR214	yellow	VSMC_M3
GO:1990266	0.62	0.56	5	74	neutrophil migration	BP	1	IL1R1,CX3CL1,LGALS3,C1QBP,JAGN1	yellow	VSMC_M3
GO:0060606	0.62	0.56	5	83	tube closure	BP	1	CTHRC1,SCRIB,DEAF1,KDM2B,MTHFR	yellow	VSMC_M3
GO:0050767	0.62	0.47	17	285	regulation of neurogenesis	BP	1	TRIM11,CUL7,DBNL,PLXND1,BAIAP2,CX3CL1,DLL4,CLCF1,LIMK1,RELA,CTDSP1,DBN1,CRABP2,EEF2K,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0051592	0.62	0.53	7	114	response to calcium ion	BP	1	ITPR3,SYT12,BAD,ANXA11,S100A16,EEF2K,JUND	yellow	VSMC_M3
GO:0003006	0.63	0.44	45	685	developmental process involved in reproduction	BP	1	BAG6,SBF1,PPARD,IFT27,CUL7,B4GALT1,PDGFRA,KRT8,SIX5,ZNF296,PAFAH1B3,DLEC1,METTL3,CEP131,DND1,YIF1B,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,MMP14,TRIM27,SLC26A6,IQCG,PLA2G3,PBX1,IDH1,SGPL1,PHB2,BAD,NANOS3,IRF2BPL,ZNF830,AKT1,HMGCS1,RFX2,SAFB2,DHCR24,NSDHL,STK11,TAZ,FAM50A,MEIG1	yellow	VSMC_M3
GO:0006469	0.63	0.50	11	172	negative regulation of protein kinase activity	BP	1	H2AFY,PLEC,SOCS5,TARBP2,CHP1,QARS,TRIM27,PKN1,MVP,AKT1,TRIB2	yellow	VSMC_M3
GO:0030330	0.63	0.57	4	63	DNA damage response, signal transduction by p53 class mediator	BP	1	SPRED2,KAT5,HIC1,ZNF385A	yellow	VSMC_M3
GO:0048523	0.63	0.40	242	3647	negative regulation of cellular process	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,ZNF608,BAG6,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,TTLL12,RING1,SREBF2,H2AFY,ITPR3,HNRNPA0,TRIM11,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,VPS28,B4GALT1,PDGFRA,SECISBP2,PHF2,SOCS5,CNOT3,KLF4,TPBG,SPRED2,RGS3,ZC3H12A,FIGNL1,PNKP,SNRNP70,CC2D1B,SNX3,MICAL1,ANXA5,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,PLXND1,EMILIN1,DMAP1,CIC,UNK,DLEC1,INSIG1,OGG1,UCP2,METTL3,CXXC5,INPPL1,DND1,PYCR1,EIF4EBP1,CAVIN3,DEAF1,TARBP2,NAT10,BCL2L1,PDE4D,TNS2,SWAP70,LRP3,ZBTB38,CAPG,PINX1,GREM1,KDM2B,PDE3B,CX3CL1,WNT10B,SOD1,PACSIN3,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,CHP1,TYRO3,YAF2,HTATIP2,PCIF1,PCBP4,KDM1B,CISH,SRSF9,DCPS,IRX1,SELENOS,GSTO1,ITPRIP,ETFBKMT,RIN3,FABP3,ZCCHC17,PDGFA,MMP14,CDK2AP2,GPX1,CORO1B,NGEF,CLCF1,QARS,TRIM27,ARPIN,EIF3A,LIMK1,PRMT2,THOC5,TWIST2,PFDN2,BRMS1,PLA2G3,STMN3,CCDC85B,PTPN23,PBX1,KAT5,RELA,SIPA1,ARNT2,LIMD1,MID1IP1,PEX5,SMARCB1,GATAD2A,PHB2,PPP1R35,IGFBP5,IFI35,CTDSP1,OTUB1,EID1,METTL13,LETM1,LGALS3,C11orf95,CD9,TNFRSF1A,BABAM1,C1QBP,AIMP2,CHERP,ZBTB49,UBXN1,WASHC1,RCC2,MTA2,CCDC22,FOXK1,SDE2,KLF3,PKN1,MIIP,MAD1L1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,CTBP1,DFFA,SP2,ARHGEF2,MVP,PER1,NFIX,CORO1A,SLX1A,IRF2BPL,RPL37,MTMR4,SMARCA4,CARM1,EEF2K,AATF,CXorf57,C19orf66,CSK,ATG3,ZNF830,AKT1,PAIP1,KHSRP,GIT1,ANKRD13B,SLC6A4,DHCR24,MYDGF,LDOC1,SIRT6,CACTIN,HMG20B,VASN,HIC1,TRAP1,AURKAIP1,MNT,CTNS,EHMT1,PGP,MBD3,MIDN,STK11,GAS8,SARS,SLC27A4,TGFBR3,MIR214,R	yellow	VSMC_M3
GO:0034644	0.63	0.55	5	77	cellular response to UV	BP	1	METTL3,ACTR5,SDE2,STK11,NSMCE3	yellow	VSMC_M3
GO:0050871	0.63	0.57	4	61	positive regulation of B cell activation	BP	1	MMP14,CLCF1,BAD,MAD2L2	yellow	VSMC_M3
GO:0150104	0.63	0.57	4	70	transport across blood-brain barrier	BP	1	SLC9A3R1,LRP3,SLC19A1,SLC27A4	yellow	VSMC_M3
GO:0002790	0.63	0.49	11	172	peptide secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0033209	0.63	0.55	5	75	tumor necrosis factor-mediated signaling pathway	BP	1	SHARPIN,KRT8,RELA,TNFRSF1A,TRADD	yellow	VSMC_M3
GO:0032526	0.63	0.55	5	84	response to retinoic acid	BP	1	KLF4,WNT10B,PHB2,SLC6A4,TWF2	yellow	VSMC_M3
GO:0010507	0.63	0.57	4	67	negative regulation of autophagy	BP	1	SNRNP70,WASHC1,FOXK1,AKT1	yellow	VSMC_M3
GO:1901216	0.63	0.55	5	78	positive regulation of neuron death	BP	1	RAPSN,BAD,AIMP2,CAPN2,CDC34	yellow	VSMC_M3
GO:0042594	0.63	0.50	10	158	response to starvation	BP	1	FNIP1,SREBF2,ZC3H12A,UCP2,EIF4EBP1,AACS,PCK2,FOXK1,WDR24,FADS1	yellow	VSMC_M3
GO:0009653	0.63	0.41	128	2050	anatomical structure morphogenesis	BP	1	NAB2,CTHRC1,PBX2,RING1,H2AFY,PACSIN1,SCRIB,PLEC,TBCC,CUL7,B4GALT1,PDGFRA,COL15A1,EPN1,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,ZC3H12A,PLEKHA4,EHD2,KRT8,SLC9A3R1,PLXND1,EMILIN1,UNK,INSIG1,METTL3,BAIAP2,INPPL1,P4HB,RIC8A,ARHGAP22,DEAF1,HOXC4,LRIG1,ARHGAP33,BCL2L1,ITGB7,SLC11A2,GREM1,KDM2B,AQP5,PDE3B,CX3CL1,WNT10B,SOD1,EGR3,DLL4,TYRO3,HTATIP2,IRX1,PDGFA,MMP14,GPX1,CORO1B,NGEF,HCCS,PLEKHO1,IGSF9,COL6A1,NECTIN1,ANPEP,ARPIN,LIMK1,PLA2G3,PBX1,RELA,RHOC,FMNL1,VPS51,LIMD1,SGPL1,PBX4,YJEFN3,PHB2,IGFBP5,C12orf57,AAMP,CD9,TNFRSF1A,C1QBP,RCC2,CNP,PKN1,DBN1,CAPN2,MTHFR,CRABP2,TMEM79,ARHGEF2,ARMC5,CORO1A,SLC39A1,S100A6,SYNE3,EEF2K,MYO19,TTC39C,ZNF358,INF2,AKT1,RFX2,SLC6A4,MYDGF,SIRT6,ANAPC2,STK11,TAZ,JMJD8,SARS,TGFBR3,PSMB10,MIR214,NDST1,TNFRSF12A,ERBB4,TWF2,RNH1,ELN,UNC13A,CDC42EP5,NSMF,ARFRP1,DUSP5	yellow	VSMC_M3
GO:0007605	0.63	0.53	6	102	sensory perception of sound	BP	1	NDUFB9,HOXA1,SLC9A3R1,LRIG1,SOD1,GPX1	yellow	VSMC_M3
GO:0071466	0.63	0.53	6	92	cellular response to xenobiotic stimulus	BP	1	GUK1,SMOX,ACSL1,GSTO1,AIP,RBM22	yellow	VSMC_M3

GO:0034097	0.63	0.43	44	659	response to cytokine	BP	1	CDK4,TTLL12,RPL3,SHARPIN,IL1R1,SOCS5,KLF4,ZC3H12A,ZYX,KRT8,RELB,METTL3,P4HB,FASN,RAB20,BCL2L1,ACSL1,DOK1,CX3CL1,LSP1,CLCF1,PCK2,IMPDH2,SLC26A6,RELA,ATIC,BAD,OTUB1,TNFRSF1A,CAPN2,PALM3,MTHFR,ARHGEF2,CORO1A,TRIM25,CDC37,C19orf66,AKT1,KHSRP,CACTIN,IRAK1,TRADD,JAGN1,CDC34	yellow	VSMC_M3
GO:0071383	0.63	0.50	10	163	cellular response to steroid hormone stimulus	BP	1	PPARD,PCK2,PRMT2,PHB2,PKN1,PER1,SMARCA4,CARM1,SAFB,SAFB2	yellow	VSMC_M3
GO:0008088	0.63	0.57	4	68	axo-dendritic transport	BP	1	SOD1,BLOC1S4,AP3D1,SPG7	yellow	VSMC_M3
GO:0098586	0.63	0.57	4	63	cellular response to virus	BP	1	ZC3H12A,RRP1B,PHB2,C1QBP	yellow	VSMC_M3
GO:0008277	0.63	0.53	6	96	regulation of G protein-coupled receptor signaling pathway	BP	1	RGS3,MGLL,ZDHHC3,GIT1,RGS16,RGS18	yellow	VSMC_M3
GO:0050868	0.63	0.55	5	76	negative regulation of T cell activation	BP	1	SCRIB,SOCS5,ZC3H12A,LGALS3,MAD1L1	yellow	VSMC_M3
GO:0007033	0.63	0.49	10	157	vacuole organization	BP	1	LAMTOR1,RAB20,HPS1,NDP,PIP4K2B,CORO1A,ATG3,PACS2,RAB34,CCDC115	yellow	VSMC_M3
GO:0005976	0.63	0.54	5	83	polysaccharide metabolic process	BP	1	ENPP1,SELENOS,AKT1,B3GNT9,NDST1	yellow	VSMC_M3
GO:0072332	0.63	0.57	4	63	intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	BAG6,ZNF385B,STK11,ZNF385A	yellow	VSMC_M3
GO:0019319	0.63	0.57	4	61	hexose biosynthetic process	BP	1	SELENOS,PCK2,PGM1,PGP	yellow	VSMC_M3
GO:0006955	0.64	0.41	68	1012	immune response	BP	1	ENPP1,GNL1,BAG6,TTLL12,TRIM11,PLEC,LGALS1,PPP1R14B,IL1R1,SSC5D,SOCS5,DBNL,ZC3H12A,ZYX,RELB,CD79A,METTL3,RAB20,TARBP2,BCL2L1,PDE4D,SWAP70,CX3CL1,DGKZ,TYRO3,RNF19B,SELENOS,GPX1,CLCF1,NECTIN1,TRIM27,LIMK1,SLC26A6,RIPK3,PSMB4,TNK2,PLA2G3,RELA,SIPA1,MAP3K14,PHB2,IFI35,OTUB1,LGALS3,TNFRSF1A,C1QBP,PKN1,MAD2L2,TBKBP1,SP2,ARHGEF2,ARMC5,CORO1A,TRIM25,CDC37,CD276,C19orf66,CSK,MID2,DOCK11,CACTIN,IRAK1,C8G,STK11,CARD9,TGFBR3,PSMB10,JAGN1	yellow	VSMC_M3
GO:0002286	0.64	0.56	4	65	T cell activation involved in immune response	BP	1	SOCS5,ZC3H12A,RELB,LGALS3	yellow	VSMC_M3
GO:0050867	0.64	0.47	15	226	positive regulation of cell activation	BP	1	LGALS1,SOCS5,EGR3,MMP14,CLCF1,PLA2G3,SART1,BAD,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1,JUND	yellow	VSMC_M3
GO:0035710	0.64	0.56	4	65	CD4-positive, alpha-beta T cell activation	BP	1	SOCS5,ZC3H12A,RELB,ARMC5	yellow	VSMC_M3
GO:0000226	0.64	0.43	33	522	microtubule cytoskeleton organization	BP	1	DCTN2,SPAG1,CUL7,FIGNL1,CEP131,NUMA1,YIF1B,CCDC57,NAT10,DCTN1,CHP1,CDK2AP2,CLIP2,PCNT,NUDC,IQCG,PLA2G3,STMN3,SAC3D1,MID1IP1,KIAA0753,CNP,EML3,ARHGEF2,RANGRF,EML1,GIT1,GAS8,NTMT1,MAP7D1,GBA2,TUBGCP2,MEIG1	yellow	VSMC_M3
GO:0022402	0.64	0.41	62	951	cell cycle process	BP	1	DCTN2,CDK4,CTDSP2,BAG6,NCAPH2,SNX9,H2AFY,PLEC,SND1,CUL7,KLF4,FIGNL1,KMT2E,SEPT9,CEP131,NUMA1,CCDC57,EIF4EBP1,NAT10,BCL2L1,RRS1,PINX1,DCTN1,WNT10B,CCAR2,RAB35,CDK2AP2,PSME2,PCNT,NUDC,PRMT2,THOC5,PBX1,RHOC,ALKBH4,SAC3D1,PHB2,CTDSP1,METTL13,KIAA0753,BABAM1,ANXA11,RCC2,EML3,SDE2,MIIP,MAD1L1,MAD2L2,MYO19,EML1,ZNF830,AKT1,SNX18,GIT1,AURKAIP1,NTMT1,MIR214,NABP2,MIS12,CDC34,FBXO6,TUBGCP2	yellow	VSMC_M3
GO:1990542	0.64	0.52	6	84	mitochondrial transmembrane transport	BP	1	UCP2,SFXN5,LETM1,ATP5PD,AKT1,ATP5F1D	yellow	VSMC_M3
GO:0010638	0.64	0.44	27	428	positive regulation of organelle organization	BP	1	SNX9,H2AFY,PNKP,SEPT9,BAIAP2,NUMA1,SWAP70,DCTN1,CX3CL1,CORO1B,TRIM27,ARPIN,LIMK1,PFDN2,RHOC,CHCHD10,BAD,ARPC1B,WASHC1,PIP4K2B,CORO1A,SLX1A,GIT1,SIRT6,NABP2,CDC42EP5,ARPC5L	yellow	VSMC_M3
GO:0010232	0.64	0.56	4	71	vascular transport	BP	1	SLC9A3R1,LRP3,SLC19A1,SLC27A4	yellow	VSMC_M3
GO:0000380	0.64	0.56	4	66	alternative mRNA splicing, via spliceosome	BP	1	RBM15B,SRSF9,RAVER1,RBM8A	yellow	VSMC_M3
GO:0060284	0.64	0.44	23	384	regulation of cell development	BP	1	TRIM11,CUL7,DBNL,PLXND1,BAIAP2,P4HB,CX3CL1,DLL4,CLCF1,LIMK1,RELA,BAD,CTDSP1,TNFRSF1A,C1QBP,RCC2,DBN1,CRABP2,EEF2K,AKT1,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0042180	0.64	0.48	10	150	cellular ketone metabolic process	BP	1	PPARD,FDXR,INSIG1,ETFBKMT,FABP3,PLA2G3,MID1IP1,HSD17B1,COQ6,AKT1	yellow	VSMC_M3
GO:0007369	0.65	0.50	8	138	gastrulation	BP	1	H2AFY,KLF4,RIC8A,MMP14,COL6A1,ARMC5,ARFRP1,DUSP5	yellow	VSMC_M3
GO:0150115	0.65	0.53	5	95	cell-substrate junction organization	BP	1	PLEC,WDPCP,GREM1,MMP14,RCC2	yellow	VSMC_M3
GO:0018193	0.65	0.41	65	997	peptidyl-amino acid modification	BP	1	BAG6,HDAC10,NELFE,FNIP1,JADE2,H2AFY,PDGFRA,SOCS5,SPRED2,MEAF6,KMT2E,DMAP1,KAT14,P4HA3,P4HB,KMT2B,PDE4D,TNKS1BP1,SETD1B,GREM1,MCRS1,FKBP11,TYRO3,ETFBKMT,STK32C,PDGFA,AIP,CLCF1,TRIM27,PRMT2,TNK2,KAT5,RELA,SCYL1,ZDHHC3,SMARCB1,TRMT112,FKBP2,EID1,TNFRSF1A,TAF6L,PKN1,MAD2L2,CTBP1,ARHGEF2,MVP,PER1,DPM3,SGF29,CARM1,CSK,AKT1,COPRS,METTL22,MAP2K2,HMG20B,EHMT1,MKNK2,CSNK1G2,MBD3,NTMT1,ERBB4,LOXL1,PIN4,THAP7	yellow	VSMC_M3
GO:0010921	0.65	0.55	4	68	regulation of phosphatase activity	BP	1	CHP1,RIPK3,PPP1R35,LGALS3	yellow	VSMC_M3
GO:0015849	0.65	0.46	13	203	organic acid transport	BP	1	PPARD,SLC9A3R1,ACSL1,SFXN5,FABP3,SLC19A1,SLC26A6,SPX,PLA2G3,SLC27A3,AKT1,CTNS,SLC27A4	yellow	VSMC_M3
GO:0040013	0.65	0.45	16	261	negative regulation of locomotion	BP	1	PPARD,KLF4,SLC9A3R1,EMILIN1,GREM1,CX3CL1,DLL4,RIN3,CORO1B,ARPIN,PTPN23,IGFBP5,MIIP,AKT1,MIR214,PTPRR	yellow	VSMC_M3
GO:0019233	0.65	0.55	4	63	sensory perception of pain	BP	1	MGLL,MMP24,SPX,TMEM120A	yellow	VSMC_M3
GO:1904951	0.65	0.45	16	257	positive regulation of establishment of protein localization	BP	1	SREBF2,PPARD,VPS28,ZC3H12A,DMAP1,MYRIP,CEP131,AACS,CHP1,PCK2,PCNT,CAPN10,PTPN23,BAD,GLUD1,RBM22	yellow	VSMC_M3
GO:0090174	0.65	0.51	6	94	organelle membrane fusion	BP	1	RAB20,CHP1,PIP4K2B,STX10,CORO1A,RAB34	yellow	VSMC_M3
GO:0006259	0.65	0.41	49	741	DNA metabolic process	BP	1	NHP2,HDAC10,FANCE,KLF4,FIGNL1,PNKP,KMT2E,MUTYH,DMAP1,OGG1,TTC5,FAAP100,SMUG1,NAT10,SWAP70,TNKS1BP1,PINX1,GREM1,MCRS1,ACTR5,KDM1B,CLCF1,CEP164,KAT5,LRWD1,ALKBH4,SMARCB1,GATAD2A,OTUB1,BABAM1,MTA2,MAD2L2,DFFA,PPP4C,SLX1A,USP43,CXorf57,ZNF830,AKT1,SIRT6,EHMT1,MBD3,TELO2,RF00024,NABP2,CDC34,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0072001	0.65	0.45	15	256	renal system development	BP	1	BAG6,MPST,IFT27,PDGFRA,WDPCP,PLXND1,SNX17,TNS2,GREM1,IRX1,PDGFA,PBX1,SGPL1,AMER1,ERBB4	yellow	VSMC_M3

GO:0050954	0.65	0.50	7	120	sensory perception of mechanical stimulus	BP	1	NDUFB9,HOXA1,SLC9A3R1,LRIG1,SOD1,GPX1,TMEM120A	yellow	VSMC_M3
GO:0001570	0.65	0.55	4	71	vasculogenesis	BP	1	CUL7,CCM2,SGPL1,TGFBR3	yellow	VSMC_M3
GO:0007416	0.65	0.50	7	132	synapse assembly	BP	1	DBNL,TPBG,PLXND1,LRFN4,NECTIN1,EEF2K,ERBB4	yellow	VSMC_M3
GO:0071479	0.65	0.55	4	64	cellular response to ionizing radiation	BP	1	EEF1D,FIGNL1,BCL2L1,TNKS1BP1	yellow	VSMC_M3
GO:0034330	0.65	0.42	31	541	cell junction organization	BP	1	PLEC,DBNL,TPBG,WDPCP,CCM2,PLXND1,BAIAP2,ARHGAP22,ARHGAP33,GREM1,DCTN1,RAPSN,CX3CL1,MMP14,NGEF,IGSF9,LRFN4,NECTIN1,PTPN23,RHOC,CHCHD10,CD9,RCC2,DBN1,EEF2K,CSK,TJP3,CLDN6,ANAPC2,ERBB4,UNC13A	yellow	VSMC_M3
GO:1902107	0.65	0.50	7	110	positive regulation of leukocyte differentiation	BP	1	SOCS5,EGR3,MMP14,PLA2G3,SART1,BAD,AP3D1	yellow	VSMC_M3
GO:1903708	0.65	0.50	7	110	positive regulation of hemopoiesis	BP	1	SOCS5,EGR3,MMP14,PLA2G3,SART1,BAD,AP3D1	yellow	VSMC_M3
GO:0014020	0.65	0.52	5	86	primary neural tube formation	BP	1	CTHRC1,SCRIB,DEAF1,KDM2B,MTHFR	yellow	VSMC_M3
GO:0048754	0.65	0.50	7	121	branching morphogenesis of an epithelial tube	BP	1	PLXND1,GREM1,DLL4,MMP14,PBX1,PHB2,SIRT6	yellow	VSMC_M3
GO:0033002	0.65	0.47	11	174	muscle cell proliferation	BP	1	PPARD,KLF4,SIX5,CX3CL1,IGFBP5,AKT1,IRAK1,TGFBR3,MIR214,ERBB4,ELN	yellow	VSMC_M3
GO:0030198	0.65	0.45	15	250	extracellular matrix organization	BP	1	B4GALT1,PDGFRA,COL15A1,COL19A1,EMILIN1,RIC8A,MMP24,GREM1,MMP14,MPZL3,TNFRSF1A,WASHC1,POMT1,LOXL1,ELN	yellow	VSMC_M3
GO:0048513	0.66	0.38	163	2529	animal organ development	BP	1	ENPP1,NAB2,CDK4,BAG6,NCAPH2,CTHRC1,FNIP1,PBX2,PDLIM4,RING1,H2AFY,TRAPPC9,PPARD,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,CUL7,PDGFRA,SECISBP2,PHF2,EPN1,COL19A1,SOCS5,TTC7A,KLF4,HOXA1,WDPCP,CCM2,FHL3,SPRED2,ZC3H12A,RCN3,PLEKHA4,KMT2E,KRT8,SIX5,RELB,SLC9A3R1,PLXND1,EMILIN1,PAFAH1B3,CIC,SNX17,CD79A,INSIG1,UCP2,METTL3,BAIAP2,INPPL1,NUMA1,FASN,EIF4EBP1,DEAF1,HOXC4,LRIG1,AACS,BCL2L1,TNS2,SLC11A2,GREM1,KDM2B,AQP5,DCTN1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,TYRO3,IRX1,PDGFA,MMP14,GPX1,HCCS,CLCF1,QARS,PCK2,IMPDH2,PIR,NECTIN1,THOC5,RIPK3,PLA2G3,SART1,PBX1,RELA,SCYL1,IDH1,ARNT2,VPS51,SGPL1,PBX4,YJEFN3,ATIC,MEF2B,PHB2,IGFBP5,C12orf57,BAD,HSD17B1,CD9,TNFRSF1A,TEAD4,AIMP2,EVC,CNP,PRXL2A,KRT10,GLUD1,FOXK1,CASP14,PKN1,MAD1L1,AMER1,MAD2L2,PRR14,TMEM79,ARMC5,MTX1,SLC39A1,S100A4,SMARCA4,EML1,CSK,TTC39C,DOCK11,ZNF830,AKT1,COPRS,HMGCS1,SAFB2,GIT1,SLC6A4,DHCR24,SIRT6,PPL,NSDHL,HMG20B,VASN,CTNS,AP3D1,MKNK2,MBD3,STK11,TAZ,APRT,GTF3C5,SLC27A4,TGFBR3,TRADD,NDST1,ERBB4,KLF13,JAGN1,IGSF8,ELN,ZNF385A,NOM1,GLIPR2,TUBGCP2	yellow	VSMC_M3
GO:0019882	0.66	0.54	4	61	antigen processing and presentation	BP	1	RELB,RAB35,RAB34,AP3D1	yellow	VSMC_M3
GO:0098542	0.66	0.41	38	574	defense response to other organism	BP	1	TTLL12,TRIM11,PPP1R14B,SSC5D,ZC3H12A,ZYX,RELB,METTL3,RAB20,TARBP2,BCL2L1,CX3CL1,TYRO3,RNF19B,TRIM27,SLC26A6,RIPK3,TNK2,RELA,MAP3K14,PHB2,IFI35,LGALS3,TNFRSF1A,C1QBP,TBKBP1,ARHGEF2,ARMC5,CORO1A,TRIM25,CDC37,C19orf66,MID2,CACTIN,IRAK1,C8G,CARD9,JAGN1	yellow	VSMC_M3
GO:0071706	0.66	0.49	7	115	tumor necrosis factor superfamily cytokine production	BP	1	ZC3H12A,CX3CL1,SELENOS,TRIM27,ARHGEF2,CACTIN,CARD9	yellow	VSMC_M3
GO:1903555	0.66	0.49	7	115	regulation of tumor necrosis factor superfamily cytokine production	BP	1	ZC3H12A,CX3CL1,SELENOS,TRIM27,ARHGEF2,CACTIN,CARD9	yellow	VSMC_M3
GO:1990845	0.66	0.48	8	132	adaptive thermogenesis	BP	1	CNOT3,UCP2,ACSL1,WNT10B,SCD,SIRT6,EHMT1,STK11	yellow	VSMC_M3
GO:0038127	0.66	0.50	6	102	ERBB signaling pathway	BP	1	SOCS5,MVB12A,MVP,AKT1,PTPRR,STUB1	yellow	VSMC_M3
GO:0034446	0.66	0.52	5	89	substrate adhesion-dependent cell spreading	BP	1	P4HB,ITGB7,TYRO3,C1QBP,RCC2	yellow	VSMC_M3
GO:0043062	0.66	0.44	15	251	extracellular structure organization	BP	1	B4GALT1,PDGFRA,COL15A1,COL19A1,EMILIN1,RIC8A,MMP24,GREM1,MMP14,MPZL3,TNFRSF1A,WASHC1,POMT1,LOXL1,ELN	yellow	VSMC_M3
GO:0048660	0.66	0.48	8	124	regulation of smooth muscle cell proliferation	BP	1	PPARD,KLF4,CX3CL1,IGFBP5,AKT1,IRAK1,MIR214,ELN	yellow	VSMC_M3
GO:0009100	0.66	0.43	19	299	glycoprotein metabolic process	BP	1	PPARD,B4GALT1,SERP2,GALNT14,PHLDA1,CHP1,SLC35C2,ST3GAL4,MANBA,TMTC1,EXTL1,MPDU1,DPM3,AATF,MAN1B1,POMT1,B3GNT9,NDST1,FBXO6	yellow	VSMC_M3
GO:0045229	0.66	0.44	15	251	external encapsulating structure organization	BP	1	B4GALT1,PDGFRA,COL15A1,COL19A1,EMILIN1,RIC8A,MMP24,GREM1,MMP14,MPZL3,TNFRSF1A,WASHC1,POMT1,LOXL1,ELN	yellow	VSMC_M3
GO:0021782	0.66	0.52	5	86	glial cell development	BP	1	HDAC10,PLEC,SOD1,CD9,AKT1	yellow	VSMC_M3
GO:0007169	0.66	0.41	30	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	ENPP1,CD63,CDK4,PDGFRA,SOCS5,SLC9A3R1,EMILIN1,BAIAP2,TNS2,GREM1,DOK1,TYRO3,PDGFA,NGEF,TNK2,RELA,SGPL1,IGFBP5,MVB12A,PIP4K2B,MVP,AKT1,GIT1,SLC27A4,TRADD,NDST1,ERBB4,PTPRR,IGFBP6,STUB1	yellow	VSMC_M3
GO:0050778	0.66	0.42	20	306	positive regulation of immune response	BP	1	BAG6,IL1R1,SOCS5,ZC3H12A,CD79A,PDE4D,DGKZ,CLCF1,LIMK1,PLA2G3,RELA,IFI35,LGALS3,C1QBP,MAD2L2,CD276,CSK,C8G,STK11,CARD9	yellow	VSMC_M3
GO:0033043	0.66	0.39	60	950	regulation of organelle organization	BP	1	SQSTM1,SNX9,SREBF2,H2AFY,CUL7,PDGFRA,DBNL,PNKP,SEPT9,BAIAP2,NUMA1,NAT10,BCL2L1,SWAP70,CAPG,PINX1,DCTN1,CX3CL1,PDGFA,CDK2AP2,GPX1,CORO1B,LRFN4,TRIM27,ARPIN,LIMK1,PFDN2,STMN3,RHOC,MID1IP1,CHCHD10,BAD,ARPC1B,WASHC1,EML3,DBN1,CAPN2,MAD1L1,PIP4K2B,MAD2L2,ARHGEF2,RANGRF,CORO1A,SLX1A,RABEP2,MYO19,ATG3,INF2,AKT1,GIT1,SIRT6,MAP2K2,AURKAIP1,MIR214,NABP2,TWF2,ELN,CDC42EP5,GBA2,ARPC5L	yellow	VSMC_M3
GO:0061041	0.66	0.50	6	96	regulation of wound healing	BP	1	PDGFRA,ST3GAL4,PDGFA,CD9,PLAU,TNFRSF12A	yellow	VSMC_M3
GO:0048709	0.66	0.53	4	67	oligodendrocyte differentiation	BP	1	HDAC10,CD9,CNP,CSK	yellow	VSMC_M3
GO:0007229	0.67	0.51	5	92	integrin-mediated signaling pathway	BP	1	CD63,CCM2,ZYX,ITGB7,RCC2	yellow	VSMC_M3
GO:0045785	0.67	0.42	19	306	positive regulation of cell adhesion	BP	1	TSTA3,LGALS1,SOCS5,EMILIN1,P4HB,CX3CL1,EGR3,ST3GAL4,SART1,PTPN23,RELA,BAD,C1QBP,CORO1A,CD276,CSK,AKT1,AP3D1,IRAK1	yellow	VSMC_M3
GO:0043542	0.67	0.44	12	195	endothelial cell migration	BP	1	TSTA3,KLF4,ZC3H12A,PLXND1,SCARB1,GREM1,EGR3,DLL4,GPX1,CORO1B,AAMP,AKT1	yellow	VSMC_M3

GO:0045087	0.67	0.40	30	459	innate immune response	BP	1	TTLL12,TRIM11,PPP1R14B,SSC5D,ZYX,RELB,METTL3,RAB20,CX3CL1,TYRO3,RNF19B,TRIM27,SLC26A6,TNK2,RELA,PHB2,IFI35,LGALS3,C1QBP,TBKBP1,ARHGEF2,CORO1A,TRIM25,CDC37,C19orf66,MID2,CACTIN,IRAK1,C8G,CARD9	yellow	VSMC_M3
GO:0010639	0.67	0.42	18	297	negative regulation of organelle organization	BP	1	NAT10,BCL2L1,SWAP70,CAPG,PINX1,GPX1,CORO1B,ARPIN,MID1IP1,MAD1L1,MAD2L2,ARHGEF2,CORO1A,SLX1A,AKT1,AURKAIP1,MIR214,TWF2	yellow	VSMC_M3
GO:0001503	0.67	0.42	20	328	ossification	BP	1	ENPP1,NAB2,CTHRC1,SND1,FIGNL1,INPPL1,FASN,LRP3,GREM1,WNT10B,MMP14,COL6A1,TWIST2,MRC2,PBX1,LIMD1,IGFBP5,AKT1,GIT1,JUND	yellow	VSMC_M3
GO:0071495	0.67	0.38	63	1018	cellular response to endogenous stimulus	BP	1	ENPP1,CDK4,PPARD,PDGFRA,KLF4,SPRED2,ZYX,SLC9A3R1,EMILIN1,INSIG1,UCP2,BAIAP2,LAMTOR1,NUMA1,BCL2L1,TNS2,ACSL1,GREM1,PDE3B,WNT10B,SOD1,EGR3,DLL4,RAB35,SELENOS,CORO1B,PCK2,COL6A1,SLC26A6,PRMT2,CAPN10,RELA,PHB2,IGFBP5,LAMTOR4,PELP1,KLF3,PKN1,CAPN2,PIP4K2B,ARHGEF2,PER1,CORO1A,MTMR4,SMARCA4,CARM1,EEF2K,CSK,AKT1,HMGCS1,SAFB,SAFB2,SLC6A4,LDOC1,VASN,STK11,APRT,SLC27A4,TGFBR3,NDST1,ERBB4,NSMF,STUB1	yellow	VSMC_M3
GO:0071674	0.67	0.47	8	126	mononuclear cell migration	BP	1	PLEC,ITGB7,GREM1,CX3CL1,RIPK3,LGALS3,C1QBP,AKT1	yellow	VSMC_M3
GO:0017038	0.67	0.45	11	174	protein import	BP	1	SAMM50,ZC3H12A,DMAP1,SEC13,CHP1,PEX5,PHB2,NUP88,RANGRF,RBM22,AKT1	yellow	VSMC_M3
GO:0071346	0.67	0.50	5	80	cellular response to interferon-gamma	BP	1	ZYX,RAB20,CX3CL1,SLC26A6,CDC37	yellow	VSMC_M3
GO:0140029	0.67	0.52	4	66	exocytic process	BP	1	SCRIB,PLA2G3,RABEPK,UNC13A	yellow	VSMC_M3
GO:0007029	0.67	0.50	5	80	endoplasmic reticulum organization	BP	1	ESYT1,BAG6,ASNA1,LMAN2,JAGN1	yellow	VSMC_M3
GO:0042060	0.67	0.41	20	329	wound healing	BP	1	PPARD,SCRIB,PLEC,B4GALT1,PDGFRA,ANXA5,SCARB1,CX3CL1,DGKZ,TYRO3,ST3GAL4,PDGFA,GPX1,CORO1B,RHOC,BLOC1S4,CD9,PLAU,PPL,TNFRSF12A	yellow	VSMC_M3
GO:0034341	0.67	0.48	6	95	response to interferon-gamma	BP	1	ZYX,RAB20,CX3CL1,SLC26A6,CDC37,C19orf66	yellow	VSMC_M3
GO:0006302	0.67	0.43	14	225	double-strand break repair	BP	1	FIGNL1,PNKP,OGG1,TNKS1BP1,ACTR5,KAT5,OTUB1,BABAM1,MAD2L2,PPP4C,SLX1A,CXorf57,SIRT6,NABP2	yellow	VSMC_M3
GO:0010257	0.68	0.52	4	53	NADH dehydrogenase complex assembly	BP	1	NDUFB9,ACAD9,NDUFS7,TAZ	yellow	VSMC_M3
GO:0032981	0.68	0.52	4	53	mitochondrial respiratory chain complex I assembly	BP	1	NDUFB9,ACAD9,NDUFS7,TAZ	yellow	VSMC_M3
GO:0050790	0.68	0.36	119	1823	regulation of catalytic activity	BP	1	NAB2,CDK4,SBF1,SNX9,FNIP1,RING1,H2AFY,SGSM3,DEF6,EEF1D,SCRIB,PLEC,PPP1R14B,PDGFRA,HSPBP1,SOCS5,KLF4,DBNL,SPRED2,RGS3,PNKP,RCN3,SNRNP70,MICAL1,ANXA5,SLC9A3R1,PLXND1,SERTAD1,ARHGEF40,LAMTOR1,ARAP3,DELE1,RIC8A,ARHGAP22,ARHGAP33,TARBP2,SCARB1,HM13,SWAP70,ACSL1,MMP24,PINX1,GREM1,CX3CL1,SOD1,DGKZ,CCAR2,HPS1,CHP1,TYRO3,CISH,ITPRIP,RRP1B,ETFBKMT,RIN3,PDGFA,PABPN1,GPX1,AIP,NGEF,QARS,PSME2,TRIM27,LIMK1,RIPK3,ADRM1,TNK2,TACO1,STMN3,SIPA1,RHOC,MID1IP1,PHB2,PPP1R35,BAD,LAMTOR4,LGALS3,AIMP2,UBXN1,WASHC1,RCC2,RAB3IL1,PKN1,PIP4K2B,MAD2L2,DFFA,ARHGEF2,MVP,RANGRF,DPM3,RABEP2,RPL37,CDC37,CSK,DOCK11,AKT1,SNX18,DENND1C,GTF2F1,RANBP3,GIT1,DHCR24,MAP2K2,ACAP3,IRAK1,MIDN,STK11,TELO2,JMJD8,CARD9,SLC27A4,VAC14,ERBB4,RNH1,TRIB2,ARHGEF1,RGS16,STUB1,RGS18	yellow	VSMC_M3
GO:0048144	0.68	0.52	4	66	fibroblast proliferation	BP	1	CDK4,PDGFRA,PDGFA,S100A6	yellow	VSMC_M3
GO:0048145	0.68	0.52	4	66	regulation of fibroblast proliferation	BP	1	CDK4,PDGFRA,PDGFA,S100A6	yellow	VSMC_M3
GO:0021700	0.68	0.43	12	204	developmental maturation	BP	1	CD63,GREM1,CX3CL1,WNT10B,SLC26A6,PLA2G3,AP1M1,TMEM79,AP3D1,ANAPC2,UNC13A,NOM1	yellow	VSMC_M3
GO:0002824	0.68	0.52	4	64	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	IL1R1,CLCF1,MAD2L2,CARD9	yellow	VSMC_M3
GO:0001764	0.68	0.48	6	113	neuron migration	BP	1	UNK,CX3CL1,ARHGEF2,ACAP3,NSMF,TUBGCP2	yellow	VSMC_M3
GO:0070997	0.68	0.41	18	288	neuron death	BP	1	BCL2L1,KDM2B,RAPSN,CX3CL1,SOD1,CHP1,TYRO3,GPX1,CLCF1,PLA2G3,BAD,AIMP2,CAPN2,CORO1A,AKT1,DHCR24,NSMF,CDC34	yellow	VSMC_M3
GO:0032386	0.68	0.41	18	290	regulation of intracellular transport	BP	1	SREBF2,EIPR1,ZC3H12A,SNX3,EHD2,DMAP1,INSIG1,CEP131,NUMA1,CHP1,PCNT,CAPN10,PLA2G3,PTPN23,RBM22,MAP2K2,STK11,PLA2G4E	yellow	VSMC_M3
GO:0016485	0.68	0.44	11	170	protein processing	BP	1	LDLRAD3,HM13,MMP14,SEC11A,BAD,PLAU,SDE2,CAPN2,DHCR24,SPG7,RCE1	yellow	VSMC_M3
GO:1905477	0.68	0.49	5	88	positive regulation of protein localization to membrane	BP	1	SQSTM1,CHP1,LGALS3,RANGRF,AKT1	yellow	VSMC_M3
GO:0034754	0.68	0.49	5	79	cellular hormone metabolic process	BP	1	PDGFRA,SCARB1,SGPL1,HSD17B1,CRABP2	yellow	VSMC_M3
GO:0042113	0.68	0.43	12	193	B cell activation	BP	1	FNIP1,LGALS1,CD79A,SWAP70,MMP14,CLCF1,PHB2,BAD,PKN1,MAD2L2,DOCK11,AKAP17A	yellow	VSMC_M3
GO:0006612	0.68	0.48	6	97	protein targeting to membrane	BP	1	ASNA1,YIF1B,CHP1,PEX5,ZDHHC3,ATG3	yellow	VSMC_M3
GO:0048638	0.68	0.42	15	257	regulation of developmental growth	BP	1	CDK4,PPARD,DBNL,SOD1,LIMK1,SGPL1,DBN1,CRABP2,AKT1,SLC6A4,ANAPC2,TGFBR3,ERBB4,TWF2,UNC13A	yellow	VSMC_M3
GO:0051963	0.68	0.51	4	79	regulation of synapse assembly	BP	1	TPBG,LRFN4,NECTIN1,EEF2K	yellow	VSMC_M3
GO:0051146	0.69	0.42	13	220	striated muscle cell differentiation	BP	1	PLEC,PDGFRA,EHD2,KRT8,GREM1,WNT10B,MMP14,GPX1,PLEKHO1,IGFBP5,CD9,CAPN2,AKT1	yellow	VSMC_M3
GO:0071675	0.69	0.49	5	81	regulation of mononuclear cell migration	BP	1	GREM1,RIPK3,LGALS3,C1QBP,AKT1	yellow	VSMC_M3
GO:0002443	0.69	0.42	14	221	leukocyte mediated immunity	BP	1	GNL1,IL1R1,KMT2E,SWAP70,RNF19B,CLCF1,RIPK3,PLA2G3,C1QBP,MAD2L2,CORO1A,C8G,CARD9,JAGN1	yellow	VSMC_M3
GO:0019079	0.69	0.47	6	99	viral genome replication	BP	1	ZC3H12A,TARBP2,BANF1,SMARCB1,CTBP1,C19orf66	yellow	VSMC_M3
GO:0060070	0.69	0.41	15	250	canonical Wnt signaling pathway	BP	1	CTHRC1,KLF4,TPBG,PLEKHA4,SLC9A3R1,RNF220,GREM1,WNT10B,CCAR2,LIMD1,AMER1,MAD2L2,CSNK1G2,STK11,IGFBP6	yellow	VSMC_M3

GO:0009605	0.69	0.35	116	1770	response to external stimulus	BP	1	CD63,CDK4,FNIP1,TTLL12,SREBF2,HNRNPA0,TRIM11,PPARD,SCRIB,PLEC,SHARPIN,PPP1R14B,PDGFRA,IL1R1,SSC5D,SOCS5,KLF4,TPBG,ZC3H12A,ZYX,SNX3,MGLL,KRT8,RELB,PLXND1,OGG1,UCP2,METTL3,BAIAP2,RAB20,EIF4EBP1,TARBP2,AACS,SCARB1,BCL2L1,SWAP70,ACSL1,MMP24,GREM1,CX3CL1,SOD1,EGR3,TYRO3,LSP1,ST3GAL4,RNF19B,DCPS,SELENOS,RRP1B,MVK,RIN3,PDGFA,MMP14,PABPN1,GPX1,CORO1B,IGSF9,PCK2,NECTIN1,TRIM27,SLC26A6,SPX,RIPK3,PSMB4,TNK2,PLA2G3,BANF1,RELA,SIPA1,TMEM120A,MAP3K14,PHB2,BAD,IFI35,LGALS3,CD9,PLAU,TNFRSF1A,C1QBP,CNP,AP1M1,FOXK1,CAPN2,PALM3,MTHFR,TBKBP1,ARHGEF2,ARMC5,PER1,CORO1A,TRIM25,CDC37,C19orf66,MID2,AKT1,HMGCS1,GTF2F1,GIT1,SLC6A4,LDOC1,SIRT6,PPL,CACTIN,AP3D1,IRAK1,MBD3,C8G,WDR24,CARD9,SLC27A4,TRADD,JUND,LOXL1,EEF1G,FADS1,JAGN1	yellow	VSMC_M3
GO:0009410	0.69	0.40	20	314	response to xenobiotic stimulus	BP	1	GUK1,LGALS1,OGG1,SMOX,AACS,ACSL1,SOD1,GSTO1,FABP3,GPX1,AIP,PPOX,RELA,BAD,MTHFR,RBM22,HMGCS1,SLC6A4,BLMH,CARD9	yellow	VSMC_M3
GO:0055088	0.69	0.46	7	116	lipid homeostasis	BP	1	SREBF2,RCN3,INSIG1,LAMTOR1,SCARB1,RALY,FABP3	yellow	VSMC_M3
GO:0043549	0.69	0.37	38	612	regulation of kinase activity	BP	1	NAB2,SNX9,H2AFY,PLEC,PDGFRA,SOCS5,KLF4,SLC9A3R1,SERTAD1,TARBP2,ACSL1,GREM1,SOD1,DGKZ,CHP1,TYRO3,CISH,PDGFA,QARS,TRIM27,RIPK3,PHB2,BAD,WASHC1,PKN1,PIP4K2B,MVP,CDC37,CSK,AKT1,MAP2K2,IRAK1,MIDN,STK11,TELO2,VAC14,ERBB4,TRIB2	yellow	VSMC_M3
GO:0006446	0.69	0.50	4	66	regulation of translational initiation	BP	1	METTL3,EIF4EBP1,EIF4B,PAIP1	yellow	VSMC_M3
GO:0033044	0.69	0.43	10	168	regulation of chromosome organization	BP	1	H2AFY,PNKP,NUMA1,NAT10,PINX1,MAD1L1,MAD2L2,SLX1A,SIRT6,NABP2	yellow	VSMC_M3
GO:0045739	0.69	0.50	4	66	positive regulation of DNA repair	BP	1	HDAC10,PNKP,BABAM1,MAD2L2	yellow	VSMC_M3
GO:0042098	0.69	0.45	8	127	T cell proliferation	BP	1	SCRIB,RIPK3,LGALS3,MAD1L1,ARMC5,CORO1A,CD276,PSMB10	yellow	VSMC_M3
GO:0045893	0.69	0.35	79	1244	positive regulation of transcription, DNA-templated	BP	1	SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,KLF4,HOXA1,ZC3H12A,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,DEAF1,HOXC4,KMT2B,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,YAF2,HTATIP2,KDM1B,CHCHD2,RRP1B,AIP,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,NDP,SSBP4,BUD31,TNFRSF1A,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,MAD2L2,ARHGEF2,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,AKT1,BRF1,GTF2F1,MYDGF,MAP2K2,AP3D1,MED16,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3
GO:1903508	0.69	0.35	79	1244	positive regulation of nucleic acid-templated transcription	BP	1	SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,KLF4,HOXA1,ZC3H12A,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,DEAF1,HOXC4,KMT2B,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,YAF2,HTATIP2,KDM1B,CHCHD2,RRP1B,AIP,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,NDP,SSBP4,BUD31,TNFRSF1A,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,MAD2L2,ARHGEF2,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,AKT1,BRF1,GTF2F1,MYDGF,MAP2K2,AP3D1,MED16,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3
GO:0033554	0.69	0.35	103	1561	cellular response to stress	BP	1	SQSTM1,GNL1,BAG6,HDAC10,FNIP1,ATF6B,SREBF2,PPARD,FANCE,PLEC,PDGFRA,SOCS5,KLF4,CCM2,SPRED2,ZC3H12A,FIGNL1,PDIA4,PNKP,RCN3,RELB,SERP2,MUTYH,TMUB1,DMAP1,INSIG1,OGG1,TTC5,UCP2,SEL1L2,METTL3,FAAP100,P4HB,PYCR1,EIF4EBP1,GSR,SMUG1,HM13,BCL2L1,ZBTB38,TNKS1BP1,AQP5,MCRS1,SOD1,ACTR5,ANKRD2,CCAR2,CHCHD2,WDR4,SELENOS,GPX1,QARS,THOC5,RIPK3,CEP164,KAT5,RELA,SIPA1,PHB2,BAD,OTUB1,LETM1,TNFRSF1A,BABAM1,UBXN1,SDE2,MAD2L2,ARHGEF2,PER1,PPP4C,SLX1A,TRIM25,USP43,EEF2K,CDC37,AATF,CXorf57,ZNF830,AKT1,ALKBH7,SIRT6,MAP2K2,VASN,HIC1,TRAP1,IRAK1,MAN1B1,STK11,WDR24,CARD9,MIR214,RF00024,NABP2,FADS1,IGFBP6,ZNF385A,TXNDC12,CDC42EP5,FBXO6,IER5,OSER1,STUB1,NSMCE3	yellow	VSMC_M3
GO:0006885	0.69	0.50	4	70	regulation of pH	BP	1	RAB20,CHP1,SLC26A6,CCDC115	yellow	VSMC_M3
GO:0051270	0.69	0.36	51	830	regulation of cellular component movement	BP	1	PPARD,TSTA3,PDGFRA,IL1R1,KLF4,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,SCARB1,PDE4D,SWAP70,GREM1,CX3CL1,DLL4,ST3GAL4,RIN3,PDGFA,MMP14,CORO1B,ARPIN,RIPK3,TWIST2,PTPN23,RHOC,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,RANGRF,CORO1A,AKT1,STK11,TGFBR3,TRADD,MIR214,ERBB4,PTPRR,CAVIN1,NSMF,GLIPR2	yellow	VSMC_M3
GO:0030334	0.69	0.36	45	735	regulation of cell migration	BP	1	PPARD,TSTA3,PDGFRA,IL1R1,KLF4,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,SCARB1,SWAP70,GREM1,CX3CL1,DLL4,ST3GAL4,RIN3,PDGFA,MMP14,CORO1B,ARPIN,RIPK3,TWIST2,PTPN23,RHOC,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,MIIP,ARHGEF2,CORO1A,AKT1,TRADD,MIR214,ERBB4,PTPRR,NSMF,GLIPR2	yellow	VSMC_M3
GO:0051054	0.69	0.42	11	176	positive regulation of DNA metabolic process	BP	1	HDAC10,KLF4,PNKP,GREM1,CLCF1,BABAM1,MAD2L2,SLX1A,AKT1,SIRT6,NABP2	yellow	VSMC_M3
GO:0007051	0.69	0.43	10	165	spindle organization	BP	1	DCTN2,NUMA1,DCTN1,PCNT,NUDC,SAC3D1,EML3,EML1,NTMT1,TUBGCP2	yellow	VSMC_M3
GO:0002821	0.69	0.50	4	66	positive regulation of adaptive immune response	BP	1	IL1R1,CLCF1,MAD2L2,CARD9	yellow	VSMC_M3
GO:0035239	0.69	0.36	42	699	tube morphogenesis	BP	1	CTHRC1,SCRIB,CUL7,B4GALT1,PDGFRA,COL15A1,EPN1,KLF4,HOXA1,CCM2,ZC3H12A,PLXND1,EMILIN1,ARHGAP22,DEAF1,GREM1,KDM2B,PDE3B,CX3CL1,EGR3,DLL4,HTATIP2,IRX1,PDGFA,MMP14,GPX1,ANPEP,PBX1,SGPL1,YJEFN3,PHB2,AAMP,MTHFR,AKT1,MYDGF,SIRT6,JMJD8,SARS,TGFBR3,MIR214,TNFRSF12A,RNH1	yellow	VSMC_M3
GO:0048659	0.70	0.44	8	128	smooth muscle cell proliferation	BP	1	PPARD,KLF4,CX3CL1,IGFBP5,AKT1,IRAK1,MIR214,ELN	yellow	VSMC_M3

GO:0030177	0.70	0.45	7	124	positive regulation of Wnt signaling pathway	BP	1	PLEKHA4,RNF220,WNT10B,CCAR2,AMER1,SMARCA4,CSNK1G2	yellow	VSMC_M3
GO:1902680	0.70	0.35	79	1246	positive regulation of RNA biosynthetic process	BP	1	SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,KLF4,HOXA1,ZC3H12A,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,DEAF1,HOXC4,KMT2B,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,YAF2,HTATIP2,KDM1B,CHCHD2,RRP1B,AIP,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,NDP,SSBP4,BUD31,TNFRSF1A,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,MAD2L2,ARHGEF2,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,AKT1,BRF1,GTF2F1,MYDGF,MAP2K2,AP3D1,MED16,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3
GO:1903008	0.70	0.46	6	101	organelle disassembly	BP	1	SQSTM1,SREBF2,PHB2,CDC37,ATG3,TAZ	yellow	VSMC_M3
GO:0009615	0.70	0.40	16	253	response to virus	BP	1	TRIM11,ZC3H12A,TARBP2,BCL2L1,RRP1B,RIPK3,BANF1,RELA,MAP3K14,PHB2,C1QBP,ARMC5,C19orf66,GTF2F1,CARD9,EEF1G	yellow	VSMC_M3
GO:0090068	0.70	0.42	11	180	positive regulation of cell cycle process	BP	1	CDK4,H2AFY,KMT2E,NUMA1,WNT10B,THOC5,PBX1,PHB2,RCC2,AKT1,MIR214	yellow	VSMC_M3
GO:0030324	0.70	0.44	8	141	lung development	BP	1	BAG6,PDGFRA,RCN3,EIF4EBP1,PDGFA,MMP14,IGFBP5,AIMP2	yellow	VSMC_M3
GO:0007589	0.70	0.49	4	68	body fluid secretion	BP	1	AQP5,MTX1,APRT,ERBB4	yellow	VSMC_M3
GO:0060322	0.70	0.36	37	624	head development	BP	1	BAG6,PBX2,TRAPPC9,SCRIB,SHARPIN,PDGFRA,SECISBP2,PAFAH1B3,CIC,METTL3,BAIAP2,KDM2B,CCDC32,TYRO3,MMP14,QARS,PBX1,ARNT2,VPS51,SGPL1,PBX4,ATIC,C12orf57,BAD,CD9,CNP,GLUD1,EML1,CSK,HMGCS1,GIT1,SLC6A4,CTNS,MBD3,NDST1,ERBB4,TUBGCP2	yellow	VSMC_M3
GO:0050708	0.70	0.41	12	200	regulation of protein secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,PTPN23,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0043067	0.70	0.35	74	1119	regulation of programmed cell death	BP	1	CDK4,SQSTM1,BAG6,FNIP1,PPARD,SCRIB,LGALS1,B4GALT1,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,SLC9A3R1,OGG1,UCP2,PHLDA1,P4HB,BCL2L1,PLEKHF1,GREM1,KDM2B,RAPSN,CX3CL1,WNT10B,SOD1,EGR3,CCAR2,TYRO3,HTATIP2,DCPS,SELENOS,ITPRIP,RRP1B,GPX1,CLCF1,QARS,PRMT2,RIPK3,TWIST2,CAPN10,BRMS1,PLA2G3,RELA,ARNT2,PHB2,BAD,LGALS3,TNFRSF1A,C1QBP,USP27X,CAPN2,NANOS3,DFFA,ARHGEF2,CORO1A,EEF2K,AATF,ZNF830,AKT1,DHCR24,MYDGF,TRAP1,MNT,CARD9,SLC27A4,TRADD,MIR214,TNFRSF12A,PTMA,ZNF385A,TXNDC12,NSMF,CDC34	yellow	VSMC_M3
GO:0035270	0.70	0.47	5	87	endocrine system development	BP	1	PDGFRA,PBX1,BAD,ARMC5,AKT1	yellow	VSMC_M3
GO:0010506	0.70	0.39	16	268	regulation of autophagy	BP	1	SREBF2,ZC3H12A,SNRNP70,PLEKHF1,TRIM27,KAT5,PHB2,BAD,WASHC1,FOXK1,PIP4K2B,MTMR4,MID2,AKT1,STK11,WDR24	yellow	VSMC_M3
GO:0050789	0.70	0.32	528	7907	regulation of biological process	BP	1	ENPP1,CD63,NAB2,NHP2,CDK4,CTDSP2,RUFY1,SQSTM1,GNL1,ZNF608,BAG6,SNX9,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,SQLE,TXNDC15,H2AFY,ITPR3,HNRNPA0,TRIM11,SGSM3,TRAPPC9,PACSIN1,DEF6,PPARD,EEF1D,TSTA3,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,BOP1,VPS28,SND1,TOM1,CUL7,PPP1R14B,DNPH1,B4GALT1,PDGFRA,IL1R1,SECISBP2,PHF2,COL15A1,EPN1,SSC5D,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,EIPR1,RGS3,ZC3H12A,FIGNL1,PNKP,ZYX,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,PLEKHA4,MGLL,EHD2,FAM120B,KMT2E,ANXA5,KRT8,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,SERP2,PLXND1,EMILIN1,RNF220,DMAP1,SLC30A3,CIC,SNX17,H3F3B,PPM1G,UNK,PLCD1,DLEC1,CD79A,INSIG1,MYRIP,SEC13,SEPT9,OGG1,SERTAD1,TTC5,PSMC4,ARHGEF40,UCP2,METTL3,PHLDA1,BAIAP2,CEP131,CXXC5,INPPL1,LAMTOR1,NUMA1,P4HB,DND1,PYCR1,CCDC57,EIF4EBP1,ARAP3,DELE1,CAVIN3,RIC8A,GSR,ARHGAP22,DEAF1,HOXC4,ARHGAP33,LDLRAD3,TARBP2,KMT2B,AACS,SCARB1,NAT10,BCL2L1,ITGB7,ZNF740,PDE4D,SPRYD3,TNS2,EIF4B,RRS1,SWAP70,LRP3,RALY,PLEKHF1,ACSL1,ZBTB38,LSM6,CAPG,TNKS1BP1,PINX1,GREM1,KDM2B,DOK1,PDE3B,MCRS1,DCTN1,TKT,RAPSN,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,CHP1,TYRO3,SCD,YAF2,HTATIP2,PCIF1,PCBP4,LSP1,RAB35,KDM1B,CHCHD2,SLC35C2,RBM15B,TSPAN5,CISH,SRSF9,ST3GAL4,RNF19B,DCPS,IRX1,DHCR7,SELENOS,GSTO1,ITPRIP,RRP1B,ETFBKMT,MVK,BRD9,RIN3,STK32C,FABP3,ZCCHC17,NKAIN1,PDGFA,MMP14,C14orf93,CDK2AP2,PABPN1,GPX1,AJP,CORO6P,NCEE,CLCA,NCDN,ERBB,PLEKHA4,TS	yellow	VSMC_M3
GO:0048646	0.70	0.35	53	877	anatomical structure formation involved in morphogenesis	BP	1	CTHRC1,H2AFY,SCRIB,PLEC,B4GALT1,PDGFRA,COL15A1,EPN1,CNOT3,KLF4,HOXA1,ZC3H12A,EHD2,KRT8,PLXND1,EMILIN1,ARHGAP22,DEAF1,GREM1,KDM2B,PDE3B,CX3CL1,WNT10B,EGR3,DLL4,HTATIP2,IRX1,PDGFA,MMP14,GPX1,PLEKHO1,COL6A1,NECTIN1,ANPEP,PLA2G3,YJEFN3,AAMP,CD9,PKN1,CAPN2,MTHFR,ARMC5,AKT1,RFX2,MYDGF,SIRT6,JMJD8,SARS,TGFBR3,MIR214,TNFRSF12A,RNH1,DUSP5	yellow	VSMC_M3
GO:0010522	0.70	0.49	4	71	regulation of calcium ion transport into cytosol	BP	1	PDE4D,CX3CL1,GSTO1,CORO1A	yellow	VSMC_M3
GO:0030856	0.70	0.45	6	106	regulation of epithelial cell differentiation	BP	1	H2AFY,SPRED2,NUMA1,WNT10B,BAD,TNFRSF1A	yellow	VSMC_M3
GO:0043502	0.70	0.49	4	71	regulation of muscle adaptation	BP	1	KLF4,IGFBP5,TNFRSF1A,MIR214	yellow	VSMC_M3
GO:0016310	0.70	0.34	91	1440	phosphorylation	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,SNX9,CERK,FNIP1,PRR5,H2AFY,GUK1,PLEC,PPP1R14B,PDGFRA,SOCS5,KLF4,SPRED2,ZC3H12A,PNKP,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SEPHS1,GALK1,SERTAD1,OGDHL,TARBP2,PDE4D,ACSL1,TNKS1BP1,GREM1,CX3CL1,SOD1,DGKZ,CHP1,TYRO3,HTATIP2,CISH,AK2,MVK,STK32C,PAPSS1,PDGFA,CLCF1,QARS,TRIM27,LIMK1,RIPK3,PSTK,TNK2,SCYL1,MEX3B,MAP3K14,LIMD1,PHB2,BAD,CTDSP1,TNFRSF1A,WASHC1,FOXK1,PKN1,PIP4K2B,MAD2L2,CTBP1,ARHGEF2,MVP,PMVK,EEF2K,CDC37,CSK,AKT1,PGM1,SGK494,GIT1,MYDGF,MAP2K2,CACTIN,CDK11B,MKNK2,CSNK1G2,IRAK1,MIDN,STK11,TELO2,JMJD8,AK1,VAC14,TGFBR3,ERBB4,TRIB2	yellow	VSMC_M3
GO:0051402	0.70	0.41	12	198	neuron apoptotic process	BP	1	BCL2L1,KDM2B,RAPSN,CX3CL1,SOD1,TYRO3,GPX1,CLCF1,PLA2G3,CORO1A,NSMF,CDC34	yellow	VSMC_M3

GO:0009719	0.70	0.34	75	1202	response to endogenous stimulus	BP	1	ENPP1,CDK4,SREBF2,PPARD,PDGFRA,SOCS5,KLF4,SPRED2,ZYX,SLC9A3R1,EMILIN1,INSIG1,UCP2,BAIAP2,INPPL1,LAMTOR1,NUMA1,BCL2L1,TNS2,ACSL1,GREM1,PDE3B,WNT10B,SOD1,EGR3,DLL4,RAB35,SELENOS,FABP3,MMP14,CORO1B,PCK2,COL6A1,SLC26A6,PRMT2,CAPN10,RELA,IDH1,PHB2,IGFBP5,BAD,LAMTOR4,ARPC1B,CD9,PELP1,KLF3,PKN1,CAPN2,PIP4K2B,ARHGEF2,PER1,CORO1A,TRIM25,MTMR4,SMARCA4,CARM1,EEF2K,CSK,AKT1,HMGCS1,SAFB,SAFB2,SLC6A4,DHCR24,LDOC1,VASN,STK11,APRT,SLC27A4,TGFBR3,NDST1,ERBB4,JUND,NSMF,STUB1	yellow	VSMC_M3
GO:0098657	0.70	0.42	9	155	import into cell	BP	1	VPS28,ACSL1,SLC11A2,FABP3,SLC19A1,SPX,AKT1,SLC6A4,SLC27A4	yellow	VSMC_M3
GO:0072330	0.70	0.42	9	144	monocarboxylic acid biosynthetic process	BP	1	MGLL,INSIG1,FASN,SCD,PLA2G3,MID1IP1,ACLY,FADS2,FADS1	yellow	VSMC_M3
GO:0048468	0.71	0.33	97	1587	cell development	BP	1	SBF1,CTHRC1,HDAC10,PBX2,TRIM11,PACSIN1,SCRIB,PLEC,LGALS1,IFT27,CUL7,B4GALT1,PDGFRA,SECISBP2,COL15A1,KLF4,DBNL,TPBG,WDPCP,CCM2,SNX3,KRT8,SIX5,SLC9A3R1,PLXND1,UNK,METTL3,BAIAP2,CEP131,P4HB,DND1,YIF1B,FASN,DEAF1,ARHGAP33,BCL2L1,ITGB7,PDE4D,SLC11A2,CX3CL1,WNT10B,SOD1,DLL4,TYRO3,RAB35,IRX1,GPX1,NGEF,CLCF1,IGSF9,NECTIN1,LIMK1,SLC26A6,PRMT2,IQCG,PLA2G3,STMN3,PBX1,RELA,SCYL1,LIMD1,PBX4,BLOC1S4,C12orf57,BAD,CTDSP1,CD9,TNFRSF1A,C1QBP,RCC2,CNP,DBN1,NANOS3,CRABP2,TMEM79,S100A6,CARM1,EEF2K,ZNF830,AKT1,RFX2,GIT1,SIRT6,TJP3,ACAP3,ANAPC2,STK11,TGFBR3,NEGR1,ERBB4,TWF2,JUND,UNC13A,ZNF385A,NSMF,GBA2,MEIG1	yellow	VSMC_M3
GO:0051604	0.71	0.39	15	230	protein maturation	BP	1	LMF2,LDLRAD3,HM13,TSPAN5,MMP14,AIP,SEC11A,BAD,PLAU,SDE2,CAPN2,DHCR24,SPG7,STUB1,RCE1	yellow	VSMC_M3
GO:0051241	0.71	0.35	47	743	negative regulation of multicellular organismal process	BP	1	ENPP1,TRIM11,PDGFRA,EPN1,SSC5D,SOCS5,KLF4,SPRED2,ZC3H12A,ANXA5,RELB,EMILIN1,PDE4D,GREM1,PDE3B,CX3CL1,WNT10B,SOD1,DLL4,SELENOS,PDGFA,TRIM27,SPX,PLA2G3,PTPN23,KAT5,YJEFN3,PHB2,IGFBP5,CTDSP1,CD9,PLAU,TNFRSF1A,C1QBP,MAD2L2,CSK,KHSRP,GIT1,SLC6A4,CACTIN,VASN,STK11,SARS,MIR214,MIR155,PTPRR,TRIB2	yellow	VSMC_M3
GO:0050890	0.71	0.40	12	214	cognition	BP	1	ITPR3,TPBG,HOXA1,CIC,RIC8A,SLC11A2,ST3GAL4,TACO1,C12orf57,GIT1,SLC6A4,CTNS	yellow	VSMC_M3
GO:0042221	0.71	0.32	192	2921	response to chemical	BP	1	ENPP1,CD63,CDK4,BAG6,ATF6B,TTLL12,SREBF2,SQLE,ITPR3,HNRNPA0,GUK1,PPARD,RPL3,SCRIB,PLEC,LGALS1,MPST,SHARPIN,PDGFRA,IL1R1,SSC5D,SOCS5,KLF4,TPBG,PTGR1,SPRED2,ZC3H12A,ZYX,RCN3,KRT8,RELB,SLC9A3R1,SERP2,PLXND1,EMILIN1,TMUB1,DMAP1,SLC30A3,INSIG1,OGG1,UCP2,SEL1L2,METTL3,BAIAP2,INPPL1,LAMTOR1,NUMA1,P4HB,PYCR1,FASN,RAB20,SMOX,EIF4EBP1,GSR,ARHGAP33,AACS,SCARB1,HM13,BCL2L1,TNS2,SWAP70,ACSL1,SLC11A2,GREM1,DOK1,AQP5,PDE3B,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,SCD,LSP1,RAB35,CHCHD2,SRSF9,DCPS,SELENOS,GSTO1,RIN3,FABP3,PDGFA,MMP14,PABPN1,GPX1,AIP,CORO1B,CLCF1,IGSF9,SYT12,PCK2,COL6A1,IMPDH2,NECTIN1,SLC26A6,PRMT2,SPX,UQCRC1,RIPK3,CAPN10,PPOX,KAT5,RELA,SIPA1,MGST3,IDH1,ARNT2,SMARCB1,ATIC,TXNRD2,PHB2,IGFBP5,BAD,LAMTOR4,OTUB1,HSD17B1,LETM1,LGALS3,ARPC1B,CD9,PLAU,TNFRSF1A,C1QBP,UBXN1,ANXA11,CNP,PRXL2A,PELP1,KLF3,PKN1,CAPN2,PALM3,MTHFR,PIP4K2B,ARHGEF2,PER1,CORO1A,PMVK,TUFM,TRIM25,MTMR4,S100A16,SMARCA4,CARM1,EEF2K,CDC37,C19orf66,CSK,RBM22,AKT1,HMGCS1,KHSRP,SAFB,SAFB2,GIT1,SLC6A4,DHCR24,BLMH,LDOC1,CACTIN,VASN,TRAP1,EHMT1,MKNK2,IRAK1,MBD3,MAN1B1,ATP5F1D,STK11,CARD9,APRT,SLC27A4,TGFBR3,TRADD,MIR214,RF00024,NDST1,ERBB4,TWF2,JUND,LOXL1,JAGN1,COL6A2,NSMF,CDC34,FBXO6,OSER1,STUB1,NSMCE3,CCDC115	yellow	VSMC_M3
GO:0060349	0.71	0.48	4	76	bone morphogenesis	BP	1	NAB2,INSIG1,INPPL1,MMP14	yellow	VSMC_M3
GO:0030901	0.71	0.48	4	69	midbrain development	BP	1	KDM2B,CNP,GLUD1,NDST1	yellow	VSMC_M3
GO:0002377	0.71	0.46	5	81	immunoglobulin production	BP	1	SWAP70,CLCF1,PHB2,PKN1,MAD2L2	yellow	VSMC_M3
GO:0098813	0.71	0.39	14	230	nuclear chromosome segregation	BP	1	DCTN2,BAG6,NCAPH2,H2AFY,NUMA1,RRS1,PINX1,NUDC,PHB2,RCC2,EML3,MAD1L1,MAD2L2,MIS12	yellow	VSMC_M3
GO:0001841	0.71	0.46	5	92	neural tube formation	BP	1	CTHRC1,SCRIB,DEAF1,KDM2B,MTHFR	yellow	VSMC_M3
GO:0016331	0.71	0.43	7	127	morphogenesis of embryonic epithelium	BP	1	CTHRC1,SCRIB,DEAF1,GREM1,KDM2B,IRX1,MTHFR	yellow	VSMC_M3
GO:0051656	0.71	0.37	20	334	establishment of organelle localization	BP	1	DCTN2,SCRIB,SLC9A3R1,NUMA1,RRS1,PINX1,DCTN1,CHP1,NUDC,PLA2G3,BLOC1S4,NUP88,EML3,MAD1L1,SYNE3,MYO19,AP3D1,STK11,TMEM201,MIS12	yellow	VSMC_M3
GO:0042981	0.71	0.33	72	1092	regulation of apoptotic process	BP	1	CDK4,SQSTM1,BAG6,FNIP1,PPARD,SCRIB,LGALS1,B4GALT1,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,SLC9A3R1,OGG1,UCP2,PHLDA1,P4HB,BCL2L1,PLEKHF1,GREM1,KDM2B,RAPSN,CX3CL1,WNT10B,SOD1,EGR3,CCAR2,TYRO3,HTATIP2,SELENOS,ITPRIP,RRP1B,GPX1,CLCF1,QARS,PRMT2,RIPK3,TWIST2,CAPN10,BRMS1,PLA2G3,RELA,ARNT2,PHB2,BAD,LGALS3,TNFRSF1A,C1QBP,USP27X,CAPN2,NANOS3,DFFA,ARHGEF2,CORO1A,EEF2K,AATF,ZNF830,AKT1,DHCR24,MYDGF,TRAP1,MNT,CARD9,SLC27A4,TRADD,TNFRSF12A,PTMA,ZNF385A,TXNDC12,NSMF,CDC34	yellow	VSMC_M3
GO:0001935	0.71	0.43	7	123	endothelial cell proliferation	BP	1	SCARB1,EGR3,DLL4,MMP14,AKT1,MYDGF,SIRT6	yellow	VSMC_M3
GO:0006323	0.71	0.43	7	119	DNA packaging	BP	1	NCAPH2,H2AFY,PHF2,H3F3B,BANF1,H3F3A,UBN1	yellow	VSMC_M3
GO:0007548	0.71	0.39	12	206	sex differentiation	BP	1	PDGFRA,BCL2L1,SOD1,TYRO3,MMP14,PBX1,IDH1,SGPL1,ZNF830,HMGCS1,SAFB2,DHCR24	yellow	VSMC_M3
GO:0002444	0.71	0.47	4	70	myeloid leukocyte mediated immunity	BP	1	KMT2E,PLA2G3,CARD9,JAGN1	yellow	VSMC_M3
GO:0042552	0.72	0.44	6	109	myelination	BP	1	NAB2,PLEC,SOD1,CD9,AKT1,MARVELD1	yellow	VSMC_M3

GO:0002764	0.72	0.37	17	278	immune response-regulating signaling pathway	BP	1	BAG6,ZC3H12A,CD79A,PDE4D,DGKZ,TYRO3,LIMK1,RELA,PHB2,IFI35,LGALS3,C1QBP,CD276,CSK,CACTIN,IRAK1,STK11	yellow	VSMC_M3
GO:0051640	0.72	0.36	27	447	organelle localization	BP	1	ESYT1,DCTN2,SCRIB,SLC9A3R1,LAMTOR1,NUMA1,RRS1,PINX1,DCTN1,CHP1,NUDC,PLA2G3,BLOC1S4,NUP88,EML3,MAD1L1,STX10,SYNE3,MYO19,PACS2,RAB34,AP3D1,STK11,TMEM201,RABEPK,MIS12,UNC13A	yellow	VSMC_M3
GO:0001655	0.72	0.38	16	283	urogenital system development	BP	1	BAG6,MPST,IFT27,PDGFRA,WDPCP,PLXND1,SNX17,TNS2,GREM1,IRX1,PDGFA,PBX1,SGPL1,AMER1,STK11,ERBB4	yellow	VSMC_M3
GO:0031497	0.72	0.45	5	84	chromatin assembly	BP	1	H2AFY,PHF2,H3F3B,H3F3A,UBN1	yellow	VSMC_M3
GO:0001656	0.72	0.47	4	74	metanephros development	BP	1	PDGFRA,GREM1,IRX1,PDGFA	yellow	VSMC_M3
GO:0048167	0.72	0.41	8	143	regulation of synaptic plasticity	BP	1	SQSTM1,ITPR3,BAIAP2,CX3CL1,SYT12,DBN1,ANAPC2,NSMF	yellow	VSMC_M3
GO:1901657	0.72	0.47	4	60	glycosyl compound metabolic process	BP	1	DNPH1,ATIC,APRT,GBA2	yellow	VSMC_M3
GO:0120034	0.72	0.45	5	92	positive regulation of plasma membrane bounded cell projection assembly	BP	1	SEPT9,WASHC1,DOCK11,TWF2,CDC42EP5	yellow	VSMC_M3
GO:2000145	0.72	0.34	47	772	regulation of cell motility	BP	1	PPARD,TSTA3,PDGFRA,IL1R1,KLF4,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,SCARB1,SWAP70,GREM1,CX3CL1,DLL4,ST3GAL4,RIN3,PDGFA,MMP14,CORO1B,ARPIN,RIPK3,TWIST2,PTPN23,RHOC,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,CORO1A,AKT1,TRADD,MIR214,ERBB4,PTPRR,CAVIN1,NSMF,GLIPR2	yellow	VSMC_M3
GO:0071478	0.72	0.40	9	150	cellular response to radiation	BP	1	EEF1D,FIGNL1,METTL3,BCL2L1,TNKS1BP1,ACTR5,SDE2,STK11,NSMCE3	yellow	VSMC_M3
GO:0048041	0.72	0.47	4	81	focal adhesion assembly	BP	1	WDPCP,GREM1,MMP14,RCC2	yellow	VSMC_M3
GO:0006952	0.72	0.33	62	949	defense response	BP	1	TTLL12,HNRNPA0,TRIM11,PPARD,SHARPIN,PPP1R14B,B4GALT1,IL1R1,SSC5D,SOCS5,KLF4,ZC3H12A,ZYX,MGLL,RELB,DLEC1,OGG1,METTL3,RAB20,SIGLEC1,TARBP2,BCL2L1,CX3CL1,SOD1,TYRO3,LSP1,RNF19B,SELENOS,MVK,GPX1,TRIM27,SLC26A6,RIPK3,PSMB4,TNK2,PLA2G3,RELA,SCYL1,MAP3K14,PHB2,IFI35,LGALS3,TNFRSF1A,C1QBP,TBKBP1,ARHGEF2,ARMC5,PER1,CORO1A,TRIM25,CDC37,C19orf66,MID2,AKT1,GIT1,CACTIN,IRAK1,C8G,CARD9,TRADD,NDST1,JAGN1	yellow	VSMC_M3
GO:0048731	0.72	0.31	226	3556	system development	BP	1	ENPP1,NAB2,CDK4,BAG6,NCAPH2,CTHRC1,HDAC10,FNIP1,PBX2,PDLIM4,RING1,H2AFY,TRIM11,TRAPPC9,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,CUL7,B4GALT1,PDGFRA,SECISBP2,PHF2,COL15A1,EPN1,COL19A1,SOCS5,TTC7A,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,ZC3H12A,RCN3,SNX3,PLEKHA4,KMT2E,KRT8,SIX5,RELB,SLC9A3R1,PLXND1,EMILIN1,RNF220,PAFAH1B3,CIC,SNX17,UNK,CD79A,INSIG1,UCP2,METTL3,BAIAP2,INPPL1,NUMA1,FASN,EIF4EBP1,RIC8A,ARHGAP22,DEAF1,TBCB,HOXC4,LRIG1,ARHGAP33,AACS,BCL2L1,TNS2,SWAP70,CAPG,SLC11A2,MMP24,GREM1,KDM2B,AQP5,PDE3B,DCTN1,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,TYRO3,HTATIP2,RAB35,APBA2,IRX1,SDHA,PAPSS1,PDGFA,MMP14,GPX1,NGEF,HCCS,CLCF1,IGSF9,QARS,LRFN4,PCK2,IMPDH2,PIR,NECTIN1,ANPEP,LIMK1,THOC5,RIPK3,EXTL1,PLA2G3,STMN3,SART1,PBX1,RELA,SCYL1,IDH1,ARNT2,VPS51,SGPL1,SMARCB1,PBX4,YJEFN3,ATIC,BLOC1S4,MEF2B,PHB2,NDP,IGFBP5,C12orf57,BAD,AAMP,CTDSP1,HSD17B1,CD9,TNFRSF1A,TEAD4,AIMP2,CHERP,EVC,CNP,PRXL2A,KRT10,GLUD1,FOXK1,CASP14,PKN1,DBN1,MAD1L1,AMER1,MTHFR,MAD2L2,PRR14,CRABP2,TMEM79,ARHGEF2,ARMC5,MTX1,IRF2BPL,SLC39A1,S100A4,S100A6,SMARCA4,CARM1,EEF2K,EML1,CSK,ZNF521,TTC39C,ZNF358,DOCK11,ZNF830,AKT1,COPRS,HMGCS1,SAFB2,GIT1,SLC6A4,DHCR24,MYDGF,SIRT6,PPL,NSDHL,HMG20B,VASN,ACAP3,CTNS,AP3D1,MKNK2,ANAPC2,MBD3,STK11,TAZ,JMJD8,SPG7,SARS,APRT,GTF3C5,SLC27A4,TGFBR3,TRADD,NEGR1,MIR214,NDST1,TNFRSF12A,ERBB4,TWF2,LOXL1,KLF13,RNH1,JAGN1,IGSF8,ELN,UNC13A,ZNF385A,NSMF,N	yellow	VSMC_M3
GO:0034612	0.72	0.39	11	181	response to tumor necrosis factor	BP	1	SHARPIN,ZC3H12A,KRT8,CX3CL1,PCK2,RELA,TNFRSF1A,ARHGEF2,AKT1,CACTIN,TRADD	yellow	VSMC_M3
GO:0006413	0.72	0.43	6	99	translational initiation	BP	1	METTL3,EIF4EBP1,EIF4B,EIF3A,EIF3G,PAIP1	yellow	VSMC_M3
GO:0031532	0.72	0.44	5	94	actin cytoskeleton reorganization	BP	1	PDLIM4,PLEC,PDGFRA,BAIAP2,CAPN10	yellow	VSMC_M3
GO:0060541	0.72	0.40	9	163	respiratory system development	BP	1	BAG6,PDGFRA,WDPCP,RCN3,EIF4EBP1,PDGFA,MMP14,IGFBP5,AIMP2	yellow	VSMC_M3
GO:0007017	0.73	0.33	44	715	microtubule-based process	BP	1	DCTN2,SPAG1,IFT27,CUL7,FIGNL1,SLC9A3R1,CEP131,NUMA1,YIF1B,CCDC57,NAT10,DCTN1,SOD1,CHP1,CDK2AP2,SRRD,CLIP2,PCNT,NUDC,IQCG,PLA2G3,STMN3,SAC3D1,MID1IP1,BLOC1S4,KIAA0753,CNP,EML3,ARHGEF2,RANGRF,EML1,GIT1,AP3D1,SSNA1,STK11,TMEM201,GAS8,SPG7,NTMT1,WDR34,MAP7D1,GBA2,TUBGCP2,MEIG1	yellow	VSMC_M3
GO:0006334	0.73	0.46	4	68	nucleosome assembly	BP	1	H2AFY,H3F3B,H3F3A,UBN1	yellow	VSMC_M3
GO:0030323	0.73	0.40	8	145	respiratory tube development	BP	1	BAG6,PDGFRA,RCN3,EIF4EBP1,PDGFA,MMP14,IGFBP5,AIMP2	yellow	VSMC_M3
GO:0012501	0.73	0.31	97	1474	programmed cell death	BP	1	CDK4,SQSTM1,BAG6,FNIP1,PPARD,SCRIB,LGALS1,SHARPIN,B4GALT1,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,KRT8,SLC9A3R1,OGG1,UCP2,PHLDA1,P4HB,DELE1,BCL2L1,PLEKHF1,GREM1,KDM2B,RAPSN,CX3CL1,WNT10B,SOD1,EGR3,CCAR2,TYRO3,HTATIP2,DCPS,SELENOS,ITPRIP,RRP1B,GPX1,CLCF1,QARS,PRMT2,RIPK3,TWIST2,CAPN10,BRMS1,PLA2G3,RELA,ARNT2,ZDHHC3,SGPL1,CHCHD10,ZNF385B,PHB2,BAD,LGALS3,TNFRSF1A,C1QBP,AIMP2,USP27X,CASP14,PKN1,CAPN2,SLTM,NANOS3,BCL7C,DFFA,TMEM79,ARHGEF2,PLEKHO2,CORO1A,EEF2K,AATF,ATG3,ZNF830,AKT1,PACS2,ALKBH7,DHCR24,MYDGF,CDK11B,HIC1,TRAP1,MNT,MKNK2,STK11,CARD9,SPG7,SLC27A4,TRADD,MIR214,TNFRSF12A,ERBB4,PTMA,ZNF385A,TXNDC12,NSMF,CDC34	yellow	VSMC_M3
GO:0060993	0.73	0.45	4	77	kidney morphogenesis	BP	1	GREM1,IRX1,PBX1,ERBB4	yellow	VSMC_M3
GO:0009408	0.73	0.43	5	84	response to heat	BP	1	SOD1,AKT1,IRAK1,IER5,STUB1	yellow	VSMC_M3

GO:0050776	0.73	0.33	34	538	regulation of immune response	BP	1	BAG6,TTLL12,IL1R1,SOCS5,ZC3H12A,CD79A,METTL3,TARBP2,PDE4D,DGKZ,TYRO3,SELENOS,GPX1,CLCF1,TRIM27,LIMK1,RIPK3,PSMB4,PLA2G3,RELA,PHB2,IFI35,LGALS3,C1QBP,PKN1,MAD2L2,CDC37,CD276,CSK,CACTIN,IRAK1,C8G,STK11,CARD9	yellow	VSMC_M3
GO:0031058	0.73	0.45	4	75	positive regulation of histone modification	BP	1	NELFE,KMT2E,SMARCB1,CTBP1	yellow	VSMC_M3
GO:0061138	0.73	0.40	8	147	morphogenesis of a branching epithelium	BP	1	PLXND1,GREM1,DLL4,PDGFA,MMP14,PBX1,PHB2,SIRT6	yellow	VSMC_M3
GO:0007275	0.73	0.29	243	3815	multicellular organism development	BP	1	ENPP1,NAB2,CDK4,BAG6,NCAPH2,CTHRC1,HDAC10,FNIP1,PBX2,PDLIM4,RING1,H2AFY,TRIM11,TRAPPC9,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,CUL7,B4GALT1,PDGFRA,SECISBP2,PHF2,COL15A1,EPN1,COL19A1,SOCS5,TTC7A,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,ZC3H12A,RCN3,SNX3,PLEKHA4,KMT2E,KRT8,SIX5,RELB,SLC9A3R1,PLXND1,EMILIN1,RNF220,PAFAH1B3,CIC,SNX17,UNK,CD79A,INSIG1,PSMC4,UCP2,METTL3,BAIAP2,INPPL1,NUMA1,FASN,RPL29,EIF4EBP1,RIC8A,ARHGAP22,DEAF1,TBCB,HOXC4,LRIG1,ARHGAP33,AACS,HM13,BCL2L1,TNS2,SWAP70,CAPG,SLC11A2,MMP24,GREM1,KDM2B,AQP5,PDE3B,DCTN1,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,TYRO3,HTATIP2,RAB35,APBA2,IRX1,SDHA,PAPSS1,PDGFA,MMP14,GPX1,NGEF,HCCS,CLCF1,IGSF9,QARS,LRFN4,PCK2,COL6A1,IMPDH2,PIR,NECTIN1,ANPEP,LIMK1,THOC5,RIPK3,EXTL1,PLA2G3,STMN3,SART1,PBX1,RELA,SCYL1,IDH1,ARNT2,VPS51,SGPL1,SMARCB1,PBX4,YJEFN3,ATIC,BLOC1S4,MEF2B,PHB2,NDP,IGFBP5,C12orf57,BAD,AAMP,CTDSP1,HSD17B1,CD9,TNFRSF1A,TEAD4,C1QBP,AIMP2,CHERP,EVC,CNP,PRXL2A,KRT10,GLUD1,FOXK1,CASP14,KLF3,PKN1,DBN1,CAPN2,MAD1L1,AMER1,MTHFR,MAD2L2,PRR14,CRABP2,TMEM79,ARHGEF2,ARMC5,MTX1,IRF2BPL,SLC39A1,S100A4,S100A6,SMARCA4,CARM1,EEF2K,EML1,AATF,CSK,ZNF521,TTC39C,ZNF358,DOCK11,ZNF830,AKT1,COPRS,HMGCS1,SAFB2,GIT1,SLC6A4,DHCR24,MYDGF,SIRT6,PPL,NSDHL,HMG20B,SLC35E2B,VASN,ACAP3,MNT,CTNS,EHMT1,AP3D1,MKNK2,ANAPC2,MBD3,STK11,TAZ,JMJD8,SPG7,SARS,APRT,GTF3C5,POMT1,SLC27A4,TGFBR3,TRADD,NEGR1,MIR214,ND	yellow	VSMC_M3
GO:0000724	0.73	0.40	7	124	double-strand break repair via homologous recombination	BP	1	FIGNL1,MAD2L2,PPP4C,SLX1A,CXorf57,SIRT6,NABP2	yellow	VSMC_M3
GO:0031328	0.73	0.30	96	1503	positive regulation of cellular biosynthetic process	BP	1	CDK4,SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,RPS9,KLF4,HOXA1,ZC3H12A,PNKP,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,METTL3,DEAF1,HOXC4,KMT2B,SCARB1,NAT10,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,RRP1B,FABP3,AIP,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,PLA2G3,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,NDP,SSBP4,MPV17L2,BUD31,TNFRSF1A,C1QBP,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,CAPN2,MAD2L2,ARHGEF2,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,AKT1,BRF1,PAIP1,GTF2F1,MYDGF,MAP2K2,AP3D1,TAZ,MED16,POMT1,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3
GO:0006941	0.73	0.40	7	128	striated muscle contraction	BP	1	ZC3H12A,PDE4D,GSTO1,SCN4A,C12orf57,RANGRF,TAZ	yellow	VSMC_M3
GO:0044092	0.73	0.31	52	806	negative regulation of molecular function	BP	1	FNIP1,H2AFY,PLEC,PPP1R14B,HSPBP1,SOCS5,KLF4,SPRED2,ZC3H12A,MICAL1,ANXA5,SLC9A3R1,TARBP2,PINX1,CCAR2,CHP1,GSTO1,ITPRIP,RRP1B,ETFBKMT,GPX1,AIP,QARS,TRIM27,LIMK1,PRMT2,BRMS1,TNK2,PHB2,PPP1R35,LGALS3,UBXN1,WASHC1,RCC2,CCDC22,PKN1,PIP4K2B,MAD2L2,DFFA,MVP,RPL37,CSK,AKT1,GTF2F1,DHCR24,CACTIN,IRAK1,MIDN,SLC27A4,RNH1,TRIB2,STUB1	yellow	VSMC_M3
GO:0048593	0.74	0.43	5	96	camera-type eye morphogenesis	BP	1	RING1,KDM2B,AQP5,NECTIN1,C12orf57	yellow	VSMC_M3
GO:0045597	0.74	0.32	39	639	positive regulation of cell differentiation	BP	1	CTHRC1,H2AFY,PPARD,CUL7,SOCS5,DBNL,ZC3H12A,WDFY2,PLXND1,BAIAP2,NUMA1,P4HB,LRP3,GREM1,CX3CL1,WNT10B,EGR3,MMP14,CLCF1,LIMK1,PLA2G3,SART1,RELA,BAD,C1QBP,DBN1,CRABP2,ARHGEF2,CARM1,EEF2K,AKT1,HMG20B,AP3D1,ANAPC2,STK11,TWF2,JUND,ZNF385A,GLIPR2	yellow	VSMC_M3
GO:0035107	0.74	0.41	6	115	appendage morphogenesis	BP	1	PBX2,WDPCP,GREM1,PBX1,CRABP2,ZNF358	yellow	VSMC_M3
GO:0035108	0.74	0.41	6	115	limb morphogenesis	BP	1	PBX2,WDPCP,GREM1,PBX1,CRABP2,ZNF358	yellow	VSMC_M3
GO:0000077	0.74	0.41	6	105	DNA damage checkpoint signaling	BP	1	CCAR2,THOC5,BABAM1,SDE2,ZNF830,FBXO6	yellow	VSMC_M3
GO:0021915	0.74	0.40	7	130	neural tube development	BP	1	CTHRC1,SCRIB,RNF220,DEAF1,KDM2B,MTHFR,ZNF358	yellow	VSMC_M3
GO:0015931	0.74	0.37	11	181	nucleobase-containing compound transport	BP	1	SEC13,SLC35C2,RBM15B,PABPN1,SLC19A1,THOC5,THOC3,NUP88,MVP,KHSRP,RBM8A	yellow	VSMC_M3
GO:0007338	0.74	0.42	5	86	single fertilization	BP	1	SPAG1,B4GALT1,GNPDA1,CD9,IGSF8	yellow	VSMC_M3
GO:0120254	0.74	0.42	5	86	olefinic compound metabolic process	BP	1	MGLL,GPX1,HSD17B1,FADS2,FADS1	yellow	VSMC_M3
GO:0055082	0.74	0.32	34	564	cellular chemical homeostasis	BP	1	ENPP1,ITPR3,PPARD,LGALS1,PDGFRA,TTC7A,SLC9A3R1,SLC30A3,UCP2,RAB20,AACS,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,CHP1,GSTO1,PCK2,SLC26A6,SMARCB1,BAD,LETM1,CHERP,CCDC22,FOXK1,CORO1A,TSPOAP1,SMARCA4,ANKRD9,PACS2,AP3D1,JAGN1,CCDC115	yellow	VSMC_M3
GO:0050680	0.74	0.41	6	108	negative regulation of epithelial cell proliferation	BP	1	PPARD,WNT10B,DLL4,PHB2,STK11,TGFBR3	yellow	VSMC_M3
GO:0008584	0.74	0.41	6	111	male gonad development	BP	1	PDGFRA,BCL2L1,MMP14,SGPL1,HMGCS1,SAFB2	yellow	VSMC_M3
GO:0040012	0.74	0.31	48	796	regulation of locomotion	BP	1	PPARD,TSTA3,PDGFRA,IL1R1,KLF4,TPBG,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,SCARB1,SWAP70,GREM1,CX3CL1,DLL4,ST3GAL4,RIN3,PDGFA,MMP14,CORO1B,ARPIN,RIPK3,TWIST2,PTPN23,RHOC,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,CORO1A,AKT1,TRADD,MIR214,ERBB4,PTPRR,CAVIN1,NSMF,GLIPR2	yellow	VSMC_M3
GO:0034763	0.74	0.42	5	88	negative regulation of transmembrane transport	BP	1	ENPP1,SLC9A3R1,SELENOS,GSTO1,AKT1	yellow	VSMC_M3
GO:0046661	0.74	0.39	7	128	male sex differentiation	BP	1	PDGFRA,BCL2L1,MMP14,SGPL1,HMGCS1,SAFB2,DHCR24	yellow	VSMC_M3
GO:0006869	0.74	0.35	16	273	lipid transport	BP	1	PQLC1,ESYT1,SREBF2,PPARD,PLEKHA8,LAMTOR1,SCARB1,ACSL1,FABP3,SPX,PLA2G3,VPS51,YJEFN3,SLC27A3,AKT1,SLC27A4	yellow	VSMC_M3

GO:0051129	0.74	0.32	34	569	negative regulation of cellular component organization	BP	1	PACSIN1,LGALS1,PHF2,EMILIN1,EIF4EBP1,NAT10,BCL2L1,SWAP70,CAPG,PINX1,PACSIN3,RIN3,MMP14,GPX1,CORO1B,NGEF,ARPIN,PFDN2,MID1IP1,PEX5,LGALS3,TNFRSF1A,RCC2,MAD1L1,MAD2L2,ARHGEF2,CORO1A,SLX1A,CARM1,AKT1,ANKRD13B,AURKAIP1,MIR214,TWF2	yellow	VSMC_M3
GO:0030968	0.74	0.44	4	69	endoplasmic reticulum unfolded protein response	BP	1	ATF6B,SERP2,SELENOS,STUB1	yellow	VSMC_M3
GO:0065007	0.74	0.28	559	8375	biological regulation	BP	1	ENPP1,PQLC1,CD63,NAB2,NHP2,CDK4,CTDSP2,RUFY1,SQSTM1,GNL1,ZNF608,BAG6,SBF1,SNX9,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,SQLE,TXNDC15,H2AFY,ITPR3,HNRNPA0,TRIM11,SGSM3,TRAPPC9,PACSIN1,DEF6,PPARD,EEF1D,TSTA3,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,BOP1,VPS28,SND1,TOM1,CUL7,PPP1R14B,DNPH1,B4GALT1,AARS2,PDGFRA,IL1R1,SECISBP2,PHF2,COL15A1,EPN1,SSC5D,HSPBP1,SOCS5,TTC7A,RPS9,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,EIPR1,RGS3,ZC3H12A,FIGNL1,PNKP,CPT1C,ZYX,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,PLEKHA4,MGLL,EHD2,FAM120B,KMT2E,ANXA5,KRT8,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,SERP2,PLXND1,EMILIN1,RNF220,DMAP1,SLC30A3,CIC,SNX17,H3F3B,PPM1G,UNK,PLCD1,DLEC1,CD79A,INSIG1,MYRIP,SEC13,SEPT9,OGG1,SERTAD1,TTC5,PSMC4,ARHGEF40,UCP2,METTL3,PHLDA1,BAIAP2,CEP131,CXXC5,INPPL1,LAMTOR1,NUMA1,P4HB,DND1,PYCR1,CCDC57,RAB20,EIF4EBP1,ARAP3,DELE1,CAVIN3,RIC8A,GSR,ARHGAP22,DEAF1,HOXC4,ARHGAP33,LDLRAD3,TARBP2,KMT2B,AACS,SCARB1,NAT10,HM13,BCL2L1,ITGB7,ZNF740,PDE4D,SPRYD3,TNS2,EIF4B,RRS1,SWAP70,LRP3,RALY,PLEKHF1,ACSL1,ZBTB38,LSM6,CAPG,SLC11A2,TNKS1BP1,MMP24,PINX1,GREM1,KDM2B,DOK1,AQP5,PDE3B,MCRS1,DCTN1,TKT,RAPSN,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,HPS1,DLL4,CHP1,TYRO3,SCD,YAF2,HTATIP2,PCIF1,PCBP4,LSP1,RAB35,KDM1B,CHCHD2,SLC35C2,RBM15B,TSPAN5,CISH,SRSF9,TMEM183A,ST3GAL4,RNF19B,DCPS,IRX1,DHCR7,SELENOS,GSTO1,ITPRIP,RRP1B,ETFBKMT,MVK,BR	yellow	VSMC_M3
GO:0019751	0.74	0.42	5	88	polyol metabolic process	BP	1	NUDT3,GALK1,PCK2,ISYNA1,PGP	yellow	VSMC_M3
GO:0003018	0.75	0.36	11	200	vascular process in circulatory system	BP	1	PPARD,PLEC,SLC9A3R1,LRP3,SOD1,GPX1,SLC19A1,AKT1,SLC6A4,TJP3,SLC27A4	yellow	VSMC_M3
GO:0051346	0.75	0.35	15	242	negative regulation of hydrolase activity	BP	1	FNIP1,KLF4,MICAL1,CHP1,RRP1B,GPX1,AIP,PPP1R35,LGALS3,UBXN1,RCC2,DFFA,AKT1,DHCR24,SLC27A4	yellow	VSMC_M3
GO:0046546	0.75	0.40	6	112	development of primary male sexual characteristics	BP	1	PDGFRA,BCL2L1,MMP14,SGPL1,HMGCS1,SAFB2	yellow	VSMC_M3
GO:0051301	0.75	0.32	32	525	cell division	BP	1	CDK4,SNX9,PLEC,CUL7,SEPT9,NUMA1,BCL2L1,DCTN1,RAB35,PDGFA,CDK2AP2,NUDC,CEP164,RHOC,ALKBH4,SAC3D1,BABAM1,ANXA11,RCC2,EML3,SDE2,MAD1L1,MAD2L2,ARHGEF2,MYO19,AATF,ZNF830,SNX18,GIT1,ANAPC2,TAZ,MIS12	yellow	VSMC_M3
GO:2001235	0.75	0.40	6	98	positive regulation of apoptotic signaling pathway	BP	1	SLC9A3R1,PLEKHF1,SOD1,RIPK3,BAD,TNFRSF12A	yellow	VSMC_M3
GO:0007098	0.75	0.40	6	115	centrosome cycle	BP	1	CEP131,CCDC57,NAT10,DCTN1,SAC3D1,KIAA0753	yellow	VSMC_M3
GO:0042129	0.75	0.40	6	102	regulation of T cell proliferation	BP	1	SCRIB,RIPK3,LGALS3,MAD1L1,CORO1A,CD276	yellow	VSMC_M3
GO:0002687	0.75	0.40	6	101	positive regulation of leukocyte migration	BP	1	IL1R1,SWAP70,CX3CL1,MMP14,LGALS3,C1QBP	yellow	VSMC_M3
GO:0030010	0.75	0.40	6	123	establishment of cell polarity	BP	1	SCRIB,WDPCP,SLC9A3R1,NUMA1,DCTN1,STK11	yellow	VSMC_M3
GO:0000725	0.75	0.38	7	126	recombinational repair	BP	1	FIGNL1,MAD2L2,PPP4C,SLX1A,CXorf57,SIRT6,NABP2	yellow	VSMC_M3
GO:2000377	0.75	0.38	7	120	regulation of reactive oxygen species metabolic process	BP	1	ZC3H12A,SOD1,RIPK3,AATF,AKT1,TRAP1,CTNS	yellow	VSMC_M3
GO:0051960	0.75	0.33	19	344	regulation of nervous system development	BP	1	TRIM11,CUL7,DBNL,TPBG,PLXND1,BAIAP2,CX3CL1,DLL4,CLCF1,LIMK1,RELA,CTDSP1,DBN1,CRABP2,EEF2K,AKT1,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0016079	0.75	0.42	4	79	synaptic vesicle exocytosis	BP	1	SCRIB,SYT12,GIT1,UNC13A	yellow	VSMC_M3
GO:0007179	0.75	0.37	8	156	transforming growth factor beta receptor signaling pathway	BP	1	SPRED2,ZYX,EMILIN1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0046879	0.75	0.35	12	206	hormone secretion	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,PLA2G3,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0043271	0.75	0.40	5	93	negative regulation of ion transport	BP	1	SLC9A3R1,PACSIN3,GSTO1,TRIM27,AKT1	yellow	VSMC_M3
GO:0009611	0.75	0.32	25	422	response to wounding	BP	1	PPARD,SCRIB,PLEC,LGALS1,B4GALT1,PDGFRA,KLF4,ANXA5,SCARB1,CX3CL1,SOD1,DGKZ,TYRO3,ST3GAL4,PDGFA,GPX1,CORO1B,RHOC,BLOC1S4,PHB2,CD9,PLAU,GIT1,PPL,TNFRSF12A	yellow	VSMC_M3
GO:0009612	0.75	0.36	10	176	response to mechanical stimulus	BP	1	PLEC,MMP14,RELA,TMEM120A,MAP3K14,BAD,TNFRSF1A,AKT1,PPL,JUND	yellow	VSMC_M3
GO:0007568	0.75	0.33	15	252	aging	BP	1	OGG1,UCP2,CX3CL1,SOD1,KAT5,RELA,IGFBP5,CNP,CARM1,AKT1,MNT,IRAK1,MBD3,RF00024,JUND	yellow	VSMC_M3
GO:0050793	0.75	0.28	115	1852	regulation of developmental process	BP	1	ENPP1,NAB2,CDK4,BAG6,CTHRC1,FNIP1,H2AFY,TRIM11,PACSIN1,PPARD,CUL7,PDGFRA,EPN1,SOCS5,CNOT3,KLF4,DBNL,TPBG,WDPCP,SPRED2,ZC3H12A,PLEKHA4,EHD2,WDFY2,SLC9A3R1,PLXND1,EMILIN1,INSIG1,METTL3,BAIAP2,NUMA1,P4HB,ARHGAP33,LRP3,GREM1,KDM2B,PDE3B,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,HTATIP2,PDGFA,MMP14,CORO1B,NGEF,CLCF1,PLEKHO1,ARPIN,LIMK1,TWIST2,PLA2G3,SART1,CCDC85B,PBX1,RELA,RHOC,FMNL1,LIMD1,SGPL1,YJEFN3,PHB2,IGFBP5,BAD,CTDSP1,EID1,TNFRSF1A,C1QBP,TAF6L,RCC2,PRXL2A,KRT10,PKN1,DBN1,CAPN2,MAD2L2,CRABP2,TMEM79,ARHGEF2,CORO1A,CARM1,SYNE3,EEF2K,MYO19,INF2,AKT1,SLC6A4,MYDGF,SIRT6,HMG20B,VASN,EHMT1,AP3D1,ANAPC2,STK11,JMJD8,SARS,TGFBR3,TRADD,MIR214,RF00024,ERBB4,TWF2,JUND,KLF13,RNH1,FADS1,UNC13A,TRIB2,ZNF385A,CDC42EP5,NSMF,GLIPR2	yellow	VSMC_M3
GO:0001938	0.76	0.42	4	78	positive regulation of endothelial cell proliferation	BP	1	EGR3,AKT1,MYDGF,SIRT6	yellow	VSMC_M3
GO:0033138	0.76	0.42	4	74	positive regulation of peptidyl-serine phosphorylation	BP	1	FNIP1,TNKS1BP1,MAD2L2,AKT1	yellow	VSMC_M3
GO:0072384	0.76	0.42	4	78	organelle transport along microtubule	BP	1	BLOC1S4,AP3D1,STK11,TMEM201	yellow	VSMC_M3
GO:1901215	0.76	0.36	9	161	negative regulation of neuron death	BP	1	BCL2L1,KDM2B,CX3CL1,SOD1,TYRO3,CLCF1,PLA2G3,CORO1A,AKT1	yellow	VSMC_M3

GO:0000075	0.76	0.35	9	155	cell cycle checkpoint signaling	BP	1	CCAR2,THOC5,BABAM1,SDE2,MAD1L1,MAD2L2,ZNF830,NABP2,FBXO6	yellow	VSMC_M3
GO:0060548	0.76	0.29	48	754	negative regulation of cell death	BP	1	BAG6,FNIP1,PPARD,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,OGG1,UCP2,PYCR1,BCL2L1,GREM1,KDM2B,CX3CL1,SOD1,EGR3,CCAR2,TYRO3,HTATIP2,DCPS,SELENOS,ITPRIP,GPX1,CLCF1,QARS,TWIST2,PLA2G3,RELA,ARNT2,PHB2,LGALS3,NANOS3,DFFA,ARHGEF2,CORO1A,EEF2K,AATF,ZNF830,AKT1,DHCR24,MYDGF,TRAP1,MNT,MIR214,PTMA,ZNF385A,TXNDC12	yellow	VSMC_M3
GO:0050670	0.76	0.36	8	137	regulation of lymphocyte proliferation	BP	1	SCRIB,CLCF1,RIPK3,LGALS3,PKN1,MAD1L1,CORO1A,CD276	yellow	VSMC_M3
GO:0055072	0.76	0.41	4	72	iron ion homeostasis	BP	1	TTC7A,SLC11A2,SOD1,CCDC115	yellow	VSMC_M3
GO:0040011	0.76	0.27	82	1349	locomotion	BP	1	CD63,CTHRC1,PPARD,TSTA3,SCRIB,PLEC,B4GALT1,PDGFRA,IL1R1,KLF4,TPBG,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,UNK,CEP131,YIF1B,RIC8A,SCARB1,ITGB7,SWAP70,GREM1,CX3CL1,DGKZ,EGR3,DLL4,TYRO3,LSP1,ST3GAL4,RIN3,PDGFA,MMP14,GPX1,CORO1B,PLEKHO1,IGSF9,NECTIN1,ARPIN,RIPK3,TWIST2,IQCG,PLA2G3,PTPN23,RHOC,FMNL1,LIMD1,SGPL1,PHB2,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,CORO1A,AKT1,ACAP3,TMEM201,GAS8,TGFBR3,TRADD,MIR214,ERBB4,PTPRR,IGFBP6,JAGN1,CAVIN1,IGSF8,NSMF,GLIPR2,TUBGCP2,MEIG1,ARPC5L	yellow	VSMC_M3
GO:0071241	0.76	0.35	9	165	cellular response to inorganic substance	BP	1	OGG1,SOD1,SYT12,BAD,HSD17B1,EEF2K,AKT1,JUND,NSMCE3	yellow	VSMC_M3
GO:0006954	0.77	0.30	31	497	inflammatory response	BP	1	HNRNPA0,PPARD,SHARPIN,B4GALT1,IL1R1,SOCS5,KLF4,ZC3H12A,ZYX,MGLL,RELB,OGG1,SIGLEC1,CX3CL1,SOD1,TYRO3,SELENOS,MVK,GPX1,PSMB4,PLA2G3,RELA,SCYL1,IFI35,TNFRSF1A,PER1,AKT1,GIT1,CARD9,TRADD,NDST1	yellow	VSMC_M3
GO:0071407	0.77	0.30	26	448	cellular response to organic cyclic compound	BP	1	CDK4,PPARD,LGALS1,KLF4,ZC3H12A,SLC9A3R1,INSIG1,AACS,WNT10B,SOD1,PCK2,SLC26A6,PRMT2,KAT5,PHB2,IGFBP5,PKN1,PER1,SMARCA4,CARM1,EEF2K,AKT1,HMGCS1,SAFB,SAFB2,SLC6A4	yellow	VSMC_M3
GO:0050794	0.77	0.26	502	7581	regulation of cellular process	BP	1	ENPP1,CD63,NAB2,CDK4,CTDSP2,RUFY1,SQSTM1,GNL1,ZNF608,BAG6,SNX9,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,TTLL12,RING1,SREBF2,SQLE,TXNDC15,H2AFY,ITPR3,HNRNPA0,TRIM11,SGSM3,TRAPPC9,PACSIN1,DEF6,PPARD,EEF1D,TSTA3,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,BOP1,VPS28,SND1,TOM1,CUL7,PPP1R14B,DNPH1,B4GALT1,PDGFRA,IL1R1,SECISBP2,PHF2,COL15A1,EPN1,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,EIPR1,RGS3,ZC3H12A,FIGNL1,PNKP,ZYX,RCN3,SNRNP70,CC2D1B,SNX3,KTI12,MICAL1,PLEKHA4,MGLL,EHD2,FAM120B,KMT2E,ANXA5,KRT8,WDFY2,SIX5,ZNF282,ZNF296,RELB,SLC9A3R1,SERP2,PLXND1,EMILIN1,RNF220,DMAP1,SLC30A3,CIC,SNX17,H3F3B,PPM1G,UNK,PLCD1,DLEC1,CD79A,INSIG1,MYRIP,SEC13,SEPT9,OGG1,SERTAD1,TTC5,PSMC4,ARHGEF40,UCP2,METTL3,PHLDA1,BAIAP2,CEP131,CXXC5,INPPL1,LAMTOR1,NUMA1,P4HB,DND1,PYCR1,CCDC57,EIF4EBP1,ARAP3,DELE1,CAVIN3,RIC8A,GSR,ARHGAP22,DEAF1,HOXC4,ARHGAP33,TARBP2,KMT2B,AACS,SCARB1,NAT10,BCL2L1,ITGB7,ZNF740,PDE4D,SPRYD3,TNS2,EIF4B,RRS1,SWAP70,LRP3,RALY,PLEKHF1,ACSL1,ZBTB38,CAPG,TNKS1BP1,PINX1,GREM1,KDM2B,DOK1,PDE3B,MCRS1,DCTN1,RAPSN,CX3CL1,WNT10B,SOD1,PACSIN3,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DNAJC17,DLL4,CHP1,TYRO3,YAF2,HTATIP2,PCIF1,PCBP4,LSP1,RAB35,KDM1B,CHCHD2,SLC35C2,RBM15B,TSPAN5,CISH,SRSF9,ST3GAL4,RNF19B,DCPS,IRX1,SELENOS,GSTO1,ITPRIP,RRP1B,ETFBKMT,BRD9,RIN3,STK32C,FABP3,ZCCHC17,PDGFA,MMP14,CDK2AP2,PABPN1,GPX1,AIP,CORO1B,NGEF,CLCF1,NGDN,SRRD,PLEKHO1,TSHZ2,IGSF9,SYT12,QARS,PRPN4,PCK2,ASB9,PSME3,RIP,NECTIN1,AND	yellow	VSMC_M3
GO:0070663	0.77	0.35	9	153	regulation of leukocyte proliferation	BP	1	SCRIB,GREM1,CLCF1,RIPK3,LGALS3,PKN1,MAD1L1,CORO1A,CD276	yellow	VSMC_M3
GO:0006664	0.77	0.39	5	87	glycolipid metabolic process	BP	1	CERK,PIGO,ST3GAL4,DPM3,GBA2	yellow	VSMC_M3
GO:1903509	0.77	0.39	5	87	liposaccharide metabolic process	BP	1	CERK,PIGO,ST3GAL4,DPM3,GBA2	yellow	VSMC_M3
GO:0010469	0.77	0.37	6	112	regulation of signaling receptor activity	BP	1	SOCS5,PDE4D,GREM1,BUD31,PLAU,GSG1L	yellow	VSMC_M3
GO:0071705	0.77	0.27	104	1609	nitrogen compound transport	BP	1	CD63,RUFY1,CCHCR1,SNX9,SAMM50,SREBF2,SGSM3,GUK1,PPARD,SCRIB,IFT27,SLC52A2,VPS28,TOM1,ASNA1,PLEKHA8,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,SLC9A3R1,SERP2,DMAP1,SNX17,INSIG1,MYRIP,SEC13,UCP2,CEP131,YIF1B,RAB20,ARHGAP33,AACS,HM13,SFXN5,CHP1,AP2A2,SNX21,RAB35,SLC35C2,RBM15B,APBA2,SELENOS,EXOC3,PABPN1,AIP,AP1G2,SYT12,PCK2,SLC19A1,PCNT,SLC26A6,THOC5,CAPN10,RHCE,PLA2G3,PTPN23,VPS51,PEX5,ZDHHC3,THOC3,PHB2,BAD,COPE,MVB12A,NUP88,WASHC1,AP1M1,RAB3IL1,CCDC22,GLUD1,SNX8,LMAN2,RAB24,CLTB,ARHGEF2,SNF8,MVP,MTX1,RANGRF,STX10,RABEP2,TMED1,CDC37,CSK,ATG3,RBM22,AKT1,SNX18,KHSRP,RANBP3,RAB34,SLC6A4,CTNS,AP3D1,MIDN,SLC44A3,RBM8A,AP5B1,JAGN1,CAVIN1,ARFRP1,TIMM22	yellow	VSMC_M3
GO:1905475	0.77	0.35	8	147	regulation of protein localization to membrane	BP	1	SQSTM1,BCL2L1,CHP1,MMP14,LGALS3,RANGRF,CSK,AKT1	yellow	VSMC_M3
GO:0008406	0.77	0.34	9	166	gonad development	BP	1	PDGFRA,BCL2L1,SOD1,MMP14,IDH1,SGPL1,ZNF830,HMGCS1,SAFB2	yellow	VSMC_M3

GO:0010557	0.77	0.27	90	1433	positive regulation of macromolecule biosynthetic process	BP	1	CDK4,SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,RPS9,KLF4,HOXA1,ZC3H12A,PNKP,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,METTL3,DEAF1,HOXC4,KMT2B,NAT10,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,RRP1B,AIP,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,NDP,SSBP4,MPV17L2,BUD31,TNFRSF1A,C1QBP,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,MAD2L2,ARHGEF2,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,AKT1,BRF1,PAIP1,GTF2F1,MYDGF,MAP2K2,AP3D1,MED16,POMT1,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3
GO:0048771	0.77	0.36	7	129	tissue remodeling	BP	1	CTHRC1,GREM1,DLL4,MMP14,IGFBP5,CSK,MIR214	yellow	VSMC_M3
GO:0065008	0.77	0.26	177	2770	regulation of biological quality	BP	1	ENPP1,PQLC1,CDK4,SQSTM1,BAG6,SNX9,SREBF2,ITPR3,HNRNPA0,PPARD,SCRIB,PLEC,LGALS1,AARS2,PDGFRA,TTC7A,RPS9,CNOT3,DBNL,TPBG,WDPCP,EIPR1,ZC3H12A,CPT1C,RCN3,KMT2E,ANXA5,SLC9A3R1,PLXND1,SLC30A3,INSIG1,MYRIP,UCP2,METTL3,BAIAP2,LAMTOR1,DND1,PYCR1,RAB20,GSR,ARHGAP22,ARHGAP33,AACS,SCARB1,BCL2L1,PDE4D,TNS2,SWAP70,RALY,ACSL1,CAPG,SLC11A2,PINX1,AQP5,DCTN1,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,CHP1,TYRO3,SCD,PCBP4,TMEM183A,ST3GAL4,DCPS,DHCR7,SELENOS,GSTO1,RIN3,FABP3,ZCCHC17,PDGFA,GPX1,CORO1B,NGEF,PLEKHO1,IGSF9,SYT12,LRFN4,PCK2,LSS,NECTIN1,ANPEP,TRIM27,ARPIN,LIMK1,SCN4A,SLC26A6,SPX,RIPK3,CAPN10,PLA2G3,RHOC,FMNL1,LIMD1,SGPL1,SMARCB1,CHCHD10,BLOC1S4,TXNRD2,PHB2,IGFBP5,BAD,PLCB3,LAMTOR4,HSD17B1,LETM1,ARPC1B,CD9,PLAU,CHERP,WASHC1,CNP,CCDC22,USP27X,GLUD1,FOXK1,PKN1,DBN1,NANOS3,CRABP2,TMEM79,SNF8,MTX1,RANGRF,DPM3,CORO1A,TSPOAP1,SMARCA4,SYNE3,EEF2K,CDC37,CSK,ANKRD9,DOCK11,ZNF830,AKT1,PACS2,PAIP1,KHSRP,ALKBH7,GIT1,SLC6A4,CARHSP1,SIRT6,TJP3,NCLN,CTNS,EHMT1,AP3D1,ANAPC2,MIDN,STK11,TELO2,CARD9,AMPD2,SPG7,APRT,TGFBR3,MIR214,ERBB4,TWF2,ARMCX1,KLF13,TENT5B,JAGN1,ELN,UNC13A,CDC42EP5,NSMF,GBA2,STUB1,CCDC115,ARPC5L,GSG1L	yellow	VSMC_M3
GO:0007264	0.77	0.30	24	437	small GTPase mediated signal transduction	BP	1	RUFY1,SQSTM1,SGSM3,DEF6,DBNL,ARHGEF40,ARHGAP22,ARHGAP33,SWAP70,DOK1,CHP1,RAB35,NGEF,LIMK1,TNK2,STMN3,SIPA1,RHOC,ARHGEF2,RANGRF,DOCK11,DHCR24,CDC42EP5,ARHGEF1	yellow	VSMC_M3
GO:0061025	0.77	0.36	7	125	membrane fusion	BP	1	RAB20,CHP1,CD9,PIP4K2B,STX10,CORO1A,RAB34	yellow	VSMC_M3
GO:0032944	0.77	0.35	8	138	regulation of mononuclear cell proliferation	BP	1	SCRIB,CLCF1,RIPK3,LGALS3,PKN1,MAD1L1,CORO1A,CD276	yellow	VSMC_M3
GO:0060326	0.77	0.33	12	206	cell chemotaxis	BP	1	PLEC,PDGFRA,TPBG,SWAP70,GREM1,CX3CL1,EGR3,RIN3,CORO1B,LGALS3,C1QBP,CORO1A	yellow	VSMC_M3
GO:0003279	0.77	0.40	4	88	cardiac septum development	BP	1	PLXND1,SNX17,TGFBR3,NDST1	yellow	VSMC_M3
GO:0043255	0.77	0.40	4	78	regulation of carbohydrate biosynthetic process	BP	1	ENPP1,SELENOS,AKT1,PGP	yellow	VSMC_M3
GO:0030522	0.77	0.32	12	217	intracellular receptor signaling pathway	BP	1	PPARD,FAM120B,PRMT2,RELA,PHB2,C1QBP,PKN1,PER1,SMARCA4,CARM1,SAFB,SAFB2	yellow	VSMC_M3
GO:0045787	0.78	0.31	14	243	positive regulation of cell cycle	BP	1	CDK4,H2AFY,KMT2E,NUMA1,CCDC57,EIF4EBP1,WNT10B,THOC5,PBX1,PHB2,RCC2,AKT1,SLC6A4,MIR214	yellow	VSMC_M3
GO:1903532	0.78	0.33	11	196	positive regulation of secretion by cell	BP	1	PPARD,MYRIP,AACS,PCK2,CAPN10,PLA2G3,PTPN23,BAD,GLUD1,SNF8,SLC6A4	yellow	VSMC_M3
GO:0030004	0.78	0.39	4	81	cellular monovalent inorganic cation homeostasis	BP	1	RAB20,CHP1,SLC26A6,CCDC115	yellow	VSMC_M3
GO:0062207	0.78	0.39	4	77	regulation of pattern recognition receptor signaling pathway	BP	1	TYRO3,IFI35,C1QBP,CACTIN	yellow	VSMC_M3
GO:0030301	0.78	0.39	4	77	cholesterol transport	BP	1	SREBF2,LAMTOR1,SCARB1,YJEFN3	yellow	VSMC_M3
GO:0002702	0.78	0.39	4	75	positive regulation of production of molecular mediator of immune response	BP	1	IL1R1,CLCF1,PHB2,MAD2L2	yellow	VSMC_M3
GO:0043281	0.78	0.33	9	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	FNIP1,KLF4,MICAL1,DELE1,GPX1,BAD,AKT1,DHCR24,CARD9	yellow	VSMC_M3
GO:0007018	0.78	0.30	16	283	microtubule-based movement	BP	1	IFT27,SLC9A3R1,CEP131,YIF1B,SOD1,IQCG,PLA2G3,BLOC1S4,AP3D1,SSNA1,STK11,TMEM201,GAS8,SPG7,WDR34,MEIG1	yellow	VSMC_M3
GO:1901888	0.78	0.34	8	165	regulation of cell junction assembly	BP	1	TPBG,WDPCP,GREM1,MMP14,LRFN4,NECTIN1,RCC2,EEF2K	yellow	VSMC_M3
GO:0006886	0.78	0.27	46	739	intracellular protein transport	BP	1	CCHCR1,SNX9,SAMM50,SREBF2,SGSM3,SCRIB,IFT27,VPS28,ASNA1,ZC3H12A,DMAP1,SNX17,INSIG1,MYRIP,SEC13,CEP131,YIF1B,RAB20,HM13,CHP1,AP2A2,SELENOS,AIP,AP1G2,PCNT,PEX5,ZDHHC3,PHB2,NUP88,AP1M1,SNX8,RAB24,CLTB,ARHGEF2,SNF8,RANGRF,STX10,TMED1,CDC37,ATG3,RBM22,AKT1,RANBP3,AP3D1,ARFRP1,TIMM22	yellow	VSMC_M3
GO:0045807	0.78	0.39	4	82	positive regulation of endocytosis	BP	1	CD63,VPS28,GREM1,EEF2K	yellow	VSMC_M3
GO:0048675	0.78	0.37	5	106	axon extension	BP	1	DBNL,LIMK1,DBN1,ANAPC2,TWF2	yellow	VSMC_M3
GO:0044272	0.78	0.35	7	127	sulfur compound biosynthetic process	BP	1	MPST,ACSL1,ST3GAL4,PAPSS1,ACLY,MTHFR,NDST1	yellow	VSMC_M3
GO:0048588	0.78	0.32	10	195	developmental cell growth	BP	1	DBNL,LIMK1,PRMT2,DBN1,CRABP2,SIRT6,ANAPC2,STK11,TWF2,UNC13A	yellow	VSMC_M3
GO:0034504	0.78	0.31	14	244	protein localization to nucleus	BP	1	ZC3H12A,DMAP1,SEC13,RRS1,PINX1,MCRS1,CHP1,CHCHD10,PHB2,NUP88,RANGRF,RBM22,AKT1,STK11	yellow	VSMC_M3
GO:0032989	0.78	0.28	33	609	cellular component morphogenesis	BP	1	PACSIN1,PLEC,CUL7,PDGFRA,DBNL,TPBG,KRT8,PLXND1,BAIAP2,ARHGAP33,BCL2L1,SLC11A2,CORO1B,NGEF,PLEKHO1,IGSF9,NECTIN1,ARPIN,LIMK1,PLA2G3,C12orf57,CD9,CNP,DBN1,CRABP2,S100A6,EEF2K,RFX2,ANAPC2,STK11,TWF2,UNC13A,NSMF	yellow	VSMC_M3
GO:0031123	0.78	0.37	5	94	RNA 3'-end processing	BP	1	NELFE,RPS21,CSTF2T,INTS1,SSU72	yellow	VSMC_M3
GO:0097530	0.78	0.37	5	91	granulocyte migration	BP	1	IL1R1,CX3CL1,LGALS3,C1QBP,JAGN1	yellow	VSMC_M3
GO:0009914	0.78	0.31	12	212	hormone transport	BP	1	PPARD,EIPR1,MYRIP,UCP2,AACS,PCK2,CAPN10,PLA2G3,BAD,GLUD1,MIDN,JAGN1	yellow	VSMC_M3
GO:0031570	0.78	0.35	6	111	DNA integrity checkpoint signaling	BP	1	CCAR2,THOC5,BABAM1,SDE2,ZNF830,FBXO6	yellow	VSMC_M3

GO:0140014	0.78	0.30	14	244	mitotic nuclear division	BP	1	DCTN2,NCAPH2,H2AFY,CUL7,NUMA1,RRS1,PINX1,NUDC,PHB2,EML3,MAD1L1,MAD2L2,AURKAIP1,MIS12	yellow	VSMC_M3
GO:1902105	0.78	0.31	11	193	regulation of leukocyte differentiation	BP	1	SOCS5,ZC3H12A,METTL3,SOD1,EGR3,MMP14,PLA2G3,SART1,BAD,PRXL2A,AP3D1	yellow	VSMC_M3
GO:0035265	0.79	0.34	7	134	organ growth	BP	1	SOD1,EVC,AKT1,SLC6A4,SIRT6,TGFBR3,ERBB4	yellow	VSMC_M3
GO:0007613	0.79	0.38	4	86	memory	BP	1	ITPR3,CIC,SLC6A4,CTNS	yellow	VSMC_M3
GO:0048736	0.79	0.34	7	140	appendage development	BP	1	PBX2,WDPCP,GREM1,PBX1,CRABP2,SLC39A1,ZNF358	yellow	VSMC_M3
GO:0060173	0.79	0.34	7	140	limb development	BP	1	PBX2,WDPCP,GREM1,PBX1,CRABP2,SLC39A1,ZNF358	yellow	VSMC_M3
GO:0007399	0.79	0.24	112	1867	nervous system development	BP	1	NAB2,BAG6,CTHRC1,HDAC10,PBX2,TRIM11,TRAPPC9,PACSIN1,PPARD,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,CUL7,SECISBP2,KLF4,DBNL,TPBG,HOXA1,WDPCP,ZC3H12A,SNX3,SLC9A3R1,PLXND1,RNF220,PAFAH1B3,CIC,UNK,METTL3,BAIAP2,DEAF1,TBCB,LRIG1,ARHGAP33,CAPG,SLC11A2,MMP24,KDM2B,DCTN1,CX3CL1,WNT10B,SOD1,EGR3,DLL4,TYRO3,RAB35,APBA2,IRX1,SDHA,MMP14,NGEF,CLCF1,IGSF9,QARS,LRFN4,NECTIN1,LIMK1,PLA2G3,STMN3,PBX1,RELA,SCYL1,ARNT2,VPS51,SMARCB1,PBX4,ATIC,BLOC1S4,NDP,C12orf57,BAD,CTDSP1,CD9,CHERP,CNP,GLUD1,DBN1,MTHFR,CRABP2,ARHGEF2,IRF2BPL,S100A6,SMARCA4,CARM1,EEF2K,EML1,CSK,ZNF521,ZNF358,AKT1,HMGCS1,GIT1,SLC6A4,HMG20B,ACAP3,CTNS,ANAPC2,MBD3,STK11,SPG7,NEGR1,NDST1,ERBB4,TWF2,IGSF8,UNC13A,NSMF,GBA2,TUBGCP2,MARVELD1	yellow	VSMC_M3
GO:0008037	0.79	0.36	5	97	cell recognition	BP	1	B4GALT1,SCARB1,IGSF9,LGALS3,CD9	yellow	VSMC_M3
GO:0050864	0.79	0.36	5	93	regulation of B cell activation	BP	1	MMP14,CLCF1,BAD,PKN1,MAD2L2	yellow	VSMC_M3
GO:0071482	0.79	0.36	5	94	cellular response to light stimulus	BP	1	METTL3,ACTR5,SDE2,STK11,NSMCE3	yellow	VSMC_M3
GO:0001763	0.79	0.32	8	157	morphogenesis of a branching structure	BP	1	PLXND1,GREM1,DLL4,PDGFA,MMP14,PBX1,PHB2,SIRT6	yellow	VSMC_M3
GO:0046631	0.79	0.36	5	97	alpha-beta T cell activation	BP	1	SOCS5,ZC3H12A,RELB,ARMC5,AP3D1	yellow	VSMC_M3
GO:0010811	0.79	0.36	5	100	positive regulation of cell-substrate adhesion	BP	1	TSTA3,EMILIN1,P4HB,CX3CL1,C1QBP	yellow	VSMC_M3
GO:1990138	0.79	0.33	7	147	neuron projection extension	BP	1	DBNL,LIMK1,DBN1,ANAPC2,STK11,TWF2,UNC13A	yellow	VSMC_M3
GO:0060041	0.79	0.35	5	108	retina development in camera-type eye	BP	1	PDGFRA,DLL4,IMPDH2,NECTIN1,SMARCA4	yellow	VSMC_M3
GO:2000278	0.79	0.35	5	95	regulation of DNA biosynthetic process	BP	1	KLF4,PNKP,NAT10,PINX1,GREM1	yellow	VSMC_M3
GO:0045137	0.79	0.31	9	170	development of primary sexual characteristics	BP	1	PDGFRA,BCL2L1,SOD1,MMP14,IDH1,SGPL1,ZNF830,HMGCS1,SAFB2	yellow	VSMC_M3
GO:0006814	0.79	0.32	8	161	sodium ion transport	BP	1	SLC9A3R1,CHP1,NKAIN1,SCN4A,PER1,RANGRF,AKT1,SLC6A4	yellow	VSMC_M3
GO:0051983	0.79	0.37	4	78	regulation of chromosome segregation	BP	1	NUMA1,RCC2,MAD1L1,MAD2L2	yellow	VSMC_M3
GO:0035637	0.79	0.35	5	114	multicellular organismal signaling	BP	1	PLEC,PDE4D,SOD1,SCN4A,RANGRF	yellow	VSMC_M3
GO:0050729	0.79	0.35	5	93	positive regulation of inflammatory response	BP	1	CX3CL1,PLA2G3,IFI35,TNFRSF1A,TRADD	yellow	VSMC_M3
GO:1902850	0.79	0.33	7	133	microtubule cytoskeleton organization involved in mitosis	BP	1	DCTN2,NUMA1,DCTN1,PCNT,NUDC,EML3,EML1	yellow	VSMC_M3
GO:0007596	0.80	0.31	9	164	blood coagulation	BP	1	PDGFRA,ANXA5,DGKZ,TYRO3,ST3GAL4,PDGFA,BLOC1S4,CD9,PLAU	yellow	VSMC_M3
GO:0007420	0.80	0.26	33	587	brain development	BP	1	BAG6,PBX2,TRAPPC9,SCRIB,SHARPIN,SECISBP2,PAFAH1B3,CIC,METTL3,BAIAP2,KDM2B,TYRO3,QARS,PBX1,ARNT2,VPS51,PBX4,ATIC,C12orf57,BAD,CD9,CNP,GLUD1,EML1,CSK,HMGCS1,GIT1,SLC6A4,CTNS,MBD3,NDST1,ERBB4,TUBGCP2	yellow	VSMC_M3
GO:0034764	0.80	0.32	8	155	positive regulation of transmembrane transport	BP	1	SLC9A3R1,ACSL1,CX3CL1,CHP1,GSTO1,SLC26A6,CAPN10,AKT1	yellow	VSMC_M3
GO:0043279	0.80	0.36	4	81	response to alkaloid	BP	1	BCL2L1,SRSF9,UQCRC1,RELA	yellow	VSMC_M3
GO:0009891	0.80	0.23	96	1533	positive regulation of biosynthetic process	BP	1	CDK4,SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,PHF2,RPS9,KLF4,HOXA1,ZC3H12A,PNKP,KMT2E,SIX5,ZNF296,SERTAD1,TTC5,METTL3,DEAF1,HOXC4,KMT2B,SCARB1,NAT10,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,CCAR2,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,RRP1B,FABP3,AIP,TRIM27,PRMT2,THOC5,RIPK3,SMARCD2,PLA2G3,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,NDP,SSBP4,MPV17L2,BUD31,TNFRSF1A,C1QBP,TAF6L,ZBTB49,MTA2,PELP1,FOXK1,PKN1,CAPN2,MAD2L2,ARHGEF2,PER1,NFIX,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,MID2,ZNF521,AKT1,BRF1,PAIP1,GTF2F1,MYDGF,MAP2K2,AP3D1,TAZ,MED16,POMT1,ERBB4,JUND,KLF13,IER5	yellow	VSMC_M3
GO:0062013	0.80	0.34	5	96	positive regulation of small molecule metabolic process	BP	1	PPARD,PLA2G3,MID1IP1,AKT1,TAZ	yellow	VSMC_M3
GO:0198738	0.80	0.27	21	374	cell-cell signaling by wnt	BP	1	CTHRC1,KLF4,TPBG,SNX3,PLEKHA4,SLC9A3R1,RNF220,GREM1,WNT10B,CCAR2,PTPN23,LIMD1,NDP,AMER1,MAD2L2,SMARCA4,HIC1,CSNK1G2,STK11,IGFBP6,APCDD1L	yellow	VSMC_M3
GO:0051050	0.80	0.25	39	660	positive regulation of transport	BP	1	CD63,SREBF2,PPARD,VPS28,EIPR1,ZC3H12A,EHD2,SLC9A3R1,DMAP1,SLC30A3,MYRIP,CEP131,NUMA1,AACS,ACSL1,GREM1,CX3CL1,SOD1,CHP1,GSTO1,FABP3,PCK2,PCNT,SLC26A6,CAPN10,PLA2G3,PTPN23,CHCHD10,BAD,LGALS3,GLUD1,LMAN2,SNF8,EEF2K,RBM22,AKT1,SLC6A4,STK11,PLA2G4E	yellow	VSMC_M3
GO:0001890	0.80	0.33	6	117	placenta development	BP	1	PPARD,CUL7,KRT8,SOD1,AKT1,NSDHL	yellow	VSMC_M3
GO:0030308	0.81	0.30	8	153	negative regulation of cell growth	BP	1	ENPP1,PPARD,GREM1,CCAR2,CCDC85B,SIPA1,SMARCA4,STK11	yellow	VSMC_M3
GO:0007599	0.81	0.30	9	166	hemostasis	BP	1	PDGFRA,ANXA5,DGKZ,TYRO3,ST3GAL4,PDGFA,BLOC1S4,CD9,PLAU	yellow	VSMC_M3
GO:0050817	0.81	0.30	9	166	coagulation	BP	1	PDGFRA,ANXA5,DGKZ,TYRO3,ST3GAL4,PDGFA,BLOC1S4,CD9,PLAU	yellow	VSMC_M3
GO:0090316	0.81	0.31	7	136	positive regulation of intracellular protein transport	BP	1	SREBF2,ZC3H12A,DMAP1,CEP131,CHP1,PCNT,RBM22	yellow	VSMC_M3
GO:1903828	0.81	0.33	5	99	negative regulation of cellular protein localization	BP	1	H2AFY,INSIG1,BCL2L1,CHP1,CSK	yellow	VSMC_M3
GO:0060048	0.81	0.33	5	103	cardiac muscle contraction	BP	1	ZC3H12A,PDE4D,GSTO1,RANGRF,TAZ	yellow	VSMC_M3
GO:0007611	0.81	0.29	9	183	learning or memory	BP	1	ITPR3,TPBG,CIC,RIC8A,SLC11A2,TACO1,GIT1,SLC6A4,CTNS	yellow	VSMC_M3

GO:0060341	0.81	0.24	40	675	regulation of cellular localization	BP	1	SQSTM1,SREBF2,H2AFY,PPARD,VPS28,EIPR1,ZC3H12A,SNX3,EHD2,DMAP1,INSIG1,UCP2,CEP131,NUMA1,BCL2L1,PDE4D,PINX1,MCRS1,CX3CL1,CHP1,GSTO1,MMP14,PCNT,CAPN10,PLA2G3,PTPN23,BAD,LGALS3,MAD1L1,RANGRF,CORO1A,CSK,RBM22,AKT1,MAP2K2,STK11,GAS8,ERBB4,PLA2G4E,JAGN1	yellow	VSMC_M3
GO:0032880	0.81	0.23	41	693	regulation of protein localization	BP	1	SQSTM1,SREBF2,H2AFY,PPARD,VPS28,WDPCP,EIPR1,ZC3H12A,SNX3,DMAP1,INSIG1,MYRIP,UCP2,CEP131,NUMA1,AACS,BCL2L1,SWAP70,PINX1,MCRS1,CHP1,MMP14,PCK2,TRIM27,PCNT,CAPN10,PTPN23,BAD,LGALS3,GLUD1,RANGRF,STX10,TRIM25,CSK,RBM22,AKT1,MIDN,STK11,GAS8,ERBB4,JAGN1	yellow	VSMC_M3
GO:0006915	0.81	0.22	92	1436	apoptotic process	BP	1	CDK4,SQSTM1,BAG6,FNIP1,PPARD,SCRIB,LGALS1,SHARPIN,B4GALT1,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,KRT8,SLC9A3R1,OGG1,UCP2,PHLDA1,P4HB,DELE1,BCL2L1,PLEKHF1,GREM1,KDM2B,RAPSN,CX3CL1,WNT10B,SOD1,EGR3,CCAR2,TYRO3,HTATIP2,SELENOS,ITPRIP,RRP1B,GPX1,CLCF1,QARS,PRMT2,RIPK3,TWIST2,CAPN10,BRMS1,PLA2G3,RELA,ARNT2,ZDHHC3,SGPL1,CHCHD10,ZNF385B,PHB2,BAD,LGALS3,TNFRSF1A,C1QBP,AIMP2,USP27X,CASP14,PKN1,CAPN2,SLTM,NANOS3,BCL7C,DFFA,ARHGEF2,PLEKHO2,CORO1A,EEF2K,AATF,ATG3,ZNF830,AKT1,PACS2,DHCR24,MYDGF,CDK11B,HIC1,TRAP1,MNT,MKNK2,STK11,CARD9,SLC27A4,TRADD,TNFRSF12A,ERBB4,PTMA,ZNF385A,TXNDC12,NSMF,CDC34	yellow	VSMC_M3
GO:0009306	0.81	0.26	15	266	protein secretion	BP	1	PPARD,EIPR1,PDIA4,RCN3,MYRIP,UCP2,AACS,PCK2,CAPN10,PTPN23,BAD,GLUD1,MIDN,JAGN1,CAVIN1	yellow	VSMC_M3
GO:0035592	0.81	0.26	15	266	establishment of protein localization to extracellular region	BP	1	PPARD,EIPR1,PDIA4,RCN3,MYRIP,UCP2,AACS,PCK2,CAPN10,PTPN23,BAD,GLUD1,MIDN,JAGN1,CAVIN1	yellow	VSMC_M3
GO:0006281	0.82	0.24	27	455	DNA repair	BP	1	HDAC10,FANCE,FIGNL1,PNKP,MUTYH,DMAP1,OGG1,TTC5,FAAP100,SMUG1,TNKS1BP1,MCRS1,ACTR5,CEP164,KAT5,OTUB1,BABAM1,MAD2L2,PPP4C,SLX1A,USP43,CXorf57,SIRT6,NABP2,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0032879	0.82	0.21	129	2074	regulation of localization	BP	1	ENPP1,CD63,NHP2,RUFY1,SQSTM1,SREBF2,H2AFY,ITPR3,PACSIN1,PPARD,TSTA3,SCRIB,VPS28,PDGFRA,IL1R1,KLF4,WDPCP,EIPR1,ZC3H12A,SNX3,MICAL1,EHD2,SLC9A3R1,PLXND1,EMILIN1,DMAP1,SLC30A3,SNX17,INSIG1,MYRIP,UCP2,CEP131,LAMTOR1,NUMA1,AACS,SCARB1,BCL2L1,PDE4D,SWAP70,ACSL1,PINX1,GREM1,MCRS1,CX3CL1,SOD1,PACSIN3,DLL4,CHP1,ST3GAL4,SELENOS,GSTO1,RIN3,FABP3,NKAIN1,PDGFA,MMP14,CORO1B,SYT12,PCK2,TRIM27,ARPIN,PCNT,SCN4A,SLC26A6,SPX,RIPK3,TWIST2,CAPN10,TNK2,TACO1,PLA2G3,PTPN23,RHOC,ZDHHC3,CHCHD10,YJEFN3,PHB2,IGFBP5,BAD,AAMP,LETM1,LGALS3,CD9,PLAU,TNFRSF1A,C1QBP,CHERP,WASHC1,RCC2,MTA2,GLUD1,ELP5,PKN1,DBN1,LMAN2,MIIP,MAD1L1,ARHGEF2,SNF8,PER1,RANGRF,STX10,CORO1A,TRIM25,EEF2K,CSK,ATG3,RBM22,AKT1,ALKBH7,GIT1,ANKRD13B,SLC6A4,MAP2K2,AP3D1,MIDN,STK11,GAS8,TGFBR3,TRADD,MIR214,ERBB4,PTPRR,PLA2G4E,JAGN1,CAVIN1,NSMF,GLIPR2,GSG1L	yellow	VSMC_M3
GO:0010817	0.82	0.25	19	331	regulation of hormone levels	BP	1	PPARD,PDGFRA,EIPR1,MYRIP,UCP2,AACS,SCARB1,DHCR7,PCK2,CAPN10,PLA2G3,SGPL1,BAD,HSD17B1,GLUD1,CRABP2,MIDN,JAGN1,STUB1	yellow	VSMC_M3
GO:0002221	0.82	0.30	7	134	pattern recognition receptor signaling pathway	BP	1	TYRO3,RELA,PHB2,IFI35,C1QBP,CACTIN,IRAK1	yellow	VSMC_M3
GO:0048666	0.82	0.23	49	877	neuron development	BP	1	CTHRC1,PBX2,PACSIN1,SCRIB,LGALS1,IFT27,CUL7,SECISBP2,KLF4,DBNL,TPBG,WDPCP,SNX3,SLC9A3R1,PLXND1,UNK,BAIAP2,ARHGAP33,SLC11A2,CX3CL1,SOD1,RAB35,NGEF,IGSF9,NECTIN1,LIMK1,PLA2G3,STMN3,PBX1,SCYL1,PBX4,BLOC1S4,C12orf57,CNP,DBN1,CRABP2,S100A6,CARM1,EEF2K,AKT1,GIT1,ACAP3,ANAPC2,STK11,NEGR1,TWF2,UNC13A,NSMF,GBA2	yellow	VSMC_M3
GO:0051234	0.82	0.20	222	3429	establishment of localization	BP	1	ENPP1,PQLC1,CD63,ESYT1,DCTN2,RUFY1,SQSTM1,CCHCR1,BAG6,SNX9,SAMM50,SREBF2,H2AFY,ITPR3,SGSM3,GUK1,PACSIN1,PPARD,SCRIB,IFT27,SLC52A2,VPS28,TOM1,EPN1,SSC5D,ASNA1,DBNL,PLEKHA8,WDPCP,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,MICAL1,EHD2,TTYH2,SLC9A3R1,SERP2,SLC16A5,DMAP1,SLC30A3,SNX17,INSIG1,MYRIP,SEC13,UCP2,CEP131,INPPL1,TSPAN10,LAMTOR1,NUMA1,YIF1B,RAB20,ARAP3,SIGLEC1,ARHGAP33,LDLRAD3,AACS,SCARB1,HM13,BCL2L1,PDE4D,RRS1,LRP3,UQCRFS1,ACSL1,SLC11A2,PINX1,GREM1,AQP5,DCTN1,RAPSN,CX3CL1,SOD1,PACSIN3,SFXN5,DNAJC17,HPS1,CHP1,TYRO3,AP2A2,SNX21,HTATIP2,RAB35,SLC35C2,RBM15B,APBA2,SELENOS,GSTO1,SLC16A14,EXOC3,RIN3,FABP3,NKAIN1,PABPN1,AIP,AP1G2,SYT12,PCK2,SLC19A1,NECTIN1,TRIM27,PCNT,LIMK1,SCN4A,SLC26A6,NUDC,SPX,THOC5,UQCRC1,CAPN10,RHCE,TNK2,TACO1,PLA2G3,PTPN23,MRC2,ATP5MC3,TMEM120A,SCYL1,LRWD1,VPS51,ZFPL1,PEX5,ZDHHC3,CHCHD10,YJEFN3,THOC3,BLOC1S4,PHB2,BAD,COPE,SCARF2,LETM1,LGALS3,CD9,TNFRSF1A,FCHO1,MVB12A,NUP88,CHERP,ANXA11,WASHC1,RCC2,CNP,AP1M1,EML3,RAB3IL1,CCDC22,GLUD1,SNX8,LMAN2,RAB24,MAD1L1,PIP4K2B,CLTB,TMEM79,ARHGEF2,SNF8,MVP,PER1,MTX1,RANGRF,STX10,CORO1A,SGF29,RABEP2,SLC39A1,ATP5PD,SLC27A3,S100A6,TMED1,SYNE3,EEF2K,CDC37,MYO19,CSK,ATG3,RBM22,AKT1,SNX18,DENND1C,KHSRP,ALKBH7,RANBP3,RAB34,GIT1,ANKRD13B,SLC6A4,MAP2K2,SLC35E2B,CTNS,AP3D1,CSNK1G2,SSNA1,NDUFS7,MIDN,ATP5F1D,STK11,TMEM201,SPG7,APRT,WDR34,SLC27A4,SLC44A3,RABEPK,NABP2,RBM8A,ERBB4,SURF1,TRAPPC5,PLA2G4E,	yellow	VSMC_M3

GO:0000165	0.82	0.23	34	579	MAPK cascade	BP	1	NELFE,PDGFRA,KLF4,TPBG,CCM2,SPRED2,ZC3H12A,SLC9A3R1,EMILIN1,LAMTOR1,CAVIN3,CX3CL1,SOD1,PDGFA,PABPN1,QARS,EIF3A,MAP3K14,PHB2,PER1,CSK,AKT1,MYDGF,MAP2K2,IRAK1,CARD9,NDST1,ERBB4,PTPRR,IGFBP6,CDC42EP5,DUSP5,GLIPR2,RCE1	yellow	VSMC_M3
GO:0070887	0.82	0.21	141	2230	cellular response to chemical stimulus	BP	1	ENPP1,CD63,CDK4,BAG6,ATF6B,TTLL12,GUK1,PPARD,RPL3,PLEC,LGALS1,SHARPIN,PDGFRA,IL1R1,SOCS5,KLF4,TPBG,SPRED2,ZC3H12A,ZYX,KRT8,RELB,SLC9A3R1,SERP2,EMILIN1,INSIG1,OGG1,UCP2,METTL3,BAIAP2,LAMTOR1,NUMA1,P4HB,PYCR1,FASN,RAB20,SMOX,EIF4EBP1,GSR,AACS,SCARB1,BCL2L1,TNS2,SWAP70,ACSL1,GREM1,DOK1,AQP5,PDE3B,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,LSP1,RAB35,CHCHD2,DCPS,SELENOS,GSTO1,RIN3,PABPN1,GPX1,AIP,CORO1B,CLCF1,SYT12,PCK2,COL6A1,IMPDH2,SLC26A6,PRMT2,RIPK3,CAPN10,KAT5,RELA,SIPA1,MGST3,SMARCB1,ATIC,TXNRD2,PHB2,IGFBP5,BAD,LAMTOR4,OTUB1,HSD17B1,LETM1,LGALS3,TNFRSF1A,C1QBP,PRXL2A,PELP1,KLF3,PKN1,CAPN2,PALM3,PIP4K2B,ARHGEF2,PER1,CORO1A,TRIM25,MTMR4,SMARCA4,CARM1,EEF2K,CDC37,CSK,RBM22,AKT1,HMGCS1,KHSRP,SAFB,SAFB2,GIT1,SLC6A4,LDOC1,CACTIN,VASN,TRAP1,MKNK2,IRAK1,STK11,APRT,SLC27A4,TGFBR3,TRADD,MIR214,RF00024,NDST1,ERBB4,TWF2,JUND,JAGN1,NSMF,CDC34,OSER1,STUB1,NSMCE3,CCDC115	yellow	VSMC_M3
GO:0009566	0.82	0.30	6	113	fertilization	BP	1	SPAG1,B4GALT1,GNPDA1,BCL2L1,CD9,IGSF8	yellow	VSMC_M3
GO:0071248	0.82	0.29	7	141	cellular response to metal ion	BP	1	OGG1,SOD1,SYT12,HSD17B1,EEF2K,AKT1,JUND	yellow	VSMC_M3
GO:0060562	0.82	0.26	14	269	epithelial tube morphogenesis	BP	1	CTHRC1,SCRIB,CCM2,PLXND1,DEAF1,GREM1,KDM2B,DLL4,IRX1,MMP14,PBX1,PHB2,MTHFR,SIRT6	yellow	VSMC_M3
GO:0031023	0.82	0.30	6	127	microtubule organizing center organization	BP	1	CEP131,CCDC57,NAT10,DCTN1,SAC3D1,KIAA0753	yellow	VSMC_M3
GO:0035150	0.82	0.31	5	100	regulation of tube size	BP	1	PPARD,SOD1,GPX1,AKT1,SLC6A4	yellow	VSMC_M3
GO:0035296	0.82	0.31	5	100	regulation of tube diameter	BP	1	PPARD,SOD1,GPX1,AKT1,SLC6A4	yellow	VSMC_M3
GO:0097746	0.82	0.31	5	100	blood vessel diameter maintenance	BP	1	PPARD,SOD1,GPX1,AKT1,SLC6A4	yellow	VSMC_M3
GO:0051173	0.82	0.20	148	2331	positive regulation of nitrogen compound metabolic process	BP	1	NAB2,CDK4,SQSTM1,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,SREBF2,SGSM3,PPARD,VPS28,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,ZC3H12A,PNKP,RCN3,SNRNP70,KMT2E,WDFY2,SIX5,ZNF296,SERTAD1,TTC5,PSMC4,METTL3,DND1,DEAF1,HOXC4,KMT2B,NAT10,ACSL1,ZBTB38,TNKS1BP1,GREM1,MCRS1,CX3CL1,WNT10B,PACSIN3,EGR3,CCAR2,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,RNF19B,DCPS,RRP1B,PDGFA,MMP14,AIP,CLCF1,ASB9,PSME2,TRIM27,PRMT2,THOC5,RIPK3,ADRM1,SMARCD2,BRMS1,BUD23,TNK2,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,PHB2,TRMT112,NDP,BAD,SSBP4,MPV17L2,BUD31,TNFRSF1A,BABAM1,C1QBP,AIMP2,TAF6L,ZBTB49,MTA2,PELP1,CCDC22,FOXK1,PKN1,CAPN2,POLR2A,AMER1,MAD2L2,NANOS3,CTBP1,ARHGEF2,SNF8,PER1,NFIX,SLX1A,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,CSK,MID2,RBM22,ZNF521,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,MYDGF,SIRT6,MAP2K2,AURKAIP1,AP3D1,IRAK1,STK11,TELO2,TAZ,MED16,CARD9,POMT1,NABP2,ERBB4,JUND,KLF13,TRIB2,NSMF,IER5,STUB1,NSMCE3	yellow	VSMC_M3
GO:0032990	0.82	0.23	28	536	cell part morphogenesis	BP	1	PACSIN1,PLEC,CUL7,DBNL,TPBG,PLXND1,BAIAP2,ARHGAP33,BCL2L1,SLC11A2,CORO1B,NGEF,PLEKHO1,IGSF9,NECTIN1,ARPIN,LIMK1,C12orf57,CNP,DBN1,CRABP2,S100A6,EEF2K,ANAPC2,STK11,TWF2,UNC13A,NSMF	yellow	VSMC_M3
GO:0032101	0.82	0.22	39	646	regulation of response to external stimulus	BP	1	TTLL12,PPARD,SHARPIN,PDGFRA,IL1R1,SOCS5,KLF4,TPBG,ZC3H12A,ZYX,MGLL,METTL3,TARBP2,SWAP70,GREM1,CX3CL1,SOD1,TYRO3,ST3GAL4,SELENOS,MVK,RIN3,PDGFA,GPX1,CORO1B,SPX,PSMB4,PLA2G3,RELA,IFI35,CD9,PLAU,TNFRSF1A,C1QBP,CDC37,GIT1,CACTIN,CARD9,TRADD	yellow	VSMC_M3
GO:0031647	0.82	0.25	14	249	regulation of protein stability	BP	1	BAG6,PINX1,WNT10B,CCAR2,CHP1,TMEM183A,LSS,PHB2,USP27X,DPM3,CDC37,NCLN,TELO2,STUB1	yellow	VSMC_M3
GO:0001906	0.82	0.33	4	78	cell killing	BP	1	BCL2L1,RNF19B,RIPK3,CORO1A	yellow	VSMC_M3
GO:0001817	0.82	0.23	29	492	regulation of cytokine production	BP	1	SCRIB,IL1R1,SSC5D,SOCS5,KLF4,ZC3H12A,RELB,PDE4D,CX3CL1,SOD1,SELENOS,TRIM27,RIPK3,PLA2G3,KAT5,RELA,C1QBP,CAPN2,ARHGEF2,PER1,CD276,CSK,GIT1,CACTIN,IRAK1,CARD9,SARS,MIR155,TRIB2	yellow	VSMC_M3
GO:1904019	0.82	0.33	4	86	epithelial cell apoptotic process	BP	1	KRT8,BCL2L1,CAPN10,BAD	yellow	VSMC_M3
GO:0051403	0.83	0.27	10	190	stress-activated MAPK cascade	BP	1	CCM2,ZC3H12A,QARS,PER1,AKT1,MAP2K2,IRAK1,CARD9,IGFBP6,CDC42EP5	yellow	VSMC_M3
GO:0050806	0.83	0.31	5	104	positive regulation of synaptic transmission	BP	1	SQSTM1,ITPR3,RAPSN,SYT12,ZDHHC3	yellow	VSMC_M3
GO:0032231	0.83	0.32	4	92	regulation of actin filament bundle assembly	BP	1	SWAP70,CX3CL1,LIMK1,RHOC	yellow	VSMC_M3
GO:0042445	0.83	0.28	7	133	hormone metabolic process	BP	1	PDGFRA,SCARB1,DHCR7,SGPL1,HSD17B1,CRABP2,STUB1	yellow	VSMC_M3
GO:0035295	0.83	0.21	49	849	tube development	BP	1	BAG6,CTHRC1,SCRIB,CUL7,B4GALT1,PDGFRA,COL15A1,EPN1,KLF4,HOXA1,CCM2,ZC3H12A,RCN3,PLXND1,EMILIN1,RNF220,EIF4EBP1,ARHGAP22,DEAF1,GREM1,KDM2B,PDE3B,CX3CL1,EGR3,DLL4,HTATIP2,IRX1,PDGFA,MMP14,GPX1,ANPEP,PBX1,SGPL1,YJEFN3,PHB2,IGFBP5,AAMP,AIMP2,MTHFR,ZNF358,AKT1,MYDGF,SIRT6,JMJD8,SARS,TGFBR3,MIR214,TNFRSF12A,RNH1	yellow	VSMC_M3
GO:0048762	0.83	0.26	10	198	mesenchymal cell differentiation	BP	1	CUL7,SPRED2,GREM1,AMER1,MAD2L2,S100A4,VASN,TGFBR3,ERBB4,GLIPR2	yellow	VSMC_M3
GO:0071692	0.83	0.24	15	271	protein localization to extracellular region	BP	1	PPARD,EIPR1,PDIA4,RCN3,MYRIP,UCP2,AACS,PCK2,CAPN10,PTPN23,BAD,GLUD1,MIDN,JAGN1,CAVIN1	yellow	VSMC_M3

GO:0002009	0.83	0.23	22	412	morphogenesis of an epithelium	BP	1	CTHRC1,SCRIB,KLF4,CCM2,PLEKHA4,SLC9A3R1,PLXND1,DEAF1,GREM1,KDM2B,DLL4,IRX1,PDGFA,MMP14,PBX1,RHOC,PHB2,IGFBP5,MTHFR,TMEM79,SIRT6,ERBB4	yellow	VSMC_M3
GO:0040017	0.83	0.23	26	462	positive regulation of locomotion	BP	1	TSTA3,PDGFRA,IL1R1,TPBG,ZC3H12A,SCARB1,SWAP70,CX3CL1,PDGFA,MMP14,TWIST2,RHOC,IGFBP5,AAMP,LGALS3,PLAU,C1QBP,WASHC1,ELP5,ARHGEF2,CORO1A,AKT1,TRADD,CAVIN1,NSMF,GLIPR2	yellow	VSMC_M3
GO:0051650	0.83	0.28	7	143	establishment of vesicle localization	BP	1	DCTN2,SCRIB,CHP1,BLOC1S4,MYO19,AP3D1,STK11	yellow	VSMC_M3
GO:0023052	0.83	0.19	271	4258	signaling	BP	1	ENPP1,CD63,CDK4,RUFY1,SQSTM1,GNL1,BAG6,CTHRC1,NELFE,FNIP1,ATF6B,PDLIM4,PRR5,TTLL12,SREBF2,TXNDC15,ITPR3,SGSM3,NUDT3,DEF6,PPARD,EEF1D,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,BOP1,TOM1,PDGFRA,IL1R1,COL15A1,EPN1,SOCS5,KLF4,DBNL,TPBG,WDPCP,CCM2,SPRED2,EIPR1,RGS3,ZC3H12A,FIGNL1,ZYX,RCN3,SNX3,MICAL1,PLEKHA4,MGLL,FAM120B,ANXA5,KRT8,RELB,SLC9A3R1,SERP2,PLXND1,EMILIN1,RNF220,SNX17,PLCD1,CD79A,INSIG1,MYRIP,SEC13,ARHGEF40,UCP2,METTL3,BAIAP2,CXXC5,LAMTOR1,NUMA1,P4HB,EIF4EBP1,ARAP3,DELE1,CAVIN3,RIC8A,ARHGAP22,ARHGAP33,AACS,SCARB1,BCL2L1,ITGB7,PDE4D,SPRYD3,TNS2,RRS1,SWAP70,PLEKHF1,ACSL1,GREM1,DOK1,PDE3B,RAPSN,CX3CL1,WNT10B,SOD1,DGKZ,EGR3,CCAR2,DLL4,CHP1,TYRO3,LSP1,RAB35,SLC35C2,TSPAN5,CISH,APBA2,SELENOS,GSTO1,ITPRIP,RIN3,STK32C,PDGFA,MMP14,PABPN1,GPX1,AIP,NGEF,CLCF1,SYT12,QARS,PCK2,ASB9,ANPEP,TRIM27,PCNT,EIF3A,LIMK1,SCN4A,PRMT2,SPX,THOC5,RIPK3,CAPN10,TNK2,PLA2G3,STMN3,PTPN23,KAT5,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,ZNF385B,YJEFN3,GNB2,PHB2,NDP,IGFBP5,BAD,PLCB3,LAMTOR4,IFI35,SH3BP2,LGALS3,BUD31,PLAU,TNFRSF1A,MVB12A,BABAM1,TEAD4,C1QBP,CHERP,EVC,RCC2,CNP,CCDC22,GLUD1,SDE2,PKN1,DBN1,MAD1L1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,TBKBP1,CRABP2,ARHGEF2,MVP,PER1,RANGRF,PPP4C,CORO1A,RABEP2,TRIM25,RPL37,MTMR4,S100A4,S100A6,SMARCA4,CARM1,TMED1,CDC37,CD276,AATF,CSK,MID2,DOCK11,ZNF830,AKT1,TEDC1,RAB34,SAFB,SAFB2,GIT1,SLC6A4,DHCR24,CARHSP1,MYDGF,MAP2K2,NSDHL,CACTIN,VAGN,HIC1,TRAPPC1,NCALD,MNT,CTNS,TPPC3	yellow	VSMC_M3
GO:0043408	0.83	0.22	29	502	regulation of MAPK cascade	BP	1	NELFE,PDGFRA,KLF4,TPBG,SPRED2,ZC3H12A,SLC9A3R1,EMILIN1,LAMTOR1,CAVIN3,CX3CL1,SOD1,PDGFA,QARS,EIF3A,PHB2,PER1,CSK,AKT1,MYDGF,MAP2K2,IRAK1,CARD9,NDST1,ERBB4,PTPRR,IGFBP6,DUSP5,GLIPR2	yellow	VSMC_M3
GO:0030595	0.83	0.27	8	150	leukocyte chemotaxis	BP	1	PLEC,SWAP70,GREM1,CX3CL1,RIN3,LGALS3,C1QBP,CORO1A	yellow	VSMC_M3
GO:0023061	0.83	0.23	18	325	signal release	BP	1	PPARD,SCRIB,EIPR1,MYRIP,UCP2,AACS,SYT12,PCK2,CAPN10,PLA2G3,PTPN23,BAD,GLUD1,GIT1,SLC6A4,MIDN,JAGN1,UNC13A	yellow	VSMC_M3
GO:0050878	0.83	0.24	15	273	regulation of body fluid levels	BP	1	PLEC,PDGFRA,ANXA5,AQP5,DGKZ,TYRO3,ST3GAL4,PDGFA,BLOC1S4,CD9,PLAU,TMEM79,MTX1,APRT,ERBB4	yellow	VSMC_M3
GO:0031398	0.83	0.29	5	102	positive regulation of protein ubiquitination	BP	1	HSPBP1,AIMP2,AMER1,STUB1,NSMCE3	yellow	VSMC_M3
GO:0051094	0.84	0.20	58	982	positive regulation of developmental process	BP	1	CTHRC1,H2AFY,PACSIN1,PPARD,CUL7,SOCS5,KLF4,DBNL,TPBG,ZC3H12A,EHD2,WDFY2,PLXND1,BAIAP2,NUMA1,P4HB,LRP3,GREM1,KDM2B,CX3CL1,WNT10B,EGR3,MMP14,CORO1B,CLCF1,LIMK1,PLA2G3,SART1,RELA,BAD,TNFRSF1A,C1QBP,KRT10,DBN1,CAPN2,MAD2L2,CRABP2,TMEM79,ARHGEF2,CARM1,EEF2K,AKT1,MYDGF,SIRT6,HMG20B,AP3D1,ANAPC2,STK11,JMJD8,TGFBR3,TRADD,MIR214,ERBB4,TWF2,JUND,UNC13A,ZNF385A,GLIPR2	yellow	VSMC_M3
GO:0031032	0.84	0.26	8	172	actomyosin structure organization	BP	1	PLEC,PDGFRA,ZYX,KRT8,LIMK1,RHOC,ALKBH4,ELN	yellow	VSMC_M3
GO:0099003	0.84	0.27	7	151	vesicle-mediated transport in synapse	BP	1	PACSIN1,SCRIB,SYT12,GIT1,AP3D1,UNC13A,GSG1L	yellow	VSMC_M3
GO:0031325	0.84	0.19	157	2483	positive regulation of cellular metabolic process	BP	1	CD63,NAB2,CDK4,SQSTM1,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,SREBF2,PPARD,SCRIB,PDGFRA,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,ZC3H12A,PNKP,RCN3,SNRNP70,KMT2E,WDFY2,SIX5,ZNF296,SERTAD1,TTC5,PSMC4,METTL3,DND1,DEAF1,HOXC4,KMT2B,SCARB1,NAT10,PLEKHF1,ACSL1,ZBTB38,TNKS1BP1,GREM1,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,DGKZ,EGR3,CCAR2,CHP1,TYRO3,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,RNF19B,DCPS,RRP1B,FABP3,PDGFA,MMP14,AIP,CLCF1,PSME2,TRIM27,PRMT2,THOC5,RIPK3,ADRM1,SMARCD2,BRMS1,BUD23,TNK2,PLA2G3,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,PHB2,TRMT112,NDP,BAD,SSBP4,MPV17L2,BUD31,TNFRSF1A,BABAM1,C1QBP,AIMP2,TAF6L,ZBTB49,MTA2,PELP1,CCDC22,FOXK1,PKN1,CAPN2,POLR2A,AMER1,PIP4K2B,MAD2L2,NANOS3,CTBP1,ARHGEF2,PER1,NFIX,SLX1A,IRF2BPL,TRIM25,SMARCA4,CARM1,AATF,CSK,MID2,RBM22,ZNF521,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,MYDGF,SIRT6,MAP2K2,AURKAIP1,AP3D1,IRAK1,STK11,TELO2,TAZ,MED16,CARD9,POMT1,VAC14,NABP2,ERBB4,JUND,KLF13,TRIB2,NSMF,IER5,STUB1,NSMCE3	yellow	VSMC_M3
GO:2000027	0.84	0.29	5	108	regulation of animal organ morphogenesis	BP	1	CTHRC1,PLEKHA4,GREM1,PDGFA,PHB2	yellow	VSMC_M3
GO:0046942	0.84	0.26	9	173	carboxylic acid transport	BP	1	SLC9A3R1,SLC16A5,SFXN5,SLC16A14,SLC19A1,SLC26A6,PLA2G3,CTNS,SLC27A4	yellow	VSMC_M3
GO:0030278	0.84	0.31	4	91	regulation of ossification	BP	1	ENPP1,GREM1,WNT10B,PBX1	yellow	VSMC_M3
GO:0007059	0.84	0.23	16	288	chromosome segregation	BP	1	DCTN2,BAG6,NCAPH2,H2AFY,NUMA1,RRS1,PINX1,NUDC,BANF1,PHB2,RCC2,EML3,MAD1L1,MAD2L2,NTMT1,MIS12	yellow	VSMC_M3
GO:0032147	0.84	0.29	5	105	activation of protein kinase activity	BP	1	GREM1,RIPK3,PHB2,IRAK1,STK11	yellow	VSMC_M3
GO:0033135	0.84	0.28	5	104	regulation of peptidyl-serine phosphorylation	BP	1	FNIP1,PDE4D,TNKS1BP1,MAD2L2,AKT1	yellow	VSMC_M3

GO:0009888	0.84	0.19	82	1389	tissue development	BP	1	ENPP1,NAB2,CDK4,CTHRC1,H2AFY,PPARD,SCRIB,PLEC,SHARPIN,CUL7,DNPH1,B4GALT1,PDGFRA,COL15A1,COL19A1,KLF4,WDPCP,CCM2,SPRED2,RCN3,PLEKHA4,SLC9A3R1,PLXND1,RNF220,NUMA1,FASN,DEAF1,AACS,PDE4D,GREM1,KDM2B,WNT10B,SOD1,DLL4,IRX1,PDGFA,MMP14,GPX1,TAGLN2,PCK2,COL6A1,NECTIN1,PBX1,RELA,RHOC,PHB2,IGFBP5,BAD,LGALS3,TNFRSF1A,AIMP2,EVC,KRT10,CASP14,AMER1,MTHFR,MAD2L2,CRABP2,TMEM79,ARMC5,S100A4,ZNF358,AKT1,SAFB2,DHCR24,SIRT6,PPL,NSDHL,TJP3,HMG20B,VASN,MBD3,TAZ,GTF3C5,TGFBR3,TRADD,ERBB4,IGSF8,ELN,NOM1,DUSP5,GLIPR2	yellow	VSMC_M3
GO:0050896	0.84	0.17	384	5876	response to stimulus	BP	1	ENPP1,CD63,CDK4,RUFY1,SQSTM1,GNL1,BAG6,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PRRS,TTLL12,SREBF2,SQLE,TXNDC15,H2AFY,ITPR3,HNRNPA0,TRIM11,SGSM3,GUK1,DEF6,PPARD,FANCE,EEF1D,RPL3,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,BOP1,TOM1,PPP1R14B,B4GALT1,PDGFRA,IL1R1,COL15A1,EPN1,SSC5D,SOCS5,KLF4,DBNL,TPBG,HOXA1,PTGR1,WDPCP,CCM2,SPRED2,RGS3,ZC3H12A,FIGNL1,PDIA4,PNKP,ZYX,RCN3,SNX3,MICAL1,PLEKHA4,MGLL,FAM120B,ANXA5,KRT8,RELB,SLC9A3R1,SERP2,MUTYH,PLXND1,EMILIN1,TMUB1,RNF220,DMAP1,SLC30A3,SNX17,PLCD1,DLEC1,CD79A,INSIG1,SEC13,OGG1,TTC5,ARHGEF40,UCP2,SEL1L2,METTL3,BAIAP2,CXXC5,INPPL1,FAAP100,LAMTOR1,NUMA1,P4HB,PYCR1,FASN,RAB20,SMOX,EIF4EBP1,ARAP3,SIGLEC1,DELE1,CAVIN3,RIC8A,GSR,ARHGAP22,SMUG1,ARHGAP33,TARBP2,AACS,SCARB1,HM13,BCL2L1,ITGB7,PDE4D,SPRYD3,TNS2,RRS1,SWAP70,PLEKHF1,ACSL1,ZBTB38,SLC11A2,TNKS1BP1,MMP24,GREM1,DOK1,AQP5,PDE3B,MCRS1,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,HPS1,DLL4,CHP1,TYRO3,SCD,LSP1,RAB35,CHCHD2,SLC35C2,TSPAN5,CISH,SRSF9,ST3GAL4,RNF19B,DCPS,WDR4,SELENOS,GSTO1,ITPRIP,RRP1B,MVK,RIN3,STK32C,FABP3,PDGFA,MMP14,PABPN1,GPX1,AIP,CORO1B,NGEF,CLCF1,IGSF9,SYT12,QARS,PCK2,ASB9,COL6A1,IMPDH2,NECTIN1,ANPEP,TRIM27,PCNT,EIF3A,LIMK1,SLC26A6,PRMT2,SPX,THOC5,UQCRC1,RIPK3,CAPN10,PSMB4,PPOX,TNK2,PLA2G3,STMN3,CEP164,BANF1,KAT5,RELA,SIPA1,MGST3,RHOC,TMEM120A,SCYL1,IDH1,MAP3K14,ARNT2,LIMD1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,ZNF385B,YJEFN3,GNB2,ATIC,BLOC1S4,TXNRD2,PHB	yellow	VSMC_M3
GO:0010941	0.84	0.19	77	1223	regulation of cell death	BP	1	CDK4,SQSTM1,BAG6,FNIP1,PPARD,SCRIB,LGALS1,B4GALT1,KLF4,ZC3H12A,FIGNL1,MICAL1,ANXA5,SLC9A3R1,OGG1,UCP2,PHLDA1,P4HB,PYCR1,BCL2L1,PLEKHF1,GREM1,KDM2B,RAPSN,CX3CL1,WNT10B,SOD1,EGR3,CCAR2,CHP1,TYRO3,HTATIP2,DCPS,SELENOS,ITPRIP,RRP1B,GPX1,CLCF1,QARS,PRMT2,RIPK3,TWIST2,CAPN10,BRMS1,PLA2G3,RELA,ARNT2,PHB2,BAD,LGALS3,TNFRSF1A,C1QBP,AIMP2,USP27X,CAPN2,NANOS3,DFFA,ARHGEF2,CORO1A,EEF2K,AATF,ZNF830,AKT1,DHCR24,MYDGF,TRAP1,MNT,CARD9,SLC27A4,TRADD,MIR214,TNFRSF12A,PTMA,ZNF385A,TXNDC12,NSMF,CDC34	yellow	VSMC_M3
GO:0045926	0.84	0.24	10	195	negative regulation of growth	BP	1	ENPP1,PPARD,GREM1,CCAR2,CCDC85B,SIPA1,IGFBP5,SMARCA4,SLC6A4,STK11	yellow	VSMC_M3
GO:0007173	0.84	0.30	4	90	epidermal growth factor receptor signaling pathway	BP	1	SOCS5,MVB12A,MVP,AKT1	yellow	VSMC_M3
GO:0007093	0.84	0.27	6	117	mitotic cell cycle checkpoint signaling	BP	1	BABAM1,SDE2,MAD1L1,MAD2L2,ZNF830,NABP2	yellow	VSMC_M3
GO:0002697	0.84	0.24	11	206	regulation of immune effector process	BP	1	IL1R1,SOCS5,ZC3H12A,CLCF1,RIPK3,PLA2G3,PHB2,LGALS3,C1QBP,PKN1,MAD2L2	yellow	VSMC_M3
GO:0050821	0.84	0.25	8	154	protein stabilization	BP	1	BAG6,WNT10B,CHP1,PHB2,USP27X,CDC37,NCLN,TELO2	yellow	VSMC_M3
GO:0051304	0.85	0.29	4	85	chromosome separation	BP	1	NCAPH2,NUMA1,MAD1L1,MAD2L2	yellow	VSMC_M3
GO:0055067	0.85	0.28	5	108	monovalent inorganic cation homeostasis	BP	1	RAB20,CHP1,SLC26A6,SPX,CCDC115	yellow	VSMC_M3
GO:0014070	0.85	0.19	41	703	response to organic cyclic compound	BP	1	CDK4,PPARD,LGALS1,KLF4,ZC3H12A,SLC9A3R1,INSIG1,OGG1,AACS,BCL2L1,ACSL1,WNT10B,SOD1,MMP14,PCK2,SLC26A6,PRMT2,KAT5,RELA,IDH1,ARNT2,PHB2,IGFBP5,BAD,ARPC1B,PKN1,MTHFR,PER1,PMVK,TRIM25,SMARCA4,CARM1,EEF2K,AKT1,HMGCS1,SAFB,SAFB2,SLC6A4,MBD3,CARD9,JUND	yellow	VSMC_M3
GO:0001932	0.85	0.19	50	845	regulation of protein phosphorylation	BP	1	ENPP1,NAB2,CTDSP2,SQSTM1,SNX9,FNIP1,PRR5,H2AFY,PLEC,SOCS5,SPRED2,ZC3H12A,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SERTAD1,TARBP2,PDE4D,ACSL1,TNKS1BP1,GREM1,CX3CL1,SOD1,CHP1,PDGFA,CLCF1,QARS,TRIM27,RIPK3,TNK2,PHB2,CTDSP1,TNFRSF1A,PKN1,MAD2L2,ARHGEF2,MVP,EEF2K,CDC37,CSK,AKT1,MYDGF,MAP2K2,CACTIN,IRAK1,STK11,TELO2,ERBB4,TRIB2	yellow	VSMC_M3
GO:0051272	0.85	0.20	26	466	positive regulation of cellular component movement	BP	1	TSTA3,PDGFRA,IL1R1,ZC3H12A,SCARB1,SWAP70,CX3CL1,PDGFA,MMP14,TWIST2,RHOC,IGFBP5,AAMP,LGALS3,PLAU,C1QBP,WASHC1,ELP5,ARHGEF2,CORO1A,AKT1,STK11,TRADD,CAVIN1,NSMF,GLIPR2	yellow	VSMC_M3
GO:0022414	0.85	0.18	63	1029	reproductive process	BP	1	SPAG1,BAG6,NCAPH2,SBF1,PPARD,IFT27,CUL7,B4GALT1,PDGFRA,EPN1,FIGNL1,KRT8,SIX5,ZNF296,PAFAH1B3,DLEC1,UCP2,METTL3,CEP131,NUMA1,DND1,YIF1B,RPL29,GNPDA1,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,MMP14,SLC19A1,TRIM27,SLC26A6,IQCG,PLA2G3,PBX1,IDH1,SGPL1,PHB2,IGFBP5,BAD,CD9,C1QBP,CAPN2,NANOS3,IRF2BPL,ZNF830,AKT1,HMGCS1,RFX2,SAFB2,SLC6A4,DHCR24,NSDHL,STK11,TAZ,FAM50A,GAS8,IGSF8,TUBGCP2,MEIG1	yellow	VSMC_M3

GO:0051247	0.85	0.18	70	1140	positive regulation of protein metabolic process	BP	1	NAB2,CDK4,SQSTM1,BAG6,SNX9,NELFE,FNIP1,PRR5,SGSM3,VPS28,HSPBP1,SOCS5,RPS9,KLF4,ZC3H12A,RCN3,KMT2E,WDFY2,PSMC4,METTL3,NAT10,ACSL1,TNKS1BP1,GREM1,CX3CL1,PACSIN3,CHP1,PCIF1,RNF19B,PDGFA,MMP14,CLCF1,ASB9,PSME2,RIPK3,ADRM1,BRMS1,TNK2,KAT5,RELA,SMARCB1,PHB2,BAD,MPV17L2,TNFRSF1A,C1QBP,AIMP2,CCDC22,AMER1,MAD2L2,CTBP1,ARHGEF2,SNF8,CSK,AKT1,PAIP1,MYDGF,SIRT6,MAP2K2,AURKAIP1,IRAK1,STK11,TELO2,CARD9,POMT1,ERBB4,TRIB2,NSMF,STUB1,NSMCE3	yellow	VSMC_M3
GO:0006887	0.85	0.22	14	266	exocytosis	BP	1	SCRIB,MICAL1,EXOC3,SYT12,PLA2G3,WASHC1,RAB3IL1,TMEM79,SNF8,CORO1A,GIT1,RABEPK,JAGN1,UNC13A	yellow	VSMC_M3
GO:0006950	0.85	0.17	175	2715	response to stress	BP	1	CDK4,SQSTM1,GNL1,BAG6,HDAC10,FNIP1,ATF6B,TTLL12,SREBF2,H2AFY,HNRNPA0,TRIM11,PPARD,FANCE,SCRIB,PLEC,LGALS1,SHARPIN,PPP1R14B,B4GALT1,PDGFRA,IL1R1,SSC5D,SOCS5,KLF4,CCM2,SPRED2,ZC3H12A,FIGNL1,PDIA4,PNKP,ZYX,RCN3,MGLL,ANXA5,KRT8,RELB,SERP2,MUTYH,TMUB1,DMAP1,DLEC1,INSIG1,OGG1,TTC5,UCP2,SEL1L2,METTL3,FAAP100,P4HB,PYCR1,RAB20,EIF4EBP1,SIGLEC1,GSR,SMUG1,TARBP2,AACS,SCARB1,HM13,BCL2L1,ZBTB38,SLC11A2,TNKS1BP1,AQP5,MCRS1,CX3CL1,SOD1,ACTR5,ANKRD2,DGKZ,CCAR2,TYRO3,LSP1,CHCHD2,ST3GAL4,RNF19B,WDR4,SELENOS,MVK,PDGFA,MMP14,GPX1,CORO1B,QARS,PCK2,TRIM27,SLC26A6,THOC5,RIPK3,PSMB4,TNK2,PLA2G3,CEP164,KAT5,RELA,SIPA1,RHOC,SCYL1,IDH1,MAP3K14,ARNT2,LIMD1,BLOC1S4,TXNRD2,PHB2,BAD,IFI35,OTUB1,LETM1,LGALS3,CD9,PLAU,TNFRSF1A,BABAM1,C1QBP,UBXN1,FOXK1,SDE2,PKN1,CAPN2,MTHFR,MAD2L2,TBKBP1,ARHGEF2,ARMC5,PER1,PPP4C,CORO1A,SLX1A,TRIM25,USP43,EEF2K,CDC37,AATF,CXorf57,C19orf66,MID2,ZNF830,AKT1,ALKBH7,GIT1,SLC6A4,DHCR24,SIRT6,PPL,MAP2K2,CACTIN,VASN,HIC1,TRAP1,IRAK1,MAN1B1,C8G,STK11,WDR24,CARD9,TGFBR3,TRADD,MIR214,RF00024,NDST1,NABP2,TNFRSF12A,FADS1,IGFBP6,JAGN1,ZNF385A,TXNDC12,CDC42EP5,FBXO6,IER5,OSER1,STUB1,NSMCE3	yellow	VSMC_M3
GO:0051047	0.85	0.23	11	211	positive regulation of secretion	BP	1	PPARD,MYRIP,AACS,PCK2,CAPN10,PLA2G3,PTPN23,BAD,GLUD1,SNF8,SLC6A4	yellow	VSMC_M3
GO:0030038	0.85	0.28	4	95	contractile actin filament bundle assembly	BP	1	ZYX,LIMK1,RHOC,ELN	yellow	VSMC_M3
GO:0043149	0.85	0.28	4	95	stress fiber assembly	BP	1	ZYX,LIMK1,RHOC,ELN	yellow	VSMC_M3
GO:0035725	0.85	0.27	5	120	sodium ion transmembrane transport	BP	1	SLC9A3R1,CHP1,SCN4A,RANGRF,SLC6A4	yellow	VSMC_M3
GO:0006928	0.85	0.17	92	1565	movement of cell or subcellular component	BP	1	CD63,CTHRC1,PPARD,TSTA3,SCRIB,PLEC,IFT27,B4GALT1,PDGFRA,IL1R1,KLF4,TPBG,WDPCP,ZC3H12A,SLC9A3R1,PLXND1,EMILIN1,UNK,CEP131,YIF1B,RIC8A,SCARB1,ITGB7,PDE4D,SWAP70,GREM1,CX3CL1,SOD1,DGKZ,EGR3,DLL4,TYRO3,ST3GAL4,RIN3,PDGFA,MMP14,GPX1,CORO1B,PLEKHO1,IGSF9,NECTIN1,ARPIN,RIPK3,TWIST2,IQCG,PLA2G3,PTPN23,RHOC,FMNL1,LIMD1,SGPL1,BLOC1S4,PHB2,IGFBP5,AAMP,LGALS3,CD9,PLAU,C1QBP,WASHC1,RCC2,MTA2,ELP5,PKN1,MIIP,ARHGEF2,RANGRF,CORO1A,MYO19,AKT1,ACAP3,AP3D1,SSNA1,STK11,TMEM201,GAS8,SPG7,WDR34,TGFBR3,TRADD,MIR214,ERBB4,PTPRR,IGFBP6,JAGN1,CAVIN1,IGSF8,NSMF,GLIPR2,TUBGCP2,MEIG1,ARPC5L	yellow	VSMC_M3
GO:0048589	0.85	0.20	27	501	developmental growth	BP	1	CDK4,PPARD,PLEC,DBNL,CCM2,TNS2,WNT10B,SOD1,GPX1,LIMK1,PRMT2,SGPL1,CD9,EVC,DBN1,CRABP2,SP2,ZNF830,AKT1,SLC6A4,SIRT6,ANAPC2,STK11,TGFBR3,ERBB4,TWF2,UNC13A	yellow	VSMC_M3
GO:0048284	0.85	0.26	6	120	organelle fusion	BP	1	RAB20,CHP1,PIP4K2B,STX10,CORO1A,RAB34	yellow	VSMC_M3
GO:0000041	0.85	0.28	4	86	transition metal ion transport	BP	1	SLC30A3,SLC11A2,NECTIN1,SLC39A1	yellow	VSMC_M3
GO:0015918	0.85	0.28	4	89	sterol transport	BP	1	SREBF2,LAMTOR1,SCARB1,YJEFN3	yellow	VSMC_M3
GO:0000003	0.85	0.18	63	1031	reproduction	BP	1	SPAG1,BAG6,NCAPH2,SBF1,PPARD,IFT27,CUL7,B4GALT1,PDGFRA,EPN1,FIGNL1,KRT8,SIX5,ZNF296,PAFAH1B3,DLEC1,UCP2,METTL3,CEP131,NUMA1,DND1,YIF1B,RPL29,GNPDA1,MORN2,DEAF1,BCL2L1,KDM2B,SOD1,TYRO3,KDM1B,MMP14,SLC19A1,TRIM27,SLC26A6,IQCG,PLA2G3,PBX1,IDH1,SGPL1,PHB2,IGFBP5,BAD,CD9,C1QBP,CAPN2,NANOS3,IRF2BPL,ZNF830,AKT1,HMGCS1,RFX2,SAFB2,SLC6A4,DHCR24,NSDHL,STK11,TAZ,FAM50A,GAS8,IGSF8,TUBGCP2,MEIG1	yellow	VSMC_M3
GO:0001816	0.85	0.19	29	504	cytokine production	BP	1	SCRIB,IL1R1,SSC5D,SOCS5,KLF4,ZC3H12A,RELB,PDE4D,CX3CL1,SOD1,SELENOS,TRIM27,RIPK3,PLA2G3,KAT5,RELA,C1QBP,CAPN2,ARHGEF2,PER1,CD276,CSK,GIT1,CACTIN,IRAK1,CARD9,SARS,MIR155,TRIB2	yellow	VSMC_M3
GO:1903322	0.85	0.26	6	121	positive regulation of protein modification by small protein conjugation or removal	BP	1	HSPBP1,ZC3H12A,AIMP2,AMER1,STUB1,NSMCE3	yellow	VSMC_M3

GO:0010033	0.85	0.17	143	2273	response to organic substance	BP	1	ENPP1,CD63,CDK4,BAG6,ATF6B,TTLL12,SREBF2,SQLE,HNRNPA0,PPARD,RPL3,LGALS1,SHARPIN,PDGFRA,IL1R1,SSC5D,SOCS5,KLF4,SPRED2,ZC3H12A,ZYX,RCN3,KRT8,RELB,SLC9A3R1,SERP2,EMILIN1,TMUB1,DMAP1,INSIG1,OGG1,UCP2,SEL1L2,METTL3,BAIAP2,INPPL1,LAMTOR1,NUMA1,P4HB,FASN,RAB20,EIF4EBP1,AACS,SCARB1,HM13,BCL2L1,TNS2,ACSL1,GREM1,DOK1,PDE3B,CX3CL1,WNT10B,SOD1,EGR3,DLL4,SCD,LSP1,RAB35,SRSF9,DCPS,SELENOS,FABP3,MMP14,PABPN1,CORO1B,CLCF1,PCK2,COL6A1,IMPDH2,SLC26A6,PRMT2,UQCRC1,CAPN10,KAT5,RELA,MGST3,IDH1,ARNT2,SMARCB1,ATIC,PHB2,IGFBP5,BAD,LAMTOR4,OTUB1,ARPC1B,CD9,TNFRSF1A,UBXN1,CNP,PELP1,KLF3,PKN1,CAPN2,PALM3,MTHFR,PIP4K2B,ARHGEF2,PER1,CORO1A,PMVK,TUFM,TRIM25,MTMR4,SMARCA4,CARM1,EEF2K,CDC37,C19orf66,CSK,AKT1,HMGCS1,KHSRP,SAFB,SAFB2,GIT1,SLC6A4,DHCR24,LDOC1,CACTIN,VASN,IRAK1,MBD3,MAN1B1,STK11,CARD9,APRT,SLC27A4,TGFBR3,TRADD,NDST1,ERBB4,TWF2,JUND,LOXL1,JAGN1,COL6A2,NSMF,CDC34,FBXO6,STUB1,NSMCE3	yellow	VSMC_M3
GO:0010604	0.85	0.17	163	2586	positive regulation of macromolecule metabolic process	BP	1	CD63,NAB2,CDK4,SQSTM1,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,SREBF2,H2AFY,HNRNPA0,SGSM3,PPARD,SCRIB,VPS28,IL1R1,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,ZC3H12A,PNKP,RCN3,SNRNP70,KMT2E,WDFY2,SIX5,ZNF296,RELB,EMILIN1,SERTAD1,TTC5,PSMC4,METTL3,DND1,DEAF1,HOXC4,KMT2B,NAT10,PDE4D,LRP3,ACSL1,ZBTB38,TNKS1BP1,GREM1,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,EGR3,CCAR2,DLL4,CHP1,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,RNF19B,DCPS,RRP1B,PDGFA,MMP14,C14orf93,AIP,CLCF1,ASB9,PSME2,TRIM27,PRMT2,THOC5,RIPK3,ADRM1,SMARCD2,BRMS1,BUD23,TNK2,PLA2G3,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,PHB2,TRMT112,NDP,BAD,SSBP4,MPV17L2,BUD31,TNFRSF1A,BABAM1,C1QBP,AIMP2,TAF6L,ZBTB49,MTA2,PELP1,CCDC22,FOXK1,PKN1,POLR2A,AMER1,MAD2L2,NANOS3,CTBP1,ARHGEF2,SNF8,PER1,NFIX,SLX1A,IRF2BPL,TRIM25,SMARCA4,CARM1,CD276,AATF,CSK,MID2,RBM22,ZNF521,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,SLC6A4,MYDGF,SIRT6,MAP2K2,AURKAIP1,AP3D1,IRAK1,STK11,TELO2,MED16,CARD9,POMT1,NABP2,ERBB4,JUND,KLF13,TENT5B,TRIB2,NSMF,IER5,STUB1,NSMCE3	yellow	VSMC_M3
GO:0060348	0.86	0.24	8	172	bone development	BP	1	NAB2,INSIG1,INPPL1,GREM1,MMP14,HSD17B1,AMER1,ZNF385A	yellow	VSMC_M3
GO:0022008	0.86	0.17	72	1272	neurogenesis	BP	1	NAB2,CTHRC1,HDAC10,PBX2,TRIM11,TRAPPC9,PACSIN1,SCRIB,PLEC,LGALS1,IFT27,CUL7,SECISBP2,KLF4,DBNL,TPBG,WDPCP,SNX3,SLC9A3R1,PLXND1,UNK,METTL3,BAIAP2,ARHGAP33,SLC11A2,MMP24,CX3CL1,WNT10B,SOD1,DLL4,RAB35,IRX1,MMP14,NGEF,CLCF1,IGSF9,NECTIN1,LIMK1,PLA2G3,STMN3,PBX1,RELA,SCYL1,PBX4,BLOC1S4,C12orf57,CTDSP1,CD9,CNP,DBN1,CRABP2,ARHGEF2,S100A6,CARM1,EEF2K,EML1,CSK,ZNF521,AKT1,GIT1,SLC6A4,HMG20B,ACAP3,ANAPC2,STK11,NEGR1,ERBB4,TWF2,UNC13A,NSMF,GBA2,TUBGCP2	yellow	VSMC_M3
GO:0050673	0.86	0.21	17	316	epithelial cell proliferation	BP	1	PPARD,B4GALT1,DEAF1,SCARB1,WNT10B,EGR3,DLL4,MMP14,GPX1,PHB2,IGFBP5,BAD,AKT1,MYDGF,SIRT6,STK11,TGFBR3	yellow	VSMC_M3
GO:0016055	0.86	0.20	20	373	Wnt signaling pathway	BP	1	CTHRC1,KLF4,TPBG,SNX3,PLEKHA4,SLC9A3R1,RNF220,GREM1,WNT10B,CCAR2,UMD1,NDP,AMER1,MAD2L2,SMARCA4,HIC1,CSNK1G2,STK11,IGFBP6,APCDD1L	yellow	VSMC_M3
GO:0043500	0.86	0.28	4	88	muscle adaptation	BP	1	KLF4,IGFBP5,TNFRSF1A,MIR214	yellow	VSMC_M3
GO:0034329	0.86	0.21	15	318	cell junction assembly	BP	1	PLEC,DBNL,TPBG,WDPCP,PLXND1,GREM1,MMP14,LRFN4,NECTIN1,RHOC,CD9,RCC2,EEF2K,CLDN6,ERBB4	yellow	VSMC_M3
GO:0010595	0.86	0.26	5	105	positive regulation of endothelial cell migration	BP	1	TSTA3,ZC3H12A,SCARB1,AAMP,AKT1	yellow	VSMC_M3
GO:2000116	0.86	0.23	9	167	regulation of cysteine-type endopeptidase activity	BP	1	FNIP1,KLF4,MICAL1,DELE1,GPX1,BAD,AKT1,DHCR24,CARD9	yellow	VSMC_M3
GO:0018107	0.86	0.28	4	98	peptidyl-threonine phosphorylation	BP	1	SPRED2,TNKS1BP1,PKN1,AKT1	yellow	VSMC_M3
GO:0120039	0.86	0.19	26	517	plasma membrane bounded cell projection morphogenesis	BP	1	PACSIN1,CUL7,DBNL,TPBG,PLXND1,BAIAP2,ARHGAP33,SLC11A2,CORO1B,NGEF,PLEKHO1,IGSF9,NECTIN1,ARPIN,LIMK1,C12orf57,CNP,DBN1,CRABP2,S100A6,EEF2K,ANAPC2,STK11,TWF2,UNC13A,NSMF	yellow	VSMC_M3
GO:0010959	0.86	0.21	14	263	regulation of metal ion transport	BP	1	CD63,SLC9A3R1,PDE4D,CX3CL1,PACSIN3,CHP1,GSTO1,NKAIN1,TRIM27,LGALS3,PER1,RANGRF,CORO1A,AKT1	yellow	VSMC_M3
GO:0045055	0.86	0.23	8	167	regulated exocytosis	BP	1	SCRIB,MICAL1,SYT12,PLA2G3,TMEM79,CORO1A,GIT1,UNC13A	yellow	VSMC_M3
GO:0032270	0.86	0.17	65	1066	positive regulation of cellular protein metabolic process	BP	1	NAB2,CDK4,SQSTM1,BAG6,SNX9,NELFE,FNIP1,PRR5,HSPBP1,SOCS5,RPS9,KLF4,ZC3H12A,RCN3,KMT2E,WDFY2,PSMC4,METTL3,NAT10,ACSL1,TNKS1BP1,GREM1,CX3CL1,PACSIN3,CHP1,PCIF1,RNF19B,PDGFA,MMP14,CLCF1,PSME2,RIPK3,ADRM1,BRMS1,TNK2,KAT5,SMARCB1,PHB2,BAD,MPV17L2,TNFRSF1A,C1QBP,AIMP2,CCDC22,AMER1,MAD2L2,CTBP1,ARHGEF2,CSK,AKT1,PAIP1,MYDGF,SIRT6,MAP2K2,AURKAIP1,IRAK1,STK11,TELO2,CARD9,POMT1,ERBB4,TRIB2,NSMF,STUB1,NSMCE3	yellow	VSMC_M3
GO:0031098	0.86	0.22	10	197	stress-activated protein kinase signaling cascade	BP	1	CCM2,ZC3H12A,QARS,PER1,AKT1,MAP2K2,IRAK1,CARD9,IGFBP6,CDC42EP5	yellow	VSMC_M3
GO:0010038	0.86	0.21	15	279	response to metal ion	BP	1	CDK4,ITPR3,SLC30A3,OGG1,SLC11A2,SOD1,SYT12,BAD,HSD17B1,ANXA11,S100A16,EEF2K,AKT1,ATP5F1D,JUND	yellow	VSMC_M3
GO:0072006	0.86	0.26	5	118	nephron development	BP	1	PDGFRA,GREM1,IRX1,PBX1,ERBB4	yellow	VSMC_M3
GO:0007626	0.86	0.25	6	132	locomotory behavior	BP	1	C12orf10,SOD1,CNP,GIT1,CTNS,NEGR1	yellow	VSMC_M3
GO:0048592	0.86	0.26	5	118	eye morphogenesis	BP	1	RING1,KDM2B,AQP5,NECTIN1,C12orf57	yellow	VSMC_M3
GO:0006997	0.86	0.26	5	112	nucleus organization	BP	1	PLEC,PHF2,TMEM43,NUMA1,DCTN1	yellow	VSMC_M3

GO:0008219	0.86	0.16	100	1587	cell death	BP	1	CDK4,SQSTM1,BAG6,FNIP1,PPARD,SCRIB,LGALS1,SHARPIN,B4GALT1,KLF4,ZC3H12A,FIGNL1,MICAL1,EMP3,ANXA5,KRT8,SLC9A3R1,OGG1,UCP2,PHLDA1,P4HB,PYCR1,DELE1,BCL2L1,PLEKHF1,GREM1,KDM2B,RAPSN,CX3CL1,WNT10B,SOD1,EGR3,CCAR2,CHP1,TYRO3,HTATIP2,DCPS,SELENOS,ITPRIP,RRP1B,GPX1,CLCF1,QARS,PRMT2,RIPK3,TWIST2,CAPN10,BRMS1,PLA2G3,RELA,ARNT2,ZDHHC3,SGPL1,CHCHD10,ZNF385B,PHB2,BAD,LGALS3,TNFRSF1A,C1QBP,AIMP2,USP27X,CASP14,PKN1,CAPN2,SLTM,NANOS3,BCL7C,DFFA,TMEM79,ARHGEF2,PLEKHO2,CORO1A,EEF2K,AATF,ATG3,ZNF830,AKT1,PACS2,ALKBH7,DHCR24,MYDGF,CDK11B,HIC1,TRAP1,MNT,MKNK2,STK11,CARD9,SPG7,SLC27A4,TRADD,MIR214,TNFRSF12A,ERBB4,PTMA,ZNF385A,TXNDC12,NSMF,CDC34	yellow	VSMC_M3
GO:2000147	0.86	0.19	25	455	positive regulation of cell motility	BP	1	TSTA3,PDGFRA,IL1R1,ZC3H12A,SCARB1,SWAP70,CX3CL1,PDGFA,MMP14,TWIST2,RHOC,IGFBP5,AAMP,LGALS3,PLAU,C1QBP,WASHC1,ELP5,ARHGEF2,CORO1A,AKT1,TRADD,CAVIN1,NSMF,GLIPR2	yellow	VSMC_M3
GO:0060249	0.86	0.21	11	218	anatomical structure homeostasis	BP	1	RCN3,DCTN1,CX3CL1,SOD1,TYRO3,CORO1A,TSPOAP1,CSK,ZNF830,TJP3,STK11	yellow	VSMC_M3
GO:0051223	0.86	0.19	23	412	regulation of protein transport	BP	1	SREBF2,PPARD,VPS28,EIPR1,ZC3H12A,SNX3,DMAP1,INSIG1,MYRIP,UCP2,CEP131,AACS,CHP1,PCK2,PCNT,CAPN10,PTPN23,BAD,GLUD1,CSK,RBM22,MIDN,JAGN1	yellow	VSMC_M3
GO:0048872	0.86	0.21	12	229	homeostasis of number of cells	BP	1	KMT2E,SLC11A2,SOD1,RIPK3,PKN1,CORO1A,DOCK11,AKT1,CARD9,TGFBR3,ARMCX1,KLF13	yellow	VSMC_M3
GO:0001936	0.86	0.25	5	111	regulation of endothelial cell proliferation	BP	1	EGR3,DLL4,AKT1,MYDGF,SIRT6	yellow	VSMC_M3
GO:0009266	0.87	0.23	7	137	response to temperature stimulus	BP	1	UCP2,MMP24,SOD1,AKT1,IRAK1,IER5,STUB1	yellow	VSMC_M3
GO:0000209	0.87	0.21	10	203	protein polyubiquitination	BP	1	SHARPIN,RNF19B,TRIM27,OTUB1,RUSC1,BLMH,ANAPC2,ZNRF1,CDC34,STUB1	yellow	VSMC_M3
GO:0002700	0.87	0.25	5	106	regulation of production of molecular mediator of immune response	BP	1	IL1R1,CLCF1,PHB2,PKN1,MAD2L2	yellow	VSMC_M3
GO:0015711	0.87	0.20	12	228	organic anion transport	BP	1	SLC52A2,PLEKHA8,SLC9A3R1,SLC16A5,SFXN5,SLC35C2,SLC16A14,SLC19A1,SLC26A6,PLA2G3,CTNS,SLC27A4	yellow	VSMC_M3
GO:0031333	0.87	0.25	5	115	negative regulation of protein-containing complex assembly	BP	1	EIF4EBP1,CAPG,PEX5,MIR214,TWF2	yellow	VSMC_M3
GO:0048858	0.87	0.18	26	520	cell projection morphogenesis	BP	1	PACSIN1,CUL7,DBNL,TPBG,PLXND1,BAIAP2,ARHGAP33,SLC11A2,CORO1B,NGEF,PLEKHO1,IGSF9,NECTIN1,ARPIN,LIMK1,C12orf57,CNP,DBN1,CRABP2,S100A6,EEF2K,ANAPC2,STK11,TWF2,UNC13A,NSMF	yellow	VSMC_M3
GO:0060560	0.87	0.22	9	200	developmental growth involved in morphogenesis	BP	1	DBNL,LIMK1,DBN1,CRABP2,SIRT6,ANAPC2,STK11,TWF2,UNC13A	yellow	VSMC_M3
GO:0090092	0.87	0.21	9	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SPRED2,EMILIN1,NUMA1,GREM1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0001501	0.87	0.18	22	413	skeletal system development	BP	1	NAB2,PDGFRA,COL19A1,HOXA1,INSIG1,INPPL1,DEAF1,HOXC4,GREM1,WNT10B,PAPSS1,MMP14,EXTL1,PBX1,SGPL1,HSD17B1,TEAD4,EVC,AMER1,SLC39A1,NDST1,ZNF385A	yellow	VSMC_M3
GO:0099504	0.87	0.23	6	138	synaptic vesicle cycle	BP	1	PACSIN1,SCRIB,SYT12,GIT1,AP3D1,UNC13A	yellow	VSMC_M3
GO:0007154	0.87	0.15	272	4300	cell communication	BP	1	ENPP1,CD63,CDK4,RUFY1,SQSTM1,GNL1,BAG6,CTHRC1,NELFE,FNIP1,ATF6B,PDLIM4,PRR5,TTLL12,SREBF2,TXNDC15,ITPR3,SGSM3,NUDT3,DEF6,PPARD,EEF1D,SCRIB,PLEC,LGALS1,IFT27,SHARPIN,BOP1,TOM1,PDGFRA,IL1R1,COL15A1,EPN1,SOCS5,KLF4,DBNL,TPBG,WDPCP,CCM2,SPRED2,EIPR1,RGS3,ZC3H12A,FIGNL1,ZYX,RCN3,SNX3,MICAL1,PLEKHA4,MGLL,FAM120B,ANXA5,KRT8,RELB,SLC9A3R1,SERP2,PLXND1,EMILIN1,RNF220,SNX17,PLCD1,CD79A,INSIG1,MYRIP,SEC13,ARHGEF40,UCP2,METTL3,BAIAP2,CXXC5,LAMTOR1,NUMA1,P4HB,EIF4EBP1,ARAP3,DELE1,CAVIN3,RIC8A,ARHGAP22,ARHGAP33,AACS,SCARB1,BCL2L1,ITGB7,PDE4D,SPRYD3,TNS2,RRS1,SWAP70,PLEKHF1,ACSL1,GREM1,DOK1,PDE3B,RAPSN,CX3CL1,WNT10B,SOD1,DGKZ,EGR3,CCAR2,DLL4,CHP1,TYRO3,LSP1,RAB35,SLC35C2,TSPAN5,CISH,APBA2,DCPS,SELENOS,GSTO1,ITPRIP,RIN3,STK32C,PDGFA,MMP14,PABPN1,GPX1,AIP,NGEF,CLCF1,SYT12,QARS,PCK2,ASB9,ANPEP,TRIM27,PCNT,EIF3A,LIMK1,SCN4A,PRMT2,SPX,THOC5,RIPK3,CAPN10,TNK2,PLA2G3,STMN3,PTPN23,KAT5,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,ZNF385B,YJEFN3,GNB2,PHB2,NDP,IGFBP5,BAD,PLCB3,LAMTOR4,IFI35,SH3BP2,LGALS3,BUD31,PLAU,TNFRSF1A,MVB12A,BABAM1,TEAD4,C1QBP,CHERP,EVC,RCC2,CNP,CCDC22,GLUD1,SDE2,PKN1,DBN1,MAD1L1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,TBKBP1,CRABP2,ARHGEF2,MVP,PER1,RANGRF,PPP4C,CORO1A,RABEP2,TRIM25,RPL37,MTMR4,S100A4,S100A6,SMARCA4,CARM1,TMED1,CDC37,CD276,AATF,CSK,MID2,DOCK11,ZNF830,AKT1,TEDC1,RAB34,SAFB,SAFB2,GIT1,SLC6A4,DHCR24,CARHSP1,MYDGF,MAP2K2,	yellow	VSMC_M3
GO:0006310	0.87	0.20	13	245	DNA recombination	BP	1	HDAC10,FIGNL1,SWAP70,MCRS1,ACTR5,CLCF1,MAD2L2,PPP4C,SLX1A,CXorf57,SIRT6,NABP2,NSMCE3	yellow	VSMC_M3
GO:1901605	0.87	0.22	8	146	alpha-amino acid metabolic process	BP	1	MPST,SEPHS1,PYCR1,THAP4,GLUD1,ILVBL,MTHFR,BLMH	yellow	VSMC_M3
GO:0030182	0.87	0.16	59	1067	neuron differentiation	BP	1	CTHRC1,PBX2,TRAPPC9,PACSIN1,SCRIB,LGALS1,IFT27,CUL7,SECISBP2,KLF4,DBNL,TPBG,WDPCP,SNX3,SLC9A3R1,PLXND1,UNK,BAIAP2,ARHGAP33,SLC11A2,CX3CL1,WNT10B,SOD1,DLL4,RAB35,IRX1,NGEF,IGSF9,NECTIN1,LIMK1,PLA2G3,STMN3,PBX1,SCYL1,PBX4,BLOC1S4,C12orf57,CTDSP1,CNP,DBN1,CRABP2,ARHGEF2,S100A6,CARM1,EEF2K,ZNF521,AKT1,GIT1,SLC6A4,HMG20B,ACAP3,ANAPC2,STK11,NEGR1,ERBB4,TWF2,UNC13A,NSMF,GBA2	yellow	VSMC_M3
GO:0032872	0.87	0.22	7	148	regulation of stress-activated MAPK cascade	BP	1	ZC3H12A,QARS,PER1,AKT1,MAP2K2,CARD9,IGFBP6	yellow	VSMC_M3
GO:0009267	0.87	0.23	6	130	cellular response to starvation	BP	1	FNIP1,SREBF2,ZC3H12A,UCP2,WDR24,FADS1	yellow	VSMC_M3
GO:0030335	0.87	0.18	24	443	positive regulation of cell migration	BP	1	TSTA3,PDGFRA,IL1R1,ZC3H12A,SCARB1,SWAP70,CX3CL1,PDGFA,MMP14,TWIST2,RHOC,IGFBP5,AAMP,LGALS3,PLAU,C1QBP,WASHC1,ELP5,ARHGEF2,CORO1A,AKT1,TRADD,NSMF,GLIPR2	yellow	VSMC_M3

GO:0033365	0.87	0.16	43	737	protein localization to organelle	BP	1	DCTN2,BAG6,SAMM50,SREBF2,H2AFY,SCRIB,VPS28,ASNA1,ZC3H12A,DMAP1,INSIG1,SEC13,CEP131,TSPAN10,NUMA1,RRS1,PINX1,MCRS1,CHP1,RAB35,AIP,LRWD1,PEX5,ZDHHC3,CHCHD10,PHB2,LAMTOR4,KIAA0753,NUP88,RCC2,SNF8,RANGRF,SGF29,MID2,RBM22,AKT1,AP3D1,STK11,GAS8,NABP2,MIS12,ARFRP1,TIMM22	yellow	VSMC_M3
GO:0002684	0.87	0.17	32	542	positive regulation of immune system process	BP	1	BAG6,LGALS1,IL1R1,SOCS5,ZC3H12A,CD79A,PDE4D,SWAP70,CX3CL1,DGKZ,EGR3,MMP14,CLCF1,LIMK1,PLA2G3,SART1,RELA,PHB2,BAD,IFI35,LGALS3,C1QBP,MAD2L2,CORO1A,CD276,CSK,AKT1,AP3D1,C8G,STK11,CARD9,JUND	yellow	VSMC_M3
GO:0007600	0.87	0.18	17	320	sensory perception	BP	1	NDUFB9,ITPR3,HOXA1,MGLL,SLC9A3R1,LRIG1,MMP24,WNT10B,SOD1,HPS1,DLL4,GPX1,RABGGTA,SPX,TMEM120A,NDP,RGS16	yellow	VSMC_M3
GO:0051716	0.87	0.14	324	5042	cellular response to stimulus	BP	1	ENPP1,CD63,CDK4,RUFY1,SQSTM1,GNL1,BAG6,CTHRC1,HDAC10,NELFE,FNIP1,ATF6B,PRR5,TTLL12,SREBF2,TXNDC15,ITPR3,SGSM3,GUK1,DEF6,PPARD,FANCE,EEF1D,RPL3,PLEC,LGALS1,IFT27,SHARPIN,BOP1,TOM1,PDGFRA,IL1R1,COL15A1,EPN1,SOCS5,KLF4,DBNL,TPBG,WDPCP,CCM2,SPRED2,RGS3,ZC3H12A,FIGNL1,PDIA4,PNKP,ZYX,RCN3,SNX3,MICAL1,PLEKHA4,MGLL,FAM120B,ANXA5,KRT8,RELB,SLC9A3R1,SERP2,MUTYH,PLXND1,EMILIN1,TMUB1,RNF220,DMAP1,SNX17,PLCD1,CD79A,INSIG1,SEC13,OGG1,TTC5,ARHGEF40,UCP2,SEL1L2,METTL3,BAIAP2,CXXC5,FAAP100,LAMTOR1,NUMA1,P4HB,PYCR1,FASN,RAB20,SMOX,EIF4EBP1,ARAP3,DELE1,CAVIN3,RIC8A,GSR,ARHGAP22,SMUG1,ARHGAP33,AACS,SCARB1,HM13,BCL2L1,ITGB7,PDE4D,SPRYD3,TNS2,RRS1,SWAP70,PLEKHF1,ACSL1,ZBTB38,TNKS1BP1,GREM1,DOK1,AQP5,PDE3B,MCRS1,CX3CL1,WNT10B,SOD1,ACTR5,ANKRD2,DGKZ,EGR3,CCAR2,DLL4,CHP1,TYRO3,LSP1,RAB35,CHCHD2,SLC35C2,TSPAN5,CISH,DCPS,WDR4,SELENOS,GSTO1,ITPRIP,RIN3,STK32C,PDGFA,MMP14,PABPN1,GPX1,AIP,CORO1B,NGEF,CLCF1,SYT12,QARS,PCK2,ASB9,COL6A1,IMPDH2,ANPEP,TRIM27,PCNT,EIF3A,LIMK1,SLC26A6,PRMT2,SPX,THOC5,RIPK3,CAPN10,TNK2,STMN3,CEP164,KAT5,RELA,SIPA1,MGST3,RHOC,MAP3K14,LIMD1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,ZNF385B,YJEFN3,GNB2,ATIC,TXNRD2,PHB2,NDP,IGFBP5,BAD,PLCB3,LAMTOR4,IFI35,OTUB1,SH3BP2,HSD17B1,LETM1,LGALS3,BUD31,CD9,PLAU,TNFRSF1A,MVB12A,BABAM1,TEAD4,C1QBP,CHERP,UBXN1,EVC,RCC2,AP1M1,PRXL2A,PELP1,CCDC22,SDE2,KLF3,PKN1,CAPN2,MAD1L1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,TBKBP1,CRAB	yellow	VSMC_M3
GO:0002244	0.87	0.25	4	96	hematopoietic progenitor cell differentiation	BP	1	FNIP1,PDGFRA,METTL3,EML1	yellow	VSMC_M3
GO:1903169	0.88	0.23	5	110	regulation of calcium ion transmembrane transport	BP	1	PDE4D,CX3CL1,GSTO1,CORO1A,AKT1	yellow	VSMC_M3
GO:0048878	0.88	0.16	48	832	chemical homeostasis	BP	1	ENPP1,SREBF2,ITPR3,PPARD,PLEC,LGALS1,PDGFRA,TTC7A,RCN3,SLC9A3R1,SLC30A3,INSIG1,UCP2,LAMTOR1,RAB20,AACS,SCARB1,PDE4D,SWAP70,RALY,SLC11A2,CX3CL1,SOD1,CHP1,GSTO1,FABP3,PCK2,SLC26A6,SPX,SMARCB1,IGFBP5,BAD,LETM1,CHERP,CCDC22,FOXK1,TMEM79,RANGRF,CORO1A,TSPOAP1,SMARCA4,ANKRD9,AKT1,PACS2,AP3D1,STK11,JAGN1,CCDC115	yellow	VSMC_M3
GO:0060047	0.88	0.21	8	172	heart contraction	BP	1	ZC3H12A,PDE4D,SOD1,GSTO1,GPX1,SPX,RANGRF,TAZ	yellow	VSMC_M3
GO:0009893	0.88	0.14	177	2815	positive regulation of metabolic process	BP	1	CD63,NAB2,CDK4,SQSTM1,BAG6,SNX9,HDAC10,NELFE,FNIP1,ATF6B,PBX2,PRR5,SREBF2,H2AFY,HNRNPA0,SGSM3,PPARD,SCRIB,VPS28,PDGFRA,IL1R1,SECISBP2,PHF2,HSPBP1,SOCS5,RPS9,CNOT3,KLF4,HOXA1,ZC3H12A,PNKP,RCN3,SNRNP70,KMT2E,WDFY2,SIX5,ZNF296,RELB,EMILIN1,SERTAD1,TTC5,PSMC4,UCP2,METTL3,DND1,DEAF1,HOXC4,KMT2B,SCARB1,NAT10,PDE4D,LRP3,PLEKHF1,ACSL1,ZBTB38,TNKS1BP1,GREM1,MCRS1,CX3CL1,WNT10B,SOD1,PACSIN3,DGKZ,EGR3,CCAR2,DLL4,CHP1,TYRO3,SCD,YAF2,HTATIP2,PCIF1,KDM1B,CHCHD2,RNF19B,DCPS,RRP1B,FABP3,PDGFA,MMP14,C14orf93,AIP,CLCF1,ASB9,PSME2,TRIM27,PRMT2,THOC5,RIPK3,ADRM1,SMARCD2,BRMS1,BUD23,TNK2,PLA2G3,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,MID1IP1,SMARCB1,CHCHD10,PBX4,UBTF,MEF2B,PHB2,TRMT112,NDP,BAD,SSBP4,MPV17L2,BUD31,TNFRSF1A,BABAM1,C1QBP,AIMP2,TAF6L,ZBTB49,MTA2,PELP1,CCDC22,FOXK1,PKN1,CAPN2,POLR2A,AMER1,PIP4K2B,MAD2L2,NANOS3,CTBP1,ARHGEF2,SNF8,PER1,NFIX,SLX1A,IRF2BPL,TRIM25,SMARCA4,CARM1,CD276,AATF,CSK,MID2,RBM22,ZNF521,AKT1,BRF1,PAIP1,KHSRP,GTF2F1,SLC6A4,MYDGF,SIRT6,MAP2K2,AURKAIP1,EHMT1,AP3D1,IRAK1,STK11,TELO2,TAZ,MED16,CARD9,POMT1,VAC14,NABP2,ERBB4,JUND,KLF13,TENT5B,TRIB2,NSMF,IER5,STUB1,NSMCE3	yellow	VSMC_M3
GO:1903305	0.88	0.24	4	95	regulation of regulated secretory pathway	BP	1	MICAL1,SYT12,PLA2G3,GIT1	yellow	VSMC_M3
GO:0045944	0.88	0.15	52	904	positive regulation of transcription by RNA polymerase II	BP	1	SQSTM1,NELFE,ATF6B,PBX2,SREBF2,PPARD,KLF4,HOXA1,ZC3H12A,SIX5,ZNF296,SERTAD1,TTC5,HOXC4,ZBTB38,GREM1,MCRS1,CX3CL1,WNT10B,EGR3,HTATIP2,KDM1B,CHCHD2,RRP1B,GMEB2,PRPF6,PBX1,KAT5,RELA,ARNT2,SMARCB1,MEF2B,SSBP4,TNFRSF1A,ZBTB49,MTA2,PELP1,ARHGEF2,PER1,NFIX,IRF2BPL,SMARCA4,AATF,ZNF521,AKT1,GTF2F1,MYDGF,AP3D1,MED16,JUND,KLF13,IER5	yellow	VSMC_M3
GO:0034620	0.88	0.24	4	86	cellular response to unfolded protein	BP	1	ATF6B,SERP2,SELENOS,STUB1	yellow	VSMC_M3
GO:0051648	0.88	0.21	7	154	vesicle localization	BP	1	DCTN2,SCRIB,CHP1,BLOC1S4,MYO19,AP3D1,STK11	yellow	VSMC_M3
GO:0006873	0.88	0.17	24	444	cellular ion homeostasis	BP	1	ENPP1,ITPR3,PDGFRA,TTC7A,SLC9A3R1,SLC30A3,RAB20,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,CHP1,GSTO1,SLC26A6,LETM1,CHERP,CCDC22,CORO1A,TSPOAP1,ANKRD9,PACS2,AP3D1,CCDC115	yellow	VSMC_M3
GO:0045766	0.88	0.21	6	133	positive regulation of angiogenesis	BP	1	KLF4,ZC3H12A,GREM1,MYDGF,SIRT6,JMJD8	yellow	VSMC_M3
GO:1904018	0.88	0.21	6	133	positive regulation of vasculature development	BP	1	KLF4,ZC3H12A,GREM1,MYDGF,SIRT6,JMJD8	yellow	VSMC_M3

GO:0048699	0.88	0.15	65	1177	generation of neurons	BP	1	CTHRC1,PBX2,TRIM11,TRAPPC9,PACSIN1,SCRIB,LGALS1,IFT27,CUL7,SECISBP2,KLF4,DBNL,TPBG,WDPCP,SNX3,SLC9A3R1,PLXND1,UNK,METTL3,BAIAP2,ARHGAP33,SLC11A2,CX3CL1,WNT10B,SOD1,DLL4,RAB35,IRX1,NGEF,CLCF1,IGSF9,NECTIN1,LIMK1,PLA2G3,STMN3,PBX1,RELA,SCYL1,PBX4,BLOC1S4,C12orf57,CTDSP1,CNP,DBN1,CRABP2,ARHGEF2,S100A6,CARM1,EEF2K,EML1,ZNF521,AKT1,GIT1,SLC6A4,HMG20B,ACAP3,ANAPC2,STK11,NEGR1,ERBB4,TWF2,UNC13A,NSMF,GBA2,TUBGCP2	yellow	VSMC_M3
GO:0035967	0.88	0.22	5	103	cellular response to topologically incorrect protein	BP	1	BAG6,ATF6B,SERP2,SELENOS,STUB1	yellow	VSMC_M3
GO:0050678	0.88	0.18	14	275	regulation of epithelial cell proliferation	BP	1	PPARD,B4GALT1,DEAF1,WNT10B,EGR3,DLL4,GPX1,PHB2,BAD,AKT1,MYDGF,SIRT6,STK11,TGFBR3	yellow	VSMC_M3
GO:0070302	0.88	0.20	7	151	regulation of stress-activated protein kinase signaling cascade	BP	1	ZC3H12A,QARS,PER1,AKT1,MAP2K2,CARD9,IGFBP6	yellow	VSMC_M3
GO:0048871	0.88	0.17	20	378	multicellular organismal homeostasis	BP	1	PLEC,CNOT3,RCN3,UCP2,TNS2,ACSL1,SLC11A2,WNT10B,SOD1,SCD,GPX1,TMEM79,CORO1A,CSK,ZNF830,SIRT6,TJP3,EHMT1,STK11,AMPD2	yellow	VSMC_M3
GO:0002682	0.88	0.14	55	915	regulation of immune system process	BP	1	BAG6,TTLL12,SCRIB,LGALS1,IL1R1,SOCS5,ZC3H12A,EMILIN1,CD79A,METTL3,TARBP2,PDE4D,SWAP70,GREM1,CX3CL1,SOD1,DGKZ,EGR3,TYRO3,ST3GAL4,SELENOS,RIN3,MMP14,GPX1,CLCF1,TRIM27,LIMK1,RIPK3,PSMB4,PLA2G3,SART1,RELA,PHB2,BAD,IFI35,LGALS3,CD9,C1QBP,PRXL2A,PKN1,MAD1L1,MAD2L2,CORO1A,CDC37,CD276,CSK,AKT1,CACTIN,AP3D1,IRAK1,C8G,STK11,CARD9,JUND,KLF13	yellow	VSMC_M3
GO:0002224	0.89	0.23	4	92	toll-like receptor signaling pathway	BP	1	TYRO3,IFI35,CACTIN,IRAK1	yellow	VSMC_M3
GO:0051179	0.89	0.13	293	4586	localization	BP	1	ENPP1,PQLC1,CD63,ESYT1,DCTN2,NHP2,RUFY1,SQSTM1,CCHCR1,BAG6,SNX9,CTHRC1,SAMM50,SREBF2,SQLE,H2AFY,ITPR3,SGSM3,GUK1,PACSIN1,PPARD,TSTA3,SCRIB,PLEC,IFT27,SLC52A2,VPS28,TOM1,B4GALT1,PDGFRA,IL1R1,EPN1,SSC5D,TTC7A,ASNA1,KLF4,DBNL,TPBG,PLEKHA8,WDPCP,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,MICAL1,EHD2,TTYH2,SLC9A3R1,SERP2,PLXND1,EMILIN1,SLC16A5,DMAP1,SLC30A3,SNX17,UNK,INSIG1,MYRIP,SEC13,SEPT9,UCP2,BAIAP2,CEP131,INPPL1,TSPAN10,LAMTOR1,NUMA1,YIF1B,RAB20,ARAP3,SIGLEC1,RIC8A,ARHGAP33,LDLRAD3,AACS,SCARB1,HM13,BCL2L1,ITGB7,PDE4D,RRS1,SWAP70,LRP3,PLEKHF1,UQCRFS1,ACSL1,SLC11A2,PINX1,GREM1,AQP5,MCRS1,DCTN1,RAPSN,CX3CL1,SOD1,PACSIN3,SFXN5,DGKZ,EGR3,DNAJC17,HPS1,DLL4,CHP1,TYRO3,AP2A2,SNX21,HTATIP2,RAB35,SLC35C2,RBM15B,TSPAN5,APBA2,ST3GAL4,SELENOS,GSTO1,SLC16A14,EXOC3,RIN3,FABP3,NKAIN1,PDGFA,MMP14,PABPN1,GPX1,AIP,AP1G2,CORO1B,PLEKHO1,SYT12,PCK2,SLC19A1,NECTIN1,TRIM27,ARPIN,PCNT,LIMK1,SCN4A,SLC26A6,NUDC,SPX,THOC5,UQCRC1,RIPK3,TWIST2,CAPN10,IQCG,RHCE,TNK2,TACO1,PLA2G3,PRPF6,PTPN23,MRC2,ATP5MC3,RHOC,TMEM120A,SCYL1,LRWD1,FMNL1,VPS51,ZFPL1,LIMD1,PEX5,ZDHHC3,SGPL1,CHCHD10,YJEFN3,THOC3,BLOC1S4,PHB2,IGFBP5,BAD,COPE,LAMTOR4,AAMP,SCARF2,LETM1,LGALS3,CD9,PLAU,TNFRSF1A,FCHO1,MVB12A,KIAA0753,C1QBP,NUP88,CHERP,ANXA11,WASHC1,RCC2,CNP,AP1M1,EML3,MTA2,RAB3IL1,CCDC22,GLUD1,ELP5,PKN1,DBN1,SNX8,LMAN2,MIIP,RAB24,MAD1L1,PIP4K2B,CLTB,TMEM79,ARHGEF2,SNF8,MVP,PER1,MTX1,RANGRF,STX10,CORO1A,SGF29,	yellow	VSMC_M3
GO:0043410	0.89	0.16	19	356	positive regulation of MAPK cascade	BP	1	NELFE,PDGFRA,TPBG,ZC3H12A,LAMTOR1,CAVIN3,CX3CL1,SOD1,PDGFA,PHB2,CSK,MYDGF,MAP2K2,IRAK1,CARD9,NDST1,ERBB4,IGFBP6,GLIPR2	yellow	VSMC_M3
GO:0009887	0.89	0.15	43	784	animal organ morphogenesis	BP	1	NAB2,CTHRC1,PBX2,RING1,SCRIB,PDGFRA,HOXA1,WDPCP,PLEKHA4,SLC9A3R1,PLXND1,INSIG1,INPPL1,HOXC4,LRIG1,GREM1,KDM2B,AQP5,WNT10B,SOD1,DLL4,IRX1,PDGFA,MMP14,HCCS,NECTIN1,PBX1,RELA,VPS51,SGPL1,PBX4,PHB2,IGFBP5,C12orf57,SLC39A1,TTC39C,SLC6A4,SIRT6,TAZ,TGFBR3,NDST1,ERBB4,ELN	yellow	VSMC_M3
GO:0048608	0.89	0.17	17	330	reproductive structure development	BP	1	PPARD,CUL7,PDGFRA,KRT8,BCL2L1,SOD1,TYRO3,MMP14,IDH1,SGPL1,ZNF830,AKT1,HMGCS1,SAFB2,DHCR24,NSDHL,STK11	yellow	VSMC_M3
GO:0060537	0.89	0.16	16	323	muscle tissue development	BP	1	PLEC,PDGFRA,COL19A1,GREM1,WNT10B,DLL4,GPX1,IGFBP5,SIRT6,HMG20B,TAZ,GTF3C5,TGFBR3,ERBB4,IGSF8,ELN	yellow	VSMC_M3
GO:0072655	0.89	0.21	5	103	establishment of protein localization to mitochondrion	BP	1	SAMM50,SREBF2,AIP,AKT1,TIMM22	yellow	VSMC_M3
GO:0010632	0.89	0.18	10	208	regulation of epithelial cell migration	BP	1	TSTA3,KLF4,ZC3H12A,SCARB1,DLL4,PTPN23,AAMP,AKT1,PTPRR,GLIPR2	yellow	VSMC_M3
GO:0051480	0.89	0.18	10	212	regulation of cytosolic calcium ion concentration	BP	1	ITPR3,PDGFRA,PDE4D,SWAP70,CX3CL1,GSTO1,LETM1,CHERP,CORO1A,TSPOAP1	yellow	VSMC_M3
GO:0006022	0.89	0.22	4	98	aminoglycan metabolic process	BP	1	ST3GAL4,AKT1,B3GNT9,NDST1	yellow	VSMC_M3
GO:0033674	0.89	0.16	19	373	positive regulation of kinase activity	BP	1	NAB2,SNX9,PDGFRA,ACSL1,GREM1,DGKZ,TYRO3,PDGFA,RIPK3,PHB2,BAD,CSK,AKT1,MAP2K2,IRAK1,STK11,TELO2,VAC14,ERBB4	yellow	VSMC_M3
GO:0018210	0.89	0.22	4	104	peptidyl-threonine modification	BP	1	SPRED2,TNKS1BP1,PKN1,AKT1	yellow	VSMC_M3
GO:0002706	0.89	0.22	4	92	regulation of lymphocyte mediated immunity	BP	1	IL1R1,CLCF1,RIPK3,MAD2L2	yellow	VSMC_M3
GO:0061458	0.89	0.16	17	333	reproductive system development	BP	1	PPARD,CUL7,PDGFRA,KRT8,BCL2L1,SOD1,TYRO3,MMP14,IDH1,SGPL1,ZNF830,AKT1,HMGCS1,SAFB2,DHCR24,NSDHL,STK11	yellow	VSMC_M3
GO:0007030	0.89	0.21	5	122	Golgi organization	BP	1	CUL7,VPS51,LMAN2,TMED1,MAP2K2	yellow	VSMC_M3
GO:0051048	0.89	0.21	5	110	negative regulation of secretion	BP	1	UCP2,SPX,TNFRSF1A,MIDN,JAGN1	yellow	VSMC_M3
GO:0006626	0.89	0.22	4	86	protein targeting to mitochondrion	BP	1	SAMM50,SREBF2,AIP,TIMM22	yellow	VSMC_M3

GO:0007165	0.89	0.12	246	3919	signal transduction	BP	1	ENPP1,CD63,CDK4,RUFY1,SQSTM1,GNL1,BAG6,CTHRC1,NELFE,FNIP1,ATF6B,PRR5,TTLL12,SREBF2,TXNDC15,ITPR3,SGSM3,DEF6,PPARD,EEF1D,LGALS1,IFT27,SHARPIN,BOP1,TOM1,PDGFRA,IL1R1,COL15A1,EPN1,SOCS5,KLF4,DBNL,TPBG,WDPCP,CCM2,SPRED2,RGS3,ZC3H12A,FIGNL1,ZYX,RCN3,SNX3,MICAL1,PLEKHA4,MGLL,FAM120B,ANXA5,KRT8,RELB,SLC9A3R1,SERP2,PLXND1,EMILIN1,RNF220,SNX17,PLCD1,CD79A,INSIG1,SEC13,ARHGEF40,METTL3,BAIAP2,CXXC5,LAMTOR1,NUMA1,P4HB,EIF4EBP1,ARAP3,DELE1,CAVIN3,RIC8A,ARHGAP22,ARHGAP33,SCARB1,BCL2L1,ITGB7,PDE4D,SPRYD3,TNS2,RRS1,SWAP70,PLEKHF1,ACSL1,GREM1,DOK1,PDE3B,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,DLL4,CHP1,TYRO3,LSP1,RAB35,SLC35C2,TSPAN5,CISH,SELENOS,GSTO1,ITPRIP,RIN3,STK32C,PDGFA,MMP14,PABPN1,GPX1,AIP,NGEF,CLCF1,QARS,ASB9,ANPEP,TRIM27,PCNT,EIF3A,LIMK1,PRMT2,SPX,THOC5,RIPK3,TNK2,STMN3,KAT5,RELA,SIPA1,RHOC,MAP3K14,LIMD1,ZDHHC3,SGPL1,SMARCB1,CHCHD10,ZNF385B,YJEFN3,GNB2,PHB2,NDP,IGFBP5,BAD,PLCB3,LAMTOR4,IFI35,SH3BP2,LGALS3,BUD31,PLAU,TNFRSF1A,MVB12A,BABAM1,TEAD4,C1QBP,CHERP,EVC,RCC2,CCDC22,SDE2,PKN1,MAD1L1,PALM3,AMER1,PIP4K2B,MAD2L2,NANOS3,TBKBP1,CRABP2,ARHGEF2,MVP,PER1,RANGRF,PPP4C,CORO1A,RABEP2,TRIM25,RPL37,MTMR4,S100A4,S100A6,SMARCA4,CARM1,TMED1,CDC37,CD276,AATF,CSK,MID2,DOCK11,ZNF830,AKT1,TEDC1,RAB34,SAFB,SAFB2,GIT1,DHCR24,CARHSP1,MYDGF,MAP2K2,NSDHL,CACTIN,VASN,HIC1,TRAP1,NCLN,MNT,CTNS,TEDC2,MKNK2,CSNK1G2,IRAK1,SSNA1,STK11,TELO2,WDR24,JMJD8,CARD9,GAS8,SLC27A4,VAC14,TG	yellow	VSMC_M3
GO:0048545	0.89	0.16	13	258	response to steroid hormone	BP	1	PPARD,PCK2,PRMT2,RELA,IDH1,PHB2,BAD,PKN1,PER1,SMARCA4,CARM1,SAFB,SAFB2	yellow	VSMC_M3
GO:0051056	0.89	0.17	11	259	regulation of small GTPase mediated signal transduction	BP	1	SQSTM1,SGSM3,DEF6,ARHGEF40,ARHGAP22,SWAP70,NGEF,STMN3,SIPA1,ARHGEF2,ARHGEF1	yellow	VSMC_M3
GO:0007204	0.90	0.18	9	194	positive regulation of cytosolic calcium ion concentration	BP	1	ITPR3,PDGFRA,PDE4D,SWAP70,CX3CL1,GSTO1,LETM1,CHERP,CORO1A	yellow	VSMC_M3
GO:0071702	0.90	0.12	117	1891	organic substance transport	BP	1	ENPP1,PQLC1,CD63,ESYT1,RUFY1,CCHCR1,SNX9,SAMM50,SREBF2,SGSM3,GUK1,PPARD,SCRIB,IFT27,SLC52A2,VPS28,TOM1,ASNA1,PLEKHA8,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,SLC9A3R1,SERP2,SLC16A5,DMAP1,SNX17,INSIG1,MYRIP,SEC13,UCP2,CEP131,LAMTOR1,YIF1B,RAB20,ARHGAP33,AACS,SCARB1,HM13,ACSL1,AQP5,SFXN5,CHP1,AP2A2,SNX21,RAB35,SLC35C2,RBM15B,APBA2,SELENOS,SLC16A14,EXOC3,FABP3,PABPN1,AIP,AP1G2,SYT12,PCK2,SLC19A1,PCNT,SLC26A6,SPX,THOC5,CAPN10,PLA2G3,PTPN23,VPS51,PEX5,ZDHHC3,YJEFN3,THOC3,PHB2,BAD,COPE,MVB12A,NUP88,WASHC1,AP1M1,RAB3IL1,CCDC22,GLUD1,SNX8,LMAN2,RAB24,CLTB,ARHGEF2,SNF8,MVP,MTX1,RANGRF,STX10,RABEP2,SLC27A3,TMED1,CDC37,CSK,ATG3,RBM22,AKT1,SNX18,KHSRP,RANBP3,RAB34,SLC6A4,CTNS,AP3D1,MIDN,SLC27A4,SLC44A3,RBM8A,AP5B1,JAGN1,CAVIN1,ARFRP1,TIMM22	yellow	VSMC_M3
GO:1904062	0.90	0.16	12	241	regulation of cation transmembrane transport	BP	1	CD63,SLC9A3R1,PDE4D,CX3CL1,CHP1,GSTO1,TACO1,PHB2,RANGRF,CORO1A,AKT1,GSG1L	yellow	VSMC_M3
GO:0007034	0.90	0.19	6	137	vacuolar transport	BP	1	VPS28,AP1G2,VPS51,MVB12A,SNF8,AP3D1	yellow	VSMC_M3
GO:0050731	0.90	0.19	6	136	positive regulation of peptidyl-tyrosine phosphorylation	BP	1	GREM1,CLCF1,TNK2,TNFRSF1A,ARHGEF2,ERBB4	yellow	VSMC_M3
GO:0014706	0.90	0.16	15	307	striated muscle tissue development	BP	1	PLEC,PDGFRA,COL19A1,GREM1,WNT10B,DLL4,GPX1,SIRT6,HMG20B,TAZ,GTF3C5,TGFBR3,ERBB4,IGSF8,ELN	yellow	VSMC_M3
GO:0065009	0.90	0.12	142	2307	regulation of molecular function	BP	1	ENPP1,NAB2,CDK4,SBF1,SNX9,CTHRC1,FNIP1,RING1,H2AFY,SGSM3,TRAPPC9,DEF6,EEF1D,SCRIB,PLEC,PPP1R14B,PDGFRA,HSPBP1,SOCS5,KLF4,DBNL,SPRED2,RGS3,ZC3H12A,PNKP,RCN3,SNRNP70,MICAL1,ANXA5,SLC9A3R1,PLXND1,SERTAD1,ARHGEF40,LAMTOR1,ARAP3,DELE1,RIC8A,ARHGAP22,ARHGAP33,TARBP2,SCARB1,HM13,PDE4D,SWAP70,ACSL1,MMP24,PINX1,GREM1,CX3CL1,WNT10B,SOD1,DGKZ,CCAR2,HPS1,CHP1,TYRO3,CISH,GSTO1,ITPRIP,RRP1B,ETFBKMT,RIN3,PDGFA,PABPN1,GPX1,AIP,NGEF,QARS,PSME2,TRIM27,LIMK1,PRMT2,RIPK3,ADRM1,BRMS1,TNK2,TACO1,STMN3,RELA,SIPA1,RHOC,MID1IP1,SMARCB1,PHB2,PPP1R35,BAD,LAMTOR4,LGALS3,BUD31,PLAU,AIMP2,UBXN1,WASHC1,RCC2,RAB3IL1,CCDC22,PKN1,PIP4K2B,MAD2L2,DFFA,ARHGEF2,MVP,RANGRF,DPM3,RABEP2,TRIM25,RPL37,SMARCA4,CARM1,CDC37,CSK,MID2,DOCK11,AKT1,SNX18,DENND1C,GTF2F1,RANBP3,GIT1,DHCR24,MAP2K2,CACTIN,ACAP3,IRAK1,MIDN,STK11,TELO2,JMJD8,CARD9,GAS8,SLC27A4,VAC14,TGFBR3,TRADD,ERBB4,RNH1,TRIB2,ARHGEF1,RGS16,STUB1,RGS18,GSG1L	yellow	VSMC_M3
GO:0046903	0.90	0.13	38	673	secretion	BP	1	PPARD,SCRIB,EIPR1,PDIA4,RCN3,MICAL1,SLC9A3R1,MYRIP,UCP2,AACS,AQP5,TYRO3,EXOC3,SYT12,PCK2,SLC26A6,SPX,CAPN10,PLA2G3,PTPN23,BAD,TNFRSF1A,WASHC1,RAB3IL1,GLUD1,TMEM79,SNF8,MTX1,CORO1A,GIT1,SLC6A4,MIDN,APRT,RABEPK,ERBB4,JAGN1,CAVIN1,UNC13A	yellow	VSMC_M3
GO:0045088	0.90	0.18	7	148	regulation of innate immune response	BP	1	TTLL12,METTL3,TYRO3,IFI35,CDC37,CACTIN,CARD9	yellow	VSMC_M3
GO:0007569	0.90	0.21	4	98	cell aging	BP	1	SOD1,KAT5,MNT,RF00024	yellow	VSMC_M3
GO:0048738	0.90	0.17	8	186	cardiac muscle tissue development	BP	1	PLEC,PDGFRA,GREM1,DLL4,SIRT6,TAZ,TGFBR3,ERBB4	yellow	VSMC_M3
GO:0003015	0.90	0.17	8	180	heart process	BP	1	ZC3H12A,PDE4D,SOD1,GSTO1,GPX1,SPX,RANGRF,TAZ	yellow	VSMC_M3
GO:1902115	0.90	0.18	7	161	regulation of organelle assembly	BP	1	SEPT9,NUMA1,LRFN4,EML3,PIP4K2B,RABEP2,ATG3	yellow	VSMC_M3

GO:0072359	0.90	0.12	49	902	circulatory system development	BP	1	PDLIM4,PPARD,PLEC,CUL7,B4GALT1,PDGFRA,COL15A1,EPN1,KLF4,HOXA1,WDPCP,CCM2,ZC3H12A,PLXND1,EMILIN1,SNX17,RIC8A,ARHGAP22,GREM1,PDE3B,CX3CL1,EGR3,DLL4,HTATIP2,PDGFA,MMP14,GPX1,ANPEP,SGPL1,YJEFN3,AAMP,TNFRSF1A,AKT1,MYDGF,SIRT6,NSDHL,MBD3,STK11,TAZ,JMJD8,SARS,TGFBR3,MIR214,NDST1,TNFRSF12A,ERBB4,LOXL1,RNH1,ELN	yellow	VSMC_M3
GO:0018108	0.90	0.15	14	287	peptidyl-tyrosine phosphorylation	BP	1	PDGFRA,SOCS5,GREM1,TYRO3,PDGFA,CLCF1,TNK2,SCYL1,TNFRSF1A,ARHGEF2,MVP,CSK,MAP2K2,ERBB4	yellow	VSMC_M3
GO:0002573	0.90	0.17	7	154	myeloid leukocyte differentiation	BP	1	RELB,FASN,PIR,THOC5,PLA2G3,PRXL2A,JAGN1	yellow	VSMC_M3
GO:0046822	0.90	0.20	4	94	regulation of nucleocytoplasmic transport	BP	1	ZC3H12A,DMAP1,CHP1,RBM22	yellow	VSMC_M3
GO:0070585	0.91	0.19	5	107	protein localization to mitochondrion	BP	1	SAMM50,SREBF2,AIP,AKT1,TIMM22	yellow	VSMC_M3
GO:0051259	0.91	0.16	8	174	protein complex oligomerization	BP	1	ZC3H12A,AQP5,CHP1,TMEM120A,LETM1,KRT10,FARSA,CARD9	yellow	VSMC_M3
GO:0042127	0.91	0.12	74	1230	regulation of cell population proliferation	BP	1	CDK4,BAG6,CTHRC1,SQLE,PPARD,SCRIB,B4GALT1,PDGFRA,RPS9,KLF4,TPBG,SIX5,SLC9A3R1,DLEC1,SERTAD1,CEP131,INPPL1,DEAF1,BCL2L1,TNS2,PINX1,GREM1,KDM2B,CX3CL1,WNT10B,EGR3,DLL4,FABP3,PDGFA,GPX1,CLCF1,RIPK3,PBX1,RELA,ARNT2,SMARCB1,PHB2,IGFBP5,BAD,IFI35,LGALS3,CD9,PLAU,AIMP2,CHERP,ZBTB49,PKN1,MAD1L1,CTBP1,ARHGEF2,CORO1A,S100A6,CARM1,CD276,CSK,AKT1,SLC6A4,DHCR24,MYDGF,LDOC1,SIRT6,MNT,IRAK1,STK11,GAS8,MVD,TGFBR3,MIR214,ERBB4,JUND,KLF13,IGFBP6,ELN,IER5	yellow	VSMC_M3
GO:2000026	0.91	0.12	57	1014	regulation of multicellular organismal development	BP	1	ENPP1,BAG6,H2AFY,TRIM11,PPARD,CUL7,EPN1,SOCS5,KLF4,DBNL,TPBG,WDPCP,SPRED2,ZC3H12A,PLXND1,EMILIN1,METTL3,BAIAP2,NUMA1,GREM1,PDE3B,CX3CL1,WNT10B,SOD1,EGR3,DLL4,HTATIP2,MMP14,CLCF1,LIMK1,PLA2G3,SART1,RELA,YJEFN3,BAD,CTDSP1,TNFRSF1A,PRXL2A,DBN1,CRABP2,EEF2K,AKT1,MYDGF,SIRT6,EHMT1,AP3D1,ANAPC2,STK11,JMJD8,SARS,TGFBR3,TRADD,MIR214,ERBB4,TWF2,KLF13,RNH1	yellow	VSMC_M3
GO:0045595	0.91	0.12	66	1153	regulation of cell differentiation	BP	1	ENPP1,CTHRC1,FNIP1,H2AFY,TRIM11,PPARD,CUL7,PDGFRA,SOCS5,KLF4,DBNL,SPRED2,ZC3H12A,WDFY2,PLXND1,INSIG1,METTL3,BAIAP2,NUMA1,P4HB,LRP3,GREM1,CX3CL1,WNT10B,SOD1,ANKRD2,EGR3,DLL4,MMP14,CLCF1,LIMK1,TWIST2,PLA2G3,SART1,CCDC85B,PBX1,RELA,LIMD1,IGFBP5,BAD,CTDSP1,EID1,TNFRSF1A,C1QBP,RCC2,PRXL2A,DBN1,MAD2L2,CRABP2,ARHGEF2,CARM1,EEF2K,AKT1,SLC6A4,HMG20B,VASN,AP3D1,ANAPC2,STK11,TWF2,JUND,KLF13,FADS1,TRIB2,ZNF385A,GLIPR2	yellow	VSMC_M3
GO:0007088	0.91	0.20	4	96	regulation of mitotic nuclear division	BP	1	CUL7,MAD1L1,MAD2L2,AURKAIP1	yellow	VSMC_M3
GO:0006810	0.91	0.11	208	3300	transport	BP	1	ENPP1,PQLC1,CD63,ESYT1,DCTN2,RUFY1,SQSTM1,CCHCR1,SNX9,SAMM50,SREBF2,ITPR3,SGSM3,GUK1,PACSIN1,PPARD,SCRIB,IFT27,SLC52A2,VPS28,TOM1,EPN1,SSC5D,ASNA1,DBNL,PLEKHA8,EIPR1,ZC3H12A,PDIA4,RCN3,SNX3,MICAL1,EHD2,TTYH2,SLC9A3R1,SERP2,SLC16A5,DMAP1,SLC30A3,SNX17,INSIG1,MYRIP,SEC13,UCP2,CEP131,INPPL1,LAMTOR1,NUMA1,YIF1B,RAB20,ARAP3,SIGLEC1,ARHGAP33,LDLRAD3,AACS,SCARB1,HM13,BCL2L1,PDE4D,RRS1,LRP3,UQCRFS1,ACSL1,SLC11A2,GREM1,AQP5,DCTN1,CX3CL1,SOD1,PACSIN3,SFXN5,DNAJC17,HPS1,CHP1,TYRO3,AP2A2,SNX21,HTATIP2,RAB35,SLC35C2,RBM15B,APBA2,SELENOS,GSTO1,SLC16A14,EXOC3,RIN3,FABP3,NKAIN1,PABPN1,AIP,AP1G2,SYT12,PCK2,SLC19A1,NECTIN1,TRIM27,PCNT,LIMK1,SCN4A,SLC26A6,SPX,THOC5,UQCRC1,CAPN10,RHCE,TNK2,TACO1,PLA2G3,PTPN23,MRC2,ATP5MC3,TMEM120A,SCYL1,VPS51,ZFPL1,PEX5,ZDHHC3,CHCHD10,YJEFN3,THOC3,BLOC1S4,PHB2,BAD,COPE,SCARF2,LETM1,LGALS3,CD9,TNFRSF1A,FCHO1,MVB12A,NUP88,CHERP,ANXA11,WASHC1,CNP,AP1M1,RAB3IL1,CCDC22,GLUD1,SNX8,LMAN2,RAB24,PIP4K2B,CLTB,TMEM79,ARHGEF2,SNF8,MVP,PER1,MTX1,RANGRF,STX10,CORO1A,RABEP2,SLC39A1,ATP5PD,SLC27A3,S100A6,TMED1,SYNE3,EEF2K,CDC37,MYO19,CSK,ATG3,RBM22,AKT1,SNX18,DENND1C,KHSRP,ALKBH7,RANBP3,RAB34,GIT1,ANKRD13B,SLC6A4,MAP2K2,SLC35E2B,CTNS,AP3D1,CSNK1G2,SSNA1,NDUFS7,MIDN,ATP5F1D,STK11,TMEM201,SPG7,APRT,WDR34,SLC27A4,SLC44A3,RABEPK,RBM8A,ERBB4,SURF1,TRAPPC5,PLA2G4E,AP5B1,JAGN1,CAVIN1,UNC13A,ARFRP1,TIMM22,PHETA2,GSG1L	yellow	VSMC_M3
GO:0051924	0.91	0.16	8	172	regulation of calcium ion transport	BP	1	PDE4D,CX3CL1,PACSIN3,GSTO1,TRIM27,LGALS3,CORO1A,AKT1	yellow	VSMC_M3
GO:0051347	0.91	0.13	23	441	positive regulation of transferase activity	BP	1	NAB2,SNX9,PDGFRA,KLF4,PNKP,ACSL1,GREM1,DGKZ,TYRO3,PDGFA,PABPN1,RIPK3,PHB2,BAD,CSK,AKT1,MAP2K2,IRAK1,STK11,TELO2,VAC14,ERBB4,STUB1	yellow	VSMC_M3
GO:0007259	0.91	0.19	4	98	receptor signaling pathway via JAK-STAT	BP	1	SOCS5,CLCF1,TNFRSF1A,ERBB4	yellow	VSMC_M3
GO:0010466	0.91	0.17	7	145	negative regulation of peptidase activity	BP	1	FNIP1,KLF4,MICAL1,GPX1,UBXN1,AKT1,DHCR24	yellow	VSMC_M3
GO:0002688	0.91	0.19	4	92	regulation of leukocyte chemotaxis	BP	1	SWAP70,GREM1,RIN3,C1QBP	yellow	VSMC_M3
GO:0015748	0.91	0.19	4	102	organophosphate ester transport	BP	1	PQLC1,PLEKHA8,SCARB1,SLC19A1	yellow	VSMC_M3
GO:0016236	0.91	0.14	13	265	macroautophagy	BP	1	SQSTM1,HDAC10,VPS28,LIX1L,PHB2,MVB12A,PIP4K2B,SNF8,CDC37,ATG3,AKT1,PACS2,TAZ	yellow	VSMC_M3
GO:0051049	0.91	0.11	75	1276	regulation of transport	BP	1	ENPP1,CD63,RUFY1,SREBF2,PACSIN1,PPARD,SCRIB,VPS28,EIPR1,ZC3H12A,SNX3,MICAL1,EHD2,SLC9A3R1,DMAP1,SLC30A3,SNX17,INSIG1,MYRIP,UCP2,CEP131,LAMTOR1,NUMA1,AACS,SCARB1,PDE4D,ACSL1,GREM1,CX3CL1,SOD1,PACSIN3,CHP1,SELENOS,GSTO1,RIN3,FABP3,NKAIN1,SYT12,PCK2,TRIM27,PCNT,SCN4A,SLC26A6,SPX,CAPN10,TNK2,TACO1,PLA2G3,PTPN23,CHCHD10,YJEFN3,PHB2,BAD,LGALS3,TNFRSF1A,GLUD1,LMAN2,SNF8,PER1,RANGRF,CORO1A,EEF2K,CSK,ATG3,RBM22,AKT1,GIT1,ANKRD13B,SLC6A4,MAP2K2,MIDN,STK11,PLA2G4E,JAGN1,GSG1L	yellow	VSMC_M3
GO:0007601	0.91	0.18	5	123	visual perception	BP	1	HPS1,DLL4,RABGGTA,NDP,RGS16	yellow	VSMC_M3

GO:0032412	0.91	0.16	8	178	regulation of ion transmembrane transporter activity	BP	1	SLC9A3R1,PDE4D,CHP1,GSTO1,TACO1,PHB2,RANGRF,GSG1L	yellow	VSMC_M3
GO:0030218	0.91	0.19	4	102	erythrocyte differentiation	BP	1	KMT2E,SLC11A2,TGFBR3,KLF13	yellow	VSMC_M3
GO:0010594	0.91	0.16	7	157	regulation of endothelial cell migration	BP	1	TSTA3,KLF4,ZC3H12A,SCARB1,DLL4,AAMP,AKT1	yellow	VSMC_M3
GO:0018212	0.91	0.14	14	290	peptidyl-tyrosine modification	BP	1	PDGFRA,SOCS5,GREM1,TYRO3,PDGFA,CLCF1,TNK2,SCYL1,TNFRSF1A,ARHGEF2,MVP,CSK,MAP2K2,ERBB4	yellow	VSMC_M3
GO:0050730	0.91	0.15	9	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	SOCS5,GREM1,PDGFA,CLCF1,TNK2,TNFRSF1A,ARHGEF2,MVP,ERBB4	yellow	VSMC_M3
GO:0002831	0.91	0.14	11	224	regulation of response to biotic stimulus	BP	1	TTLL12,ZC3H12A,METTL3,TARBP2,CX3CL1,TYRO3,IFI35,C1QBP,CDC37,CACTIN,CARD9	yellow	VSMC_M3
GO:0071695	0.91	0.16	7	163	anatomical structure maturation	BP	1	GREM1,CX3CL1,WNT10B,SLC26A6,PLA2G3,TMEM79,NOM1	yellow	VSMC_M3
GO:0051345	0.91	0.12	23	440	positive regulation of hydrolase activity	BP	1	SNX9,SGSM3,SCRIB,PDGFRA,RCN3,ARAP3,ARHGAP22,CX3CL1,NGEF,PSME2,RIPK3,ADRM1,SIPA1,RHOC,PHB2,BAD,RCC2,DOCK11,AKT1,SNX18,CARD9,SLC27A4,RGS16	yellow	VSMC_M3
GO:0071496	0.91	0.14	13	267	cellular response to external stimulus	BP	1	FNIP1,SREBF2,PLEC,ZC3H12A,UCP2,DCPS,SIPA1,MAP3K14,BAD,TNFRSF1A,AKT1,WDR24,FADS1	yellow	VSMC_M3
GO:0010562	0.92	0.11	36	669	positive regulation of phosphorus metabolic process	BP	1	NAB2,SQSTM1,SNX9,FNIP1,PRR5,PDGFRA,WDFY2,ACSL1,TNKS1BP1,GREM1,CX3CL1,DGKZ,CHP1,TYRO3,FABP3,PDGFA,CLCF1,RIPK3,TNK2,PHB2,BAD,TNFRSF1A,CAPN2,MAD2L2,ARHGEF2,CSK,AKT1,MYDGF,MAP2K2,IRAK1,STK11,TELO2,TAZ,VAC14,ERBB4,NSMF	yellow	VSMC_M3
GO:0045937	0.92	0.11	36	669	positive regulation of phosphate metabolic process	BP	1	NAB2,SQSTM1,SNX9,FNIP1,PRR5,PDGFRA,WDFY2,ACSL1,TNKS1BP1,GREM1,CX3CL1,DGKZ,CHP1,TYRO3,FABP3,PDGFA,CLCF1,RIPK3,TNK2,PHB2,BAD,TNFRSF1A,CAPN2,MAD2L2,ARHGEF2,CSK,AKT1,MYDGF,MAP2K2,IRAK1,STK11,TELO2,TAZ,VAC14,ERBB4,NSMF	yellow	VSMC_M3
GO:0051225	0.92	0.18	4	101	spindle assembly	BP	1	NUMA1,SAC3D1,EML3,TUBGCP2	yellow	VSMC_M3
GO:0070201	0.92	0.12	23	436	regulation of establishment of protein localization	BP	1	SREBF2,PPARD,VPS28,EIPR1,ZC3H12A,SNX3,DMAP1,INSIG1,MYRIP,UCP2,CEP131,AACS,CHP1,PCK2,PCNT,CAPN10,PTPN23,BAD,GLUD1,CSK,RBM22,MIDN,JAGN1	yellow	VSMC_M3
GO:0007292	0.92	0.18	4	101	female gamete generation	BP	1	NCAPH2,METTL3,NANOS3,ZNF830	yellow	VSMC_M3
GO:0010628	0.92	0.11	46	803	positive regulation of gene expression	BP	1	CDK4,H2AFY,HNRNPA0,PPARD,SCRIB,IL1R1,SECISBP2,PHF2,RPS9,KLF4,ZC3H12A,SNRNP70,RELB,EMILIN1,SERTAD1,METTL3,DND1,NAT10,PDE4D,LRP3,CX3CL1,SOD1,DLL4,PCIF1,MMP14,C14orf93,CLCF1,TRIM27,PLA2G3,RELA,PHB2,MPV17L2,C1QBP,POLR2A,MAD2L2,ARHGEF2,SNF8,CD276,RBM22,AKT1,PAIP1,SLC6A4,MAP2K2,IRAK1,CARD9,TENT5B	yellow	VSMC_M3
GO:0090287	0.92	0.14	10	230	regulation of cellular response to growth factor stimulus	BP	1	CD63,SPRED2,EMILIN1,NUMA1,GREM1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0098662	0.92	0.11	29	541	inorganic cation transmembrane transport	BP	1	CD63,ITPR3,SLC9A3R1,SLC30A3,UCP2,PDE4D,UQCRFS1,SLC11A2,CX3CL1,CHP1,GSTO1,SCN4A,UQCRC1,RHCE,TACO1,ATP5MC3,PHB2,LETM1,CHERP,RANGRF,CORO1A,SLC39A1,ATP5PD,AKT1,SLC6A4,CTNS,NDUFS7,ATP5F1D,SURF1	yellow	VSMC_M3
GO:0050953	0.92	0.16	5	126	sensory perception of light stimulus	BP	1	HPS1,DLL4,RABGGTA,NDP,RGS16	yellow	VSMC_M3
GO:0003205	0.92	0.16	5	135	cardiac chamber development	BP	1	PLXND1,SNX17,DLL4,TGFBR3,NDST1	yellow	VSMC_M3
GO:0010634	0.92	0.15	6	143	positive regulation of epithelial cell migration	BP	1	TSTA3,ZC3H12A,SCARB1,AAMP,AKT1,GLIPR2	yellow	VSMC_M3
GO:0002274	0.92	0.14	7	156	myeloid leukocyte activation	BP	1	ZC3H12A,KMT2E,RELB,CX3CL1,PLA2G3,IFI35,JUND	yellow	VSMC_M3
GO:0032940	0.92	0.10	31	574	secretion by cell	BP	1	PPARD,SCRIB,EIPR1,PDIA4,RCN3,MICAL1,MYRIP,UCP2,AACS,TYRO3,EXOC3,SYT12,PCK2,CAPN10,PLA2G3,PTPN23,BAD,TNFRSF1A,WASHC1,RAB3IL1,GLUD1,TMEM79,SNF8,CORO1A,GIT1,SLC6A4,MIDN,RABEPK,JAGN1,CAVIN1,UNC13A	yellow	VSMC_M3
GO:0043270	0.92	0.14	8	182	positive regulation of ion transport	BP	1	SLC9A3R1,CX3CL1,CHP1,GSTO1,PLA2G3,LGALS3,AKT1,SLC6A4	yellow	VSMC_M3
GO:0031401	0.93	0.10	41	747	positive regulation of protein modification process	BP	1	NAB2,SQSTM1,SNX9,NELFE,FNIP1,PRR5,HSPBP1,ZC3H12A,KMT2E,WDFY2,ACSL1,TNKS1BP1,GREM1,CX3CL1,CHP1,PDGFA,CLCF1,RIPK3,BRMS1,TNK2,KAT5,SMARCB1,PHB2,TNFRSF1A,AIMP2,AMER1,MAD2L2,CTBP1,ARHGEF2,CSK,AKT1,MYDGF,MAP2K2,IRAK1,STK11,TELO2,POMT1,ERBB4,NSMF,STUB1,NSMCE3	yellow	VSMC_M3
GO:1903531	0.93	0.16	4	99	negative regulation of secretion by cell	BP	1	UCP2,TNFRSF1A,MIDN,JAGN1	yellow	VSMC_M3
GO:0048729	0.93	0.11	24	490	tissue morphogenesis	BP	1	CTHRC1,SCRIB,KLF4,CCM2,PLEKHA4,SLC9A3R1,PLXND1,DEAF1,GREM1,KDM2B,DLL4,IRX1,PDGFA,MMP14,PBX1,RHOC,PHB2,IGFBP5,MTHFR,TMEM79,ARMC5,SIRT6,TGFBR3,ERBB4	yellow	VSMC_M3
GO:0031175	0.93	0.10	40	784	neuron projection development	BP	1	CTHRC1,PACSIN1,SCRIB,LGALS1,IFT27,CUL7,KLF4,DBNL,TPBG,SNX3,SLC9A3R1,PLXND1,BAIAP2,ARHGAP33,SLC11A2,CX3CL1,SOD1,RAB35,NGEF,IGSF9,NECTIN1,LIMK1,PLA2G3,STMN3,BLOC1S4,C12orf57,CNP,DBN1,CRABP2,S100A6,CARM1,EEF2K,AKT1,ACAP3,ANAPC2,STK11,NEGR1,TWF2,UNC13A,NSMF	yellow	VSMC_M3
GO:0002440	0.93	0.14	6	138	production of molecular mediator of immune response	BP	1	IL1R1,SWAP70,CLCF1,PHB2,PKN1,MAD2L2	yellow	VSMC_M3
GO:0007417	0.93	0.10	42	795	central nervous system development	BP	1	BAG6,HDAC10,PBX2,TRAPPC9,SCRIB,MPST,SHARPIN,SECISBP2,PAFAH1B3,CIC,METTL3,BAIAP2,CAPG,KDM2B,DCTN1,DLL4,TYRO3,CLCF1,QARS,PBX1,SCYL1,ARNT2,VPS51,PBX4,ATIC,C12orf57,BAD,CD9,CNP,GLUD1,EML1,CSK,AKT1,HMGCS1,GIT1,SLC6A4,CTNS,MBD3,NDST1,ERBB4,GBA2,TUBGCP2	yellow	VSMC_M3

GO:0008283	0.93	0.09	86	1442	cell population proliferation	BP	1	CDK4,BAG6,CTHRC1,SQLE,PPARD,SCRIB,BOP1,B4GALT1,PDGFRA,RPS9,KLF4,TPBG,FIGNL1,SIX5,SLC9A3R1,DLEC1,CD79A,SERTAD1,CEP131,INPPL1,DEAF1,SCARB1,BCL2L1,TNS2,PINX1,GREM1,KDM2B,CX3CL1,WNT10B,EGR3,DLL4,FABP3,PDGFA,MMP14,GPX1,CLCF1,IMPDH2,RIPK3,PBX1,RELA,ARNT2,SMARCB1,YJEFN3,PHB2,IGFBP5,BAD,IFI35,LGALS3,CD9,PLAU,AIMP2,CHERP,ZBTB49,PKN1,DBN1,MAD1L1,CTBP1,ARHGEF2,ARMC5,CORO1A,S100A6,CARM1,CD276,EML1,CSK,AKT1,SLC6A4,DHCR24,MYDGF,LDOC1,SIRT6,MNT,IRAK1,STK11,GAS8,MVD,TGFBR3,PSMB10,MIR214,NDST1,ERBB4,JUND,KLF13,IGFBP6,ELN,IER5	yellow	VSMC_M3
GO:0030003	0.93	0.10	22	434	cellular cation homeostasis	BP	1	ITPR3,PDGFRA,TTC7A,SLC30A3,RAB20,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,CHP1,GSTO1,SLC26A6,LETM1,CHERP,CCDC22,CORO1A,TSPOAP1,ANKRD9,PACS2,AP3D1,CCDC115	yellow	VSMC_M3
GO:0006875	0.93	0.11	19	381	cellular metal ion homeostasis	BP	1	ITPR3,PDGFRA,TTC7A,SLC30A3,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,GSTO1,LETM1,CHERP,CCDC22,CORO1A,TSPOAP1,ANKRD9,PACS2,AP3D1,CCDC115	yellow	VSMC_M3
GO:0008217	0.93	0.14	5	122	regulation of blood pressure	BP	1	PDE4D,SOD1,ANPEP,SPX,PLCB3	yellow	VSMC_M3
GO:0071560	0.93	0.13	8	199	cellular response to transforming growth factor beta stimulus	BP	1	SPRED2,ZYX,EMILIN1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0045859	0.93	0.10	27	513	regulation of protein kinase activity	BP	1	NAB2,SNX9,H2AFY,PLEC,SOCS5,SLC9A3R1,SERTAD1,TARBP2,ACSL1,GREM1,SOD1,CHP1,PDGFA,QARS,TRIM27,RIPK3,PHB2,PKN1,MVP,CDC37,CSK,AKT1,MAP2K2,IRAK1,STK11,TELO2,TRIB2	yellow	VSMC_M3
GO:0031668	0.93	0.12	9	205	cellular response to extracellular stimulus	BP	1	FNIP1,SREBF2,PLEC,ZC3H12A,UCP2,DCPS,SIPA1,WDR24,FADS1	yellow	VSMC_M3
GO:0021953	0.93	0.15	4	116	central nervous system neuron differentiation	BP	1	DLL4,SCYL1,C12orf57,GBA2	yellow	VSMC_M3
GO:0002699	0.93	0.13	6	142	positive regulation of immune effector process	BP	1	IL1R1,SOCS5,CLCF1,PLA2G3,PHB2,MAD2L2	yellow	VSMC_M3
GO:0071310	0.93	0.08	105	1784	cellular response to organic substance	BP	1	ENPP1,CD63,CDK4,BAG6,ATF6B,TTLL12,PPARD,RPL3,LGALS1,SHARPIN,PDGFRA,IL1R1,SOCS5,KLF4,SPRED2,ZC3H12A,ZYX,KRT8,SLC9A3R1,SERP2,EMILIN1,INSIG1,UCP2,METTL3,BAIAP2,LAMTOR1,NUMA1,P4HB,FASN,RAB20,AACS,SCARB1,BCL2L1,TNS2,ACSL1,GREM1,DOK1,PDE3B,CX3CL1,WNT10B,SOD1,EGR3,DLL4,LSP1,RAB35,DCPS,SELENOS,PABPN1,CORO1B,CLCF1,PCK2,COL6A1,IMPDH2,SLC26A6,PRMT2,CAPN10,KAT5,RELA,SMARCB1,ATIC,PHB2,IGFBP5,BAD,LAMTOR4,OTUB1,TNFRSF1A,PELP1,KLF3,PKN1,CAPN2,PALM3,PIP4K2B,ARHGEF2,PER1,CORO1A,TRIM25,MTMR4,SMARCA4,CARM1,EEF2K,CDC37,CSK,AKT1,HMGCS1,KHSRP,SAFB,SAFB2,GIT1,SLC6A4,LDOC1,CACTIN,VASN,IRAK1,STK11,APRT,SLC27A4,TGFBR3,TRADD,NDST1,ERBB4,TWF2,JAGN1,NSMF,CDC34,STUB1	yellow	VSMC_M3
GO:0043393	0.93	0.13	7	162	regulation of protein binding	BP	1	CTHRC1,PLXND1,AKT1,GTF2F1,GAS8,TGFBR3,STUB1	yellow	VSMC_M3
GO:0072593	0.93	0.12	8	176	reactive oxygen species metabolic process	BP	1	ZC3H12A,SOD1,GPX1,RIPK3,AATF,AKT1,TRAP1,CTNS	yellow	VSMC_M3
GO:0022898	0.93	0.12	8	186	regulation of transmembrane transporter activity	BP	1	SLC9A3R1,PDE4D,CHP1,GSTO1,TACO1,PHB2,RANGRF,GSG1L	yellow	VSMC_M3
GO:0007269	0.93	0.15	4	110	neurotransmitter secretion	BP	1	SCRIB,SYT12,GIT1,UNC13A	yellow	VSMC_M3
GO:0099643	0.93	0.15	4	110	signal release from synapse	BP	1	SCRIB,SYT12,GIT1,UNC13A	yellow	VSMC_M3
GO:0015698	0.94	0.15	4	113	inorganic anion transport	BP	1	ENPP1,ASNA1,TTYH2,SLC26A6	yellow	VSMC_M3
GO:0097696	0.94	0.14	4	105	receptor signaling pathway via STAT	BP	1	SOCS5,CLCF1,TNFRSF1A,ERBB4	yellow	VSMC_M3
GO:1903827	0.94	0.09	23	454	regulation of cellular protein localization	BP	1	SQSTM1,SREBF2,H2AFY,VPS28,ZC3H12A,DMAP1,INSIG1,CEP131,NUMA1,BCL2L1,PINX1,MCRS1,CHP1,MMP14,PCNT,LGALS3,RANGRF,CSK,RBM22,AKT1,STK11,GAS8,ERBB4	yellow	VSMC_M3
GO:0010951	0.94	0.13	6	137	negative regulation of endopeptidase activity	BP	1	FNIP1,KLF4,MICAL1,GPX1,AKT1,DHCR24	yellow	VSMC_M3
GO:0071902	0.94	0.12	7	170	positive regulation of protein serine/threonine kinase activity	BP	1	ACSL1,PDGFA,CSK,AKT1,MAP2K2,IRAK1,TELO2	yellow	VSMC_M3
GO:0030162	0.94	0.09	30	538	regulation of proteolysis	BP	1	BAG6,SNX9,FNIP1,HSPBP1,SOCS5,KLF4,ZC3H12A,RCN3,MICAL1,PSMC4,DELE1,LDLRAD3,WNT10B,PACSIN3,CCAR2,RNF19B,MMP14,GPX1,PSME2,ADRM1,BAD,UBXN1,CCDC22,AKT1,DHCR24,SIRT6,AURKAIP1,CARD9,TRIB2,STUB1	yellow	VSMC_M3
GO:0030902	0.94	0.14	4	116	hindbrain development	BP	1	SCRIB,KDM2B,ATIC,SLC6A4	yellow	VSMC_M3
GO:0048812	0.94	0.09	23	503	neuron projection morphogenesis	BP	1	PACSIN1,CUL7,DBNL,TPBG,PLXND1,BAIAP2,ARHGAP33,SLC11A2,NGEF,IGSF9,NECTIN1,LIMK1,C12orf57,CNP,DBN1,CRABP2,S100A6,EEF2K,ANAPC2,STK11,TWF2,UNC13A,NSMF	yellow	VSMC_M3
GO:1905114	0.94	0.09	22	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	CTHRC1,KLF4,TPBG,SNX3,PLEKHA4,SLC9A3R1,RNF220,BAIAP2,GREM1,WNT10B,CCAR2,LIMD1,NDP,AMER1,MAD2L2,SMARCA4,AKT1,HIC1,CSNK1G2,STK11,IGFBP6,APCDD1L	yellow	VSMC_M3
GO:0071559	0.94	0.11	8	205	response to transforming growth factor beta	BP	1	SPRED2,ZYX,EMILIN1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0051336	0.94	0.08	41	754	regulation of hydrolase activity	BP	1	SBF1,SNX9,FNIP1,SGSM3,SCRIB,PDGFRA,KLF4,RCN3,SNRNP70,MICAL1,PLXND1,ARAP3,DELE1,ARHGAP22,CX3CL1,SOD1,CHP1,RRP1B,GPX1,AIP,NGEF,PSME2,RIPK3,ADRM1,STMN3,SIPA1,RHOC,PHB2,PPP1R35,BAD,LGALS3,UBXN1,RCC2,DFFA,DOCK11,AKT1,SNX18,DHCR24,CARD9,SLC27A4,RGS16	yellow	VSMC_M3
GO:0046467	0.94	0.12	5	120	membrane lipid biosynthetic process	BP	1	PIGO,ST3GAL4,SGPL1,DPM3,CSNK1G2	yellow	VSMC_M3
GO:0060485	0.94	0.10	10	235	mesenchyme development	BP	1	CUL7,SPRED2,GREM1,AMER1,MAD2L2,S100A4,VASN,TGFBR3,ERBB4,GLIPR2	yellow	VSMC_M3
GO:0098660	0.94	0.08	30	574	inorganic ion transmembrane transport	BP	1	CD63,ITPR3,SLC9A3R1,SLC30A3,UCP2,PDE4D,UQCRFS1,SLC11A2,CX3CL1,CHP1,GSTO1,SCN4A,SLC26A6,UQCRC1,RHCE,TACO1,ATP5MC3,PHB2,LETM1,CHERP,RANGRF,CORO1A,SLC39A1,ATP5PD,AKT1,SLC6A4,CTNS,NDUFS7,ATP5F1D,SURF1	yellow	VSMC_M3
GO:0007254	0.94	0.12	5	134	JNK cascade	BP	1	PER1,AKT1,IRAK1,CARD9,CDC42EP5	yellow	VSMC_M3
GO:0034101	0.94	0.13	4	111	erythrocyte homeostasis	BP	1	KMT2E,SLC11A2,TGFBR3,KLF13	yellow	VSMC_M3
GO:0050920	0.94	0.11	7	167	regulation of chemotaxis	BP	1	PDGFRA,TPBG,SWAP70,GREM1,RIN3,CORO1B,C1QBP	yellow	VSMC_M3

GO:0042592	0.94	0.07	74	1295	homeostatic process	BP	1	ENPP1,SREBF2,ITPR3,PPARD,PLEC,LGALS1,PDGFRA,TTC7A,CNOT3,RCN3,KMT2E,SLC9A3R1,SLC30A3,INSIG1,UCP2,LAMTOR1,RAB20,GSR,AACS,SCARB1,PDE4D,TNS2,SWAP70,RALY,ACSL1,SLC11A2,DCTN1,CX3CL1,WNT10B,SOD1,CHP1,TYRO3,SCD,SELENOS,GSTO1,FABP3,GPX1,PCK2,SLC26A6,SPX,RIPK3,SMARCB1,TXNRD2,IGFBP5,BAD,LETM1,CHERP,CCDC22,FOXK1,PKN1,TMEM79,RANGRF,CORO1A,TSPOAP1,SMARCA4,CSK,ANKRD9,DOCK11,ZNF830,AKT1,PACS2,GIT1,SIRT6,TJP3,EHMT1,AP3D1,STK11,CARD9,AMPD2,TGFBR3,ARMCX1,KLF13,JAGN1,CCDC115	yellow	VSMC_M3
GO:0032501	0.94	0.06	311	5003	multicellular organismal process	BP	1	ENPP1,NAB2,CDK4,BAG6,NCAPH2,SBF1,CTHRC1,HDAC10,FNIP1,PBX2,PDLIM4,RING1,NDUFB9,H2AFY,ITPR3,TRIM11,TRAPPC9,PACSIN1,PPARD,TSTA3,SCRIB,PLEC,LGALS1,MPST,IFT27,SHARPIN,SND1,CUL7,B4GALT1,PDGFRA,IL1R1,SECISBP2,PHF2,GRHPR,COL15A1,EPN1,COL19A1,SSC5D,SOCS5,TTC7A,CNOT3,KLF4,DBNL,TPBG,HOXA1,WDPCP,CCM2,FHL3,SPRED2,ZC3H12A,FIGNL1,RCN3,SNX3,PLEKHA4,MGLL,KMT2E,ANXA5,KRT8,SIX5,ZNF296,RELB,SLC9A3R1,PLXND1,EMILIN1,RNF220,PAFAH1B3,CIC,SNX17,UNK,DLEC1,CD79A,INSIG1,PSMC4,UCP2,METTL3,BAIAP2,CEP131,INPPL1,NUMA1,DND1,YIF1B,FASN,RPL29,EIF4EBP1,MORN2,CAVIN3,RIC8A,ARHGAP22,DEAF1,TBCB,HOXC4,LRIG1,ARHGAP33,AACS,SCARB1,HM13,BCL2L1,PDE4D,TNS2,SWAP70,LRP3,ACSL1,CAPG,SLC11A2,MMP24,GREM1,KDM2B,AQP5,PDE3B,DCTN1,CX3CL1,WNT10B,SOD1,ANKRD2,DGKZ,EGR3,HPS1,DLL4,TYRO3,SCD,HTATIP2,RAB35,KDM1B,APBA2,ST3GAL4,IRX1,SELENOS,GSTO1,SDHA,PAPSS1,PDGFA,MMP14,PABPN1,GPX1,CORO1B,NGEF,HCCS,CLCF1,IGSF9,QARS,LRFN4,PCK2,SLC19A1,COL6A1,IMPDH2,PIR,NECTIN1,ANPEP,TRIM27,LIMK1,SCN4A,SLC26A6,RABGGTA,SPX,THOC5,RIPK3,TWIST2,EXTL1,IQCG,MPZL3,TACO1,PLA2G3,STMN3,SART1,PTPN23,MRC2,PBX1,KAT5,RELA,TMEM120A,SCYL1,IDH1,ARNT2,VPS51,LIMD1,SGPL1,SMARCB1,PBX4,YJEFN3,ATIC,BLOC1S4,MEF2B,PHB2,NDP,IGFBP5,C12orf57,BAD,PLCB3,AAMP,CTDSP1,HSD17B1,CD9,PLAU,TNFRSF1A,TEAD4,C1QBP,AIMP2,TAF6L,CHERP,EVC,CNP,PRXL2A,KRT10,GLUD1,FOXK1,CASP14,KLF3,PKN1,DBN1,CAPN2,MAD1L1,AMER1,MTHFR,MAD2L2,NANOS3,PRR14,CRABP2,SP2,TMEM79,ARHGEF2,ARMC5,PER1,	yellow	VSMC_M3
GO:0050804	0.94	0.09	14	317	modulation of chemical synaptic transmission	BP	1	SQSTM1,ITPR3,BAIAP2,RAPSN,CX3CL1,DGKZ,SYT12,ZDHHC3,DBN1,GIT1,SLC6A4,ANAPC2,UNC13A,NSMF	yellow	VSMC_M3
GO:0003013	0.95	0.08	21	437	circulatory system process	BP	1	PPARD,PLEC,ZC3H12A,SLC9A3R1,PDE4D,LRP3,SOD1,DLL4,GSTO1,GPX1,SLC19A1,ANPEP,SPX,PLCB3,RANGRF,AKT1,SLC6A4,TJP3,TAZ,SLC27A4,ELN	yellow	VSMC_M3
GO:0007266	0.95	0.12	4	116	Rho protein signal transduction	BP	1	LIMK1,ARHGEF2,CDC42EP5,ARHGEF1	yellow	VSMC_M3
GO:0006508	0.95	0.07	77	1295	proteolysis	BP	1	SQSTM1,BAG6,SNX9,FNIP1,SHARPIN,VPS28,CUL7,HSPBP1,SOCS5,KLF4,JOSD2,PSMB3,ZC3H12A,RCN3,MICAL1,TMUB1,PSMC4,SEL1L2,DELE1,LDLRAD3,HM13,PEPD,MMP24,WNT10B,PACSIN3,CCAR2,RNF19B,SELENOS,MMP14,APEH,GPX1,PSME2,ANPEP,ADRM1,DPP3,CAPN10,PSMB4,SEC11A,PTPN23,KAT5,BAD,OTUB1,COPS6,PLAU,MVB12A,BABAM1,UBXN1,CCDC22,USP27X,SDE2,CASP14,CAPN2,FBXL19,SNF8,TRIM25,USP43,SENP8,ANKRD9,AKT1,DHCR24,BLMH,SIRT6,AURKAIP1,NCLN,ANAPC2,SPSB3,MAN1B1,CARD9,SPG7,ZNRF1,PSMB10,CTRL,TRIB2,CDC34,FBXO6,STUB1,RCE1	yellow	VSMC_M3
GO:0099177	0.95	0.09	14	318	regulation of trans-synaptic signaling	BP	1	SQSTM1,ITPR3,BAIAP2,RAPSN,CX3CL1,DGKZ,SYT12,ZDHHC3,DBN1,GIT1,SLC6A4,ANAPC2,UNC13A,NSMF	yellow	VSMC_M3
GO:0035051	0.95	0.12	4	119	cardiocyte differentiation	BP	1	PLEC,PDGFRA,GREM1,TGFBR3	yellow	VSMC_M3
GO:1903706	0.95	0.09	12	258	regulation of hemopoiesis	BP	1	SOCS5,ZC3H12A,METTL3,SOD1,EGR3,MMP14,PLA2G3,SART1,BAD,PRXL2A,AP3D1,KLF13	yellow	VSMC_M3
GO:0050679	0.95	0.11	6	154	positive regulation of epithelial cell proliferation	BP	1	B4GALT1,EGR3,BAD,AKT1,MYDGF,SIRT6	yellow	VSMC_M3
GO:2000241	0.95	0.12	4	105	regulation of reproductive process	BP	1	B4GALT1,METTL3,C1QBP,STK11	yellow	VSMC_M3
GO:0034767	0.95	0.12	4	114	positive regulation of ion transmembrane transport	BP	1	SLC9A3R1,CX3CL1,CHP1,GSTO1	yellow	VSMC_M3
GO:0021537	0.95	0.10	7	184	telencephalon development	BP	1	TRAPPC9,SECISBP2,KDM2B,ATIC,C12orf57,BAD,ERBB4	yellow	VSMC_M3
GO:0002262	0.95	0.11	5	134	myeloid cell homeostasis	BP	1	KMT2E,SLC11A2,SOD1,TGFBR3,KLF13	yellow	VSMC_M3
GO:0051093	0.95	0.07	35	676	negative regulation of developmental process	BP	1	ENPP1,TRIM11,PPARD,EPN1,SOCS5,KLF4,SPRED2,ZC3H12A,EMILIN1,INSIG1,LRP3,GREM1,PDE3B,WNT10B,ANKRD2,NGEF,ARPIN,TWIST2,CCDC85B,PBX1,LIMD1,YJEFN3,IGFBP5,CTDSP1,RCC2,MAD2L2,CARM1,SLC6A4,VASN,STK11,SARS,MIR214,RF00024,KLF13,TRIB2	yellow	VSMC_M3
GO:0006820	0.95	0.08	15	319	anion transport	BP	1	ENPP1,SLC52A2,ASNA1,PLEKHA8,TTYH2,SLC9A3R1,SLC16A5,SFXN5,SLC35C2,SLC16A14,SLC19A1,SLC26A6,PLA2G3,CTNS,SLC27A4	yellow	VSMC_M3
GO:0042327	0.95	0.07	31	612	positive regulation of phosphorylation	BP	1	NAB2,SQSTM1,SNX9,FNIP1,PRR5,PDGFRA,WDFY2,ACSL1,TNKS1BP1,GREM1,CX3CL1,DGKZ,TYRO3,PDGFA,CLCF1,RIPK3,TNK2,PHB2,BAD,TNFRSF1A,MAD2L2,ARHGEF2,CSK,AKT1,MYDGF,MAP2K2,IRAK1,STK11,TELO2,VAC14,ERBB4	yellow	VSMC_M3
GO:0006986	0.95	0.10	5	124	response to unfolded protein	BP	1	ATF6B,SERP2,SELENOS,FBXO6,STUB1	yellow	VSMC_M3
GO:0098771	0.95	0.07	25	502	inorganic ion homeostasis	BP	1	ENPP1,ITPR3,PDGFRA,TTC7A,SLC9A3R1,SLC30A3,RAB20,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,CHP1,GSTO1,SLC26A6,SPX,LETM1,CHERP,CCDC22,CORO1A,TSPOAP1,ANKRD9,PACS2,AP3D1,CCDC115	yellow	VSMC_M3
GO:0048469	0.95	0.11	4	116	cell maturation	BP	1	CX3CL1,SLC26A6,PLA2G3,TMEM79	yellow	VSMC_M3
GO:0006836	0.96	0.10	5	139	neurotransmitter transport	BP	1	SCRIB,SYT12,GIT1,SLC6A4,UNC13A	yellow	VSMC_M3
GO:0007163	0.96	0.09	7	189	establishment or maintenance of cell polarity	BP	1	SCRIB,WDPCP,SLC9A3R1,NUMA1,DCTN1,RHOC,STK11	yellow	VSMC_M3
GO:0006936	0.96	0.08	11	256	muscle contraction	BP	1	ZC3H12A,PDE4D,SOD1,ANKRD2,GSTO1,PABPN1,SCN4A,SPX,C12orf57,RANGRF,TAZ	yellow	VSMC_M3
GO:0007409	0.96	0.07	14	341	axonogenesis	BP	1	DBNL,PLXND1,BAIAP2,IGSF9,NECTIN1,LIMK1,C12orf57,CNP,DBN1,CRABP2,S100A6,ANAPC2,STK11,TWF2	yellow	VSMC_M3

GO:0006643	0.96	0.09	7	164	membrane lipid metabolic process	BP	1	CERK,PIGO,ST3GAL4,SGPL1,DPM3,CSNK1G2,GBA2	yellow	VSMC_M3
GO:0008015	0.96	0.07	17	369	blood circulation	BP	1	PPARD,PLEC,ZC3H12A,PDE4D,SOD1,DLL4,GSTO1,GPX1,ANPEP,SPX,PLCB3,RANGRF,AKT1,SLC6A4,TJP3,TAZ,ELN	yellow	VSMC_M3
GO:0035966	0.96	0.09	6	143	response to topologically incorrect protein	BP	1	BAG6,ATF6B,SERP2,SELENOS,FBXO6,STUB1	yellow	VSMC_M3
GO:0051239	0.96	0.05	112	1937	regulation of multicellular organismal process	BP	1	ENPP1,CDK4,BAG6,H2AFY,TRIM11,PPARD,TSTA3,SCRIB,CUL7,PDGFRA,IL1R1,EPN1,SSC5D,SOCS5,CNOT3,KLF4,DBNL,TPBG,WDPCP,SPRED2,ZC3H12A,MGLL,ANXA5,RELB,SLC9A3R1,PLXND1,EMILIN1,UCP2,METTL3,BAIAP2,NUMA1,SCARB1,PDE4D,ACSL1,GREM1,KDM2B,PDE3B,CX3CL1,WNT10B,SOD1,EGR3,DLL4,SCD,HTATIP2,ST3GAL4,SELENOS,GSTO1,PDGFA,MMP14,CLCF1,TRIM27,LIMK1,SCN4A,SPX,RIPK3,PLA2G3,SART1,PTPN23,PBX1,KAT5,RELA,SGPL1,YJEFN3,PHB2,IGFBP5,C12orf57,BAD,AAMP,CTDSP1,CD9,PLAU,TNFRSF1A,C1QBP,TAF6L,PRXL2A,DBN1,CAPN2,MAD2L2,CRABP2,ARHGEF2,PER1,RANGRF,EEF2K,CD276,CSK,AKT1,KHSRP,GIT1,SLC6A4,MYDGF,SIRT6,CACTIN,VASN,EHMT1,AP3D1,IRAK1,ANAPC2,STK11,JMJD8,CARD9,SARS,TGFBR3,TRADD,MIR214,MIR155,ERBB4,TWF2,PTPRR,KLF13,RNH1,TRIB2,GLIPR2	yellow	VSMC_M3
GO:0032409	0.96	0.08	8	198	regulation of transporter activity	BP	1	SLC9A3R1,PDE4D,CHP1,GSTO1,TACO1,PHB2,RANGRF,GSG1L	yellow	VSMC_M3
GO:0051302	0.96	0.09	5	138	regulation of cell division	BP	1	BCL2L1,PDGFA,CDK2AP2,MYO19,GIT1	yellow	VSMC_M3
GO:0050877	0.96	0.06	34	678	nervous system process	BP	1	NDUFB9,ITPR3,PLEC,TPBG,HOXA1,MGLL,SLC9A3R1,CIC,BAIAP2,RIC8A,LRIG1,SLC11A2,MMP24,DCTN1,WNT10B,SOD1,HPS1,DLL4,ST3GAL4,GSTO1,GPX1,SCN4A,RABGGTA,SPX,TACO1,TMEM120A,BLOC1S4,NDP,C12orf57,AKT1,GIT1,SLC6A4,CTNS,RGS16	yellow	VSMC_M3
GO:0008016	0.96	0.09	5	144	regulation of heart contraction	BP	1	ZC3H12A,PDE4D,GSTO1,SPX,RANGRF	yellow	VSMC_M3
GO:0051240	0.96	0.05	57	1050	positive regulation of multicellular organismal process	BP	1	H2AFY,SCRIB,CUL7,IL1R1,SOCS5,CNOT3,KLF4,DBNL,TPBG,ZC3H12A,PLXND1,UCP2,BAIAP2,NUMA1,PDE4D,ACSL1,GREM1,KDM2B,CX3CL1,WNT10B,SOD1,EGR3,SCD,ST3GAL4,GSTO1,MMP14,CLCF1,TRIM27,LIMK1,SPX,PLA2G3,SART1,RELA,BAD,C1QBP,DBN1,MAD2L2,CRABP2,ARHGEF2,EEF2K,CD276,AKT1,MYDGF,SIRT6,EHMT1,AP3D1,IRAK1,ANAPC2,STK11,JMJD8,CARD9,TGFBR3,TRADD,MIR214,ERBB4,TWF2,GLIPR2	yellow	VSMC_M3
GO:0003012	0.96	0.07	15	332	muscle system process	BP	1	KLF4,ZC3H12A,PDE4D,SOD1,ANKRD2,GSTO1,PABPN1,SCN4A,SPX,IGFBP5,C12orf57,TNFRSF1A,RANGRF,TAZ,MIR214	yellow	VSMC_M3
GO:0098739	0.96	0.10	4	123	import across plasma membrane	BP	1	SLC9A3R1,ACSL1,SLC19A1,AKT1	yellow	VSMC_M3
GO:0033157	0.96	0.08	8	196	regulation of intracellular protein transport	BP	1	SREBF2,ZC3H12A,DMAP1,INSIG1,CEP131,CHP1,PCNT,RBM22	yellow	VSMC_M3
GO:0051606	0.96	0.09	5	135	detection of stimulus	BP	1	SSC5D,PNKP,SCARB1,MMP24,TMEM120A	yellow	VSMC_M3
GO:0031669	0.96	0.08	7	182	cellular response to nutrient levels	BP	1	FNIP1,SREBF2,ZC3H12A,UCP2,DCPS,WDR24,FADS1	yellow	VSMC_M3
GO:0002703	0.96	0.09	5	136	regulation of leukocyte mediated immunity	BP	1	IL1R1,CLCF1,RIPK3,PLA2G3,MAD2L2	yellow	VSMC_M3
GO:0045664	0.96	0.09	5	145	regulation of neuron differentiation	BP	1	PBX1,CTDSP1,ARHGEF2,SLC6A4,HMG20B	yellow	VSMC_M3
GO:0006605	0.96	0.07	12	262	protein targeting	BP	1	SAMM50,SREBF2,ASNA1,YIF1B,CHP1,AIP,PEX5,ZDHHC3,CDC37,ATG3,AP3D1,TIMM22	yellow	VSMC_M3
GO:0018105	0.96	0.07	10	249	peptidyl-serine phosphorylation	BP	1	FNIP1,PDE4D,TNKS1BP1,STK32C,PKN1,MAD2L2,AKT1,MAP2K2,MKNK2,CSNK1G2	yellow	VSMC_M3
GO:0007167	0.96	0.05	37	752	enzyme linked receptor protein signaling pathway	BP	1	ENPP1,CD63,CDK4,PDGFRA,SOCS5,SPRED2,ZYX,SLC9A3R1,EMILIN1,BAIAP2,NUMA1,TNS2,GREM1,DOK1,TYRO3,PDGFA,NGEF,TNK2,RELA,SGPL1,IGFBP5,MVB12A,PIP4K2B,MVP,MTMR4,AKT1,GIT1,VASN,STK11,SLC27A4,TGFBR3,TRADD,NDST1,ERBB4,PTPRR,IGFBP6,STUB1	yellow	VSMC_M3
GO:0018209	0.96	0.07	11	267	peptidyl-serine modification	BP	1	FNIP1,PDE4D,TNKS1BP1,STK32C,PKN1,MAD2L2,AKT1,MAP2K2,MKNK2,CSNK1G2,NTMT1	yellow	VSMC_M3
GO:1903530	0.96	0.06	19	399	regulation of secretion by cell	BP	1	PPARD,EIPR1,MICAL1,MYRIP,UCP2,AACS,SYT12,PCK2,CAPN10,PLA2G3,PTPN23,BAD,TNFRSF1A,GLUD1,SNF8,GIT1,SLC6A4,MIDN,JAGN1	yellow	VSMC_M3
GO:0051783	0.96	0.09	4	114	regulation of nuclear division	BP	1	CUL7,MAD1L1,MAD2L2,AURKAIP1	yellow	VSMC_M3
GO:0051046	0.96	0.06	21	434	regulation of secretion	BP	1	PPARD,EIPR1,MICAL1,SLC9A3R1,MYRIP,UCP2,AACS,SYT12,PCK2,SPX,CAPN10,PLA2G3,PTPN23,BAD,TNFRSF1A,GLUD1,SNF8,GIT1,SLC6A4,MIDN,JAGN1	yellow	VSMC_M3
GO:0070588	0.96	0.07	8	211	calcium ion transmembrane transport	BP	1	ITPR3,PDE4D,CX3CL1,GSTO1,LETM1,CHERP,CORO1A,AKT1	yellow	VSMC_M3
GO:0007166	0.96	0.04	111	1935	cell surface receptor signaling pathway	BP	1	ENPP1,CD63,CDK4,BAG6,CTHRC1,TTLL12,SREBF2,TXNDC15,IFT27,SHARPIN,PDGFRA,IL1R1,EPN1,SOCS5,KLF4,TPBG,WDPCP,CCM2,SPRED2,ZC3H12A,ZYX,SNX3,PLEKHA4,KRT8,SLC9A3R1,PLXND1,EMILIN1,RNF220,CD79A,METTL3,BAIAP2,NUMA1,P4HB,DELE1,SCARB1,BCL2L1,ITGB7,PDE4D,SPRYD3,TNS2,ACSL1,GREM1,DOK1,CX3CL1,WNT10B,DGKZ,CCAR2,DLL4,TYRO3,SLC35C2,TSPAN5,ITPRIP,PDGFA,MMP14,GPX1,NGEF,CLCF1,LIMK1,TNK2,RELA,LIMD1,ZDHHC3,SGPL1,YJEFN3,PHB2,NDP,IGFBP5,BAD,LGALS3,TNFRSF1A,MVB12A,EVC,RCC2,PALM3,AMER1,PIP4K2B,MAD2L2,ARHGEF2,MVP,CORO1A,MTMR4,SMARCA4,CDC37,CD276,CSK,AKT1,TEDC1,RAB34,GIT1,NSDHL,CACTIN,VASN,HIC1,TEDC2,MKNK2,CSNK1G2,IRAK1,SSNA1,STK11,GAS8,SLC27A4,TGFBR3,TRADD,NDST1,TNFRSF12A,ERBB4,PTPRR,IGFBP6,JAGN1,APCDD1L,STUB1	yellow	VSMC_M3
GO:0015850	0.97	0.07	7	179	organic hydroxy compound transport	BP	1	SREBF2,LAMTOR1,SCARB1,SYT12,SLC26A6,YJEFN3,SLC6A4	yellow	VSMC_M3
GO:0030900	0.97	0.06	11	282	forebrain development	BP	1	TRAPPC9,SECISBP2,METTL3,KDM2B,TYRO3,ATIC,C12orf57,BAD,CNP,NDST1,ERBB4	yellow	VSMC_M3
GO:0007610	0.97	0.05	18	406	behavior	BP	1	ITPR3,TPBG,HOXA1,CIC,RIC8A,C12orf10,SLC11A2,DCTN1,SOD1,TACO1,C12orf57,CNP,CAPN2,GIT1,SLC6A4,CTNS,APRT,NEGR1	yellow	VSMC_M3
GO:0042692	0.97	0.06	13	303	muscle cell differentiation	BP	1	PLEC,PDGFRA,EHD2,KRT8,GREM1,WNT10B,MMP14,GPX1,PLEKHO1,IGFBP5,CD9,CAPN2,AKT1	yellow	VSMC_M3

GO:0043269	0.97	0.05	21	444	regulation of ion transport	BP	1	CD63,SLC9A3R1,PDE4D,CX3CL1,PACSIN3,CHP1,GSTO1,NKAIN1,SYT12,TRIM27,SCN4A,TACO1,PLA2G3,PHB2,LGALS3,PER1,RANGRF,CORO1A,AKT1,SLC6A4,GSG1L	yellow	VSMC_M3
GO:0034762	0.97	0.05	18	396	regulation of transmembrane transport	BP	1	ENPP1,CD63,SLC9A3R1,PDE4D,ACSL1,CX3CL1,CHP1,SELENOS,GSTO1,SCN4A,SLC26A6,CAPN10,TACO1,PHB2,RANGRF,CORO1A,AKT1,GSG1L	yellow	VSMC_M3
GO:0055001	0.97	0.07	5	150	muscle cell development	BP	1	PLEC,PDGFRA,KRT8,WNT10B,GPX1	yellow	VSMC_M3
GO:0031345	0.97	0.07	5	150	negative regulation of cell projection organization	BP	1	LGALS1,NGEF,ARPIN,CARM1,MIR214	yellow	VSMC_M3
GO:0045596	0.97	0.05	23	489	negative regulation of cell differentiation	BP	1	ENPP1,TRIM11,PPARD,SOCS5,SPRED2,ZC3H12A,INSIG1,LRP3,GREM1,WNT10B,ANKRD2,TWIST2,CCDC85B,PBX1,LIMD1,IGFBP5,CTDSP1,RCC2,MAD2L2,SLC6A4,VASN,KLF13,TRIB2	yellow	VSMC_M3
GO:0001505	0.97	0.07	5	147	regulation of neurotransmitter levels	BP	1	SCRIB,SYT12,GIT1,SLC6A4,UNC13A	yellow	VSMC_M3
GO:0007265	0.97	0.06	12	296	Ras protein signal transduction	BP	1	SQSTM1,SGSM3,DBNL,DOK1,RAB35,LIMK1,STMN3,ARHGEF2,RANGRF,DHCR24,CDC42EP5,ARHGEF1	yellow	VSMC_M3
GO:0031214	0.97	0.08	4	126	biomineral tissue development	BP	1	ENPP1,GREM1,WNT10B,NECTIN1	yellow	VSMC_M3
GO:0045165	0.97	0.07	6	172	cell fate commitment	BP	1	KLF4,WNT10B,DLL4,ARHGEF2,ZNF521,ERBB4	yellow	VSMC_M3
GO:0072503	0.97	0.05	13	306	cellular divalent inorganic cation homeostasis	BP	1	ITPR3,PDGFRA,SLC30A3,PDE4D,SWAP70,CX3CL1,GSTO1,LETM1,CHERP,CORO1A,TSPOAP1,PACS2,AP3D1	yellow	VSMC_M3
GO:0140352	0.97	0.04	31	618	export from cell	BP	1	PPARD,SCRIB,EIPR1,PDIA4,RCN3,MICAL1,MYRIP,UCP2,AACS,TYRO3,EXOC3,SYT12,PCK2,CAPN10,PLA2G3,PTPN23,BAD,TNFRSF1A,WASHC1,RAB3IL1,GLUD1,TMEM79,SNF8,CORO1A,GIT1,SLC6A4,MIDN,RABEPK,JAGN1,CAVIN1,UNC13A	yellow	VSMC_M3
GO:0110148	0.97	0.07	4	127	biomineralization	BP	1	ENPP1,GREM1,WNT10B,NECTIN1	yellow	VSMC_M3
GO:0045860	0.97	0.05	13	305	positive regulation of protein kinase activity	BP	1	NAB2,SNX9,ACSL1,GREM1,PDGFA,RIPK3,PHB2,CSK,AKT1,MAP2K2,IRAK1,STK11,TELO2	yellow	VSMC_M3
GO:0001894	0.97	0.06	7	189	tissue homeostasis	BP	1	RCN3,SOD1,CORO1A,CSK,ZNF830,TJP3,STK11	yellow	VSMC_M3
GO:0045861	0.97	0.05	9	213	negative regulation of proteolysis	BP	1	BAG6,FNIP1,KLF4,MICAL1,CCAR2,GPX1,UBXN1,AKT1,DHCR24	yellow	VSMC_M3
GO:0071363	0.97	0.04	25	545	cellular response to growth factor stimulus	BP	1	CD63,PDGFRA,KLF4,SPRED2,ZYX,EMILIN1,BAIAP2,NUMA1,GREM1,EGR3,DLL4,RAB35,CORO1B,RELA,CORO1A,MTMR4,EEF2K,AKT1,VASN,STK11,TGFBR3,NDST1,ERBB4,TWF2,STUB1	yellow	VSMC_M3
GO:0050801	0.97	0.04	26	542	ion homeostasis	BP	1	ENPP1,ITPR3,PDGFRA,TTC7A,SLC9A3R1,SLC30A3,RAB20,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,CHP1,GSTO1,SLC26A6,SPX,LETM1,CHERP,CCDC22,RANGRF,CORO1A,TSPOAP1,ANKRD9,PACS2,AP3D1,CCDC115	yellow	VSMC_M3
GO:0007268	0.97	0.04	21	471	chemical synaptic transmission	BP	1	SQSTM1,PDLIM4,ITPR3,SCRIB,TPBG,BAIAP2,RAPSN,CX3CL1,DGKZ,EGR3,APBA2,SYT12,ZDHHC3,CNP,DBN1,AKT1,GIT1,SLC6A4,ANAPC2,UNC13A,NSMF	yellow	VSMC_M3
GO:0098916	0.97	0.04	21	471	anterograde trans-synaptic signaling	BP	1	SQSTM1,PDLIM4,ITPR3,SCRIB,TPBG,BAIAP2,RAPSN,CX3CL1,DGKZ,EGR3,APBA2,SYT12,ZDHHC3,CNP,DBN1,AKT1,GIT1,SLC6A4,ANAPC2,UNC13A,NSMF	yellow	VSMC_M3
GO:0017157	0.97	0.06	5	147	regulation of exocytosis	BP	1	MICAL1,SYT12,PLA2G3,SNF8,GIT1	yellow	VSMC_M3
GO:0006935	0.97	0.04	19	426	chemotaxis	BP	1	SCRIB,PLEC,PDGFRA,TPBG,PLXND1,SWAP70,GREM1,CX3CL1,EGR3,LSP1,RIN3,PDGFA,CORO1B,IGSF9,NECTIN1,LGALS3,PLAU,C1QBP,CORO1A	yellow	VSMC_M3
GO:0001934	0.97	0.04	26	543	positive regulation of protein phosphorylation	BP	1	NAB2,SQSTM1,SNX9,FNIP1,PRR5,WDFY2,ACSL1,TNKS1BP1,GREM1,CX3CL1,PDGFA,CLCF1,RIPK3,TNK2,PHB2,TNFRSF1A,MAD2L2,ARHGEF2,CSK,AKT1,MYDGF,MAP2K2,IRAK1,STK11,TELO2,ERBB4	yellow	VSMC_M3
GO:0042330	0.97	0.04	19	427	taxis	BP	1	SCRIB,PLEC,PDGFRA,TPBG,PLXND1,SWAP70,GREM1,CX3CL1,EGR3,LSP1,RIN3,PDGFA,CORO1B,IGSF9,NECTIN1,LGALS3,PLAU,C1QBP,CORO1A	yellow	VSMC_M3
GO:0006665	0.97	0.07	4	120	sphingolipid metabolic process	BP	1	CERK,SGPL1,CSNK1G2,GBA2	yellow	VSMC_M3
GO:0006468	0.97	0.03	65	1223	protein phosphorylation	BP	1	ENPP1,NAB2,CDK4,CTDSP2,SQSTM1,SNX9,FNIP1,PRR5,H2AFY,PLEC,PDGFRA,SOCS5,SPRED2,ZC3H12A,MICAL1,WDFY2,SLC9A3R1,EMILIN1,SERTAD1,TARBP2,PDE4D,ACSL1,TNKS1BP1,GREM1,CX3CL1,SOD1,CHP1,TYRO3,HTATIP2,STK32C,PDGFA,CLCF1,QARS,TRIM27,LIMK1,RIPK3,TNK2,SCYL1,MEX3B,MAP3K14,PHB2,CTDSP1,TNFRSF1A,PKN1,MAD2L2,CTBP1,ARHGEF2,MVP,EEF2K,CDC37,CSK,AKT1,SGK494,MYDGF,MAP2K2,CACTIN,CDK11B,MKNK2,CSNK1G2,IRAK1,STK11,TELO2,TGFBR3,ERBB4,TRIB2	yellow	VSMC_M3
GO:0019932	0.98	0.05	8	218	second-messenger-mediated signaling	BP	1	ITPR3,SLC9A3R1,PDE4D,PDE3B,CHP1,GSTO1,CHERP,CDC34	yellow	VSMC_M3
GO:0009952	0.98	0.06	5	150	anterior/posterior pattern specification	BP	1	RING1,HOXC4,KDM2B,PBX1,HOXC5	yellow	VSMC_M3
GO:0000280	0.98	0.04	16	355	nuclear division	BP	1	DCTN2,BAG6,NCAPH2,H2AFY,CUL7,FIGNL1,NUMA1,RRS1,PINX1,NUDC,PHB2,EML3,MAD1L1,MAD2L2,AURKAIP1,MIS12	yellow	VSMC_M3
GO:0003002	0.98	0.05	10	251	regionalization	BP	1	PBX2,RING1,RNF220,HOXC4,GREM1,KDM2B,DLL4,IRX1,PBX1,HOXC5	yellow	VSMC_M3
GO:0051260	0.98	0.06	4	128	protein homooligomerization	BP	1	AQP5,TMEM120A,LETM1,CARD9	yellow	VSMC_M3
GO:0061564	0.98	0.04	15	380	axon development	BP	1	KLF4,DBNL,PLXND1,BAIAP2,IGSF9,NECTIN1,LIMK1,C12orf57,CNP,DBN1,CRABP2,S100A6,ANAPC2,STK11,TWF2	yellow	VSMC_M3
GO:0055065	0.98	0.04	20	438	metal ion homeostasis	BP	1	ITPR3,PDGFRA,TTC7A,SLC30A3,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,GSTO1,SPX,LETM1,CHERP,CCDC22,CORO1A,TSPOAP1,ANKRD9,PACS2,AP3D1,CCDC115	yellow	VSMC_M3
GO:0070848	0.98	0.03	26	570	response to growth factor	BP	1	CD63,PDGFRA,KLF4,SPRED2,ZYX,EMILIN1,BAIAP2,NUMA1,GREM1,EGR3,DLL4,RAB35,CORO1B,RELA,CORO1A,MTMR4,EEF2K,AKT1,VASN,STK11,TGFBR3,NDST1,ERBB4,TWF2,CDC34,STUB1	yellow	VSMC_M3
GO:0055080	0.98	0.03	23	494	cation homeostasis	BP	1	ITPR3,PDGFRA,TTC7A,SLC30A3,RAB20,PDE4D,SWAP70,SLC11A2,CX3CL1,SOD1,CHP1,GSTO1,SLC26A6,SPX,LETM1,CHERP,CCDC22,CORO1A,TSPOAP1,ANKRD9,PACS2,AP3D1,CCDC115	yellow	VSMC_M3
GO:0099537	0.98	0.04	21	477	trans-synaptic signaling	BP	1	SQSTM1,PDLIM4,ITPR3,SCRIB,TPBG,BAIAP2,RAPSN,CX3CL1,DGKZ,EGR3,APBA2,SYT12,ZDHHC3,CNP,DBN1,AKT1,GIT1,SLC6A4,ANAPC2,UNC13A,NSMF	yellow	VSMC_M3

GO:0099536	0.98	0.03	22	494	synaptic signaling	BP	1	SQSTM1,PDLIM4,ITPR3,SCRIB,TPBG,BAIAP2,RAPSN,CX3CL1,DGKZ,EGR3,APBA2,SYT12,RELA,ZDHHC3,CNP,DBN1,AKT1,GIT1,SLC6A4,ANAPC2,UNC13A,NSMF	yellow	VSMC_M3
GO:1903522	0.98	0.05	6	179	regulation of blood circulation	BP	1	ZC3H12A,PDE4D,GSTO1,SPX,RANGRF,AKT1	yellow	VSMC_M3
GO:0006816	0.98	0.04	11	282	calcium ion transport	BP	1	ITPR3,PDE4D,CX3CL1,PACSIN3,GSTO1,TRIM27,LETM1,LGALS3,CHERP,CORO1A,AKT1	yellow	VSMC_M3
GO:0030099	0.98	0.04	12	293	myeloid cell differentiation	BP	1	KMT2E,RELB,FASN,SLC11A2,PIR,THOC5,PLA2G3,PRXL2A,TGFBR3,KLF13,JAGN1,ZNF385A	yellow	VSMC_M3
GO:0010952	0.98	0.05	5	142	positive regulation of peptidase activity	BP	1	RCN3,PSME2,ADRM1,BAD,CARD9	yellow	VSMC_M3
GO:0007267	0.98	0.03	60	1146	cell-cell signaling	BP	1	SQSTM1,CTHRC1,PDLIM4,ITPR3,NUDT3,PPARD,SCRIB,KLF4,TPBG,EIPR1,ZYX,SNX3,PLEKHA4,SLC9A3R1,RNF220,MYRIP,UCP2,BAIAP2,AACS,GREM1,RAPSN,CX3CL1,WNT10B,DGKZ,EGR3,CCAR2,APBA2,PDGFA,SYT12,PCK2,CAPN10,PLA2G3,PTPN23,RELA,LIMD1,ZDHHC3,NDP,BAD,CNP,GLUD1,DBN1,AMER1,MAD2L2,RANGRF,SMARCA4,TMED1,AKT1,GIT1,SLC6A4,HIC1,CSNK1G2,ANAPC2,MIDN,STK11,FADS1,IGFBP6,JAGN1,UNC13A,NSMF,APCDD1L	yellow	VSMC_M3
GO:0007178	0.98	0.04	10	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SPRED2,ZYX,EMILIN1,NUMA1,GREM1,MTMR4,VASN,STK11,TGFBR3,STUB1	yellow	VSMC_M3
GO:0051100	0.98	0.05	4	129	negative regulation of binding	BP	1	MAD2L2,AKT1,GTF2F1,STUB1	yellow	VSMC_M3
GO:0061448	0.98	0.04	7	203	connective tissue development	BP	1	CDK4,PPARD,AACS,GREM1,WNT10B,EVC,AMER1	yellow	VSMC_M3
GO:0071103	0.98	0.04	7	200	DNA conformation change	BP	1	NCAPH2,H2AFY,PHF2,H3F3B,BANF1,H3F3A,UBN1	yellow	VSMC_M3
GO:0072507	0.98	0.03	13	323	divalent inorganic cation homeostasis	BP	1	ITPR3,PDGFRA,SLC30A3,PDE4D,SWAP70,CX3CL1,GSTO1,LETM1,CHERP,CORO1A,TSPOAP1,PACS2,AP3D1	yellow	VSMC_M3
GO:0048285	0.98	0.03	18	401	organelle fission	BP	1	DCTN2,BAG6,NCAPH2,H2AFY,CUL7,FIGNL1,NUMA1,RRS1,PINX1,NUDC,PHB2,EML3,MAD1L1,MAD2L2,MYO19,INF2,AURKAIP1,MIS12	yellow	VSMC_M3
GO:0006874	0.98	0.03	11	283	cellular calcium ion homeostasis	BP	1	ITPR3,PDGFRA,PDE4D,SWAP70,CX3CL1,GSTO1,LETM1,CHERP,CORO1A,TSPOAP1,PACS2	yellow	VSMC_M3
GO:0052547	0.98	0.03	13	294	regulation of peptidase activity	BP	1	FNIP1,KLF4,RCN3,MICAL1,DELE1,GPX1,PSME2,ADRM1,BAD,UBXN1,AKT1,DHCR24,CARD9	yellow	VSMC_M3
GO:0098655	0.98	0.03	30	623	cation transmembrane transport	BP	1	CD63,ITPR3,SLC9A3R1,SLC30A3,UCP2,PDE4D,UQCRFS1,SLC11A2,CX3CL1,CHP1,GSTO1,SCN4A,UQCRC1,RHCE,TACO1,ATP5MC3,PHB2,LETM1,CHERP,RANGRF,CORO1A,SLC39A1,ATP5PD,AKT1,SLC6A4,CTNS,NDUFS7,ATP5F1D,SURF1,GSG1L	yellow	VSMC_M3
GO:0034765	0.98	0.03	13	323	regulation of ion transmembrane transport	BP	1	CD63,SLC9A3R1,PDE4D,CX3CL1,CHP1,GSTO1,SCN4A,TACO1,PHB2,RANGRF,CORO1A,AKT1,GSG1L	yellow	VSMC_M3
GO:0006261	0.98	0.05	4	137	DNA-dependent DNA replication	BP	1	PNKP,LRWD1,ZNF830,CDC34	yellow	VSMC_M3
GO:0010950	0.98	0.04	4	127	positive regulation of endopeptidase activity	BP	1	PSME2,ADRM1,BAD,CARD9	yellow	VSMC_M3
GO:0043085	0.98	0.02	44	875	positive regulation of catalytic activity	BP	1	NAB2,SNX9,SGSM3,SCRIB,PDGFRA,KLF4,PNKP,RCN3,ARAP3,ARHGAP22,SCARB1,ACSL1,GREM1,CX3CL1,SOD1,DGKZ,TYRO3,PDGFA,PABPN1,NGEF,PSME2,RIPK3,ADRM1,SIPA1,RHOC,MID1IP1,PHB2,BAD,AIMP2,RCC2,CSK,DOCK11,AKT1,SNX18,MAP2K2,IRAK1,STK11,TELO2,CARD9,SLC27A4,VAC14,ERBB4,RGS16,STUB1	yellow	VSMC_M3
GO:0003007	0.99	0.03	6	197	heart morphogenesis	BP	1	PLXND1,DLL4,SIRT6,TAZ,TGFBR3,ELN	yellow	VSMC_M3
GO:0044093	0.99	0.02	60	1151	positive regulation of molecular function	BP	1	NAB2,SNX9,CTHRC1,SGSM3,TRAPPC9,SCRIB,PDGFRA,KLF4,PNKP,RCN3,PLXND1,ARAP3,ARHGAP22,SCARB1,ACSL1,PINX1,GREM1,CX3CL1,WNT10B,SOD1,DGKZ,CHP1,TYRO3,GSTO1,PDGFA,PABPN1,NGEF,PSME2,TRIM27,RIPK3,ADRM1,RELA,SIPA1,RHOC,MID1IP1,SMARCB1,PHB2,BAD,BUD31,AIMP2,RCC2,ARHGEF2,TRIM25,SMARCA4,CSK,MID2,DOCK11,AKT1,SNX18,MAP2K2,IRAK1,STK11,TELO2,CARD9,SLC27A4,VAC14,TRADD,ERBB4,RGS16,STUB1	yellow	VSMC_M3
GO:0031349	0.99	0.03	6	177	positive regulation of defense response	BP	1	CX3CL1,PLA2G3,IFI35,TNFRSF1A,CARD9,TRADD	yellow	VSMC_M3
GO:0055074	0.99	0.03	11	291	calcium ion homeostasis	BP	1	ITPR3,PDGFRA,PDE4D,SWAP70,CX3CL1,GSTO1,LETM1,CHERP,CORO1A,TSPOAP1,PACS2	yellow	VSMC_M3
GO:0043405	0.99	0.03	4	146	regulation of MAP kinase activity	BP	1	PDGFA,CSK,IRAK1,TRIB2	yellow	VSMC_M3
GO:0008284	0.99	0.02	33	681	positive regulation of cell population proliferation	BP	1	CDK4,CTHRC1,PPARD,B4GALT1,PDGFRA,RPS9,SERTAD1,CEP131,BCL2L1,GREM1,CX3CL1,WNT10B,EGR3,DLL4,PDGFA,CLCF1,PBX1,RELA,ARNT2,IGFBP5,BAD,CORO1A,S100A6,CARM1,CD276,AKT1,MYDGF,SIRT6,IRAK1,MVD,TGFBR3,MIR214,ERBB4	yellow	VSMC_M3
GO:0006811	0.99	0.02	53	1026	ion transport	BP	1	ENPP1,CD63,ITPR3,SLC52A2,ASNA1,PLEKHA8,TTYH2,SLC9A3R1,SLC16A5,SLC30A3,UCP2,PDE4D,UQCRFS1,SLC11A2,CX3CL1,PACSIN3,SFXN5,CHP1,SLC35C2,GSTO1,SLC16A14,NKAIN1,SYT12,SLC19A1,NECTIN1,TRIM27,SCN4A,SLC26A6,UQCRC1,RHCE,TACO1,PLA2G3,ATP5MC3,TMEM120A,PHB2,LETM1,LGALS3,CHERP,PER1,RANGRF,CORO1A,SLC39A1,ATP5PD,S100A6,AKT1,SLC6A4,CTNS,NDUFS7,ATP5F1D,SLC27A4,SLC44A3,SURF1,GSG1L	yellow	VSMC_M3
GO:0052548	0.99	0.02	11	270	regulation of endopeptidase activity	BP	1	FNIP1,KLF4,MICAL1,DELE1,GPX1,PSME2,ADRM1,BAD,AKT1,DHCR24,CARD9	yellow	VSMC_M3
GO:0001819	0.99	0.02	12	304	positive regulation of cytokine production	BP	1	SCRIB,IL1R1,PDE4D,CX3CL1,SOD1,TRIM27,PLA2G3,RELA,ARHGEF2,CD276,IRAK1,CARD9	yellow	VSMC_M3
GO:0046578	0.99	0.03	4	161	regulation of Ras protein signal transduction	BP	1	SQSTM1,SGSM3,STMN3,ARHGEF2	yellow	VSMC_M3
GO:0006812	0.99	0.02	39	796	cation transport	BP	1	CD63,ITPR3,SLC9A3R1,SLC30A3,UCP2,PDE4D,UQCRFS1,SLC11A2,CX3CL1,PACSIN3,CHP1,GSTO1,NKAIN1,SYT12,NECTIN1,TRIM27,SCN4A,UQCRC1,RHCE,TACO1,PLA2G3,ATP5MC3,PHB2,LETM1,LGALS3,CHERP,PER1,RANGRF,CORO1A,SLC39A1,ATP5PD,AKT1,SLC6A4,CTNS,NDUFS7,ATP5F1D,SLC44A3,SURF1,GSG1L	yellow	VSMC_M3
GO:0044057	0.99	0.02	16	398	regulation of system process	BP	1	KLF4,ZC3H12A,MGLL,SLC9A3R1,BAIAP2,PDE4D,SOD1,GSTO1,SCN4A,SPX,IGFBP5,C12orf57,TNFRSF1A,RANGRF,AKT1,MIR214	yellow	VSMC_M3
GO:0042391	0.99	0.02	11	302	regulation of membrane potential	BP	1	UCP2,BAIAP2,PYCR1,BCL2L1,SOD1,SCN4A,CHCHD10,BAD,RANGRF,AKT1,CTNS	yellow	VSMC_M3
GO:0051099	0.99	0.03	4	141	positive regulation of binding	BP	1	CTHRC1,KLF4,PLXND1,PINX1	yellow	VSMC_M3
GO:0051321	0.99	0.02	6	192	meiotic cell cycle	BP	1	BAG6,NCAPH2,FIGNL1,METTL3,NUMA1,TUBGCP2	yellow	VSMC_M3
GO:0071900	0.99	0.01	11	300	regulation of protein serine/threonine kinase activity	BP	1	H2AFY,SERTAD1,ACSL1,PDGFA,CDC37,CSK,AKT1,MAP2K2,IRAK1,TELO2,TRIB2	yellow	VSMC_M3

GO:0007186	0.99	0.01	19	458	G protein-coupled receptor signaling pathway	BP	1	ITPR3,RGS3,MGLL,SLC9A3R1,RIC8A,PDE4D,PDE3B,CX3CL1,DGKZ,TYRO3,CISH,ZDHHC3,GNB2,PLCB3,AKT1,GIT1,ARHGEF1,RGS16,RGS18	yellow	VSMC_M3
GO:0051098	0.99	0.01	11	296	regulation of binding	BP	1	CTHRC1,KLF4,PLXND1,PINX1,MAD2L2,CARM1,AKT1,GTF2F1,GAS8,TGFBR3,STUB1	yellow	VSMC_M3
GO:0034220	0.99	0.01	36	765	ion transmembrane transport	BP	1	CD63,ITPR3,SLC9A3R1,SLC30A3,UCP2,PDE4D,UQCRFS1,SLC11A2,CX3CL1,SFXN5,CHP1,SLC35C2,GSTO1,SLC19A1,SCN4A,SLC26A6,UQCRC1,RHCE,TACO1,ATP5MC3,TMEM120A,PHB2,LETM1,CHERP,RANGRF,CORO1A,SLC39A1,ATP5PD,S100A6,AKT1,SLC6A4,CTNS,NDUFS7,ATP5F1D,SURF1,GSG1L	yellow	VSMC_M3
GO:0007507	0.99	0.01	18	474	heart development	BP	1	PDLIM4,PPARD,PLEC,PDGFRA,CCM2,PLXND1,EMILIN1,SNX17,GREM1,DLL4,TNFRSF1A,SIRT6,MBD3,TAZ,TGFBR3,NDST1,ERBB4,ELN	yellow	VSMC_M3
GO:0006260	0.99	0.01	7	230	DNA replication	BP	1	PNKP,ZBTB38,LRWD1,SDE2,NFIX,ZNF830,CDC34	yellow	VSMC_M3
GO:0048863	1.00	0.01	4	171	stem cell differentiation	BP	1	PDGFRA,METTL3,GREM1,ERBB4	yellow	VSMC_M3
GO:0007389	1.00	0.01	11	329	pattern specification process	BP	1	PBX2,RING1,RNF220,HOXC4,GREM1,KDM2B,DLL4,IRX1,PBX1,ERBB4,HOXC5	yellow	VSMC_M3
GO:0055085	1.00	0.00	50	1047	transmembrane transport	BP	1	ENPP1,CD63,ITPR3,PPARD,SLC9A3R1,SLC16A5,SLC30A3,UCP2,SCARB1,PDE4D,UQCRFS1,ACSL1,SLC11A2,AQP5,CX3CL1,SFXN5,CHP1,SLC35C2,SELENOS,GSTO1,SLC16A14,SLC19A1,SCN4A,SLC26A6,UQCRC1,CAPN10,RHCE,TACO1,ATP5MC3,TMEM120A,PEX5,PHB2,LETM1,CHERP,RANGRF,CORO1A,SLC39A1,ATP5PD,S100A6,AKT1,SLC6A4,SLC35E2B,CTNS,NDUFS7,ATP5F1D,SLC27A4,SLC44A3,SURF1,TIMM22,GSG1L	yellow	VSMC_M3
GO:0030001	1.00	0.00	23	587	metal ion transport	BP	1	CD63,ITPR3,SLC9A3R1,SLC30A3,PDE4D,SLC11A2,CX3CL1,PACSIN3,CHP1,GSTO1,NKAIN1,NECTIN1,TRIM27,SCN4A,LETM1,LGALS3,CHERP,PER1,RANGRF,CORO1A,SLC39A1,AKT1,SLC6A4	yellow	VSMC_M3
GO:0003008	1.00	0.00	58	1240	system process	BP	1	NDUFB9,ITPR3,PPARD,PLEC,GRHPR,KLF4,TPBG,HOXA1,ZC3H12A,MGLL,SLC9A3R1,CIC,BAIAP2,RIC8A,LRIG1,SCARB1,PDE4D,LRP3,SLC11A2,MMP24,AQP5,DCTN1,WNT10B,SOD1,ANKRD2,HPS1,DLL4,ST3GAL4,GSTO1,PABPN1,GPX1,SLC19A1,ANPEP,SCN4A,SLC26A6,RABGGTA,SPX,TACO1,TMEM120A,BLOC1S4,NDP,IGFBP5,C12orf57,PLCB3,TNFRSF1A,PKN1,RANGRF,ZNF830,AKT1,GIT1,SLC6A4,TJP3,CTNS,TAZ,SLC27A4,MIR214,ELN,RGS16	yellow	VSMC_M3
GO:0032103	1.00	0.00	9	286	positive regulation of response to external stimulus	BP	1	TPBG,SWAP70,CX3CL1,PLA2G3,IFI35,TNFRSF1A,C1QBP,CARD9,TRADD	yellow	VSMC_M3
GO:0099537	0.00	1.00	288	477	trans-synaptic signaling	BP	1	STAC3,KIF5A,PDE7B,SNCAIP,MAPK8IP2,SLC12A2,RIMS2,PRRT1,PRKN,AGER,SYNGAP1,AKAP7,GRM4,EXOC4,ATF4,SYNGR1,NTRK2,PLA2G6,PICK1,BTBD9,CHRNA3,LRRC4,GRM8,CHRNA5,SRF,GABRA1,APBA1,PHF24,USP46,KIT,SLC1A1,ROR2,GABBR2,BRSK1,PRKCE,RIMS1,RIMS3,ACP4,SHANK1,PPT1,CRHR2,SLC1A4,PTN,DGKI,EGFR,NCDN,GRIK2,DLGAP3,AMPH,SDCBP,SLC7A11,PPFIA3,LIN7B,NTF4,PRKAR2B,GRIN2D,MTMR2,NAPA,SLC8A2,GAD2,CACNB2,DLG2,PCDH8,GRIK5,NAPB,PLAT,CHRNA6,FARP1,FCHSD2,SYT1,CACNB4,RAB5A,LIN7A,PLCB1,PLCL2,RAC3,PRNP,FCHSD1,P2RX2,PTPRA,STX2,SYT9,SNPH,EPHB1,PLK2,HTR7,FAM107A,NR4A1,PXK,ABHD6,CLSTN2,P2RX3,CHRM5,ERC2,MEF2C,ASIC1,P2RX7,DLGAP4,GUCY1A1,GUCY1B1,CUX2,P2RY1,PTK2B,MME,RAPGEF2,EIF2AK4,SYNJ1,HOMER1,CHRM4,F2R,VPS18,SLC6A2,GLS,ITPKA,CYFIP1,DTNBP1,SLC12A5,KCNIP2,CHRM3,LZTS1,SYT8,GRM2,BDNF,SLC4A10,NEURL1,DNM1L,SLC6A3,SORCS3,PPP3CA,SLC12A7,ADRA2A,IGSF11,ADARB1,SNAP23,DAG1,NLGN4Y,SSH1,STAU1,KCNB1,KRAS,BSN,ADNP,DISC1,GPER1,GRIK4,AGT,ATP1A2,NFATC4,RPS6KA1,SYAP1,STX1A,TMEM25,NPAS4,NTSR1,YTHDF1,CNIH2,BACE1,DNAJC5,GLUL,CSPG5,DLG1,CREB1,YWHAG,HTR3B,SPG11,MAPT,RAP1B,BLOC1S6,SRGN,VGF,EIF4EBP2,TNR,NRXN2,CASK,MPP2,BCHE,PNKD,CRTC1,PPP3CB,RAB3A,PINK1,KCNN1,SYN1,SNAP29,STAT3,KCNA1,CD38,NPTX2,MAPK1,CHRM1,TMOD2,NSG1,DAGLB,MINK1,RAB8A,HAP1,EPHA4,RNF216,DLG4,SYT7,IQSEC2,NLGN2,CHRNB1,CNIH3,RGS14,CACNB1,SYNJ2BP,HRH2,CPLX1,STX1B,STX4,PSEN1,CACNA1A,SYT11,NLGN3,KCTD13,MYCBPAP,CACNA1G,AC138894.1,CHRNB2,RAB11A,DGKE,CALM1,	grey	VSMC_M10
GO:0007268	0.00	1.00	284	471	chemical synaptic transmission	BP	1	STAC3,KIF5A,PDE7B,SNCAIP,MAPK8IP2,SLC12A2,RIMS2,PRRT1,PRKN,AGER,SYNGAP1,AKAP7,GRM4,EXOC4,ATF4,SYNGR1,NTRK2,PLA2G6,PICK1,BTBD9,CHRNA3,LRRC4,GRM8,CHRNA5,SRF,GABRA1,APBA1,PHF24,USP46,KIT,SLC1A1,ROR2,GABBR2,BRSK1,PRKCE,RIMS1,RIMS3,ACP4,SHANK1,PPT1,CRHR2,SLC1A4,PTN,DGKI,EGFR,NCDN,GRIK2,DLGAP3,AMPH,SDCBP,SLC7A11,PPFIA3,LIN7B,NTF4,PRKAR2B,GRIN2D,MTMR2,NAPA,SLC8A2,GAD2,CACNB2,DLG2,PCDH8,GRIK5,NAPB,PLAT,CHRNA6,FCHSD2,SYT1,CACNB4,RAB5A,LIN7A,PLCB1,PLCL2,RAC3,PRNP,FCHSD1,P2RX2,PTPRA,STX2,SYT9,SNPH,EPHB1,PLK2,HTR7,FAM107A,NR4A1,PXK,ABHD6,CLSTN2,P2RX3,CHRM5,ERC2,MEF2C,ASIC1,P2RX7,DLGAP4,GUCY1A1,GUCY1B1,CUX2,P2RY1,PTK2B,MME,RAPGEF2,EIF2AK4,SYNJ1,HOMER1,CHRM4,F2R,VPS18,SLC6A2,GLS,ITPKA,CYFIP1,DTNBP1,SLC12A5,KCNIP2,CHRM3,LZTS1,SYT8,GRM2,BDNF,SLC4A10,NEURL1,DNM1L,SLC6A3,SORCS3,PPP3CA,SLC12A7,ADRA2A,IGSF11,ADARB1,SNAP23,NLGN4Y,SSH1,STAU1,KCNB1,KRAS,BSN,ADNP,DISC1,GPER1,GRIK4,AGT,ATP1A2,NFATC4,RPS6KA1,SYAP1,STX1A,TMEM25,NPAS4,NTSR1,YTHDF1,CNIH2,BACE1,DNAJC5,GLUL,CSPG5,DLG1,CREB1,YWHAG,HTR3B,SPG11,MAPT,RAP1B,BLOC1S6,SRGN,VGF,EIF4EBP2,TNR,NRXN2,CASK,MPP2,BCHE,PNKD,CRTC1,PPP3CB,RAB3A,PINK1,KCNN1,SYN1,SNAP29,STAT3,KCNA1,CD38,NPTX2,MAPK1,CHRM1,TMOD2,NSG1,MINK1,RAB8A,HAP1,EPHA4,RNF216,DLG4,SYT7,IQSEC2,NLGN2,CHRNB1,CNIH3,RGS14,CACNB1,SYNJ2BP,HRH2,CPLX1,STX1B,STX4,PSEN1,CACNA1A,SYT11,NLGN3,KCTD13,MYCBPAP,CACNA1G,AC138894.1,CHRNB2,RAB11A,DGKE,CALM1,SNAPIN,PRKCB,RIT2,	grey	VSMC_M10

GO:0098916	0.00	1.00	284	471	anterograde trans-synaptic signaling	BP	1	STAC3,KIF5A,PDE7B,SNCAIP,MAPK8IP2,SLC12A2,RIMS2,PRRT1,PRKN,AGER,SYNGAP1,AKAP7,GRM4,EXOC4,ATF4,SYNGR1,NTRK2,PLA2G6,PICK1,BTBD9,CHRNA3,LRRC4,GRM8,CHRNA5,SRF,GABRA1,APBA1,PHF24,USP46,KIT,SLC1A1,ROR2,GABBR2,BRSK1,PRKCE,RIMS1,RIMS3,ACP4,SHANK1,PPT1,CRHR2,SLC1A4,PTN,DGKI,EGFR,NCDN,GRIK2,DLGAP3,AMPH,SDCBP,SLC7A11,PPFIA3,LIN7B,NTF4,PRKAR2B,GRIN2D,MTMR2,NAPA,SLC8A2,GAD2,CACNB2,DLG2,PCDH8,GRIK5,NAPB,PLAT,CHRNA6,FCHSD2,SYT1,CACNB4,RAB5A,LIN7A,PLCB1,PLCL2,RAC3,PRNP,FCHSD1,P2RX2,PTPRA,STX2,SYT9,SNPH,EPHB1,PLK2,HTR7,FAM107A,NR4A1,PXK,ABHD6,CLSTN2,P2RX3,CHRM5,ERC2,MEF2C,ASIC1,P2RX7,DLGAP4,GUCY1A1,GUCY1B1,CUX2,P2RY1,PTK2B,MME,RAPGEF2,EIF2AK4,SYNJ1,HOMER1,CHRM4,F2R,VPS18,SLC6A2,GLS,ITPKA,CYFIP1,DTNBP1,SLC12A5,KCNIP2,CHRM3,LZTS1,SYT8,GRM2,BDNF,SLC4A10,NEURL1,DNM1L,SLC6A3,SORCS3,PPP3CA,SLC12A7,ADRA2A,IGSF11,ADARB1,SNAP23,NLGN4Y,SSH1,STAU1,KCNB1,KRAS,BSN,ADNP,DISC1,GPER1,GRIK4,AGT,ATP1A2,NFATC4,RPS6KA1,SYAP1,STX1A,TMEM25,NPAS4,NTSR1,YTHDF1,CNIH2,BACE1,DNAJC5,GLUL,CSPG5,DLG1,CREB1,YWHAG,HTR3B,SPG11,MAPT,RAP1B,BLOC1S6,SRGN,VGF,EIF4EBP2,TNR,NRXN2,CASK,MPP2,BCHE,PNKD,CRTC1,PPP3CB,RAB3A,PINK1,KCNN1,SYN1,SNAP29,STAT3,KCNA1,CD38,NPTX2,MAPK1,CHRM1,TMOD2,NSG1,MINK1,RAB8A,HAP1,EPHA4,RNF216,DLG4,SYT7,IQSEC2,NLGN2,CHRNB1,CNIH3,RGS14,CACNB1,SYNJ2BP,HRH2,CPLX1,STX1B,STX4,PSEN1,CACNA1A,SYT11,NLGN3,KCTD13,MYCBPAP,CACNA1G,AC138894.1,CHRNB2,RAB11A,DGKE,CALM1,SNAPIN,PRKCB,RIT2	grey	VSMC_M10
GO:0099536	0.00	1.00	297	494	synaptic signaling	BP	1	STAC3,KIF5A,PDE7B,SNCAIP,MAPK8IP2,SLC12A2,RIMS2,PRRT1,PRKN,AGER,SYNGAP1,AKAP7,GRM4,LY6E,EXOC4,ATF4,SYNGR1,NTRK2,PLA2G6,PICK1,BTBD9,CHRNA3,LRRC4,GRM8,CHRNA5,SRF,GABRA1,APBA1,PHF24,USP46,KIT,SLC1A1,ROR2,GABBR2,BRSK1,PRKCE,RIMS1,RIMS3,ACP4,SHANK1,PPT1,CRHR2,SLC1A4,PTN,DGKI,EGFR,NCDN,GRIK2,DLGAP3,AMPH,SDCBP,SLC7A11,PPFIA3,LIN7B,NTF4,PRKAR2B,GRIN2D,MTMR2,NAPA,SLC8A2,GAD2,CACNB2,DLG2,PCDH8,GRIK5,NAPB,PLAT,KPNA2,CHRNA6,FARP1,FCHSD2,SYT1,CACNB4,RAB5A,LIN7A,PLCB1,PLCL2,RAC3,PRNP,FCHSD1,P2RX2,NRG1,PTPRA,STX2,SYT9,SNPH,EPHB1,PLK2,HTR7,FAM107A,NR4A1,PXK,ABHD6,CLSTN2,P2RX3,CHRM5,ERC2,MEF2C,ASIC1,P2RX7,DLGAP4,GUCY1A1,GUCY1B1,CUX2,P2RY1,PTK2B,MME,RAPGEF2,EIF2AK4,SYNJ1,HOMER1,CHRM4,F2R,VPS18,SLC6A2,GLS,ITPKA,CYFIP1,DTNBP1,SLC12A5,KCNIP2,CHRM3,LZTS1,SYT8,GRM2,BDNF,SLC4A10,NEURL1,DNM1L,SLC6A3,SORCS3,PPP3CA,SLC12A7,ADRA2A,IGSF11,ADARB1,SNAP23,DAG1,NLGN4Y,SSH1,STAU1,KCNB1,KRAS,BSN,ADNP,GRK2,DISC1,GPER1,GRIK4,AGT,ATP1A2,NFATC4,RPS6KA1,SYAP1,STX1A,TMEM25,NPAS4,NTSR1,YTHDF1,CNIH2,BACE1,DNAJC5,GLUL,CSPG5,DLG1,CREB1,YWHAG,HTR3B,SPG11,MAPT,RAP1B,BLOC1S6,SRGN,VGF,EIF4EBP2,TNR,NRXN2,CASK,MPP2,BCHE,PNKD,CRTC1,PPP3CB,RAB3A,PINK1,KCNN1,SYN1,SNAP29,STAT3,KCNA1,CD38,NPTX2,MAPK1,CHRM1,TMOD2,NSG1,DAGLB,MINK1,RAB8A,HAP1,EPHA4,RNF216,DLG4,SYT7,IQSEC2,NLGN2,CHRNB1,CNIH3,RGS14,CACNB1,SYNJ2BP,HRH2,CPLX1,STX1B,STX4,PSEN1,CACNA1A,SYT11,NLGN3,KCTD13,MYCBPAP,CACNA1G,AC138894.1,CHRNB2,RAB11A,DGKE,CALM1,SNAPIN,PRKCB,RIT2	grey	VSMC_M10
GO:0009063	0.00	1.00	60	84	cellular amino acid catabolic process	BP	1	GLS2,SHMT2,ALDH8A1,RIDA,GPT,CARNMT1,PPAT,HMGCLL1,IL4I1,DDO,BCAT2,GAD2,HNMT,IDO2,IDO1,AMDHD1,CSAD,AHCY,MCCC2,SDSL,IVD,HOGA1,HIBCH,GLS,ACAD8,MTRR,ALDH5A1,CBSL,HGD,AMT,MCCC1,ACADSB,OAT,HMGCL,GLUL,FAH,PRODH,HDC,ALDH4A1,MAT1A,ASRGL1,HSD17B10,SLC25A44,ALDH6A1,GSTZ1,CRYM,SHMT1,ENOSF1,NOS2,PIPOX,ABAT,SARDH,GCSH,KYAT1,KYAT3,MIR21,HIBADH,SLC25A21,AUH,HYKK	grey	VSMC_M10
GO:0007031	0.00	1.00	26	32	peroxisome organization	BP	1	PEX7,PEX3,PEX6,PEX1,ZFAND6,HACL1,MAVS,PEX2,PEX16,LONP2,DNM1L,PEX11B,PEX19,FIS1,SEC16B,PLA2G16,PEX26,PEX14,ABCD4,RAB8B,PEX11G,PEX10,ABCD3,PJVK,PEX11A,PEX12	grey	VSMC_M10
GO:0055085	0.00	1.00	604	1047	transmembrane transport	BP	1	TIMM21,SLC39A5,NEDD4L,ATP8B1,MIP,SLC18B1,STAC3,SLC2A12,SLC26A10,PEX7,SLC16A7,ATP5MGL,NIPAL2,MAPK8IP2,CPT1B,SLC12A2,KCNV1,PRRT1,RNF5,TAP1,SLC22A4,CALHM4,GOPC,SLC35F1,SMDT1,BAK1,CATSPER3,PKD2L2,KCNK9,MAPK14,TOMM22,KCNJ4,PLA2G6,PIM1,SLC39A4,ATP6V1F,MFSD3,CHRNA3,CHRNA5,PEX6,TRPM6,ABCB1,SLC25A40,ABCC10,STEAP2,GABRA1,CNGA1,SLC41A2,TMEM63B,PEX1,SLC35B2,CLIC5,SLC25A27,SLC1A1,SLC25A13,TRAM2,WNK2,MFSD14C,CNNM4,TSPAN13,ABCG5,ABCG8,SEC61B,SLC3A1,PRKCE,ATP6V1E2,ABCB5,TMC4,TMEM30A,KCNQ4,IBTK,PNPT1,SHANK1,SLC4A4,SLC46A2,SLC35A1,AQP1,GJA10,SLC1A4,SLC31A2,SLC13A4,GRB10,SEC61G,ATP6V1C2,HECW1,TCAF2,GRIK2,GJB5,CLCN1,KEL,UCP1,ATG5,TRPM4,SLC7A11,OSR1,MFSD8,FGF21,BRAF,MFSD4B,MFSD2B,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,PANX1,SLC26A5,ATP7B,KCNRG,CACNB2,ANO10,SLC39A12,SLC25A30,ATP6V0E2,SLC4A2,DNAJC15,ASIC3,STAC,ATP6V0B,AQP11,PRKAG2,GRIK5,ATP1A3,CCT8L2,OXSR1,TMEM163,SLC22A13,ATP5F1C,SCN5A,SCN1A,SLC25A38,SEC62,SLC24A3,AKT2,GPD1L,ABCC4,CHRNA6,TIMM50,SLC20A2,SLC4A7,SLC38A10,CACNB4,ASPSCR1,RYR1,NALCN,SLC6A15,SLC25A15,SLC23A2,PRNP,DIAPH1,P2RX2,CLIC1,TMCO3,GAS6,RASA3,ARL6IP5,COX7A1,SLC7A1,SLC25A26,SLC46A3,SLC38A9,MICU3,KCNIP3,ANO4,SLC5A8,ATP6V1H,TRIB3,COX4I2,SLC35A4,CYB5A,SLCO6A1,PIK3R1,ABCB9,SLMAP,SLC43A1,ATP5F1A,SLC43A3,GLRX,P2RX3,TRPC4AP,SLC9A9,RYR3,ORAI1,SORBS1,MEF2C,ASIC1,PEX2,P2RX7,HVCN1,KCNH3,TMEM144,PTK2B,SLC39A13,KCNJ11,SLC33A1,TMEM150C,TPCN1,SLC8B1,HOMER1,IFNGR2,SL	grey	VSMC_M10
GO:0006625	0.00	1.00	15	17	protein targeting to peroxisome	BP	1	PEX7,PEX3,PEX6,PEX1,ZFAND6,HACL1,PEX2,PEX16,LONP2,PEX19,PEX26,PEX14,RAB8B,PEX10,PEX12	grey	VSMC_M10

GO:0072662	0.00	1.00	15	17	protein localization to peroxisome	BP	1	PEX7,PEX3,PEX6,PEX1,ZFAND6,HACL1,PEX2,PEX16,LONP2,PEX19,PEX26,PEX14,RAB8B,PEX10,PEX12	grey	VSMC_M10
GO:0072663	0.00	1.00	15	17	establishment of protein localization to peroxisome	BP	1	PEX7,PEX3,PEX6,PEX1,ZFAND6,HACL1,PEX2,PEX16,LONP2,PEX19,PEX26,PEX14,RAB8B,PEX10,PEX12	grey	VSMC_M10
GO:0080154	0.00	1.00	9	9	regulation of fertilization	BP	1	MYH9,CFAP69,NLRP5,PLAT,PLCB1,INTS13,CCDC87,ZP2,LHFPL2	grey	VSMC_M10
GO:0043574	0.00	1.00	17	20	peroxisomal transport	BP	1	PEX7,PEX3,PEX6,PEX1,ZFAND6,HACL1,PEX2,PEX16,LONP2,PEX19,PEX26,PEX14,ABCD4,RAB8B,PEX10,ABCD3,PEX12	grey	VSMC_M10
GO:0006813	0.00	1.00	90	140	potassium ion transport	BP	1	VPS4B,NEDD4L,SLC12A2,KCNV1,KCNK9,KCNJ4,WNK2,KCNQ4,AQP1,KEL,KCNJ14,KCNRG,ATP1A3,CCT8L2,OXSR1,SLC24A3,NALCN,PRNP,KCNIP3,SLC9A9,KCNH3,PTK2B,KCNJ11,KCNJ3,ANO6,KCNK15,KCNE2,PKD2,CASQ2,KCNJ15,SLC12A5,KCNIP2,KCNJ2,SLC12A7,ADRA2A,KCNB1,SLC9A8,KCNK1,KCNG1,ANK2,KLHL24,ATP1A2,SLC9A1,CCDC51,SLC12A8,KCNK2,NOS1AP,CDKN1B,DLG1,KCNK7,NSF,SLC12A9,KCNK4,SLC9A7,KCNN1,ATP1B1,KCNA1,KCNMA1,KCNH4,KCND1,WNK3,ATP1B2,KCNAB3,KCNIP1,HCN3,KCNN3,DNM2,KCNJ18,SLC9A6,RNF207,KCNC4,AMIGO1,TSC1,WWP2,SLC12A4,SLC9A5,MIR21,KCNK3,KCNH2,KCNK5,NETO2,CRBN,RGS4,KCNA6,KCNJ8,KCNT2,HCN4,KCNMB4,KCNG2,KCNJ9	grey	VSMC_M10
GO:0046395	0.00	1.00	116	182	carboxylic acid catabolic process	BP	1	GLS2,HSD17B4,SHMT2,ALDH8A1,AIG1,RIDA,CPT1B,PPARA,MCAT,ECHDC1,GPT,CARNMT1,CROT,GNPDA2,PPAT,HMGCLL1,ETFB,IL4I1,LPIN1,DDO,BCAT2,FAAH,HADHA,GAD2,AKR1A1,ACOX1,XYLB,HNMT,AKT2,IDO2,IDO1,HACL1,AMDHD1,ACOXL,CSAD,ACOX2,AHCY,MCCC2,PEX2,ETFDH,SDSL,IVD,LPIN3,HOGA1,ECI2,HIBCH,GLS,ACAD8,ADTRP,LONP2,MTRR,MCEE,ALDH5A1,IRS1,CBSL,CPT1A,BDH2,HGD,AMT,ABHD2,MCCC1,ABCB11,ACADSB,OAT,HMGCL,GLUL,EHHADH,ACADL,FAH,MTHFS,TYSND1,PRODH,HDC,ALDH4A1,MAT1A,ASRGL1,ACADVL,HSD17B10,SLC25A44,ALDH6A1,ABCD4,GCDH,GSTZ1,CRYM,ABHD3,SHMT1,ENOSF1,LPIN2,NOS2,PIPOX,ACAA2,ABAT,DECR2,SARDH,ACSF3,CEL,MLYCD,GCSH,KYAT1,ABCD3,KYAT3,PLA2G15,ACADM,MIR21,PHYH,ACOT4,HIBADH,SLC25A21,HADHB,AMACR,NUDT19,IDNK,ALDH1L1,ECI1,AUH,HYKK	grey	VSMC_M10
GO:0098659	0.00	1.00	49	71	inorganic cation import across plasma membrane	BP	1	SLC39A5,SLC12A2,KCNK9,KCNJ4,SLC39A4,STEAP2,WNK2,TRPM4,KCNJ14,SLC8A2,SLC39A12,ATP1A3,PRNP,SLC9A9,KCNJ11,KCNJ3,KCNE2,KCNJ15,SLC12A5,KCNJ2,SLC12A7,TRPV4,ISCU,ATP1A2,SLC9A1,SLC12A8,DLG1,SLC12A9,SLC9A7,ATP1B1,WNK3,ATP1B2,FAM155B,SLC5A2,SLC39A6,TRPV2,KCNJ18,SLC9A6,TRPV3,TRPV1,P2RX1,LCN2,SLC12A4,SLC9A5,MIR24-1,KCNH2,KCNJ8,HCN4,KCNJ9	grey	VSMC_M10
GO:0099587	0.00	1.00	49	71	inorganic ion import across plasma membrane	BP	1	SLC39A5,SLC12A2,KCNK9,KCNJ4,SLC39A4,STEAP2,WNK2,TRPM4,KCNJ14,SLC8A2,SLC39A12,ATP1A3,PRNP,SLC9A9,KCNJ11,KCNJ3,KCNE2,KCNJ15,SLC12A5,KCNJ2,SLC12A7,TRPV4,ISCU,ATP1A2,SLC9A1,SLC12A8,DLG1,SLC12A9,SLC9A7,ATP1B1,WNK3,ATP1B2,FAM155B,SLC5A2,SLC39A6,TRPV2,KCNJ18,SLC9A6,TRPV3,TRPV1,P2RX1,LCN2,SLC12A4,SLC9A5,MIR24-1,KCNH2,KCNJ8,HCN4,KCNJ9	grey	VSMC_M10
GO:0003333	0.00	1.00	46	66	amino acid transmembrane transport	BP	1	SLC22A4,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC25A38,SLC38A10,SLC6A15,SLC25A15,ARL6IP5,SLC7A1,SLC38A9,SLC43A1,SLC38A4,SLC38A2,SLC38A1,SFXN2,SLC38A11,SLC38A3,SLC7A7,AGT,ACE2,ATP1A2,PER2,NTSR1,PQLC2,SLC38A5,ARL6IP1,SLC3A2,SLC38A6,PRAF2,CLN8,PSEN1,SLC7A3,SLC6A7,LRRC8E,SLC1A7,SLC7A5,LRRC8A,SLC7A6,SLC36A1,LRRC8D,SLC6A19,RGS4,SLC25A29	grey	VSMC_M10
GO:0045956	0.01	1.00	11	12	positive regulation of calcium ion-dependent exocytosis	BP	1	SYT1,SYT9,HYAL3,KCNB1,STX1A,SYT7,CACNA1G,SCAMP5,CACNA1H,STXBP1,DOC2B	grey	VSMC_M10
GO:0071805	0.01	1.00	84	131	potassium ion transmembrane transport	BP	1	NEDD4L,SLC12A2,KCNV1,KCNK9,KCNJ4,WNK2,KCNQ4,AQP1,KEL,KCNJ14,KCNRG,ATP1A3,CCT8L2,OXSR1,SLC24A3,NALCN,PRNP,KCNIP3,SLC9A9,KCNH3,KCNJ11,KCNJ3,ANO6,KCNK15,KCNE2,PKD2,CASQ2,KCNJ15,SLC12A5,KCNIP2,KCNJ2,SLC12A7,KCNB1,SLC9A8,KCNK1,KCNG1,ANK2,KLHL24,ATP1A2,SLC9A1,CCDC51,SLC12A8,KCNK2,NOS1AP,DLG1,KCNK7,SLC12A9,KCNK4,SLC9A7,KCNN1,ATP1B1,KCNA1,KCNMA1,KCNH4,KCND1,WNK3,ATP1B2,KCNAB3,KCNIP1,HCN3,KCNN3,DNM2,KCNJ18,SLC9A6,RNF207,KCNC4,AMIGO1,WWP2,SLC12A4,SLC9A5,MIR21,KCNK3,KCNH2,KCNK5,NETO2,CRBN,RGS4,KCNA6,KCNJ8,KCNT2,HCN4,KCNMB4,KCNG2,KCNJ9	grey	VSMC_M10
GO:0035435	0.01	1.00	11	12	phosphate ion transmembrane transport	BP	1	SLC25A30,SLC20A2,ADAMTS8,SLC37A1,SLC37A2,SLC37A4,XPR1,ANKH,SLC25A11,SLC25A14,SLC25A3	grey	VSMC_M10
GO:1990573	0.01	1.00	26	35	potassium ion import across plasma membrane	BP	1	SLC12A2,KCNK9,KCNJ4,WNK2,KCNJ14,ATP1A3,KCNJ11,KCNJ3,KCNE2,KCNJ15,SLC12A5,KCNJ2,SLC12A7,ATP1A2,SLC12A8,DLG1,SLC12A9,ATP1B1,WNK3,ATP1B2,KCNJ18,SLC12A4,KCNH2,KCNJ8,HCN4,KCNJ9	grey	VSMC_M10

GO:0016054	0.01	1.00	117	186	organic acid catabolic process	BP	1	GLS2,HSD17B4,SHMT2,ALDH8A1,AIG1,RIDA,CPT1B,PPARA,MCAT,ECHDC1,GPT,CARNMT1,CROT,GNPDA2,PPAT,HMGCLL1,ETFB,IL4I1,LPIN1,DDO,BCAT2,FAAH,HADHA,GAD2,AKR1A1,ACOX1,XYLB,HNMT,AKT2,IDO2,IDO1,HACL1,AMDHD1,ACOXL,CSAD,ACOX2,THNSL2,AHCY,MCCC2,PEX2,ETFDH,SDSL,IVD,LPIN3,HOGA1,ECI2,HIBCH,GLS,ACAD8,ADTRP,LONP2,MTRR,MCEE,ALDH5A1,IRS1,CBSL,CPT1A,BDH2,HGD,AMT,ABHD2,MCC1,ABCB11,ACADSB,OAT,HMGCL,GLUL,EHHADH,ACADL,FAH,MTHFS,TYSND1,PRODH,HDC,ALDH4A1,MAT1A,ASRGL1,ACADVL,HSD17B10,SLC25A44,ALDH6A1,ABCD4,GCDH,GSTZ1,CRYM,ABHD3,SHMT1,ENOSF1,LPIN2,NOS2,PIPOX,ACAA2,ABAT,DECR2,SARDH,ACSF3,CEL,MLYCD,GCSH,KYAT1,ABCD3,KYAT3,PLA2G15,ACADM,MIR21,PHYH,ACOT4,HIBADH,SLC25A21,HADHB,AMACR,NUDT19,IDNK,ALDH1L1,ECI1,AUH,HYKK	grey	VSMC_M10
GO:0006817	0.01	1.00	15	18	phosphate ion transport	BP	1	SFRP4,SLC25A30,SLC20A2,CRY2,ADAMTS8,SLC37A1,SLC37A2,IP6K2,SLC37A4,XPR1,ANKH,SLC25A11,SLC25A14,SLC25A3,CEBPB	grey	VSMC_M10
GO:1903825	0.01	1.00	69	106	organic acid transmembrane transport	BP	1	SLC16A7,CPT1B,SLC22A4,ABCB1,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC25A30,SLC25A38,AKT2,SLC38A10,SLC6A15,SLC25A15,SLC23A2,ARL6IP5,SLC7A1,SLC38A9,SLC5A8,SLC43A1,SLC38A4,SLC38A2,SLC38A1,SFXN2,SLC38A11,SLC38A3,CPT1A,ACSL5,SLC7A7,AGT,SLC25A20,ABCC5,ACE2,ATP1A2,PER2,NTSR1,SLC16A1,PQLC2,SLC27A1,SLC38A5,MPC2,ARL6IP1,SLC3A2,SLC38A6,PRAF2,SLC25A11,SLC29A4,CLN8,PSEN1,SLC7A3,ABCD4,SLC6A7,LRRC8E,EMB,SLC46A1,SLC25A14,SLC1A7,SLC7A5,LRRC8A,ABCD3,SLC7A6,SLC36A1,LRRC8D,SLC6A19,SLC25A21,SLC25A32,RGS4,SLC25A29	grey	VSMC_M10
GO:0015919	0.01	1.00	15	18	peroxisomal membrane transport	BP	1	PEX7,PEX3,PEX6,PEX1,PEX2,PEX16,LONP2,PEX19,PEX26,PEX14,ABCD4,RAB8B,PEX10,ABCD3,PEX12	grey	VSMC_M10
GO:0042789	0.01	1.00	10	11	mRNA transcription by RNA polymerase II	BP	1	ATF4,FOXE3,C5AR1,TFCP2,AP3B1,STAT3,ZBTB1,MED1,SREBF1,SUPT6H	grey	VSMC_M10
GO:0007494	0.01	1.00	10	11	midgut development	BP	1	SMO,EGFR,RET,CPS1,ALDH1A2,DAB1,FOXL1,FOXF1,ASS1,WNT5A	grey	VSMC_M10
GO:0015807	0.01	1.00	34	48	L-amino acid transport	BP	1	SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC25A15,ARL6IP5,SLC7A1,SLC38A9,SLC43A1,SERINC5,SLC38A2,SLC38A1,SLC38A3,SLC7A7,AGT,ACE2,ATP1A2,PER2,NTSR1,SLC11A1,PQLC2,SLC38A5,ARL6IP1,SLC3A2,PRAF2,CLN8,PSEN1,SLC7A3,SLC1A7,SLC7A5,SLC7A6,SLC36A1,SLC25A29	grey	VSMC_M10
GO:0061025	0.01	0.99	80	125	membrane fusion	BP	1	STX7,SEPT8,TSNARE1,TGFBRAP1,STX17,RIMS1,SPACA6,VPS41,HACE1,IZUMO1,NAPA,RAB7A,PIP4K2A,RUBCNL,NECTIN2,GRIK5,TBC1D4,AKT2,YIPF4,SYT1,GAS6,BET1L,STX2,SYT9,NSFL1C,ANKRD27,MYOF,CHMP2B,DYSF,VPS39,RAB7B,DNM1L,SEC22B,VTI1A,SNAP23,MFN1,RCC1L,C2CD5,STX1A,STX6,VPS8,LYZL6,NSF,SPG11,PIKFYVE,BLOC1S6,ANXA7,RAB3A,VAMP1,SNAP29,ANKFY1,STX5,STX18,RAB8A,ATP13A2,CPLANE2,SYT7,ANXA2,CPLX1,STX1B,STX4,BNIP1,SYT11,RAB8B,AC138894.1,SOX30,STX8,SPESP1,NOX5,SNAPIN,NAPG,GNAI3,VAV3,STXBP1,VPS4A,SNAP47,DOC2B,RABIF,VAMP3,RAB39A	grey	VSMC_M10
GO:1905039	0.01	0.99	68	105	carboxylic acid transmembrane transport	BP	1	SLC16A7,CPT1B,SLC22A4,ABCB1,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC25A30,SLC25A38,AKT2,SLC38A10,SLC6A15,SLC25A15,SLC23A2,ARL6IP5,SLC7A1,SLC38A9,SLC5A8,SLC43A1,SLC38A4,SLC38A2,SLC38A1,SFXN2,SLC38A11,SLC38A3,CPT1A,ACSL5,SLC7A7,AGT,SLC25A20,ABCC5,ACE2,ATP1A2,PER2,NTSR1,SLC16A1,PQLC2,SLC27A1,SLC38A5,MPC2,ARL6IP1,SLC3A2,SLC38A6,PRAF2,SLC25A11,CLN8,PSEN1,SLC7A3,ABCD4,SLC6A7,LRRC8E,EMB,SLC46A1,SLC25A14,SLC1A7,SLC7A5,LRRC8A,ABCD3,SLC7A6,SLC36A1,LRRC8D,SLC6A19,SLC25A21,SLC25A32,RGS4,SLC25A29	grey	VSMC_M10
GO:0034220	0.01	0.99	439	765	ion transmembrane transport	BP	1	SLC39A5,NEDD4L,ATP8B1,STAC3,SLC26A10,SLC16A7,ATP5MGL,NIPAL2,MAPK8IP2,SLC12A2,KCNV1,PRRT1,SLC22A4,CALHM4,GOPC,SMDT1,BAK1,CATSPER3,PKD2L2,KCNK9,KCNJ4,PLA2G6,SLC39A4,ATP6V1F,MFSD3,CHRNA3,CHRNA5,TRPM6,ABCB1,STEAP2,GABRA1,CNGA1,SLC41A2,TMEM63B,SLC35B2,CLIC5,SLC1A1,SLC25A13,WNK2,CNNM4,TSPAN13,SLC3A1,PRKCE,ATP6V1E2,TMC4,KCNQ4,IBTK,SHANK1,SLC4A4,SLC35A1,AQP1,SLC1A4,SLC31A2,SLC13A4,ATP6V1C2,HECW1,TCAF2,GRIK2,CLCN1,KEL,UCP1,ATG5,TRPM4,SLC7A11,OSR1,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,PANX1,SLC26A5,ATP7B,KCNRG,CACNB2,ANO10,SLC39A12,SLC25A30,ATP6V0E2,SLC4A2,ASIC3,STAC,ATP6V0B,GRIK5,ATP1A3,CCT8L2,OXSR1,TMEM163,ATP5F1C,SCN5A,SCN1A,SLC25A38,SLC24A3,GPD1L,ABCC4,CHRNA6,SLC20A2,SLC4A7,CACNB4,RYR1,NALCN,SLC6A15,SLC25A15,SLC23A2,PRNP,DIAPH1,P2RX2,CLIC1,TMCO3,GAS6,RASA3,ARL6IP5,COX7A1,SLC7A1,SLC25A26,SLC38A9,MICU3,KCNIP3,ANO4,SLC5A8,ATP6V1H,COX4I2,CYB5A,SLMAP,SLC43A1,ATP5F1A,GLRX,P2RX3,TRPC4AP,SLC9A9,RYR3,ORAI1,MEF2C,ASIC1,P2RX7,HVCN1,KCNH3,PTK2B,SLC39A13,KCNJ11,SLC33A1,TMEM150C,TPCN1,SLC8B1,HOMER1,IFNGR2,SLC25A37,OPA1,KCNJ3,F2R,TESC,RIPK1,SLC40A1,ANO6,SLC6A2,ZDHHC13,COX15,KCNK15,ABCC2,KCNE2,PKD2,NIPA1,CASQ2,KCNJ15,MCUR1,SLC12A5,KCNIP2,CHRM3,ADAMTS8,RYR2,FAM173B,ATP6V1B2,PM20D1,SLC41A1,COX6B1,SLC4A10,SFXN2,TRPM1,SLC37A1,CALHM2,CALHM1,SLC6A3,LCK,SLC2A10,HECW2,KCNJ2,SLC38A3,SLC9B1,SLC12A7,TRPV4,SLC9B2,ADRA2A,SLC30A10,SLC37A2,TCIRG1,COX17,SCN2A,ISCU,KCNB1,SHROOM2,MC	grey	VSMC_M10

GO:1902475	0.01	1.00	32	45	L-alpha-amino acid transmembrane transport	BP	1	SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC25A38,SLC25A15,ARL6IP5,SLC7A1,SLC38A9,SLC43A1,SLC38A1,SLC38A3,SLC7A7,AGT,ACE2,ATP1A2,PER2,NTSR1,PQLC2,SLC38A5,ARL6IP1,SLC3A2,PRAF2,CLN8,PSEN1,SLC7A3,SLC1A7,SLC7A5,SLC7A6,RGS4,SLC25A29	grey	VSMC_M10
GO:0006858	0.01	1.00	22	29	extracellular transport	BP	1	LRRC6,RFX3,DNAH11,NEK10,DNAH5,DPCD,ROPN1L,CFAP43,JHY,OFD1,CFAP45,DNAAF2,SPAG16,STK36,ADCY10,TTC25,DNAAF4,SPEF2,CFAP53,ARRDC1,WWP2,SPA17	grey	VSMC_M10
GO:0045741	0.01	1.00	10	11	positive regulation of epidermal growth factor-activated receptor activity	BP	1	EPGN,AREG,TGFA,HBEGF,FBXW7,NEURL1,ADRA2A,NCF1,EGF,EREG	grey	VSMC_M10
GO:0018410	0.01	1.00	10	11	C-terminal protein amino acid modification	BP	1	ATG12,AGTPBP1,ATG5,TTL,GPLD1,ATG16L1,WIPI2,LCMT1,FOLH1,IRGM	grey	VSMC_M10
GO:0001505	0.01	0.99	92	147	regulation of neurotransmitter levels	BP	1	SNCAIP,RIMS2,PRKN,GRM4,AGTPBP1,CHRNA3,CHRNA5,APBA1,BRSK1,RIMS1,RIMS3,PPT1,PPFIA3,LIN7B,NAPA,GAD2,CACNB2,GRIK5,NAPB,HNMT,ZNF219,SYT1,LRTOMT,AP000812.5,RAB5A,LIN7A,STX2,SYT9,SNPH,NR4A1,ERC2,MEF2C,ASIC1,P2RY1,SYNJ1,SLC38A1,VPS18,SLC6A2,DTNBP1,SYT8,ALDH5A1,DNM1L,SLC6A3,ADRA2A,SNAP23,GPER1,ATP1A2,PER2,STX1A,SLC29A2,BACE1,DNAJC5,CSPG5,RAP1B,BLOC1S6,COMT,NRXN2,CASK,BCHE,PNKD,RAB3A,SYN1,SNAP29,DAGLB,SLC29A4,SYT7,CLN8,CPLX1,STX1B,STX4,PSEN1,SYT11,AC138894.1,CALM1,SNAPIN,PRKCB,CAMK2A,STXBP2,ABAT,FMR1,SLC1A7,PIP5K1C,P2RX1,BAIAP3,PARK7,STXBP1,CHRNB4,SNAP47,PDZD11,DOC2B,KCNMB4,PRIMA1	grey	VSMC_M10
GO:0044282	0.01	0.99	172	284	small molecule catabolic process	BP	1	GLS2,HSD17B4,SHMT2,ALDH8A1,CYP27B1,AIG1,RIDA,MIOX,CPT1B,SYNJ2,PPARA,MCAT,ECHDC1,APOBEC3H,GPT,CARNMT1,GDA,CROT,GNPDA2,GALT,ENPP4,SRD5A3,PPAT,HMGCLL1,ADH5,ETFB,IL4I1,LPIN1,INPP4B,DHDH,DDO,BCAT2,MTMR2,FAAH,HADHA,GAD2,CDADC1,ESD,AKR1A1,GLB1,NUDT5,ACOX1,XYLB,HNMT,RBKS,AKT2,PFKP,IDO2,IDO1,HACL1,FUT10,AMDHD1,MTMR7,ACOXL,CSAD,CYP7A1,ACOX2,THNSL2,AHCY,GK5,MCCC2,PEX2,ETFDH,PFKM,SYNJ1,SDSL,IVD,ENTPD4,LPIN3,HOGA1,NQO2,ECI2,HIBCH,GLS,CBR3,ACAD8,GLYCTK,ADTRP,LONP2,MTRR,MCEE,ALDH5A1,IRS1,CBSL,CPT1A,BDH2,INPP5A,ALDH3B2,HGD,AMT,PFKFB2,ABHD2,MCCC1,ABCB11,ACTN3,ACADSB,NTSR1,OAT,MGAT1,INPP5J,HMGCL,GLUL,EHHADH,SORD,RPE,UPB1,ACADL,HK1,FAH,MTHFS,TYSND1,PRODH,PNKD,CYP27A1,HDC,ALDH4A1,MAT1A,ASRGL1,ACADVL,TKFC,HSD17B10,SLC25A44,ALDH6A1,ABCD4,GCDH,GSTZ1,CRYM,CYP46A1,ABHD3,SHMT1,ENOSF1,LPIN2,OXCT1,NOS2,IMPA2,PIPOX,ACAA2,ABAT,INPP5K,TKTL1,PARK7,DECR2,ALDH2,SARDH,ACSF3,CEL,MLYCD,GCSH,KYAT1,ABCD3,KYAT3,PLA2G15,ACADM,MIR21,PHYH,ACOT4,FUT4,HIBADH,SLC25A21,TIGAR,HADHB,AMACR,NUDT19,IDNK,ALDH1L1,ECI1,AUH,HYKK,INPP1,ADH4,PDXP,UPP1	grey	VSMC_M10
GO:0003351	0.01	1.00	20	26	epithelial cilium movement involved in extracellular fluid movement	BP	1	LRRC6,RFX3,DNAH11,NEK10,DNAH5,DPCD,ROPN1L,CFAP43,JHY,OFD1,CFAP45,DNAAF2,SPAG16,STK36,ADCY10,TTC25,DNAAF4,SPEF2,CFAP53,SPA17	grey	VSMC_M10
GO:0007631	0.01	0.99	32	45	feeding behavior	BP	1	ADM2,MCHR1,NTRK2,CNTFR,USP46,NAPEPLD,DACH1,POU4F1,TCF15,HAND2,CFAP20,P2RY1,EIF2AK4,GLS,CPT1A,GIGYF2,TTC21B,OPRD1,AGT,ACE2,PYY,GDF15,STAT3,FOS,UBE2Q1,NMUR2,STRA6,SGIP1,LEPR,NPB,MRAP2,DERL2	grey	VSMC_M10
GO:0099177	0.01	0.99	188	318	regulation of trans-synaptic signaling	BP	1	SNCAIP,MAPK8IP2,SLC12A2,RIMS2,PRRT1,PRKN,AGER,SYNGAP1,AKAP7,GRM4,ATF4,SYNGR1,NTRK2,PLA2G6,PICK1,BTBD9,CHRNA3,LRRC4,GRM8,CHRNA5,SRF,APBA1,PHF24,USP46,KIT,SLC1A1,ROR2,BRSK1,PRKCE,RIMS1,RIMS3,ACP4,SHANK1,CRHR2,PTN,DGKI,EGFR,NCDN,GRIK2,DLGAP3,SLC7A11,PPFIA3,NTF4,PRKAR2B,GRIN2D,MTMR2,SLC8A2,CACNB2,GRIK5,SYT1,RAB5A,PLCB1,PLCL2,PRNP,PTPRA,EPHB1,PLK2,FAM107A,PXK,ABHD6,CLSTN2,P2RX3,ERC2,MEF2C,ASIC1,DLGAP4,CUX2,P2RY1,PTK2B,MME,RAPGEF2,EIF2AK4,HOMER1,VPS18,ITPKA,CYFIP1,DTNBP1,LZTS1,GRM2,BDNF,SLC4A10,NEURL1,DNM1L,SORCS3,PPP3CA,ADRA2A,IGSF11,NLGN4Y,SSH1,STAU1,KCNB1,KRAS,ADNP,DISC1,GPER1,GRIK4,AGT,ATP1A2,NFATC4,SYAP1,STX1A,TMEM25,NPAS4,YTHDF1,CNIH2,BACE1,GLUL,CSPG5,CREB1,YWHAG,MAPT,RAP1B,SRGN,VGF,EIF4EBP2,TNR,CASK,MPP2,BCHE,PNKD,CRTC1,PPP3CB,RAB3A,PINK1,SYN1,STAT3,CD38,NPTX2,MAPK1,NSG1,RAB8A,HAP1,EPHA4,DLG4,SYT7,IQSEC2,NLGN2,RGS14,CPLX1,STX1B,STX4,PSEN1,CACNA1A,SYT11,NLGN3,KCTD13,AC138894.1,CHRNB2,RAB11A,DGKE,CALM1,SNAPIN,PRKCB,CYP46A1,BEGAIN,CAMK2A,CCL2,DLGAP1,ABR,FMR1,LRP8,P2RX1,CACNA1B,PRKCZ,RAB26,MECP2,TPRG1L,BAIAP3,CEL,NTNG2,JPH3,ZDHHC12,CNTNAP4,STXBP1,FABP5,CHRNB4,CNTN2,GRID2,CACNG7,RGS4,CRH,YWHAH,HRAS,SHISA8,CACNG5,KCNMB4,MAP1A,LRRTM2	grey	VSMC_M10
GO:0030878	0.01	1.00	14	17	thyroid gland development	BP	1	SRF,RAF1,PAX8,HOXD3,RAP1GAP,MAPK1,THRA,MAPK3,MAP2K1,SMAD3,HOXB3,SIX1,NKX2-5,HOXA3	grey	VSMC_M10
GO:0000289	0.01	1.00	21	28	nuclear-transcribed mRNA poly(A) tail shortening	BP	1	PAN2,CNOT2,CNOT6,PABPC1,PNLDC1,AGO2,TNRC6B,TUT7,TUT4,MLH1,TNRC6C,PAN3,CNOT1,CNOT6L,TENT4B,EIF4ENIF1,SAMD4A,POLR2G,TOB1,TNRC6A,PARN	grey	VSMC_M10
GO:0006307	0.01	1.00	7	7	DNA dealkylation involved in DNA repair	BP	1	ASCC3,ALKBH3,FTO,ALKBH2,MGMT,ALKBH1,MPG	grey	VSMC_M10
GO:0110095	0.01	1.00	7	7	cellular detoxification of aldehyde	BP	1	ALDH1A1,ADH5,ESD,AKR1A1,RDH11,PARK7,ADH4	grey	VSMC_M10

GO:0050804	0.01	0.99	187	317	modulation of chemical synaptic transmission	BP	1	SNCAIP,MAPK8IP2,SLC12A2,RIMS2,PRRT1,PRKN,AGER,SYNGAP1,AKAP7,GRM4,ATF4,SYNGR1,NTRK2,PLA2G6,PICK1,BTBD9,CHRNA3,LRRC4,GRM8,CHRNA5,SRF,APBA1,PHF24,USP46,KIT,SLC1A1,ROR2,BRSK1,PRKCE,RIMS1,RIMS3,ACP4,SHANK1,CRHR2,PTN,DGKI,EGFR,NCDN,GRIK2,DLGAP3,SLC7A11,PPFIA3,NTF4,PRKAR2B,GRIN2D,MTMR2,SLC8A2,CACNB2,GRIK5,SYT1,RAB5A,PLCB1,PLCL2,PRNP,PTPRA,EPHB1,PLK2,FAM107A,PXK,ABHD6,CLSTN2,P2RX3,ERC2,MEF2C,ASIC1,DLGAP4,CUX2,P2RY1,PTK2B,MME,RAPGEF2,EIF2AK4,HOMER1,VPS18,ITPKA,CYFIP1,DTNBP1,LZTS1,GRM2,BDNF,SLC4A10,NEURL1,DNM1L,SORCS3,PPP3CA,ADRA2A,IGSF11,NLGN4Y,SSH1,STAU1,KCNB1,KRAS,ADNP,DISC1,GPER1,GRIK4,AGT,ATP1A2,NFATC4,SYAP1,STX1A,TMEM25,NPAS4,YTHDF1,CNIH2,BACE1,GLUL,CSPG5,CREB1,YWHAG,MAPT,RAP1B,SRGN,VGF,EIF4EBP2,TNR,CASK,MPP2,BCHE,PNKD,CRTC1,PPP3CB,RAB3A,PINK1,SYN1,STAT3,CD38,NPTX2,MAPK1,NSG1,RAB8A,HAP1,EPHA4,DLG4,SYT7,IQSEC2,NLGN2,RGS14,CPLX1,STX1B,STX4,PSEN1,CACNA1A,SYT11,NLGN3,KCTD13,AC138894.1,CHRNB2,RAB11A,DGKE,CALM1,SNAPIN,PRKCB,CYP46A1,BEGAIN,CAMK2A,CCL2,DLGAP1,ABR,FMR1,LRP8,P2RX1,CACNA1B,PRKCZ,RAB26,MECP2,TPRG1L,BAIAP3,CEL,NTNG2,JPH3,ZDHHC12,CNTNAP4,STXBP1,CHRNB4,CNTN2,GRID2,CACNG7,RGS4,CRH,YWHAH,HRAS,SHISA8,CACNG5,KCNMB4,MAP1A,LRRTM2	grey	VSMC_M10
GO:0042908	0.02	0.99	21	28	xenobiotic transport	BP	1	ATP8B1,SLC22A4,ABCB1,ABCC10,ABCB5,TMEM30A,ATP7B,EBP,ABCC4,ABCC2,ABCG2,ABCB11,ABCC5,SLC29A4,ABCC3,RALBP1,ABCA3,SLC7A5,SLC22A5,ABCA8,CLDN1	grey	VSMC_M10
GO:0035278	0.02	1.00	16	20	miRNA mediated inhibition of translation	BP	1	AGO2,TNRC6B,AGO1,TNRC6C,EIF4E2,DDX6,EIF4ENIF1,STAT3,TNRC6A,MIR29A,MIR21,MIR222,MIR125B1,MIR27B,MIR27A,AGO4	grey	VSMC_M10
GO:0040033	0.02	1.00	16	20	negative regulation of translation, ncRNA-mediated	BP	1	AGO2,TNRC6B,AGO1,TNRC6C,EIF4E2,DDX6,EIF4ENIF1,STAT3,TNRC6A,MIR29A,MIR21,MIR222,MIR125B1,MIR27B,MIR27A,AGO4	grey	VSMC_M10
GO:0045974	0.02	1.00	16	20	regulation of translation, ncRNA-mediated	BP	1	AGO2,TNRC6B,AGO1,TNRC6C,EIF4E2,DDX6,EIF4ENIF1,STAT3,TNRC6A,MIR29A,MIR21,MIR222,MIR125B1,MIR27B,MIR27A,AGO4	grey	VSMC_M10
GO:0001539	0.02	0.99	52	79	cilium or flagellum-dependent cell motility	BP	1	UBE2B,CATSPER3,LRRC6,CFAP69,RFX3,EFHC1,DNAJA1,DNAH11,CABS1,ARMC2,APOB,ADCY3,DRC1,RSPH6A,TTC21A,TTLL3,MKKS,ING2,DNAH6,WDR66,CFAP20,CCDC65,DNAH1,PLTP,DNAH5,DPCD,ROPN1L,NEURL1,CFAP43,SLC9B1,SLC9B2,CFAP46,INTS13,CFAP45,ENO4,TSSK4,CELF3,CATSPER2,SORD,TTC12,DNAAF2,SPAG16,EFHC2,MNS1,DNAH2,DNAH3,TEKT3,SPEF2,CATSPERD,TPGS1,WDR63,CCSAP	grey	VSMC_M10
GO:0060285	0.02	0.99	52	79	cilium-dependent cell motility	BP	1	UBE2B,CATSPER3,LRRC6,CFAP69,RFX3,EFHC1,DNAJA1,DNAH11,CABS1,ARMC2,APOB,ADCY3,DRC1,RSPH6A,TTC21A,TTLL3,MKKS,ING2,DNAH6,WDR66,CFAP20,CCDC65,DNAH1,PLTP,DNAH5,DPCD,ROPN1L,NEURL1,CFAP43,SLC9B1,SLC9B2,CFAP46,INTS13,CFAP45,ENO4,TSSK4,CELF3,CATSPER2,SORD,TTC12,DNAAF2,SPAG16,EFHC2,MNS1,DNAH2,DNAH3,TEKT3,SPEF2,CATSPERD,TPGS1,WDR63,CCSAP	grey	VSMC_M10
GO:0007368	0.02	0.99	58	90	determination of left/right symmetry	BP	1	TBC1D32,LRRC6,SMO,DAAM2,FOXH1,IFT74,SRF,RFX3,ANKS6,DYNC2LI1,DNAH11,ARMC4,BBS7,SETDB2,DRC1,MEGF8,GALNT11,IFT172,FOXJ1,TGFBR2,OVOL2,ACVR2A,MKKS,KIF3B,HAND2,MEF2C,IFT52,RPGRIP1L,PKD2,DNAH5,DPCD,SUFU,OFD1,CFAP45,AP1B1,BICC1,MMP21,DNAAF2,PKD1L1,NKX3-2,TTC25,DNAAF4,PSEN1,TMEM107,SMAD3,CCDC151,MKS1,TBX2,MIB1,CFAP53,RNF207,FOXF1,ENG,PSKH1,LBX1,WNT5A,C2CD3,NKX2-5	grey	VSMC_M10
GO:0045591	0.02	1.00	9	10	positive regulation of regulatory T cell differentiation	BP	1	HLA-DRA,IL4I1,SOX12,DUSP10,BCL6,VSIR,FOXP3,SOCS1,CD46	grey	VSMC_M10
GO:0031547	0.02	1.00	6	6	brain-derived neurotrophic factor receptor signaling pathway	BP	1	FSTL4,NTRK2,RAPGEF2,BDNF,NFATC4,SLC2A4	grey	VSMC_M10
GO:0006855	0.02	1.00	6	6	xenobiotic transmembrane transport	BP	1	ATP8B1,TMEM30A,ABCC2,ABCB11,ABCC3,ABCA3	grey	VSMC_M10
GO:0098656	0.02	0.99	99	161	anion transmembrane transport	BP	1	SLC26A10,SLC16A7,SLC12A2,GOPC,ABCB1,GABRA1,SLC35B2,SLC1A1,SLC25A13,SLC3A1,SLC4A4,SLC35A1,SLC1A4,SLC13A4,TCAF2,CLCN1,SLC7A11,SLC26A5,SLC25A30,SLC4A2,SLC25A38,SLC24A3,ABCC4,SLC20A2,SLC4A7,SLC25A15,SLC23A2,PRNP,ARL6IP5,SLC7A1,SLC38A9,ANO4,SLC5A8,SLC43A1,SLC9A9,RIPK1,ANO6,SLC12A5,ADAMTS8,SLC4A10,SFXN2,SLC37A1,SLC38A3,SLC12A7,SLC37A2,SLC9A8,AGT,ABCC5,ACE2,ATP1A2,SLC9A1,SLC37A4,PER2,SLC12A8,NTSR1,XPR1,SLC16A1,SLC12A9,ANKH,SLC25A42,MFSD10,SLC9A7,PQLC2,SLC27A1,SLC38A5,MPC2,ARL6IP1,SLC3A2,SLC35A2,SLC4A3,PRAF2,SLC25A11,CLN8,SLC26A1,PSEN1,SLC7A3,SLC35B1,SLC26A2,LRRC8E,EMB,SLC25A41,SLC46A1,SLC25A14,SLC9A6,GABRE,GABRA3,SLC1A7,CLCN7,SLC7A5,LRRC8A,SLC12A4,SLC9A5,SLC25A3,LRRC8D,LRRC8B,SLC25A21,SLC25A32,RGS4,SLC25A29	grey	VSMC_M10
GO:0010603	0.02	1.00	6	6	regulation of cytoplasmic mRNA processing body assembly	BP	1	PAN2,CNOT2,CNOT6,PAN3,CNOT1,CNOT6L	grey	VSMC_M10
GO:0010606	0.02	1.00	6	6	positive regulation of cytoplasmic mRNA processing body assembly	BP	1	PAN2,CNOT2,CNOT6,PAN3,CNOT1,CNOT6L	grey	VSMC_M10

GO:0044106	0.02	0.99	49	74	cellular amine metabolic process	BP	1	SNCAIP,ALDH7A1,PRKN,LY6E,AKR1B1,GPR37,SLC1A1,EPAS1,DDC,IL4I1,SLC7A11,NAPEPLD,AANAT,HNMT,IDO2,IDO1,LRTOMT,AP000812.5,NR1H4,HAND2,CHDH,NR4A2,ABCC2,SIRT4,AZIN2,SLC6A3,TGFB2,CHKA,SLC7A7,SMS,COMT,PNKD,GCH1,HDC,SLC29A4,ITGAM,GDPD3,GCDH,AC138894.1,CHRNB2,GDPD1,GDE1,ABAT,OAZ1,MECP2,PARK7,MIR21,NNMT,AOC2	grey	VSMC_M10
GO:0009855	0.02	0.99	62	97	determination of bilateral symmetry	BP	1	TBC1D32,LRRC6,SMO,DAAM2,FOXH1,IFT74,SRF,RFX3,SOSTDC1,ANKS6,DYNC2LI1,DNAH11,ARMC4,BBS7,SETDB2,DRC1,MEGF8,GALNT11,IFT172,FOXJ1,TGFBR2,OVOL2,ACVR2A,MKKS,KIF3B,HAND2,MEF2C,IFT52,RPGRIP1L,PKD2,DNAH5,DPCD,SUFU,OFD1,CFAP45,AP1B1,BICC1,MMP21,AIDA,DNAAF2,PKD1L1,NKX3-2,TTC25,DNAAF4,ALDH1A2,PSEN1,TMEM107,SMAD3,CCDC151,MKS1,TBX2,MIB1,CFAP53,RNF207,FOXF1,ENG,PSKH1,LBX1,WNT5A,DDIT3,C2CD3,NKX2-5	grey	VSMC_M10
GO:0071467	0.02	1.00	13	16	cellular response to pH	BP	1	ASIC1,HVCN1,RAB11FIP5,GPLD1,HYAL1,SLC38A3,SLC9A1,KCNK4,GPR68,TRPV1,PKD1L3,INSRR,IMPACT	grey	VSMC_M10
GO:1900019	0.02	1.00	6	6	regulation of protein kinase C activity	BP	1	ROR2,EGFR,TCIM,CEMIP,WNT5A,C3orf58	grey	VSMC_M10
GO:1900020	0.02	1.00	6	6	positive regulation of protein kinase C activity	BP	1	ROR2,EGFR,TCIM,CEMIP,WNT5A,C3orf58	grey	VSMC_M10
GO:0097164	0.02	1.00	11	13	ammonium ion metabolic process	BP	1	TPH2,ALDH7A1,BTBD9,DDC,HNMT,CHDH,SRD5A1,CHKA,BCHE,HDC,SLC29A4	grey	VSMC_M10
GO:0033278	0.02	1.00	6	6	cell proliferation in midbrain	BP	1	FZD6,RYK,FZD3,WNT5A,PITX3,WNT2	grey	VSMC_M10
GO:0110096	0.02	1.00	9	10	cellular response to aldehyde	BP	1	AKR1B1,ALDH1A1,ADH5,ESD,AKR1A1,RDH11,SCNN1B,PARK7,ADH4	grey	VSMC_M10
GO:0098734	0.02	1.00	11	13	macromolecule depalmitoylation	BP	1	ABHD16A,PPT2,ABHD17B,PPT1,LYPLA1,LYPLAL1,ABHD12B,ABHD17A,ABHD10,ABHD17C,LYPLA2	grey	VSMC_M10
GO:0006884	0.02	0.99	18	24	cell volume homeostasis	BP	1	SLC12A2,AQP1,CLNS1A,AQP11,P2RX7,ANO6,SLC12A5,SLC12A7,TRPV4,SLC12A8,SLC12A9,GNB3,KCNMA1,WNK3,AC138894.1,LRRC8E,LRRC8A,SLC12A4	grey	VSMC_M10
GO:0035095	0.02	1.00	6	6	behavioral response to nicotine	BP	1	PPARA,CHRNA3,CHRNA5,GRM2,CHRNB1,CHRNB2	grey	VSMC_M10
GO:1901678	0.02	1.00	11	13	iron coordination entity transport	BP	1	PGRMC2,ASIC3,HPX,SLC48A1,ABCC5,ABCB6,FLVCR2,SLC46A1,C1orf194,LCN2,SLC22A17	grey	VSMC_M10
GO:0060456	0.02	1.00	6	6	positive regulation of digestive system process	BP	1	AQP1,NR1H2,LPCAT3,TRPV1,SLC22A5,CRH	grey	VSMC_M10
GO:0007269	0.02	0.99	69	110	neurotransmitter secretion	BP	1	SNCAIP,RIMS2,PRKN,GRM4,CHRNA3,CHRNA5,APBA1,BRSK1,RIMS1,RIMS3,PPT1,PPFIA3,LIN7B,NAPA,CACNB2,GRIK5,NAPB,SYT1,RAB5A,LIN7A,STX2,SYT9,SNPH,NR4A1,ERC2,MEF2C,ASIC1,P2RY1,SYNJ1,VPS18,DTNBP1,SYT8,DNM1L,ADRA2A,SNAP23,GPER1,STX1A,BACE1,DNAJC5,CSPG5,RAP1B,BLOC1S6,NRXN2,CASK,PNKD,RAB3A,SYN1,SNAP29,SYT7,CPLX1,STX1B,STX4,PSEN1,SYT11,CALM1,SNAPIN,PRKCB,CAMK2A,STXBP2,FMR1,PIP5K1C,P2RX1,BAIAP3,STXBP1,CHRNB4,SNAP47,PDZD11,DOC2B,KCNMB4	grey	VSMC_M10
GO:0099643	0.02	0.99	69	110	signal release from synapse	BP	1	SNCAIP,RIMS2,PRKN,GRM4,CHRNA3,CHRNA5,APBA1,BRSK1,RIMS1,RIMS3,PPT1,PPFIA3,LIN7B,NAPA,CACNB2,GRIK5,NAPB,SYT1,RAB5A,LIN7A,STX2,SYT9,SNPH,NR4A1,ERC2,MEF2C,ASIC1,P2RY1,SYNJ1,VPS18,DTNBP1,SYT8,DNM1L,ADRA2A,SNAP23,GPER1,STX1A,BACE1,DNAJC5,CSPG5,RAP1B,BLOC1S6,NRXN2,CASK,PNKD,RAB3A,SYN1,SNAP29,SYT7,CPLX1,STX1B,STX4,PSEN1,SYT11,CALM1,SNAPIN,PRKCB,CAMK2A,STXBP2,FMR1,PIP5K1C,P2RX1,BAIAP3,STXBP1,CHRNB4,SNAP47,PDZD11,DOC2B,KCNMB4	grey	VSMC_M10
GO:0048241	0.02	1.00	6	6	epinephrine transport	BP	1	LY6E,ADRA2B,ADRA2A,ADRA2C,SLC29A4,CRH	grey	VSMC_M10
GO:0048304	0.02	1.00	6	6	positive regulation of isotype switching to IgG isotypes	BP	1	MSH2,MLH1,PAXIP1,CD40,CD28,TBX21	grey	VSMC_M10
GO:1903307	0.02	0.99	26	37	positive regulation of regulated secretory pathway	BP	1	SPHK2,CACNB2,GAB2,UNC13D,SYT1,SYT9,F2RL1,DNM1L,HYAL3,KCNB1,FGR,STX1A,SNX4,RAB3A,SYT7,RAB15,STX4,ITGAM,CACNA1G,RAB3D,IL4R,SCAMP5,CACNA1H,STXBP1,AP1G1,DOC2B	grey	VSMC_M10
GO:0006584	0.02	0.99	23	32	catecholamine metabolic process	BP	1	SNCAIP,PRKN,LY6E,AKR1B1,GPR37,SLC1A1,EPAS1,DDC,LRTOMT,AP000812.5,HAND2,NR4A2,SLC6A3,TGFB2,COMT,PNKD,GCH1,HDC,ITGAM,CHRNB2,ABAT,PARK7,AOC2	grey	VSMC_M10
GO:0009712	0.02	0.99	23	32	catechol-containing compound metabolic process	BP	1	SNCAIP,PRKN,LY6E,AKR1B1,GPR37,SLC1A1,EPAS1,DDC,LRTOMT,AP000812.5,HAND2,NR4A2,SLC6A3,TGFB2,COMT,PNKD,GCH1,HDC,ITGAM,CHRNB2,ABAT,PARK7,AOC2	grey	VSMC_M10
GO:0070471	0.02	1.00	6	6	uterine smooth muscle contraction	BP	1	ADRA2B,GPER1,AGT,ADRA2C,SETD3,ABAT	grey	VSMC_M10
GO:0051937	0.03	0.99	30	43	catecholamine transport	BP	1	PRKN,LY6E,MAPK15,SYT1,SYT9,ADRA2B,CHRM5,P2RY1,SLC6A2,DTNBP1,SYT8,GRM2,SLC6A3,ADRA2A,KCNB1,GRK2,AGT,STX1A,ADRA2C,RAB3A,PINK1,ACTB,SLC29A4,SYT7,SYT11,CHRNB2,ABAT,PARK7,CHGA,CRH	grey	VSMC_M10
GO:0009799	0.03	0.98	62	98	specification of symmetry	BP	1	TBC1D32,LRRC6,SMO,DAAM2,FOXH1,IFT74,SRF,RFX3,SOSTDC1,ANKS6,DYNC2LI1,DNAH11,ARMC4,BBS7,SETDB2,DRC1,MEGF8,GALNT11,IFT172,FOXJ1,TGFBR2,OVOL2,ACVR2A,MKKS,KIF3B,HAND2,MEF2C,IFT52,RPGRIP1L,PKD2,DNAH5,DPCD,SUFU,OFD1,CFAP45,AP1B1,BICC1,MMP21,AIDA,DNAAF2,PKD1L1,NKX3-2,TTC25,DNAAF4,ALDH1A2,PSEN1,TMEM107,SMAD3,CCDC151,MKS1,TBX2,MIB1,CFAP53,RNF207,FOXF1,ENG,PSKH1,LBX1,WNT5A,DDIT3,C2CD3,NKX2-5	grey	VSMC_M10
GO:0090174	0.03	0.98	60	94	organelle membrane fusion	BP	1	STX7,SEPT8,TSNARE1,TGFBRAP1,STX17,VPS41,RAB7A,PIP4K2A,RUBCNL,GRIK5,TBC1D4,AKT2,YIPF4,SYT1,STX2,SYT9,ANKRD27,CHMP2B,DYSF,VPS39,RAB7B,SEC22B,VTI1A,SNAP23,MFN1,RCC1L,C2CD5,STX1A,STX6,VPS8,SPG11,PIKFYVE,RAB3A,VAMP1,SNAP29,ANKFY1,STX5,RAB8A,ATP13A2,CPLANE2,SYT7,ANXA2,CPLX1,STX1B,STX4,BNIP1,SYT11,RAB8B,AC138894.1,SOX30,STX8,SNAPIN,GNAI3,VAV3,STXBP1,VPS4A,SNAP47,DOC2B,VAMP3,RAB39A	grey	VSMC_M10

GO:0098660	0.03	0.98	329	574	inorganic ion transmembrane transport	BP	1	SLC39A5,NEDD4L,STAC3,SLC26A10,ATP5MGL,NIPAL2,SLC12A2,KCNV1,SMDT1,CATSPER3,PKD2L2,KCNK9,KCNJ4,PLA2G6,SLC39A4,ATP6V1F,MFSD3,TRPM6,STEAP2,GABRA1,SLC41A2,SLC1A1,WNK2,CNNM4,TSPAN13,PRKCE,ATP6V1E2,KCNQ4,IBTK,SLC4A4,AQP1,SLC31A2,SLC13A4,ATP6V1C2,HECW1,CLCN1,KEL,UCP1,ATG5,TRPM4,OSR1,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,PANX1,SLC26A5,ATP7B,KCNRG,CACNB2,SLC39A12,SLC25A30,ATP6V0E2,ASIC3,STAC,ATP6V0B,ATP1A3,CCT8L2,OXSR1,TMEM163,ATP5F1C,SCN5A,SCN1A,SLC24A3,GPD1L,SLC20A2,SLC4A7,CACNB4,RYR1,NALCN,SLC6A15,PRNP,DIAPH1,TMCO3,GAS6,RASA3,COX7A1,MICU3,KCNIP3,ANO4,ATP6V1H,COX4I2,CYB5A,SLMAP,ATP5F1A,GLRX,P2RX3,TRPC4AP,SLC9A9,RYR3,ORAI1,ASIC1,P2RX7,HVCN1,KCNH3,PTK2B,SLC39A13,KCNJ11,SLC33A1,TPCN1,SLC8B1,SLC25A37,OPA1,KCNJ3,F2R,TESC,SLC40A1,ANO6,SLC6A2,ZDHHC13,COX15,KCNK15,ABCC2,KCNE2,PKD2,NIPA1,CASQ2,KCNJ15,MCUR1,SLC12A5,KCNIP2,ADAMTS8,RYR2,FAM173B,ATP6V1B2,PM20D1,SLC41A1,COX6B1,SLC4A10,TRPM1,SLC37A1,CALHM1,SLC6A3,LCK,SLC2A10,HECW2,KCNJ2,SLC9B1,SLC12A7,TRPV4,SLC9B2,ADRA2A,SLC30A10,SLC37A2,TCIRG1,COX17,SCN2A,ISCU,KCNB1,SHROOM2,MCUB,SLC9A8,CLCN4,KCNK1,KCNG1,SCN7A,UBASH3B,ANK2,GPER1,KLHL24,RHCG,TRPM8,ABCC5,ATP1A2,SLC9A1,SLC37A4,C4orf3,CASQ1,CCDC51,SLC12A8,KCNK2,NTSR1,XPR1,SCN4B,DNAJC30,NIPAL3,NOS1AP,CATSPER2,DLG1,KCNK7,TMCO1,COX6A1,SLC30A4,CEMIP,SLC12A9,SESTD1,ATP5S,ANKH,PTPN6,KCNK4,MICU1,MCU,SLC11A1,HTT,PKD1L1,COX8A,SLC9A7,ATP6V0A1,KCNN1,ABCB6,TRPM7,ATP1B1,KCNA1,BH	grey	VSMC_M10
GO:0098655	0.03	0.98	356	623	cation transmembrane transport	BP	1	SLC39A5,NEDD4L,STAC3,ATP5MGL,NIPAL2,MAPK8IP2,SLC12A2,KCNV1,PRRT1,SLC22A4,CALHM4,SMDT1,CATSPER3,PKD2L2,KCNK9,KCNJ4,PLA2G6,SLC39A4,ATP6V1F,MFSD3,TRPM6,STEAP2,CNGA1,SLC41A2,TMEM63B,SLC1A1,WNK2,CNNM4,TSPAN13,PRKCE,ATP6V1E2,KCNQ4,IBTK,SHANK1,SLC4A4,AQP1,SLC1A4,SLC31A2,ATP6V1C2,HECW1,KEL,UCP1,ATG5,TRPM4,OSR1,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,PANX1,ATP7B,KCNRG,CACNB2,ANO10,SLC39A12,ATP6V0E2,ASIC3,STAC,ATP6V0B,ATP1A3,CCT8L2,OXSR1,TMEM163,ATP5F1C,SCN5A,SCN1A,SLC25A38,SLC24A3,GPD1L,SLC20A2,SLC4A7,CACNB4,RYR1,NALCN,SLC6A15,SLC25A15,PRNP,DIAPH1,P2RX2,TMCO3,GAS6,RASA3,COX7A1,SLC7A1,SLC25A26,SLC38A9,MICU3,KCNIP3,ATP6V1H,COX4I2,CYB5A,SLMAP,SLC43A1,ATP5F1A,GLRX,P2RX3,TRPC4AP,SLC9A9,RYR3,ORAI1,MEF2C,ASIC1,P2RX7,HVCN1,KCNH3,PTK2B,SLC39A13,KCNJ11,SLC33A1,TPCN1,SLC8B1,HOMER1,IFNGR2,SLC25A37,OPA1,KCNJ3,F2R,TESC,SLC40A1,ANO6,SLC6A2,ZDHHC13,COX15,KCNK15,ABCC2,KCNE2,PKD2,NIPA1,CASQ2,KCNJ15,MCUR1,SLC12A5,KCNIP2,RYR2,FAM173B,ATP6V1B2,PM20D1,SLC41A1,COX6B1,SLC4A10,SFXN2,TRPM1,CALHM2,CALHM1,SLC6A3,LCK,SLC2A10,HECW2,KCNJ2,SLC38A3,SLC9B1,SLC12A7,TRPV4,SLC9B2,ADRA2A,SLC30A10,TCIRG1,COX17,SCN2A,ISCU,KCNB1,SHROOM2,MCUB,SLC9A8,CLCN4,KCNK1,KCNG1,SCN7A,UBASH3B,ANK2,GPER1,KLHL24,RHCG,TRPM8,AGT,SLC25A20,ABCC5,ACE2,ATP1A2,SLC9A1,C4orf3,CASQ1,CCDC51,SLC12A8,KCNK2,NTSR1,SCN4B,CNIH2,DNAJC30,NIPAL3,NOS1AP,CATSPER2,DLG1,KCNK7,TMCO1,COX6A1,SLC30A4,UNC80,CEMIP,SLC12A9,SESTD1,ATP5S,	grey	VSMC_M10
GO:0010257	0.03	0.99	37	53	NADH dehydrogenase complex assembly	BP	1	TIMM21,NDUFA6,NDUFB2,NDUFB6,TMEM126B,NDUFC2,DMAC2,NDUFS8,NDUFAF7,NDUFA12,NDUFAF2,NDUFS3,NDUFAF6,FOXRED1,OXA1L,NDUFB4,NDUFB3,NDUFS2,NUBPL,NDUFB11,BCS1L,NDUFA9,NDUFAB1,NDUFB10,MT-ND1,MT-ND2,MT-ND6,NDUFA5,NDUFC1,NDUFAF8,DMAC1,NDUFA3,NDUFB5,NDUFA8,NDUFS5,TMEM126A,COA1	grey	VSMC_M10
GO:0032981	0.03	0.99	37	53	mitochondrial respiratory chain complex I assembly	BP	1	TIMM21,NDUFA6,NDUFB2,NDUFB6,TMEM126B,NDUFC2,DMAC2,NDUFS8,NDUFAF7,NDUFA12,NDUFAF2,NDUFS3,NDUFAF6,FOXRED1,OXA1L,NDUFB4,NDUFB3,NDUFS2,NUBPL,NDUFB11,BCS1L,NDUFA9,NDUFAB1,NDUFB10,MT-ND1,MT-ND2,MT-ND6,NDUFA5,NDUFC1,NDUFAF8,DMAC1,NDUFA3,NDUFB5,NDUFA8,NDUFS5,TMEM126A,COA1	grey	VSMC_M10
GO:0035871	0.03	1.00	8	9	protein K11-linked deubiquitination	BP	1	TNFAIP3,OTUD7A,USP30,YOD1,OTUD7B,USP37,OTUD3,OTUB2	grey	VSMC_M10
GO:2000647	0.03	1.00	6	6	negative regulation of stem cell proliferation	BP	1	FBLN1,OVOL2,FERMT1,KDF1,OVOL1,MIR222	grey	VSMC_M10

GO:0050877	0.03	0.98	384	678	nervous system process	BP	1	RDH5,ATP8B1,MIP,MYO1A,EYA4,STAC3,MAPK8IP2,ALDH7A1,RIMS2,PRRT1,PRKN,AGER,HLA-DRA,COL11A2,SYNGAP1,LRRC6,AGTPBP1,NTRK2,PLA2G6,SOX10,BTBD9,OPN1SW,GUCA1B,RBFOX2,CHRNA3,PRPH2,GRM8,CHRNA5,RORB,SRF,TTBK1,CFAP69,GABRA1,CNGA1,PHF24,CLIC5,KIT,SLC1A1,ADGRF1,TNFRSF21,CNNM4,CLDN19,BRSK1,TNNI3,EPAS1,RIMS1,DNAH11,KCNQ4,GSDME,SHANK1,PPT1,GJA10,MYH14,SLC1A4,WHRN,PTN,EGFR,GRIK2,DLGAP3,CLCN1,LPIN1,SOBP,SLC7A11,NTF4,FIG4,TULP2,PRKAR2B,GRIN2D,ADCY3,MTMR2,BBS7,SLC8A2,C5AR1,SLC26A5,MYO3A,CST7,MYO7B,EML2,OPA3,CACNB2,USH1G,ASIC3,XRCC1,STAC,B4GALT2,CRYGN,ZNF513,GRIK5,SCN5A,SCN1A,MYO7A,MYCBP2,METTL23,POU4F1,SPRY2,CHRNA6,CHD8,MKKS,FSCN2,PDE6G,LRTOMT,AP000812.5,PLCB1,TMTC4,RAC3,PRNP,DDHD2,KERA,LUM,DIAPH1,SPART,P2RX2,ARL6IP5,FAM19A4,ATXN7,TUB,TCF15,EPHB1,PLK2,FAM107A,GPI,NR4A1,CAMK4,CASP3,CHMP2B,MARVELD2,EYA1,P2RX3,CHRM5,CEP250,CCDC66,ADGRV1,MEF2C,ASIC1,P2RX7,NCAM2,JAM2,DLGAP4,CUX2,P2RY1,KIFC3,PTK2B,MME,KCNJ11,EIF2AK4,TMEM150C,NBN,USH1C,SYNJ1,HOMER1,OPA1,AMFR,F2R,NQO2,TNNC1,GLS,IMPG2,CBR3,DOP1B,TFAP2A,PAX2,CYFIP1,SLC12A5,ATXN1,FAM173B,BDNF,SLC4A10,TRPM1,RNF10,CABP1,CALHM1,CFAP43,SLC6A3,ALDH1A3,SORCS3,PPP3CA,LINS1,KCNJ2,PGAP1,TNNI1,SYNM,IGSF11,VTI1A,ADARB1,PDE6D,SCN2A,DAG1,NLGN4Y,SSH1,KRAS,GIGYF2,RRH,LRIT3,ADNP,MYH7,ZFHX2,SCN7A,OPRD1,JHY,GPER1,CFAP45,CRYBA4,NRL,EYA3,TRPM8,AGT,ACE2,ATP1A2,SLC9A1,NIPSNAP1,NFATC4,CASQ1,MYO3B,ACTN3,BBS1,KCNK2,STX1A,T	grey	VSMC_M10
GO:0045066	0.03	0.99	14	18	regulatory T cell differentiation	BP	1	HLA-DRA,IL4I1,SOX12,TOX,CD28,DUSP10,BCL6,VSIR,LAG3,FOXP3,SOCS1,DROSHA,MIR21,CD46	grey	VSMC_M10
GO:0098719	0.03	0.99	10	12	sodium ion import across plasma membrane	BP	1	SLC12A2,TRPM4,SLC9A9,SLC9A1,SLC9A7,SLC5A2,SLC9A6,SLC9A5,MIR24-1,HCN4	grey	VSMC_M10
GO:0045055	0.03	0.98	101	167	regulated exocytosis	BP	1	RIMS2,SYNGR1,RAC2,MYH9,CHRNA5,STEAP2,APBA1,KIT,NLRP5,RIMS1,RIMS3,PLEK,VPS41,PPFIA3,SPHK2,NAPA,RAB10,CACNB2,GAB2,GRIK5,UNC13D,NAPB,ABCC4,SYT1,RAB5A,NCKAP1L,STX2,SYT9,SNPH,HCK,FER,ERC2,P2RY1,RASGRP1,RAB11FIP5,SYNJ1,F2RL1,VPS18,DMTN,DTNBP1,SYT8,DNM1L,HYAL3,ADRA2A,SNAP23,KCNB1,RAB11FIP2,LAT2,FGR,CBL,STX1A,SNX4,BACE1,DNAJC5,CSPG5,RAP1B,BLOC1S6,ABCA12,CASK,PTGDR,PPP3CB,RAB3A,SYN1,SNAP29,C12orf4,SYT7,RAB15,CPLX1,STX1B,STX4,PSEN1,ITGAM,SYT11,TMED10,CACNA1G,LAT,RAB3D,IL4R,CALM1,SNAPIN,S100A13,PRKCB,BTK,SCAMP5,STXBP2,PRAM1,FMR1,PIP5K1C,SDF4,PDPK1,P2RX1,RAB26,BAIAP3,CACNA1H,FOXF1,STXBP1,AP1G1,CHGA,SNAP47,DOC2B,VAMP3	grey	VSMC_M10
GO:0003341	0.03	0.98	65	103	cilium movement	BP	1	UBE2B,CATSPER3,LRRC6,CFAP69,RFX3,DNAJA1,DNAH11,CABS1,ARMC2,ARMC4,APOB,ADCY3,DRC1,RSPH6A,TTC21A,CFAP61,TTLL3,MKKS,NEK10,SPEF1,ING2,WDR66,CFAP20,CCDC65,DNAH1,PLTP,DNAH5,DPCD,ROPN1L,NEURL1,CFAP43,ZMYND10,SLC9B1,SLC9B2,CFAP46,INTS13,JHY,OFD1,CFAP45,ENO4,TSSK4,CELF3,CATSPER2,SORD,TTC12,DNAAF2,SPAG16,CFAP70,STK36,ADCY10,TTC25,DNAAF4,MNS1,CCDC151,TEKT3,CAMSAP3,SPEF2,CATSPERD,CFAP53,TPGS1,CELSR2,HYDIN,WDR63,CCSAP,SPA17	grey	VSMC_M10
GO:1901606	0.03	0.98	43	65	alpha-amino acid catabolic process	BP	1	GLS2,SHMT2,ALDH8A1,RIDA,GPT,PPAT,IL4I1,DDO,BCAT2,GAD2,IDO2,IDO1,CSAD,THNSL2,AHCY,SDSL,HOGA1,GLS,MTRR,CBSL,HGD,AMT,ACADSB,OAT,GLUL,FAH,PRODH,ALDH4A1,MAT1A,ASRGL1,HSD17B10,GSTZ1,CRYM,SHMT1,NOS2,PIPOX,SARDH,GCSH,KYAT1,KYAT3,MIR21,SLC25A21,HYKK	grey	VSMC_M10
GO:0046461	0.03	0.99	19	26	neutral lipid catabolic process	BP	1	ABHD16A,PNPLA3,PNPLA5,APOB,FGF21,FAAH,ABHD5,LIPE,DDHD2,ABHD6,GPLD1,ABHD2,SORL1,CPS1,ABHD12B,DAGLB,LIPC,PNPLA4,LYPLA2	grey	VSMC_M10
GO:0046464	0.03	0.99	19	26	acylglycerol catabolic process	BP	1	ABHD16A,PNPLA3,PNPLA5,APOB,FGF21,FAAH,ABHD5,LIPE,DDHD2,ABHD6,GPLD1,ABHD2,SORL1,CPS1,ABHD12B,DAGLB,LIPC,PNPLA4,LYPLA2	grey	VSMC_M10
GO:0002717	0.03	0.99	10	12	positive regulation of natural killer cell mediated immunity	BP	1	CD226,NECTIN2,PVR,RASGRP1,CADM1,IL12A,LAG3,STAT5B,VAV1,AP1G1	grey	VSMC_M10
GO:0045954	0.03	0.99	10	12	positive regulation of natural killer cell mediated cytotoxicity	BP	1	CD226,NECTIN2,PVR,RASGRP1,CADM1,IL12A,LAG3,STAT5B,VAV1,AP1G1	grey	VSMC_M10
GO:0032816	0.03	0.99	12	15	positive regulation of natural killer cell activation	BP	1	IL15,IL15RA,GAS6,TOX,RASGRP1,BLOC1S6,IL12A,STAT5B,ZBTB1,TICAM1,AP1G1,BLOC1S3	grey	VSMC_M10
GO:0033604	0.03	1.00	8	9	negative regulation of catecholamine secretion	BP	1	ADRA2B,P2RY1,ADRA2A,ADRA2C,SYT11,ABAT,CHGA,CRH	grey	VSMC_M10
GO:0140042	0.03	1.00	8	9	lipid droplet formation	BP	1	CDS2,AUP1,CDS1,FITM2,FITM1,ZFYVE1,TMEM159,BSCL2	grey	VSMC_M10
GO:0015802	0.03	0.99	12	15	basic amino acid transport	BP	1	SLC3A1,SLC7A1,SLC38A9,SLC38A3,SLC7A7,AGT,SLC11A1,PQLC2,SLC7A3,AC138894.1,SLC7A6,SLC25A29	grey	VSMC_M10
GO:0055075	0.03	0.99	15	20	potassium ion homeostasis	BP	1	SLC12A2,TFAP2B,ATP1A3,SLC12A5,KCNJ2,SLC12A7,ATP1A2,SLC12A8,SLC12A9,ATP1B1,KCNMA1,ATP1B2,SCNN1B,SLC12A4,KCNH2	grey	VSMC_M10
GO:0016558	0.03	0.99	10	12	protein import into peroxisome matrix	BP	1	PEX7,PEX6,PEX1,PEX2,PEX16,LONP2,PEX26,PEX14,PEX10,PEX12	grey	VSMC_M10
GO:0033344	0.03	0.98	29	42	cholesterol efflux	BP	1	LRP1,APOM,PTCH1,TTC39B,ABCG5,ABCG8,NR1H2,APOB,APOC1,TSKU,SOAT2,NR1H3,PLTP,ABCA5,EGF,ABCG4,SOAT1,ZDHHC8,ABCA12,GPS2,NAXE,NPC1,ABCA3,ABCA7,RXRA,MIR27B,MIR27A,ABCA8,MIR33B	grey	VSMC_M10

GO:0006865	0.03	0.98	62	99	amino acid transport	BP	1	SLC12A2,SLC22A4,NTRK2,APBA1,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,LLGL2,SLC25A38,SLC38A10,SLC6A15,SLC25A15,ARL6IP5,SLC7A1,SLC38A9,SLC43A1,SERINC5,SLC38A4,SLC38A2,SLC38A1,OCA2,GRM2,SFXN2,SLC38A11,SLC38A3,SLC7A7,AGT,ACE2,ATP1A2,PER2,NTSR1,SLC11A1,PQLC2,SLC38A5,ARL6IP1,SLC3A2,SLC38A6,PRAF2,CLN8,PSEN1,SLC25A44,SLC7A3,AC138894.1,SLC25A47,SLC6A7,LRRC8E,ABAT,SLC1A7,TRPV1,SLC7A5,LRRC8A,STXBP1,SLC7A6,SLC36A1,LRRC8D,SLC6A19,SLC25A45,XK,RGS4,SLC25A29	grey	VSMC_M10
GO:0046330	0.03	0.98	44	68	positive regulation of JNK cascade	BP	1	MAP3K5,STK3,AGER,GADD45G,MTURN,NOD1,TLR4,TRAF1,SDCBP,MYD88,PLCB1,SEMA3A,SH3RF2,MFHAS1,TRAF6,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,TRPV4,NCF1,TRAF5,FZD7,MAP3K11,MBIP,MAP4K2,DUSP19,LTBR,MINK1,TAOK2,TRAF3,TAOK1,SERPINF2,MAPK8IP3,TRAF2,DAB2IP,ZNF622,WNT5A,GADD45A,DUSP22,HRAS	grey	VSMC_M10
GO:0033238	0.04	0.99	17	23	regulation of cellular amine metabolic process	BP	1	PRKN,GPR37,SLC7A11,NR1H4,NR4A2,SIRT4,SLC6A3,SLC7A7,COMT,PNKD,ITGAM,AC138894.1,CHRNB2,ABAT,PARK7,MIR21,NNMT	grey	VSMC_M10
GO:0046185	0.04	1.00	8	9	aldehyde catabolic process	BP	1	ADH5,ESD,AKR1A1,HOGA1,PNKD,PARK7,ADH4,PDXP	grey	VSMC_M10
GO:0006639	0.04	0.98	58	92	acylglycerol metabolic process	BP	1	AVIL,ABHD16A,TNXB,SLC22A4,PNPLA3,PNPLA5,CAT,MBOAT7,NR1H2,DGKI,LPIN1,APOB,FGF21,FAAH,ABHD5,APOC1,LIPE,DDHD2,PANK2,ABHD6,GK5,PLCE1,FBXW7,NR1H3,LPIN3,FITM2,GPLD1,SIK1,CPT1A,GPAM,ABHD2,SORL1,DGKD,LPGAT1,DGKG,PLA2G4A,MOGAT3,CPS1,ABHD12B,GNB3,PLA2G16,SLC27A1,DAGLB,LIPC,DGKQ,APOBR,SEL1L,DGKE,LDLR,SREBF1,LPIN2,C3,LMF1,PLA2G15,PNPLA4,CNEP1R1,LYPLA2,INSIG2	grey	VSMC_M10
GO:0072235	0.04	1.00	5	5	metanephric distal tubule development	BP	1	POU3F3,PAX8,PKD2,PAX2,PKD1	grey	VSMC_M10
GO:0000414	0.04	1.00	5	5	regulation of histone H3-K36 methylation	BP	1	IWS1,PAXIP1,NSD3,BCOR,NSD1	grey	VSMC_M10
GO:0006906	0.04	0.98	57	90	vesicle fusion	BP	1	STX7,SEPT8,TSNARE1,TGFBRAP1,STX17,VPS41,RAB7A,PIP4K2A,RUBCNL,GRIK5,TBC1D4,AKT2,YIPF4,SYT1,STX2,SYT9,ANKRD27,CHMP2B,DYSF,VPS39,RAB7B,SEC22B,VTI1A,SNAP23,C2CD5,STX1A,STX6,VPS8,SPG11,PIKFYVE,RAB3A,VAMP1,SNAP29,ANKFY1,STX5,RAB8A,ATP13A2,CPLANE2,SYT7,ANXA2,CPLX1,STX1B,STX4,SYT11,RAB8B,AC138894.1,SOX30,STX8,SNAPIN,GNAI3,VAV3,STXBP1,VPS4A,SNAP47,DOC2B,VAMP3,RAB39A	grey	VSMC_M10
GO:0071294	0.04	1.00	8	9	cellular response to zinc ion	BP	1	TSPO,MTF1,HVCN1,CREB1,ATP13A2,PARP1,KCNK3,MT1X	grey	VSMC_M10
GO:0006576	0.04	0.98	42	64	cellular biogenic amine metabolic process	BP	1	SNCAIP,ALDH7A1,PRKN,LY6E,AKR1B1,GPR37,SLC1A1,EPAS1,DDC,IL4I1,NAPEPLD,AANAT,HNMT,IDO2,IDO1,LRTOMT,AP000812.5,HAND2,CHDH,NR4A2,AZIN2,SLC6A3,TGFB2,CHKA,SMS,COMT,PNKD,GCH1,HDC,SLC29A4,ITGAM,GDPD3,GCDH,CHRNB2,GDPD1,GDE1,ABAT,OAZ1,MECP2,PARK7,NNMT,AOC2	grey	VSMC_M10
GO:0050957	0.04	1.00	5	5	equilibrioception	BP	1	USH1G,MYO7A,POU4F1,USH1C,CDH23	grey	VSMC_M10
GO:0031064	0.04	1.00	5	5	negative regulation of histone deacetylation	BP	1	SPHK2,KDM5A,FOXP3,SKI,PRMT6	grey	VSMC_M10
GO:0060073	0.04	1.00	5	5	micturition	BP	1	CHRNA3,KCNMA1,CHRNB2,TRPV1,CHRNB4	grey	VSMC_M10
GO:0050774	0.04	1.00	5	5	negative regulation of dendrite morphogenesis	BP	1	TLX2,RAPGEF2,PPP3CA,NFATC4,YWHAH	grey	VSMC_M10
GO:1902816	0.04	1.00	5	5	regulation of protein localization to microtubule	BP	1	ABHD17B,TTBK2,ABHD17A,ABHD17C,MAP1A	grey	VSMC_M10
GO:1902817	0.04	1.00	5	5	negative regulation of protein localization to microtubule	BP	1	ABHD17B,TTBK2,ABHD17A,ABHD17C,MAP1A	grey	VSMC_M10
GO:0050953	0.04	0.97	77	126	sensory perception of light stimulus	BP	1	RDH5,MIP,EYA4,OPN1SW,GUCA1B,PRPH2,GRM8,RORB,CNGA1,CLIC5,CNNM4,CLDN19,EPAS1,RIMS1,PPT1,GJA10,WHRN,TULP2,BBS7,MYO3A,EML2,OPA3,CACNB2,USH1G,CRYGN,ZNF513,MYO7A,MKKS,FSCN2,PDE6G,KERA,LUM,ATXN7,CEP250,CCDC66,ADGRV1,KIFC3,USH1C,OPA1,IMPG2,PAX2,SLC4A10,TRPM1,CABP1,PDE6D,RRH,LRIT3,CRYBA4,NRL,EYA3,MYO3B,BBS1,OAT,PDE6H,HMCN1,CDH23,ROM1,CLN8,DHRS3,GUCY2D,CHRNB2,LCTL,CLN6,MYO9A,UNC119,SLC45A2,PITPNA,GNAT2,LAMC3,HSF4,CRYZ,REEP6,DRAM2,LRAT,AOC2,BBS10,DNAJC19	grey	VSMC_M10
GO:0010804	0.04	0.99	12	15	negative regulation of tumor necrosis factor-mediated signaling pathway	BP	1	GAS6,F2RL1,PELI3,GPS2,PYDC1,PTPN2,PIAS4,MIR27B,MIR24-1,NOL3,CCDC3,HIST1H2BJ	grey	VSMC_M10
GO:0007158	0.04	0.99	11	14	neuron cell-cell adhesion	BP	1	RET,NCAM2,NLGN4Y,TNR,NRXN2,NINJ2,NLGN2,NLGN3,CDK5R1,CEL,NRXN3	grey	VSMC_M10
GO:0021937	0.04	1.00	5	5	cerebellar Purkinje cell-granule cell precursor cell signaling involved in regulation of granule cell precursor cell proliferation	BP	1	GLI1,SMO,GLI2,ZNF423,LHX1	grey	VSMC_M10

GO:0006811	0.04	0.96	574	1026	ion transport	BP	1	VPS4B,SLC39A5,NEDD4L,ATP8B1,STAC3,SLC26A10,CYP27B1,SLC16A7,ATP5MGL,NIPAL2,MAPK8IP2,SLC12A2,SLC27A6,KCNV1,PRRT1,PRKN,SLC22A4,CALHM4,TSPO,GOPC,SMDT1,BAK1,CATSPER3,KLHL3,MCHR1,PKD2L2,KCNK9,MAPK15,NTRK2,KCNJ4,PLA2G6,SLC39A4,ATP6V1F,MFSD3,CHRNA3,CHRNA5,TRPM6,ABCB1,ABCC10,STEAP2,GABRA1,APBA1,CNGA1,SLC41A2,TMEM63B,SLC35B2,CLIC5,SLC1A1,SLC25A13,WNK2,CNNM4,TSPAN13,SLC3A1,PRKCE,ATP6V1E2,TMC4,KCNQ4,IBTK,SHANK1,SLC4A4,CYB5R4,SLC35A1,AQP1,SLC1A4,SLC31A2,BSPRY,SLC13A4,ATP6V1C2,HECW1,TCAF2,GRIK2,CLCN1,SFRP4,KEL,UCP1,ATG5,TRPM4,SLC7A11,OSR1,PGRMC2,MFSD4B,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,COMMD3,PANX1,SLC26A5,HEPHL1,ATP7B,KCNRG,CACNB2,ANO10,SLC39A12,SLC25A30,ATP6V0E2,SLC4A2,ASIC3,STAC,LLGL2,ATP6V0B,CLNS1A,STEAP3,GRIK5,ATP1A3,CCT8L2,OXSR1,TMEM163,SLC2A13,ATP5F1C,SCN5A,SCN1A,SLC25A38,SEC14L1,SLC24A3,GPD1L,ABCC4,CHRNA6,SLC20A2,SLC4A7,SLC38A10,SYT1,CACNB4,EFHB,RYR1,NALCN,SLC6A15,SLC25A15,SLC23A2,PRNP,TAF7,DIAPH1,P2RX2,CLIC1,TMCO3,GAS6,HPX,RASA3,ARL6IP5,COX7A1,SLC7A1,SLC25A26,SYT9,COMMD9,SLC38A9,MICU3,KCNIP3,ANO4,SLC5A8,ATP6V1H,MFSD5,COX4I2,CYP7A1,CYB5A,PXK,SLCO6A1,SLMAP,SLC43A1,ATP5F1A,GLRX,P2RX3,TRPC4AP,CHRM5,SLC9A9,RYR3,ORAI1,MEF2C,ASIC1,TMBIM6,P2RX7,HVCN1,KCNH3,P2RY1,PTK2B,SLC39A13,KCNJ11,SLC33A1,PLLP,SERINC5,TMEM150C,TPCN1,SLC8B1,HOMER1,IFNGR2,VDR,STC1,SLC25A37,OPA1,SLC48A1,KCNJ3,SLC38A4,SLC38A2,F2R,SLC38A1,TESC,RIPK1,SLC40A1,SLC22A23,ANO6,CRY2,SLC6A2,ZDHHC1	grey	VSMC_M10
GO:0048284	0.04	0.97	74	120	organelle fusion	BP	1	STX7,PRKN,SEPT8,BAK1,TSNARE1,TGFBRAP1,STX17,VPS41,RAB7A,PIP4K2A,RUBCNL,GRIK5,TBC1D4,AKT2,YIPF4,SYT1,VPS16,STX2,SYT9,ANKRD27,CHMP2B,DYSF,OPA1,VPS18,VPS39,RAB7B,DNM1L,SEC22B,ZDHHC6,VTI1A,SNAP23,USP30,MFN1,RCC1L,C2CD5,STX1A,STX6,VPS8,SPG11,PIKFYVE,FIS1,RAB3A,MUL1,VAMP1,SNAP29,ANKFY1,STX5,RAB8A,ATP13A2,CPLANE2,SYT7,MFN2,ANXA2,CPLX1,STX1B,STX4,BNIP1,SYT11,RAB8B,AC138894.1,ADCK1,THG1L,SOX30,STX8,SNAPIN,GNAI3,VAV3,MIGA2,STXBP1,VPS4A,SNAP47,DOC2B,VAMP3,RAB39A	grey	VSMC_M10
GO:0007343	0.04	1.00	5	5	egg activation	BP	1	MYH9,NLRP5,PLAT,PLCB1,ZP2	grey	VSMC_M10
GO:0002420	0.04	1.00	5	5	natural killer cell mediated cytotoxicity directed against tumor cell target	BP	1	CD226,NECTIN2,PVR,IL12A,HAVCR2	grey	VSMC_M10
GO:0002423	0.04	1.00	5	5	natural killer cell mediated immune response to tumor cell	BP	1	CD226,NECTIN2,PVR,IL12A,HAVCR2	grey	VSMC_M10
GO:0002855	0.04	1.00	5	5	regulation of natural killer cell mediated immune response to tumor cell	BP	1	CD226,NECTIN2,PVR,IL12A,HAVCR2	grey	VSMC_M10
GO:0002858	0.04	1.00	5	5	regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	BP	1	CD226,NECTIN2,PVR,IL12A,HAVCR2	grey	VSMC_M10
GO:0080144	0.04	1.00	5	5	amino acid homeostasis	BP	1	SLC1A1,SLC7A11,GLS,GRM2,PQLC2	grey	VSMC_M10
GO:0098739	0.04	0.97	75	123	import across plasma membrane	BP	1	SLC39A5,SLC12A2,SLC22A4,KCNK9,KCNJ4,SLC39A4,STEAP2,SLC1A1,WNK2,SLC1A4,TRPM4,SLC7A11,KCNJ14,SLC8A2,SLC39A12,ATP1A3,AKT2,PRNP,ARL6IP5,SLC7A1,SLC43A1,SLC9A9,KCNJ11,KCNJ3,KCNE2,KCNJ15,SLC12A5,SLC2A10,KCNJ2,SLC12A7,TRPV4,ACSL5,ISCU,AGT,ACE2,ATP1A2,SLC9A1,PER2,SLC12A8,NTSR1,DLG1,SLC12A9,SLC9A7,ATP1B1,SLC27A1,ARL6IP1,SLC3A2,CLN8,WNK3,ATP1B2,FAM155B,PSEN1,SLC7A3,SLC5A2,SLC39A6,TRPV2,LRRC8E,KCNJ18,SLC46A1,SLC9A6,TRPV3,TRPV1,P2RX1,SLC7A5,LRRC8A,LCN2,SLC12A4,SLC9A5,MIR24-1,SLC36A1,KCNH2,RGS4,KCNJ8,HCN4,KCNJ9	grey	VSMC_M10
GO:0045217	0.04	0.99	11	14	cell-cell junction maintenance	BP	1	MTSS1,WHRN,KIFC3,PLEKHA7,F2RL1,F2R,NLGN2,CSF1R,CAMSAP3,INAVA,PARD6A	grey	VSMC_M10
GO:0060332	0.04	1.00	5	5	positive regulation of response to interferon-gamma	BP	1	HPX,NLRC5,PARP9,MED1,IRGM	grey	VSMC_M10
GO:0060335	0.04	1.00	5	5	positive regulation of interferon-gamma-mediated signaling pathway	BP	1	HPX,NLRC5,PARP9,MED1,IRGM	grey	VSMC_M10
GO:0072174	0.04	1.00	5	5	metanephric tubule formation	BP	1	SOX9,PAX8,PAX2,WNT4,SOX8	grey	VSMC_M10
GO:0001910	0.04	0.98	26	38	regulation of leukocyte mediated cytotoxicity	BP	1	CD226,STX7,AGER,HLA-DRA,NECTIN2,PVR,SLC22A13,NCKAP1L,RASGRP1,F2RL1,CADM1,IL12A,LAG3,PPP3CB,STAT5B,ITGAM,VAV1,NOS2,IL7R,CRK,DNASE1,AP1G1,FADD,CXCL6,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0070472	0.04	1.00	5	5	regulation of uterine smooth muscle contraction	BP	1	ADRA2B,GPER1,ADRA2C,SETD3,ABAT	grey	VSMC_M10
GO:0045663	0.04	0.99	13	17	positive regulation of myoblast differentiation	BP	1	MAPK14,AKIRIN1,PLCB1,BTG1,SMYD1,MEF2C,HIF1AN,RBM24,CDON,RANBP3L,LRRC8A,MIR199A1,XKR8	grey	VSMC_M10
GO:0045589	0.04	0.99	13	17	regulation of regulatory T cell differentiation	BP	1	HLA-DRA,IL4I1,SOX12,CD28,DUSP10,BCL6,VSIR,LAG3,FOXP3,SOCS1,DROSHA,MIR21,CD46	grey	VSMC_M10
GO:0006376	0.04	0.98	20	28	mRNA splice site selection	BP	1	SF3A3,PUF60,YTHDC1,SRSF10,CELF2,CELF1,SRSF6,CELF3,PRPF39,KHDC4,LUC7L3,SLU7,CELF5,LUC7L,RNVU1-6,NOL3,RNU4ATAC,RF00003,SNRPC,SRSF12	grey	VSMC_M10
GO:0010815	0.04	1.00	5	5	bradykinin catabolic process	BP	1	IDE,CPN1,XPNPEP1,CTSH,ECE1	grey	VSMC_M10
GO:0051938	0.04	0.99	9	11	L-glutamate import	BP	1	SLC1A1,SLC7A11,ARL6IP5,ATP1A2,PER2,NTSR1,ARL6IP1,CLN8,PSEN1	grey	VSMC_M10
GO:0098712	0.04	0.99	9	11	L-glutamate import across plasma membrane	BP	1	SLC1A1,SLC7A11,ARL6IP5,ATP1A2,PER2,NTSR1,ARL6IP1,CLN8,PSEN1	grey	VSMC_M10
GO:0048278	0.05	0.98	33	50	vesicle docking	BP	1	STX7,TSNARE1,EXOC4,SCFD2,STX17,PLEK,BVES,PPFIA3,RAB10,SYTL2,RALB,SYT1,STX2,SNPH,VPS18,KCNB1,STX1A,STX6,NSF,BLOC1S6,RAB3A,STX5,RAB8A,RAB15,STX1B,STX4,RAB8B,AC138894.1,STX8,RAB3D,STXBP2,STXBP1,VAMP3	grey	VSMC_M10
GO:0048242	0.05	1.00	5	5	epinephrine secretion	BP	1	LY6E,ADRA2B,ADRA2A,ADRA2C,CRH	grey	VSMC_M10
GO:0046039	0.05	0.99	13	17	GTP metabolic process	BP	1	NME1,GTPBP1,IMPDH1,RAB23,OPA1,NME4,MFN1,EFL1,NME7,NME3,GNAI3,RHOA,NME6	grey	VSMC_M10

GO:0006836	0.05	0.97	84	139	neurotransmitter transport	BP	1	SNCAIP,RIMS2,PRKN,GRM4,CHRNA3,CHRNA5,APBA1,SLC1A1,BRSK1,RIMS1,RIMS3,PPT1,DDC,PPFIA3,LIN7B,NAPA,CACNB2,GRIK5,NAPB,SYT1,RAB5A,LIN7A,SLC6A15,STX2,SYT9,SNPH,NR4A1,ERC2,MEF2C,ASIC1,P2RY1,SYNJ1,SLC38A2,SLC38A1,VPS18,SLC6A2,DTNBP1,SYT8,DNM1L,SLC6A3,ADRA2A,SNAP23,GPER1,ATP1A2,PER2,STX1A,SLC29A2,BACE1,DNAJC5,CSPG5,RAP1B,BLOC1S6,NRXN2,CASK,PNKD,RAB3A,SYN1,SNAP29,SLC29A4,SYT7,CLN8,CPLX1,STX1B,STX4,PSEN1,SYT11,CALM1,SNAPIN,PRKCB,CAMK2A,SLC6A7,STXBP2,FMR1,SLC1A7,PIP5K1C,P2RX1,BAIAP3,PARK7,STXBP1,CHRNB4,SNAP47,PDZD11,DOC2B,KCNMB4	grey	VSMC_M10
GO:0010700	0.05	1.00	5	5	negative regulation of norepinephrine secretion	BP	1	ADRA2B,P2RY1,ADRA2A,ADRA2C,CRH	grey	VSMC_M10
GO:0060259	0.05	0.99	7	8	regulation of feeding behavior	BP	1	NAPEPLD,CFAP20,EIF2AK4,TTC21B,STAT3,SGIP1,LEPR	grey	VSMC_M10
GO:0098662	0.05	0.96	308	541	inorganic cation transmembrane transport	BP	1	SLC39A5,NEDD4L,STAC3,ATP5MGL,NIPAL2,SLC12A2,KCNV1,SMDT1,CATSPER3,PKD2L2,KCNK9,KCNJ4,PLA2G6,SLC39A4,ATP6V1F,MFSD3,TRPM6,STEAP2,SLC41A2,SLC1A1,WNK2,CNNM4,TSPAN13,PRKCE,ATP6V1E2,KCNQ4,IBTK,SLC4A4,AQP1,SLC31A2,ATP6V1C2,HECW1,KEL,UCP1,ATG5,TRPM4,OSR1,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,PANX1,ATP7B,KCNRG,CACNB2,SLC39A12,ATP6V0E2,ASIC3,STAC,ATP6V0B,ATP1A3,CCT8L2,OXSR1,TMEM163,ATP5F1C,SCN5A,SCN1A,SLC24A3,GPD1L,SLC20A2,SLC4A7,CACNB4,RYR1,NALCN,SLC6A15,PRNP,DIAPH1,TMCO3,GAS6,RASA3,COX7A1,MICU3,KCNIP3,ATP6V1H,COX4I2,CYB5A,SLMAP,ATP5F1A,GLRX,P2RX3,TRPC4AP,SLC9A9,RYR3,ORAI1,ASIC1,P2RX7,HVCN1,KCNH3,PTK2B,SLC39A13,KCNJ11,SLC33A1,TPCN1,SLC8B1,SLC25A37,OPA1,KCNJ3,F2R,TESC,SLC40A1,ANO6,SLC6A2,ZDHHC13,COX15,KCNK15,ABCC2,KCNE2,PKD2,NIPA1,CASQ2,KCNJ15,MCUR1,SLC12A5,KCNIP2,RYR2,FAM173B,ATP6V1B2,PM20D1,SLC41A1,COX6B1,SLC4A10,TRPM1,CALHM1,SLC6A3,LCK,SLC2A10,HECW2,KCNJ2,SLC9B1,SLC12A7,TRPV4,SLC9B2,ADRA2A,SLC30A10,TCIRG1,COX17,SCN2A,ISCU,KCNB1,SHROOM2,MCUB,SLC9A8,CLCN4,KCNK1,KCNG1,SCN7A,UBASH3B,ANK2,GPER1,KLHL24,RHCG,TRPM8,ABCC5,ATP1A2,SLC9A1,C4orf3,CASQ1,CCDC51,SLC12A8,KCNK2,NTSR1,SCN4B,DNAJC30,NIPAL3,NOS1AP,CATSPER2,DLG1,KCNK7,TMCO1,COX6A1,SLC30A4,CEMIP,SLC12A9,SESTD1,ATP5S,PTPN6,KCNK4,MICU1,MCU,SLC11A1,HTT,PKD1L1,COX8A,SLC9A7,ATP6V0A1,KCNN1,ABCB6,TRPM7,ATP1B1,KCNA1,BHLHA15,KCNMA1,SLC3A2,ASIC4,KCNH4,SLC2A9,GNB5,KCND1,HAP1,PSEN2,ATP6V1D,WNK3,STAC2,CACNB1,ANXA2,A	grey	VSMC_M10
GO:0006638	0.05	0.97	58	93	neutral lipid metabolic process	BP	1	AVIL,ABHD16A,TNXB,SLC22A4,PNPLA3,PNPLA5,CAT,MBOAT7,NR1H2,DGKI,LPIN1,APOB,FGF21,FAAH,ABHD5,APOC1,LIPE,DDHD2,PANK2,ABHD6,GK5,PLCE1,FBXW7,NR1H3,LPIN3,FITM2,GPLD1,SIK1,CPT1A,GPAM,ABHD2,SORL1,DGKD,LPGAT1,DGKG,PLA2G4A,MOGAT3,CPS1,ABHD12B,GNB3,PLA2G16,SLC27A1,DAGLB,LIPC,DGKQ,APOBR,SEL1L,DGKE,LDLR,SREBF1,LPIN2,C3,LMF1,PLA2G15,PNPLA4,CNEP1R1,LYPLA2,INSIG2	grey	VSMC_M10
GO:0021940	0.05	0.99	7	8	positive regulation of cerebellar granule cell precursor proliferation	BP	1	GLI1,SMO,GLI2,ZNF423,EGF,LHX1,GPR37L1	grey	VSMC_M10
GO:0000965	0.05	1.00	5	5	mitochondrial RNA 3'-end processing	BP	1	PNPT1,TRNT1,SUPV3L1,HSD17B10,TRMT10C	grey	VSMC_M10
GO:0042219	0.05	0.98	17	23	cellular modified amino acid catabolic process	BP	1	ABHD16A,CHAC2,GGACT,AHCY,HOGA1,ACADL,GGT2,MTHFS,PRODH,ABHD12B,ALDH4A1,PCYOX1L,SARDH,DIO3,ALDH1L1,GGT5,DIO2	grey	VSMC_M10
GO:0006643	0.05	0.97	99	164	membrane lipid metabolic process	BP	1	KDSR,ORMDL2,B4GALNT1,A4GALT,PLA2G6,GPAA1,HACD4,LARGE1,CWH43,KIT,SPTLC1,TMEM246,PIGF,PPP2R1A,PPT1,MGST2,SMPD2,AGK,SPHK2,PRKD2,GLB1,ACER3,ELOVL1,NEU3,SPTLC3,PGAP2,SIRT3,NSMAF,ELOVL7,ASAH1,PIGU,ST8SIA4,HTRA2,SERINC5,ST3GAL6,ORMDL1,COL4A3BP,PIGT,GPLD1,A3GALT2,PGAP1,ST8SIA2,SGMS2,ALDH3B2,B3GALT1,TEX2,B3GNT5,CERS6,PIGM,HACD2,CERS2,PIGV,PIGX,GAL3ST3,PIGZ,ABCA12,PPM1L,B3GALNT1,GAL3ST4,PIGC,SMPD4,SGMS1,SCCPDH,FADS3,TECR,CLN8,PGAP3,DEGS1,PIGH,ALOXE3,HACD3,GALC,CLN6,ST8SIA5,GLA,HEXA,GM2A,PIGL,MPPE1,P2RX1,GBGT1,CEL,ST6GALNAC4,ST3GAL2,PLA2G15,ST6GALNAC5,CYP4F22,ABCA8,ELOVL3,PEMT,ACER2,PYURF,CPTP,NEU2,PIGB,B4GALT3,PIGA,SGPP1,ST8SIA6	grey	VSMC_M10
GO:0051289	0.05	0.98	30	45	protein homotetramerization	BP	1	MIP,SHMT2,CBY1,GNMT,TRPM4,SSBP1,RYR1,APIP,CBR4,RYR3,USP16,GLS,PKD2,SYCP1,ALDH1A3,KCNJ2,OSBPL2,UPB1,CRTC1,MAT1A,HSD17B10,ALDH1A2,THG1L,CRTC2,EVL,ACACA,SHMT1,TRPV1,CRYZ,VASP	grey	VSMC_M10
GO:0043011	0.05	0.99	11	14	myeloid dendritic cell differentiation	BP	1	TGFBR2,TRAF6,CAMK4,ITGB6,BATF2,LTBR,RBPJ,PSEN1,BATF,DHRS2,BATF3	grey	VSMC_M10
GO:0009308	0.05	0.97	49	77	amine metabolic process	BP	1	SNCAIP,ALDH7A1,PRKN,LY6E,AKR1B1,GPR37,SLC1A1,EPAS1,DDC,IL4I1,SLC7A11,NAPEPLD,AANAT,HNMT,IDO2,IDO1,LRTOMT,AP000812.5,NR1H4,HAND2,CHDH,NR4A2,ABCC2,SIRT4,AZIN2,SLC6A3,TGFB2,CHKA,SLC7A7,SMS,COMT,PNKD,GCH1,HDC,SLC29A4,ITGAM,GDPD3,GCDH,AC138894.1,CHRNB2,GDPD1,GDE1,ABAT,OAZ1,MECP2,PARK7,MIR21,NNMT,AOC2	grey	VSMC_M10
GO:0032823	0.05	0.99	7	8	regulation of natural killer cell differentiation	BP	1	IL15,IL15RA,GAS6,TOX,RASGRP1,STAT5B,ZBTB1	grey	VSMC_M10
GO:0032825	0.05	0.99	7	8	positive regulation of natural killer cell differentiation	BP	1	IL15,IL15RA,GAS6,TOX,RASGRP1,STAT5B,ZBTB1	grey	VSMC_M10
GO:0021591	0.05	0.98	19	27	ventricular system development	BP	1	CCDC134,CDK6,MBOAT7,AQP1,SLC7A11,ARMC4,NUMBL,TSKU,RAPGEF2,RPGRIP1L,DNAH5,DPCD,TTC21B,SEMA6D,ATP1B2,MECP2,CELSR2,AK8,HYDIN	grey	VSMC_M10

GO:0048167	0.05	0.97	86	143	regulation of synaptic plasticity	BP	1	RIMS2,PRRT1,AGER,SYNGAP1,ATF4,SYNGR1,NTRK2,PICK1,SRF,KIT,SLC1A1,BRSK1,RIMS1,RIMS3,ACP4,CRHR2,PTN,NCDN,GRIK2,PPFIA3,GRIN2D,SLC8A2,RAB5A,PRNP,PLK2,FAM107A,ABHD6,P2RX3,ERC2,MEF2C,PTK2B,MME,RAPGEF2,EIF2AK4,ITPKA,LZTS1,SLC4A10,NEURL1,SORCS3,IGSF11,SSH1,STAU1,KCNB1,KRAS,AGT,NFATC4,SYAP1,NPAS4,YTHDF1,CREB1,YWHAG,MAPT,VGF,EIF4EBP2,TNR,MPP2,CRTC1,PPP3CB,RAB3A,CD38,MAPK1,NSG1,RAB8A,EPHA4,DLG4,SYT7,RGS14,STX4,PSEN1,AC138894.1,RAB11A,CYP46A1,CAMK2A,FMR1,PRKCZ,MECP2,JPH3,STXBP1,CNTN2,GRID2,CRH,YWHAH,HRAS,SHISA8,MAP1A,LRRTM2	grey	VSMC_M10
GO:0015844	0.05	0.97	32	48	monoamine transport	BP	1	PRKN,LY6E,MAPK15,PICK1,SYT1,SYT9,ADRA2B,CHRM5,P2RY1,SLC6A2,DTNBP1,SYT8,GRM2,SLC6A3,ADRA2A,KCNB1,GRK2,AGT,STX1A,ADRA2C,RAB3A,PINK1,ACTB,SLC29A4,SYT7,SYT11,CHRNB2,ABAT,P2RX1,PARK7,CHGA,CRH	grey	VSMC_M10
GO:0042754	0.05	0.99	9	11	negative regulation of circadian rhythm	BP	1	CRY1,SUV39H2,CRY2,PER2,CIPC,SFPQ,SIN3A,CRH,PASD1	grey	VSMC_M10
GO:0072173	0.05	0.99	7	8	metanephric tubule morphogenesis	BP	1	SOX9,PAX8,PAX2,CXCR2,WNT4,PKD1,SOX8	grey	VSMC_M10
GO:0051560	0.05	0.98	18	25	mitochondrial calcium ion homeostasis	BP	1	SMDT1,SLC25A27,MICU3,IMMT,C19orf12,SLC8B1,MCUR1,RAP1GDS1,MCUB,DISC1,PDZD8,FIS1,MICU1,MCU,ATP2A1,SLC25A23,MAIP1,BCAP31	grey	VSMC_M10
GO:0021559	0.05	0.99	7	8	trigeminal nerve development	BP	1	PLXNA4,POU4F1,SEMA3A,TFAP2A,SEMA3F,ISL1,PLXNA3	grey	VSMC_M10
GO:1990822	0.05	0.99	9	11	basic amino acid transmembrane transport	BP	1	SLC3A1,SLC7A1,SLC38A9,SLC7A7,AGT,PQLC2,SLC7A3,SLC7A6,SLC25A29	grey	VSMC_M10
GO:0019323	0.05	1.00	5	5	pentose catabolic process	BP	1	DHDH,NUDT5,XYLB,RBKS,RPE	grey	VSMC_M10
GO:0050905	0.05	0.97	63	103	neuromuscular process	BP	1	STAC3,PRKN,AGTPBP1,RBFOX2,TNNI3,SHANK1,MYH14,GRIN2D,USH1G,XRCC1,STAC,MYO7A,MYCBP2,POU4F1,CHD8,RAC3,SPART,TCF15,NR4A1,TMEM150C,NBN,USH1C,HOMER1,TNNC1,SLC6A3,ALDH1A3,KCNJ2,TNNI1,SYNM,VTI1A,ADARB1,GIGYF2,MYH7,CASQ1,ACTN3,BACE1,CDH23,TNR,PNKD,CNTNAP1,GCH1,KCNA1,DLG4,NLGN2,CHRNB1,CLN8,TCAP,STAC2,AC138894.1,IGDCC3,ATP2A1,STRA6,GM2A,MECP2,JPH3,AARS,DMD,GRID2,TNNC2,FXN,POMK,GPR88,MAP1A	grey	VSMC_M10
GO:0046655	0.05	0.99	9	11	folic acid metabolic process	BP	1	SHMT2,DHFR,MTHFD2,MTRR,MTHFS,SHMT1,SLC46A1,MTHFD2L,SLC25A32	grey	VSMC_M10
GO:0060287	0.05	0.99	7	8	epithelial cilium movement involved in determination of left/right asymmetry	BP	1	LRRC6,RFX3,DNAH11,OFD1,CFAP45,TTC25,CFAP53	grey	VSMC_M10
GO:0030001	0.05	0.96	331	587	metal ion transport	BP	1	VPS4B,SLC39A5,NEDD4L,STAC3,CYP27B1,NIPAL2,SLC12A2,KCNV1,SLC22A4,TSPO,SMDT1,BAK1,CATSPER3,KLHL3,MCHR1,PKD2L2,KCNK9,KCNJ4,PLA2G6,SLC39A4,TRPM6,STEAP2,SLC41A2,SLC1A1,WNK2,CNNM4,TSPAN13,PRKCE,KCNQ4,IBTK,SLC4A4,AQP1,SLC31A2,BSPRY,SLC13A4,HECW1,KEL,ATG5,TRPM4,OSR1,PGRMC2,MFSD4B,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,COMMD3,PANX1,HEPHL1,ATP7B,KCNRG,CACNB2,SLC39A12,ASIC3,STAC,STEAP3,ATP1A3,CCT8L2,OXSR1,TMEM163,SCN5A,SCN1A,SLC24A3,GPD1L,SLC20A2,SLC4A7,SLC38A10,CACNB4,EFHB,RYR1,NALCN,SLC6A15,SLC23A2,PRNP,DIAPH1,P2RX2,GAS6,HPX,RASA3,COMMD9,MICU3,KCNIP3,SLC5A8,SLMAP,GLRX,P2RX3,TRPC4AP,SLC9A9,RYR3,ORAI1,ASIC1,TMBIM6,P2RX7,KCNH3,PTK2B,SLC39A13,KCNJ11,TPCN1,SLC8B1,HOMER1,VDR,STC1,SLC25A37,OPA1,SLC48A1,KCNJ3,SLC38A4,SLC38A2,F2R,SLC38A1,TESC,SLC40A1,ANO6,SLC6A2,ZDHHC13,SLC10A6,KCNK15,CUTC,ABCC2,KCNE2,PKD2,NIPA1,CASQ2,KCNJ15,MCUR1,CNTN1,SLC12A5,KCNIP2,RYR2,SLC41A1,SLC4A10,TRPM1,CALHM1,PKP2,DNM1L,SLC6A3,SIK1,LCK,PPP3CA,SLC38A11,HECW2,KCNJ2,SLC38A3,SLC9B1,SLC12A7,TRPV4,SLC9B2,ADRA2A,SLC30A10,COX17,SCN2A,ISCU,KCNB1,SHROOM2,MCUB,SLC9A8,EGF,KCNK1,KCNG1,SCN7A,EPB41,OPRD1,UBASH3B,ANK2,GPER1,KLHL24,TRPM8,AGT,ABCC5,ATP1A2,SLC9A1,PLPP4,C4orf3,CASQ1,CCDC51,SLC12A8,KCNK2,NTSR1,SCN4B,NIPAL3,NOS1AP,MELTF,HOMER2,CATSPER2,CDKN1B,DLG1,KCNK7,TMCO1,NSF,SLC30A4,IL16,CEMIP,SLC12A9,SESTD1,CDH23,CASK,PTPN6,KCNK4,MICU1,MCU,SLC11A1,HTT,PKD1L1,CALCRL,SLC9A7,RAMP2,KCNN1,ABCB6,CAMK2G,TRPM7	grey	VSMC_M10
GO:0090184	0.05	0.99	7	8	positive regulation of kidney development	BP	1	MYC,SOX9,RET,PAX2,WNT4,SOX8,NOG	grey	VSMC_M10
GO:0045006	0.05	1.00	5	5	DNA deamination	BP	1	APOBEC3H,EXOSC4,EXOSC3,CDADC1,EXOSC5	grey	VSMC_M10
GO:0042416	0.05	0.99	7	8	dopamine biosynthetic process	BP	1	GPR37,DDC,NR4A2,SLC6A3,TGFB2,GCH1,PARK7	grey	VSMC_M10
GO:0006835	0.05	0.97	36	56	dicarboxylic acid transport	BP	1	SLC26A10,SLC12A2,NTRK2,APBA1,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC26A5,SLC25A30,ARL6IP5,ABCC2,GRM2,ABCC5,ATP1A2,PER2,NTSR1,ARL6IP1,PRAF2,SLC25A11,CLN8,SLC26A1,PSEN1,SLC26A2,LRRC8E,SLC46A1,SLC25A14,ABAT,SLC1A7,TRPV1,LRRC8A,STXBP1,LRRC8D,SLC25A21,SLC25A32	grey	VSMC_M10
GO:0002715	0.05	0.98	14	19	regulation of natural killer cell mediated immunity	BP	1	CD226,NECTIN2,PVR,RASGRP1,CD96,CADM1,IL12A,LAG3,STAT5B,VAV1,CRK,AP1G1,SERPINB9,HAVCR2	grey	VSMC_M10
GO:1903959	0.05	0.98	14	19	regulation of anion transmembrane transport	BP	1	GOPC,ABCB1,TCAF2,PRNP,ARL6IP5,SLC43A1,RIPK1,AGT,ACE2,ATP1A2,PER2,ARL6IP1,PSEN1,RGS4	grey	VSMC_M10
GO:0051262	0.06	0.97	42	66	protein tetramerization	BP	1	MIP,SHMT2,CPSF6,STK3,HSD17B8,CBY1,GNMT,TRPM6,TRPM4,SSBP1,RYR1,APIP,CBR4,RYR3,USP16,HOMER1,GLS,CUTC,PKD2,STK4,SYCP1,TRPM1,ALDH1A3,KCNJ2,OXA1L,OSBPL2,UPB1,CRTC1,TRPM7,MAT1A,FARSB,HSD17B10,ALDH1A2,THG1L,CRTC2,EVL,ACACA,SHMT1,TRPV1,PKD1,CRYZ,VASP	grey	VSMC_M10
GO:0048172	0.06	0.99	9	11	regulation of short-term neuronal synaptic plasticity	BP	1	SYNGR1,GRIK2,PPFIA3,SLC8A2,SLC4A10,SYAP1,RAB3A,AC138894.1,SHISA8	grey	VSMC_M10
GO:1901186	0.06	0.97	22	32	positive regulation of ERBB signaling pathway	BP	1	RTN4,EPGN,AREG,TGFA,NEU3,HBEGF,PDE6G,HIP1R,FBXW7,NEURL1,ADRA2A,NCF1,EGF,GPER1,DGKD,AGT,CBL,PDE6H,HAP1,RBPJ,MIR29A,EREG	grey	VSMC_M10
GO:0009299	0.06	0.98	12	16	mRNA transcription	BP	1	ATF4,HSF1,FOXE3,CSAR1,TFCP2,AP3B1,STAT3,ZBTB1,MED1,SREBF1,SUPT6H,EREG	grey	VSMC_M10
GO:0042430	0.06	0.99	9	11	indole-containing compound metabolic process	BP	1	TPH2,BTBD9,DDC,IL4I1,AANAT,IDO2,IDO1,SRD5A1,GCDH	grey	VSMC_M10

GO:0021536	0.06	0.97	31	47	diencephalon development	BP	1	GLI1,UQCRQ,PITX1,SMO,PTN,NDNF,GLI2,POU4F1,SEMA3A,NR4A2,SALL1,SRD5A1,SLC6A3,SOX2,GBX2,CREB1,WNT4,TBX19,HAP1,BMPR1A,RBPJ,ALDH1A2,CHRNB2,ISL1,UBB,NOG,WNT5A,POU3F2,OTX1,CRH,TAL2	grey	VSMC_M10
GO:0036480	0.06	0.99	7	8	neuron intrinsic apoptotic signaling pathway in response to oxidative stress	BP	1	PRKN,FBXW7,MCL1,NONO,PINK1,PARP1,PARK7	grey	VSMC_M10
GO:1903376	0.06	0.99	7	8	regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	BP	1	PRKN,FBXW7,MCL1,NONO,PINK1,PARP1,PARK7	grey	VSMC_M10
GO:0046471	0.06	0.98	19	27	phosphatidylglycerol metabolic process	BP	1	SERAC1,PLA2G6,HADHA,TAMM41,CRLS1,CDS2,PLA2G4B,LPCAT1,GPAM,LPGAT1,THEM5,PLA2G4A,SLC27A1,ABCA3,MECP2,PLA2G15,LCLAT1,PTPMT1,DNAJC19	grey	VSMC_M10
GO:1905244	0.06	0.99	9	11	regulation of modification of synaptic structure	BP	1	CTTNBP2,CHMP2B,TIAM1,CYFIP1,CAMKV,GRIPAP1,EPHA4,AC138894.1,RHOA	grey	VSMC_M10
GO:0035270	0.06	0.96	54	87	endocrine system development	BP	1	ONECUT2,GLI1,TSPO,BAK1,PITX1,LY6E,SMO,SRF,CDK6,RFX3,SOX9,GIPR,GLI2,RAF1,MNX1,WNT11,PAX8,DKK3,ARNTL,NKX6-1,ZBED6,SALL1,SRD5A1,SLC6A3,SOX2,SIDT2,HOXD3,CREB1,MEN1,WNT4,RAP1GAP,TBX19,MAPK1,BMPR1A,THRA,RBPJ,ALDH1A2,MAPK3,IL6R,MAP2K1,SMAD3,STRA6,GATA6,ISL1,PDPK1,FSTL3,SOX4,HOXB3,NOG,WNT5A,POU3F2,SIX1,NKX2-5,HOXA3	grey	VSMC_M10
GO:0031629	0.06	0.98	14	19	synaptic vesicle fusion to presynaptic active zone membrane	BP	1	GRIK5,SYT1,STX2,SYT9,SNAP23,STX1A,RAB3A,SNAP29,CPLX1,STX1B,STX4,SNAPIN,STXBP1,SNAP47	grey	VSMC_M10
GO:0099500	0.06	0.98	14	19	vesicle fusion to plasma membrane	BP	1	GRIK5,SYT1,STX2,SYT9,SNAP23,STX1A,RAB3A,SNAP29,CPLX1,STX1B,STX4,SNAPIN,STXBP1,SNAP47	grey	VSMC_M10
GO:0042417	0.06	0.98	17	24	dopamine metabolic process	BP	1	SNCAIP,PRKN,GPR37,SLC1A1,DDC,LRTOMT,AP000812.5,NR4A2,SLC6A3,TGFB2,COMT,PNKD,GCH1,ITGAM,CHRNB2,ABAT,PARK7	grey	VSMC_M10
GO:0045637	0.06	0.96	91	152	regulation of myeloid cell differentiation	BP	1	NME1,HSPA1B,BRD1,IL5,TRIB1,MYC,TOB2,MAPK14,HSF1,ZNF16,RBFOX2,CDK6,ROR2,SMAP1,HOXA7,MTURN,CNOT4,TLR4,FOXO3,POU4F1,ACVR2A,JAG1,NCKAP1L,FOXP1,MITF,PRKDC,IRF7,TRAF6,ACVR1B,CAMK4,PIK3R1,FBXW7,MEF2C,PTK2B,TESC,RIPK1,LDB1,RAB7B,SLC9B2,GPR137B,PIAS3,ACIN1,TCTA,HCLS1,UBASH3B,CIB1,ARNT,THPO,ZBTB46,CREB1,WDR61,ESRRA,GPR137,FBN1,STAT3,STAT5B,LEO1,INHA,TFE3,MED1,HOXB8,KAT7,FOS,HAX1,GPR68,RCOR1,CD74,PPARGC1B,EVI2B,PTPN2,JUN,ATP6AP1,MIR222,MIR125B1,PRMT6,FSTL3,ANKRD54,MAFB,FADD,CASP8,CA2,BGLAP,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H4D,FAM210B,LIF,CEBPB,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0016559	0.06	0.99	7	8	peroxisome fission	BP	1	DNM1L,PEX11B,PEX19,FIS1,SEC16B,PEX11G,PEX11A	grey	VSMC_M10
GO:0006812	0.06	0.95	446	796	cation transport	BP	1	VPS4B,SLC39A5,NEDD4L,STAC3,CYP27B1,ATP5MGL,NIPAL2,MAPK8IP2,SLC12A2,KCNV1,PRRT1,PRKN,SLC22A4,CALHM4,TSPO,SMDT1,BAK1,CATSPER3,KLHL3,MCHR1,PKD2L2,KCNK9,MAPK15,KCNJ4,PLA2G6,SLC39A4,ATP6V1F,MFSD3,CHRNA3,TRPM6,STEAP2,CNGA1,SLC41A2,TMEM63B,SLC1A1,WNK2,CNNM4,TSPAN13,PRKCE,ATP6V1E2,KCNQ4,IBTK,SHANK1,SLC4A4,AQP1,SLC1A4,SLC31A2,BSPRY,SLC13A4,ATP6V1C2,HECW1,KEL,UCP1,ATG5,TRPM4,OSR1,PGRMC2,MFSD4B,SPHK2,KCNJ14,GRIN2D,TRPC3,SLC8A2,COMMD3,PANX1,HEPHL1,ATP7B,KCNRG,CACNB2,ANO10,SLC39A12,ATP6V0E2,ASIC3,STAC,ATP6V0B,STEAP3,ATP1A3,CCT8L2,OXSR1,TMEM163,ATP5F1C,SCN5A,SCN1A,SLC25A38,SEC14L1,SLC24A3,GPD1L,SLC20A2,SLC4A7,SLC38A10,SYT1,CACNB4,EFHB,RYR1,NALCN,SLC6A15,SLC25A15,SLC23A2,PRNP,TAF7,DIAPH1,P2RX2,TMCO3,GAS6,HPX,RASA3,COX7A1,SLC7A1,SLC25A26,SYT9,COMMD9,SLC38A9,MICU3,KCNIP3,SLC5A8,ATP6V1H,COX4I2,CYB5A,SLMAP,SLC43A1,ATP5F1A,GLRX,P2RX3,TRPC4AP,CHRM5,SLC9A9,RYR3,ORAI1,MEF2C,ASIC1,TMBIM6,P2RX7,HVCN1,KCNH3,PTK2B,SLC39A13,KCNJ11,SLC33A1,SERINC5,TPCN1,SLC8B1,HOMER1,IFNGR2,VDR,STC1,SLC25A37,OPA1,SLC48A1,KCNJ3,SLC38A4,SLC38A2,F2R,SLC38A1,TESC,SLC40A1,ANO6,SLC6A2,ZDHHC13,SLC10A6,COX15,KCNK15,CUTC,ABCC2,KCNE2,PKD2,NIPA1,CASQ2,KCNJ15,MCUR1,CNTN1,DTNBP1,SLC12A5,KCNIP2,RYR2,SYT8,FAM173B,GRM2,ATP6V1B2,PM20D1,SLC41A1,COX6B1,SLC4A10,SFXN2,TRPM1,CALHM2,CALHM1,PKP2,DNM1L,SLC6A3,SIK1,LCK,SLC2A10,PPP3CA,SLC38A11,HECW2,KCNJ2,SLC38A3,SLC9B1,SLC12A7,TRPV4,SLC9B2,ADRA2A,SLC	grey	VSMC_M10
GO:0008045	0.06	0.98	17	24	motor neuron axon guidance	BP	1	PLXNA4,RAC2,HOXA2,MYCBP2,KIF5C,SEMA3A,SLIT1,ALCAM,SEMA3F,EPHA4,NTN1,RNF165,LHX1,NTN3,PLXNA3,NOG,CHN1	grey	VSMC_M10
GO:0007274	0.06	0.98	15	21	neuromuscular synaptic transmission	BP	1	STAC3,CHRNA3,FCHSD2,FCHSD1,P2RX2,P2RX3,ERC2,ADARB1,RAB3A,CHRM1,CHRNB1,CHRNB2,DTNA,STXBP1,CHRNB4	grey	VSMC_M10
GO:0051259	0.06	0.95	103	174	protein complex oligomerization	BP	1	MIP,SHMT2,CPSF6,STK3,KCNV1,HSD17B8,CBY1,PRPH2,GNMT,TRPM6,NINJ1,CHMP2A,PNPT1,TRPM4,SSBP1,VSTM5,KCNRG,KCTD2,KCTD21,AQP11,HGSNAT,TMEM173,SYT1,RYR1,PRNP,ATL2,APIP,KCTD6,KCTD15,CBR4,P2RX3,RYR3,TMEM120B,ASIC1,USP16,HOMER1,OPA1,GLS,CUTC,PKD2,STK4,SYCP1,TWNK,TRPM1,CALHM1,DNM1L,ALDH1A3,KCNJ2,KCTD18,OXA1L,KCNB1,KCNG1,TIFA,HSCB,SLC9A1,OSBPL2,UPB1,EHD1,MPP2,ATL1,MICU1,MCU,CRTC1,TRPM7,KCNA1,KCND1,ROM1,MAT1A,ZBTB1,FARSB,HSD17B10,CARD11,ALDH1A2,KCTD13,THG1L,CRTC2,EVL,ACACA,CD74,SHMT1,RNF135,TNFAIP1,TRPV1,KCTD5,ABCA3,PKD1,KCNC4,LRRC8A,ZNHIT6,BCL10,KCTD19,CRYZ,LRRC8D,NOL3,VASP,BEND3,CLDN1,KCTD1,KCNA6,IKZF4,CLYBL,TRMT61B,KCNG2	grey	VSMC_M10
GO:0000959	0.06	0.97	29	44	mitochondrial RNA metabolic process	BP	1	TFB1M,MTERF1,LRPPRC,MTO1,PNPT1,TRIT1,C6orf203,FOXO3,FASTK,TRNT1,TWNK,WARS2,RPUSD4,YARS2,TARS2,TFAM,FASTKD1,KIAA0391,SUPV3L1,DARS2,TRMT5,HSD17B10,EARS2,PPARGC1B,METTL4,TEFM,SLC25A33,TRMT10C,TRMT61B	grey	VSMC_M10

GO:0033630	0.06	0.98	12	16	positive regulation of cell adhesion mediated by integrin	BP	1	PODXL,IFT74,FERMT1,RAC3,NCKAP1L,RET,TGFB2,CIB1,PTPN6,CCL5,PIEZO1,LIF	grey	VSMC_M10
GO:0072017	0.06	0.99	8	10	distal tubule development	BP	1	KLHL3,TFAP2B,POU3F3,JAG1,PAX8,PKD2,PAX2,PKD1	grey	VSMC_M10
GO:0001912	0.06	0.97	17	24	positive regulation of leukocyte mediated cytotoxicity	BP	1	CD226,STX7,HLA-DRA,NECTIN2,PVR,SLC22A13,RASGRP1,F2RL1,CADM1,IL12A,LAG3,STAT5B,ITGAM,VAV1,NOS2,AP1G1,FADD	grey	VSMC_M10
GO:0050433	0.06	0.97	22	32	regulation of catecholamine secretion	BP	1	PRKN,SYT1,SYT9,ADRA2B,P2RY1,DTNBP1,SYT8,GRM2,ADRA2A,KCNB1,GRK2,AGT,STX1A,ADRA2C,RAB3A,PINK1,SYT7,SYT11,CHRNB2,ABAT,CHGA,CRH	grey	VSMC_M10
GO:0006814	0.06	0.95	95	161	sodium ion transport	BP	1	NEDD4L,SLC12A2,SLC22A4,CATSPER3,KLHL3,WNK2,CNNM4,PRKCE,SLC4A4,SLC13A4,HECW1,TRPM4,OSR1,MFSD4B,SLC8A2,COMMD3,ASIC3,ATP1A3,SCN5A,SCN1A,SLC24A3,GPD1L,SLC20A2,SLC4A7,SLC38A10,NALCN,SLC6A15,SLC23A2,COMMD9,SLC5A8,SLMAP,GLRX,SLC9A9,ASIC1,P2RX7,TPCN1,SLC8B1,SLC38A4,SLC38A2,SLC38A1,TESC,ANO6,SLC6A2,SLC10A6,PKD2,CNTN1,SLC41A1,SLC4A10,PKP2,SLC6A3,SIK1,SLC38A11,HECW2,SLC38A3,SLC9B1,SLC9B2,SCN2A,SHROOM2,SLC9A8,KCNK1,SCN7A,KLHL24,ATP1A2,SLC9A1,SCN4B,DLG1,SLC9A7,ATP1B1,NDUFA9,SLC3A2,ASIC4,SLC38A6,WNK3,ATP1B2,SLC5A2,HCN3,CACNA1G,SLC5A11,DNM2,SCNN1B,SLC6A7,ASIC2,SLC9A6,CACNA1H,SLC9A5,MIR24-1,DMD,SLC22A5,SLC6A19,FGF11,SCN2B,NETO2,YWHAH,HCN4,NKX2-5	grey	VSMC_M10
GO:0007601	0.07	0.96	74	123	visual perception	BP	1	RDH5,MIP,EYA4,OPN1SW,GUCA1B,PRPH2,GRM8,RORB,CNGA1,CLIC5,CNNM4,CLDN19,EPAS1,RIMS1,PPT1,GJA10,TULP2,BBS7,MYO3A,EML2,OPA3,CACNB2,CRYGN,ZNF513,MYO7A,MKKS,FSCN2,PDE6G,KERA,LUM,ATXN7,CEP250,CCDC66,ADGRV1,KIFC3,OPA1,IMPG2,PAX2,SLC4A10,TRPM1,CABP1,PDE6D,RRH,LRIT3,CRYBA4,NRL,EYA3,MYO3B,BBS1,OAT,PDE6H,HMCN1,CDH23,ROM1,CLN8,DHRS3,GUCY2D,CHRNB2,LCTL,CLN6,MYO9A,UNC119,SLC45A2,PITPNA,GNAT2,LAMC3,HSF4,CRYZ,REEP6,DRAM2,LRAT,AOC2,BBS10,DNAJC19	grey	VSMC_M10
GO:0007611	0.07	0.95	107	183	learning or memory	BP	1	MAPK8IP2,PRRT1,PRKN,AGER,SYNGAP1,NTRK2,PLA2G6,BTBD9,SRF,TTBK1,KIT,SLC1A1,ADGRF1,BRSK1,DNAH11,SHANK1,PPT1,PTN,EGFR,SLC7A11,NTF4,PRKAR2B,ADCY3,SLC8A2,B4GALT2,PLCB1,PRNP,DDHD2,ARL6IP5,PLK2,GPI,CAMK4,CASP3,MEF2C,ASIC1,CUX2,MME,EIF2AK4,SYNJ1,AMFR,NQO2,SLC12A5,ATXN1,BDNF,SORCS3,SCN2A,NLGN4Y,KRAS,ADNP,AGT,ATP1A2,NFATC4,KCNK2,NPAS4,NTSR1,YTHDF1,FZD9,CREB1,MAPT,C1QL1,EIF4EBP2,COMT,TNR,NRXN2,KCNK4,BCHE,CRTC1,HTT,PPP3CB,NPTX2,MAPK1,TMOD2,DLG4,SLC2A4,THRA,CLN8,RGS14,PSEN1,SYT11,ITGA3,NLGN3,FOS,AC138894.1,CHRNB2,LDLR,GPRASP2,BHLHB9,STRA6,GM2A,INSR,IFT20,JUN,AFF2,PRKCZ,MECP2,ABCA7,JPH3,LHX8,ATXN1L,CNTN2,POMK,CRH,GPR88,NRXN3,CEBPB,MAP1A,FOXO6	grey	VSMC_M10
GO:0030004	0.07	0.96	50	81	cellular monovalent inorganic cation homeostasis	BP	1	NEDD4L,SLC12A2,TFAP2B,SLC4A4,PPT1,RAB7A,ATP6V0E2,LACC1,SLC4A2,AQP11,ATP1A3,SLC4A7,TMEM106B,MAFG,ATP6V1H,TM9SF4,IL1A,SLC9A9,HVCN1,SLC4A10,KCNJ2,SLC9B1,TMEM9,TCIRG1,SLC9A8,SLAMF8,AGT,ATP1A2,SLC9A1,CLIC4,SLC11A1,SLC9A7,ATP6V0A1,ATP1B1,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP1B2,MAPK3,AC138894.1,CLN6,SNAPIN,C7,TMEM199,SLC9A6,ATP6AP1,SLC9A5,CA2,RAB39A	grey	VSMC_M10
GO:0042157	0.07	0.95	68	111	lipoprotein metabolic process	BP	1	LRP1,ATG12,APOM,ZDHHC14,PPARA,GPAA1,ZDHHC21,APOL4,APOL6,ABHD17B,CWH43,TMEM246,PIGF,PPT1,ATG5,APOB,APOC1,PGAP2,LYPLA1,ZDHHC20,PIGU,ATG10,GOLGA7B,ZDHHC13,PIGT,GPLD1,PGAP1,ZDHHC23,LYPLAL1,ZDHHC6,RABL3,ATG16L1,PIGM,HHAT,ZDHHC18,PIGV,ZDHHC24,PIGX,GLUL,PIGZ,APOLD1,APOD,OLR1,NMT1,ZDHHC8,PIGC,PPM1A,ZDHHC4,WIPI2,PGAP3,PIGH,ZDHHC15,LDLR,PIGL,MPPE1,ABHD17A,ZDHHC12,ZDHHC1,ZDHHC11,ABHD10,PEMT,IRGM,ABHD17C,PYURF,LYPLA2,PIGB,PIGA,MAP6D1	grey	VSMC_M10
GO:0060294	0.07	0.96	43	68	cilium movement involved in cell motility	BP	1	UBE2B,CATSPER3,LRRC6,CFAP69,DNAJA1,DNAH11,CABS1,ARMC2,APOB,ADCY3,RSPH6A,TTC21A,TTLL3,MKKS,ING2,WDR66,CFAP20,DNAH1,PLTP,DNAH5,DPCD,ROPN1L,NEURL1,CFAP43,SLC9B1,SLC9B2,CFAP46,INTS13,CFAP45,ENO4,TSSK4,CELF3,CATSPER2,SORD,TTC12,SPAG16,MNS1,TEKT3,SPEF2,CATSPERD,TPGS1,WDR63,CCSAP	grey	VSMC_M10
GO:0046467	0.07	0.95	73	120	membrane lipid biosynthetic process	BP	1	KDSR,ORMDL2,B4GALNT1,A4GALT,PLA2G6,GPAA1,HACD4,LARGE1,CWH43,SPTLC1,TMEM246,PIGF,SMPD2,AGK,SPHK2,PRKD2,ACER3,ELOVL1,SPTLC3,PGAP2,SIRT3,ELOVL7,ASAH1,PIGU,ST8SIA4,ORMDL1,PIGT,A3GALT2,PGAP1,ST8SIA2,SGMS2,ALDH3B2,B3GALT1,B3GNT5,CERS6,PIGM,HACD2,CERS2,PIGV,PIGX,GAL3ST3,PIGZ,PPM1L,GAL3ST4,PIGC,SMPD4,SGMS1,SCCPDH,CLN8,PGAP3,DEGS1,PIGH,ALOXE3,HACD3,ST8SIA5,PIGL,MPPE1,P2RX1,GBGT1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,CYP4F22,ABCA8,ELOVL3,PEMT,ACER2,PYURF,PIGB,B4GALT3,PIGA,SGPP1,ST8SIA6	grey	VSMC_M10
GO:0086016	0.07	0.99	6	7	AV node cell action potential	BP	1	TRPM4,CACNB2,SCN5A,RYR2,SCN4B,CACNA1G	grey	VSMC_M10
GO:0086027	0.07	0.99	6	7	AV node cell to bundle of His cell signaling	BP	1	TRPM4,CACNB2,SCN5A,RYR2,SCN4B,CACNA1G	grey	VSMC_M10

GO:0006520	0.07	0.95	132	224	cellular amino acid metabolic process	BP	1	GLS2,SHMT2,ALDH8A1,MARS,GFPT2,TPH2,RIDA,DPYS,ATF4,PYCR3,PSAT1,GPT,MTAP,CARNMT1,GNMT,ALDH1A1,SLC25A13,AASDH,PPAT,HMGCLL1,RIMKLA,DDC,IL4I1,QRSL1,SLC7A11,DDO,BCAT2,DHFR,GAD2,HPDL,HNMT,IDO2,IDO1,HARS,HARS2,CARS2,AMDHD1,LARS,NR1H4,APIP,CSAD,THNSL2,AHCY,GSS,MCCC2,MSRA,GMPS,SERINC5,ENOPH1,SDSL,IVD,HOGA1,NIT2,BPHL,ASNSD1,HIBCH,GLS,ACAD8,WARS2,MTRR,PM20D1,SIRT4,GATC,ASL,ALDH5A1,AZIN2,MTR,YARS2,CBSL,SLC7A7,HGD,AMT,MCCC1,TARS2,DALRD3,CTPS2,ACADSB,OAT,HMGCL,GLUL,SMS,UPB1,PLOD3,FAH,CPS1,MTHFS,LARS2,PRODH,COMT,DARS2,AASDHPPT,NAT8L,HDC,ALDH4A1,MAT1A,ASRGL1,FARSB,HSD17B10,SLC25A44,ALDH6A1,GCDH,AC138894.1,GSTZ1,EARS2,CRYM,SHMT1,ADSSL1,ENOSF1,NOS2,PIPOX,ABAT,MECP2,LRRC47,PARK7,SARDH,ASS1,GCSH,KYAT1,KARS,AARS,KYAT3,MIR21,MARS2,MTHFD2L,PEMT,HIBADH,SLC25A21,GGT5,AUH,HYKK,PHGDH,PCBD2	grey	VSMC_M10
GO:0050884	0.07	0.98	10	13	neuromuscular process controlling posture	BP	1	POU4F1,TCF15,TMEM150C,ADARB1,PNKD,CNTNAP1,GCH1,CLN8,MECP2,FXN	grey	VSMC_M10
GO:1902953	0.07	1.00	4	4	positive regulation of ER to Golgi vesicle-mediated transport	BP	1	PGAP1,SORL1,STX18,TBC1D20	grey	VSMC_M10
GO:0050771	0.07	0.96	33	52	negative regulation of axonogenesis	BP	1	SEMA6A,FSTL4,SYNGAP1,SEMA4D,SEMA4C,RTN4,RUFY3,EPHA7,SEMA3D,SPART,SEMA3A,ULK1,RYK,SEMA4F,SEMA3G,SPP1,SEMA4G,KIAA0319,SEMA3F,WNT3,SEMA6D,TNR,PSEN1,SEMA4A,TRIM46,NTN1,CDK5R1,DAB1,ARHGAP4,PLXNA3,THY1,WNT5A,EFNB3	grey	VSMC_M10
GO:0034331	0.07	0.97	19	28	cell junction maintenance	BP	1	SYNGAP1,MTSS1,WHRN,ERC2,KIFC3,PLEKHA7,F2RL1,F2R,BSN,DLG1,C1QL1,RAB3A,NLGN2,CSF1R,CAMSAP3,SDF4,CLDN1,INAVA,PARD6A	grey	VSMC_M10
GO:0006400	0.07	0.95	53	85	tRNA modification	BP	1	ADAT2,TRMU,TRMT11,C9orf64,MTO1,ELP1,PUS10,TRIT1,DUS4L,NSUN6,THUMPD3,DPH3,TRMT6,THUMPD2,TRMT9B,ELP4,ELP3,BCDIN3D,TPRKB,NSUN3,OSGEPL1,CDKAL1,RPUSD4,TRMT10A,QTRT2,TYW1B,TYW5,TRUB1,DALRD3,LCMT2,METTL8,ELP6,METTL2B,TRMT1L,ALKBH8,TRMT5,HSD17B10,MTFMT,ALKBH1,THG1L,QTRT1,ELP2,THUMPD1,METTL6,PUSL1,AARS,DUS2,CTU1,TRMT10B,TRMT61A,TRMT10C,TRMT61B,TYW3	grey	VSMC_M10
GO:0003010	0.07	1.00	4	4	voluntary skeletal muscle contraction	BP	1	SYNM,MYH7,ACTN3,ATP2A1	grey	VSMC_M10
GO:0014721	0.07	1.00	4	4	twitch skeletal muscle contraction	BP	1	SYNM,MYH7,ACTN3,ATP2A1	grey	VSMC_M10
GO:0035562	0.07	0.99	6	7	negative regulation of chromatin binding	BP	1	FBH1,BTAF1,PPP3CA,NFATC4,MEPCE,ZNF304	grey	VSMC_M10
GO:0021936	0.07	0.98	8	10	regulation of cerebellar granule cell precursor proliferation	BP	1	GLI1,SMO,GLI2,ZNF423,EGF,LHX1,GPR37L1,CEND1	grey	VSMC_M10
GO:0030317	0.07	0.96	37	58	flagellated sperm motility	BP	1	UBE2B,CATSPER3,LRRC6,CFAP69,DNAJA1,DNAH11,CABS1,ARMC2,APOB,ADCY3,TTC21A,TTLL3,ING2,WDR66,DNAH1,PLTP,DNAH5,DPCD,ROPN1L,NEURL1,CFAP43,SLC9B1,SLC9B2,INTS13,CFAP45,ENO4,TSSK4,CELF3,CATSPER2,SORD,TTC12,SPAG16,MNS1,TEKT3,SPEF2,CATSPERD,TPGS1	grey	VSMC_M10
GO:0097722	0.07	0.96	37	58	sperm motility	BP	1	UBE2B,CATSPER3,LRRC6,CFAP69,DNAJA1,DNAH11,CABS1,ARMC2,APOB,ADCY3,TTC21A,TTLL3,ING2,WDR66,DNAH1,PLTP,DNAH5,DPCD,ROPN1L,NEURL1,CFAP43,SLC9B1,SLC9B2,INTS13,CFAP45,ENO4,TSSK4,CELF3,CATSPER2,SORD,TTC12,SPAG16,MNS1,TEKT3,SPEF2,CATSPERD,TPGS1	grey	VSMC_M10
GO:0071806	0.07	0.96	35	54	protein transmembrane transport	BP	1	TIMM21,PEX7,TOMM22,PEX6,PEX1,TRAM2,SEC61B,SEC61G,DNAJC15,SEC62,AKT2,TIMM50,PEX2,PEX16,LONP2,C2CD5,MCL1,TOMM40L,GRPEL1,AP4M1,ZFAND2B,TIMM17B,PEX26,PEX14,TMED10,PAM16,PEX10,HSPA5,BLOC1S3,TIMM23B,TRAM1L1,GRPEL2,PEX12,DNAJC19,SEC61A2	grey	VSMC_M10
GO:0048934	0.07	0.98	8	10	peripheral nervous system neuron differentiation	BP	1	ONECUT2,NTRK2,ETV1,POU4F1,HAND2,RUNX3,ISL1,ISL2	grey	VSMC_M10
GO:0048935	0.07	0.98	8	10	peripheral nervous system neuron development	BP	1	ONECUT2,NTRK2,ETV1,POU4F1,HAND2,RUNX3,ISL1,ISL2	grey	VSMC_M10
GO:0060033	0.07	0.98	8	10	anatomical structure regression	BP	1	GLI1,SMAD5,GLI2,FLT1,AMHR2,SLC6A3,BMPR1A,CD248	grey	VSMC_M10
GO:0050432	0.07	0.96	23	34	catecholamine secretion	BP	1	PRKN,LY6E,SYT1,SYT9,ADRA2B,P2RY1,DTNBP1,SYT8,GRM2,ADRA2A,KCNB1,GRK2,AGT,STX1A,ADRA2C,RAB3A,PINK1,SYT7,SYT11,CHRNB2,ABAT,CHGA,CRH	grey	VSMC_M10
GO:0010586	0.07	0.97	16	23	miRNA metabolic process	BP	1	AGO2,TUT7,XPO5,PNPT1,TUT4,BCDIN3D,TENT2,TENT4B,DIS3L2,RC3H1,ZSWIM8,PARN,DROSHA,AGO4,HRAS,RC3H2	grey	VSMC_M10
GO:0042053	0.07	0.98	10	13	regulation of dopamine metabolic process	BP	1	PRKN,GPR37,NR4A2,SLC6A3,COMT,PNKD,ITGAM,CHRNB2,ABAT,PARK7	grey	VSMC_M10
GO:0042069	0.07	0.98	10	13	regulation of catecholamine metabolic process	BP	1	PRKN,GPR37,NR4A2,SLC6A3,COMT,PNKD,ITGAM,CHRNB2,ABAT,PARK7	grey	VSMC_M10
GO:0072289	0.07	1.00	4	4	metanephric nephron tubule formation	BP	1	SOX9,PAX8,PAX2,SOX8	grey	VSMC_M10
GO:0060896	0.07	0.99	6	7	neural plate pattern specification	BP	1	PTCH1,FUZ,BMPR1A,CELSR2,NOG,C2CD3	grey	VSMC_M10
GO:0015874	0.08	0.98	12	16	norepinephrine transport	BP	1	ADRA2B,P2RY1,SLC6A2,SLC6A3,ADRA2A,KCNB1,AGT,STX1A,ADRA2C,ACTB,SLC29A4,CRH	grey	VSMC_M10
GO:0015837	0.08	0.96	37	58	amine transport	BP	1	SLC12A2,PRKN,CHRNA3,DDC,SYT1,ARL6IP5,SYT9,ADRA2B,SLC43A1,P2RY1,DTNBP1,SYT8,GRM2,SLC38A3,ADRA2A,KCNB1,GRK2,RHCG,AGT,ACE2,ATP1A2,PER2,STX1A,NTSR1,ADRA2C,RAB3A,PINK1,ARL6IP1,SYT7,PSEN1,SYT11,CHRNB2,ABAT,STXBP1,CHGA,RGS4,CRH	grey	VSMC_M10
GO:0021938	0.08	1.00	4	4	smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell proliferation	BP	1	GLI1,SMO,GLI2,ZNF423	grey	VSMC_M10
GO:0046726	0.08	1.00	4	4	positive regulation by virus of viral protein levels in host cell	BP	1	STAU1,DDB1,HACD3,TBC1D20	grey	VSMC_M10
GO:0006904	0.08	0.96	21	31	vesicle docking involved in exocytosis	BP	1	EXOC4,SCFD2,PLEK,PPFIA3,RAB10,SYTL2,RALB,SNPH,VPS18,KCNB1,STX1A,BLOC1S6,RAB3A,RAB8A,RAB15,STX1B,RAB8B,RAB3D,STXBP2,STXBP1,VAMP3	grey	VSMC_M10

GO:0042391	0.08	0.94	173	302	regulation of membrane potential	BP	1	NEDD4L,HEBP2,MAPK8IP2,RIMS2,PRKN,TSPO,BAK1,KCNK9,NTRK2,CHRNA3,CHRNA5,GABRA1,SLC25A27,CLDN19,RIMS1,ABCB5,RIMS3,SHANK1,SLC4A4,MYH14,PTN,GRIK2,BVES,CLCN1,TRPM4,DLD,WISP3,GRIN2D,MTMR2,SLC8A2,SLC26A5,CACNB2,GRIK5,ATP1A3,PRDX3,SCN5A,SCN1A,AKT2,GPD1L,CHRNA6,NALCN,DCN,PANK2,SPART,P2RX2,RNF122,CLIC1,ARL6IP5,FAM19A4,RGS7BP,PXK,SLMAP,GLRX,P2RX3,MEF2C,ASIC1,P2RX7,KCNH3,CUX2,PTK2B,KCNJ11,SLC8B1,KCNJ3,TBX5,KCNK15,KCNE2,DSP,CASQ2,KCNIP2,RYR2,PKP2,PPP3CA,KCNJ2,IGSF11,PPA2,SCN2A,SSH1,MFN1,PIAS3,KCNB1,KCNK1,SCN7A,OPRD1,ANK2,GPER1,GRIK4,IFI6,ATP1A2,SLC9A1,KCNK2,STX1A,TMEM25,NPAS4,NTSR1,SCN4B,CNIH2,NOS1AP,FZD9,DLG1,PPP2R3C,KCNK7,HTR3B,MAPT,STOX1,BCO2,MPP2,KCNK4,CRTC1,CNTNAP1,PINK1,MUL1,ATP1B1,KCNA1,KCNMA1,CHRM1,KCNH4,SLC4A3,DLG4,PARP1,NLGN2,CHRNB1,CNIH3,ATP1B2,STX1B,PSEN1,HCN3,NLGN3,CACNA1G,AC138894.1,CHRNB2,CALM1,DSG2,ASIC2,SEZ6,JUN,ABAT,FMR1,GABRE,GABRA3,GNA15,TRPV1,P2RX1,PRKCZ,MECP2,RNF207,CACNA1H,PARK7,SLC25A33,PIEZO1,PIP5KL1,WWP2,KCNK3,UBB,DMD,GPR35,CHRNB4,MLLT11,CHRNA10,CHRNG,GRID2,BNIP3L,KCNH2,SCN2B,KCNK5,RGS4,GPR88,POPDC2,INSYN1,YWHAH,KCNJ8,GNA14,HCN4,KCNMB4	grey	VSMC_M10
GO:0015747	0.08	1.00	4	4	urate transport	BP	1	SLC22A13,ABCC4,ABCG2,SLC2A9	grey	VSMC_M10
GO:0035907	0.08	0.98	8	10	dorsal aorta development	BP	1	SRF,NKX3-1,BMPR1A,RBPJ,NGFR,ENG,ACVRL1,HEY2	grey	VSMC_M10
GO:0035249	0.08	0.96	36	57	synaptic transmission, glutamatergic	BP	1	MAPK8IP2,PRKN,GRM4,PLA2G6,GRM8,ROR2,SLC1A4,DGKI,EGFR,GRIK2,NAPA,GRIK5,NAPB,SYT1,MEF2C,PTK2B,HOMER1,GRM2,DISC1,GRIK4,ATP1A2,CNIH2,GLUL,TNR,NLGN2,CNIH3,PSEN1,NLGN3,AC138894.1,CCL2,P2RX1,TPRG1L,STXBP1,GRID2,CACNG7,CACNG5	grey	VSMC_M10
GO:0060467	0.08	1.00	4	4	negative regulation of fertilization	BP	1	MYH9,NLRP5,PLAT,ZP2	grey	VSMC_M10
GO:0060468	0.08	1.00	4	4	prevention of polyspermy	BP	1	MYH9,NLRP5,PLAT,ZP2	grey	VSMC_M10
GO:0009452	0.08	0.99	6	7	7-methylguanosine RNA capping	BP	1	RNMT,CMTR1,RNGTT,TGS1,NCBP3,CMTR2	grey	VSMC_M10
GO:0036260	0.08	0.99	6	7	RNA capping	BP	1	RNMT,CMTR1,RNGTT,TGS1,NCBP3,CMTR2	grey	VSMC_M10
GO:0035864	0.08	0.98	8	10	response to potassium ion	BP	1	SLC12A2,HSF1,SLC26A5,DLG2,CARF,DLG4,CACNA1H,ADAMTS13	grey	VSMC_M10
GO:0031034	0.08	1.00	4	4	myosin filament assembly	BP	1	RAP1GDS1,TTN,TCAP,MYH11	grey	VSMC_M10
GO:0006577	0.08	0.98	10	13	amino-acid betaine metabolic process	BP	1	CPT1B,ALDH7A1,SLC22A4,CROT,CHDH,CPT1A,POR,ACADL,TMLHE,ACADM	grey	VSMC_M10
GO:0002857	0.08	1.00	4	4	positive regulation of natural killer cell mediated immune response to tumor cell	BP	1	CD226,NECTIN2,PVR,IL12A	grey	VSMC_M10
GO:0002860	0.08	1.00	4	4	positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	BP	1	CD226,NECTIN2,PVR,IL12A	grey	VSMC_M10
GO:1901656	0.08	1.00	4	4	glycoside transport	BP	1	SLC5A2,SLC50A1,ABCC3,RALBP1	grey	VSMC_M10
GO:0032324	0.08	1.00	4	4	molybdopterin cofactor biosynthetic process	BP	1	MOCS1,GPHN,MOCOS,MOCS2	grey	VSMC_M10
GO:0042269	0.08	0.97	13	18	regulation of natural killer cell mediated cytotoxicity	BP	1	CD226,NECTIN2,PVR,RASGRP1,CADM1,IL12A,LAG3,STAT5B,VAV1,CRK,AP1G1,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0090461	0.08	1.00	4	4	glutamate homeostasis	BP	1	SLC1A1,SLC7A11,GLS,GRM2	grey	VSMC_M10
GO:0002834	0.08	0.98	8	10	regulation of response to tumor cell	BP	1	CD226,IL4I1,NECTIN2,PVR,SLC22A13,IL12A,FBXO38,HAVCR2	grey	VSMC_M10
GO:0002837	0.08	0.98	8	10	regulation of immune response to tumor cell	BP	1	CD226,IL4I1,NECTIN2,PVR,SLC22A13,IL12A,FBXO38,HAVCR2	grey	VSMC_M10
GO:0045576	0.08	0.96	31	48	mast cell activation	BP	1	CD226,ENPP3,RAC2,KIT,SPHK2,CD300LF,NECTIN2,GAB2,UNC13D,FER,RASGRP1,SNAP23,LAT2,FGR,CBL,SNX4,PTGDR,C12orf4,LCP2,LAT,IL4R,S100A13,BTK,STXBP2,PDPK1,FOXF1,STXBP1,S100A12,HAVCR1,CHGA,TSLP	grey	VSMC_M10
GO:0009235	0.08	0.98	8	10	cobalamin metabolic process	BP	1	MMACHC,MMAA,MTR,MMAB,ABCD4,CD320,MMADHC,CLYBL	grey	VSMC_M10
GO:2001225	0.08	1.00	4	4	regulation of chloride transport	BP	1	ATP8B1,ABCB1,PRNP,GABRE	grey	VSMC_M10
GO:0060750	0.08	1.00	4	4	epithelial cell proliferation involved in mammary gland duct elongation	BP	1	ESR1,AREG,MED1,WNT5A	grey	VSMC_M10
GO:0060751	0.08	1.00	4	4	branch elongation involved in mammary gland duct branching	BP	1	ESR1,AREG,MED1,WNT5A	grey	VSMC_M10
GO:0033198	0.08	0.97	16	23	response to ATP	BP	1	TRPM4,TRPC3,PANX1,P2RX2,P2RX3,RYR3,P2RX7,P2RY1,KCNJ11,SSH1,DGKQ,PKLR,TAF1,TRPV1,P2RX1,PDXP	grey	VSMC_M10
GO:0050915	0.08	1.00	4	4	sensory perception of sour taste	BP	1	ASIC3,ASIC1,ASIC2,PKD1L3	grey	VSMC_M10
GO:1990809	0.08	1.00	4	4	endoplasmic reticulum tubular network membrane organization	BP	1	RTN4,ATL2,ATL1,ARL6IP1	grey	VSMC_M10
GO:0019433	0.08	0.97	13	18	triglyceride catabolic process	BP	1	PNPLA3,PNPLA5,APOB,FGF21,ABHD5,LIPE,DDHD2,GPLD1,SORL1,CPS1,DAGLB,LIPC,PNPLA4	grey	VSMC_M10
GO:0060075	0.08	0.99	6	7	regulation of resting membrane potential	BP	1	ATP1A3,NALCN,KCNJ2,KCNK1,PSEN1,KCNK5	grey	VSMC_M10
GO:0015809	0.08	0.98	8	10	arginine transport	BP	1	SLC7A1,SLC38A9,AGT,SLC11A1,PQLC2,SLC7A3,AC138894.1,SLC25A29	grey	VSMC_M10
GO:0098953	0.08	1.00	4	4	receptor diffusion trapping	BP	1	DLG4,GPHN,CACNG7,CACNG5	grey	VSMC_M10
GO:0098970	0.08	1.00	4	4	postsynaptic neurotransmitter receptor diffusion trapping	BP	1	DLG4,GPHN,CACNG7,CACNG5	grey	VSMC_M10
GO:0099628	0.08	1.00	4	4	neurotransmitter receptor diffusion trapping	BP	1	DLG4,GPHN,CACNG7,CACNG5	grey	VSMC_M10
GO:0015858	0.08	1.00	4	4	nucleoside transport	BP	1	SLC29A2,SLC29A3,SLC29A4,RSC1A1	grey	VSMC_M10
GO:1904177	0.08	1.00	4	4	regulation of adipose tissue development	BP	1	TRPM4,SORL1,KLF7,PLA2G16	grey	VSMC_M10
GO:0036444	0.08	0.98	10	13	calcium import into the mitochondrion	BP	1	SMDT1,MICU3,OPA1,MCUR1,MCUB,MICU1,MCU,PSEN2,SLC25A23,MAIP1	grey	VSMC_M10
GO:0070973	0.08	0.99	6	7	protein localization to endoplasmic reticulum exit site	BP	1	BCAP29,GBF1,MIA3,SEC16B,BCAP31,SEC16A	grey	VSMC_M10
GO:0014060	0.08	1.00	4	4	regulation of epinephrine secretion	BP	1	ADRA2B,ADRA2A,ADRA2C,CRH	grey	VSMC_M10
GO:0032811	0.08	1.00	4	4	negative regulation of epinephrine secretion	BP	1	ADRA2B,ADRA2A,ADRA2C,CRH	grey	VSMC_M10

GO:0035194	0.08	0.94	69	112	post-transcriptional gene silencing by RNA	BP	1	ZC3H10,ESR1,CNOT6,MOV10L1,AGO2,TNRC6B,TUT7,XPO5,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,TNRC6C,CLP1,BCDIN3D,CNOT1,CELF1,EIF4E2,RIPK1,PPP3CA,TERT,AJUBA,DDX6,EIF4ENIF1,PRKRA,DDX3X,STAT3,MAP2K1,SMAD3,NRDE2,TNRC6A,CNOT8,NCOR1,DROSHA,FMR1,SPOUT1,MIRLET7A2,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR425,MIR125B1,MIR32,MIR22,MIR27B,MIR24-1,MIR7-1,MIR199A2,MIRLET7D,MIR27A,MIR23B,MIR365B,MIR25,MIR491,MIR24-2,MIRLET7A3,AGO4,MIR33B,MIR339,MIR125A,MIR99B,MIR940,MIR1249,MIR1180	grey	VSMC_M10
GO:1903706	0.08	0.93	149	258	regulation of hemopoiesis	BP	1	NME1,HSPA1B,BRD1,AGER,HLA-DRA,IL5,TCF7,XRCC6,TRIB1,MYC,TOB2,MAPK14,HSF1,ZNF16,RBFOX2,FBXO7,CDK6,ROR2,SMAP1,HOXA7,SLC46A2,MTURN,CNOT4,PTN,IL4I1,TLR4,IL15,FOXO3,CLPTM1,GLI2,FOXJ1,POU4F1,IL15RA,TGFBR2,ACVR2A,JAG1,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,TRAF6,SOX12,TOX,ZC3H8,ACVR1B,CAMK4,PIK3R1,FBXW7,MEF2C,TMEM131L,IL7,PTK2B,RASGRP1,RIPK2,AP3B1,TESC,RIPK1,SOX13,LDB1,RAB7B,SLC9B2,GPR137B,PIAS3,HLX,ACIN1,TCTA,HCLS1,UBASH3B,SLAMF8,CIB1,ARNT,THPO,CD28,RUNX3,ZBTB46,PPP2R3C,ADAM8,CREB1,DUSP10,BCL6,WDR61,VSIR,RC3H1,ESRRA,PTPN6,GPR137,FBN1,TNFSF18,LAG3,STAT3,STAT5B,LEO1,INHA,TFE3,FOXP3,ZBTB1,CARD11,MED1,TBX21,HOXB8,KAT7,FOS,ZBTB7B,HAX1,IL4R,GPR68,BTK,RCOR1,CD74,PPARGC1B,NKAP,EVI2B,IL7R,PTPN2,JUN,SOCS1,DROSHA,PRKCZ,ATP6AP1,MIR21,MIR222,MIR125B1,RHOA,PRMT6,FSTL3,ANKRD54,SOX4,MAFB,FADD,CD46,CASP8,CA2,BGLAP,HIST1H4B,HIST2H4A,HIST1H4H,FGL2,TNFSF9,HIST1H4D,FAM210B,LIF,ZFP36L2,CEBPB,HIST1H4A,IL17D,HIST1H4F,RC3H2	grey	VSMC_M10
GO:0006578	0.08	1.00	4	4	amino-acid betaine biosynthetic process	BP	1	ALDH7A1,CHDH,TMLHE,ACADM	grey	VSMC_M10
GO:0072177	0.08	0.99	6	7	mesonephric duct development	BP	1	OSR1,WNT11,PKD2,LHX1,GPC3,PKD1	grey	VSMC_M10
GO:1905616	0.08	0.99	6	7	regulation of miRNA mediated inhibition of translation	BP	1	AGO2,TNRC6B,EIF4E2,DDX6,EIF4ENIF1,STAT3	grey	VSMC_M10
GO:1905618	0.08	0.99	6	7	positive regulation of miRNA mediated inhibition of translation	BP	1	AGO2,TNRC6B,EIF4E2,DDX6,EIF4ENIF1,STAT3	grey	VSMC_M10
GO:0097201	0.08	0.98	8	10	negative regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	NCK2,SIRT2,TMBIM6,HIF1AN,BAG3,DNAJB1,JUN,IMPACT	grey	VSMC_M10
GO:1900747	0.08	0.98	8	10	negative regulation of vascular endothelial growth factor signaling pathway	BP	1	SEMA6A,SPRY2,DCN,PIK3CB,IL12A,DAB2IP,MIR199A1,CADM4	grey	VSMC_M10
GO:0001773	0.08	0.97	13	18	myeloid dendritic cell activation	BP	1	TGFBR2,TRAF6,CAMK4,ITGB6,BATF2,LTBR,RBPJ,PSEN1,DOCK2,BATF,DHRS2,HAVCR2,BATF3	grey	VSMC_M10
GO:0061739	0.08	1.00	4	4	protein lipidation involved in autophagosome assembly	BP	1	ATG5,ATG16L1,WIPI2,IRGM	grey	VSMC_M10
GO:0032730	0.08	1.00	4	4	positive regulation of interleukin-1 alpha production	BP	1	PANX1,IL16,S100A13,ISL1	grey	VSMC_M10
GO:0070291	0.08	1.00	4	4	N-acylethanolamine metabolic process	BP	1	NAPEPLD,GDPD3,GDPD1,GDE1	grey	VSMC_M10
GO:0019230	0.08	1.00	4	4	proprioception	BP	1	POU4F1,TMEM150C,MECP2,FXN	grey	VSMC_M10
GO:1904505	0.08	1.00	4	4	regulation of telomere maintenance in response to DNA damage	BP	1	ERCC1,XRCC1,RTEL1,ERCC4	grey	VSMC_M10
GO:1904506	0.08	1.00	4	4	negative regulation of telomere maintenance in response to DNA damage	BP	1	ERCC1,XRCC1,RTEL1,ERCC4	grey	VSMC_M10
GO:0051952	0.08	0.95	35	55	regulation of amine transport	BP	1	SLC12A2,PRKN,CHRNA3,SYT1,ARL6IP5,SYT9,ADRA2B,SLC43A1,P2RY1,DTNBP1,SYT8,GRM2,SLC38A3,ADRA2A,KCNB1,GRK2,AGT,ACE2,ATP1A2,PER2,STX1A,NTSR1,ADRA2C,RAB3A,PINK1,ARL6IP1,SYT7,PSEN1,SYT11,CHRNB2,ABAT,STXBP1,CHGA,RGS4,CRH	grey	VSMC_M10
GO:0006063	0.08	1.00	4	4	uronic acid metabolic process	BP	1	PRKCE,AKR1A1,XYLB,ABHD10	grey	VSMC_M10
GO:0019585	0.08	1.00	4	4	glucuronate metabolic process	BP	1	PRKCE,AKR1A1,XYLB,ABHD10	grey	VSMC_M10
GO:0002084	0.09	0.98	8	10	protein depalmitoylation	BP	1	ABHD17B,PPT1,LYPLA1,LYPLAL1,ABHD17A,ABHD10,ABHD17C,LYPLA2	grey	VSMC_M10
GO:0006572	0.09	1.00	4	4	tyrosine catabolic process	BP	1	IL4I1,HGD,FAH,GSTZ1	grey	VSMC_M10
GO:0000964	0.09	1.00	4	4	mitochondrial RNA 5'-end processing	BP	1	PNPT1,KIAA0391,HSD17B10,TRMT10C	grey	VSMC_M10
GO:0002836	0.09	0.99	6	7	positive regulation of response to tumor cell	BP	1	CD226,NECTIN2,PVR,SLC22A13,IL12A,FBXO38	grey	VSMC_M10
GO:0002839	0.09	0.99	6	7	positive regulation of immune response to tumor cell	BP	1	CD226,NECTIN2,PVR,SLC22A13,IL12A,FBXO38	grey	VSMC_M10
GO:0002275	0.09	0.95	39	62	myeloid cell activation involved in immune response	BP	1	ENPP3,RAC2,KIT,PRKCE,SPHK2,GAB2,UNC13D,MYD88,NMI,FER,RASGRP1,DYSF,F2RL1,SNAP23,LAT2,FGR,CBL,SNX4,FCER1G,PTGDR,C12orf4,STX4,ITGAM,DOCK2,LAT,IL4R,S100A13,BTK,SCNN1B,STXBP2,PRAM1,TICAM1,DNASE1,PDPK1,FOXF1,KARS,STXBP1,CHGA,HAVCR2	grey	VSMC_M10
GO:0048570	0.09	0.99	6	7	notochord morphogenesis	BP	1	GLI1,GLI2,WNT11,EFNA1,NOG,WNT5A	grey	VSMC_M10
GO:0006844	0.09	1.00	4	4	acyl carnitine transport	BP	1	SLC25A20,SLC25A47,SLC25A45,SLC25A29	grey	VSMC_M10
GO:0051694	0.09	0.99	6	7	pointed-end actin filament capping	BP	1	LMOD2,TMOD1,LMOD3,LMOD1,TMOD4,TMOD2	grey	VSMC_M10
GO:0006548	0.09	1.00	4	4	histidine catabolic process	BP	1	CARNMT1,HNMT,AMDHD1,HDC	grey	VSMC_M10
GO:0018200	0.09	0.97	15	21	peptidyl-glutamic acid modification	BP	1	AGTPBP1,AGBL3,TTLL3,AGBL2,CFAP20,TTLL13P,TTLL4,PARP1,TTLL5,TPGS2,NAA10,TPGS1,TTLL11,TTLL7,FOLH1	grey	VSMC_M10
GO:0071651	0.09	1.00	4	4	positive regulation of chemokine (C-C motif) ligand 5 production	BP	1	MAVS,TRPV4,DDX3X,DEFB124	grey	VSMC_M10
GO:1903826	0.09	0.99	6	7	arginine transmembrane transport	BP	1	SLC7A1,SLC38A9,AGT,PQLC2,SLC7A3,SLC25A29	grey	VSMC_M10
GO:0006000	0.09	0.98	8	10	fructose metabolic process	BP	1	AKR1B1,KHK,GLYCTK,PFKFB2,PFKFB4,SORD,ALDOC,FBP2	grey	VSMC_M10
GO:0009744	0.09	1.00	4	4	response to sucrose	BP	1	PNPLA3,ERCC1,KHK,CALCRL	grey	VSMC_M10
GO:0034285	0.09	1.00	4	4	response to disaccharide	BP	1	PNPLA3,ERCC1,KHK,CALCRL	grey	VSMC_M10

GO:0008033	0.09	0.94	71	117	tRNA processing	BP	1	ADAT2,RPP21,TRMU,TRMT11,C9orf64,MTO1,TSEN34,ELP1,PUS10,TRIT1,DUS4L,NSUN6,THUMPD3,DPH3,TRMT6,TRNT1,THUMPD2,TRMT9B,ELP4,POP4,CLP1,ELP3,BCDIN3D,TPRKB,NSUN3,OSGEPL1,RPP40,CDKAL1,POP5,RPUSD4,TRMT10A,ZBTB8OS,QTRT2,TYW1B,TYW5,TRUB1,RTRAF,DALRD3,LCMT2,METTL8,ELP6,METTL2B,KIAA0391,TRMT1L,POP7,TRPT1,ALKBH8,TRMT5,HSD17B10,MTFMT,ALKBH1,THG1L,QTRT1,ELP2,THUMPD1,METTL6,PUSL1,POLR3K,KARS,ADAT1,AARS,DUS2,CTU1,RPP38,TRMT10B,TP53RK,TRMT61A,TRMT10C,RPP30,TRMT61B,TYW3	grey	VSMC_M10
GO:0036017	0.09	1.00	4	4	response to erythropoietin	BP	1	KIT,CD40,EPOR,MT1X	grey	VSMC_M10
GO:0036018	0.09	1.00	4	4	cellular response to erythropoietin	BP	1	KIT,CD40,EPOR,MT1X	grey	VSMC_M10
GO:1903146	0.09	0.96	20	30	regulation of autophagy of mitochondrion	BP	1	PRKN,TSPO,FBXO7,USP36,FBXW7,HTRA2,CSNK2A2,DNM1L,USP30,FZD5,HTT,PINK1,ATP13A2,VPS13D,VPS13C,HAX1,SREBF1,PARK7,BNIP3L,TIGAR	grey	VSMC_M10
GO:0042538	0.09	0.98	8	10	hyperosmotic salinity response	BP	1	XRCC6,AKR1B1,TRPV4,XRCC5,MICU1,SLC25A23,MT-CYB,CLDN1	grey	VSMC_M10
GO:0090207	0.09	0.96	19	28	regulation of triglyceride metabolic process	BP	1	MBOAT7,NR1H2,LPIN1,FGF21,ABHD5,PANK2,FBXW7,NR1H3,FITM2,GPLD1,SIK1,SORL1,GNB3,SLC27A1,DAGLB,LDLR,SREBF1,C3,CNEP1R1	grey	VSMC_M10
GO:0001754	0.09	0.96	20	30	eye photoreceptor cell differentiation	BP	1	AGTPBP1,NTRK2,RORB,RDH13,PTN,SOX9,MYO7A,DZANK1,FSCN2,CEP290,USH1C,RPGRIP1L,NKD1,NRL,STAT3,ROM1,SOX8,OLFM3,THY1,DIO3	grey	VSMC_M10
GO:0015886	0.09	0.98	8	10	heme transport	BP	1	PGRMC2,HPX,SLC48A1,ABCC5,ABCB6,FLVCR2,SLC46A1,C1orf194	grey	VSMC_M10
GO:0033091	0.09	1.00	4	4	positive regulation of immature T cell proliferation	BP	1	BMI1,IL1A,RIPK2,FOXP3	grey	VSMC_M10
GO:0006552	0.09	0.99	6	7	leucine catabolic process	BP	1	HMGCLL1,MCCC2,IVD,MCCC1,HMGCL,AUH	grey	VSMC_M10
GO:1905395	0.09	1.00	4	4	response to flavonoid	BP	1	DNM1L,IP6K2,FIS1,NQO1	grey	VSMC_M10
GO:0002923	0.09	0.99	6	7	regulation of humoral immune response mediated by circulating immunoglobulin	BP	1	FOXJ1,HPX,NOD2,PTPN6,CD46,FCER2	grey	VSMC_M10
GO:0071609	0.09	0.99	6	7	chemokine (C-C motif) ligand 5 production	BP	1	MAVS,OAS3,TRPV4,DDX3X,MUL1,DEFB124	grey	VSMC_M10
GO:0071649	0.09	0.99	6	7	regulation of chemokine (C-C motif) ligand 5 production	BP	1	MAVS,OAS3,TRPV4,DDX3X,MUL1,DEFB124	grey	VSMC_M10
GO:0045656	0.09	0.99	6	7	negative regulation of monocyte differentiation	BP	1	MYC,CDK6,HOXA7,ZBTB46,GPR68,MIR125B1	grey	VSMC_M10
GO:0140029	0.09	0.94	41	66	exocytic process	BP	1	EXOC4,SCFD2,PLEK,PPFIA3,NAPA,RAB10,SYTL2,RALB,GRIK5,NAPB,SYT1,STX2,SYT9,SNPH,ERC2,EXOC6B,SYNJ1,VPS18,DMTN,SNAP23,KCNB1,STX1A,SNX4,BLOC1S6,RAB3A,SNAP29,RAB8A,RAB15,CPLX1,STX1B,STX4,PSEN1,RAB8B,RAB3D,SNAPIN,BTK,STXBP2,P2RX1,STXBP1,SNAP47,VAMP3	grey	VSMC_M10
GO:0015850	0.09	0.93	105	179	organic hydroxy compound transport	BP	1	VPS4B,ATP8B1,LRP1,SLC16A7,APOM,SERAC1,PRKN,TSPO,PTCH1,LY6E,MAPK15,TTC39B,ABCG5,ABCG8,AQP1,NR1H2,APOB,PIP4K2A,APOC1,ASIC3,AQP11,TSKU,ABCC4,C1QTNF1,SYT1,SYT9,ADRA2B,SLC5A8,SOAT2,CYP7A1,OSBP,CHRM5,LIMA1,P2RY1,NR1H3,SLC6A2,SLC10A6,ABCC2,SPP1,PLTP,DTNBP1,SLC2A13,SYT8,GRM2,SLC6A3,ABCA5,ADRA2A,KCNB1,EGF,GRAMD1B,GRK2,ABCB11,AGT,ABCG4,SLCO1A2,SLCO1C1,OSBPL2,STX1A,OSBP2,SLC16A1,STARD5,OSBPL6,SOAT1,OSBPL1A,ZDHHC8,ABCA12,LPCAT3,ADRA2C,MFSD10,RAB3A,PINK1,ACTB,SLC29A4,SYT7,GPS2,LIPC,ANXA2,OSBPL7,NAXE,SYT11,CHRNB2,ABCC3,SLC5A11,LDLR,STRA6,NPC1,EMB,RALBP1,ABAT,P2RX1,ABCA3,ABCA7,PARK7,RXRA,CEL,ABCD3,VPS4A,MIR27B,MIR27A,CHGA,ABCA8,MIR33B,LDLRAP1,CRH,STARD4	grey	VSMC_M10
GO:0042531	0.09	0.95	26	40	positive regulation of tyrosine phosphorylation of STAT protein	BP	1	HSF1,KIT,IL15,HDAC2,PIBF1,HPX,OSBP,ARL2BP,CD40,HDAC1,HCLS1,PARP9,PARP14,OSM,IL12A,TNFSF18,FGFR3,CTF1,IL6R,CCL5,CSF1R,ISL1,GHR,CNTF,LIF,TSLP	grey	VSMC_M10
GO:0014061	0.09	0.98	8	10	regulation of norepinephrine secretion	BP	1	ADRA2B,P2RY1,ADRA2A,KCNB1,AGT,STX1A,ADRA2C,CRH	grey	VSMC_M10
GO:0042182	0.09	0.98	8	10	ketone catabolic process	BP	1	ALDH8A1,NQO2,CBR3,PNKD,OXCT1,PARK7,KYAT1,KYAT3	grey	VSMC_M10
GO:0060292	0.09	0.96	14	20	long-term synaptic depression	BP	1	PRRT1,AGER,PICK1,SRF,PLK2,ABHD6,PTK2B,SORCS3,KCNB1,MAPT,CD38,FMR1,STXBP1,GRID2	grey	VSMC_M10
GO:0010984	0.09	0.97	12	16	regulation of lipoprotein particle clearance	BP	1	FGF21,APOC1,NR1H4,MYLIP,GPLD1,LRPAP1,ANXA2,MIR199A1,MIR27B,MIR27A,MIR33B,LDLRAP1	grey	VSMC_M10
GO:0099159	0.09	0.99	6	7	regulation of modification of postsynaptic structure	BP	1	CTTNBP2,CHMP2B,TIAM1,CYFIP1,CAMKV,RHOA	grey	VSMC_M10
GO:0050890	0.09	0.93	123	214	cognition	BP	1	MAPK8IP2,PRRT1,PRKN,AGER,HLA-DRA,SYNGAP1,NTRK2,PLA2G6,BTBD9,SRF,TTBK1,KIT,SLC1A1,ADGRF1,BRSK1,DNAH11,SHANK1,PPT1,SLC1A4,PTN,EGFR,SOBP,SLC7A11,NTF4,PRKAR2B,ADCY3,SLC8A2,C5AR1,B4GALT2,METTL23,PLCB1,PRNP,DDHD2,ARL6IP5,PLK2,FAM107A,GPI,CAMK4,CASP3,CHMP2B,MEF2C,ASIC1,CUX2,MME,EIF2AK4,SYNJ1,AMFR,NQO2,CBR3,DOP1B,CYFIP1,SLC12A5,ATXN1,BDNF,SORCS3,LINS1,SCN2A,NLGN4Y,KRAS,ADNP,AGT,ATP1A2,NFATC4,KCNK2,NPAS4,NTSR1,YTHDF1,FZD9,NSUN5,GPR155,CREB1,MAPT,C1QL1,EIF4EBP2,COMT,TNR,NRXN2,KCNK4,BCHE,CRTC1,HTT,PPP3CB,NPTX2,MAPK1,CHRM1,TMOD2,DLG4,SHROOM4,SLC2A4,THRA,CLN8,RGS14,PSEN1,SYT11,ITGA3,NLGN3,FOS,AC138894.1,CHRNB2,LDLR,GPRASP2,BHLHB9,STRA6,GM2A,INSR,IFT20,JUN,AFF2,PRKCZ,MECP2,ABCA7,JPH3,LHX8,ATXN1L,CNTN2,RP9,POMK,CRH,GPR88,NRXN3,CEBPB,MAP1A,FOXO6	grey	VSMC_M10
GO:0046503	0.09	0.95	30	47	glycerolipid catabolic process	BP	1	ABHD16A,PNPLA3,PNPLA5,PLA2G6,APOB,FGF21,FAAH,ABHD5,APOC1,LIPE,DDHD2,ABHD6,PLA2G4B,GPLD1,ABHD2,SORL1,PLA2G4A,CPS1,ABHD12B,SMPD4,DAGLB,LIPC,GDPD3,LDLR,GDPD1,GDE1,PNPLA6,PLA2G15,PNPLA4,LYPLA2	grey	VSMC_M10
GO:0036135	0.09	1.00	4	4	Schwann cell migration	BP	1	LRP1,TIAM1,CERS2,MIR222	grey	VSMC_M10
GO:1900147	0.09	1.00	4	4	regulation of Schwann cell migration	BP	1	LRP1,TIAM1,CERS2,MIR222	grey	VSMC_M10
GO:0008535	0.09	0.96	15	21	respiratory chain complex IV assembly	BP	1	TIMM21,COA5,COX15,COX17,OXA1L,COA6,COA3,BCS1L,COX10,MT-CO3,COX16,APOPT1,COX14,COA1,SCO1	grey	VSMC_M10

GO:0016079	0.10	0.94	48	79	synaptic vesicle exocytosis	BP	1	RIMS2,CHRNA5,APBA1,RIMS1,RIMS3,PPFIA3,NAPA,CACNB2,GRIK5,NAPB,SYT1,RAB5A,STX2,SYT9,SNPH,ERC2,P2RY1,SYNJ1,VPS18,DTNBP1,SYT8,DNM1L,ADRA2A,SNAP23,STX1A,BACE1,DNAJC5,CSPG5,RAP1B,BLOC1S6,CASK,RAB3A,SYN1,SNAP29,SYT7,CPLX1,STX1B,STX4,PSEN1,CALM1,SNAPIN,PRKCB,FMR1,PIP5K1C,P2RX1,STXBP1,SNAP47,DOC2B	grey	VSMC_M10
GO:0048875	0.10	0.97	9	12	chemical homeostasis within a tissue	BP	1	EPAS1,HOMER1,ITGB6,LPCAT1,HOMER2,CTSH,ABCA12,ABCA3,OAS1	grey	VSMC_M10
GO:0006501	0.10	0.99	6	7	C-terminal protein lipidation	BP	1	ATG12,ATG5,GPLD1,ATG16L1,WIPI2,IRGM	grey	VSMC_M10
GO:0009066	0.10	0.95	28	43	aspartate family amino acid metabolic process	BP	1	RIDA,ATF4,MTAP,GNMT,SLC25A13,DDO,APIP,MSRA,ENOPH1,SDSL,NIT2,ASNSD1,MTRR,MTR,SMS,PLOD3,AASDHPPT,NAT8L,MAT1A,ASRGL1,CRYM,ADSSL1,PIPOX,ASS1,MTHFD2L,SLC25A21,HYKK,PHGDH	grey	VSMC_M10
GO:0045670	0.10	0.95	27	42	regulation of osteoclast differentiation	BP	1	TOB2,TLR4,POU4F1,MITF,TRAF6,CAMK4,PIK3R1,FBXW7,SLC9B2,GPR137B,PIAS3,TCTA,UBASH3B,CREB1,ESRRA,GPR137,FBN1,TFE3,FOS,GPR68,PPARGC1B,ATP6AP1,FSTL3,MAFB,CA2,BGLAP,CEBPB	grey	VSMC_M10
GO:0090141	0.10	0.96	14	20	positive regulation of mitochondrial fission	BP	1	PRKN,VPS35,DDHD2,DCN,DNM1L,FIS1,MCU,DDHD1,PINK1,MUL1,MIEF2,RALBP1,RALA,MIEF1	grey	VSMC_M10
GO:0006183	0.10	0.99	6	7	GTP biosynthetic process	BP	1	NME1,IMPDH1,NME4,NME7,NME3,NME6	grey	VSMC_M10
GO:0045742	0.10	0.95	20	30	positive regulation of epidermal growth factor receptor signaling pathway	BP	1	EPGN,AREG,TGFA,NEU3,HBEGF,PDE6G,HIP1R,FBXW7,NEURL1,ADRA2A,NCF1,EGF,GPER1,DGKD,AGT,CBL,PDE6H,HAP1,MIR29A,EREG	grey	VSMC_M10
GO:0006767	0.10	0.94	30	47	water-soluble vitamin metabolic process	BP	1	SHMT2,PSAT1,DHFR,AKR1A1,MMACHC,BTD,SLC23A2,PANK2,MMAA,MTHFD2,MTRR,MTR,MMAB,THTPA,MCCC1,MTHFS,AASDHPPT,PNPO,ABCD4,SHMT1,CD320,SLC46A1,TKTL1,TPK1,MTHFD2L,SLC25A32,MMADHC,NNMT,CLYBL,PDXP	grey	VSMC_M10
GO:0021983	0.10	0.96	17	25	pituitary gland development	BP	1	GLI1,PITX1,GLI2,SALL1,SRD5A1,SLC6A3,SOX2,CREB1,WNT4,TBX19,BMPR1A,RBPJ,ALDH1A2,ISL1,NOG,WNT5A,POU3F2	grey	VSMC_M10
GO:0007259	0.10	0.93	59	98	receptor signaling pathway via JAK-STAT	BP	1	IL5,AKR1B1,HSF1,OCIAD1,KIT,PPP2R1A,IL15,HDAC2,PIBF1,NMI,HPX,RET,FER,PIGU,OSBP,PTK2B,ARL2BP,F2R,PKD2,CD40,HDAC1,MST1,EGF,HCLS1,PARP9,PARP14,AGT,OSM,IL10RA,IL12A,TNFSF18,FGFR3,STAT3,STAT5B,CTF1,IL6R,STAT2,ELP2,CCL5,CSF1R,CCL2,CDK5R1,ISL1,SUZ12,GHR,JAK1,NLK,PTPN2,SOCS1,DAB1,DOT1L,PKD1,CNTF,MIR125A,STAMBP,GADD45A,LIF,TSLP,LEPROT	grey	VSMC_M10
GO:0070509	0.10	0.94	36	58	calcium ion import	BP	1	SMDT1,SPHK2,SLC8A2,CACNB2,PRNP,MICU3,ORAI1,HOMER1,STC1,OPA1,PKD2,MCUR1,TRPV4,MCUB,EGF,PLPP4,CASK,MICU1,MCU,PSEN2,WNK3,FAM155B,CACNA1A,CACNA1G,ATP2A1,TRPV2,CCL2,SLC25A23,MAIP1,TRPV3,TRPV1,P2RX1,CACNA1B,CACNA1H,ATP2C2,CRH	grey	VSMC_M10
GO:0050885	0.10	0.95	22	34	neuromuscular process controlling balance	BP	1	RBFOX2,SHANK1,USH1G,MYO7A,POU4F1,RAC3,NBN,USH1C,ALDH1A3,GIGYF2,CDH23,TNR,CNTNAP1,DLG4,NLGN2,CLN8,AC138894.1,IGDCC3,GM2A,JPH3,AARS,GPR88	grey	VSMC_M10
GO:0006629	0.10	0.91	545	982	lipid metabolic process	BP	1	RDH5,KDSR,ORMDL2,APOF,ATP8B1,RDH16,HSD17B4,LRP1,ALDH8A1,PIP4K2C,PEX7,B4GALNT1,AGAP2,CYP27B1,AVIL,AIG1,LTC4S,ESR1,CPT1B,ABHD16A,SYNJ2,SERAC1,SLC27A6,ALG12,CYP21A2,TNXB,AGPAT4,AGPAT1,QKI,PPARA,ACSL6,SLC22A4,PNPLA3,PNPLA5,SULT4A1,TSPO,MCAT,HSD17B8,A4GALT,ECHDC1,PTK2,HSD17B3,AKR1B1,GOLM1,MAPK14,PLA2G6,GPAA1,TTC39B,HACD4,APOL4,TEK,LARGE1,ALDH1A1,CROT,CWH43,KIT,PLPP6,SRD5A3,SPTLC1,AASDH,HINT2,LIPT1,HMGCLL1,INPP4A,ADH5,CAT,ALG2,PLPPR1,TMEM246,TMEM86B,PRKCE,PIGF,RDH13,MBOAT7,PPP2R1A,FPR2,ETFB,JAZF1,PPT1,PLEK,NR1H2,MBOAT2,DGKI,EGFR,LPIN1,INPP4B,DKKL1,MGST2,SMPD2,DLD,FIG4,LDAH,APOB,AGK,HSD17B14,FGF21,PRKAR2B,SPHK2,TPRA1,MTMR2,RAB7A,PIP4K2A,NAPEPLD,ALG11,FAAH,PRKD2,HADHA,EBP,SELENOI,EBPL,SOX9,OPA3,ABHD5,RUBCNL,CUBN,APOC1,GLB1,DNAJC15,LIPE,ECHDC3,PRKAG2,GDPD4,ACOX1,TAMM41,SLC22A13,PIBF1,ITPKC,CYGB,ACER3,TSKU,ELOVL1,ALK,AKT2,GDPD5,PIP4P1,NEU3,MTMR14,SPTLC3,SIRT2,NR1D2,PLCB1,PLCL2,PGAP2,CRLS1,HACL1,CDS2,PLPP5,DDHD2,PANK2,PDK1,SIRT3,FLT1,NR1H4,MTMR7,TRIB3,LYPLA1,SDR16C5,ACOXL,SOAT2,CYP7A1,NSMAF,ELOVL7,ASAH1,CYP7B1,ACOX2,ABHD6,CEBPA,THNSL2,CBR4,PIGU,PIK3CB,OSBP,PITPNM2,ST8SIA4,PIK3R1,TMEM150A,GK5,RETSAT,DKK3,ATP5F1A,HPGD,PLCE1,CHRM5,MTMR9,FBXW7,LIMA1,SORBS1,GPD1,PEX2,HTRA2,EPHX2,CYP2R1,SLA2,PTK2B,ETFDH,ACOT12,PLCH1,PRKAG1,NR1H3,SERINC5,SYNJ1,COQ2,IVD,LPIN3,CDS1,ST3GAL6,FITM2,ORMDL1,ECI2,COL4A3BP,HSD17B13,ITPKA,SPP1,ERLIN1,PIGT,PLA2G4B,ACAD8,ADTRP,NOD2,PRMT	grey	VSMC_M10
GO:0099563	0.10	0.96	14	20	modification of synaptic structure	BP	1	CTTNBP2,DLGAP3,WASF1,CHMP2B,TIAM1,CYFIP1,CAMKV,STAU1,GRIPAP1,EPHA4,AC138894.1,MYH10,ARHGAP44,RHOA	grey	VSMC_M10
GO:0002708	0.10	0.94	38	61	positive regulation of lymphocyte mediated immunity	BP	1	CD226,STX7,HLA-DRA,EXOSC3,MSH2,RSAD2,HMCES,NECTIN2,PVR,MLH1,SLC22A13,PAXIP1,SHLD1,HPX,TRAF6,RASGRP1,NOD2,CD40,DENND1B,CD28,CADM1,FZD5,IL12A,LAG3,STAT5B,FOXP3,ZBTB1,SHLD2,TBX21,BTK,FBXO38,VAV1,C3,PRKCZ,TRAF2,AP1G1,FADD,FCER2	grey	VSMC_M10
GO:0048745	0.10	0.96	12	17	smooth muscle tissue development	BP	1	PTCH1,SMO,ZFAND5,SRF,OSR1,SOX9,PKD2,EFEMP2,DLG1,STRA6,ENG,SIX1	grey	VSMC_M10
GO:0034308	0.10	0.94	38	61	primary alcohol metabolic process	BP	1	RDH5,RDH16,AKR1B1,ALDH1A1,ADH5,RDH13,NAPEPLD,AKR1A1,LIPE,SDR16C5,CBR4,RETSAT,DKK3,GPD1,ALDH1A3,CHKA,ALDH3B2,THTPA,DHRS9,PECR,WNT4,DHRS3,RDH11,ALDH1A2,DGKQ,GDPD3,GDPD1,SCNN1B,GDE1,TKTL1,CACNA1H,PARK7,ALDH2,TPK1,PNPLA4,LRAT,RDH14,ADH4	grey	VSMC_M10
GO:0001914	0.10	0.97	11	15	regulation of T cell mediated cytotoxicity	BP	1	STX7,AGER,HLA-DRA,NECTIN2,PVR,SLC22A13,NCKAP1L,IL12A,PPP3CB,IL7R,FADD	grey	VSMC_M10
GO:0038183	0.10	0.97	9	12	bile acid signaling pathway	BP	1	ABCG5,ABCG8,ABCC4,NR1H4,CYP7A1,VDR,ABCC2,CIDEB,GPBAR1	grey	VSMC_M10

GO:0098661	0.10	0.94	32	51	inorganic anion transmembrane transport	BP	1	SLC26A10,SLC12A2,GABRA1,SLC1A1,SLC13A4,CLCN1,SLC26A5,SLC25A30,SLC20A2,PRNP,ANO4,ANO6,SLC12A5,ADAMTS8,SLC37A1,SLC12A7,SLC37A2,SLC37A4,SLC12A8,XPR1,SLC12A9,ANKH,SLC25A11,SLC26A1,SLC26A2,SLC25A14,GABRE,GABRA3,CLCN7,LRRC8A,SLC12A4,SLC25A3	grey	VSMC_M10
GO:0015698	0.10	0.93	67	113	inorganic anion transport	BP	1	ATP8B1,SLC26A10,SLC12A2,TSPO,ABCB1,ABCC10,GABRA1,CLIC5,SLC1A1,SLC4A4,SLC1A4,SLC13A4,CLCN1,SFRP4,SLC26A5,ANO10,SLC25A30,SLC4A2,CLNS1A,CCT8L2,ABCC4,SLC20A2,SLC4A7,PRNP,CLIC1,ANO4,MFSD5,ANO6,CRY2,ABCC2,SLC12A5,ADAMTS8,SLC4A10,SLC37A1,SLC12A7,SLC37A2,CLCN4,ABCC5,IP6K2,TMEM206,SLC37A4,SLC12A8,XPR1,CLIC4,SLC12A9,ANKH,SLC11A1,ANO8,SLC4A3,SLC25A11,TTYH3,SLC26A1,ABCC3,NMUR2,SLC26A2,LRRC8E,SLC25A14,GABRE,GABRA3,CLCN7,LRRC8A,CLCA2,SLC12A4,SLC25A3,LRRC8D,LRRC8B,CEBPB	grey	VSMC_M10
GO:0046328	0.10	0.93	62	104	regulation of JNK cascade	BP	1	PHLPP1,MAP3K5,STK3,MAPK8IP2,PRKN,AGER,GADD45G,KLHL31,DNAJA1,FKTN,MTURN,NOD1,EGFR,TLR4,TRAF1,SDCBP,MYD88,ZMYND11,PLCB1,SEMA3A,SH3RF2,MFHAS1,TRAF6,EPHB1,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,TRPV4,PDCD4,NCF1,TRAF5,FZD7,MAGI3,MAP3K11,AIDA,DUSP10,MBIP,MEN1,MAP4K2,DUSP19,PINK1,LTBR,MINK1,GPS2,TAOK2,NCOR1,TRAF3,TAOK1,SERPINF2,MAPK8IP3,TRAF2,MARVELD3,DAB2IP,ZNF622,WNT5A,GADD45A,DUSP22,HRAS	grey	VSMC_M10
GO:0031063	0.10	0.95	18	27	regulation of histone deacetylation	BP	1	C6orf89,SPHK2,PRKD2,TADA3,SDR16C5,ING2,BCL6,PINK1,KDM5A,FOXP3,AKAP8L,AKAP8,JDP2,ZBTB7B,SREBF1,SKI,PRMT6,SAP30BP	grey	VSMC_M10
GO:2000353	0.10	0.96	11	15	positive regulation of endothelial cell apoptotic process	BP	1	FOXO3,ANO6,CD40,PDCD4,GPER1,ITGA4,CCL2,MIR24-1,MIR125A,CD248,RGCC	grey	VSMC_M10
GO:0034381	0.10	0.95	21	31	plasma lipoprotein particle clearance	BP	1	APOM,APOB,FGF21,APOC1,NR1H4,SOAT2,MYLIP,GPLD1,SOAT1,EHD1,LRPAP1,LIPA,LIPC,ANXA2,LDLR,MIR199A1,MIR27B,MIR27A,MIR33B,NCEH1,LDLRAP1	grey	VSMC_M10
GO:0017004	0.10	0.95	21	31	cytochrome complex assembly	BP	1	TIMM21,LYRM7,COA5,UQCC1,COX15,COX17,OXA1L,COA6,COA3,BCS1L,COX10,SLC25A33,CYBA,MT-CO3,COX16,C12orf73,APOPT1,COX14,COA1,UQCC2,SCO1	grey	VSMC_M10
GO:0010803	0.11	0.95	23	35	regulation of tumor necrosis factor-mediated signaling pathway	BP	1	TNFAIP3,HSPA1B,PRKN,TRIM32,IKBKB,GAS6,OTULIN,F2RL1,SPATA2,PELI3,SPPL2A,GPS2,PYDC1,PTPN2,PIAS4,SPPL2B,TRAF2,MIR27B,MIR24-1,NOL3,CASP8,CCDC3,HIST1H2BJ	grey	VSMC_M10
GO:0006641	0.11	0.93	43	70	triglyceride metabolic process	BP	1	TNXB,SLC22A4,PNPLA3,PNPLA5,CAT,MBOAT7,NR1H2,LPIN1,APOB,FGF21,ABHD5,APOC1,LIPE,DDHD2,PANK2,GK5,FBXW7,NR1H3,LPIN3,FITM2,GPLD1,SIK1,CPT1A,GPAM,SORL1,LPGAT1,MOGAT3,CPS1,GNB3,PLA2G16,SLC27A1,DAGLB,LIPC,APOBR,SEL1L,LDLR,SREBF1,LPIN2,C3,LMF1,PNPLA4,CNEP1R1,INSIG2	grey	VSMC_M10
GO:0006541	0.11	0.96	14	20	glutamine metabolic process	BP	1	GLS2,GFPT2,PPAT,GMPS,NIT2,ASNSD1,GLS,SIRT4,CTPS2,GLUL,CPS1,ADSSL1,MECP2,PHGDH	grey	VSMC_M10
GO:0016441	0.11	0.92	70	115	posttranscriptional gene silencing	BP	1	ZC3H10,ESR1,CNOT6,MOV10L1,AGO2,TNRC6B,TUT7,XPO5,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,TNRC6C,CLP1,BCDIN3D,CNOT1,CELF1,EIF4E2,RIPK1,PPP3CA,TERT,AJUBA,GIGYF2,DDX6,EIF4ENIF1,PRKRA,DDX3X,STAT3,MAP2K1,SMAD3,NRDE2,TNRC6A,CNOT8,NCOR1,DROSHA,FMR1,SPOUT1,MIRLET7A2,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR425,MIR125B1,MIR32,MIR22,MIR27B,MIR24-1,MIR7-1,MIR199A2,MIRLET7D,MIR27A,MIR23B,MIR365B,MIR25,MIR491,MIR24-2,MIRLET7A3,AGO4,MIR33B,MIR339,MIR125A,MIR99B,MIR940,MIR1249,MIR1180	grey	VSMC_M10
GO:1902548	0.11	0.97	9	12	negative regulation of cellular response to vascular endothelial growth factor stimulus	BP	1	SEMA6A,SPRY2,DCN,PIK3CB,IL12A,ADAMTS12,DAB2IP,MIR199A1,CADM4	grey	VSMC_M10
GO:0048002	0.11	0.95	20	30	antigen processing and presentation of peptide antigen	BP	1	HLA-DRA,HLA-DOB,TAP1,HLA-DMA,HLA-DPB1,IKBKB,TRAF6,MARCH8,IDE,ABCB9,ERAP1,MFSD6,FCER1G,PIKFYVE,SLC11A1,CTSV,TAPBPL,DNM2,CD74,ERAP2	grey	VSMC_M10
GO:0030534	0.11	0.93	54	90	adult behavior	BP	1	PRKN,PPARA,AGTPBP1,BTBD9,CHRNA3,CHRNA5,ADAM22,USP46,SLC1A1,TMOD1,SHANK1,PPT1,SLC7A11,NTF4,GRIN2D,HDAC2,ALK,MAFG,LGI4,PREX2,HTRA2,HOMER1,NR4A2,GRM2,GIGYF2,ZFHX2,OPRD1,ATP1A2,SPTBN2,NTSR1,EPS8,HOMER2,NRXN2,EPHA4,SDK1,CHRNB1,CLN8,HOXB8,NLGN3,CHRNB2,NPC1,SEZ6,DAB1,ABAT,MECP2,PARK7,TPGS1,TSC1,CNTN2,FADD,CEND1,FXN,NRXN3,EFNB3	grey	VSMC_M10
GO:1904862	0.11	0.98	7	9	inhibitory synapse assembly	BP	1	GABRA1,SEMA4D,NPAS4,NLGN2,LGI2,SEMA4A,WNT5A	grey	VSMC_M10
GO:0002097	0.11	0.96	14	20	tRNA wobble base modification	BP	1	ADAT2,TRMU,MTO1,ELP1,DPH3,TRMT9B,ELP4,ELP3,NSUN3,ELP6,ALKBH8,ALKBH1,ELP2,CTU1	grey	VSMC_M10
GO:0002761	0.11	0.93	52	86	regulation of myeloid leukocyte differentiation	BP	1	NME1,IL5,TRIB1,MYC,TOB2,HSF1,CDK6,ROR2,HOXA7,TLR4,POU4F1,FOXP1,MITF,IRF7,TRAF6,CAMK4,PIK3R1,FBXW7,TESC,RIPK1,SLC9B2,GPR137B,PIAS3,ACIN1,TCTA,HCLS1,UBASH3B,ZBTB46,CREB1,ESRRA,GPR137,FBN1,INHA,TFE3,FOS,HAX1,GPR68,CD74,PPARGC1B,EVI2B,PTPN2,JUN,ATP6AP1,MIR125B1,FSTL3,MAFB,FADD,CASP8,CA2,BGLAP,LIF,CEBPB	grey	VSMC_M10
GO:0060078	0.11	0.93	51	85	regulation of postsynaptic membrane potential	BP	1	MAPK8IP2,RIMS2,CHRNA3,CHRNA5,GABRA1,RIMS1,SHANK1,GRIK2,GRIN2D,MTMR2,SLC8A2,GRIK5,CHRNA6,P2RX2,RGS7BP,P2RX3,MEF2C,P2RX7,CUX2,PTK2B,PPP3CA,IGSF11,SSH1,GRIK4,STX1A,TMEM25,NPAS4,NTSR1,MPP2,KCNA1,CHRM1,DLG4,NLGN2,CHRNB1,STX1B,NLGN3,CHRNB2,SEZ6,ABAT,GABRE,GABRA3,TRPV1,P2RX1,PRKCZ,MECP2,CHRNB4,CHRNA10,CHRNG,GRID2,RGS4,INSYN1	grey	VSMC_M10

GO:0045639	0.11	0.93	47	77	positive regulation of myeloid cell differentiation	BP	1	HSPA1B,BRD1,IL5,TRIB1,MAPK14,HSF1,ZNF16,ROR2,SMAP1,MTURN,FOXO3,POU4F1,ACVR2A,JAG1,NCKAP1L,PRKDC,TRAF6,ACVR1B,TESC,RIPK1,RAB7B,SLC9B2,ACIN1,HCLS1,ARNT,THPO,CREB1,STAT3,STAT5B,MED1,KAT7,FOS,HAX1,GPR68,RCOR1,CD74,PPARGC1B,EVI2B,JUN,ATP6AP1,MIR222,ANKRD54,FADD,CASP8,CA2,FAM210B,LIF	grey	VSMC_M10
GO:0035640	0.11	0.96	12	17	exploration behavior	BP	1	PRKCE,SLC4A10,ATP1A2,ABL2,TNR,DLG4,NLGN2,ITGA3,ABAT,JPH3,DPP4,CRBN	grey	VSMC_M10
GO:0016578	0.11	0.95	15	22	histone deubiquitination	BP	1	USP15,USP49,SUPT3H,USP36,TAF10,ATXN7,ASXL1,USP16,SART3,USP21,ENY2,ATXN7L3,UIMC1,EPOP,BRCC3	grey	VSMC_M10
GO:0010958	0.11	0.97	9	12	regulation of amino acid import across plasma membrane	BP	1	ARL6IP5,SLC43A1,AGT,ACE2,ATP1A2,PER2,ARL6IP1,PSEN1,RGS4	grey	VSMC_M10
GO:1903789	0.11	0.97	9	12	regulation of amino acid transmembrane transport	BP	1	ARL6IP5,SLC43A1,AGT,ACE2,ATP1A2,PER2,ARL6IP1,PSEN1,RGS4	grey	VSMC_M10
GO:0009247	0.11	0.93	38	61	glycolipid biosynthetic process	BP	1	B4GALNT1,A4GALT,GPAA1,LARGE1,CWH43,TMEM246,PIGF,PGAP2,PIGU,ST8SIA4,PIGT,A3GALT2,PGAP1,ST8SIA2,B3GALT1,B3GNT5,PIGM,PIGV,PIGX,GAL3ST3,PIGZ,GAL3ST4,PIGC,SCCPDH,PGAP3,PIGH,ST8SIA5,PIGL,MPPE1,GBGT1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,PYURF,PIGB,B4GALT3,PIGA,ST8SIA6	grey	VSMC_M10
GO:0060831	0.11	0.97	9	12	smoothened signaling pathway involved in dorsal/ventral neural tube patterning	BP	1	TBC1D32,PTCH1,GLI2,SUFU,GORAB,GPR161,TULP3,WDR19,MKS1	grey	VSMC_M10
GO:0030301	0.11	0.93	47	77	cholesterol transport	BP	1	VPS4B,LRP1,APOM,SERAC1,TSPO,PTCH1,TTC39B,ABCG5,ABCG8,NR1H2,APOB,PIP4K2A,APOC1,TSKU,SOAT2,OSBP,LIMA1,NR1H3,PLTP,ABCA5,EGF,ABCG4,OSBPL2,STARD5,OSBPL6,SOAT1,ZDHHC8,ABCA12,LPCAT3,SYT7,GPS2,LIPC,ANXA2,NAXE,LDLR,NPC1,ABCA3,ABCA7,RXRA,CEL,VPS4A,MIR27B,MIR27A,ABCA8,MIR33B,LDLRAP1,STARD4	grey	VSMC_M10
GO:0018958	0.11	0.93	40	65	phenol-containing compound metabolic process	BP	1	TPH2,SNCAIP,PRKN,LY6E,AKR1B1,BTBD9,GPR37,SLC1A1,EPAS1,DDC,SLC7A11,LRTOMT,AP000812.5,PAX8,HAND2,RAPGEF2,NR4A2,OCA2,SRD5A1,SLC6A3,TGFB2,SLCO1C1,DUOX1,FAH,COMT,PNKD,GCH1,HDC,MED1,ITGAM,CITED1,CHRNB2,CRYM,SLC45A2,ABAT,PARK7,WNT5A,DIO3,AOC2,DIO2	grey	VSMC_M10
GO:0006264	0.11	0.97	9	12	mitochondrial DNA replication	BP	1	SSBP1,MGME1,PRIMPOL,TWNK,POLG2,POLG,LIG3,METTL4,DNAJA3	grey	VSMC_M10
GO:0009583	0.11	0.94	21	32	detection of light stimulus	BP	1	OPN1SW,PRPH2,CAMKMT,GJA10,TRPC3,PLEKHB1,CEP250,CCDC66,CDS1,PITPNM1,RRH,SAG,NMT1,GRK4,ROM1,GUCY2D,ASIC2,UNC119,GNAT2,REEP6,GPR88	grey	VSMC_M10
GO:0009713	0.11	0.97	9	12	catechol-containing compound biosynthetic process	BP	1	GPR37,DDC,HAND2,NR4A2,SLC6A3,TGFB2,GCH1,HDC,PARK7	grey	VSMC_M10
GO:0042423	0.11	0.97	9	12	catecholamine biosynthetic process	BP	1	GPR37,DDC,HAND2,NR4A2,SLC6A3,TGFB2,GCH1,HDC,PARK7	grey	VSMC_M10
GO:0099116	0.11	0.96	11	15	tRNA 5'-end processing	BP	1	RPP21,POP4,RPP40,POP5,KIAA0391,POP7,HSD17B10,THG1L,RPP38,TRMT10C,RPP30	grey	VSMC_M10
GO:0099550	0.11	0.97	7	9	trans-synaptic signaling, modulating synaptic transmission	BP	1	NTRK2,PLAT,GUCY1A1,GUCY1B1,F2R,CSPG5,EFNB3	grey	VSMC_M10
GO:0009205	0.11	0.93	36	57	purine ribonucleoside triphosphate metabolic process	BP	1	NME1,ATP5MGL,PPARA,GTPBP1,IMPDH1,SLC25A13,RAB23,SPHK2,PRKAG2,ATP5F1C,ATP5F1A,DGUOK,OPA1,FAM173B,NME4,MFN1,DNAJC30,EFL1,ATP5S,PINK1,STAT3,NME7,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,GNAI3,MT-ATP8,MT-ATP6,RHOA,ATP5ME,ATP5MF,NME6,NUDT2	grey	VSMC_M10
GO:0033108	0.11	0.92	52	83	mitochondrial respiratory chain complex assembly	BP	1	TIMM21,LYRM7,NDUFA6,COA5,SDHAF4,NDUFB2,NDUFB6,TMEM126B,NDUFC2,DMAC2,NDUFS8,NDUFAF7,NDUFA12,NDUFAF2,UQCC1,NDUFS3,NDUFAF6,FOXRED1,COX17,OXA1L,NDUFB4,NDUFB3,TFAM,NDUFS2,NUBPL,COA3,NDUFB11,BCS1L,NDUFA9,NDUFAB1,NDUFB10,SLC25A33,MT-ND1,MT-ND2,MT-ND6,NDUFA5,NDUFC1,COX16,NDUFAF8,DMAC1,NDUFA3,NDUFB5,NDUFA8,SDHAF2,C12orf73,NDUFS5,APOPT1,TMEM126A,COX14,COA1,UQCC2,SCO1	grey	VSMC_M10
GO:0010587	0.12	0.97	7	9	miRNA catabolic process	BP	1	PNPT1,TUT4,TENT2,TENT4B,DIS3L2,ZSWIM8,PARN	grey	VSMC_M10
GO:0002577	0.12	0.97	9	12	regulation of antigen processing and presentation	BP	1	HLA-DOB,NOD1,NOD2,YTHDF1,SLC11A1,TAPBPL,WAS,CD74,FGL2	grey	VSMC_M10
GO:1903025	0.12	0.97	9	12	regulation of RNA polymerase II regulatory region sequence-specific DNA binding	BP	1	DDRGK1,FBXW7,NSD1,TAF1,ZBTB7C,LAMTOR5,DDIT3,ZNF593,LIF	grey	VSMC_M10
GO:0010866	0.12	0.96	12	17	regulation of triglyceride biosynthetic process	BP	1	NR1H2,LPIN1,FBXW7,NR1H3,FITM2,GPLD1,SIK1,SLC27A1,LDLR,SREBF1,C3,CNEP1R1	grey	VSMC_M10
GO:0031343	0.12	0.94	18	27	positive regulation of cell killing	BP	1	CD226,STX7,HLA-DRA,NECTIN2,PVR,SLC22A13,RASGRP1,F2RL1,CADM1,IL12A,LAG3,STAT5B,ITGAM,VAV1,NOS2,AP1G1,FADD,FCER2	grey	VSMC_M10
GO:0090646	0.12	0.96	9	12	mitochondrial tRNA processing	BP	1	MTO1,TRIT1,TRNT1,RPUSD4,KIAA0391,TRMT5,HSD17B10,TRMT10C,TRMT61B	grey	VSMC_M10
GO:0044242	0.12	0.91	96	164	cellular lipid catabolic process	BP	1	HSD17B4,LRP1,AIG1,CPT1B,ABHD16A,PPARA,PNPLA3,PNPLA5,MCAT,ECHDC1,PLA2G6,CROT,SRD5A3,ETFB,PPT1,LPIN1,MGST2,SMPD2,APOB,FGF21,NAPEPLD,FAAH,HADHA,ABHD5,APOC1,LIPE,ACOX1,ACER3,AKT2,NEU3,SIRT2,HACL1,DDHD2,ACOXL,ASAH1,ACOX2,ABHD6,PEX2,ETFDH,IVD,LPIN3,ECI2,PLA2G4B,ADTRP,LONP2,GPLD1,MCEE,IRS1,CPT1A,BDH2,ABHD2,SORL1,ABCB11,PLBD1,EHHADH,PLA2G4A,ACADL,BCO2,CPS1,TYSND1,ABHD12B,SMPD4,DAGLB,ACADVL,HSD17B10,LIPC,ABCD4,GDPD3,GCDH,GALC,LDLR,GDPD1,GLA,HEXA,GM2A,GDE1,ABHD3,PNPLA6,LPIN2,ACAA2,DECR2,CEL,MLYCD,ABCD3,PLA2G15,ACADM,PHYH,PNPLA4,HADHB,AMACR,ACER2,NUDT19,ECI1,AUH,LYPLA2,NEU2	grey	VSMC_M10
GO:0051954	0.12	0.95	15	22	positive regulation of amine transport	BP	1	SLC12A2,SYT1,SLC38A3,KCNB1,GRK2,AGT,ACE2,STX1A,NTSR1,PINK1,ARL6IP1,PSEN1,CHRNB2,ABAT,STXBP1	grey	VSMC_M10

GO:0070103	0.12	0.98	6	7	regulation of interleukin-6-mediated signaling pathway	BP	1	RIPK1,PTPN2,GFI1,MIR125B1,MIR125A,C1QTNF4	grey	VSMC_M10
GO:0035725	0.12	0.91	70	120	sodium ion transmembrane transport	BP	1	NEDD4L,SLC12A2,WNK2,CNNM4,PRKCE,SLC4A4,HECW1,TRPM4,OSR1,SLC8A2,ASIC3,ATP1A3,SCN5A,SCN1A,SLC24A3,GPD1L,SLC20A2,SLC4A7,NALCN,SLC6A15,SLMAP,GLRX,SLC9A9,ASIC1,TPCN1,SLC8B1,TESC,ANO6,SLC6A2,PKD2,SLC41A1,SLC4A10,SLC6A3,HECW2,SLC9B1,SLC9B2,SCN2A,SHROOM2,SLC9A8,KCNK1,SCN7A,KLHL24,ATP1A2,SLC9A1,SCN4B,DLG1,SLC9A7,ATP1B1,SLC3A2,ASIC4,WNK3,ATP1B2,SLC5A2,HCN3,CACNA1G,DNM2,SCNN1B,SLC6A7,ASIC2,SLC9A6,CACNA1H,SLC9A5,MIR24-1,DMD,SLC6A19,FGF11,SCN2B,NETO2,YWHAH,HCN4	grey	VSMC_M10
GO:0048490	0.12	0.95	12	17	anterograde synaptic vesicle transport	BP	1	AP3S1,AP3M2,AP3B1,DTNBP1,CNIH2,BLOC1S6,AP3M1,TRIM46,SNAPIN,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0099514	0.12	0.95	12	17	synaptic vesicle cytoskeletal transport	BP	1	AP3S1,AP3M2,AP3B1,DTNBP1,CNIH2,BLOC1S6,AP3M1,TRIM46,SNAPIN,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0099517	0.12	0.95	12	17	synaptic vesicle transport along microtubule	BP	1	AP3S1,AP3M2,AP3B1,DTNBP1,CNIH2,BLOC1S6,AP3M1,TRIM46,SNAPIN,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0070525	0.12	0.96	9	12	tRNA threonylcarbamoyladenosine metabolic process	BP	1	MTO1,TRIT1,TPRKB,OSGEPL1,RPUSD4,TRMT5,HSD17B10,TP53RK,TRMT61B	grey	VSMC_M10
GO:0070071	0.12	0.96	9	12	proton-transporting two-sector ATPase complex assembly	BP	1	ATP23,ATPAF1,PIP4P1,TM9SF4,TMEM9,OXA1L,ATPAF2,TMEM199,VMA21	grey	VSMC_M10
GO:0065002	0.12	0.93	30	47	intracellular protein transmembrane transport	BP	1	TIMM21,PEX7,PEX6,PEX1,TRAM2,SEC61B,SEC61G,DNAJC15,SEC62,AKT2,TIMM50,PEX2,PEX16,LONP2,C2CD5,TOMM40L,GRPEL1,ZFAND2B,TIMM17B,PEX26,PEX14,PAM16,PEX10,HSPA5,TIMM23B,TRAM1L1,GRPEL2,PEX12,DNAJC19,SEC61A2	grey	VSMC_M10
GO:0032814	0.12	0.95	15	22	regulation of natural killer cell activation	BP	1	IL15,PIBF1,IL15RA,GAS6,TOX,RASGRP1,FGR,BLOC1S6,IL12A,STAT5B,ZBTB1,TICAM1,AP1G1,BLOC1S3,HAVCR2	grey	VSMC_M10
GO:0007216	0.12	0.97	7	9	G protein-coupled glutamate receptor signaling pathway	BP	1	GRM4,GRM8,HOMER1,GRM2,TRPM1,HOMER2,DAGLB	grey	VSMC_M10
GO:0003263	0.12	0.97	7	9	cardioblast proliferation	BP	1	PIM1,HAND2,EYA1,TBX5,MKS1,ISL1,SIX1	grey	VSMC_M10
GO:0003264	0.12	0.97	7	9	regulation of cardioblast proliferation	BP	1	PIM1,HAND2,EYA1,TBX5,MKS1,ISL1,SIX1	grey	VSMC_M10
GO:0048712	0.12	0.97	7	9	negative regulation of astrocyte differentiation	BP	1	MYCN,KDM4A,LDLR,MBD1,DAB1,GPR37L1,NOG	grey	VSMC_M10
GO:0007602	0.12	0.95	15	22	phototransduction	BP	1	OPN1SW,CAMKMT,TRPC3,PLEKHB1,CDS1,PITPNM1,RRH,SAG,NMT1,GRK4,GUCY2D,ASIC2,UNC119,GNAT2,GPR88	grey	VSMC_M10
GO:0007600	0.12	0.90	181	320	sensory perception	BP	1	RDH5,ATP8B1,MIP,MYO1A,EYA4,ALDH7A1,COL11A2,BTBD9,OPN1SW,GUCA1B,PRPH2,GRM8,RORB,CFAP69,CNGA1,PHF24,CLIC5,KIT,CNNM4,CLDN19,EPAS1,RIMS1,KCNQ4,GSDME,SHANK1,PPT1,GJA10,MYH14,WHRN,GRIK2,SOBP,TULP2,GRIN2D,ADCY3,BBS7,C5AR1,SLC26A5,MYO3A,MYO7B,EML2,OPA3,CACNB2,USH1G,ASIC3,CRYGN,ZNF513,SCN1A,MYO7A,POU4F1,SPRY2,MKKS,FSCN2,PDE6G,LRTOMT,AP000812.5,TMTC4,KERA,LUM,DIAPH1,P2RX2,FAM19A4,ATXN7,TUB,EPHB1,CASP3,MARVELD2,EYA1,P2RX3,CEP250,CCDC66,ADGRV1,ASIC1,P2RX7,NCAM2,P2RY1,KIFC3,MME,TMEM150C,USH1C,OPA1,F2R,IMPG2,TFAP2A,PAX2,FAM173B,SLC4A10,TRPM1,CABP1,CALHM1,SLC6A3,PGAP1,PDE6D,RRH,LRIT3,ZFHX2,OPRD1,CRYBA4,NRL,EYA3,TRPM8,SLC9A1,NIPSNAP1,MYO3B,BBS1,NTSR1,OAT,COCH,PDE6H,BACE1,STRC,HOMER2,CDKN1B,LRIG2,HMCN1,CEMIP,RTP4,CDH23,COMT,KCNK4,ADRA2C,RAB3A,KCNA1,MAPK1,ROM1,NLGN2,CLN8,DHRS3,HOXB8,GUCY2D,ALOXE3,MAPK3,CHRNB2,LCTL,TMEM100,POU3F4,CLN6,MYO9A,SCNN1B,OTOA,BDKRB1,PDE4A,CRYM,NMUR2,TRPV2,CCL2,ASIC2,UNC119,GNAL,SLC45A2,PITPNA,GNB1,TRPV1,MECP2,GNG13,GNAT2,LAMC3,CDC14A,PKD1L3,HSF4,CRYZ,SRRM4,REEP6,FABP5,PJVK,CHRNA10,TAS2R3,EPS8L2,FXN,SIX1,POMK,DDIT3,DRAM2,OTOR,OR5AN1,LRAT,AOC2,PTGES,TIMM8B,BBS10,OTOS,DNAJC19	grey	VSMC_M10
GO:0006665	0.12	0.91	71	120	sphingolipid metabolic process	BP	1	KDSR,ORMDL2,B4GALNT1,A4GALT,PLA2G6,HACD4,LARGE1,KIT,SPTLC1,PPP2R1A,PPT1,SMPD2,AGK,SPHK2,PRKD2,GLB1,ACER3,ELOVL1,NEU3,SPTLC3,SIRT3,NSMAF,ELOVL7,ASAH1,ST8SIA4,HTRA2,SERINC5,ORMDL1,COL4A3BP,A3GALT2,ST8SIA2,SGMS2,ALDH3B2,B3GALT1,TEX2,CERS6,HACD2,CERS2,ABCA12,PPM1L,B3GALNT1,SMPD4,SGMS1,FADS3,TECR,CLN8,DEGS1,ALOXE3,HACD3,GALC,CLN6,ST8SIA5,GLA,HEXA,GM2A,P2RX1,CEL,ST6GALNAC4,ST3GAL2,PLA2G15,ST6GALNAC5,CYP4F22,ABCA8,ELOVL3,PEMT,ACER2,CPTP,NEU2,B4GALT3,SGPP1,ST8SIA6	grey	VSMC_M10
GO:0015740	0.12	0.95	13	19	C4-dicarboxylate transport	BP	1	SLC12A2,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC25A30,NTSR1,SLC25A11,LRRC8E,SLC25A14,ABAT,LRRC8A,LRRC8D	grey	VSMC_M10
GO:0140053	0.12	0.91	61	101	mitochondrial gene expression	BP	1	SHMT2,TSFM,RMND1,TFB1M,MTERF1,LRPPRC,MTO1,MTIF2,PNPT1,TRIT1,QRSL1,C6orf203,FOXO3,FASTK,MTRF1,MRPS12,HARS,TRNT1,MRPS27,MRPS28,NSUN3,TWNK,WARS2,MRPS17,GATC,RPUSD4,YARS2,MRPS35,MRPL52,RCC1L,MRPS11,MRPS21,TARS2,TFAM,FASTKD1,MTG2,KIAA0391,SUPV3L1,LARS2,DARS2,COA3,TRMT5,MRPL44,HSD17B10,ALKBH1,EARS2,PPARGC1B,METTL4,TEFM,NDUFA7,MRPS34,SLC25A33,MRPS2,MRPS6,RPUSD3,MRPL57,MRPL51,UQCC2,TRMT10C,MRPL16,TRMT61B	grey	VSMC_M10
GO:0097151	0.12	0.98	5	6	positive regulation of inhibitory postsynaptic potential	BP	1	RIMS2,RIMS1,NTSR1,NLGN2,ABAT	grey	VSMC_M10
GO:0098828	0.12	0.98	5	6	modulation of inhibitory postsynaptic potential	BP	1	RIMS2,RIMS1,NTSR1,NLGN2,ABAT	grey	VSMC_M10
GO:0061029	0.12	0.97	7	9	eyelid development in camera-type eye	BP	1	OSR2,SRF,HDAC2,TFAP2A,HDAC1,GRHL3,STRA6	grey	VSMC_M10
GO:0014014	0.12	0.94	19	29	negative regulation of gliogenesis	BP	1	TSPO,SOX10,DAAM2,PTN,MYCN,KDM4A,SIRT2,NKX6-1,RNF10,CERS2,DLX1,DUSP10,LDLR,MBD1,DAB1,SKI,GPR37L1,NOG,PITX3	grey	VSMC_M10

GO:0006654	0.12	0.94	19	29	phosphatidic acid biosynthetic process	BP	1	AGPAT4,AGPAT1,PNPLA3,LPIN1,ABHD5,NR1H4,LPCAT1,GPAM,ACP6,ABHD4,GNPAT,DGKD,DGKG,SLC27A1,ABHD8,DGKQ,DGKE,AGPAT2,LCLAT1	grey	VSMC_M10
GO:0002706	0.12	0.91	55	92	regulation of lymphocyte mediated immunity	BP	1	CD226,STX7,AGER,HLA-DRA,EXOSC3,MSH2,RSAD2,IL4I1,TRPM4,HMCES,NECTIN2,PVR,MLH1,SLC22A13,FOXJ1,PAXIP1,SHLD1,NCKAP1L,HPX,TRAF6,RASGRP1,NOD2,CD40,CD96,DENND1B,CD28,CADM1,FZD5,BCL6,IL12A,PTPN6,LAG3,PPP3CB,STAT5B,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,TBX21,BTK,FBXO38,VAV1,C3,IL7R,SUPT6H,CRK,PRKCZ,TRAF2,AP1G1,FADD,CD46,FCER2,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0072282	0.12	0.98	5	6	metanephric nephron tubule morphogenesis	BP	1	SOX9,PAX8,PAX2,PKD1,SOX8	grey	VSMC_M10
GO:0007187	0.12	0.94	15	22	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	BP	1	PTGIR,HTR7,CHRM5,NPY1R,CHRM4,CHRM3,OPRD1,AGT,PTH1R,CALCRL,CHRM1,HRH2,HRH4,CCL2,HTR1D	grey	VSMC_M10
GO:0035195	0.13	0.91	65	107	gene silencing by miRNA	BP	1	ZC3H10,ESR1,CNOT6,AGO2,TNRC6B,TUT7,XPO5,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,TNRC6C,BCDIN3D,CNOT1,EIF4E2,RIPK1,PPP3CA,TERT,AJUBA,DDX6,EIF4ENIF1,PRKRA,DDX3X,STAT3,MAP2K1,SMAD3,TNRC6A,CNOT8,NCOR1,DROSHA,FMR1,SPOUT1,MIRLET7A2,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR425,MIR125B1,MIR32,MIR22,MIR27B,MIR24-1,MIR7-1,MIR199A2,MIRLET7D,MIR27A,MIR23B,MIR365B,MIR25,MIR491,MIR24-2,MIRLET7A3,AGO4,MIR33B,MIR339,MIR125A,MIR99B,MIR940,MIR1249,MIR1180	grey	VSMC_M10
GO:0015813	0.13	0.95	13	19	L-glutamate transmembrane transport	BP	1	SLC1A1,SLC25A13,SLC3A1,SLC7A11,ARL6IP5,ATP1A2,PER2,NTSR1,ARL6IP1,PRAF2,CLN8,PSEN1,SLC1A7	grey	VSMC_M10
GO:0071285	0.13	0.97	7	9	cellular response to lithium ion	BP	1	TPH2,CEBPA,XRCC4,ADCY7,FABP4,NFATC4,CDKN1B	grey	VSMC_M10
GO:0006551	0.13	0.97	7	9	leucine metabolic process	BP	1	HMGCLL1,BCAT2,MCCC2,IVD,MCCC1,HMGCL,AUH	grey	VSMC_M10
GO:0030299	0.13	0.97	7	9	intestinal cholesterol absorption	BP	1	ABCG5,ABCG8,SOAT2,LIMA1,LPCAT3,LDLR,CEL	grey	VSMC_M10
GO:0044241	0.13	0.97	7	9	lipid digestion	BP	1	ABCG5,ABCG8,SOAT2,LIMA1,LPCAT3,LDLR,CEL	grey	VSMC_M10
GO:0006505	0.13	0.93	21	32	GPI anchor metabolic process	BP	1	GPAA1,CWH43,TMEM246,PIGF,PGAP2,PIGU,PIGT,GPLD1,PGAP1,PIGM,PIGV,PIGX,PIGZ,PIGC,PGAP3,PIGH,PIGL,MPPE1,PYURF,PIGB,PIGA	grey	VSMC_M10
GO:0006612	0.13	0.91	58	97	protein targeting to membrane	BP	1	PEX3,ZDHHC14,SIL1,MICALL1,ZDHHC21,SLC1A1,TRAM2,SEC61B,ITGB1BP1,SEC61G,TCAF2,SDCBP,AQP11,SEC62,AKT2,PRNP,SRP14,ZDHHC20,SSR3,GOLGA7B,PEX16,DMTN,SRPRA,ZDHHC23,ZDHHC6,KCNB1,NCF1,C2CD5,CIB1,ZDHHC18,PEX19,ZDHHC24,VPS37D,PIKFYVE,FIS1,CEMIP,RTP4,ZFAND2B,ARL6IP1,ZDHHC4,PEX26,ITGAM,SSR2,RAB8B,TAOK2,ZDHHC15,MIEF2,CDK5R1,INPP5K,SGTA,ZDHHC12,HSPA5,ZDHHC1,ZDHHC11,TRAM1L1,HRAS,MIEF1,SEC61A2	grey	VSMC_M10
GO:1901605	0.13	0.91	86	146	alpha-amino acid metabolic process	BP	1	GLS2,SHMT2,ALDH8A1,GFPT2,RIDA,ATF4,PYCR3,PSAT1,GPT,MTAP,GNMT,SLC25A13,PPAT,RIMKLA,IL4I1,SLC7A11,DDO,BCAT2,DHFR,GAD2,IDO2,IDO1,AMDHD1,NR1H4,APIP,CSAD,THNSL2,AHCY,MSRA,GMPS,SERINC5,ENOPH1,SDSL,HOGA1,NIT2,ASNSD1,GLS,MTRR,SIRT4,ASL,ALDH5A1,AZIN2,MTR,CBSL,SLC7A7,HGD,AMT,CTPS2,ACADSB,OAT,GLUL,SMS,PLOD3,FAH,CPS1,MTHFS,PRODH,COMT,AASDHPPT,NAT8L,ALDH4A1,MAT1A,ASRGL1,HSD17B10,GCDH,AC138894.1,GSTZ1,CRYM,SHMT1,ADSSL1,NOS2,PIPOX,MECP2,PARK7,SARDH,ASS1,GCSH,KYAT1,KYAT3,MIR21,MTHFD2L,PEMT,SLC25A21,HYKK,PHGDH,PCBD2	grey	VSMC_M10
GO:0032228	0.13	0.95	13	19	regulation of synaptic transmission, GABAergic	BP	1	PHF24,USP46,PRKCE,PLCL2,KRAS,NPAS4,HAP1,NLGN2,AC138894.1,BAIAP3,ZDHHC12,CNTNAP4,STXBP1	grey	VSMC_M10
GO:0051260	0.13	0.91	75	128	protein homooligomerization	BP	1	MIP,SHMT2,KCNV1,CBY1,PRPH2,GNMT,NINJ1,CHMP2A,PNPT1,TRPM4,SSBP1,VSTM5,KCNRG,KCTD2,KCTD21,AQP11,RYR1,PRNP,ATL2,APIP,KCTD6,KCTD15,CBR4,P2RX3,RYR3,ASIC1,USP16,GLS,PKD2,SYCP1,CALHM1,ALDH1A3,KCNJ2,KCTD18,KCNB1,KCNG1,TIFA,OSBPL2,UPB1,EHD1,MPP2,ATL1,MICU1,CRTC1,KCNA1,KCND1,ROM1,MAT1A,ZBTB1,HSD17B10,CARD11,ALDH1A2,KCTD13,THG1L,CRTC2,EVL,ACACA,SHMT1,RNF135,TNFAIP1,TRPV1,KCTD5,ABCA3,KCNC4,BCL10,KCTD19,CRYZ,VASP,BEND3,KCTD1,KCNA6,IKZF4,CLYBL,TRMT61B,KCNG2	grey	VSMC_M10
GO:0070935	0.13	0.96	10	14	3'-UTR-mediated mRNA stabilization	BP	1	MAPK14,MYD88,TENT4B,RBM24,MAPKAPK2,ANGEL2,YBX3,RBM10,TARDBP,METTL16	grey	VSMC_M10
GO:1901160	0.13	0.97	7	9	primary amino compound metabolic process	BP	1	TPH2,BTBD9,DDC,SRD5A1,AZIN2,CHKA,GDE1	grey	VSMC_M10
GO:0042976	0.13	0.97	7	9	activation of Janus kinase activity	BP	1	PIBF1,PTK2B,AGT,IL6R,CCL5,GHR,SOCS1	grey	VSMC_M10
GO:0089718	0.13	0.93	20	31	amino acid import across plasma membrane	BP	1	SLC22A4,SLC1A1,SLC1A4,SLC7A11,ARL6IP5,SLC7A1,SLC43A1,AGT,ACE2,ATP1A2,PER2,NTSR1,ARL6IP1,SLC3A2,CLN8,PSEN1,SLC7A3,SLC7A5,SLC36A1,RGS4	grey	VSMC_M10
GO:0060304	0.13	0.98	5	6	regulation of phosphatidylinositol dephosphorylation	BP	1	MTMR2,CHRM5,MTMR9,MTMR3,MTMR1	grey	VSMC_M10
GO:1902107	0.13	0.91	65	110	positive regulation of leukocyte differentiation	BP	1	AGER,HLA-DRA,IL5,XRCC6,TRIB1,HSF1,ROR2,IL4I1,IL15,GLI2,POU4F1,IL15RA,TGFBR2,NCKAP1L,GAS6,PRKDC,TRAF6,SOX12,TOX,IL7,RASGRP1,RIPK2,AP3B1,TESC,RIPK1,SOX13,SLC9B2,HLX,ACIN1,HCLS1,RUNX3,ZBTB46,PPP2R3C,ADAM8,CREB1,DUSP10,BCL6,VSIR,STAT5B,FOXP3,ZBTB1,FOS,ZBTB7B,HAX1,IL4R,GPR68,BTK,CD74,PPARGC1B,NKAP,EVI2B,IL7R,JUN,SOCS1,PRKCZ,ATP6AP1,MIR21,RHOA,SOX4,FADD,CD46,CASP8,CA2,TNFSF9,LIF	grey	VSMC_M10

GO:1903708	0.13	0.91	65	110	positive regulation of hemopoiesis	BP	1	AGER,HLA-DRA,IL5,XRCC6,TRIB1,HSF1,ROR2,IL4I1,IL15,GLI2,POU4F1,IL15RA,TGFBR2,NCKAP1L,GAS6,PRKDC,TRAF6,SOX12,TOX,IL7,RASGRP1,RIPK2,AP3B1,TESC,RIPK1,SOX13,SLC9B2,HLX,ACIN1,HCLS1,RUNX3,ZBTB46,PPP2R3C,ADAM8,CREB1,DUSP10,BCL6,VSIR,STAT5B,FOXP3,ZBTB1,FOS,ZBTB7B,HAX1,IL4R,GPR68,BTK,CD74,PPARGC1B,NKAP,EVI2B,IL7R,JUN,SOCS1,PRKCZ,ATP6AP1,MIR21,RHOA,SOX4,FADD,CD46,CASP8,CA2,TNFSF9,LIF	grey	VSMC_M10
GO:0006370	0.13	0.98	5	6	7-methylguanosine mRNA capping	BP	1	RNMT,CMTR1,RNGTT,NCBP3,CMTR2	grey	VSMC_M10
GO:0003016	0.13	0.93	19	29	respiratory system process	BP	1	ZFAND5,ADH5,YWHAZ,NEK10,TCF15,AP3B1,TNNC1,FTO,GLS,CFAP43,ATP1A2,MTG2,SPAG16,RAB3A,TTC25,NLGN2,NLGN3,JAG2,MECP2	grey	VSMC_M10
GO:0051606	0.13	0.90	79	135	detection of stimulus	BP	1	TSPO,PKD2L2,PTK2,SMO,OPN1SW,PRPH2,PHF24,KIT,MRPS9,CAMKMT,DNAJA1,CYB5R4,NOD1,GJA10,WHRN,TLR4,GRIK2,TRPC3,ASIC3,DACH1,SCN1A,PLEKHB1,MKKS,SYT1,P2RX2,MRPS26,EPHB1,CEP250,CCDC66,ADGRV1,PTPRJ,NKX6-1,CDS1,PKD2,CASQ2,NOD2,KCNIP2,RYR2,FAP,MRPS35,PITPNM1,MRPS11,RRH,SAG,TRPM8,NTSR1,BACE1,STRC,CADM1,NMT1,RTP4,TTN,KCNK4,GRK4,PKD1L1,KCNA1,ROM1,PARP1,TCAP,GUCY2D,NGFR,TMEM107,CALM1,ASIC2,UNC119,TRPV1,PKD1,GNAT2,PIEZO1,FOXF1,PKD1L3,REEP6,PJVK,CHRNA10,TAS2R3,SOX4,OR5AN1,GPR88,KCNMB4	grey	VSMC_M10
GO:1902105	0.13	0.90	111	193	regulation of leukocyte differentiation	BP	1	NME1,AGER,HLA-DRA,IL5,TCF7,XRCC6,TRIB1,MYC,TOB2,HSF1,FBXO7,CDK6,ROR2,HOXA7,SLC46A2,IL4I1,TLR4,IL15,CLPTM1,GLI2,FOXJ1,POU4F1,IL15RA,TGFBR2,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,TRAF6,SOX12,TOX,ZC3H8,CAMK4,PIK3R1,FBXW7,TMEM131L,IL7,RASGRP1,RIPK2,AP3B1,TESC,RIPK1,SOX13,SLC9B2,GPR137B,PIAS3,HLX,ACIN1,TCTA,HCLS1,UBASH3B,SLAMF8,CD28,RUNX3,ZBTB46,PPP2R3C,ADAM8,CREB1,DUSP10,BCL6,VSIR,RC3H1,ESRRA,PTPN6,GPR137,FBN1,TNFSF18,LAG3,STAT5B,INHA,TFE3,FOXP3,ZBTB1,CARD11,TBX21,FOS,ZBTB7B,HAX1,IL4R,GPR68,BTK,CD74,PPARGC1B,NKAP,EVI2B,IL7R,PTPN2,JUN,SOCS1,DROSHA,PRKCZ,ATP6AP1,MIR21,MIR125B1,RHOA,FSTL3,SOX4,MAFB,FADD,CD46,CASP8,CA2,BGLAP,FGL2,TNFSF9,LIF,ZFP36L2,CEBPB,RC3H2	grey	VSMC_M10
GO:0019884	0.13	0.94	15	22	antigen processing and presentation of exogenous antigen	BP	1	HLA-DRA,HLA-DOB,TAP1,HLA-DMA,HLA-DPB1,IKBKB,TRAF6,AP3B1,MFSD6,PSME1,FCER1G,PIKFYVE,CTSV,DNM2,CD74	grey	VSMC_M10
GO:0000353	0.13	1.00	4	4	formation of quadruple SL/U4/U5/U6 snRNP	BP	1	RNU5E-1,RNU5B-1,RNU4-2,RNU4-1	grey	VSMC_M10
GO:0000365	0.13	1.00	4	4	mRNA trans splicing, via spliceosome	BP	1	RNU5E-1,RNU5B-1,RNU4-2,RNU4-1	grey	VSMC_M10
GO:0045291	0.13	1.00	4	4	mRNA trans splicing, SL addition	BP	1	RNU5E-1,RNU5B-1,RNU4-2,RNU4-1	grey	VSMC_M10
GO:0050919	0.13	0.92	25	40	negative chemotaxis	BP	1	SEMA6A,PLXNA4,SEMA4D,SEMA4C,EPHA7,SEMA3D,SEMA3A,NRG1,RYK,ROBO1,ROBO2,SEMA4F,SLIT1,SEMA3G,SEMA4G,LGR6,SEMA3F,SEMA6D,LRTM2,SEMA4A,NTN1,PLXNA3,RHOA,DPP4,WNT5A	grey	VSMC_M10
GO:0031047	0.13	0.90	77	129	gene silencing by RNA	BP	1	ZC3H10,ESR1,CNOT2,CNOT6,PABPC1,MOV10L1,AGO2,TNRC6B,TUT7,XPO5,CNOT11,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,TNRC6C,TEX15,CLP1,BCDIN3D,CNOT1,CELF1,CNOT6L,EIF4E2,RIPK1,EXD1,PPP3CA,TERT,AJUBA,DDX6,TDRKH,NCBP2,EIF4ENIF1,PRKRA,DDX3X,STAT3,MAP2K1,SMAD3,NRDE2,TNRC6A,CNOT8,NCOR1,DROSHA,FMR1,SPOUT1,MIRLET7A2,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR425,MIR125B1,MIR32,MIR22,MIR27B,MIR24-1,MIR7-1,MIR199A2,MIRLET7D,MIR27A,MIR23B,MIR365B,MIR25,MIR491,MIR24-2,MIRLET7A3,AGO4,MIR33B,MIR339,MIR125A,MIR99B,MIR940,MIR1249,MIR1180	grey	VSMC_M10
GO:0009145	0.13	0.92	30	47	purine nucleoside triphosphate biosynthetic process	BP	1	NME1,ATP5MGL,PPARA,IMPDH1,SLC25A13,SPHK2,PRKAG2,ATP5F1C,ATP5F1A,DGUOK,FAM173B,NME4,DNAJC30,ATP5S,PINK1,STAT3,NME7,ADK,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,NME6,NUDT2	grey	VSMC_M10
GO:0015822	0.13	0.98	5	6	ornithine transport	BP	1	SLC25A15,SLC7A1,SLC7A3,SLC7A6,SLC25A29	grey	VSMC_M10
GO:0001547	0.13	0.98	5	6	antral ovarian follicle growth	BP	1	ESR1,FOXO3,BMPR1B,GAS2,EREG	grey	VSMC_M10
GO:0031290	0.13	0.95	11	16	retinal ganglion cell axon guidance	BP	1	EPHA7,EPHB1,ROBO2,SEMA4F,SLIT1,ALCAM,BMPR1B,PTPRO,EPHB3,ISL1,ISL2	grey	VSMC_M10
GO:0014883	0.13	0.98	5	6	transition between fast and slow fiber	BP	1	TNNC1,PPP3CA,TNNI1,MYH7,ACTN3	grey	VSMC_M10
GO:0043576	0.13	0.95	10	14	regulation of respiratory gaseous exchange	BP	1	NR4A2,FTO,GLS,ATP1A2,MTG2,NTSR1,PASK,NLGN2,NLGN3,MECP2	grey	VSMC_M10
GO:0031058	0.14	0.91	45	75	positive regulation of histone modification	BP	1	SNW1,PHF1,C6orf89,RNF20,SPHK2,PRKD2,PAXIP1,ARRB1,CHTOP,NSD3,SDR16C5,DNMT3B,ING2,RTF1,JARID2,AUTS2,SART3,TET1,BCL6,WDR61,TADA2B,NELFA,PINK1,FOXP3,AKAP8L,AKAP8,KAT7,MUC1,JDP2,MAPK3,ZBTB7B,OGT,NAP1L2,RPS6KA5,SREBF1,ISL1,FMR1,GLYR1,MECP2,MTF2,SAP30BP,ZNF304,UBE2N,LIF,RPS6KA4	grey	VSMC_M10
GO:0043954	0.14	0.92	29	47	cellular component maintenance	BP	1	SYNGAP1,MTSS1,PICK1,ABHD17B,WHRN,VPS35,MTMR2,PRNP,ERC2,KIFC3,PLEKHA7,HOMER1,F2RL1,F2R,ITPKA,BSN,DLG1,C1QL1,RAB3A,NLGN2,ITGA3,INSR,CSF1R,CAMSAP3,SDF4,PJVK,CLDN1,INAVA,PARD6A	grey	VSMC_M10
GO:0120040	0.14	0.98	5	6	regulation of macrophage proliferation	BP	1	PTK2,MAPK1,MAPK3,CSF1R,IL33	grey	VSMC_M10
GO:0099010	0.14	0.95	10	14	modification of postsynaptic structure	BP	1	CTTNBP2,WASF1,CHMP2B,TIAM1,CYFIP1,CAMKV,STAU1,MYH10,ARHGAP44,RHOA	grey	VSMC_M10
GO:0006120	0.14	0.92	30	46	mitochondrial electron transport, NADH to ubiquinone	BP	1	NDUFA6,DLD,NDUFB2,NDUFB6,DNAJC15,NDUFC2,NDUFS8,NDUFS3,NDUFV3,NDUFB4,ISCU,NDUFB3,NDUFS2,PINK1,NDUFA9,NDUFAB1,NDUFA7,NDUFV2,NDUFB10,PARK7,MT-ND1,MT-ND2,MT-ND6,NDUFA5,NDUFC1,NDUFA3,NDUFB5,NDUFS6,NDUFA8,NDUFS5	grey	VSMC_M10

GO:0032148	0.14	0.94	16	24	activation of protein kinase B activity	BP	1	SLC1A1,ITGB1BP1,NRG1,GAS6,ADRA2B,ADRA2A,ADRA2C,PINK1,INSR,PDPK1,PRKCZ,PARK7,MIR21,WNT5A,TXN,FGF1	grey	VSMC_M10
GO:0045653	0.14	0.97	7	9	negative regulation of megakaryocyte differentiation	BP	1	CIB1,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0030316	0.14	0.91	41	68	osteoclast differentiation	BP	1	TOB2,MAPK14,CD109,TLR4,OSTM1,GAB2,POU4F1,FOXP1,MITF,TRAF6,CAMK4,PIK3R1,FBXW7,SH3PXD2A,LRRK1,SLC9B2,TCIRG1,GPR137B,PIAS3,TCTA,UBASH3B,FARP2,CREB1,ESRRA,GPR137,FBN1,TFE3,ANXA2,FOS,GPR68,CSF1R,PPARGC1B,GPC3,ATP6AP1,FSTL3,MAFB,CA2,BGLAP,SNX10,GLO1,CEBPB	grey	VSMC_M10
GO:0042159	0.14	0.95	10	14	lipoprotein catabolic process	BP	1	ABHD17B,PPT1,APOB,LYPLA1,LYPLAL1,LDLR,ABHD17A,ABHD10,ABHD17C,LYPLA2	grey	VSMC_M10
GO:0009071	0.14	0.97	7	9	serine family amino acid catabolic process	BP	1	SHMT2,CSAD,THNSL2,CBSL,AMT,SHMT1,GCSH	grey	VSMC_M10
GO:0009144	0.14	0.91	39	63	purine nucleoside triphosphate metabolic process	BP	1	NME1,ATP5MGL,PPARA,GTPBP1,IMPDH1,SLC25A13,RAB23,SPHK2,NUDT15,PRKAG2,ATP5F1C,NUDT16,ATP5F1A,DGUOK,OPA1,FAM173B,NME4,MFN1,DNAJC30,EFL1,ATP5S,PINK1,STAT3,NME7,ADK,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,GNAI3,MT-ATP8,MT-ATP6,RHOA,ATP5ME,ATP5MF,NME6,NUDT2	grey	VSMC_M10
GO:0045652	0.14	0.93	16	24	regulation of megakaryocyte differentiation	BP	1	ZNF16,MTURN,CNOT4,MEF2C,TESC,RAB7B,CIB1,THPO,RCOR1,PRMT6,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0009581	0.14	0.90	50	84	detection of external stimulus	BP	1	PKD2L2,PTK2,OPN1SW,PRPH2,PHF24,KIT,CAMKMT,GJA10,WHRN,GRIK2,TRPC3,ASIC3,SCN1A,PLEKHB1,MKKS,EPHB1,CEP250,CCDC66,ADGRV1,CDS1,PKD2,PITPNM1,RRH,SAG,TRPM8,NTSR1,BACE1,STRC,NMT1,TTN,KCNK4,GRK4,PKD1L1,KCNA1,ROM1,TCAP,GUCY2D,NGFR,ASIC2,UNC119,TRPV1,PKD1,GNAT2,PIEZO1,FOXF1,PKD1L3,REEP6,PJVK,CHRNA10,GPR88	grey	VSMC_M10
GO:1903764	0.14	0.98	5	6	regulation of potassium ion export across plasma membrane	BP	1	ANO6,KCNIP2,DLG1,MIR21,KCNH2	grey	VSMC_M10
GO:0021904	0.14	0.94	13	19	dorsal/ventral neural tube patterning	BP	1	TBC1D32,PTCH1,SMO,GLI2,SUFU,FKBP8,GORAB,GPR161,TULP3,WDR19,PSEN1,MKS1,GSC	grey	VSMC_M10
GO:0002036	0.14	0.98	5	6	regulation of L-glutamate import across plasma membrane	BP	1	ARL6IP5,ATP1A2,PER2,ARL6IP1,PSEN1	grey	VSMC_M10
GO:0021794	0.14	0.96	7	9	thalamus development	BP	1	UQCRQ,SMO,PTN,SRD5A1,GBX2,CHRNB2,TAL2	grey	VSMC_M10
GO:0046473	0.14	0.93	20	31	phosphatidic acid metabolic process	BP	1	AGPAT4,AGPAT1,PNPLA3,PLA2G6,LPIN1,ABHD5,NR1H4,LPCAT1,GPAM,ACP6,ABHD4,GNPAT,DGKD,DGKG,SLC27A1,ABHD8,DGKQ,DGKE,AGPAT2,LCLAT1	grey	VSMC_M10
GO:0043379	0.14	0.98	5	6	memory T cell differentiation	BP	1	HLA-DRA,BCL6,TSC1,CD46,FGL2	grey	VSMC_M10
GO:0021785	0.14	0.98	5	6	branchiomotor neuron axon guidance	BP	1	PLXNA4,MYCBP2,SEMA3A,SEMA3F,PLXNA3	grey	VSMC_M10
GO:0070534	0.14	0.91	31	50	protein K63-linked ubiquitination	BP	1	PRKN,RNF5,UBE2B,PELI1,TRAF1,TRAF3IP2,UBE2E2,UBE2O,TRAF6,ZFP91,NOD2,MAGEL2,RNF115,ARIH2,TRAF5,PELI3,RNF168,DDX3X,RNF4,GPS2,PRPF19,OTUB2,TRAF3,RNF135,TRAF2,RNF126,WWP2,UBE2G1,RNF8,UBE2N,RNF152	grey	VSMC_M10
GO:0072087	0.14	0.94	13	19	renal vesicle development	BP	1	SMO,SIX2,OSR1,SOX9,PAX8,FMN1,PAX2,SALL1,WNT4,CITED1,LHX1,SOX8,LIF	grey	VSMC_M10
GO:0050907	0.14	0.96	7	9	detection of chemical stimulus involved in sensory perception	BP	1	ASIC3,RTP4,TRPV1,GNAT2,PKD1L3,TAS2R3,OR5AN1	grey	VSMC_M10
GO:0019228	0.14	0.93	15	23	neuronal action potential	BP	1	MYH14,SCN5A,SCN1A,P2RX3,SCN2A,SCN7A,GPER1,KCNA1,CACNA1G,FMR1,P2RX1,CACNA1H,GPR35,GPR88,KCNMB4	grey	VSMC_M10
GO:0000963	0.14	0.94	13	19	mitochondrial RNA processing	BP	1	MTO1,PNPT1,TRIT1,FASTK,TRNT1,RPUSD4,FASTKD1,KIAA0391,SUPV3L1,TRMT5,HSD17B10,TRMT10C,TRMT61B	grey	VSMC_M10
GO:0014832	0.14	0.98	5	6	urinary bladder smooth muscle contraction	BP	1	PLA2G6,P2RX2,P2RX3,KCNMA1,TRPV1	grey	VSMC_M10
GO:0006362	0.14	0.98	5	6	transcription elongation from RNA polymerase I promoter	BP	1	ERCC2,ERCC3,POU4F1,ERCC6,GTF2H5	grey	VSMC_M10
GO:0070070	0.14	0.98	5	6	proton-transporting V-type ATPase complex assembly	BP	1	PIP4P1,TM9SF4,TMEM9,TMEM199,VMA21	grey	VSMC_M10
GO:0006544	0.14	0.96	7	9	glycine metabolic process	BP	1	SHMT2,RIDA,DHFR,AMT,SHMT1,GCSH,PHGDH	grey	VSMC_M10
GO:0034067	0.14	0.93	18	28	protein localization to Golgi apparatus	BP	1	BICD2,ARL5B,OPTN,ARL5A,PAQR3,GBF1,SORL1,PACS1,OBSL1,VPS13D,ARL5C,GAK,VPS13C,TMED10,ZDHHC15,COG7,IFT20,RIPOR1	grey	VSMC_M10
GO:1903400	0.14	0.98	5	6	L-arginine transmembrane transport	BP	1	SLC7A1,SLC38A9,AGT,SLC7A3,SLC25A29	grey	VSMC_M10
GO:0090280	0.14	0.95	10	14	positive regulation of calcium ion import	BP	1	SPHK2,STC1,CASK,ATP2A1,TRPV2,CCL2,TRPV3,P2RX1,ATP2C2,CRH	grey	VSMC_M10
GO:1902022	0.14	0.98	5	6	L-lysine transport	BP	1	SLC7A1,AGT,PQLC2,SLC7A3,SLC25A29	grey	VSMC_M10
GO:1903401	0.14	0.98	5	6	L-lysine transmembrane transport	BP	1	SLC7A1,AGT,PQLC2,SLC7A3,SLC25A29	grey	VSMC_M10
GO:0043583	0.14	0.89	93	162	ear development	BP	1	ATP8B1,EYA4,OSR2,FZD6,PTK7,SLC25A27,ROR2,DLX5,SIX2,KCNQ4,GSDME,HOXA2,HOXA13,MYCL,BMPER,WHRN,ATG5,MYCN,SOBP,OSR1,SLC26A5,MYO3A,SOX9,USH1G,GLI2,MYO7A,TSKU,SPRY2,SLC4A7,JAG1,LRTOMT,AP000812.5,LIN7A,FREM2,CEP290,TCF15,PAX8,CEBPA,EYA1,PLS1,ADGRV1,FZD3,USH1C,OPA1,RPGRIP1L,TFAP2A,PAX2,ALDH1A3,TGFB2,TRIP11,SHROOM2,MAPKAPK2,SOX2,GBX2,MYO3B,KCNK2,GRHL3,STRC,CDKN1B,STOX1,PRKRA,CDH23,ECE1,NKX3-2,MAPK1,EPHA4,DVL2,WDR19,TCAP,RBPJ,MAPK3,ESRRB,POU3F4,NTN1,MKS1,GSC,STRA6,JAG2,IFT20,MCOLN3,KCNK3,PJVK,CHRNA10,FOXG1,MAFB,NOG,WNT5A,OTX1,SIX1,BCL2L11,INSIG2,HEY2,ZIC1	grey	VSMC_M10
GO:0090036	0.14	0.95	10	14	regulation of protein kinase C signaling	BP	1	PLA2G6,SPHK2,WNT11,GPD1L,ADGRV1,CD40,DGKD,DGKG,SEZ6,WNT5A	grey	VSMC_M10
GO:0060330	0.14	0.95	10	14	regulation of response to interferon-gamma	BP	1	NR1H2,HPX,NR1H3,NLRC5,PARP9,PARP14,MED1,PTPN2,SOCS1,IRGM	grey	VSMC_M10
GO:0060334	0.14	0.95	10	14	regulation of interferon-gamma-mediated signaling pathway	BP	1	NR1H2,HPX,NR1H3,NLRC5,PARP9,PARP14,MED1,PTPN2,SOCS1,IRGM	grey	VSMC_M10

GO:0097696	0.14	0.90	62	105	receptor signaling pathway via STAT	BP	1	IL5,AKR1B1,HSF1,OCIAD1,KIT,PPP2R1A,IL15,HDAC2,PIBF1,NMI,HPX,RET,FER,PIGU,OSBP,PTK2B,ARL2BP,F2R,PKD2,CD40,HDAC1,MST1,EGF,HCLS1,PARP9,PARP14,AGT,OSM,THPO,IL10RA,IL12A,TNFSF18,FGFR3,STAT3,STAT5B,CTF1,IL6R,STAT2,ELP2,CCL5,CSF1R,CCL2,CDK5R1,ISL1,SUZ12,GHR,JAK1,NLK,IL7R,PTPN2,SOCS1,DAB1,DOT1L,PKD1,MIR125B1,CNTF,MIR125A,STAMBP,GADD45A,LIF,TSLP,LEPROT	grey	VSMC_M10
GO:1904263	0.14	0.95	10	14	positive regulation of TORC1 signaling	BP	1	RRAGD,PIP4P1,LARS,GPR137B,SIK3,GPR137,OTUD5,RRAGB,CLEC16A,LAMTOR5	grey	VSMC_M10
GO:0044803	0.14	0.98	5	6	multi-organism membrane organization	BP	1	NECTIN2,FCHSD2,FCHSD1,GAS6,PI4KA	grey	VSMC_M10
GO:0034383	0.14	0.93	15	22	low-density lipoprotein particle clearance	BP	1	APOB,FGF21,NR1H4,SOAT2,MYLIP,SOAT1,EHD1,LIPA,ANXA2,LDLR,MIR199A1,MIR27B,MIR27A,NCEH1,LDLRAP1	grey	VSMC_M10
GO:0051966	0.14	0.92	25	40	regulation of synaptic transmission, glutamatergic	BP	1	MAPK8IP2,GRM4,PLA2G6,GRM8,ROR2,DGKI,EGFR,SYT1,MEF2C,PTK2B,HOMER1,GRM2,DISC1,ATP1A2,GLUL,TNR,NLGN2,PSEN1,NLGN3,AC138894.1,CCL2,TPRG1L,STXBP1,CACNG7,CACNG5	grey	VSMC_M10
GO:0045836	0.15	0.96	7	9	positive regulation of meiotic nuclear division	BP	1	UBE2B,SIRT2,PLCB1,NPM2,WNT4,OOEP,WNT5A	grey	VSMC_M10
GO:0002430	0.15	0.98	5	6	complement receptor mediated signaling pathway	BP	1	FPR2,C5AR2,C5AR1,GPLD1,CMKLR1	grey	VSMC_M10
GO:0050806	0.15	0.90	61	104	positive regulation of synaptic transmission	BP	1	RIMS2,PRRT1,AGER,NTRK2,SLC1A1,ROR2,PRKCE,RIMS1,RIMS3,CRHR2,PTN,EGFR,GRIK2,GRIN2D,SLC8A2,CACNB2,SYT1,PRNP,PLK2,FAM107A,CLSTN2,PTK2B,MME,EIF2AK4,DTNBP1,DNM1L,IGSF11,STAU1,GPER1,NFATC4,STX1A,YTHDF1,GLUL,CREB1,TNR,MPP2,CRTC1,PINK1,MAPK1,NSG1,HAP1,EPHA4,DLG4,NLGN2,RGS14,STX1B,STX4,NLGN3,KCTD13,CYP46A1,CCL2,FMR1,PRKCZ,MECP2,BAIAP3,ZDHHC12,STXBP1,CACNG7,CRH,CACNG5,LRRTM2	grey	VSMC_M10
GO:0036446	0.15	0.98	5	6	myofibroblast differentiation	BP	1	TSKU,TP53INP1,PDCD4,PARP1,MIR21	grey	VSMC_M10
GO:1904760	0.15	0.98	5	6	regulation of myofibroblast differentiation	BP	1	TSKU,TP53INP1,PDCD4,PARP1,MIR21	grey	VSMC_M10
GO:0070584	0.15	0.94	13	19	mitochondrion morphogenesis	BP	1	PNPT1,MYH14,WASF1,SSBP1,PANK2,OPA1,COL4A3BP,DNM1L,POLG2,NUBPL,FIS1,SUPV3L1,MTM1	grey	VSMC_M10
GO:0045046	0.15	0.98	5	6	protein import into peroxisome membrane	BP	1	PEX3,PEX16,PEX19,PEX26,RAB8B	grey	VSMC_M10
GO:0002703	0.15	0.89	79	136	regulation of leukocyte mediated immunity	BP	1	CD226,STX7,AGER,HLA-DRA,RAC2,KIT,EXOSC3,MSH2,RSAD2,IL4I1,TLR4,TRPM4,SPHK2,HMCES,NECTIN2,PVR,GAB2,MLH1,UNC13D,SLC22A13,FOXJ1,PAXIP1,SHLD1,MAVS,NCKAP1L,HPX,TRAF6,FER,RASGRP1,F2RL1,NOD2,CD40,CD96,DENND1B,FGR,SNX4,CD28,CADM1,FZD5,BCL6,IL12A,PTPN6,LAG3,PPP3CB,C12orf4,STAT5B,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,TBX21,STX4,ITGAM,IL4R,BTK,STXBP2,FBXO38,PRAM1,VAV1,C3,NOS2,IL7R,SUPT6H,TICAM1,CRK,DNASE1,PDPK1,PRKCZ,TRAF2,FOXF1,STXBP1,AP1G1,FADD,CXCL6,CD46,FCER2,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0007197	0.15	0.98	5	6	adenylate cyclase-inhibiting G protein-coupled acetylcholine receptor signaling pathway	BP	1	CHRM5,CHRM4,CHRM3,CHRM1,HRH4	grey	VSMC_M10
GO:0046034	0.15	0.88	128	219	ATP metabolic process	BP	1	SHMT2,ENPP3,ATP5MGL,HSPA1B,PPARA,TSPO,UQCRQ,NDUFA6,PRXL2C,SLC25A13,GAPDH,MSH2,SLC4A4,BPGM,DLD,NDUFB2,SPHK2,NDUFB6,DNAJC15,NUDT5,DHTKD1,NDUFC2,PRKAG2,ATP5F1C,PFKP,NDUFS8,NDUFA12,COX7A1,COX4I2,GPI,ATP5F1A,GPD1,P2RX7,NDUFS3,DGUOK,PRKAG1,PFKM,UQCRB,COX15,FAM173B,ATP6V1B2,COX6B1,NDUFV3,DNM1L,ZBTB20,FAM20C,NDUFB4,ISCU,COA6,PFKFB2,MYH7,HSPA8,ENO4,NDUFB3,ARNT,ATP1A2,ACTN3,HDAC4,NDUFS2,DNAJC30,MLXIPL,SDHC,OLA1,COX6A1,FIS1,HK1,ATP5S,COX8A,PRKAG3,PINK1,STAT3,ATP1B1,NDUFA9,ENO3,PARP1,PSEN1,COX6A2,PKLR,OGT,NDUFAB1,ADPGK,UQCRC2,COX5A,NCOR1,INSR,TEFM,NDUFA7,SLC25A23,NDUFV2,ALDOC,NADK,ATP6V0C,NDUFB10,UQCR11,PARK7,SLC25A33,ATP5PB,SLC2A6,VPS9D1,SLC25A25,MT-ND1,MT-ND2,MT-ATP8,MT-ATP6,MT-CO3,MT-ND6,MT-CYB,RHOA,ATP5ME,ATP5MF,NDUFA5,ENTPD5,NDUFC1,BEND3,COX7A2,TIGAR,FXN,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,UQCC2,NUDT2,COX7A2L,PPIF,NMNAT1	grey	VSMC_M10
GO:0021670	0.15	0.95	8	11	lateral ventricle development	BP	1	CDK6,AQP1,NUMBL,TSKU,RPGRIP1L,DNAH5,DPCD,ATP1B2	grey	VSMC_M10
GO:0018198	0.15	0.91	27	43	peptidyl-cysteine modification	BP	1	ZDHHC14,NCOA7,ZDHHC21,GAPDH,ADH5,PRDX3,ZDHHC20,GOLGA7B,ZDHHC23,ZDHHC6,HHAT,ZDHHC18,ZDHHC24,NOS1AP,ZDHHC8,ZDHHC4,ZDHHC15,RAB3D,S100A8,NOS2,PARK7,ZDHHC12,ZDHHC1,DMD,ZDHHC11,TXN,MAP6D1	grey	VSMC_M10
GO:0042439	0.15	0.98	5	6	ethanolamine-containing compound metabolic process	BP	1	NAPEPLD,CHKA,GDPD3,GDPD1,GDE1	grey	VSMC_M10
GO:0055088	0.15	0.89	68	116	lipid homeostasis	BP	1	ORMDL2,APOM,PNPLA3,PNPLA5,TTC39B,SLC25A27,ABCG5,ABCG8,RTN4,NR1H2,APOB,CNBP,ABHD5,ACOX1,GCKR,TSKU,NR1D2,COMMD9,NR1H4,USF2,ACOXL,SOAT2,CYP7A1,CYP7B1,ACOX2,CEBPA,FBXW7,LIMA1,EPHX2,NR1H3,FITM2,ORMDL1,COL4A3BP,ITGB6,MYLIP,ABCA5,ZBTB20,GPAM,ABHD4,NR5A2,FABP4,GRAMD1B,ABCB11,ABCG4,USF1,MLXIPL,SOAT1,EHD1,DDX3X,ABCA12,ABHD8,ATP13A2,CLN8,FGFR4,LIPC,ADCK1,LDLR,ACSM3,ACACA,NPC1,TMEM97,FAM57A,ABCA3,MIR27B,MIR33B,PNPLA4,LDLRAP1,TLCD1	grey	VSMC_M10
GO:0055064	0.15	0.95	8	11	chloride ion homeostasis	BP	1	SLC12A2,CKB,ABCC2,SLC12A5,SLC12A7,SLC12A8,SLC12A9,SLC12A4	grey	VSMC_M10
GO:0055083	0.15	0.95	8	11	monovalent inorganic anion homeostasis	BP	1	SLC12A2,CKB,ABCC2,SLC12A5,SLC12A7,SLC12A8,SLC12A9,SLC12A4	grey	VSMC_M10
GO:0006555	0.15	0.95	10	14	methionine metabolic process	BP	1	MTAP,GNMT,APIP,MSRA,ENOPH1,MTRR,MTR,SMS,MAT1A,MTHFD2L	grey	VSMC_M10
GO:0072378	0.15	0.98	5	6	blood coagulation, fibrin clot formation	BP	1	FBLN1,FN1,SERPINC1,F12,FGA	grey	VSMC_M10
GO:0032610	0.15	0.98	5	6	interleukin-1 alpha production	BP	1	IL1R2,PANX1,IL16,S100A13,ISL1	grey	VSMC_M10
GO:0032650	0.15	0.98	5	6	regulation of interleukin-1 alpha production	BP	1	IL1R2,PANX1,IL16,S100A13,ISL1	grey	VSMC_M10

GO:0071500	0.15	0.98	5	6	cellular response to nitrosative stress	BP	1	DNAJA1,ATG5,STOX1,PARK7,DDIT3	grey	VSMC_M10
GO:0044255	0.15	0.87	412	743	cellular lipid metabolic process	BP	1	RDH5,KDSR,ORMDL2,RDH16,HSD17B4,LRP1,ALDH8A1,PIP4K2C,PEX7,B4GALNT1,AVIL,AIG1,LTC4S,CPT1B,ABHD16A,SYNJ2,SERAC1,SLC27A6,ALG12,TNXB,AGPAT4,AGPAT1,QKI,PPARA,ACSL6,SLC22A4,PNPLA3,PNPLA5,MCAT,HSD17B8,A4GALT,ECHDC1,AKR1B1,MAPK14,PLA2G6,GPAA1,HACD4,LARGE1,ALDH1A1,CROT,CWH43,KIT,PLPP6,SRD5A3,SPTLC1,AASDH,INPP4A,ADH5,CAT,ALG2,PLPPR1,TMEM246,TMEM86B,PIGF,RDH13,MBOAT7,PPP2R1A,ETFB,PPT1,PLEK,NR1H2,MBOAT2,DGKI,EGFR,LPIN1,INPP4B,MGST2,SMPD2,DLD,FIG4,APOB,AGK,FGF21,PRKAR2B,SPHK2,MTMR2,PIP4K2A,NAPEPLD,ALG11,FAAH,PRKD2,HADHA,SELENOI,SOX9,ABHD5,APOC1,GLB1,LIPE,ECHDC3,PRKAG2,ACOX1,TAMM41,SLC22A13,PIBF1,ITPKC,CYGB,ACER3,ELOVL1,AKT2,PIP4P1,NEU3,MTMR14,SPTLC3,SIRT2,PLCB1,PGAP2,CRLS1,HACL1,CDS2,PLPP5,DDHD2,PANK2,PDK1,SIRT3,NR1H4,MTMR7,TRIB3,LYPLA1,SDR16C5,ACOXL,SOAT2,CYP7A1,NSMAF,ELOVL7,ASAH1,ACOX2,ABHD6,THNSL2,CBR4,PIGU,PIK3CB,PITPNM2,ST8SIA4,PIK3R1,TMEM150A,GK5,RETSAT,HPGD,PLCE1,CHRM5,MTMR9,FBXW7,GPD1,PEX2,HTRA2,EPHX2,SLA2,ETFDH,ACOT12,PRKAG1,NR1H3,SERINC5,SYNJ1,COQ2,IVD,LPIN3,CDS1,ST3GAL6,FITM2,ORMDL1,ECI2,COL4A3BP,ITPKA,ERLIN1,PIGT,PLA2G4B,ADTRP,PRMT3,PRKAB1,LONP2,PM20D1,SIRT4,GPLD1,SRD5A1,MCEE,A3GALT2,IRS1,ALG10,LPCAT1,SIK1,ALDH1A3,PGAP1,CPT1A,BDH2,GPAM,ACSL5,CHKA,PLA1A,ACP6,INPP5A,ABHD4,ST8SIA2,SGMS2,CYP2U1,ALDH3B2,AJUBA,GGPS1,PITPNM1,ABHD2,MSMO1,MTMR11,MECR,B3GALT1,SORL1,TEX2,GNPAT,DGKD,B3GNT5,CERS6,PIGM,FITM1,ABCB11,DHRS9,BMX,AGT,HACD2,FAM126B,IP6K2,LPGAT1,SERS2,PIGV,PPAGT1,PLPP1,MTMR3,PERP,ALG3	grey	VSMC_M10
GO:0099565	0.15	0.90	44	74	chemical synaptic transmission, postsynaptic	BP	1	MAPK8IP2,RIMS2,CHRNA3,CHRNA5,RIMS1,SHANK1,GRIK2,GRIN2D,MTMR2,SLC8A2,GRIK5,CHRNA6,P2RX2,P2RX3,MEF2C,P2RX7,CUX2,PTK2B,PPP3CA,IGSF11,SSH1,STX1A,TMEM25,NPAS4,NTSR1,MPP2,DLG4,NLGN2,CHRNB1,STX1B,NLGN3,CHRNB2,SEZ6,ABAT,TRPV1,P2RX1,PRKCZ,MECP2,CHRNB4,CHRNA10,CHRNG,GRID2,RGS4,INSYN1	grey	VSMC_M10
GO:0002922	0.15	0.98	5	6	positive regulation of humoral immune response	BP	1	PHB,HPX,NOD2,C3,FCER2	grey	VSMC_M10
GO:0048168	0.15	0.91	24	38	regulation of neuronal synaptic plasticity	BP	1	SYNGAP1,SYNGR1,KIT,ACP4,NCDN,GRIK2,PPFIA3,SLC8A2,RAB5A,SLC4A10,NEURL1,KRAS,AGT,SYAP1,RAB3A,RAB8A,DLG4,AC138894.1,RAB11A,CAMK2A,JPH3,CNTN2,HRAS,SHISA8	grey	VSMC_M10
GO:0060080	0.15	0.95	8	11	inhibitory postsynaptic potential	BP	1	RIMS2,RIMS1,NPAS4,NTSR1,NLGN2,NLGN3,ABAT,INSYN1	grey	VSMC_M10
GO:1903793	0.15	0.92	17	26	positive regulation of anion transport	BP	1	SLC12A2,PLA2G6,ABCB1,PLA2R1,SLC38A3,MAP2K6,ABCB11,AGT,ACE2,NTSR1,PLA2G4A,ARL6IP1,PSEN1,ABAT,STXBP1,PTGES,CEBPB	grey	VSMC_M10
GO:0006547	0.15	0.98	5	6	histidine metabolic process	BP	1	CARNMT1,HNMT,AMDHD1,HDC,MTHFD2L	grey	VSMC_M10
GO:0010624	0.15	0.98	5	6	regulation of Schwann cell proliferation	BP	1	SOX10,RNF10,CERS2,SKI,MIR222	grey	VSMC_M10
GO:0050687	0.15	0.93	14	21	negative regulation of defense response to virus	BP	1	C6orf106,SEC14L1,NPLOC4,PCBP2,RNF26,NLRX1,TRAF3IP1,HTRA1,MUL1,FOXP3,TKFC,TSPAN6,RIOK3,FGL2	grey	VSMC_M10
GO:0046839	0.15	0.91	25	40	phospholipid dephosphorylation	BP	1	SYNJ2,PLPP6,PLPPR1,INPP4B,FIG4,MTMR2,PIP4P1,PLPP5,MTMR7,CHRM5,MTMR9,EPHX2,SYNJ1,INPP5A,MTMR11,PLPP4,MTMR3,INPP5J,SACM1L,PLPPR2,MTMR12,MTM1,MTMR1,INPP5K,SGPP1	grey	VSMC_M10
GO:0018243	0.15	0.98	5	6	protein O-linked glycosylation via threonine	BP	1	GALNT11,EOGT,GALNT2,GALNT16,GALNT1	grey	VSMC_M10
GO:0048640	0.15	0.89	53	90	negative regulation of developmental growth	BP	1	SEMA6A,STK3,PPARA,FSTL4,PTCH1,PI16,SEMA4D,SEMA4C,RTN4,EPHA7,TGFBR2,SEMA3D,SPART,SEMA3A,ULK1,RYK,SEMA4F,TLL2,TBX5,SEMA3G,SPP1,STK4,SEMA4G,NKD1,JARID2,KIAA0319,SEMA3F,KCNK2,CDKN1B,WNT3,DUSP10,SEMA6D,TNR,SAV1,MYOZ1,GDF15,FGFR3,SEMA4A,TRIM46,WWC1,NTN1,YY1,CDK5R1,RAI1,ARHGAP4,PLXNA3,MIR199A1,MIR25,NOG,WNT5A,FXN,RGS4,PLAC8	grey	VSMC_M10
GO:0006887	0.15	0.88	150	266	exocytosis	BP	1	VPS4B,RAB21,RIMS2,PRKN,EXOC4,SYNGR1,PLA2G6,RAC2,MYH9,CHRNA5,STEAP2,APBA1,SCFD2,KIT,CHMP2A,NLRP5,STX17,RIMS1,RIMS3,SCRN1,PLEK,VPS41,SDCBP,PPFIA3,LIN7B,SPHK2,NAPA,RAB7A,RAB10,CACNB2,SYTL2,CLASP2,GAB2,LLGL2,RALB,GRIK5,UNC13D,NAPB,ABCC4,ANK1,SYT1,RAB5A,LIN7A,NCKAP1L,STX2,SYT9,SNPH,HCK,FER,TRAPPC11,ERC2,P2RY1,RASGRP1,RAB11FIP5,EXOC6B,SYNJ1,F2RL1,VPS18,LGI3,DMTN,DTNBP1,SYT8,DNM1L,HYAL3,ADRA2A,SNAP23,KCNB1,RAB11FIP2,LAT2,FGR,CBL,SYTL1,PRSS12,STX1A,SNX4,SEPT2,BACE1,DNAJC5,CSPG5,NSF,MIA3,RAP1B,BLOC1S6,ABCA12,CASK,PTGDR,PPP3CB,RAB3A,SYN1,SNAP29,EXOC5,C12orf4,RAB8A,ATP13A2,HAP1,CPLANE2,SYT7,RAB15,RSC1A1,SEPT1,WASHC3,CPLX1,STX1B,STX4,PSEN1,RAB25,ITGAM,SYT11,RAB8B,TMED10,CACNA1G,RAB11A,LAT,RAB3D,IL4R,CALM1,SYTL4,SNAPIN,S100A13,PRKCB,BTK,ARHGAP44,SCAMP5,CCL5,TNFAIP2,STXBP2,PRAM1,FMR1,RPH3AL,PIP5K1C,SDF4,PDPK1,P2RX1,RAB26,ATP6AP1,BAIAP3,CACNA1H,FOXF1,STXBP1,AP1G1,VPS4A,FGA,CHGA,SNAP47,TMEM167A,TMEM167B,DOC2B,RALA,VAMP3,EXOC3L4	grey	VSMC_M10
GO:1903350	0.15	0.90	34	56	response to dopamine	BP	1	PRKN,ATF4,SLC1A1,VPS35,HDAC2,ALK,HTR7,CHRM5,CHRM4,DTNBP1,CHRM3,CALY,HTR3B,MAPK1,CHRM1,GNB5,NSG1,HRH2,HCN3,MAPK3,DNM2,SIN3A,HRH4,GNAL,GNB1,GNA15,PALM,GNAI3,FUK,HTR1D,RGS4,GNA14,GNG2,ARPP19	grey	VSMC_M10
GO:0086067	0.15	0.96	6	8	AV node cell to bundle of His cell communication	BP	1	TRPM4,CACNB2,SCN5A,RYR2,SCN4B,CACNA1G	grey	VSMC_M10
GO:0002227	0.15	0.97	5	6	innate immune response in mucosa	BP	1	NOD2,NOS2,HIST1H2BK,HIST1H2BF,HIST1H2BJ	grey	VSMC_M10
GO:0042220	0.15	0.91	22	35	response to cocaine	BP	1	SLC1A1,HDAC2,DNMT3A,HNMT,DNMT3B,PTK2B,TIAM1,HOMER1,GRM2,SLC6A3,HOMER2,SDK1,CHRNB2,DNM2,MBD1,ABAT,HSPA5,MT-ND6,FADD,RGS4,CRH,PITX3	grey	VSMC_M10
GO:0046856	0.16	0.92	18	28	phosphatidylinositol dephosphorylation	BP	1	SYNJ2,INPP4B,FIG4,MTMR2,PIP4P1,MTMR7,CHRM5,MTMR9,SYNJ1,INPP5A,MTMR11,MTMR3,INPP5J,SACM1L,MTMR12,MTM1,MTMR1,INPP5K	grey	VSMC_M10

GO:0002448	0.16	0.91	25	40	mast cell mediated immunity	BP	1	RAC2,KIT,SPHK2,GAB2,UNC13D,FER,RASGRP1,SNAP23,LAT2,FGR,CBL,SNX4,PTGDR,C12orf4,SPON2,LAT,IL4R,S100A13,BTK,STXBP2,PDPK1,FOXF1,STXBP1,CHGA,SERPINB9	grey	VSMC_M10
GO:0002478	0.16	0.93	13	19	antigen processing and presentation of exogenous peptide antigen	BP	1	HLA-DRA,HLA-DOB,TAP1,HLA-DMA,HLA-DPB1,IKBKB,TRAF6,MFSD6,FCER1G,PIKFYVE,CTSV,DNM2,CD74	grey	VSMC_M10
GO:1904429	0.16	0.97	5	6	regulation of t-circle formation	BP	1	ERCC1,RTEL1,XRCC5,SLX4,TERF2	grey	VSMC_M10
GO:0032874	0.16	0.89	57	97	positive regulation of stress-activated MAPK cascade	BP	1	MAP3K5,STK3,MAPK8IP2,MAP3K4,AGER,GADD45G,SEMA4C,EMC10,MTURN,NOD1,TLR4,TRAF1,SDCBP,MYD88,PLCB1,EIF2AK2,RELL2,SEMA3A,SH3RF2,ARL6IP5,MFHAS1,TRAF6,HAND2,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,TRPV4,TGFB2,NCF1,TRAF5,FZD7,MAP3K3,MAP3K11,MBIP,MAP4K2,DUSP19,PDCD10,LTBR,MINK1,RELL1,TAOK2,TRAF3,TAOK1,SERPINF2,MAPK8IP3,TRAF2,DAB2IP,ZNF622,WNT5A,GADD45A,INAVA,DUSP22,HRAS	grey	VSMC_M10
GO:0097623	0.16	0.95	8	11	potassium ion export across plasma membrane	BP	1	ANO6,KCNE2,KCNIP2,DLG1,MIR21,KCNH2,KCNK5,KCNT2	grey	VSMC_M10
GO:0051930	0.16	0.93	14	21	regulation of sensory perception of pain	BP	1	GRIN2D,FAM19A4,P2RX3,F2R,FAM173B,ZFHX2,OPRD1,SLC9A1,NTSR1,COMT,ADRA2C,TMEM100,NMUR2,FABP5	grey	VSMC_M10
GO:0098657	0.16	0.88	89	155	import into cell	BP	1	SLC39A5,SLC12A2,PRKN,SLC22A4,KCNK9,MAPK15,KCNJ4,SLC39A4,STEAP2,SLC1A1,WNK2,SLC1A4,TRPM4,SLC7A11,KCNJ14,SLC8A2,SLC39A12,ATP1A3,AKT2,PRNP,ARL6IP5,SLC7A1,SLC43A1,SLC9A9,KCNJ11,KCNJ3,SLC38A1,SLC6A2,KCNE2,KCNJ15,SLC12A5,SLC6A3,SLC2A10,KCNJ2,SLC12A7,TRPV4,ACSL5,ISCU,AGT,ACE2,ATP1A2,SLC9A1,PER2,SLC12A8,NTSR1,SLC29A2,IL10RA,DLG1,SLC12A9,ITGA4,SLC9A7,ATP1B1,SLC27A1,ARL6IP1,SLC3A2,ACTB,SLC29A4,CLN8,WNK3,ATP1B2,FAM155B,PSEN1,NEURL1B,SLC7A3,SLC5A2,NOX5,SLC39A6,TRPV2,LRRC8E,KCNJ18,SLC46A1,SLC9A6,SLC1A7,TRPV3,TRPV1,P2RX1,PARK7,SLC7A5,LRRC8A,LCN2,SLC12A4,SLC9A5,MIR24-1,SLC36A1,KCNH2,RGS4,KCNJ8,HCN4,KCNJ9	grey	VSMC_M10
GO:0072170	0.16	0.94	11	16	metanephric tubule development	BP	1	POU3F3,OSR1,SOX9,PAX8,PKD2,PAX2,CXCR2,WNT4,PKD1,SOX8,LIF	grey	VSMC_M10
GO:0002418	0.16	0.95	8	11	immune response to tumor cell	BP	1	CD226,IL4I1,NECTIN2,PVR,SLC22A13,IL12A,FBXO38,HAVCR2	grey	VSMC_M10
GO:0042135	0.16	0.95	8	11	neurotransmitter catabolic process	BP	1	HNMT,LRTOMT,AP000812.5,ALDH5A1,COMT,BCHE,ABAT,PRIMA1	grey	VSMC_M10
GO:0097186	0.16	0.94	11	16	amelogenesis	BP	1	PPARA,CNNM4,KLK4,SLC4A2,RELT,ITGB6,TCIRG1,FAM20A,FAM20C,AMELX,PERP	grey	VSMC_M10
GO:1903361	0.16	0.97	5	6	protein localization to basolateral plasma membrane	BP	1	LIN7B,RAB10,LIN7A,AP4M1,PDZD11	grey	VSMC_M10
GO:0048681	0.16	0.95	8	11	negative regulation of axon regeneration	BP	1	SPP1,KIAA0319,KREMEN1,CERS2,LRIG2,TNR,EPHA4,RTN4RL1	grey	VSMC_M10
GO:1900424	0.16	0.95	8	11	regulation of defense response to bacterium	BP	1	SIRT2,FOXP1,F2RL1,MAPKBP1,NOD2,SYT11,CYBA,HAVCR2	grey	VSMC_M10
GO:0002762	0.16	0.91	22	35	negative regulation of myeloid leukocyte differentiation	BP	1	NME1,TRIB1,MYC,TOB2,CDK6,HOXA7,TLR4,PIK3R1,FBXW7,GPR137B,PIAS3,TCTA,UBASH3B,ZBTB46,GPR137,FBN1,INHA,GPR68,PTPN2,MIR125B1,FSTL3,MAFB	grey	VSMC_M10
GO:0043922	0.16	0.95	8	11	negative regulation by host of viral transcription	BP	1	HDAC1,ZNF639,POU2F3,PSMC3,TARDBP,CCL5,JUN,INPP5K	grey	VSMC_M10
GO:0006506	0.16	0.91	20	31	GPI anchor biosynthetic process	BP	1	GPAA1,CWH43,TMEM246,PIGF,PGAP2,PIGU,PIGT,PGAP1,PIGM,PIGV,PIGX,PIGZ,PIGC,PGAP3,PIGH,PIGL,MPPE1,PYURF,PIGB,PIGA	grey	VSMC_M10
GO:0045921	0.16	0.89	38	63	positive regulation of exocytosis	BP	1	VPS4B,PLA2G6,CHMP2A,SDCBP,SPHK2,RAB7A,CACNB2,CLASP2,GAB2,UNC13D,SYT1,RAB5A,SYT9,F2RL1,DNM1L,HYAL3,KCNB1,FGR,STX1A,SNX4,RAB3A,ATP13A2,SYT7,RAB15,STX4,ITGAM,CACNA1G,RAB3D,IL4R,SYTL4,SCAMP5,ATP6AP1,CACNA1H,STXBP1,AP1G1,VPS4A,FGA,DOC2B	grey	VSMC_M10
GO:0051151	0.16	0.93	11	16	negative regulation of smooth muscle cell differentiation	BP	1	NFATC1,ANKRD17,PDCD4,FOXO4,RBPMS2,MECP2,NFATC3,MIR21,PRDM6,EREG,HEY2	grey	VSMC_M10
GO:0000038	0.16	0.92	18	28	very long-chain fatty acid metabolic process	BP	1	HSD17B4,SLC27A6,ACSL6,HACD4,ACOX1,ELOVL1,ELOVL7,ACOX2,PEX2,HACD2,ACSBG1,TECR,ACOT2,ABCD4,HACD3,ABCD3,ACOT4,ELOVL3	grey	VSMC_M10
GO:0006521	0.16	0.95	8	11	regulation of cellular amino acid metabolic process	BP	1	SLC7A11,NR1H4,SIRT4,SLC7A7,COMT,AC138894.1,PARK7,MIR21	grey	VSMC_M10
GO:0009582	0.16	0.89	49	83	detection of abiotic stimulus	BP	1	PKD2L2,PTK2,OPN1SW,PRPH2,PHF24,KIT,CAMKMT,GJA10,WHRN,GRIK2,TRPC3,ASIC3,SCN1A,PLEKHB1,MKS,EPHB1,CEP250,CCDC66,ADGRV1,CDS1,PKD2,PITPNM1,RRH,SAG,TRPM8,NTSR1,BACE1,STRC,NMT1,TTN,KCNK4,GRK4,PKD1L1,KCNA1,ROM1,TCAP,GUCY2D,NGFR,ASIC2,UNC119,TRPV1,PKD1,GNAT2,PIEZO1,PKD1L3,REEP6,PJVK,CHRNA10,GPR88	grey	VSMC_M10
GO:0060079	0.16	0.89	41	69	excitatory postsynaptic potential	BP	1	MAPK8IP2,RIMS2,CHRNA3,CHRNA5,RIMS1,SHANK1,GRIK2,GRIN2D,MTMR2,SLC8A2,GRIK5,CHRNA6,P2RX2,P2RX3,MEF2C,P2RX7,CUX2,PTK2B,PPP3CA,IGSF11,SSH1,STX1A,TMEM25,NPAS4,MPP2,DLG4,NLGN2,CHRNB1,STX1B,NLGN3,CHRNB2,SEZ6,TRPV1,P2RX1,PRKCZ,MECP2,CHRNB4,CHRNA10,CHRNG,GRID2,RGS4	grey	VSMC_M10
GO:0009206	0.16	0.90	29	46	purine ribonucleoside triphosphate biosynthetic process	BP	1	NME1,ATP5MGL,PPARA,IMPDH1,SLC25A13,SPHK2,PRKAG2,ATP5F1C,ATP5F1A,DGUOK,FAM173B,NME4,DNAJC30,ATP5S,PINK1,STAT3,NME7,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,NME6,NUDT2	grey	VSMC_M10
GO:1902358	0.16	0.95	8	11	sulfate transmembrane transport	BP	1	SLC26A10,SLC13A4,SLC26A5,SLC25A30,SLC25A11,SLC26A1,SLC26A2,SLC25A14	grey	VSMC_M10
GO:0014012	0.16	0.97	5	6	peripheral nervous system axon regeneration	BP	1	TSPO,TNC,CERS2,APOD,MIR222	grey	VSMC_M10
GO:0019883	0.16	0.95	8	11	antigen processing and presentation of endogenous antigen	BP	1	HLA-DRA,TAP1,ATG5,IDE,ABCB9,ERAP1,CD74,ERAP2	grey	VSMC_M10
GO:0002082	0.16	0.93	13	19	regulation of oxidative phosphorylation	BP	1	SHMT2,DNAJC15,COX7A1,ACTN3,MLXIPL,PINK1,SLC25A23,SLC25A33,RHOA,COX7A2,UQCC2,COX7A2L,PPIF	grey	VSMC_M10

GO:0090181	0.16	0.91	18	28	regulation of cholesterol metabolic process	BP	1	TTC39B,APOB,NR1H4,CYP7A1,EPHX2,ERLIN1,FMO5,SCAP,POR,ACADL,LPCAT3,GNB3,ACADVL,DGKQ,LDLR,SREBF1,LDLRAP1,FGF1	grey	VSMC_M10
GO:0051953	0.16	0.93	11	16	negative regulation of amine transport	BP	1	ARL6IP5,ADRA2B,SLC43A1,P2RY1,ADRA2A,ADRA2C,SYT11,ABAT,CHGA,RGS4,CRH	grey	VSMC_M10
GO:0140056	0.16	0.89	40	67	organelle localization by membrane tethering	BP	1	STX7,TSNARE1,EXOC4,SCFD2,STX17,PLEK,BVES,PPFIA3,RAB10,SYTL2,RALB,SYT1,CEP290,STX2,SNPH,VPS18,KCNB1,PDZD8,STX1A,STX6,NSF,BLOC1S6,MOSPD3,RAB3A,SNAP29,STX5,RAB8A,PSEN2,RAB15,STX1B,STX4,RAB8B,AC138894.1,STX8,RAB3D,CALM1,VMP1,STXBP2,STXBP1,VAMP3	grey	VSMC_M10
GO:0007610	0.17	0.86	225	406	behavior	BP	1	MAPK8IP2,ADM2,PRRT1,PRKN,AGER,PPARA,TSPO,SYNGAP1,MCHR1,AGTPBP1,NTRK2,PLA2G6,BTBD9,CHRNA3,CHRNA5,GPR37,SRF,TTBK1,ADAM22,CFAP69,APBA1,CNTFR,USP46,KIT,SLC1A1,ADGRF1,ETV1,TMOD1,BRSK1,PRKCE,DNAH11,SHANK1,PPT1,MYH14,PTN,FOXP2,EGFR,SOBP,SLC7A11,NTF4,FIG4,DDO,PRKAR2B,GRIN2D,HDAC2,ADCY3,SLC8A2,NAPEPLD,B4GALT2,DACH1,POU4F1,ALK,CHD8,MKKS,RPTOR,NR1D2,PLCB1,MAFG,PRNP,DDHD2,P2RX2,NRG1,ARL6IP5,TCF15,PLK2,NPHP1,LGI4,GPI,CAMK4,AHCY,PREX2,CASP3,NCOA2,HAND2,P2RX3,MEF2C,ASIC1,HTRA2,CFAP20,CUX2,P2RY1,MME,EIF2AK4,SYNJ1,HOMER1,AMFR,NR4A2,NQO2,GLS,SLC12A5,ATXN1,GRM2,BDNF,SLC4A10,SRD5A1,SLC6A3,ALDH1A3,SORCS3,CPT1A,ADARB1,SCN2A,NLGN4Y,KRAS,GIGYF2,ADNP,TTC21B,ZFHX2,OPRD1,CIART,USP2,AGT,ACE2,ATP1A2,SPTBN2,NFATC4,HDAC4,KCNK2,NPAS4,NTSR1,EPS8,YTHDF1,FZD9,HOMER2,C3orf70,SLC16A1,CREB1,TRMT1L,SPG11,MAPT,ABL2,C1QL1,EIF4EBP2,ZDHHC8,CDH23,COMT,ANKH,TNR,NRXN2,PYY,KCNK4,BCHE,CRTC1,HTT,PPP3CB,GDF15,STAT3,NPTX2,MAPK1,TMOD2,ASIC4,EPHA4,DLG4,SLC2A4,THRA,SDK1,NLGN2,CHRNB1,CLN8,RGS14,ATP1B2,PSEN1,HOXB8,SYT11,ITGA3,NLGN3,FOS,AC138894.1,CHRNB2,UBE2Q1,CLN6,LDLR,GPRASP2,BHLHB9,NMUR2,STRA6,GM2A,NCOR1,INSR,NPC1,SGIP1,LEPR,IFT20,SEZ6,JUN,DAB1,ABAT,AFF2,VWA1,TRPV1,PRKCZ,MECP2,ABCA7,PER3,PARK7,TPGS1,GPR157,TSC1,JPH3,CNTNAP4,STRBP,ZFHX3,MCOLN3,LHX8,HTR1D,ATXN1L,CNTN2,FADD,DPP4,NPB,CEND1,FXN,CRBN,POMK,CRH,GPR88,NRXN3,APH1B,EFNB3,CEBPB,PITX3,MRAP2,MAP1A,FOXO6,DERL2,RASD2	grey	VSMC_M10
GO:0002501	0.17	0.97	5	6	peptide antigen assembly with MHC protein complex	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TAPBPL	grey	VSMC_M10
GO:0006228	0.17	0.97	5	6	UTP biosynthetic process	BP	1	NME1,NME4,NME7,NME3,NME6	grey	VSMC_M10
GO:0080009	0.17	0.93	11	16	mRNA methylation	BP	1	CMTR1,TRMT6,WTAP,METTL8,METTL16,CMTR2,METTL14,TRMT61A,TRMT10C,TRMT61B,CBLL1	grey	VSMC_M10
GO:0006165	0.17	0.89	43	72	nucleoside diphosphate phosphorylation	BP	1	NME1,PPARA,PRXL2C,GAPDH,SLC4A4,BPGM,CMPK1,DHTKD1,PRKAG2,PFKP,GPI,GPD1,P2RX7,PRKAG1,PFKM,NME4,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,DTYMK,HK1,PRKAG3,STAT3,NME7,ENO3,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,NME3,SLC2A6,AK8,ENTPD5,CMPK2,TIGAR,NME6	grey	VSMC_M10
GO:0009249	0.17	0.97	5	6	protein lipoylation	BP	1	LIPT1,NNAT,LIAS,NDUFAB1,GCSH	grey	VSMC_M10
GO:0010692	0.17	0.96	6	8	regulation of alkaline phosphatase activity	BP	1	SEMA4D,MEF2C,GPLD1,TGFB2,SMAD3,PPARGC1B	grey	VSMC_M10
GO:0048247	0.17	0.91	21	33	lymphocyte chemotaxis	BP	1	SLC12A2,CCL27,OXSR1,GAS6,CYP7B1,PTK2B,CCL17,SLC8B1,ADAM8,CH25H,PADI2,CXCL16,TMEM102,CCL14,CCL5,CCL7,CCL2,CCL25,CCL16,WNT5A,CCL22	grey	VSMC_M10
GO:0099633	0.17	0.95	8	11	protein localization to postsynaptic specialization membrane	BP	1	ADAM22,DAG1,DLG1,DLG4,IQSEC2,PRKCZ,CACNG7,HRAS	grey	VSMC_M10
GO:0099645	0.17	0.95	8	11	neurotransmitter receptor localization to postsynaptic specialization membrane	BP	1	ADAM22,DAG1,DLG1,DLG4,IQSEC2,PRKCZ,CACNG7,HRAS	grey	VSMC_M10
GO:0046710	0.17	0.95	8	11	GDP metabolic process	BP	1	DLG2,ENTPD4,NUDT18,MAGI3,DLG1,CASK,CARD11,MPP1	grey	VSMC_M10
GO:0015801	0.17	0.95	8	11	aromatic amino acid transport	BP	1	SLC7A1,OCA2,SLC38A3,ACE2,SLC38A5,SLC3A2,SLC7A5,SLC25A29	grey	VSMC_M10
GO:0009437	0.17	0.95	8	11	carnitine metabolic process	BP	1	CPT1B,SLC22A4,CROT,CPT1A,POR,ACADL,TMLHE,ACADM	grey	VSMC_M10
GO:1905809	0.17	0.96	6	8	negative regulation of synapse organization	BP	1	EPHA7,PTN,ROBO2,SLIT1,NFATC4,WNT5A	grey	VSMC_M10
GO:1903707	0.17	0.88	43	72	negative regulation of hemopoiesis	BP	1	NME1,TRIB1,MYC,TOB2,FBXO7,CDK6,HOXA7,TLR4,FOXJ1,ZC3H8,PIK3R1,FBXW7,TMEM131L,GPR137B,PIAS3,HLX,TCTA,UBASH3B,RUNX3,ZBTB46,BCL6,RC3H1,GPR137,FBN1,TNFSF18,LAG3,INHA,FOXP3,TBX21,ZBTB7B,IL4R,GPR68,CD74,PTPN2,SOCS1,MIR21,MIR222,MIR125B1,FSTL3,MAFB,FGL2,IL17D,RC3H2	grey	VSMC_M10
GO:0048708	0.17	0.89	36	60	astrocyte differentiation	BP	1	LRP1,AGER,SMO,TTBK1,CDK6,ROR2,FPR2,EGFR,TLR4,MYCN,C5AR1,SOX9,KDM4A,TSPAN2,KRAS,TTC21B,MAPT,STAT3,MAPK1,EPHA4,PRPF19,PSEN1,MAPK3,MAP2K1,LDLR,S100A8,MBD1,DAB1,SOX8,LAMC3,CNTN2,CNTF,GPR37L1,NOG,POU3F2,LIF	grey	VSMC_M10
GO:0007612	0.17	0.87	60	104	learning	BP	1	MAPK8IP2,PRKN,SYNGAP1,NTRK2,SRF,KIT,SLC1A1,BRSK1,SHANK1,PPT1,PTN,SLC7A11,PRKAR2B,ADCY3,SLC8A2,B4GALT2,DDHD2,ASIC1,EIF2AK4,SYNJ1,SLC12A5,ATXN1,SORCS3,NLGN4Y,KRAS,AGT,ATP1A2,NPAS4,NTSR1,YTHDF1,CREB1,C1QL1,COMT,TNR,NRXN2,BCHE,HTT,PPP3CB,NPTX2,DLG4,CLN8,RGS14,SYT11,NLGN3,FOS,AC138894.1,CHRNB2,STRA6,INSR,IFT20,JUN,MECP2,ABCA7,JPH3,ATXN1L,CNTN2,CRH,GPR88,NRXN3,MAP1A	grey	VSMC_M10

GO:0016458	0.17	0.87	98	169	gene silencing	BP	1	ZC3H10,BAZ2A,ESR1,CNOT2,CNOT6,PABPC1,MOV10L1,AGO2,H3F3C,TNRC6B,TUT7,XPO5,CNOT11,SCMH1,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,DNMT3A,SETDB2,TNRC6C,SIRT2,TEX15,CLP1,FAM208A,BCDIN3D,CNOT1,CELF1,CNOT6L,EIF4E2,BAHD1,RIPK1,EXD1,PPHLN1,HDAC1,PPP3CA,TERT,AJUBA,ZNFX1,GIGYF2,DDX6,TDRKH,NCBP2,EIF4ENIF1,TET1,PRKRA,DDX3X,STAT3,PHF8,MAP2K1,SMAD3,NRDE2,TNRC6A,CNOT8,NCOR1,SMCHD1,DROSHA,FMR1,CHMP1A,SPOUT1,MIRLET7A2,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR425,MIR125B1,MIR32,MIR22,MIR27B,MIR24-1,MIR7-1,MIR199A2,MIRLET7D,MIR27A,MIR23B,MIR365B,MIR25,MIR491,MIR24-2,MIRLET7A3,SETDB1,AGO4,MIR33B,MIR339,MIR125A,MIR99B,MIR940,MIR1249,MIR1180,BEND3,HIST1H3F,HIST1H3H,ZNF304	grey	VSMC_M10
GO:0060900	0.17	0.96	6	8	embryonic camera-type eye formation	BP	1	FRS2,TFAP2A,PAX2,ALDH1A3,STRA6,WNT5A	grey	VSMC_M10
GO:0002385	0.17	0.94	8	11	mucosal immune response	BP	1	NOD2,OTUD7B,RAB17,NOS2,HIST1H2BK,IFNLR1,HIST1H2BF,HIST1H2BJ	grey	VSMC_M10
GO:0051446	0.17	0.93	11	16	positive regulation of meiotic cell cycle	BP	1	YTHDC2,UBE2B,MAPK15,TOPAZ1,SIRT2,PLCB1,NPM2,OVOL1,WNT4,OOEP,WNT5A	grey	VSMC_M10
GO:0009451	0.17	0.87	82	141	RNA modification	BP	1	RNMT,ADAT2,TFB1M,TRMU,TRMT11,APOBEC3H,C9orf64,CMTR1,MTO1,ELP1,PUS10,TRIT1,DUS4L,NSUN6,THUMPD3,DPH3,TRMT6,BAG4,NUDT16,WTAP,THUMPD2,ALKBH3,TRMT9B,TGS1,DIMT1,ELP4,ELP3,BCDIN3D,TPRKB,NSUN3,RPUSD2,OSGEPL1,FTO,PUS7L,CDKAL1,RPUSD4,TRMT10A,QTRT2,TYW1B,TYW5,ADARB1,GAR1,TRUB1,DALRD3,LCMT2,METTL8,ELP6,NSUN5,METTL2B,TRMT1L,MEPCE,ALKBH8,TRMT5,HSD17B10,MRM2,ZCCHC4,MTFMT,ALKBH1,THG1L,QTRT1,ELP2,THUMPD1,ALKBH5,METTL4,METTL6,PARN,MRM3,PUSL1,METTL16,RPUSD1,AARS,CMTR2,DUS2,CTU1,METTL14,TRMT10B,TRMT61A,RPUSD3,TRMT10C,TRMT61B,CBLL1,TYW3	grey	VSMC_M10
GO:0006490	0.17	0.93	11	16	oligosaccharide-lipid intermediate biosynthetic process	BP	1	ALG12,SRD5A3,ALG2,ALG11,ALG10,DPAGT1,ALG3,ALG9,ALG6,ALG1,DHDDS	grey	VSMC_M10
GO:0018345	0.17	0.91	18	28	protein palmitoylation	BP	1	ZDHHC14,ZDHHC21,ZDHHC20,GOLGA7B,ZDHHC13,ZDHHC23,ZDHHC6,HHAT,ZDHHC18,ZDHHC24,GLUL,ZDHHC8,ZDHHC4,ZDHHC15,ZDHHC12,ZDHHC1,ZDHHC11,MAP6D1	grey	VSMC_M10
GO:0050768	0.17	0.87	59	102	negative regulation of neurogenesis	BP	1	SEMA6A,TSPO,FSTL4,SYNGAP1,SOX10,DAAM2,SEMA4D,SEMA4C,RTN4,RUFY3,EPHA7,PTN,MYCN,KDM4A,HOOK3,SIRT2,SEMA3D,SPART,SEMA3A,ULK1,RYK,SEMA4F,TLX2,RAPGEF2,NKX6-1,SEMA3G,SPP1,SEMA4G,RNF10,KIAA0319,PPP3CA,SEMA3F,SORL1,CERS2,NFATC4,DLX1,WNT3,DUSP10,SEMA6D,TNR,BMPR1A,PSEN1,SEMA4A,TRIM46,NTN1,LDLR,CDK5R1,MBD1,DAB1,SKI,ARHGAP4,PLXNA3,GPR37L1,NOG,THY1,WNT5A,YWHAH,EFNB3,PITX3	grey	VSMC_M10
GO:0009199	0.17	0.88	39	64	ribonucleoside triphosphate metabolic process	BP	1	NME1,ATP5MGL,PPARA,GTPBP1,IMPDH1,SLC25A13,RAB23,SPHK2,PRKAG2,ATP5F1C,ATP5F1A,DGUOK,OPA1,ENTPD4,FAM173B,NME4,MFN1,CTPS2,DNAJC30,EFL1,ATP5S,PINK1,STAT3,NME7,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,GNAI3,UCK1,MT-ATP8,MT-ATP6,RHOA,ATP5ME,ATP5MF,NME6,NUDT2	grey	VSMC_M10
GO:0031065	0.17	0.92	12	18	positive regulation of histone deacetylation	BP	1	C6orf89,PRKD2,SDR16C5,ING2,BCL6,PINK1,AKAP8L,AKAP8,JDP2,ZBTB7B,SREBF1,SAP30BP	grey	VSMC_M10
GO:0003009	0.17	0.90	19	30	skeletal muscle contraction	BP	1	STAC3,TNNI3,MYH14,STAC,NR4A1,HOMER1,TNNC1,KCNJ2,TNNI1,SYNM,MYH7,CASQ1,ACTN3,CHRNB1,TCAP,STAC2,ATP2A1,DMD,TNNC2	grey	VSMC_M10
GO:0018095	0.18	0.94	8	11	protein polyglutamylation	BP	1	CFAP20,TTLL13P,TTLL4,TTLL5,TPGS2,TPGS1,TTLL11,TTLL7	grey	VSMC_M10
GO:0048243	0.18	0.94	8	11	norepinephrine secretion	BP	1	ADRA2B,P2RY1,ADRA2A,KCNB1,AGT,STX1A,ADRA2C,CRH	grey	VSMC_M10
GO:0051561	0.18	0.94	8	11	positive regulation of mitochondrial calcium ion concentration	BP	1	MCUR1,RAP1GDS1,FIS1,MICU1,MCU,ATP2A1,SLC25A23,BCAP31	grey	VSMC_M10
GO:0015872	0.18	0.91	18	28	dopamine transport	BP	1	PRKN,MAPK15,SYT1,SYT9,CHRM5,SLC6A2,DTNBP1,SYT8,GRM2,SLC6A3,RAB3A,PINK1,SLC29A4,SYT7,SYT11,CHRNB2,ABAT,PARK7	grey	VSMC_M10
GO:0021801	0.18	0.92	12	18	cerebral cortex radial glia-guided migration	BP	1	SUN2,MBOAT7,RTN4,SRGAP2C,DISC1,CDK5R1,DAB1,LRP8,DAB2IP,ADGRG1,FOXG1,LAMB1	grey	VSMC_M10
GO:0022030	0.18	0.92	12	18	telencephalon glial cell migration	BP	1	SUN2,MBOAT7,RTN4,SRGAP2C,DISC1,CDK5R1,DAB1,LRP8,DAB2IP,ADGRG1,FOXG1,LAMB1	grey	VSMC_M10
GO:0002705	0.18	0.88	45	76	positive regulation of leukocyte mediated immunity	BP	1	CD226,STX7,HLA-DRA,KIT,EXOSC3,MSH2,RSAD2,HMCES,NECTIN2,PVR,MLH1,SLC22A13,PAXIP1,SHLD1,MAVS,HPX,TRAF6,RASGRP1,F2RL1,NOD2,CD40,DENND1B,CD28,CADM1,FZD5,IL12A,LAG3,STAT5B,FOXP3,ZBTB1,SHLD2,TBX21,STX4,ITGAM,BTK,FBXO38,VAV1,C3,NOS2,TICAM1,PRKCZ,TRAF2,AP1G1,FADD,FCER2	grey	VSMC_M10
GO:0006907	0.18	0.92	12	18	pinocytosis	BP	1	PPT1,NR1H2,SNX5,NR1H3,MAPKAPK3,CARMIL1,MAPKAPK2,ANKFY1,STX1B,DOCK2,AC138894.1,DNM2	grey	VSMC_M10
GO:0061098	0.18	0.89	27	44	positive regulation of protein tyrosine kinase activity	BP	1	ERBB3,EPGN,AREG,TGFA,ABI1,HBEGF,PRNP,NRG1,GAS6,ERCC6,FBXW7,NEURL1,ADRA2A,NCF1,EGF,CASS4,AGT,DOK7,EPHA4,DLG4,DVL2,EFNA1,CCL5,CSF1R,UNC119,LRP8,EREG	grey	VSMC_M10
GO:0009062	0.18	0.87	51	86	fatty acid catabolic process	BP	1	HSD17B4,AIG1,CPT1B,PPARA,MCAT,ECHDC1,CROT,ETFB,LPIN1,FAAH,HADHA,ACOX1,AKT2,HACL1,ACOXL,ACOX2,PEX2,ETFDH,IVD,LPIN3,ECI2,ADTRP,LONP2,MCEE,IRS1,CPT1A,BDH2,ABHD2,ABCB11,EHHADH,ACADL,TYSND1,ACADVL,HSD17B10,ABCD4,GCDH,ABHD3,LPIN2,ACAA2,DECR2,CEL,MLYCD,ABCD3,PLA2G15,ACADM,PHYH,HADHB,AMACR,NUDT19,ECI1,AUH	grey	VSMC_M10

GO:1901184	0.18	0.88	40	67	regulation of ERBB signaling pathway	BP	1	RTN4,ACP4,EPGN,AREG,TGFA,EGFR,RAB7A,NEU3,SNX5,HBEGF,PDE6G,FER,HIP1R,FBXW7,PTPRJ,WDR54,NEURL1,ADRA2A,RNF115,NCF1,EGF,GPER1,DGKD,IFI6,AGT,CBL,PDE6H,SNX6,ZFYVE28,SOCS4,HAP1,RBPJ,PSEN1,PTPN2,RNF126,MVB12B,DAB2IP,MIR29A,MIR21,EREG	grey	VSMC_M10
GO:0048499	0.18	0.91	15	23	synaptic vesicle membrane organization	BP	1	SYNGR1,GRIK5,SYT1,STX2,SYT9,SNAP23,STX1A,RAB3A,SNAP29,CPLX1,STX1B,STX4,SNAPIN,STXBP1,SNAP47	grey	VSMC_M10
GO:0048312	0.18	0.95	6	8	intracellular distribution of mitochondria	BP	1	ARMC1,OPA1,DNM1L,MAPT,BHLHA15,CLUH	grey	VSMC_M10
GO:2000311	0.18	0.92	12	18	regulation of AMPA receptor activity	BP	1	MAPK8IP2,PRRT1,SHANK1,MEF2C,CNIH2,MINK1,NLGN2,CNIH3,NLGN3,CACNG7,SHISA8,CACNG5	grey	VSMC_M10
GO:0044275	0.18	0.90	19	30	cellular carbohydrate catabolic process	BP	1	MIOX,MGAM,PYGB,PPP1CB,PPP1R3B,GK5,PFKM,PPP1R3D,TREH,SORD,PYGM,PYGL,TKFC,ENOSF1,AGL,ABHD10,TIGAR,IDNK,NEU2	grey	VSMC_M10
GO:0009072	0.18	0.92	11	16	aromatic amino acid family metabolic process	BP	1	TPH2,IL4I1,HPDL,IDO2,IDO1,HGD,FAH,GCDH,GSTZ1,PARK7,PCBD2	grey	VSMC_M10
GO:0015696	0.18	0.95	6	8	ammonium transport	BP	1	SLC12A2,AQP1,SLC12A7,RHCG,RHBG,SLC12A4	grey	VSMC_M10
GO:0072488	0.18	0.95	6	8	ammonium transmembrane transport	BP	1	SLC12A2,AQP1,SLC12A7,RHCG,RHBG,SLC12A4	grey	VSMC_M10
GO:0051961	0.18	0.87	61	106	negative regulation of nervous system development	BP	1	SEMA6A,TSPO,FSTL4,SYNGAP1,SOX10,DAAM2,SEMA4D,SEMA4C,RTN4,RUFY3,EPHA7,PTN,MYCN,KDM4A,HOOK3,SIRT2,SEMA3D,SPART,SEMA3A,ULK1,RYK,ROBO2,SEMA4F,TLX2,RAPGEF2,SLIT1,NKX6-1,SEMA3G,SPP1,SEMA4G,RNF10,KIAA0319,PPP3CA,SEMA3F,SORL1,CERS2,NFATC4,DLX1,WNT3,DUSP10,SEMA6D,TNR,BMPR1A,PSEN1,SEMA4A,TRIM46,NTN1,LDLR,CDK5R1,MBD1,DAB1,SKI,ARHGAP4,PLXNA3,GPR37L1,NOG,THY1,WNT5A,YWHAH,EFNB3,PITX3	grey	VSMC_M10
GO:0072329	0.18	0.87	56	95	monocarboxylic acid catabolic process	BP	1	HSD17B4,AIG1,CPT1B,PPARA,MCAT,ECHDC1,CROT,ETFB,LPIN1,FAAH,HADHA,AKR1A1,ACOX1,XYLB,AKT2,HACL1,ACOXL,ACOX2,PEX2,ETFDH,IVD,LPIN3,HOGA1,ECI2,ADTRP,LONP2,MCEE,IRS1,CPT1A,BDH2,ABHD2,ABCB11,EHHADH,ACADL,FAH,TYSND1,ACADVL,HSD17B10,ABCD4,GCDH,ABHD3,LPIN2,ACAA2,DECR2,CEL,MLYCD,ABCD3,PLA2G15,ACADM,PHYH,HADHB,AMACR,NUDT19,IDNK,ECI1,AUH	grey	VSMC_M10
GO:0007613	0.18	0.87	50	86	memory	BP	1	PLA2G6,BTBD9,SRF,SLC1A1,ADGRF1,SHANK1,PTN,NTF4,SLC8A2,B4GALT2,PLCB1,PRNP,PLK2,CAMK4,ASIC1,CUX2,EIF2AK4,NQO2,ATXN1,BDNF,SORCS3,SCN2A,ADNP,NFATC4,KCNK2,NPAS4,YTHDF1,CREB1,MAPT,EIF4EBP2,COMT,KCNK4,CRTC1,PPP3CB,SLC2A4,RGS14,PSEN1,SYT11,ITGA3,CHRNB2,LDLR,INSR,PRKCZ,MECP2,ABCA7,JPH3,ATXN1L,CEBPB,MAP1A,FOXO6	grey	VSMC_M10
GO:1900452	0.18	0.95	6	8	regulation of long-term synaptic depression	BP	1	AGER,SORCS3,KCNB1,MAPT,FMR1,GRID2	grey	VSMC_M10
GO:0021795	0.18	0.90	20	32	cerebral cortex cell migration	BP	1	SUN2,EFHC1,MBOAT7,RTN4,POU3F3,ROBO1,SRGAP2C,DISC1,DIXDC1,PSEN1,NDEL1,CDK5R1,DAB1,LRP8,DAB2IP,RHOA,ADGRG1,FOXG1,LAMB1,POU3F2	grey	VSMC_M10
GO:0030641	0.18	0.88	38	64	regulation of cellular pH	BP	1	SLC4A4,PPT1,RAB7A,ATP6V0E2,LACC1,SLC4A2,AQP11,SLC4A7,TMEM106B,MAFG,ATP6V1H,TM9SF4,SLC9A9,HVCN1,SLC4A10,SLC9B1,TMEM9,TCIRG1,SLC9A8,SLAMF8,SLC9A1,CLIC4,SLC11A1,SLC9A7,ATP6V0A1,MAPK1,DMXL2,SLC4A3,MAPK3,AC138894.1,CLN6,SNAPIN,TMEM199,SLC9A6,ATP6AP1,SLC9A5,CA2,RAB39A	grey	VSMC_M10
GO:0051127	0.18	0.93	9	13	positive regulation of actin nucleation	BP	1	WASF1,FCHSD2,FMN1,CYFIP1,MAGEL2,WASF2,WHAMM,NCKAP1,WAS	grey	VSMC_M10
GO:0002495	0.18	0.92	11	16	antigen processing and presentation of peptide antigen via MHC class II	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TRAF6,MARCH8,FCER1G,PIKFYVE,CTSV,DNM2,CD74	grey	VSMC_M10
GO:0003266	0.18	0.95	6	8	regulation of secondary heart field cardioblast proliferation	BP	1	HAND2,EYA1,TBX5,MKS1,ISL1,SIX1	grey	VSMC_M10
GO:0035912	0.18	0.95	6	8	dorsal aorta morphogenesis	BP	1	SRF,BMPR1A,RBPJ,ENG,ACVRL1,HEY2	grey	VSMC_M10
GO:1903351	0.18	0.88	33	55	cellular response to dopamine	BP	1	PRKN,ATF4,SLC1A1,VPS35,HDAC2,ALK,HTR7,CHRM5,CHRM4,DTNBP1,CHRM3,CALY,HTR3B,MAPK1,CHRM1,GNB5,NSG1,HRH2,HCN3,MAPK3,DNM2,SIN3A,HRH4,GNAL,GNB1,GNA15,PALM,GNAI3,HTR1D,RGS4,GNA14,GNG2,ARPP19	grey	VSMC_M10
GO:0060213	0.18	0.93	9	13	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	BP	1	PABPC1,AGO2,TNRC6B,TNRC6C,CNOT1,EIF4ENIF1,POLR2G,TOB1,TNRC6A	grey	VSMC_M10
GO:0010807	0.18	0.95	6	8	regulation of synaptic vesicle priming	BP	1	NAPA,NAPB,STX1A,RAB3A,STX1B,STXBP1	grey	VSMC_M10
GO:0009311	0.18	0.89	27	44	oligosaccharide metabolic process	BP	1	ST6GAL2,MGAM,BRAF,NEU3,ST8SIA4,MOGS,ST3GAL6,GANC,ST8SIA2,B3GALT1,TREH,GAL3ST3,MGAT2,B3GALNT1,GAL3ST4,IDUA,ST8SIA5,GLA,GM2A,ST6GALNAC4,ST3GAL2,CTBS,ST6GALNAC5,FBP2,FUT4,NEU2,ST8SIA6	grey	VSMC_M10
GO:1902106	0.18	0.87	41	69	negative regulation of leukocyte differentiation	BP	1	NME1,TRIB1,MYC,TOB2,FBXO7,CDK6,HOXA7,TLR4,FOXJ1,ZC3H8,PIK3R1,FBXW7,TMEM131L,GPR137B,PIAS3,HLX,TCTA,UBASH3B,RUNX3,ZBTB46,BCL6,RC3H1,GPR137,FBN1,TNFSF18,LAG3,INHA,FOXP3,TBX21,ZBTB7B,IL4R,GPR68,CD74,PTPN2,SOCS1,MIR21,MIR125B1,FSTL3,MAFB,FGL2,RC3H2	grey	VSMC_M10
GO:0072176	0.18	0.93	9	13	nephric duct development	BP	1	EPHA7,OSR1,WNT11,PKD2,PAX2,EPHA4,LHX1,GPC3,PKD1	grey	VSMC_M10
GO:0007215	0.18	0.89	21	34	glutamate receptor signaling pathway	BP	1	GRM4,GRM8,SLC1A1,GRIK2,GRIN2D,GRIK5,PLCB1,PRNP,PTK2B,TIAM1,HOMER1,GRM2,TRPM1,KCNB1,GRIK4,HOMER2,DAGLB,AC138894.1,CDK5R1,FMR1,GRID2	grey	VSMC_M10
GO:0000820	0.19	0.95	6	8	regulation of glutamine family amino acid metabolic process	BP	1	SLC7A11,NR1H4,SIRT4,SLC7A7,AC138894.1,MIR21	grey	VSMC_M10
GO:0030890	0.19	0.90	19	30	positive regulation of B cell proliferation	BP	1	IL5,TNFRSF13C,PELI1,TLR4,BMI1,NCKAP1L,MEF2C,IL7,CD40,BCL6,CD38,BST1,CARD11,CHRNB2,CD74,CD320,TICAM1,VAV3,TNFSF13B	grey	VSMC_M10
GO:0014848	0.19	0.95	6	8	urinary tract smooth muscle contraction	BP	1	PLA2G6,P2RX2,P2RX3,KCNMA1,TBX2,TRPV1	grey	VSMC_M10
GO:0046341	0.19	0.93	9	13	CDP-diacylglycerol metabolic process	BP	1	AGPAT4,AGPAT1,TAMM41,CDS2,CDS1,GPAM,AGPAT2,LCLAT1,CDIPT	grey	VSMC_M10
GO:0000272	0.19	0.93	9	13	polysaccharide catabolic process	BP	1	MGAM,PYGB,PPP1CB,PPP1R3B,PFKM,PPP1R3D,PYGM,PYGL,AGL	grey	VSMC_M10
GO:0009251	0.19	0.93	9	13	glucan catabolic process	BP	1	MGAM,PYGB,PPP1CB,PPP1R3B,PFKM,PPP1R3D,PYGM,PYGL,AGL	grey	VSMC_M10

GO:0044247	0.19	0.93	9	13	cellular polysaccharide catabolic process	BP	1	MGAM,PYGB,PPP1CB,PPP1R3B,PFKM,PPP1R3D,PYGM,PYGL,AGL	grey	VSMC_M10
GO:0046530	0.19	0.89	25	41	photoreceptor cell differentiation	BP	1	AGTPBP1,NTRK2,PRPH2,RORB,RDH13,PTN,SOX9,MYO7A,DZANK1,FSCN2,CEP290,USH1C,C8orf37,RPGRIP1L,NKD1,NRL,DLX1,STAT3,ROM1,IFT20,SOX8,OLFM3,CNTF,THY1,DIO3	grey	VSMC_M10
GO:0002753	0.19	0.88	32	53	cytoplasmic pattern recognition receptor signaling pathway	BP	1	TNFAIP3,USP15,HSPA1B,ANKRD17,SLC46A2,TLR4,PUM2,PHB,LACC1,SEC14L1,CLPB,NPLOC4,IRF7,TRAF6,OAS3,RIPK2,OTULIN,NOD2,IFIH1,OASL,MAP2K6,TIFA,ALPK1,NLRX1,BIRC3,TKFC,TSPAN6,RIOK3,RNF135,ZCCHC3,IRGM,INAVA	grey	VSMC_M10
GO:0042796	0.19	0.95	6	8	snRNA transcription by RNA polymerase III	BP	1	SNAPC3,ZC3H8,ELL,ICE2,SNAPC5,SNAPC4	grey	VSMC_M10
GO:0015701	0.19	0.91	13	20	bicarbonate transport	BP	1	SLC26A10,SLC4A4,CYB5R4,SLC26A5,SLC4A2,SLC4A7,SLC4A10,CYB5R1,SLC4A3,SLC26A1,CA4,SLC26A2,CYB5RL	grey	VSMC_M10
GO:0001911	0.19	0.95	6	8	negative regulation of leukocyte mediated cytotoxicity	BP	1	NCKAP1L,PPP3CB,IL7R,CRK,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0090037	0.19	0.95	6	8	positive regulation of protein kinase C signaling	BP	1	PLA2G6,SPHK2,WNT11,ADGRV1,CD40,WNT5A	grey	VSMC_M10
GO:0035561	0.19	0.91	13	20	regulation of chromatin binding	BP	1	ZNF618,MED25,FBH1,BTAF1,HMBOX1,EBF2,PPP3CA,PARP9,DTX3L,NFATC4,MEPCE,DDX11,ZNF304	grey	VSMC_M10
GO:0036230	0.19	0.90	18	28	granulocyte activation	BP	1	ENPP3,CXCL8,IL15,TRAF3IP2,MYD88,F2RL1,FCER1G,CXCR2,STX4,ITGAM,SCNN1B,CCL5,STXBP2,PRAM1,DNASE1,KARS,CXCL6,MIR125A	grey	VSMC_M10
GO:0035865	0.19	0.95	6	8	cellular response to potassium ion	BP	1	SLC12A2,HSF1,DLG2,CARF,DLG4,CACNA1H	grey	VSMC_M10
GO:0072033	0.19	0.95	6	8	renal vesicle formation	BP	1	SMO,SOX9,FMN1,SALL1,WNT4,SOX8	grey	VSMC_M10
GO:0034315	0.19	0.91	12	18	regulation of Arp2/3 complex-mediated actin nucleation	BP	1	PICK1,WASF1,FCHSD2,ARFIP2,HIP1R,CYFIP1,AP1AR,WASF2,NCKAP1,WAS,WDR63,GMFG	grey	VSMC_M10
GO:0072077	0.19	0.91	12	18	renal vesicle morphogenesis	BP	1	SMO,SIX2,SOX9,PAX8,FMN1,PAX2,SALL1,WNT4,CITED1,LHX1,SOX8,LIF	grey	VSMC_M10
GO:0015849	0.19	0.85	115	203	organic acid transport	BP	1	ATP8B1,SLC26A10,SLC16A7,CPT1B,SLC12A2,SLC27A6,PPARA,SLC22A4,NTRK2,PLA2G6,PLIN2,CROT,ABCB1,APBA1,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC26A5,SLC25A30,LLGL2,SLC22A13,SLC25A38,AKT2,ABCC4,SLC38A10,SLC6A15,SLC25A15,SLC23A2,ARL6IP5,SLC7A1,SLC38A9,SLC5A8,CYP7A1,SLC43A1,SERINC5,SLC38A4,SLC38A2,SLC38A1,SLC10A6,ABCC2,PLA2R1,ABCG2,OCA2,GRM2,SFXN2,SLC38A11,SLC38A3,CPT1A,MAP2K6,ACSL5,SLC7A7,FABP4,ABCB11,AGT,SLC25A20,ABCC5,ACE2,ATP1A2,SLCO1A2,SLCO1C1,PER2,NTSR1,SLC16A1,PLA2G4A,FIS1,SLC11A1,PQLC2,SLC27A1,SLC38A5,MPC2,ARL6IP1,SLC3A2,SLC38A6,PRAF2,SLC25A11,SLC29A4,CLN8,SLC26A1,PSEN1,SLC25A44,SLC7A3,ABCD4,AC138894.1,ABCC3,NMUR2,SLC25A47,SLC6A7,SLC26A2,LRRC8E,EMB,SLC46A1,SLC25A14,PROCA1,ABAT,SLC1A7,TRPV1,SLC7A5,LRRC8A,ABCD3,STXBP1,SLC7A6,FABP5,SLC36A1,LRRC8D,SLC6A19,SLC25A45,XK,PLA2G2C,SLC25A21,SLC25A32,RGS4,SLC25A29,PTGES	grey	VSMC_M10
GO:0006497	0.19	0.87	48	81	protein lipidation	BP	1	ATG12,ZDHHC14,GPAA1,ZDHHC21,CWH43,TMEM246,PIGF,ATG5,PGAP2,ZDHHC20,PIGU,ATG10,GOLGA7B,ZDHHC13,PIGT,GPLD1,PGAP1,ZDHHC23,ZDHHC6,RABL3,ATG16L1,PIGM,HHAT,ZDHHC18,PIGV,ZDHHC24,PIGX,GLUL,PIGZ,NMT1,ZDHHC8,PIGC,PPM1A,ZDHHC4,WIPI2,PGAP3,PIGH,ZDHHC15,PIGL,MPPE1,ZDHHC12,ZDHHC1,ZDHHC11,IRGM,PYURF,PIGB,PIGA,MAP6D1	grey	VSMC_M10
GO:0070571	0.19	0.93	9	13	negative regulation of neuron projection regeneration	BP	1	SPP1,KIAA0319,KREMEN1,CERS2,LRIG2,TNR,EPHA4,RTN4RL1,THY1	grey	VSMC_M10
GO:0006672	0.19	0.87	46	78	ceramide metabolic process	BP	1	ORMDL2,B4GALNT1,PLA2G6,SPTLC1,PPP2R1A,SMPD2,AGK,SPHK2,ACER3,ELOVL1,NEU3,SPTLC3,SIRT3,NSMAF,ASAH1,ST8SIA4,HTRA2,ORMDL1,COL4A3BP,ST8SIA2,SGMS2,B3GALT1,CERS6,CERS2,ABCA12,SMPD4,SGMS1,CLN8,DEGS1,ALOXE3,GALC,CLN6,GLA,HEXA,GM2A,P2RX1,CEL,ST6GALNAC4,ST3GAL2,PLA2G15,ST6GALNAC5,CYP4F22,ACER2,NEU2,B4GALT3,ST8SIA6	grey	VSMC_M10
GO:0006820	0.19	0.84	178	319	anion transport	BP	1	ATP8B1,SLC26A10,SLC16A7,SLC12A2,SLC27A6,TSPO,GOPC,NTRK2,PLA2G6,ABCB1,ABCC10,GABRA1,APBA1,SLC35B2,CLIC5,SLC1A1,SLC25A13,SLC3A1,SLC4A4,CYB5R4,SLC35A1,SLC1A4,SLC13A4,TCAF2,CLCN1,SFRP4,SLC7A11,SLC26A5,ANO10,SLC25A30,SLC4A2,ASIC3,LLGL2,CLNS1A,CCT8L2,SLC22A13,SLC25A38,SLC24A3,ABCC4,SLC20A2,SLC4A7,SLC6A15,SLC25A15,SLC23A2,PRNP,CLIC1,ARL6IP5,SLC7A1,SLC38A9,ANO4,SLC5A8,MFSD5,CYP7A1,SLCO6A1,SLC43A1,SLC9A9,SLC33A1,SERINC5,STC1,SLC38A2,SLC38A1,RIPK1,ANO6,CRY2,SLC10A6,COL4A3BP,ABCC2,PLA2R1,ABCG2,SLC12A5,ADAMTS8,GRM2,SLC4A10,SFXN2,CYB5R1,SLC37A1,CALHM1,SLC2A10,SLC38A3,MAP2K6,SLC12A7,SLC37A2,SLC16A6,SLC7A7,SLCO3A1,SLC9A8,CLCN4,ABCB11,AGT,ABCC5,ACE2,IP6K2,ATP1A2,SLC9A1,TMEM206,SLCO1A2,SLCO1C1,SLC37A4,PER2,SLC12A8,NTSR1,XPR1,CLIC4,SLC16A1,PLA2G4A,SLC12A9,ANKH,SLC25A42,SLC11A1,MFSD10,SLC9A7,SLC2A2,PQLC2,SLC27A1,SLC38A5,MPC2,ANO8,ARL6IP1,SLC3A2,SLC2A9,SLC38A6,SLC35A2,SLC4A3,PRAF2,SLC25A11,SLC16A13,CLN8,TTYH3,SLC26A1,PSEN1,SLC7A3,SLC35B1,AC138894.1,ABCC3,NMUR2,CA4,SLC6A7,SLC26A2,LRRC8E,EMB,NOS2,SLC25A23,SLC25A41,SLC46A1,SLC25A14,PROCA1,SLC9A6,ABAT,CYB5RL,GABRE,GABRA3,SLC1A7,TRPV1,CLCN7,SLC2A6,SLC16A4,SLC7A5,LRRC8A,SLC25A25,ABCD3,STXBP1,CLCA2,SLC7A6,SLC12A4,SLC9A5,SLC25A3,SLC36A1,LRRC8D,LRRC8B,CA2,PLA2G2C,SLC25A21,SLC25A32,RGS4,CPTP,SLC25A29,PTGES,CEBPB	grey	VSMC_M10

GO:0009132	0.19	0.86	55	94	nucleoside diphosphate metabolic process	BP	1	NME1,PPARA,PRXL2C,GAPDH,SLC4A4,NT5E,BPGM,CMPK1,ENTPD6,DLG2,NUDT5,DHTKD1,PRKAG2,PFKP,NUDT16,GPI,GPD1,P2RX7,PRKAG1,PFKM,ENTPD4,NUDT18,NME4,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,DTYMK,MAGI3,DLG1,HK1,CASK,PRKAG3,STAT3,NME7,ENO3,CARD11,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,NME3,MPP1,SLC2A6,AK8,ENTPD5,CMPK2,TIGAR,NME6	grey	VSMC_M10
GO:1902023	0.19	0.95	6	8	L-arginine transport	BP	1	SLC7A1,SLC38A9,AGT,SLC11A1,SLC7A3,SLC25A29	grey	VSMC_M10
GO:0090205	0.19	0.95	6	8	positive regulation of cholesterol metabolic process	BP	1	CYP7A1,SCAP,POR,SREBF1,LDLRAP1,FGF1	grey	VSMC_M10
GO:0018242	0.19	0.95	6	8	protein O-linked glycosylation via serine	BP	1	MGAT5B,POGLUT1,GALNT2,KDELC2,GALNT16,GALNT1	grey	VSMC_M10
GO:0007413	0.19	0.91	13	20	axonal fasciculation	BP	1	TNFRSF21,RTN4,NRCAM,MEGF8,SEMA3A,CASP3,NCAM2,CRTAC1,EPHB3,EPHA4,CDK5R1,AMIGO1,CNTN2	grey	VSMC_M10
GO:0106030	0.19	0.91	13	20	neuron projection fasciculation	BP	1	TNFRSF21,RTN4,NRCAM,MEGF8,SEMA3A,CASP3,NCAM2,CRTAC1,EPHB3,EPHA4,CDK5R1,AMIGO1,CNTN2	grey	VSMC_M10
GO:0033605	0.19	0.95	6	8	positive regulation of catecholamine secretion	BP	1	SYT1,KCNB1,GRK2,STX1A,PINK1,CHRNB2	grey	VSMC_M10
GO:0090219	0.19	0.95	6	8	negative regulation of lipid kinase activity	BP	1	PIP4K2C,PIP4K2A,PPP2R5A,RUBCN,PIK3IP1,DAB2IP	grey	VSMC_M10
GO:0007260	0.19	0.88	32	53	tyrosine phosphorylation of STAT protein	BP	1	HSF1,KIT,PPP2R1A,IL15,HDAC2,PIBF1,HPX,FER,OSBP,ARL2BP,CD40,HDAC1,HCLS1,PARP9,PARP14,OSM,IL12A,TNFSF18,FGFR3,CTF1,IL6R,CCL5,CSF1R,ISL1,SUZ12,GHR,PTPN2,SOCS1,CNTF,MIR125A,LIF,TSLP	grey	VSMC_M10
GO:0007210	0.19	0.93	9	13	serotonin receptor signaling pathway	BP	1	HTR7,CHRM5,CHRM4,CHRM3,HTR3B,CHRM1,HRH2,HRH4,HTR1D	grey	VSMC_M10
GO:0086046	0.19	0.97	4	5	membrane depolarization during SA node cell action potential	BP	1	SCN5A,ANK2,CACNA1G,HCN4	grey	VSMC_M10
GO:0051957	0.19	0.93	9	13	positive regulation of amino acid transport	BP	1	SLC12A2,SLC38A3,AGT,ACE2,NTSR1,ARL6IP1,PSEN1,ABAT,STXBP1	grey	VSMC_M10
GO:0070536	0.19	0.89	20	32	protein K63-linked deubiquitination	BP	1	SHMT2,TNFAIP3,OTUD1,OTUD4,USP25,USP16,ABRAXAS1,OTUD7A,USP13,SPATA2,YOD1,OTUD7B,ABRAXAS2,OTUD5,STAMBPL1,UIMC1,OTUB2,USP20,STAMBP,BRCC3	grey	VSMC_M10
GO:0019321	0.19	0.93	8	11	pentose metabolic process	BP	1	UXS1,DHDH,NUDT5,XYLB,RBKS,RPE,FGGY,RPIA	grey	VSMC_M10
GO:0002634	0.19	0.95	6	8	regulation of germinal center formation	BP	1	TNFAIP3,FOXJ1,MEF2C,BCL6,RC3H1,TNFSF13B	grey	VSMC_M10
GO:0002279	0.19	0.88	24	39	mast cell activation involved in immune response	BP	1	ENPP3,RAC2,KIT,SPHK2,GAB2,UNC13D,FER,RASGRP1,SNAP23,LAT2,FGR,CBL,SNX4,PTGDR,C12orf4,LAT,IL4R,S100A13,BTK,STXBP2,PDPK1,FOXF1,STXBP1,CHGA	grey	VSMC_M10
GO:0030517	0.19	0.89	22	36	negative regulation of axon extension	BP	1	SEMA6A,SEMA4D,SEMA4C,RTN4,SEMA3D,SEMA3A,RYK,SEMA4F,SEMA3G,SEMA4G,KIAA0319,SEMA3F,WNT3,SEMA6D,TNR,SEMA4A,TRIM46,NTN1,CDK5R1,ARHGAP4,PLXNA3,WNT5A	grey	VSMC_M10
GO:0060914	0.19	0.90	17	27	heart formation	BP	1	LEMD2,PIM1,FOXH1,WNT11,HAND2,EYA1,ROBO1,ROBO2,MEF2C,TBX5,AXIN2,BMPR1A,RBPJ,MKS1,ISL1,WNT5A,SIX1	grey	VSMC_M10
GO:0055081	0.19	0.90	17	27	anion homeostasis	BP	1	SLC12A2,CKB,SLC1A1,TFAP2B,SFRP4,SLC7A11,GLS,ABCC2,SLC12A5,GRM2,SLC12A7,SLC12A8,XPR1,CPS1,SLC12A9,FGFR4,SLC12A4	grey	VSMC_M10
GO:0031341	0.19	0.88	28	46	regulation of cell killing	BP	1	CD226,STX7,AGER,HLA-DRA,NECTIN2,PVR,SLC22A13,NCKAP1L,P2RX7,RASGRP1,F2RL1,CADM1,IL12A,LAG3,PPP3CB,STAT5B,ITGAM,VAV1,NOS2,IL7R,CRK,DNASE1,AP1G1,FADD,CXCL6,FCER2,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0042058	0.19	0.87	37	62	regulation of epidermal growth factor receptor signaling pathway	BP	1	EPGN,AREG,TGFA,EGFR,RAB7A,NEU3,SNX5,HBEGF,PDE6G,FER,HIP1R,FBXW7,PTPRJ,WDR54,NEURL1,ADRA2A,RNF115,NCF1,EGF,GPER1,DGKD,IFI6,AGT,CBL,PDE6H,SNX6,ZFYVE28,SOCS4,HAP1,PSEN1,PTPN2,RNF126,MVB12B,DAB2IP,MIR29A,MIR21,EREG	grey	VSMC_M10
GO:0001696	0.19	0.95	6	8	gastric acid secretion	BP	1	CCKBR,HIP1R,CHRM5,HRH2,TRPV1,SNX10	grey	VSMC_M10
GO:0042462	0.19	0.91	13	20	eye photoreceptor cell development	BP	1	NTRK2,RORB,RDH13,MYO7A,DZANK1,FSCN2,CEP290,USH1C,RPGRIP1L,NRL,OLFM3,THY1,DIO3	grey	VSMC_M10
GO:0046928	0.19	0.87	39	66	regulation of neurotransmitter secretion	BP	1	SNCAIP,PRKN,CHRNA3,CHRNA5,APBA1,RIMS1,RIMS3,CACNB2,SYT1,RAB5A,MEF2C,ASIC1,P2RY1,VPS18,DTNBP1,DNM1L,ADRA2A,GPER1,STX1A,BACE1,CSPG5,RAP1B,CASK,PNKD,RAB3A,SYN1,CPLX1,STX1B,SYT11,CALM1,SNAPIN,PRKCB,CAMK2A,FMR1,P2RX1,BAIAP3,STXBP1,CHRNB4,KCNMB4	grey	VSMC_M10
GO:0010667	0.19	0.90	15	23	negative regulation of cardiac muscle cell apoptotic process	BP	1	PPP1R10,RGL2,HSF1,PAX8,HAND2,SIRT5,SIRT4,NFE2L2,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,NKX2-5,HEY2	grey	VSMC_M10
GO:0021513	0.19	0.95	6	8	spinal cord dorsal/ventral patterning	BP	1	SMO,INTU,GLI2,SUFU,CHRD,TULP3	grey	VSMC_M10
GO:0031630	0.19	0.95	6	8	regulation of synaptic vesicle fusion to presynaptic active zone membrane	BP	1	GRIK5,SYT1,SYT9,RAB3A,CPLX1,STXBP1	grey	VSMC_M10
GO:1901632	0.19	0.95	6	8	regulation of synaptic vesicle membrane organization	BP	1	GRIK5,SYT1,SYT9,RAB3A,CPLX1,STXBP1	grey	VSMC_M10
GO:1904896	0.19	0.95	6	8	ESCRT complex disassembly	BP	1	VPS4B,CHMP2A,CHMP2B,CHMP7,CHMP1A,VPS4A	grey	VSMC_M10
GO:1904903	0.19	0.95	6	8	ESCRT III complex disassembly	BP	1	VPS4B,CHMP2A,CHMP2B,CHMP7,CHMP1A,VPS4A	grey	VSMC_M10
GO:0051125	0.20	0.90	16	25	regulation of actin nucleation	BP	1	WASHC5,PICK1,WASF1,FCHSD2,ARFIP2,HIP1R,FMN1,CYFIP1,MAGEL2,AP1AR,WASF2,WHAMM,NCKAP1,WAS,WDR63,GMFG	grey	VSMC_M10
GO:0071468	0.20	0.95	6	8	cellular response to acidic pH	BP	1	RAB11FIP5,SLC38A3,SLC9A1,TRPV1,PKD1L3,IMPACT	grey	VSMC_M10
GO:1900029	0.20	0.92	9	13	positive regulation of ruffle assembly	BP	1	EPS8L1,CYFIP1,EPS8,NDEL1,EPS8L3,DEF8,CARMIL2,EPS8L2,HRAS	grey	VSMC_M10
GO:0002468	0.20	0.95	6	8	dendritic cell antigen processing and presentation	BP	1	HLA-DRA,NOD1,NOD2,SLC11A1,CD74,FGL2	grey	VSMC_M10
GO:0090660	0.20	0.95	6	8	cerebrospinal fluid circulation	BP	1	LRRC6,CFAP43,JHY,CFAP45,SPAG16,TTC25	grey	VSMC_M10
GO:0002091	0.20	0.92	9	13	negative regulation of receptor internalization	BP	1	SDCBP,MTMR2,WDR54,ANKRD13A,ANKRD13D,LRPAP1,DLG4,MIR199A1,LRRTM2	grey	VSMC_M10
GO:0044070	0.20	0.87	34	57	regulation of anion transport	BP	1	ATP8B1,SLC12A2,GOPC,PLA2G6,ABCB1,TCAF2,SFRP4,PRNP,ARL6IP5,SLC43A1,STC1,RIPK1,CRY2,ABCC2,PLA2R1,GRM2,SLC38A3,MAP2K6,ABCB11,AGT,ACE2,ATP1A2,PER2,NTSR1,PLA2G4A,ARL6IP1,PSEN1,ABAT,GABRE,STXBP1,CA2,RGS4,PTGES,CEBPB	grey	VSMC_M10

GO:0010874	0.20	0.89	19	30	regulation of cholesterol efflux	BP	1	LRP1,PTCH1,TTC39B,NR1H2,NR1H3,PLTP,ABCA5,EGF,ZDHHC8,ABCA12,GPS2,NAXE,ABCA3,ABCA7,RXRA,MIR27B,MIR27A,ABCA8,MIR33B	grey	VSMC_M10
GO:0006851	0.20	0.91	12	18	mitochondrial calcium ion transmembrane transport	BP	1	SMDT1,MICU3,SLC8B1,OPA1,MCUR1,MCUB,MICU1,MCU,BHLHA15,PSEN2,SLC25A23,MAIP1	grey	VSMC_M10
GO:0051932	0.20	0.89	17	27	synaptic transmission, GABAergic	BP	1	GABRA1,PHF24,USP46,PRKCE,PLCL2,RAC3,KRAS,NPAS4,HAP1,NLGN2,AC138894.1,GABRE,GABRA3,BAIAP3,ZDHHC12,CNTNAP4,STXBP1	grey	VSMC_M10
GO:0045821	0.20	0.92	10	15	positive regulation of glycolytic process	BP	1	PRXL2C,SLC4A4,GPD1,P2RX7,ZBTB20,ARNT,MLXIPL,PSEN1,INSR,ENTPD5	grey	VSMC_M10
GO:0070900	0.20	0.95	6	8	mitochondrial tRNA modification	BP	1	MTO1,TRIT1,RPUSD4,TRMT5,HSD17B10,TRMT61B	grey	VSMC_M10
GO:1900864	0.20	0.95	6	8	mitochondrial RNA modification	BP	1	MTO1,TRIT1,RPUSD4,TRMT5,HSD17B10,TRMT61B	grey	VSMC_M10
GO:0086045	0.20	0.97	4	5	membrane depolarization during AV node cell action potential	BP	1	TRPM4,CACNB2,SCN5A,CACNA1G	grey	VSMC_M10
GO:0034058	0.20	0.95	6	8	endosomal vesicle fusion	BP	1	TGFBRAP1,VPS41,VPS39,VPS8,ANKFY1,VPS4A	grey	VSMC_M10
GO:0042133	0.20	0.90	13	20	neurotransmitter metabolic process	BP	1	AGTPBP1,GAD2,HNMT,LRTOMT,AP000812.5,ALDH5A1,SLC6A3,COMT,BCHE,DAGLB,AC138894.1,ABAT,PRIMA1	grey	VSMC_M10
GO:0046689	0.20	0.94	6	8	response to mercury ion	BP	1	SLC1A1,AQP1,ABCC2,PARK7,BSG,MT-CYB	grey	VSMC_M10
GO:0010988	0.20	0.93	8	11	regulation of low-density lipoprotein particle clearance	BP	1	FGF21,NR1H4,MYLIP,ANXA2,MIR199A1,MIR27B,MIR27A,LDLRAP1	grey	VSMC_M10
GO:0019627	0.20	0.94	6	8	urea metabolic process	BP	1	SLC25A15,NR1H4,CEBPA,ASL,CPS1,ASS1	grey	VSMC_M10
GO:0071941	0.20	0.94	6	8	nitrogen cycle metabolic process	BP	1	SLC25A15,NR1H4,CEBPA,ASL,CPS1,ASS1	grey	VSMC_M10
GO:0014010	0.20	0.94	6	8	Schwann cell proliferation	BP	1	SNW1,SOX10,RNF10,CERS2,SKI,MIR222	grey	VSMC_M10
GO:0090158	0.20	0.92	9	13	endoplasmic reticulum membrane organization	BP	1	RTN4,ATL2,MOSPD3,LPCAT3,ATL1,ARL6IP1,STX18,BNIP1,CXorf56	grey	VSMC_M10
GO:0050688	0.20	0.87	30	50	regulation of defense response to virus	BP	1	TNFAIP3,C6orf106,IL15,TRAF3IP2,SEC14L1,TMEM173,NPLOC4,MAVS,PCBP2,TRIM44,EIF2AK4,HERC5,PARP9,DTX3L,RNF26,NLRX1,TRAF3IP1,HTRA1,MUL1,FOXP3,RNF216,TKFC,TSPAN6,SIN3A,TRAF3,RIOK3,ZDHHC1,ZDHHC11,IFNLR1,FGL2	grey	VSMC_M10
GO:0055067	0.20	0.85	62	108	monovalent inorganic cation homeostasis	BP	1	NEDD4L,SLC12A2,TFAP2B,SLC4A4,PPT1,RAB7A,ATP6V0E2,LACC1,SLC4A2,AQP11,ATP1A3,SNX5,SLC4A7,TMEM106B,MAFG,CCKBR,ATP6V1H,TM9SF4,IL1A,SLC9A9,HVCN1,SLC12A5,SLC4A10,KCNJ2,SLC9B1,SLC12A7,TMEM9,TCIRG1,SLC9A8,SCN7A,SLAMF8,RHCG,AGT,ATP1A2,SLC9A1,SLC12A8,CLIC4,SLC12A9,COMT,SLC11A1,SLC9A7,ATP6V0A1,ATP1B1,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP1B2,MAPK3,AC138894.1,CLN6,SNAPIN,SCNN1B,C7,TMEM199,SLC9A6,ATP6AP1,SLC12A4,SLC9A5,CA2,KCNH2,RAB39A	grey	VSMC_M10
GO:0021534	0.20	0.91	10	15	cell proliferation in hindbrain	BP	1	GLI1,SMO,C5AR1,GLI2,ZNF423,EGF,GBX2,LHX1,GPR37L1,CEND1	grey	VSMC_M10
GO:0003338	0.20	0.89	17	27	metanephros morphogenesis	BP	1	SMO,SIX2,SOX9,FOXJ1,PAX8,FMN1,FRAS1,PKD2,PAX2,SALL1,WNT4,CITED1,LHX1,PKD1,SOX8,BASP1,LIF	grey	VSMC_M10
GO:0033683	0.20	0.94	6	8	nucleotide-excision repair, DNA incision	BP	1	ERCC1,ERCC2,ERCC3,FAN1,ERCC4,NTHL1	grey	VSMC_M10
GO:0034389	0.20	0.90	13	20	lipid droplet organization	BP	1	PNPLA3,CIDEC,CDS2,DDHD2,SPART,AUP1,CDS1,FITM2,FITM1,ZFYVE1,TMEM159,BSCL2,TBC1D20	grey	VSMC_M10
GO:0035082	0.20	0.86	33	55	axoneme assembly	BP	1	UBE2B,LRRC6,CFAP69,WDR92,ARMC2,ARMC4,TTC26,DRC1,RSPH6A,FOXJ1,TTLL3,SPEF1,CCDC65,DNAH1,DNAH5,NEURL1,CFAP43,ZMYND10,CFAP46,JHY,TTC12,TOGARAM1,DNAAF2,SPAG16,TTC25,DNAAF4,MNS1,CCDC151,SPEF2,C16orf71,TPGS1,HYDIN,WDR63	grey	VSMC_M10
GO:0006664	0.20	0.85	51	87	glycolipid metabolic process	BP	1	B4GALNT1,A4GALT,GPAA1,LARGE1,CWH43,KIT,TMEM246,PIGF,GLB1,NEU3,PGAP2,PIGU,ST8SIA4,ST3GAL6,PIGT,GPLD1,A3GALT2,PGAP1,ST8SIA2,B3GALT1,B3GNT5,PIGM,PIGV,PIGX,GAL3ST3,PIGZ,B3GALNT1,GAL3ST4,PIGC,SCCPDH,PGAP3,PIGH,GALC,CLN6,ST8SIA5,GLA,HEXA,GM2A,PIGL,MPPE1,GBGT1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,PYURF,CPTP,NEU2,PIGB,B4GALT3,PIGA,ST8SIA6	grey	VSMC_M10
GO:1903509	0.20	0.85	51	87	liposaccharide metabolic process	BP	1	B4GALNT1,A4GALT,GPAA1,LARGE1,CWH43,KIT,TMEM246,PIGF,GLB1,NEU3,PGAP2,PIGU,ST8SIA4,ST3GAL6,PIGT,GPLD1,A3GALT2,PGAP1,ST8SIA2,B3GALT1,B3GNT5,PIGM,PIGV,PIGX,GAL3ST3,PIGZ,B3GALNT1,GAL3ST4,PIGC,SCCPDH,PGAP3,PIGH,GALC,CLN6,ST8SIA5,GLA,HEXA,GM2A,PIGL,MPPE1,GBGT1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,PYURF,CPTP,NEU2,PIGB,B4GALT3,PIGA,ST8SIA6	grey	VSMC_M10
GO:0060211	0.20	0.91	10	15	regulation of nuclear-transcribed mRNA poly(A) tail shortening	BP	1	PABPC1,AGO2,TNRC6B,TNRC6C,CNOT1,TENT4B,EIF4ENIF1,POLR2G,TOB1,TNRC6A	grey	VSMC_M10
GO:0033079	0.20	0.94	6	8	immature T cell proliferation	BP	1	BMI1,IL1A,TMEM131L,RIPK2,WNT4,FOXP3	grey	VSMC_M10
GO:0002251	0.20	0.92	9	13	organ or tissue specific immune response	BP	1	NOD2,OTUD7B,RAB17,IL6R,NOS2,HIST1H2BK,IFNLR1,HIST1H2BF,HIST1H2BJ	grey	VSMC_M10
GO:0098917	0.20	0.94	6	8	retrograde trans-synaptic signaling	BP	1	FARP1,PLCB1,GUCY1A1,DAG1,DAGLB,FABP5	grey	VSMC_M10
GO:0030516	0.20	0.85	48	83	regulation of axon extension	BP	1	LRP1,SEMA6A,RAB21,PLXNA4,SRF,SEMA4D,SEMA4C,RTN4,RUFY3,NRCAM,GOLGA4,MEGF8,SEMA3D,SEMA3A,RYK,TTL,SEMA4F,DPYSL2,NKX6-1,ZFYVE27,SEMA3G,CYFIP1,SEMA4G,KIAA0319,SEMA3F,ADNP,DISC1,CDKL5,WNT3,MAPT,SEMA6D,TNR,FN1,SEMA4A,TRIM46,NDEL1,RAB11A,NTN1,DNM2,SIN3A,TRPV2,CDK5R1,L1CAM,ARHGAP4,PLXNA3,BARHL2,WNT5A,OLFM1	grey	VSMC_M10
GO:0015669	0.20	0.94	6	8	gas transport	BP	1	MYC,AQP1,CYGB,NGB,CA2,HBA2	grey	VSMC_M10
GO:0098971	0.21	0.96	4	5	anterograde dendritic transport of neurotransmitter receptor complex	BP	1	KIF5A,KIF5C,KIF3B,KIF17	grey	VSMC_M10
GO:0043090	0.21	0.88	22	36	amino acid import	BP	1	SLC22A4,SLC1A1,SLC1A4,SLC7A11,SLC25A38,ARL6IP5,SLC7A1,SLC43A1,SFXN2,AGT,ACE2,ATP1A2,PER2,NTSR1,ARL6IP1,SLC3A2,CLN8,PSEN1,SLC7A3,SLC7A5,SLC36A1,RGS4	grey	VSMC_M10
GO:0045837	0.21	0.92	9	13	negative regulation of membrane potential	BP	1	HEBP2,SLC25A27,PTN,RNF122,ARL6IP5,MAPT,TRPV1,PIP5KL1,BNIP3L	grey	VSMC_M10
GO:0051964	0.21	0.96	4	5	negative regulation of synapse assembly	BP	1	EPHA7,ROBO2,SLIT1,WNT5A	grey	VSMC_M10
GO:0006563	0.21	0.94	6	8	L-serine metabolic process	BP	1	SHMT2,PSAT1,SERINC5,CBSL,SHMT1,PHGDH	grey	VSMC_M10
GO:0043129	0.21	0.93	7	10	surfactant homeostasis	BP	1	EPAS1,ITGB6,LPCAT1,CTSH,ABCA12,ABCA3,OAS1	grey	VSMC_M10
GO:0045198	0.21	0.91	10	15	establishment of epithelial cell apical/basal polarity	BP	1	PTK7,SYNE4,TCF15,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,WNT5A	grey	VSMC_M10

GO:0006513	0.21	0.86	36	61	protein monoubiquitination	BP	1	NEDD4L,PRKN,SKP1,UBE2B,RNF20,UBE3D,FANCL,BMI1,FBXL2,WDR48,UBE2O,UBE2E1,RYBP,KBTBD8,DDB2,MARCH7,PCGF6,KLHL12,NEURL1,PEF1,PDCD6,DTX3L,CBL,RNF168,BCOR,ATXN7L3,LEO1,DDB1,PCGF3,TRIM37,CUL4B,MGRN1,RNF126,UBB,UBE2R2,PEX12	grey	VSMC_M10
GO:0060371	0.21	0.96	4	5	regulation of atrial cardiac muscle cell membrane depolarization	BP	1	SCN5A,TBX5,CACNA1G,SCN2B	grey	VSMC_M10
GO:0090279	0.21	0.89	17	27	regulation of calcium ion import	BP	1	SPHK2,PRNP,HOMER1,STC1,PKD2,EGF,PLPP4,CASK,PSEN2,WNK3,ATP2A1,TRPV2,CCL2,TRPV3,P2RX1,ATP2C2,CRH	grey	VSMC_M10
GO:0032787	0.21	0.82	225	404	monocarboxylic acid metabolic process	BP	1	ATP8B1,HSD17B4,ALDH8A1,AIG1,LTC4S,CPT1B,SLC27A6,TNXB,QKI,PPARA,ACSL6,PNPLA3,MCAT,HSD17B8,ECHDC1,PRXL2C,AKR1B1,MAPK14,HACD4,ALDH1A1,CROT,KIT,GAPDH,AASDH,ADH5,PRKCE,ETFB,SLC4A4,ME1,BPGM,NR1H2,IL4I1,LPIN1,DLD,PRKAR2B,FAAH,HADHA,SOX9,ABHD5,AKR1A1,APOC1,DHTKD1,ECHDC3,PRKAG2,ACOX1,SLC22A13,XYLB,PIBF1,CYGB,HYI,ELOVL1,AKT2,PFKP,BTD,HACL1,PANK2,PDK1,AMDHD1,NR1H4,PDHX,TRIB3,LYPLA1,ACOXL,CYP7A1,ELOVL7,ASAH1,CYP7B1,ACOX2,GPI,ABHD6,THNSL2,CBR4,OSBP,HPGD,GPD1,PEX2,P2RX7,ETFDH,ACOT12,PRKAG1,NR1H3,PFKM,IVD,LPIN3,HOGA1,ECI2,ABCC2,ERLIN1,PLA2G4B,ADTRP,PRMT3,PRKAB1,LONP2,PM20D1,SIRT4,MCEE,ALDH5A1,IRS1,ALDH1A3,CPT1A,BDH2,ZBTB20,GPAM,ACSL5,NR5A2,CYP2U1,PFKFB2,ABHD2,MSMO1,MECR,MCCC1,GNPAT,ENO4,ABCB11,DHRS9,PC,HACD2,ARNT,LPGAT1,PER2,ACTN3,HDAC4,OSBPL2,ACADSB,THEM5,THEM4,MLXIPL,SCAP,EHHADH,POR,PDK3,PLA2G4A,OSBPL6,ACADL,HK1,FAH,BCO2,MTHFS,TYSND1,OSBPL1A,ACSBG1,PECR,PNKD,AASDHPPT,CYP27A1,PRKAG3,STAT3,SLC27A1,MPC2,DAGLB,ENO3,FADS3,LIAS,ACADVL,EPHX1,TECR,HSD17B10,DEGS1,ALDH1A2,FGFR4,LIPC,OSBPL7,PSEN1,ACOT2,AC005520.1,ABCD4,ALOXE3,PKLR,GCDH,MAPK3,OGT,HACD3,SCPEP1,NDUFAB1,ADPGK,CYP46A1,ACSM3,ACACA,NCOR1,CD74,INSR,NPC1,ABHD3,SREBF1,LPIN2,C3,ACSBG2,ALDOC,CYP2J2,ACAA2,ACOT11,ABAT,GAMT,PARK7,DECR2,SLC2A6,ACSF3,CEL,MLYCD,PTGES2,ABCD3,PLA2G15,CES2,ACADM,PHYH,ACOT4,FABP5,FADS6,ENTPD5,ELOVL3,ABHD10,TIGAR,HADHB,AMACR,NUDT19,IDNK,GGT5,ECI1,AUH,LYPLA2,STARD4,PTGES,INSIG2,PH	grey	VSMC_M10
GO:0002822	0.21	0.84	59	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	CD226,STX7,TNFAIP3,AGER,HLA-DRA,EXOSC3,MSH2,RSAD2,IL4I1,TRPM4,HMCES,NECTIN2,PVR,MLH1,SLC22A13,FOXJ1,PAXIP1,SHLD1,NCKAP1L,HPX,TRAF6,MEF2C,RIPK2,NOD2,CD40,HLX,DENND1B,CD28,FZD5,PLA2G4A,BCL6,IL12A,RC3H1,PTPN6,TNFSF18,SLC11A1,PPP3CB,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,TBX21,ZBTB7B,IL4R,BTK,FBXO38,C3,IL7R,SUPT6H,PRKCZ,TRAF2,MIR21,FADD,CD46,FCER2,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0002714	0.21	0.88	17	27	positive regulation of B cell mediated immunity	BP	1	CD226,EXOSC3,MSH2,HMCES,NECTIN2,MLH1,PAXIP1,SHLD1,HPX,NOD2,CD40,CD28,SHLD2,TBX21,BTK,C3,FCER2	grey	VSMC_M10
GO:0002891	0.21	0.88	17	27	positive regulation of immunoglobulin mediated immune response	BP	1	CD226,EXOSC3,MSH2,HMCES,NECTIN2,MLH1,PAXIP1,SHLD1,HPX,NOD2,CD40,CD28,SHLD2,TBX21,BTK,C3,FCER2	grey	VSMC_M10
GO:0030854	0.21	0.94	6	8	positive regulation of granulocyte differentiation	BP	1	IL5,TRIB1,TESC,HCLS1,HAX1,EVI2B	grey	VSMC_M10
GO:0019646	0.21	0.85	46	75	aerobic electron transport chain	BP	1	UQCRQ,NDUFA6,DLD,NDUFB2,NDUFB6,DNAJC15,NDUFC2,NDUFS8,COX7A1,COX4I2,NDUFS3,UQCRB,COX15,NDUFV3,NDUFB4,ISCU,NDUFB3,NDUFS2,SDHC,COX6A1,COX8A,PINK1,NDUFA9,COX6A2,NDUFAB1,COX5A,NDUFA7,NDUFV2,NDUFB10,UQCR11,PARK7,MT-ND1,MT-ND2,MT-CO3,MT-ND6,MT-CYB,NDUFA5,NDUFC1,COX7A2,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,COX7A2L	grey	VSMC_M10
GO:0086029	0.21	0.96	4	5	Purkinje myocyte to ventricular cardiac muscle cell signaling	BP	1	TRPM4,SCN5A,CASQ2,RYR2	grey	VSMC_M10
GO:0086068	0.21	0.96	4	5	Purkinje myocyte to ventricular cardiac muscle cell communication	BP	1	TRPM4,SCN5A,CASQ2,RYR2	grey	VSMC_M10
GO:0009074	0.21	0.94	6	8	aromatic amino acid family catabolic process	BP	1	IL4I1,IDO2,IDO1,HGD,FAH,GSTZ1	grey	VSMC_M10
GO:0098935	0.21	0.93	7	10	dendritic transport	BP	1	KIF5A,WASF1,KIF5C,PURA,KIF3B,KIF17,SFPQ	grey	VSMC_M10
GO:0014733	0.21	0.93	7	10	regulation of skeletal muscle adaptation	BP	1	TNNC1,PPP3CA,TNNI1,MYH7,GTF2IRD1,ACTN3,CAMK2G	grey	VSMC_M10
GO:0042572	0.21	0.88	17	27	retinol metabolic process	BP	1	RDH5,RDH16,AKR1B1,ALDH1A1,RDH13,LIPE,SDR16C5,RETSAT,ALDH1A3,DHRS9,DHRS3,RDH11,ALDH1A2,PNPLA4,LRAT,RDH14,ADH4	grey	VSMC_M10
GO:0002072	0.21	0.96	4	5	optic cup morphogenesis involved in camera-type eye development	BP	1	TFAP2A,PAX2,ALDH1A3,WNT5A	grey	VSMC_M10
GO:0070633	0.21	0.89	14	22	transepithelial transport	BP	1	SLC12A2,ABCB1,SLC1A1,CLDN19,AQP1,ACTG1,SLC23A2,ABCC2,ABCG2,GPLD1,RHCG,ACTB,RHBG,SCNN1B	grey	VSMC_M10
GO:0000395	0.21	0.94	6	8	mRNA 5'-splice site recognition	BP	1	PRPF39,RNVU1-6,RNU4ATAC,RF00003,SNRPC,SRSF12	grey	VSMC_M10
GO:0014854	0.21	0.94	6	8	response to inactivity	BP	1	CAT,SCN5A,DAG1,CASQ1,ACTN3,HDAC4	grey	VSMC_M10
GO:0048261	0.21	0.89	16	25	negative regulation of receptor-mediated endocytosis	BP	1	SDCBP,MTMR2,APOC1,NEU3,WDR54,ANKRD13A,ANKRD13D,SH3GL3,LRPAP1,DLG4,SYT11,UNC119,MIR199A1,MIR27B,MIR27A,LRRTM2	grey	VSMC_M10
GO:0001778	0.21	0.93	7	10	plasma membrane repair	BP	1	MYH9,MYOF,DYSF,RAB3A,SYT7,SYT11,SYTL4	grey	VSMC_M10
GO:0090399	0.21	0.91	10	15	replicative senescence	BP	1	CDKN2A,ERCC1,WRN,ATR,MME,PLA2R1,TERT,CHEK2,CTC1,MIR21	grey	VSMC_M10
GO:0001961	0.21	0.86	26	43	positive regulation of cytokine-mediated signaling pathway	BP	1	HSPA1B,PRKN,AGPAT1,TRIM32,CD300LF,MAVS,GAS6,HPX,IRF7,TRIM44,IL7,NLRC5,RIPK2,RIPK1,PARP9,PARP14,MED1,CD74,TRAF2,AGPAT2,GFI1,FADD,IRGM,WNT5A,C1QTNF4,TSLP	grey	VSMC_M10
GO:0070120	0.21	0.96	4	5	ciliary neurotrophic factor-mediated signaling pathway	BP	1	CNTFR,IL6R,LIFR,CNTF	grey	VSMC_M10
GO:0043171	0.21	0.89	14	22	peptide catabolic process	BP	1	LVRN,CHAC2,IDE,ERAP1,CPN1,XPNPEP1,ENPEP,GGT2,CTSH,ECE1,NPEPPS,ADAMTS13,ERAP2,GGT5	grey	VSMC_M10
GO:0071622	0.21	0.87	25	41	regulation of granulocyte chemotaxis	BP	1	PTK2,RAC2,CXCL8,AKIRIN1,C5AR2,C5AR1,NCKAP1L,NOD2,DNM1L,TRPV4,CMKLR1,MOSPD2,MCU,TNFSF18,CXCR2,BST1,MAPK1,DAPK2,MAPK3,S100A14,CD74,CCL5,CSF1R,MPP1,DPP4	grey	VSMC_M10

GO:0072567	0.22	0.91	10	15	chemokine (C-X-C motif) ligand 2 production	BP	1	LRP1,TLR4,MYD88,FOXP1,OAS3,F2RL1,HDAC1,MAP2K5,CD74,OAS1	grey	VSMC_M10
GO:2000341	0.22	0.91	10	15	regulation of chemokine (C-X-C motif) ligand 2 production	BP	1	LRP1,TLR4,MYD88,FOXP1,OAS3,F2RL1,HDAC1,MAP2K5,CD74,OAS1	grey	VSMC_M10
GO:0042795	0.22	0.91	10	15	snRNA transcription by RNA polymerase II	BP	1	SNAPC3,ZC3H8,ZNF143,CDK7,MEPCE,ELL,CC2D1A,ICE2,SNAPC5,SNAPC4	grey	VSMC_M10
GO:2000628	0.22	0.93	7	10	regulation of miRNA metabolic process	BP	1	PNPT1,TENT2,RC3H1,ZSWIM8,DROSHA,HRAS,RC3H2	grey	VSMC_M10
GO:0016052	0.22	0.83	65	113	carbohydrate catabolic process	BP	1	MIOX,PPARA,PRXL2C,GALT,GAPDH,SLC4A4,BPGM,MGAM,DHDH,PYGB,GLB1,NUDT5,DHTKD1,PRKAG2,XYLB,RBKS,PPP1CB,NEU3,PFKP,FUT10,PPP1R3B,GPI,GK5,GPD1,P2RX7,PRKAG1,PFKM,GLYCTK,ZBTB20,PFKFB2,ENO4,ARNT,PPP1R3D,TREH,ACTN3,HDAC4,MLXIPL,SORD,RPE,HK1,PYGM,PYGL,PRKAG3,STAT3,ENO3,TKFC,PSEN1,PKLR,OGT,ADPGK,GM2A,NCOR1,INSR,ENOSF1,ALDOC,TKTL1,SLC2A6,AGL,CTBS,FUT4,ENTPD5,ABHD10,TIGAR,IDNK,NEU2	grey	VSMC_M10
GO:0007351	0.22	0.93	7	10	tripartite regional subdivision	BP	1	FRS2,FAM208A,HOXD8,FZD5,WDR77,WNT5A,BASP1	grey	VSMC_M10
GO:0008595	0.22	0.93	7	10	anterior/posterior axis specification, embryo	BP	1	FRS2,FAM208A,HOXD8,FZD5,WDR77,WNT5A,BASP1	grey	VSMC_M10
GO:0060897	0.22	0.96	4	5	neural plate regionalization	BP	1	FUZ,BMPR1A,CELSR2,NOG	grey	VSMC_M10
GO:0070304	0.22	0.84	57	99	positive regulation of stress-activated protein kinase signaling cascade	BP	1	MAP3K5,STK3,MAPK8IP2,MAP3K4,AGER,GADD45G,SEMA4C,EMC10,MTURN,NOD1,TLR4,TRAF1,SDCBP,MYD88,PLCB1,EIF2AK2,RELL2,SEMA3A,SH3RF2,ARL6IP5,MFHAS1,TRAF6,HAND2,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,TRPV4,TGFB2,NCF1,TRAF5,FZD7,MAP3K3,MAP3K11,MBIP,MAP4K2,DUSP19,PDCD10,LTBR,MINK1,RELL1,TAOK2,TRAF3,TAOK1,SERPINF2,MAPK8IP3,TRAF2,DAB2IP,ZNF622,WNT5A,GADD45A,INAVA,DUSP22,HRAS	grey	VSMC_M10
GO:0021603	0.22	0.96	4	5	cranial nerve formation	BP	1	ATP8B1,TFAP2A,PAX2,MAFB	grey	VSMC_M10
GO:0015804	0.22	0.87	22	36	neutral amino acid transport	BP	1	SLC1A1,SLC3A1,SLC1A4,LLGL2,SLC25A38,SLC6A15,SLC38A9,SLC43A1,SERINC5,SLC38A2,SLC38A1,SFXN2,SLC38A3,ACE2,SLC38A5,SLC3A2,SLC38A6,SLC6A7,SLC7A5,SLC36A1,SLC6A19,RGS4	grey	VSMC_M10
GO:0006119	0.22	0.83	71	119	oxidative phosphorylation	BP	1	SHMT2,UQCRQ,NDUFA6,MSH2,DLD,NDUFB2,NDUFB6,DNAJC15,NDUFC2,ATP5F1C,NDUFS8,NDUFA12,COX7A1,COX4I2,ATP5F1A,NDUFS3,DGUOK,UQCRB,COX15,FAM173B,COX6B1,NDUFV3,NDUFB4,ISCU,COA6,NDUFB3,ACTN3,NDUFS2,DNAJC30,MLXIPL,SDHC,COX6A1,COX8A,PINK1,NDUFA9,COX6A2,NDUFAB1,UQCRC2,COX5A,TEFM,NDUFA7,SLC25A23,NDUFV2,NDUFB10,UQCR11,PARK7,SLC25A33,ATP5PB,MT-ND1,MT-ND2,MT-ATP8,MT-ATP6,MT-CO3,MT-ND6,MT-CYB,RHOA,ATP5ME,ATP5MF,NDUFA5,NDUFC1,COX7A2,FXN,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,UQCC2,COX7A2L,PPIF	grey	VSMC_M10
GO:0002709	0.22	0.86	26	43	regulation of T cell mediated immunity	BP	1	STX7,AGER,HLA-DRA,RSAD2,IL4I1,TRPM4,NECTIN2,PVR,SLC22A13,NCKAP1L,TRAF6,NOD2,DENND1B,FZD5,IL12A,PPP3CB,WAS,FOXP3,ZBTB1,TNFRSF1B,TBX21,FBXO38,IL7R,PRKCZ,TRAF2,FADD	grey	VSMC_M10
GO:0010759	0.22	0.90	10	15	positive regulation of macrophage chemotaxis	BP	1	PTK2,AKIRIN1,C5AR1,TRPV4,CMKLR1,TNFSF18,MAPK1,MAPK3,CCL5,CSF1R	grey	VSMC_M10
GO:0033005	0.22	0.90	10	15	positive regulation of mast cell activation	BP	1	CD226,SPHK2,NECTIN2,GAB2,FGR,SNX4,IL4R,STXBP1,HAVCR1,TSLP	grey	VSMC_M10
GO:0098814	0.22	0.92	7	10	spontaneous synaptic transmission	BP	1	SLC12A2,RIMS2,PRKN,AGER,SYT1,NSG1,STX1B	grey	VSMC_M10
GO:0060221	0.22	0.92	7	10	retinal rod cell differentiation	BP	1	NTRK2,RORB,PTN,SOX9,RPGRIP1L,NRL,SOX8	grey	VSMC_M10
GO:0010793	0.22	0.96	4	5	regulation of mRNA export from nucleus	BP	1	IWS1,SETD2,AKAP8L,SUPT6H	grey	VSMC_M10
GO:0120041	0.22	0.96	4	5	positive regulation of macrophage proliferation	BP	1	PTK2,MAPK1,MAPK3,CSF1R	grey	VSMC_M10
GO:0003431	0.22	0.96	4	5	growth plate cartilage chondrocyte development	BP	1	COL27A1,SOX9,TSKU,TGFBR2	grey	VSMC_M10
GO:0030488	0.22	0.86	24	39	tRNA methylation	BP	1	TRMT11,MTO1,NSUN6,THUMPD3,TRMT6,THUMPD2,TRMT9B,BCDIN3D,NSUN3,TRMT10A,DALRD3,LCMT2,METTL8,METTL2B,TRMT1L,ALKBH8,TRMT5,HSD17B10,METTL6,TRMT10B,TRMT61A,TRMT10C,TRMT61B,TYW3	grey	VSMC_M10
GO:0030913	0.22	0.96	4	5	paranodal junction assembly	BP	1	ANK2,GNPAT,CNTNAP1,EPB41L3	grey	VSMC_M10
GO:1901097	0.22	0.96	4	5	negative regulation of autophagosome maturation	BP	1	TMEM39A,RUBCN,PHF23,CLEC16A	grey	VSMC_M10
GO:0006390	0.22	0.90	10	15	mitochondrial transcription	BP	1	TFB1M,MTERF1,C6orf203,FOXO3,TWNK,TFAM,PPARGC1B,METTL4,TEFM,SLC25A33	grey	VSMC_M10
GO:0003056	0.22	0.92	7	10	regulation of vascular associated smooth muscle contraction	BP	1	ZDHHC21,ADRA2B,DOCK5,CHRM3,P2RX1,MIR21,RHOA	grey	VSMC_M10
GO:0003139	0.22	0.92	7	10	secondary heart field specification	BP	1	FOXH1,WNT11,MEF2C,AXIN2,RBPJ,ISL1,WNT5A	grey	VSMC_M10
GO:0050910	0.22	0.92	7	10	detection of mechanical stimulus involved in sensory perception of sound	BP	1	KIT,WHRN,MKKS,ADGRV1,STRC,PJVK,CHRNA10	grey	VSMC_M10
GO:0010359	0.22	0.96	4	5	regulation of anion channel activity	BP	1	GOPC,ABCB1,TCAF2,PRNP	grey	VSMC_M10
GO:0007340	0.22	0.89	14	22	acrosome reaction	BP	1	TRIM36,RIMS1,ADCY3,PLCB1,STX2,HYAL3,ABHD2,CCDC87,PLCD4,RAB3A,AKAP3,SPESP1,CACNA1H,STXBP1	grey	VSMC_M10
GO:1904478	0.22	0.96	4	5	regulation of intestinal absorption	BP	1	ABCG5,ABCG8,EPB41,LPCAT3	grey	VSMC_M10
GO:1902455	0.22	0.96	4	5	negative regulation of stem cell population maintenance	BP	1	ZNF706,PAX8,LOXL2,PAX2	grey	VSMC_M10
GO:0033564	0.22	0.96	4	5	anterior/posterior axon guidance	BP	1	LHX9,UNC5A,NTN1,LHX1	grey	VSMC_M10
GO:0010626	0.22	0.96	4	5	negative regulation of Schwann cell proliferation	BP	1	SOX10,RNF10,CERS2,SKI	grey	VSMC_M10
GO:0035524	0.22	0.96	4	5	proline transmembrane transport	BP	1	SLC1A4,ACE2,SLC6A7,SLC36A1	grey	VSMC_M10
GO:0046835	0.22	0.88	14	22	carbohydrate phosphorylation	BP	1	IPPK,KHK,XYLB,RBKS,PFKM,ITPK1,PFKFB2,PFKFB4,HK1,TKFC,FGGY,GNPTG,FUK,POMK	grey	VSMC_M10
GO:0097070	0.22	0.96	4	5	ductus arteriosus closure	BP	1	TFAP2B,HPGD,STRA6,FOXF1	grey	VSMC_M10
GO:0045745	0.22	0.90	10	15	positive regulation of G protein-coupled receptor signaling pathway	BP	1	KLK14,PHB,PDE6G,GPER1,PDE6H,TMOD2,C3,CNTN2,CHGA,MRAP2	grey	VSMC_M10
GO:0060729	0.22	0.96	4	5	intestinal epithelial structure maintenance	BP	1	TLR4,SOX9,SLC22A5,INAVA	grey	VSMC_M10
GO:0045648	0.22	0.87	18	29	positive regulation of erythrocyte differentiation	BP	1	HSPA1B,BRD1,MAPK14,ZNF16,SMAP1,FOXO3,ACVR2A,NCKAP1L,PRKDC,ACVR1B,ARNT,STAT3,STAT5B,MED1,KAT7,MIR222,ANKRD54,FAM210B	grey	VSMC_M10
GO:1903352	0.22	0.96	4	5	L-ornithine transmembrane transport	BP	1	SLC25A15,SLC7A1,SLC7A3,SLC25A29	grey	VSMC_M10

GO:1900186	0.22	0.96	4	5	negative regulation of clathrin-dependent endocytosis	BP	1	NEU3,SH3GL3,SYT11,UNC119	grey	VSMC_M10
GO:0071716	0.22	0.96	4	5	leukotriene transport	BP	1	ABCC10,ABCC4,ABCC2,ABCC3	grey	VSMC_M10
GO:0061669	0.22	0.96	4	5	spontaneous neurotransmitter secretion	BP	1	RIMS2,PRKN,SYT1,STX1B	grey	VSMC_M10
GO:0060478	0.22	0.96	4	5	acrosomal vesicle exocytosis	BP	1	RIMS1,HYAL3,RAB3A,STXBP1	grey	VSMC_M10
GO:0016042	0.22	0.81	127	225	lipid catabolic process	BP	1	HSD17B4,LRP1,CYP27B1,AIG1,CPT1B,ABHD16A,PPARA,PNPLA3,PNPLA5,MCAT,ECHDC1,PLA2G6,CROT,SRD5A3,HINT2,PRKCE,ETFB,PPT1,LPIN1,MGST2,SMPD2,LDAH,APOB,HSD17B14,FGF21,RAB7A,NAPEPLD,FAAH,HADHA,ABHD5,APOC1,LIPE,ACOX1,ACER3,ALK,AKT2,NEU3,SIRT2,PLCB1,HACL1,DDHD2,ACOXL,CYP7A1,ASAH1,ACOX2,ABHD6,PLCE1,PEX2,ETFDH,PLCH1,IVD,LPIN3,ECI2,SPP1,PLA2G4B,ADTRP,LONP2,GPLD1,SRD5A1,MCEE,PLCXD2,IRS1,CPT1A,BDH2,ADRA2A,PLA1A,ABHD4,ABHD2,SORL1,HSD11B1,ABCB11,PAFAH2,PLBD1,EHHADH,PLA2G4A,ACADL,BCO2,CPS1,TYSND1,ABHD12B,PLCD4,DDHD1,CYP27A1,SMPD4,PLA2G16,LIPA,DAGLB,ACADVL,THRA,HSD17B10,LIPC,ABCD4,GDPD3,GCDH,GALC,LDLR,GDPD1,GLA,HEXA,CYP46A1,GM2A,GDE1,ABHD3,PNPLA6,LPIN2,ACAA2,DECR2,CEL,MLYCD,ABCD3,PLA2G15,ACADM,PHYH,BSCL2,LIPJ,PNPLA4,PLA2G2C,NCEH1,HADHB,AMACR,ACER2,NUDT19,ECI1,AUH,LYPLA2,NEU2,YWHAH	grey	VSMC_M10
GO:0030320	0.22	0.96	4	5	cellular monovalent inorganic anion homeostasis	BP	1	SLC12A2,CKB,ABCC2,SLC12A5	grey	VSMC_M10
GO:0030644	0.22	0.96	4	5	cellular chloride ion homeostasis	BP	1	SLC12A2,CKB,ABCC2,SLC12A5	grey	VSMC_M10
GO:0048489	0.22	0.86	23	38	synaptic vesicle transport	BP	1	AP3S1,KIF5A,PRKN,AP3M2,KIF5C,LIN7A,TMEM230,SYNJ1,AP3B1,DTNBP1,CNIH2,SPG11,BLOC1S6,RAB3A,PINK1,AP3M1,SLC2A4,TRIM46,SNAPIN,DNM2,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:1903205	0.22	0.89	13	20	regulation of hydrogen peroxide-induced cell death	BP	1	GPR37,MET,FOXO3,PAWR,RIPK1,PDE8A,NFE2L2,PINK1,STK26,PARK7,MIR21,GPR37L1,TXN	grey	VSMC_M10
GO:0009448	0.23	0.96	4	5	gamma-aminobutyric acid metabolic process	BP	1	ALDH1A1,ALDH5A1,ABAT,PHGDH	grey	VSMC_M10
GO:0044743	0.23	0.87	20	32	protein transmembrane import into intracellular organelle	BP	1	TIMM21,PEX7,PEX6,PEX1,DNAJC15,TIMM50,PEX2,PEX16,LONP2,TOMM40L,GRPEL1,TIMM17B,PEX26,PEX14,PAM16,PEX10,TIMM23B,GRPEL2,PEX12,DNAJC19	grey	VSMC_M10
GO:0061643	0.23	0.96	4	5	chemorepulsion of axon	BP	1	PLXNA4,RYK,NTN1,WNT5A	grey	VSMC_M10
GO:0048843	0.23	0.88	15	24	negative regulation of axon extension involved in axon guidance	BP	1	SEMA6A,SEMA4D,SEMA4C,SEMA3D,SEMA3A,RYK,SEMA4F,SEMA3G,SEMA4G,SEMA3F,WNT3,SEMA6D,SEMA4A,PLXNA3,WNT5A	grey	VSMC_M10
GO:0061087	0.23	0.96	4	5	positive regulation of histone H3-K27 methylation	BP	1	PHF1,OGT,MTF2,ZNF304	grey	VSMC_M10
GO:0006366	0.23	0.79	1005	1862	transcription by RNA polymerase II	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ONECUT2,TCF4,TBPL1,GLI1,HIVEP2,PLAGL1,MAML1,ZBTB2,ESR1,CNOT2,OSR2,SNW1,ARID1B,ZBTB12,ZBED4,PRKN,PPARA,MED30,BRD2,TAF2,RXRB,VGLL2,HSF2,TCF7,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,KDM3B,PTCH1,ATF4,RPAP2,CBX7,MAPK14,KDM4C,SOX10,NRF1,TMPRSS6,SMO,SNAPC3,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,ZNF16,JFT74,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,NFX1,NFXL1,SUPT3H,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,RFX8,DLX5,PHF14,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,ZNF268,ZNF667,ZNF787,ZNF691,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,ZNF189,EPAS1,EPCAM,SP4,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,AKIRIN2,BACH2,ZNF692,AKIRIN1,MTF1,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,NOBOX,TLR4,CCNC,BCL2L12,SCAF1,LPIN1,UCP1,CREM,TEAD2,SDCBP,MYCN,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,MAMSTR,ATAD2B,KDM7A,ZNF438,FOXE3,HDAC2,PHF10,MAML2,BBS7,MLLT10,DNMT3A,BMI1,C5AR1,ZC3H4,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,ZNF467,EED,ERCC2,ERCC3,GTF2F2,PCF11,SUV39H2,UTF1,ZNF404,PLK3,SUMO2,ZNF575,GLI2,ZNF526,RSF1,ZNF513,ZNF574,RAF1,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,GZF1,METTL23,MNX1,POU4F1,MED8,SS18L2,TADA3,KLF6,ZNF662,ARRB1,THAP1,EID2,OVOL2,ZNF219,ACVR2A,EOMES,IKBKB,MED29,CBX4,BHLHE40,CHD8,JAG1,SIRT2,TOX4,NMI,ZMYND11,TMEM173,R	grey	VSMC_M10
GO:0051931	0.23	0.88	14	22	regulation of sensory perception	BP	1	GRIN2D,FAM19A4,P2RX3,F2R,FAM173B,ZFHX2,OPRD1,SLC9A1,NTSR1,COMT,ADRA2C,TMEM100,NMUR2,FABP5	grey	VSMC_M10
GO:0030277	0.23	0.92	7	10	maintenance of gastrointestinal epithelium	BP	1	KIAA1211,TLR4,SOX9,NOD2,PBLD,SLC22A5,INAVA	grey	VSMC_M10
GO:0016082	0.23	0.89	11	17	synaptic vesicle priming	BP	1	NAPA,NAPB,ERC2,SYNJ1,SNAP23,STX1A,RAB3A,SNAP29,STX1B,STXBP1,SNAP47	grey	VSMC_M10
GO:1904251	0.23	0.92	7	10	regulation of bile acid metabolic process	BP	1	KIT,PANK2,NR1H4,CYP7A1,ABCB11,FGFR4,STARD4	grey	VSMC_M10
GO:0036301	0.23	0.96	4	5	macrophage colony-stimulating factor production	BP	1	FOXP1,ISL1,TSLP,HAVCR2	grey	VSMC_M10
GO:1901256	0.23	0.96	4	5	regulation of macrophage colony-stimulating factor production	BP	1	FOXP1,ISL1,TSLP,HAVCR2	grey	VSMC_M10
GO:0042509	0.23	0.85	31	52	regulation of tyrosine phosphorylation of STAT protein	BP	1	HSF1,KIT,PPP2R1A,IL15,HDAC2,PIBF1,HPX,OSBP,ARL2BP,CD40,HDAC1,HCLS1,PARP9,PARP14,OSM,IL12A,TNFSF18,FGFR3,CTF1,IL6R,CCL5,CSF1R,ISL1,SUZ12,GHR,PTPN2,SOCS1,CNTF,MIR125A,LIF,TSLP	grey	VSMC_M10
GO:1903578	0.23	0.84	39	66	regulation of ATP metabolic process	BP	1	SHMT2,PPARA,TSPO,PRXL2C,SLC4A4,SPHK2,DNAJC15,PRKAG2,COX7A1,GPD1,P2RX7,PRKAG1,FAM173B,DNM1L,ZBTB20,ARNT,ACTN3,HDAC4,DNAJC30,MLXIPL,FIS1,PINK1,STAT3,PARP1,PSEN1,OGT,NCOR1,INSR,SLC25A23,SLC25A33,SLC2A6,RHOA,ENTPD5,BEND3,COX7A2,TIGAR,UQCC2,COX7A2L,PPIF	grey	VSMC_M10

GO:0030258	0.23	0.82	97	171	lipid modification	BP	1	HSD17B4,B4GALNT1,CPT1B,SYNJ2,PPARA,MCAT,ECHDC1,MAPK14,CROT,PLPP6,ADH5,PLPPR1,MBOAT7,ETFB,MBOAT2,DGKI,INPP4B,FIG4,AGK,SPHK2,MTMR2,HADHA,SOX9,APOC1,PRKAG2,ACOX1,CYGB,AKT2,PIP4P1,HACL1,PLPP5,MTMR7,ACOXL,SOAT2,ACOX2,CHRM5,MTMR9,PEX2,EPHX2,ETFDH,SYNJ1,IVD,ECI2,LONP2,SIRT4,A3GALT2,IRS1,CPT1A,BDH2,INPP5A,MTMR11,B3GALT1,DGKD,ABCB11,AGT,PLPP4,MTMR3,INPP5J,EHHADH,APOD,POR,DGKG,ACADL,SOAT1,SACM1L,TYSND1,LPCAT3,ACADVL,HSD17B10,DGKQ,ABCD4,GCDH,DGKE,PLPPR2,MTMR12,ACAA2,MTM1,MTMR1,INPP5K,DECR2,ABO,GBGT1,MLYCD,ABCD3,ST3GAL2,ACADM,MIR27B,MIR27A,PHYH,HADHB,AMACR,ECI1,AUH,STARD4,ADH4,SLC35C1,SGPP1	grey	VSMC_M10
GO:0001923	0.23	0.96	4	5	B-1 B cell differentiation	BP	1	CMTM7,PLCL2,SLAMF8,CD19	grey	VSMC_M10
GO:1990166	0.23	0.96	4	5	protein localization to site of double-strand break	BP	1	SLF1,XRCC4,SLF2,IFFO1	grey	VSMC_M10
GO:0001782	0.23	0.87	18	29	B cell homeostasis	BP	1	TNFAIP3,BAK1,TRAF3IP2,NCKAP1L,GAPT,CASP3,MEF2C,DOCK10,PPP2R3C,RC3H1,FOXP3,CD74,BCL10,CAMLG,BCL2L11,SH2B2,TNFSF13B,RC3H2	grey	VSMC_M10
GO:0006498	0.23	0.96	4	5	N-terminal protein lipidation	BP	1	HHAT,NMT1,PPM1A,MAP6D1	grey	VSMC_M10
GO:0022029	0.23	0.86	24	40	telencephalon cell migration	BP	1	SUN2,SRF,EFHC1,MBOAT7,RTN4,POU3F3,NRG1,ROBO1,SRGAP2C,DISC1,DIXDC1,TNR,PSEN1,NDEL1,CDK5R1,DAB1,LRP8,DAB2IP,RHOA,ADGRG1,CNTN2,FOXG1,LAMB1,POU3F2	grey	VSMC_M10
GO:0010469	0.23	0.83	64	112	regulation of signaling receptor activity	BP	1	MAPK8IP2,PRRT1,PPARA,LY6E,NCK2,SHANK1,EPGN,AREG,TGFA,DLGAP3,DKKL1,HDAC2,HBEGF,FAM19A4,ADRA2B,DKK3,FBXW7,MEF2C,DLGAP4,P2RY1,PTK2B,HOMER1,IFNGR2,NEURL1,HDAC1,ADRA2A,DKK2,NCF1,EGF,KLHL24,CBL,ACE2,CNIH2,SNX6,PPP2R5B,ADRA2C,LRPAP1,ZFYVE28,SOCS4,PINK1,NPTX2,GREM2,MINK1,DLG4,NLGN2,CNIH3,PSEN1,NLGN3,TAF1,WFIKKN2,BEGAIN,CCL2,DLGAP1,WFIKKN1,PARK7,MIR125A,NOG,NETO2,CACNG7,CRH,SHISA8,EREG,CNRIP1,CACNG5	grey	VSMC_M10
GO:0048645	0.23	0.84	33	56	animal organ formation	BP	1	FRS2,LEMD2,PIM1,FOXH1,NTF4,SPRY1,GLI2,WNT11,TGFBR2,PAX8,HAND2,EYA1,ROBO1,ROBO2,MEF2C,TBX5,PAX2,AXIN2,NKX3-2,MAPK1,BMPR1A,RBPJ,MAPK3,MAP2K1,MKS1,GATA6,ISL1,NOG,WNT5A,SIX1,FGF1,WNT2,HOXA3	grey	VSMC_M10
GO:0019184	0.23	0.90	10	15	nonribosomal peptide biosynthetic process	BP	1	SLC1A1,AASDH,CHAC2,MGST2,SLC7A11,GSS,BDH2,NFE2L2,GGT6,GGT5	grey	VSMC_M10
GO:0035771	0.23	0.96	4	5	interleukin-4-mediated signaling pathway	BP	1	CD300LF,PARP14,IL4R,PTPN2	grey	VSMC_M10
GO:0031033	0.23	0.96	4	5	myosin filament organization	BP	1	RAP1GDS1,TTN,TCAP,MYH11	grey	VSMC_M10
GO:0032792	0.23	0.96	4	5	negative regulation of CREB transcription factor activity	BP	1	EIF2AK4,SIK1,FOXP3,DDIT3	grey	VSMC_M10
GO:0019233	0.23	0.84	37	63	sensory perception of pain	BP	1	PHF24,GRIN2D,ASIC3,SCN1A,FAM19A4,EPHB1,P2RX3,P2RX7,P2RY1,MME,F2R,FAM173B,ZFHX2,OPRD1,SLC9A1,NIPSNAP1,NTSR1,BACE1,COMT,KCNK4,ADRA2C,KCNA1,MAPK1,NLGN2,HOXB8,ALOXE3,MAPK3,CHRNB2,TMEM100,BDKRB1,NMUR2,CCL2,TRPV1,MECP2,FABP5,POMK,PTGES	grey	VSMC_M10
GO:1903297	0.23	0.96	4	5	regulation of hypoxia-induced intrinsic apoptotic signaling pathway	BP	1	TMBIM6,HYOU1,PINK1,NOL3	grey	VSMC_M10
GO:1903298	0.23	0.96	4	5	negative regulation of hypoxia-induced intrinsic apoptotic signaling pathway	BP	1	TMBIM6,HYOU1,PINK1,NOL3	grey	VSMC_M10
GO:0008361	0.23	0.82	88	157	regulation of cell size	BP	1	LRP1,SEMA6A,RAB21,PRR16,SLC12A2,FSTL4,PLXNA4,SRF,SEMA4D,SEMA4C,RTN4,RUFY3,AQP1,PLEK,EPHA7,KEL,NRCAM,SLC26A5,GOLGA4,MEGF8,CLNS1A,AQP11,RPTOR,SEMA3D,SPART,SEMA3A,LARS,ULK1,RYK,RET,TTL,SEMA4F,P2RX7,DPYSL2,NKX6-1,ZFYVE27,ANO6,SEMA3G,SPP1,CYFIP1,SEMA4G,SLC12A5,BDNF,KIAA0319,SLC12A7,TRPV4,SEMA3F,ADNP,DISC1,SLC12A8,CDKL5,WNT3,CREB1,MAPT,SEMA6D,SLC12A9,TNR,FN1,GNB3,KCNMA1,CLN8,WNK3,SEMA4A,TRIM46,NDEL1,AC138894.1,RAB11A,NTN1,DNM2,SIN3A,TRPV2,LRRC8E,CDK5R1,VAV1,IL7R,RAP1GAP2,L1CAM,ARHGAP4,PLXNA3,TSC1,LAMTOR5,VAV3,LRRC8A,BARHL2,SLC12A4,RHOA,WNT5A,OLFM1	grey	VSMC_M10
GO:0051386	0.23	0.92	7	10	regulation of neurotrophin TRK receptor signaling pathway	BP	1	WASF1,SPRY1,SPRY2,CYFIP1,DOK5,AGT,PPP2R5B	grey	VSMC_M10
GO:0070170	0.23	0.96	4	5	regulation of tooth mineralization	BP	1	SLC4A2,TFAP2A,AMELX,BCOR	grey	VSMC_M10
GO:0050879	0.23	0.86	24	40	multicellular organismal movement	BP	1	STAC3,TNNI3,MYH14,XRCC1,STAC,NR4A1,HOMER1,TNNC1,KCNJ2,TNNI1,SYNM,VTI1A,GIGYF2,MYH7,CASQ1,ACTN3,CHRNB1,CLN8,TCAP,STAC2,ATP2A1,DMD,TNNC2,MAP1A	grey	VSMC_M10
GO:0050881	0.23	0.86	24	40	musculoskeletal movement	BP	1	STAC3,TNNI3,MYH14,XRCC1,STAC,NR4A1,HOMER1,TNNC1,KCNJ2,TNNI1,SYNM,VTI1A,GIGYF2,MYH7,CASQ1,ACTN3,CHRNB1,CLN8,TCAP,STAC2,ATP2A1,DMD,TNNC2,MAP1A	grey	VSMC_M10
GO:0061734	0.23	0.96	4	5	parkin-mediated stimulation of mitophagy in response to mitochondrial depolarization	BP	1	PRKN,OPTN,MFN2,VPS13C	grey	VSMC_M10
GO:0009138	0.23	0.96	4	5	pyrimidine nucleoside diphosphate metabolic process	BP	1	CMPK1,ENTPD4,DTYMK,CMPK2	grey	VSMC_M10
GO:0019695	0.23	0.96	4	5	choline metabolic process	BP	1	ALDH7A1,CHDH,CHKA,BCHE	grey	VSMC_M10
GO:0042428	0.23	0.96	4	5	serotonin metabolic process	BP	1	TPH2,BTBD9,DDC,SRD5A1	grey	VSMC_M10
GO:2000465	0.23	0.96	4	5	regulation of glycogen (starch) synthase activity	BP	1	EPM2AIP1,IGF2,PPP1R3F,INPP5K	grey	VSMC_M10
GO:0035502	0.23	0.96	4	5	metanephric part of ureteric bud development	BP	1	FOXJ1,PKD2,LHX1,BASP1	grey	VSMC_M10
GO:1905563	0.23	0.96	4	5	negative regulation of vascular endothelial cell proliferation	BP	1	FLT1,MEF2C,CCL2,MIR24-1	grey	VSMC_M10
GO:0070669	0.23	0.96	4	5	response to interleukin-2	BP	1	STAT5B,CITED1,JAK1,PTPN2	grey	VSMC_M10
GO:0006349	0.23	0.92	7	10	regulation of gene expression by genetic imprinting	BP	1	DNMT3A,IGF2,PCGF3,MECP2,PRMT7,CTCF,ARID4A	grey	VSMC_M10
GO:0018230	0.23	0.88	14	22	peptidyl-L-cysteine S-palmitoylation	BP	1	ZDHHC14,ZDHHC21,ZDHHC20,GOLGA7B,ZDHHC23,ZDHHC6,ZDHHC18,ZDHHC24,ZDHHC8,ZDHHC4,ZDHHC15,ZDHHC12,ZDHHC1,ZDHHC11	grey	VSMC_M10
GO:0018231	0.23	0.88	14	22	peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-cysteine	BP	1	ZDHHC14,ZDHHC21,ZDHHC20,GOLGA7B,ZDHHC23,ZDHHC6,ZDHHC18,ZDHHC24,ZDHHC8,ZDHHC4,ZDHHC15,ZDHHC12,ZDHHC1,ZDHHC11	grey	VSMC_M10

GO:0016540	0.23	0.90	10	15	protein autoprocessing	BP	1	MYRFL,HTRA2,PIDD1,HJV,SPRTN,PISD,PARP1,F12,FXN,FAM111A	grey	VSMC_M10
GO:0034505	0.23	0.89	11	17	tooth mineralization	BP	1	PPARA,CNNM4,SLC4A2,TFAP2A,ITGB6,TCIRG1,FAM20A,FAM20C,AMELX,BCOR,ALPL	grey	VSMC_M10
GO:0042158	0.23	0.83	49	84	lipoprotein biosynthetic process	BP	1	ATG12,ZDHHC14,GPAA1,ZDHHC21,CWH43,TMEM246,PIGF,ATG5,APOB,PGAP2,ZDHHC20,PIGU,ATG10,GOLGA7B,ZDHHC13,PIGT,GPLD1,PGAP1,ZDHHC23,ZDHHC6,RABL3,ATG16L1,PIGM,HHAT,ZDHHC18,PIGV,ZDHHC24,PIGX,GLUL,PIGZ,NMT1,ZDHHC8,PIGC,PPM1A,ZDHHC4,WIPI2,PGAP3,PIGH,ZDHHC15,PIGL,MPPE1,ZDHHC12,ZDHHC1,ZDHHC11,IRGM,PYURF,PIGB,PIGA,MAP6D1	grey	VSMC_M10
GO:0086015	0.23	0.94	5	7	SA node cell action potential	BP	1	SCN5A,RYR2,ANK2,CACNA1G,HCN4	grey	VSMC_M10
GO:0086018	0.23	0.94	5	7	SA node cell to atrial cardiac muscle cell signaling	BP	1	SCN5A,RYR2,ANK2,CACNA1G,HCN4	grey	VSMC_M10
GO:0050908	0.23	0.92	7	10	detection of light stimulus involved in visual perception	BP	1	PRPH2,GJA10,CEP250,CCDC66,ROM1,GNAT2,REEP6	grey	VSMC_M10
GO:0050962	0.23	0.92	7	10	detection of light stimulus involved in sensory perception	BP	1	PRPH2,GJA10,CEP250,CCDC66,ROM1,GNAT2,REEP6	grey	VSMC_M10
GO:2000427	0.23	0.96	4	5	positive regulation of apoptotic cell clearance	BP	1	CD300LF,CCL2,C3,ABCA7	grey	VSMC_M10
GO:0006488	0.23	0.90	10	15	dolichol-linked oligosaccharide biosynthetic process	BP	1	ALG12,SRD5A3,ALG2,ALG10,DPAGT1,ALG3,ALG9,ALG6,ALG1,DHDDS	grey	VSMC_M10
GO:0009137	0.23	0.96	4	5	purine nucleoside diphosphate catabolic process	BP	1	NT5E,NUDT16,ENTPD4,NUDT18	grey	VSMC_M10
GO:0009181	0.23	0.96	4	5	purine ribonucleoside diphosphate catabolic process	BP	1	NT5E,NUDT16,ENTPD4,NUDT18	grey	VSMC_M10
GO:0033127	0.23	0.92	7	10	regulation of histone phosphorylation	BP	1	UBE2B,AKAP8L,AKAP8,MAPK3,RPS6KA5,FMR1,RPS6KA4	grey	VSMC_M10
GO:0043303	0.23	0.86	23	38	mast cell degranulation	BP	1	RAC2,KIT,SPHK2,GAB2,UNC13D,FER,RASGRP1,SNAP23,LAT2,FGR,CBL,SNX4,PTGDR,C12orf4,LAT,IL4R,S100A13,BTK,STXBP2,PDPK1,FOXF1,STXBP1,CHGA	grey	VSMC_M10
GO:0015985	0.23	0.89	12	18	energy coupled proton transport, down electrochemical gradient	BP	1	ATP5MGL,ATP5F1C,ATP5F1A,FAM173B,DNAJC30,ATP6V0C,ATP5PB,VPS9D1,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF	grey	VSMC_M10
GO:0015986	0.23	0.89	12	18	ATP synthesis coupled proton transport	BP	1	ATP5MGL,ATP5F1C,ATP5F1A,FAM173B,DNAJC30,ATP6V0C,ATP5PB,VPS9D1,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF	grey	VSMC_M10
GO:0043380	0.23	0.96	4	5	regulation of memory T cell differentiation	BP	1	HLA-DRA,BCL6,CD46,FGL2	grey	VSMC_M10
GO:0051409	0.23	0.92	7	10	response to nitrosative stress	BP	1	ADH5,DNAJA1,ATG5,DUSP6,STOX1,PARK7,DDIT3	grey	VSMC_M10
GO:0070493	0.23	0.92	7	10	thrombin-activated receptor signaling pathway	BP	1	PLEK,MET,HPGD,F2RL1,F2R,IQGAP2,DGKQ	grey	VSMC_M10
GO:0097237	0.23	0.83	50	85	cellular response to toxic substance	BP	1	LTC4S,APOM,PRKN,PRXL2C,KDM3B,FANCC,PIM1,ALDH1A1,TXNRD1,PRDX1,ADH5,CAT,ALB,PXDN,MGST2,TXNRD3,DHFR,ESD,AKR1A1,GSTK1,PRDX3,CYGB,PXDNL,ABTB2,GLRX,GPX8,TP53INP1,ABCG2,FBLN5,MARC2,MARC1,OPRD1,NFE2L2,DUOX1,FIS1,GCH1,PINK1,ABCB6,RDH11,SOD3,GSTZ1,MPO,TXNDC2,PARK7,NQO1,MIR21,HBA2,TXN,PTGES,ADH4	grey	VSMC_M10
GO:0030240	0.23	0.96	4	5	skeletal muscle thin filament assembly	BP	1	LMOD3,ACTC1,TTN,TCAP	grey	VSMC_M10
GO:0006004	0.23	0.92	7	10	fucose metabolic process	BP	1	FUCA2,FUT10,POFUT1,FUOM,FUT4,FPGT,POFUT2	grey	VSMC_M10
GO:0031640	0.23	0.88	13	20	killing of cells of other organism	BP	1	GAPDH,MYD88,P2RX7,F2RL1,SCNN1B,NOS2,S100A12,HIST1H2BK,CHGA,CXCL6,FCER2,SERPINB9,HIST1H2BJ	grey	VSMC_M10
GO:1901623	0.23	0.90	10	15	regulation of lymphocyte chemotaxis	BP	1	CCL27,OXSR1,PTK2B,SLC8B1,PADI2,TMEM102,CCL5,CCL7,CCL2,WNT5A	grey	VSMC_M10
GO:0003071	0.24	0.89	10	15	renal system process involved in regulation of systemic arterial blood pressure	BP	1	GAS6,F2RL1,F2R,AGT,PTPRO,CORO2B,SERPINF2,CYBA,HSD11B2,RHOA	grey	VSMC_M10
GO:0046618	0.24	0.92	7	10	xenobiotic export	BP	1	ABCB1,ATP7B,ABCC2,ABCB11,RALBP1,ABCA3,SLC22A5	grey	VSMC_M10
GO:0035518	0.24	0.89	11	17	histone H2A monoubiquitination	BP	1	SKP1,BMI1,RYBP,DDB2,PCGF6,RNF168,BCOR,DDB1,PCGF3,TRIM37,CUL4B	grey	VSMC_M10
GO:0003228	0.24	0.96	4	5	atrial cardiac muscle tissue development	BP	1	ENG,NOG,NKX2-5,WNT2	grey	VSMC_M10
GO:1901668	0.24	0.96	4	5	regulation of superoxide dismutase activity	BP	1	SZT2,SIRT3,PARK7,MIR21	grey	VSMC_M10
GO:0044065	0.24	0.92	7	10	regulation of respiratory system process	BP	1	FTO,GLS,ATP1A2,MTG2,NLGN2,NLGN3,MECP2	grey	VSMC_M10
GO:0002579	0.24	0.96	4	5	positive regulation of antigen processing and presentation	BP	1	NOD1,NOD2,SLC11A1,CD74	grey	VSMC_M10
GO:0002606	0.24	0.96	4	5	positive regulation of dendritic cell antigen processing and presentation	BP	1	NOD1,NOD2,SLC11A1,CD74	grey	VSMC_M10
GO:0018298	0.24	0.96	4	5	protein-chromophore linkage	BP	1	OPN1SW,CRY1,CRY2,RRH	grey	VSMC_M10
GO:0031054	0.24	0.90	8	12	pre-miRNA processing	BP	1	AGO2,TUT7,AGO1,TUT4,BCDIN3D,PRKRA,DROSHA,AGO4	grey	VSMC_M10
GO:0035608	0.24	0.96	4	5	protein deglutamylation	BP	1	AGTPBP1,AGBL3,AGBL2,FOLH1	grey	VSMC_M10
GO:0030259	0.24	0.92	7	10	lipid glycosylation	BP	1	B4GALNT1,A3GALT2,B3GALT1,ABO,GBGT1,ST3GAL2,SLC35C1	grey	VSMC_M10
GO:0021636	0.24	0.96	4	5	trigeminal nerve morphogenesis	BP	1	PLXNA4,SEMA3A,SEMA3F,PLXNA3	grey	VSMC_M10
GO:0021637	0.24	0.96	4	5	trigeminal nerve structural organization	BP	1	PLXNA4,SEMA3A,SEMA3F,PLXNA3	grey	VSMC_M10
GO:0009637	0.24	0.96	4	5	response to blue light	BP	1	CPT1B,CRY1,CRY2,LCN2	grey	VSMC_M10
GO:0001967	0.24	0.91	7	10	suckling behavior	BP	1	CNTFR,DACH1,POU4F1,HAND2,GLS,UBE2Q1,DERL2	grey	VSMC_M10
GO:0032700	0.24	0.91	7	10	negative regulation of interleukin-17 production	BP	1	TLR4,PRNP,NCKAP1L,IL12A,VSIR,FOXP3,DDIT3	grey	VSMC_M10
GO:1905515	0.24	0.84	31	53	non-motile cilium assembly	BP	1	TBC1D32,IFT74,TMEM17,FUZ,MAPRE1,INTU,BBS7,PIBF1,IFT172,CCDC13,MKKS,CEP290,TMEM80,CEP250,IFT52,RPGRIP1L,CLCN4,DISC1,BBS1,TOGARAM1,GORAB,CEP126,EXOC5,HAP1,TMEM107,MKS1,DNM2,WRAP73,C2CD3,CC2D2B,BBS10	grey	VSMC_M10
GO:0001977	0.24	0.91	7	10	renal system process involved in regulation of blood volume	BP	1	GAS6,F2RL1,F2R,PTPRO,CORO2B,CYBA,HSD11B2	grey	VSMC_M10
GO:0070672	0.24	0.95	4	5	response to interleukin-15	BP	1	IL15,IL15RA,PLCB1,STAT5B	grey	VSMC_M10
GO:0034754	0.24	0.83	46	79	cellular hormone metabolic process	BP	1	RDH5,RDH16,HSD17B4,ALDH8A1,ESR1,CYP21A2,TSPO,HSD17B8,HSD17B3,AKR1B1,ALDH1A1,SRD5A3,RDH13,IL4I1,LIPE,AANAT,SDR16C5,RETSAT,DKK3,SPP1,PRMT3,SRD5A1,ALDH1A3,DHRS9,HSD17B7,BCO2,COMT,WNT4,ECE1,STAT5B,HSD17B10,DHRS3,MED1,RDH11,ALDH1A2,DGKQ,SCPEP1,SCNN1B,CYP46A1,DHRS11,CACNA1H,DHRS2,PNPLA4,LRAT,RDH14,ADH4	grey	VSMC_M10
GO:0099541	0.24	0.95	4	5	trans-synaptic signaling by lipid	BP	1	PLCB1,F2R,DAGLB,FABP5	grey	VSMC_M10
GO:0099542	0.24	0.95	4	5	trans-synaptic signaling by endocannabinoid	BP	1	PLCB1,F2R,DAGLB,FABP5	grey	VSMC_M10
GO:0048291	0.24	0.91	7	10	isotype switching to IgG isotypes	BP	1	MSH2,MLH1,PAXIP1,CD40,CD28,FOXP3,TBX21	grey	VSMC_M10
GO:0048302	0.24	0.91	7	10	regulation of isotype switching to IgG isotypes	BP	1	MSH2,MLH1,PAXIP1,CD40,CD28,FOXP3,TBX21	grey	VSMC_M10

GO:1904528	0.24	0.95	4	5	positive regulation of microtubule binding	BP	1	HSF1,MAPRE1,MAPRE3,PPP2CB	grey	VSMC_M10
GO:0017156	0.24	0.84	26	44	calcium-ion regulated exocytosis	BP	1	RIMS2,MYH9,NLRP5,RIMS1,RIMS3,SYT1,SYT9,SYT8,HYAL3,ADRA2A,KCNB1,STX1A,RAP1B,PPP3CB,RAB3A,SYT7,STX1B,SYT11,CACNA1G,SCAMP5,SDF4,BAIAP3,CACNA1H,STXBP1,DOC2B,VAMP3	grey	VSMC_M10
GO:1902177	0.24	0.95	4	5	positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	BP	1	FBXW7,MCL1,SFPQ,PARK7	grey	VSMC_M10
GO:0033003	0.24	0.86	19	31	regulation of mast cell activation	BP	1	CD226,ENPP3,RAC2,SPHK2,CD300LF,NECTIN2,GAB2,UNC13D,FER,FGR,SNX4,C12orf4,IL4R,STXBP2,PDPK1,FOXF1,STXBP1,HAVCR1,TSLP	grey	VSMC_M10
GO:0061387	0.24	0.82	54	95	regulation of extent of cell growth	BP	1	LRP1,SEMA6A,RAB21,FSTL4,PLXNA4,SRF,SEMA4D,SEMA4C,RTN4,RUFY3,EPHA7,NRCAM,GOLGA4,MEGF8,SEMA3D,SPART,SEMA3A,ULK1,RYK,TTL,SEMA4F,DPYSL2,NKX6-1,ZFYVE27,SEMA3G,SPP1,CYFIP1,SEMA4G,BDNF,KIAA0319,SEMA3F,ADNP,DISC1,CDKL5,WNT3,MAPT,SEMA6D,TNR,FN1,SEMA4A,TRIM46,NDEL1,RAB11A,NTN1,DNM2,SIN3A,TRPV2,CDK5R1,L1CAM,ARHGAP4,PLXNA3,BARHL2,WNT5A,OLFM1	grey	VSMC_M10
GO:0021910	0.24	0.95	4	5	smoothened signaling pathway involved in ventral spinal cord patterning	BP	1	SMO,GLI2,SUFU,TULP3	grey	VSMC_M10
GO:0120197	0.24	0.95	4	5	mucociliary clearance	BP	1	NEK10,CFAP43,SPAG16,TTC25	grey	VSMC_M10
GO:0002221	0.24	0.81	76	134	pattern recognition receptor signaling pathway	BP	1	TNFAIP3,USP15,ESR1,HSPA1B,GRAMD4,LRRC14,NINJ1,PRKCE,RTN4,ANKRD17,SLC46A2,NOD1,PELI1,RSAD2,TLR4,PUM2,PHB,CD300LF,LACC1,MYD88,IRAK2,SEC14L1,NMI,CLPB,NPLOC4,IRF7,MFHAS1,TRAF6,NR1H4,OTUD4,NR1H3,OAS3,RIPK2,OTULIN,AP3B1,F2RL1,NOD2,CD40,RAB7B,MAPKAPK3,IFIH1,OASL,MAP2K6,UNC93B1,TLR5,MAPKAPK2,TIFA,ALPK1,RAB11FIP2,NLRX1,DDX3X,TNIP2,BIRC3,GPS2,TKFC,WDFY1,TSPAN6,S100A14,BTK,TNIP1,TRAF3,RIOK3,COLEC12,RNF135,GPR108,TICAM1,PDPK1,CYBA,GFI1,BCL10,DAB2IP,OAS1,ZCCHC3,IRGM,INAVA,HAVCR2	grey	VSMC_M10
GO:0009083	0.24	0.89	10	15	branched-chain amino acid catabolic process	BP	1	BCAT2,IVD,HIBCH,ACAD8,ACADSB,HSD17B10,SLC25A44,ALDH6A1,HIBADH,AUH	grey	VSMC_M10
GO:0060760	0.24	0.84	29	49	positive regulation of response to cytokine stimulus	BP	1	HSPA1B,PRKN,AGPAT1,TRIM32,TLR4,CD300LF,MAVS,GAS6,HPX,IRF7,TRIM44,TAF9,IL7,NLRC5,RIPK2,RIPK1,IFIH1,PARP9,PARP14,MED1,CD74,TRAF2,AGPAT2,GFI1,FADD,IRGM,WNT5A,C1QTNF4,TSLP	grey	VSMC_M10
GO:0022038	0.24	0.90	8	12	corpus callosum development	BP	1	TSKU,SZT2,RYK,RPGRIP1L,EPHB3,NSUN5,NIN,RTN4RL1	grey	VSMC_M10
GO:0006528	0.24	0.95	4	5	asparagine metabolic process	BP	1	ATF4,NIT2,ASNSD1,ASRGL1	grey	VSMC_M10
GO:0017157	0.24	0.81	83	147	regulation of exocytosis	BP	1	VPS4B,RAB21,RIMS2,PRKN,PLA2G6,RAC2,CHRNA5,APBA1,CHMP2A,RIMS3,SDCBP,SPHK2,RAB7A,RAB10,CACNB2,CLASP2,GAB2,UNC13D,SYT1,RAB5A,NCKAP1L,SYT9,FER,P2RY1,F2RL1,VPS18,LGI3,DTNBP1,SYT8,DNM1L,HYAL3,ADRA2A,KCNB1,FGR,STX1A,SNX4,SEPT2,BACE1,CSPG5,NSF,RAP1B,CASK,RAB3A,SYN1,C12orf4,RAB8A,ATP13A2,HAP1,CPLANE2,SYT7,RAB15,RSC1A1,SEPT1,CPLX1,STX1B,STX4,ITGAM,SYT11,RAB8B,CACNA1G,RAB3D,IL4R,CALM1,SYTL4,SNAPIN,PRKCB,SCAMP5,STXBP2,PRAM1,FMR1,RPH3AL,PDPK1,P2RX1,RAB26,ATP6AP1,CACNA1H,FOXF1,STXBP1,AP1G1,VPS4A,FGA,DOC2B,RALA	grey	VSMC_M10
GO:0097202	0.24	0.91	7	10	activation of cysteine-type endopeptidase activity	BP	1	BAK1,ASPH,RIPK2,CIDEB,FADD,CASP8,PERP	grey	VSMC_M10
GO:0086005	0.24	0.86	16	26	ventricular cardiac muscle cell action potential	BP	1	NEDD4L,TRPM4,SCN5A,GPD1L,KCNJ3,KCNE2,DSP,RYR2,PKP2,ANK2,NOS1AP,DLG1,DSG2,RNF207,KCNH2,KCNJ8	grey	VSMC_M10
GO:1900426	0.24	0.95	4	5	positive regulation of defense response to bacterium	BP	1	F2RL1,NOD2,CYBA,HAVCR2	grey	VSMC_M10
GO:0039694	0.24	0.87	15	24	viral RNA genome replication	BP	1	APOBEC3H,CXCL8,PCBP1,ATG5,PHB,FBXL2,ATG16L2,RAB5A,PCBP2,FAM208A,ATG16L1,PI4KA,FMR1,INPP5K,SETDB1	grey	VSMC_M10
GO:0006559	0.24	0.95	4	5	L-phenylalanine catabolic process	BP	1	IL4I1,HGD,FAH,GSTZ1	grey	VSMC_M10
GO:1902222	0.24	0.95	4	5	erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process	BP	1	IL4I1,HGD,FAH,GSTZ1	grey	VSMC_M10
GO:0045048	0.24	0.88	13	20	protein insertion into ER membrane	BP	1	EMC2,TRAM2,EMC10,EMC3,EMC4,GET4,EMC6,SGTA,UBL4A,WDR83OS,CAMLG,EMC7,TRAM1L1	grey	VSMC_M10
GO:0070944	0.24	0.95	4	5	neutrophil-mediated killing of bacterium	BP	1	MYD88,F2RL1,SCNN1B,CXCL6	grey	VSMC_M10
GO:0046939	0.24	0.82	43	74	nucleotide phosphorylation	BP	1	NME1,PPARA,PRXL2C,GAPDH,SLC4A4,BPGM,CMPK1,DHTKD1,PRKAG2,PFKP,GPI,GPD1,P2RX7,PRKAG1,PFKM,NME4,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,DTYMK,HK1,PRKAG3,STAT3,NME7,ENO3,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,NME3,SLC2A6,AK8,ENTPD5,CMPK2,TIGAR,NME6	grey	VSMC_M10
GO:0051620	0.24	0.95	4	5	norepinephrine uptake	BP	1	SLC6A2,SLC6A3,ACTB,SLC29A4	grey	VSMC_M10
GO:0032048	0.24	0.89	10	15	cardiolipin metabolic process	BP	1	PLA2G6,HADHA,TAMM41,CRLS1,THEM5,SLC27A1,MECP2,LCLAT1,PTPMT1,DNAJC19	grey	VSMC_M10
GO:0050796	0.24	0.81	72	127	regulation of insulin secretion	BP	1	LRP1,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,BMP8A,TRPM4,GIPR,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,OSBP,ARNTL,KCNJ11,NNAT,TIAM1,PFKM,SLC8B1,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,PER2,STX1A,GLUL,SIDT2,SLC16A1,KLF7,ENY2,ABCA12,MCU,PPP3CB,CD38,MPC2,SYT7,NLGN2,TARDBP,STX4,SYTL4,GPR68,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,LRRC8A,CHGA,SOX4,DPP4,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:0007214	0.24	0.90	8	12	gamma-aminobutyric acid signaling pathway	BP	1	SLC12A2,GABRA1,PHF24,GABBR2,PLCL2,GPR156,GABRE,GABRA3	grey	VSMC_M10
GO:0001916	0.24	0.91	7	10	positive regulation of T cell mediated cytotoxicity	BP	1	STX7,HLA-DRA,NECTIN2,PVR,SLC22A13,IL12A,FADD	grey	VSMC_M10
GO:0015671	0.24	0.95	4	5	oxygen transport	BP	1	MYC,CYGB,NGB,HBA2	grey	VSMC_M10
GO:0006655	0.24	0.91	7	10	phosphatidylglycerol biosynthetic process	BP	1	PLA2G6,TAMM41,CRLS1,CDS2,GPAM,SLC27A1,PTPMT1	grey	VSMC_M10
GO:0019886	0.24	0.89	10	15	antigen processing and presentation of exogenous peptide antigen via MHC class II	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TRAF6,FCER1G,PIKFYVE,CTSV,DNM2,CD74	grey	VSMC_M10
GO:0015697	0.25	0.91	7	10	quaternary ammonium group transport	BP	1	SLC22A4,SLC38A2,SLC25A20,SLC25A47,SLC22A5,SLC25A45,SLC25A29	grey	VSMC_M10

GO:0071377	0.25	0.95	4	5	cellular response to glucagon stimulus	BP	1	FGF21,CYSLTR2,CPS1,ASS1	grey	VSMC_M10
GO:0044058	0.25	0.88	11	17	regulation of digestive system process	BP	1	ABCG5,ABCG8,AQP1,NR1H2,HIP1R,NR1H3,EPB41,LPCAT3,TRPV1,SLC22A5,CRH	grey	VSMC_M10
GO:0099601	0.25	0.84	26	44	regulation of neurotransmitter receptor activity	BP	1	MAPK8IP2,PRRT1,SHANK1,DLGAP3,MEF2C,DLGAP4,PTK2B,HOMER1,IFNGR2,KLHL24,CNIH2,PINK1,NPTX2,MINK1,DLG4,NLGN2,CNIH3,NLGN3,BEGAIN,CCL2,DLGAP1,NETO2,CACNG7,CRH,SHISA8,CACNG5	grey	VSMC_M10
GO:0045655	0.25	0.88	11	17	regulation of monocyte differentiation	BP	1	MYC,CDK6,HOXA7,FOXP1,IRF7,ACIN1,ZBTB46,GPR68,CD74,JUN,MIR125B1	grey	VSMC_M10
GO:0035965	0.25	0.95	4	5	cardiolipin acyl-chain remodeling	BP	1	PLA2G6,HADHA,THEM5,LCLAT1	grey	VSMC_M10
GO:1905274	0.25	0.95	4	5	regulation of modification of postsynaptic actin cytoskeleton	BP	1	CTTNBP2,TIAM1,CYFIP1,RHOA	grey	VSMC_M10
GO:1902956	0.25	0.95	4	5	regulation of mitochondrial electron transport, NADH to ubiquinone	BP	1	DNAJC15,ISCU,PINK1,PARK7	grey	VSMC_M10
GO:1903377	0.25	0.95	4	5	negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	BP	1	PRKN,NONO,PINK1,PARK7	grey	VSMC_M10
GO:0032732	0.25	0.84	24	40	positive regulation of interleukin-1 production	BP	1	AGER,NOD1,TLR4,HDAC2,PANX1,MYD88,P2RX7,RIPK2,F2RL1,NOD2,HDAC1,FZD5,IL16,HK1,STAT3,PYDC1,TMED10,SMAD3,S100A13,ISL1,CASP8,WNT5A,INAVA,HAVCR2	grey	VSMC_M10
GO:0035513	0.25	0.95	4	5	oxidative RNA demethylation	BP	1	ALKBH3,FTO,ALKBH1,ALKBH5	grey	VSMC_M10
GO:0006801	0.25	0.83	32	54	superoxide metabolic process	BP	1	FANCC,SLC1A1,PRDX1,FPR2,CYB5R4,EGFR,DHFR,FAM19A4,HVCN1,F2RL1,SH3PXD2A,FBLN5,NCF1,AGT,NCF2,NFE2L2,MAPT,DUOX1,GCH1,BST1,SOD3,ITGAM,MPO,NOX5,NOS2,NOXA1,GNAI3,CYBA,NQO1,MIR21,MIR27B,NRROS	grey	VSMC_M10
GO:0010390	0.25	0.86	16	26	histone monoubiquitination	BP	1	SKP1,RNF20,BMI1,UBE2E1,RYBP,DDB2,PCGF6,DTX3L,RNF168,BCOR,ATXN7L3,LEO1,DDB1,PCGF3,TRIM37,CUL4B	grey	VSMC_M10
GO:0002920	0.25	0.88	11	17	regulation of humoral immune response	BP	1	PHB,FOXJ1,HPX,NOD2,PPP2R3C,PTPN6,GATA6,C3,CD46,A2M,FCER2	grey	VSMC_M10
GO:0010533	0.25	0.95	4	5	regulation of activation of Janus kinase activity	BP	1	AGT,IL6R,CCL5,SOCS1	grey	VSMC_M10
GO:0021799	0.25	0.86	16	26	cerebral cortex radially oriented cell migration	BP	1	SUN2,MBOAT7,RTN4,POU3F3,SRGAP2C,DISC1,DIXDC1,NDEL1,CDK5R1,DAB1,LRP8,DAB2IP,ADGRG1,FOXG1,LAMB1,POU3F2	grey	VSMC_M10
GO:0050805	0.25	0.84	25	42	negative regulation of synaptic transmission	BP	1	PRRT1,PRKN,AGER,PLA2G6,PICK1,SRF,MTMR2,PLK2,ABHD6,ASIC1,PTK2B,SORCS3,KCNB1,ADNP,TMEM25,MAPT,RAP1B,TNR,BCHE,PNKD,CD38,SYT11,FMR1,STXBP1,GRID2	grey	VSMC_M10
GO:0070257	0.25	0.95	4	5	positive regulation of mucus secretion	BP	1	PRKCE,EGFR,ATG5,CYBA	grey	VSMC_M10
GO:0006574	0.25	0.95	4	5	valine catabolic process	BP	1	HIBCH,ACAD8,ALDH6A1,HIBADH	grey	VSMC_M10
GO:0042776	0.25	0.90	9	13	mitochondrial ATP synthesis coupled proton transport	BP	1	ATP5F1C,ATP5F1A,FAM173B,DNAJC30,ATP5PB,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF	grey	VSMC_M10
GO:0048169	0.25	0.88	11	17	regulation of long-term neuronal synaptic plasticity	BP	1	SYNGAP1,SYNGR1,KIT,RAB5A,NEURL1,KRAS,AGT,RAB8A,DLG4,RAB11A,HRAS	grey	VSMC_M10
GO:0019336	0.25	0.91	7	10	phenol-containing compound catabolic process	BP	1	LRTOMT,AP000812.5,SLC6A3,FAH,COMT,DIO3,DIO2	grey	VSMC_M10
GO:0050912	0.25	0.95	4	5	detection of chemical stimulus involved in sensory perception of taste	BP	1	RTP4,GNAT2,PKD1L3,TAS2R3	grey	VSMC_M10
GO:0045671	0.25	0.87	12	19	negative regulation of osteoclast differentiation	BP	1	TOB2,TLR4,PIK3R1,FBXW7,GPR137B,PIAS3,TCTA,UBASH3B,GPR137,FBN1,FSTL3,MAFB	grey	VSMC_M10
GO:0009142	0.25	0.82	37	62	nucleoside triphosphate biosynthetic process	BP	1	NME1,TBPL1,ATP5MGL,PPARA,IMPDH1,SLC25A13,SPHK2,CMPK1,PRKAG2,ATP5F1C,ATP5F1A,DGUOK,FAM173B,NME4,CTPS2,DNAJC30,DTYMK,ATP5S,PINK1,STAT3,NME7,ADK,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,AK8,UCK1,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,CMPK2,NME6,NUDT2	grey	VSMC_M10
GO:0030148	0.25	0.81	48	83	sphingolipid biosynthetic process	BP	1	KDSR,ORMDL2,B4GALNT1,A4GALT,PLA2G6,HACD4,LARGE1,SPTLC1,SMPD2,AGK,SPHK2,PRKD2,ACER3,ELOVL1,SPTLC3,SIRT3,ELOVL7,ASAH1,ST8SIA4,ORMDL1,A3GALT2,ST8SIA2,SGMS2,ALDH3B2,B3GALT1,CERS6,HACD2,CERS2,PPM1L,SMPD4,SGMS1,CLN8,DEGS1,ALOXE3,HACD3,ST8SIA5,P2RX1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,CYP4F22,ABCA8,ELOVL3,PEMT,ACER2,B4GALT3,SGPP1,ST8SIA6	grey	VSMC_M10
GO:0034334	0.25	0.93	5	7	adherens junction maintenance	BP	1	MTSS1,KIFC3,PLEKHA7,CAMSAP3,INAVA	grey	VSMC_M10
GO:0032373	0.25	0.86	16	26	positive regulation of sterol transport	BP	1	LRP1,PTCH1,NR1H2,NR1H3,PLTP,ABCA5,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,ABCA3,ABCA7,RXRA,ABCA8,LDLRAP1	grey	VSMC_M10
GO:0032376	0.25	0.86	16	26	positive regulation of cholesterol transport	BP	1	LRP1,PTCH1,NR1H2,NR1H3,PLTP,ABCA5,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,ABCA3,ABCA7,RXRA,ABCA8,LDLRAP1	grey	VSMC_M10
GO:0009148	0.25	0.89	10	15	pyrimidine nucleoside triphosphate biosynthetic process	BP	1	NME1,TBPL1,NME4,CTPS2,DTYMK,NME7,NME3,UCK1,CMPK2,NME6	grey	VSMC_M10
GO:0006241	0.25	0.91	7	10	CTP biosynthetic process	BP	1	NME1,NME4,CTPS2,NME7,NME3,UCK1,NME6	grey	VSMC_M10
GO:0050821	0.25	0.80	87	154	protein stabilization	BP	1	TRIM39,RAB21,STK3,ZNF207,HSPA1B,PRKN,UBE2B,PIM1,SMO,PEX6,BAG1,CDC37L1,GAPDH,PDCL3,RTN4,AAK1,PHB,CRTAP,USP36,MCM8,BAG4,TRIM44,PIK3R1,CDK7,HIP1R,TAF9,CTNND1,PARVA,MTMR9,FBXW7,CCNH,TESC,MARCH7,STK4,MORC3,RPL23,TBRG1,RABL3,USP13,USP19,HPS4,ANK2,CHEK2,USP2,DVL3,BAG3,PEX19,RPL11,CREB1,PRKRA,SYVN1,MFSD1,SAV1,PDCD10,TNIP2,PINK1,MUL1,OTUD3,ATP1B1,PIM2,EPHA4,ATP1B2,TMEM88,AHSP,EFNA1,TAF1,TAF9B,SEL1L,SMAD3,SWSAP1,COG7,LAMP2,NLK,NAPG,HCFC1,MAPK8IP3,SEC16A,PER3,PARK7,TSC1,STXBP1,SOX4,BAG2,IRGM,SUGT1,CAMLG,APOPT1	grey	VSMC_M10
GO:0048679	0.25	0.86	15	24	regulation of axon regeneration	BP	1	LRP1,PTN,PTPRF,SPP1,KIAA0319,KREMEN1,CERS2,LRIG2,TNR,EPHA4,NDEL1,MAP2K1,MIR222,CNTF,RTN4RL1	grey	VSMC_M10
GO:0050873	0.25	0.84	24	40	brown fat cell differentiation	BP	1	MAPK14,PIM1,UCP1,NAPEPLD,CEBPA,EBF2,FTO,RREB1,SOX13,TRPV4,FABP4,LAMB3,DUSP10,TFE3,SLC2A4,ALDH6A1,ZBTB7B,PRDM16,SIX1,PLAC8,PEX11A,SH2B2,CEBPB,DIO2	grey	VSMC_M10

GO:0034765	0.25	0.78	178	323	regulation of ion transmembrane transport	BP	1	NEDD4L,STAC3,MAPK8IP2,KCNV1,PRRT1,GOPC,CATSPER3,KCNJ4,PLA2G6,ABCB1,CLIC5,WNK2,TSPAN13,PRKCE,KCNQ4,SHANK1,SLC31A2,HECW1,TCAF2,CLCN1,KEL,ATG5,OSR1,SPHK2,KCNJ14,SLC26A5,KCNRG,CACNB2,STAC,OXSR1,SCN5A,SCN1A,GPD1L,CACNB4,NALCN,PRNP,DIAPH1,CLIC1,ARL6IP5,KCNIP3,SLMAP,SLC43A1,GLRX,MEF2C,P2RX7,HVCN1,KCNH3,PTK2B,KCNJ11,TPCN1,HOMER1,IFNGR2,KCNJ3,F2R,TESC,RIPK1,ANO6,KCNK15,KCNE2,PKD2,CASQ2,KCNJ15,KCNIP2,CHRM3,RYR2,FAM173B,PM20D1,CALHM1,HECW2,KCNJ2,ADRA2A,TCIRG1,COX17,SCN2A,ISCU,KCNB1,KCNG1,SCN7A,UBASH3B,ANK2,GPER1,KLHL24,AGT,ACE2,ATP1A2,SLC9A1,PER2,C4orf3,CASQ1,NTSR1,SCN4B,CNIH2,CLIC4,DNAJC30,NOS1AP,CATSPER2,DLG1,KCNK7,CEMIP,SESTD1,PTPN6,KCNK4,HTT,PINK1,ATP1B1,KCNA1,ARL6IP1,KCNMA1,KCNH4,GNB5,KCND1,MINK1,HAP1,DLG4,PSEN2,NLGN2,CNIH3,WNK3,STAC2,CACNB1,ATP1B2,PSEN1,KCNAB3,CACNA1A,KCNIP1,HCN3,NLGN3,CACNA1G,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,CCL2,ASIC2,KCNJ18,FMR1,PDPK1,P2RX1,CACNA1B,RNF207,CACNA1H,PARK7,KCNC4,AMIGO1,CYBA,JPH3,LCN2,WWP2,RRAD,MIR21,MIR24-1,DMD,GPR35,JPH2,KCNH2,FGF11,THY1,SCN2B,KCNK5,NETO2,CACNG7,CRBN,RGS4,CRH,KCNA6,APOPT1,YWHAH,TMEM109,SHISA8,KCNJ8,CACNG5,HCN4,GEM,PPIF,KCNG2,KCNJ9	grey	VSMC_M10
GO:0014029	0.25	0.90	8	12	neural crest formation	BP	1	FUZ,SOX9,KBTBD8,KLHL12,PEF1,PDCD6,GSC,TCOF1	grey	VSMC_M10
GO:0009202	0.25	0.95	4	5	deoxyribonucleoside triphosphate biosynthetic process	BP	1	TBPL1,DTYMK,ADK,CMPK2	grey	VSMC_M10
GO:1903026	0.25	0.95	4	5	negative regulation of RNA polymerase II regulatory region sequence-specific DNA binding	BP	1	FBXW7,TAF1,DDIT3,ZNF593	grey	VSMC_M10
GO:0016024	0.25	0.89	8	12	CDP-diacylglycerol biosynthetic process	BP	1	AGPAT4,AGPAT1,TAMM41,CDS2,CDS1,GPAM,AGPAT2,LCLAT1	grey	VSMC_M10
GO:0005980	0.25	0.89	8	12	glycogen catabolic process	BP	1	PYGB,PPP1CB,PPP1R3B,PFKM,PPP1R3D,PYGM,PYGL,AGL	grey	VSMC_M10
GO:0006357	0.26	0.76	961	1784	regulation of transcription by RNA polymerase II	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ONECUT2,TCF4,GLI1,HIVEP2,PLAGL1,MAML1,ZBTB2,ESR1,CNOT2,OSR2,SNW1,ARID1B,ZBTB12,ZBED4,PRKN,PPARA,MED30,BRD2,RXRB,VGLL2,HSF2,TCF7,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,KDM3B,PTCH1,ATF4,RPAP2,CBX7,MAPK14,KDM4C,SOX10,NRF1,TMPRSS6,SMO,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,ZNF16,IFT74,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,NFX1,NFXL1,SUPT3H,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,RFX8,DLX5,PHF14,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,ZNF268,ZNF667,ZNF787,ZNF691,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,ZNF189,EPAS1,EPCAM,SP4,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,AKIRIN2,BACH2,ZNF692,AKIRIN1,MTF1,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,NOBOX,TLR4,CCNC,BCL2L12,LPIN1,UCP1,CREM,TEAD2,SDCBP,MYCN,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,MAMSTR,ATAD2B,KDM7A,ZNF438,FOXE3,HDAC2,PHF10,MAML2,BBS7,MLLT10,DNMT3A,BMI1,ZC3H4,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,ZNF467,EED,SUV39H2,UTF1,ZNF404,PLK3,SUMO2,ZNF575,GLI2,ZNF526,RSF1,ZNF513,ZNF574,RAF1,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,GZF1,METTL23,MNX1,POU4F1,MED8,SS18L2,TADA3,KLF6,ZNF662,ARRB1,THAP1,EID2,OVOL2,ZNF219,ACVR2A,EOMES,IKBKB,MED29,CBX4,BHLHE40,CHD8,JAG1,SIRT2,TOX4,TMEM173,RARB,PURA,NR1D2,PAWR,ZIC5,SIRT7,MAFG,DPF1,ALX1,TAF7,LUM,DCN,MAVS,SOHLH	grey	VSMC_M10
GO:0010986	0.26	0.95	4	5	positive regulation of lipoprotein particle clearance	BP	1	GPLD1,ANXA2,MIR33B,LDLRAP1	grey	VSMC_M10
GO:0002763	0.26	0.84	24	40	positive regulation of myeloid leukocyte differentiation	BP	1	IL5,TRIB1,HSF1,ROR2,POU4F1,TRAF6,TESC,RIPK1,SLC9B2,ACIN1,HCLS1,CREB1,FOS,HAX1,GPR68,CD74,PPARGC1B,EVI2B,JUN,ATP6AP1,FADD,CASP8,CA2,LIF	grey	VSMC_M10
GO:0031062	0.26	0.85	17	28	positive regulation of histone methylation	BP	1	SNW1,PHF1,RNF20,PAXIP1,CHTOP,NSD3,DNMT3B,RTF1,JARID2,AUTS2,TET1,WDR61,NELFA,OGT,MECP2,MTF2,ZNF304	grey	VSMC_M10
GO:0007176	0.26	0.85	16	26	regulation of epidermal growth factor-activated receptor activity	BP	1	NCK2,EPGN,AREG,TGFA,HBEGF,FBXW7,NEURL1,ADRA2A,NCF1,EGF,CBL,SNX6,ZFYVE28,SOCS4,PSEN1,EREG	grey	VSMC_M10
GO:0035641	0.26	0.89	8	12	locomotory exploration behavior	BP	1	PRKCE,SLC4A10,ATP1A2,TNR,DLG4,NLGN2,DPP4,CRBN	grey	VSMC_M10
GO:0021889	0.26	0.93	5	7	olfactory bulb interneuron differentiation	BP	1	DLX5,ROBO1,ROBO2,SALL1,WNT5A	grey	VSMC_M10
GO:0070166	0.26	0.89	8	12	enamel mineralization	BP	1	PPARA,CNNM4,SLC4A2,ITGB6,TCIRG1,FAM20A,FAM20C,AMELX	grey	VSMC_M10
GO:0002098	0.26	0.87	11	17	tRNA wobble uridine modification	BP	1	TRMU,MTO1,ELP1,DPH3,TRMT9B,ELP4,ELP3,ELP6,ALKBH8,ELP2,CTU1	grey	VSMC_M10
GO:0072205	0.26	0.92	5	7	metanephric collecting duct development	BP	1	PTCH1,AKR1B1,PAX8,PAX2,PKD1	grey	VSMC_M10
GO:0060333	0.26	0.86	15	24	interferon-gamma-mediated signaling pathway	BP	1	NR1H2,NMI,HPX,HCK,NR1H3,NLRC5,IFNGR2,SP100,PARP9,PARP14,MED1,JAK1,PTPN2,SOCS1,IRGM	grey	VSMC_M10
GO:0030219	0.26	0.83	26	44	megakaryocyte differentiation	BP	1	MPIG6B,ZNF16,SRF,KIT,IL11,MTURN,CNOT4,PIP4K2A,ABI1,MEF2C,TESC,RAB7B,CIB1,WASF2,THPO,SP3,PTPN6,MED1,RCOR1,PRMT6,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0002467	0.26	0.89	8	12	germinal center formation	BP	1	TNFAIP3,UNC13D,FOXJ1,MEF2C,NFKB2,BCL6,RC3H1,TNFSF13B	grey	VSMC_M10
GO:0010875	0.26	0.87	12	19	positive regulation of cholesterol efflux	BP	1	LRP1,PTCH1,NR1H2,NR1H3,PLTP,ZDHHC8,ABCA12,GPS2,ABCA3,ABCA7,RXRA,ABCA8	grey	VSMC_M10
GO:0043299	0.26	0.82	30	51	leukocyte degranulation	BP	1	RAC2,KIT,SPHK2,GAB2,UNC13D,NCKAP1L,HCK,FER,RASGRP1,F2RL1,SNAP23,LAT2,FGR,CBL,SNX4,PTGDR,C12orf4,STX4,ITGAM,LAT,IL4R,S100A13,BTK,STXBP2,PRAM1,PDPK1,FOXF1,STXBP1,AP1G1,CHGA	grey	VSMC_M10

GO:0002791	0.26	0.79	80	142	regulation of peptide secretion	BP	1	LRP1,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,BMP8A,EGFR,TRPM4,GIPR,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,KCNJ11,NNAT,TIAM1,PFKM,SLC8B1,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,PER2,STX1A,PASK,GLUL,SIDT2,SLC16A1,KLF7,ENY2,ABCA12,MCU,PPP3CB,CD38,MPC2,SYT7,NLGN2,TARDBP,STX4,RAB8B,SYTL4,GPR68,S100A8,CD74,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,LRRC8A,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:0015918	0.26	0.80	51	89	sterol transport	BP	1	VPS4B,LRP1,APOM,SERAC1,TSPO,PTCH1,TTC39B,ABCG5,ABCG8,NR1H2,APOB,PIP4K2A,APOC1,TSKU,SOAT2,OSBP,LIMA1,NR1H3,PLTP,ABCA5,EGF,GRAMD1B,ABCG4,OSBPL2,OSBP2,STARD5,OSBPL6,SOAT1,OSBPL1A,ZDHHC8,ABCA12,LPCAT3,SYT7,GPS2,LIPC,ANXA2,OSBPL7,NAXE,LDLR,NPC1,ABCA3,ABCA7,RXRA,CEL,VPS4A,MIR27B,MIR27A,ABCA8,MIR33B,LDLRAP1,STARD4	grey	VSMC_M10
GO:0002399	0.26	0.95	4	5	MHC class II protein complex assembly	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1	grey	VSMC_M10
GO:0002503	0.26	0.95	4	5	peptide antigen assembly with MHC class II protein complex	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1	grey	VSMC_M10
GO:2000660	0.26	0.95	4	5	negative regulation of interleukin-1-mediated signaling pathway	BP	1	IL1R2,OTUD4,MIR21,MIR27A	grey	VSMC_M10
GO:0035235	0.26	0.88	9	14	ionotropic glutamate receptor signaling pathway	BP	1	GRIK2,GRIN2D,GRIK5,PTK2B,TIAM1,GRIK4,AC138894.1,CDK5R1,GRID2	grey	VSMC_M10
GO:1903305	0.26	0.80	54	95	regulation of regulated secretory pathway	BP	1	RAC2,CHRNA5,APBA1,RIMS3,SPHK2,CACNB2,GAB2,UNC13D,SYT1,RAB5A,NCKAP1L,SYT9,FER,P2RY1,F2RL1,VPS18,DTNBP1,SYT8,DNM1L,HYAL3,ADRA2A,KCNB1,FGR,STX1A,SNX4,BACE1,CSPG5,RAP1B,CASK,RAB3A,SYN1,C12orf4,SYT7,RAB15,STX4,ITGAM,SYT11,CACNA1G,RAB3D,IL4R,CALM1,SNAPIN,PRKCB,SCAMP5,STXBP2,PRAM1,FMR1,PDPK1,P2RX1,CACNA1H,FOXF1,STXBP1,AP1G1,DOC2B	grey	VSMC_M10
GO:0042461	0.26	0.85	17	28	photoreceptor cell development	BP	1	NTRK2,PRPH2,RORB,RDH13,MYO7A,DZANK1,FSCN2,CEP290,USH1C,C8orf37,RPGRIP1L,NRL,ROM1,IFT20,OLFM3,THY1,DIO3	grey	VSMC_M10
GO:0031103	0.26	0.83	25	42	axon regeneration	BP	1	LRP1,TSPO,PTN,TNC,DHFR,PTPRF,CHL1,SPP1,KIAA0319,MTR,GAP43,DAG1,KREMEN1,CERS2,LRIG2,APOD,TNR,EPHA4,NDEL1,MAP2K1,ISL1,MAPK8IP3,MIR222,CNTF,RTN4RL1	grey	VSMC_M10
GO:0000288	0.26	0.82	31	53	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	BP	1	PAN2,CNOT2,CNOT6,PABPC1,PNLDC1,AGO2,TNRC6B,TUT7,EXOSC3,TUT4,MLH1,TNRC6C,LSM1,PAN3,CNOT1,CNOT6L,TENT4B,EIF4ENIF1,RC3H1,SAMD4A,POLR2G,NT5C3B,DCP1B,TOB1,TNRC6A,CNOT8,PARN,NANOS1,ZFP36L2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0046645	0.26	0.92	5	7	positive regulation of gamma-delta T cell activation	BP	1	NCKAP1L,SOX13,NOD2,STAT5B,SOX4	grey	VSMC_M10
GO:1901018	0.26	0.88	9	14	positive regulation of potassium ion transmembrane transporter activity	BP	1	KCNIP2,ANK2,NOS1AP,ATP1B1,KCNA1,ATP1B2,DNM2,RNF207,AMIGO1	grey	VSMC_M10
GO:0016198	0.26	0.92	5	7	axon choice point recognition	BP	1	ROBO1,ROBO2,GAP43,FOXG1,EFNB3	grey	VSMC_M10
GO:0008089	0.26	0.83	26	44	anterograde axonal transport	BP	1	AP3S1,KIF5A,RAB21,KIF3A,AGTPBP1,MGARP,DLG2,AP3M2,KIF5C,KIF3B,AP3B1,DTNBP1,CNIH2,CALY,BLOC1S6,AP3M1,KIF1C,HAP1,TRIM46,SNAPIN,MAPK8IP3,TERF2,BLOC1S3,BORCS5,AP3S2,MAP1A	grey	VSMC_M10
GO:0030322	0.26	0.89	8	12	stabilization of membrane potential	BP	1	KCNK9,KCNK15,KCNK1,KCNK2,KCNK7,KCNK4,KCNK3,KCNK5	grey	VSMC_M10
GO:0098664	0.26	0.89	8	12	G protein-coupled serotonin receptor signaling pathway	BP	1	HTR7,CHRM5,CHRM4,CHRM3,CHRM1,HRH2,HRH4,HTR1D	grey	VSMC_M10
GO:0097120	0.26	0.82	27	46	receptor localization to synapse	BP	1	STX7,KIF5A,ADAM22,DLG2,KIF5C,ANKS1B,KIF3B,DAG1,CNIH2,DLG1,KIF17,NSG1,GRIPAP1,RAB8A,DLG4,IQSEC2,GPHN,SYNJ2BP,CPLX1,STX1B,RAB11A,ARHGAP44,PRKCZ,CEP112,CACNG7,HRAS,CACNG5	grey	VSMC_M10
GO:0048793	0.26	0.92	5	7	pronephros development	BP	1	OSR1,CEP290,PAX8,PAX2,LHX1	grey	VSMC_M10
GO:0071816	0.26	0.88	10	15	tail-anchored membrane protein insertion into ER membrane	BP	1	EMC2,EMC10,EMC3,EMC4,GET4,EMC6,SGTA,UBL4A,CAMLG,EMC7	grey	VSMC_M10
GO:0008272	0.26	0.89	8	12	sulfate transport	BP	1	SLC26A10,SLC13A4,SLC26A5,SLC25A30,SLC25A11,SLC26A1,SLC26A2,SLC25A14	grey	VSMC_M10
GO:1903818	0.26	0.92	5	7	positive regulation of voltage-gated potassium channel activity	BP	1	KCNIP2,NOS1AP,KCNA1,RNF207,AMIGO1	grey	VSMC_M10
GO:0021884	0.26	0.86	12	19	forebrain neuron development	BP	1	UQCRQ,NDNF,SEMA3A,DCLK2,RAPGEF2,SLC4A10,DISC1,GBX2,PLXNA3,LHX8,UBB,FOXG1	grey	VSMC_M10
GO:0099640	0.26	0.92	5	7	axo-dendritic protein transport	BP	1	KIF5A,DLG2,KIF5C,MAPK8IP3,MAP1A	grey	VSMC_M10
GO:0099641	0.26	0.92	5	7	anterograde axonal protein transport	BP	1	KIF5A,DLG2,KIF5C,MAPK8IP3,MAP1A	grey	VSMC_M10
GO:0048791	0.27	0.88	9	14	calcium ion-regulated exocytosis of neurotransmitter	BP	1	RIMS2,RIMS1,RIMS3,SYT1,SYT8,SYT7,STX1B,STXBP1,DOC2B	grey	VSMC_M10
GO:0043266	0.27	0.81	34	59	regulation of potassium ion transport	BP	1	NEDD4L,WNK2,KEL,KCNRG,OXSR1,PRNP,KCNIP3,PTK2B,ANO6,KCNE2,CASQ2,KCNIP2,KCNJ2,ADRA2A,KCNG1,ANK2,KLHL24,NOS1AP,DLG1,ATP1B1,KCNA1,WNK3,ATP1B2,KCNAB3,KCNIP1,DNM2,RNF207,AMIGO1,WWP2,MIR21,KCNH2,NETO2,CRBN,RGS4	grey	VSMC_M10
GO:0061014	0.27	0.80	47	82	positive regulation of mRNA catabolic process	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,PNLDC1,AGO2,TNRC6B,TUT7,GTPBP1,EXOSC3,PNPT1,TUT4,ZC3HAV1,MLH1,TNRC6C,LSM1,PAN3,CNOT1,CELF1,CNOT6L,FTO,TENT4B,RBM24,DIS3L2,GIGYF2,YTHDF2,YTHDF1,EIF4ENIF1,RC3H1,UPF1,SAMD4A,POLR2G,NT5C3B,DCP1B,TARDBP,TOB1,TNRC6A,CNOT8,PARN,METTL16,PLEKHN1,METTL14,NANOS1,ZFP36L2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0002756	0.27	0.89	8	12	MyD88-independent toll-like receptor signaling pathway	BP	1	PRKCE,TLR4,CD300LF,IRF7,CD40,RAB11FIP2,TRAF3,TICAM1	grey	VSMC_M10

GO:0090087	0.27	0.79	81	144	regulation of peptide transport	BP	1	LRP1,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,BMP8A,EGFR,TRPM4,GIPR,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,KCNJ11,NNAT,TIAM1,PFKM,SLC8B1,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,PER2,STX1A,PASK,GLUL,SIDT2,SLC16A1,KLF7,ENY2,ABCA12,MCU,PPP3CB,CD38,MPC2,SYT7,NLGN2,TARDBP,STX4,RAB8B,SYTL4,GPR68,S100A8,CD74,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,LRRC8A,FGA,CHGA,SOX4,DPP4,CA2,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:0046513	0.27	0.82	30	51	ceramide biosynthetic process	BP	1	ORMDL2,B4GALNT1,PLA2G6,SPTLC1,SMPD2,AGK,SPHK2,ELOVL1,SPTLC3,SIRT3,ASAH1,ST8SIA4,ORMDL1,ST8SIA2,SGMS2,B3GALT1,CERS6,CERS2,SMPD4,SGMS1,CLN8,DEGS1,ALOXE3,P2RX1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,CYP4F22,B4GALT3,ST8SIA6	grey	VSMC_M10
GO:0015824	0.27	0.92	5	7	proline transport	BP	1	SLC1A4,SLC6A15,ACE2,SLC6A7,SLC36A1	grey	VSMC_M10
GO:0015820	0.27	0.92	5	7	leucine transport	BP	1	LLGL2,SLC6A15,SLC43A1,SLC3A2,SLC7A5	grey	VSMC_M10
GO:0002819	0.27	0.79	63	111	regulation of adaptive immune response	BP	1	CD226,STX7,TNFAIP3,AGER,HLA-DRA,EXOSC3,MSH2,RSAD2,IL4I1,TRPM4,HMCES,NECTIN2,PVR,MLH1,SLC22A13,FOXJ1,PAXIP1,SHLD1,NCKAP1L,HPX,IRF7,TRAF6,MEF2C,EIF2AK4,RIPK2,NOD2,ADCY7,CD40,HLX,DENND1B,CD28,FZD5,DUSP10,PLA2G4A,BCL6,IL12A,RC3H1,PTPN6,TNFSF18,SLC11A1,PPP3CB,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,TBX21,ZBTB7B,IL4R,BTK,FBXO38,C3,IL7R,SUPT6H,PRKCZ,TRAF2,MIR21,FADD,CD46,FCER2,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0099111	0.27	0.78	92	165	microtubule-based transport	BP	1	AP3S1,KIF5A,RAB21,KIF3A,LRRC6,AGTPBP1,SUN2,COPG2,IFT74,APBA1,RFX3,BICD2,DYNC2LI1,LRPPRC,DNAH11,MGARP,WASF1,TTC26,KIF3C,ARHGAP21,COPG1,KLC3,DLG2,IFT172,TTC21A,WDR60,AP3M2,KIF5C,NEK10,PURA,TUB,KIF3B,IFT81,RASGRP1,OPA1,AP3B1,IFT52,DNAH5,DTNBP1,DPCD,ROPN1L,KIF13A,BICDL1,CFAP43,TTC21B,HSPA8,JHY,OFD1,CFAP45,BAG3,TRAF3IP1,CNIH2,CALY,TTC30A,SPG11,MAPT,BLOC1S6,DNAAF2,SPAG16,MREG,HTT,STK36,KIF17,UXT,AP3M1,ADCY10,KIF1C,TTC25,HAP1,DNAAF4,WDR19,PEX14,TRIM46,NDEL1,AC138894.1,SNAPIN,SFPQ,CAMSAP3,IFT20,SPEF2,CFAP53,HSPB11,BICDL2,PRKCZ,MAPK8IP3,TERF2,UBB,BLOC1S3,BORCS5,AP3S2,MAP1A,SPA17	grey	VSMC_M10
GO:0050779	0.27	0.80	47	82	RNA destabilization	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,DXO,PNLDC1,AGO2,TNRC6B,TUT7,EXOSC3,PNPT1,TUT4,MLH1,TNRC6C,LSM1,PAN3,CNOT1,CELF1,CNOT6L,FTO,TENT4B,RBM24,DIS3L2,GIGYF2,YTHDF2,YTHDF1,EIF4ENIF1,RC3H1,UPF1,SAMD4A,POLR2G,NT5C3B,DCP1B,TNFRSF1B,TARDBP,TOB1,TNRC6A,CNOT8,PARN,METTL16,PLEKHN1,METTL14,NANOS1,ZFP36L2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0010839	0.27	0.89	8	12	negative regulation of keratinocyte proliferation	BP	1	CD109,INTU,VDR,KDF1,SFN,CASK,MED1,MIR125B1	grey	VSMC_M10
GO:0032620	0.27	0.85	15	24	interleukin-17 production	BP	1	TLR4,IL15,PHB,MYD88,PRNP,NCKAP1L,NR1H4,NOD2,OSM,IL12A,VSIR,FOXP3,ZBTB7B,SLC7A5,DDIT3	grey	VSMC_M10
GO:0032660	0.27	0.85	15	24	regulation of interleukin-17 production	BP	1	TLR4,IL15,PHB,MYD88,PRNP,NCKAP1L,NR1H4,NOD2,OSM,IL12A,VSIR,FOXP3,ZBTB7B,SLC7A5,DDIT3	grey	VSMC_M10
GO:0046460	0.27	0.83	22	37	neutral lipid biosynthetic process	BP	1	AVIL,PNPLA3,NR1H2,LPIN1,PLCE1,FBXW7,NR1H3,LPIN3,FITM2,GPLD1,SIK1,GPAM,LPGAT1,PLA2G4A,MOGAT3,SLC27A1,LDLR,SREBF1,LPIN2,C3,PLA2G15,CNEP1R1	grey	VSMC_M10
GO:0046463	0.27	0.83	22	37	acylglycerol biosynthetic process	BP	1	AVIL,PNPLA3,NR1H2,LPIN1,PLCE1,FBXW7,NR1H3,LPIN3,FITM2,GPLD1,SIK1,GPAM,LPGAT1,PLA2G4A,MOGAT3,SLC27A1,LDLR,SREBF1,LPIN2,C3,PLA2G15,CNEP1R1	grey	VSMC_M10
GO:0071868	0.27	0.81	38	66	cellular response to monoamine stimulus	BP	1	PRKN,ATF4,SLC1A1,VPS35,HDAC2,ALK,SIRT2,HTR7,CHRM5,CHRM4,DTNBP1,CHRM3,RYR2,SRD5A1,SLC9A1,CALY,HTR3B,MAPK1,CHRM1,GNB5,NSG1,HRH2,PKLR,HCN3,MAPK3,DNM2,SIN3A,HRH4,GNAL,GNB1,GNA15,PALM,GNAI3,HTR1D,RGS4,GNA14,GNG2,ARPP19	grey	VSMC_M10
GO:0071870	0.27	0.81	38	66	cellular response to catecholamine stimulus	BP	1	PRKN,ATF4,SLC1A1,VPS35,HDAC2,ALK,SIRT2,HTR7,CHRM5,CHRM4,DTNBP1,CHRM3,RYR2,SRD5A1,SLC9A1,CALY,HTR3B,MAPK1,CHRM1,GNB5,NSG1,HRH2,PKLR,HCN3,MAPK3,DNM2,SIN3A,HRH4,GNAL,GNB1,GNA15,PALM,GNAI3,HTR1D,RGS4,GNA14,GNG2,ARPP19	grey	VSMC_M10
GO:0009220	0.27	0.87	11	17	pyrimidine ribonucleotide biosynthetic process	BP	1	NME1,CMPK1,NME4,CTPS2,NME7,UPRT,NME3,UCK1,DHODH,NME6,UPP1	grey	VSMC_M10
GO:0015800	0.27	0.83	23	39	acidic amino acid transport	BP	1	SLC12A2,NTRK2,APBA1,SLC1A1,SLC25A13,SLC3A1,SLC7A11,ARL6IP5,GRM2,ATP1A2,PER2,NTSR1,ARL6IP1,PRAF2,CLN8,PSEN1,LRRC8E,ABAT,SLC1A7,TRPV1,LRRC8A,STXBP1,LRRC8D	grey	VSMC_M10
GO:0072234	0.27	0.88	9	14	metanephric nephron tubule development	BP	1	POU3F3,OSR1,SOX9,PAX8,PKD2,PAX2,PKD1,SOX8,LIF	grey	VSMC_M10
GO:0010665	0.27	0.83	20	33	regulation of cardiac muscle cell apoptotic process	BP	1	MAP3K5,PPP1R10,RGL2,HSF1,PAX8,HAND2,SIRT5,SIRT4,AGT,NFE2L2,CXCR2,CAMK2A,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,TIGAR,NKX2-5,HEY2	grey	VSMC_M10
GO:0007172	0.27	0.92	5	7	signal complex assembly	BP	1	MAPK8IP2,PTK2,NCK2,PTK2B,PXN	grey	VSMC_M10
GO:0036148	0.27	0.92	5	7	phosphatidylglycerol acyl-chain remodeling	BP	1	SERAC1,CRLS1,PLA2G4B,LPCAT1,LPGAT1	grey	VSMC_M10
GO:0006766	0.27	0.80	41	71	vitamin metabolic process	BP	1	SHMT2,CYP27B1,PSAT1,DHFR,AKR1A1,MMACHC,BTD,SLC23A2,PANK2,MMAA,CYP2R1,MTHFD2,CBR3,PRMT3,PLTP,MTRR,MTR,MMAB,SNAI1,THTPA,MCCC1,MTHFS,AASDHPPT,CYP27A1,ALDH1A2,PNPO,ABCD4,SHMT1,CD320,SLC46A1,PIAS4,TKTL1,GFI1,TPK1,MTHFD2L,SLC25A32,MMADHC,LRAT,NNMT,CLYBL,PDXP	grey	VSMC_M10
GO:0051890	0.27	0.92	5	7	regulation of cardioblast differentiation	BP	1	TBX5,PRICKLE1,TGFB2,GATA6,NKX2-5	grey	VSMC_M10

GO:0044458	0.27	0.83	20	33	motile cilium assembly	BP	1	UBE2B,LRRC6,CFAP69,ARMC2,INTU,SPATA6,RSPH6A,FOXJ1,DNAH1,NEURL1,CFAP43,ZMYND10,IHY,TTC12,SPAG16,MNS1,BBOF1,MKS1,SPEF2,TPGS1	grey	VSMC_M10
GO:0002576	0.27	0.92	5	7	platelet degranulation	BP	1	PLEK,ABCC4,DMTN,P2RX1,STXBP1	grey	VSMC_M10
GO:0070498	0.27	0.84	16	26	interleukin-1-mediated signaling pathway	BP	1	IL1R2,VRK2,MYD88,IRAK2,IKBKB,PLCB1,ST18,TRAF6,OTUD4,TOLLIP,TNIP2,MAPK3,RPS6KA5,MIR21,MIR27A,RPS6KA4	grey	VSMC_M10
GO:1904354	0.27	0.92	5	7	negative regulation of telomere capping	BP	1	ERCC1,XRCC1,NBN,ERCC4,TERF2	grey	VSMC_M10
GO:0021924	0.27	0.88	9	14	cell proliferation in external granule layer	BP	1	GLI1,SMO,GLI2,ZNF423,EGF,GBX2,LHX1,GPR37L1,CEND1	grey	VSMC_M10
GO:0021930	0.27	0.88	9	14	cerebellar granule cell precursor proliferation	BP	1	GLI1,SMO,GLI2,ZNF423,EGF,GBX2,LHX1,GPR37L1,CEND1	grey	VSMC_M10
GO:0150094	0.27	0.92	5	7	amyloid-beta clearance by cellular catabolic process	BP	1	LRP1,IDE,MME,LDLR,ABCA7	grey	VSMC_M10
GO:0071639	0.27	0.92	5	7	positive regulation of monocyte chemotactic protein-1 production	BP	1	AGER,OAS3,NOD2,TRPV4,OAS1	grey	VSMC_M10
GO:0007254	0.27	0.78	75	134	JNK cascade	BP	1	PHLPP1,MAP3K5,STK3,MAPK8IP2,PRKN,AGER,TRIB1,ROR2,GADD45G,KLHL31,DNAJA1,FKTN,MTURN,NOD1,EGFR,TLR4,TRAF1,SDCBP,MYD88,ZMYND11,PLCB1,MAP4K1,GPS1,SEMA3A,SH3RF2,ERCC6,MFHAS1,TRAF6,EPHB1,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,TRPV4,PDCD4,NCF1,TRAF5,STRADB,FZD7,MAGI3,MAP3K11,AIDA,DUSP10,MBIP,MEN1,MAP4K2,DUSP19,PINK1,LTBR,MINK1,GPS2,TAOK2,HACD3,SMAD3,NCOR1,TRAF3,ADORA2B,SH2D3A,PTGER4,TAOK1,ARHGEF6,SERPINF2,MAPK8IP3,TRAF2,MARVELD3,DAB2IP,ZNF622,WNT5A,GADD45A,DUSP22,HRAS,MAP2K7	grey	VSMC_M10
GO:0017014	0.27	0.88	8	12	protein nitrosylation	BP	1	NCOA7,GAPDH,ADH5,NOS1AP,S100A8,NOS2,DMD,TXN	grey	VSMC_M10
GO:0018119	0.27	0.88	8	12	peptidyl-cysteine S-nitrosylation	BP	1	NCOA7,GAPDH,ADH5,NOS1AP,S100A8,NOS2,DMD,TXN	grey	VSMC_M10
GO:1903748	0.27	0.92	5	7	negative regulation of establishment of protein localization to mitochondrion	BP	1	DNAJA1,BAG4,BAG3,MAPT,C11orf65	grey	VSMC_M10
GO:0006082	0.27	0.75	378	689	organic acid metabolic process	BP	1	ATP8B1,GLS2,HSD17B4,SHMT2,ALDH8A1,MARS,AIG1,LTC4S,GFPT2,TPH2,RIDA,CPT1B,DPYS,SLC27A6,TNXB,QKI,PPARA,ACSL6,PNPLA3,MCAT,HSD17B8,ECHDC1,ACO2,PRXL2C,AKR1B1,ATF4,PYCR3,MAPK14,PSAT1,GPT,HACD4,MTAP,CARNMT1,GNMT,ALDH1A1,CROT,ABCC10,GNPDA2,SLC35B2,KIT,SLC25A13,GAPDH,AASDH,PPAT,LIPT1,HMGCLL1,ADH5,RIMKLA,PRKCE,ETFB,SLC4A4,ME1,BPGM,NR1H2,DDC,IL4I1,LPIN1,MGST2,QRSL1,SLC7A11,DLD,DDO,BCAT2,NANP,PRKAR2B,DHFR,FAAH,HADHA,GAD2,SOX9,ABHD5,AKR1A1,APOC1,HPDL,DHTKD1,ECHDC3,PRKAG2,ACOX1,SLC22A13,XYLB,PIBF1,CYGB,GCKR,HYI,HNMT,ELOVL1,CSGALNACT1,AKT2,PFKP,IDO2,IDO1,MDH2,HARS,HARS2,BTD,HACL1,SLC23A2,CARS2,PANK2,PDK1,AMDHD1,LARS,SUCLG2,NR1H4,PDHX,APIP,TRIB3,LYPLA1,ACOXL,CSAD,CYP7A1,ELOVL7,ASAH1,CYP7B1,ACOX2,GPI,ABHD6,THNSL2,AHCY,CBR4,OSBP,GSS,MCCC2,HPGD,MSRA,GPD1,PEX2,P2RX7,CYP2R1,ETFDH,ACOT12,MTHFD2,PRKAG1,GMPS,NR1H3,SERINC5,ENOPH1,PFKM,SDSL,IVD,LPIN3,HOGA1,NIT2,BPHL,ASNSD1,ECI2,HIBCH,GLS,ABCC2,ERLIN1,ABCG2,PLA2G4B,ACAD8,ADTRP,PRMT3,PRKAB1,WARS2,LONP2,MTRR,PM20D1,SIRT4,GATC,ASL,MCEE,ALDH5A1,AZIN2,IRS1,MTR,YARS2,CARMIL1,CBSL,ALDH1A3,CPT1A,TPST1,BDH2,ZBTB20,GPAM,PPA2,ACSL5,NR5A2,SLC7A7,CYP2U1,HGD,MARC2,MARC1,MAPKAPK2,AMT,PFKFB2,ABHD2,MSMO1,MECR,MCCC1,GNPAT,CMAS,ENO4,TARS2,DALRD3,ABCB11,DHRS9,PC,HACD2,ARNT,LPGAT1,CTPS2,PER2,ACTN3,HDAC4,OSBPL2,ACADSB,OAT,THEM5,THEM4,MLXIPL,HMGCL,GLUL,D2HGDH,SCAP,EHHADH,SMS,MDH1B,POR,PDK3,PLA2G4A,OSBPL6,UPB1,ACADL,PLOD3,GCT3,UK1,FAU,PCO2,CBS1,ATIH5,TYSND1,LARS2,OSB	grey	VSMC_M10
GO:0090715	0.27	0.92	5	7	immunological memory formation process	BP	1	HLA-DRA,BCL6,TSC1,CD46,FGL2	grey	VSMC_M10
GO:0035701	0.27	0.92	5	7	hematopoietic stem cell migration	BP	1	KIT,GAS6,JAM2,GPLD1,BCL11B	grey	VSMC_M10
GO:0036151	0.27	0.88	8	12	phosphatidylcholine acyl-chain remodeling	BP	1	TMEM86B,MBOAT7,NR1H2,MBOAT2,NR1H3,LPCAT1,PLA2G4A,LPCAT3	grey	VSMC_M10
GO:0033622	0.27	0.85	13	21	integrin activation	BP	1	TLN1,PLEK,ITGB1BP1,FERMT1,CDH17,COL16A1,FARP2,RAP1B,FN1,FERMT3,FBLIM1,PTGER4,PIEZO1	grey	VSMC_M10
GO:0032239	0.27	0.87	9	14	regulation of nucleobase-containing compound transport	BP	1	CPSF6,IWS1,RIPK1,NCBP2,SETD2,AKAP8L,RSC1A1,NRDE2,SUPT6H	grey	VSMC_M10
GO:0032418	0.27	0.80	36	62	lysosome localization	BP	1	RAC2,TFEB,MYH9,KIT,SPHK2,GAB2,UNC13D,PIP4P1,TMEM106B,FER,RASGRP1,SNAP23,LAT2,FGR,CBL,SNX4,KLC2,PTGDR,KXD1,RAB3A,C12orf4,BORCS6,NDEL1,LAT,IL4R,SYTL4,SNAPIN,S100A13,BTK,STXBP2,PDPK1,DEF8,FOXF1,STXBP1,CHGA,BORCS5	grey	VSMC_M10
GO:0034393	0.27	0.88	8	12	positive regulation of smooth muscle cell apoptotic process	BP	1	CDKN2A,ARRB1,STK4,PDCD4,IL12A,RBM10,MFN2,MIR24-1	grey	VSMC_M10
GO:0009084	0.28	0.88	8	12	glutamine family amino acid biosynthetic process	BP	1	GLS2,PYCR3,GLS,ASL,OAT,GLUL,AC138894.1,ASS1	grey	VSMC_M10
GO:1901381	0.28	0.84	15	25	positive regulation of potassium ion transmembrane transport	BP	1	WNK2,ANO6,KCNIP2,KCNJ2,ANK2,NOS1AP,ATP1B1,KCNA1,WNK3,ATP1B2,DNM2,RNF207,AMIGO1,MIR21,KCNH2	grey	VSMC_M10
GO:0060242	0.28	0.92	5	7	contact inhibition	BP	1	TSPO,SMO,DACH1,PTPRJ,FAP	grey	VSMC_M10
GO:0060245	0.28	0.92	5	7	detection of cell density	BP	1	TSPO,SMO,DACH1,PTPRJ,FAP	grey	VSMC_M10
GO:0048537	0.28	0.92	5	7	mucosa-associated lymphoid tissue development	BP	1	RET,TOX,STAT5B,FOXL1,ARTN	grey	VSMC_M10
GO:0048541	0.28	0.92	5	7	Peyer's patch development	BP	1	RET,TOX,STAT5B,FOXL1,ARTN	grey	VSMC_M10
GO:0046036	0.28	0.88	8	12	CTP metabolic process	BP	1	NME1,ENTPD4,NME4,CTPS2,NME7,NME3,UCK1,NME6	grey	VSMC_M10
GO:0006221	0.28	0.84	15	24	pyrimidine nucleotide biosynthetic process	BP	1	NME1,TBPL1,CMPK1,NME4,CTPS2,DTYMK,NME7,UPRT,NME3,UCK1,DHODH,CMPK2,NME6,DCTD,UPP1	grey	VSMC_M10
GO:0042501	0.28	0.92	5	7	serine phosphorylation of STAT protein	BP	1	RET,CDK5R1,NLK,GADD45A,LIF	grey	VSMC_M10
GO:0032372	0.28	0.89	7	10	negative regulation of sterol transport	BP	1	ABCG5,ABCG8,APOC1,EGF,MIR27B,MIR27A,MIR33B	grey	VSMC_M10
GO:0032375	0.28	0.89	7	10	negative regulation of cholesterol transport	BP	1	ABCG5,ABCG8,APOC1,EGF,MIR27B,MIR27A,MIR33B	grey	VSMC_M10
GO:0015803	0.28	0.92	5	7	branched-chain amino acid transport	BP	1	SLC38A9,SLC43A1,SLC3A2,SLC25A44,SLC7A5	grey	VSMC_M10
GO:1900246	0.28	0.92	5	7	positive regulation of RIG-I signaling pathway	BP	1	USP15,ANKRD17,PUM2,OASL,ZCCHC3	grey	VSMC_M10

GO:0010758	0.28	0.85	13	21	regulation of macrophage chemotaxis	BP	1	PTK2,AKIRIN1,C5AR1,MTUS1,PTK2B,TRPV4,CMKLR1,SLAMF8,TNFSF18,MAPK1,MAPK3,CCL5,CSF1R	grey	VSMC_M10
GO:0045717	0.28	0.88	8	12	negative regulation of fatty acid biosynthetic process	BP	1	APOC1,PIBF1,TRIB3,CYP7A1,ERLIN1,ACADL,ACADVL,INSIG2	grey	VSMC_M10
GO:0050996	0.28	0.88	8	12	positive regulation of lipid catabolic process	BP	1	PPARA,PRKCE,FGF21,ABHD5,AKT2,IRS1,CPT1A,DAGLB	grey	VSMC_M10
GO:0010917	0.28	0.88	8	12	negative regulation of mitochondrial membrane potential	BP	1	HEBP2,SLC25A27,RNF122,ARL6IP5,MAPT,TRPV1,PIP5KL1,BNIP3L	grey	VSMC_M10
GO:0033235	0.28	0.88	8	12	positive regulation of protein sumoylation	BP	1	TOLLIP,PIAS3,ARNT,HDAC4,MUL1,PIAS4,RWDD3,RASD2	grey	VSMC_M10
GO:0006885	0.28	0.79	40	70	regulation of pH	BP	1	SLC4A4,PPT1,RAB7A,ATP6V0E2,LACC1,SLC4A2,AQP11,SLC4A7,TMEM106B,MAFG,CCKBR,ATP6V1H,TM9SF4,SLC9A9,HVCN1,SLC4A10,SLC9B1,TMEM9,TCIRG1,SLC9A8,SLAMF8,RHCG,SLC9A1,CLIC4,SLC11A1,SLC9A7,ATP6V0A1,MAPK1,DMXL2,SLC4A3,MAPK3,AC138894.1,CLN6,SNAPIN,TMEM199,SLC9A6,ATP6AP1,SLC9A5,CA2,RAB39A	grey	VSMC_M10
GO:0097250	0.28	0.94	4	5	mitochondrial respirasome assembly	BP	1	HIGD1A,COX7A1,COX7A2,COX7A2L	grey	VSMC_M10
GO:2000785	0.28	0.82	22	37	regulation of autophagosome assembly	BP	1	PIP4K2C,RNF5,PIP4K2A,RALB,RAB5A,FEZ2,ULK1,TBC1D12,SEC22B,TMEM39A,ADPRH,MTMR3,RAB1B,PIKFYVE,TBC1D14,PINK1,PHF23,SMCR8,IFT20,MTM1,KIAA1324,SH3GLB1	grey	VSMC_M10
GO:0002573	0.28	0.77	86	154	myeloid leukocyte differentiation	BP	1	NME1,IL5,TRIB1,MYC,TOB2,L3MBTL3,MAPK14,HSF1,MYH9,CDK6,KIT,ROR2,CD109,HOXA7,TLR4,IL15,OSTM1,GAB2,POU4F1,TGFBR2,FOXP1,MITF,IRF7,TRAF6,CAMK4,CEBPA,PIK3R1,FBXW7,AP3B1,F2RL1,TESC,RIPK1,TSPAN2,ITGB6,SH3PXD2A,LRRK1,SLC9B2,TCIRG1,GPR137B,PIAS3,ACIN1,TCTA,HCLS1,UBASH3B,FARP2,ZBTB46,SP3,CREB1,BATF2,ESRRA,GPR137,FBN1,LTBR,INHA,TFE3,PARP1,RBPJ,MED1,ANXA2,PSEN1,FOS,BATF,HAX1,GPR68,CD74,CSF1R,PPARGC1B,EVI2B,PTPN2,GPC3,JUN,ATP6AP1,MIR125B1,FSTL3,MAFB,FADD,CASP8,CA2,DHRS2,BGLAP,SNX10,GLO1,NRROS,LIF,CEBPB,BATF3	grey	VSMC_M10
GO:0010664	0.28	0.84	16	26	negative regulation of striated muscle cell apoptotic process	BP	1	PPP1R10,RGL2,HSF1,PAX8,HAND2,SIRT5,SIRT4,BAG3,NFE2L2,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,NKX2-5,HEY2	grey	VSMC_M10
GO:0061909	0.28	0.91	5	7	autophagosome-lysosome fusion	BP	1	PIP4K2A,RUBCNL,VPS39,ATP13A2,AC138894.1	grey	VSMC_M10
GO:0009201	0.28	0.80	31	52	ribonucleoside triphosphate biosynthetic process	BP	1	NME1,ATP5MGL,PPARA,IMPDH1,SLC25A13,SPHK2,PRKAG2,ATP5F1C,ATP5F1A,DGUOK,FAM173B,NME4,CTPS2,DNAJC30,ATP5S,PINK1,STAT3,NME7,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,UCK1,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,NME6,NUDT2	grey	VSMC_M10
GO:0070127	0.28	0.91	5	7	tRNA aminoacylation for mitochondrial protein translation	BP	1	WARS2,YARS2,TARS2,DARS2,EARS2	grey	VSMC_M10
GO:0045542	0.28	0.91	5	7	positive regulation of cholesterol biosynthetic process	BP	1	CYP7A1,SCAP,POR,SREBF1,FGF1	grey	VSMC_M10
GO:0106120	0.28	0.91	5	7	positive regulation of sterol biosynthetic process	BP	1	CYP7A1,SCAP,POR,SREBF1,FGF1	grey	VSMC_M10
GO:0002824	0.28	0.80	37	64	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	CD226,STX7,HLA-DRA,EXOSC3,MSH2,RSAD2,HMCES,NECTIN2,PVR,MLH1,SLC22A13,PAXIP1,SHLD1,HPX,TRAF6,RIPK2,NOD2,CD40,DENND1B,CD28,FZD5,PLA2G4A,IL12A,SLC11A1,FOXP3,ZBTB1,SHLD2,TBX21,BTK,FBXO38,C3,PRKCZ,TRAF2,MIR21,FADD,FCER2,TNFSF13B	grey	VSMC_M10
GO:1903961	0.28	0.91	5	7	positive regulation of anion transmembrane transport	BP	1	ABCB1,AGT,ACE2,ARL6IP1,PSEN1	grey	VSMC_M10
GO:0007350	0.28	0.87	9	14	blastoderm segmentation	BP	1	FRS2,SEMA3A,FAM208A,SEMA3F,HOXD8,FZD5,WDR77,WNT5A,BASP1	grey	VSMC_M10
GO:0010662	0.28	0.82	21	35	regulation of striated muscle cell apoptotic process	BP	1	MAP3K5,PPP1R10,RGL2,HSF1,PAX8,HAND2,SIRT5,SIRT4,AGT,BAG3,NFE2L2,CXCR2,CAMK2A,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,TIGAR,NKX2-5,HEY2	grey	VSMC_M10
GO:0000244	0.28	0.86	11	17	spliceosomal tri-snRNP complex assembly	BP	1	PRPF31,SRSF10,AAR2,SART3,PRPF19,RNU5E-1,RNU5B-1,RNU4ATAC,RNU4-2,SRSF12,RNU4-1	grey	VSMC_M10
GO:0030388	0.28	0.91	5	7	fructose 1,6-bisphosphate metabolic process	BP	1	PFKP,PFKM,ALDOC,FBP2,TIGAR	grey	VSMC_M10
GO:0072044	0.28	0.89	6	9	collecting duct development	BP	1	PTCH1,AKR1B1,TFAP2B,PAX8,PAX2,PKD1	grey	VSMC_M10
GO:1903792	0.28	0.87	9	14	negative regulation of anion transport	BP	1	GOPC,TCAF2,SFRP4,ARL6IP5,SLC43A1,PLA2R1,ABAT,GABRE,RGS4	grey	VSMC_M10
GO:0002604	0.28	0.91	5	7	regulation of dendritic cell antigen processing and presentation	BP	1	NOD1,NOD2,SLC11A1,CD74,FGL2	grey	VSMC_M10
GO:0035666	0.29	0.91	5	7	TRIF-dependent toll-like receptor signaling pathway	BP	1	TLR4,CD300LF,CD40,TRAF3,TICAM1	grey	VSMC_M10
GO:0071379	0.29	0.86	10	16	cellular response to prostaglandin stimulus	BP	1	PRKCE,TNC,APOB,PTGER2,AKAP8,ACACA,PTGER4,GNB1,PTGFR,GNG2	grey	VSMC_M10
GO:1900746	0.29	0.84	13	21	regulation of vascular endothelial growth factor signaling pathway	BP	1	SEMA6A,PTP4A3,ADAMTS3,TSPAN12,SPRY2,DCN,PIK3CB,ROBO1,IL12A,DAB2IP,MIR199A1,MIR21,CADM4	grey	VSMC_M10
GO:0071318	0.29	0.87	9	14	cellular response to ATP	BP	1	TRPM4,P2RX3,RYR3,P2RX7,P2RY1,SSH1,TAF1,TRPV1,PDXP	grey	VSMC_M10
GO:0021532	0.29	0.83	17	28	neural tube patterning	BP	1	TBC1D32,PTCH1,SMO,BMI1,GLI2,RPGRIP1L,SUFU,GBX2,FKBP8,GORAB,GPR161,TULP3,WDR19,PSEN1,TMEM107,MKS1,GSC	grey	VSMC_M10
GO:1904415	0.29	0.91	5	7	regulation of xenophagy	BP	1	NOD1,OPTN,RIPK2,NOD2,MAPK3	grey	VSMC_M10
GO:1904417	0.29	0.91	5	7	positive regulation of xenophagy	BP	1	NOD1,OPTN,RIPK2,NOD2,MAPK3	grey	VSMC_M10
GO:0009191	0.29	0.91	5	7	ribonucleoside diphosphate catabolic process	BP	1	NT5E,NUDT5,NUDT16,ENTPD4,NUDT18	grey	VSMC_M10
GO:0001956	0.29	0.87	9	14	positive regulation of neurotransmitter secretion	BP	1	CACNB2,SYT1,DTNBP1,DNM1L,GPER1,STX1A,STX1B,BAIAP3,STXBP1	grey	VSMC_M10
GO:0043029	0.29	0.83	17	28	T cell homeostasis	BP	1	SLC46A2,NCKAP1L,ZC3H8,CASP3,GPAM,TCIRG1,PPP2R3C,RC3H1,PPP3CB,STAT5B,FOXP3,DNAJA3,FADD,TSC22D3,BCL2L11,SLC39A3,RC3H2	grey	VSMC_M10
GO:0002821	0.29	0.79	38	66	positive regulation of adaptive immune response	BP	1	CD226,STX7,HLA-DRA,EXOSC3,MSH2,RSAD2,HMCES,NECTIN2,PVR,MLH1,SLC22A13,PAXIP1,SHLD1,HPX,TRAF6,EIF2AK4,RIPK2,NOD2,CD40,DENND1B,CD28,FZD5,PLA2G4A,IL12A,SLC11A1,FOXP3,ZBTB1,SHLD2,TBX21,BTK,FBXO38,C3,PRKCZ,TRAF2,MIR21,FADD,FCER2,TNFSF13B	grey	VSMC_M10
GO:1990314	0.29	0.91	5	7	cellular response to insulin-like growth factor stimulus	BP	1	SYAP1,CREB1,FBN1,CRK,SLC25A33	grey	VSMC_M10

GO:2000638	0.29	0.91	5	7	regulation of SREBP signaling pathway	BP	1	C12orf49,FBXW7,AMFR,ZBTB7B,INSIG2	grey	VSMC_M10
GO:0045623	0.29	0.86	9	14	negative regulation of T-helper cell differentiation	BP	1	HLX,BCL6,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,RC3H2	grey	VSMC_M10
GO:0014874	0.29	0.88	8	12	response to stimulus involved in regulation of muscle adaptation	BP	1	SCN5A,DAG1,AGT,CASQ1,ACTN3,HDAC4,PRKAG3,NOL3	grey	VSMC_M10
GO:0038030	0.29	0.91	5	7	non-canonical Wnt signaling pathway via MAPK cascade	BP	1	NKD1,DVL3,FZD7,WNT4,WNT5A	grey	VSMC_M10
GO:0090324	0.29	0.91	5	7	negative regulation of oxidative phosphorylation	BP	1	DNAJC15,ACTN3,MLXIPL,RHOA,PPIF	grey	VSMC_M10
GO:0010896	0.29	0.91	5	7	regulation of triglyceride catabolic process	BP	1	FGF21,ABHD5,GPLD1,SORL1,DAGLB	grey	VSMC_M10
GO:0033083	0.29	0.91	5	7	regulation of immature T cell proliferation	BP	1	BMI1,IL1A,TMEM131L,RIPK2,FOXP3	grey	VSMC_M10
GO:0033617	0.29	0.85	11	17	mitochondrial cytochrome c oxidase assembly	BP	1	TIMM21,COA5,COX17,OXA1L,COA3,BCS1L,COX16,APOPT1,COX14,COA1,SCO1	grey	VSMC_M10
GO:1901029	0.29	0.91	5	7	negative regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	BP	1	TMEM14A,FZD9,ACAA2,SLC35F6,AC140504.1	grey	VSMC_M10
GO:0070831	0.29	0.86	9	14	basement membrane assembly	BP	1	PXDN,CLASP2,DAG1,LAMB3,PHLDB1,PLOD3,RAMP2,NTNG2,LAMB1	grey	VSMC_M10
GO:0033240	0.29	0.91	5	7	positive regulation of cellular amine metabolic process	BP	1	GPR37,NR1H4,COMT,ABAT,PARK7	grey	VSMC_M10
GO:0022900	0.29	0.76	86	149	electron transport chain	BP	1	RDH16,P4HA2,UQCRQ,NDUFA6,AKR1B1,SLC25A13,ADH5,ETFB,ME1,DLD,NDUFB2,NDUFB6,AKR1A1,DNAJC15,NDUFC2,IDO1,NDUFS8,NDUFA12,COX7A1,COX4I2,ASPH,CYB5A,GPD1,NDUFS3,ETFDH,CIAPIN1,DGUOK,LOXL2,NQO2,UQCRB,COX15,COX6B1,SRD5A1,NDUFV3,GLRX2,NDUFB4,ISCU,NCF1,COA6,POLG2,PDIA5,NDUFB3,NDUFS2,SDHC,NCF2,POR,COX6A1,FDX1,COX8A,PINK1,NDUFA9,ALDH4A1,SDHB,DHRS3,DEGS1,COX6A2,COX11,NDUFAB1,COX5A,NDUFA7,NDUFV2,ENOX2,NDUFB10,UQCR11,PARK7,ALDH2,CYBA,MT-ND1,MT-ND2,MT-CO3,MT-ND6,MT-CYB,NDUFA5,DHRS2,NDUFC1,COX7A2,ETFRF1,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,AOC2,PHGDH,COX7A2L	grey	VSMC_M10
GO:0072273	0.29	0.83	14	23	metanephric nephron morphogenesis	BP	1	SMO,SIX2,SOX9,PAX8,FMN1,PKD2,PAX2,SALL1,WNT4,CITED1,LHX1,PKD1,SOX8,LIF	grey	VSMC_M10
GO:0098754	0.29	0.78	52	90	detoxification	BP	1	LTC4S,APOM,PRXL2C,KDM3B,FANCC,PIM1,ALDH1A1,ABCB1,TXNRD1,PRDX1,ADH5,CAT,ALB,PXDN,MGST2,TXNRD3,DHFR,ATP7B,ESD,AKR1A1,GSTK1,PRDX3,CYGB,PXDNL,GLRX,GPX8,TP53INP1,ABCC2,ABCG2,SLC30A10,FBLN5,MARC2,MARC1,NFE2L2,DUOX1,GCH1,ABCB6,RDH11,SOD3,GSTZ1,MPO,RALBP1,TXNDC2,PARK7,NQO1,MIR21,MT1X,SLC22A5,HBA2,TXN,PTGES,ADH4	grey	VSMC_M10
GO:0051683	0.29	0.91	5	7	establishment of Golgi localization	BP	1	YWHAZ,ARHGAP21,COPG1,PDCD10,RIPOR1	grey	VSMC_M10
GO:0042368	0.29	0.91	5	7	vitamin D biosynthetic process	BP	1	CYP27B1,CYP2R1,SNAI1,CYP27A1,GFI1	grey	VSMC_M10
GO:0010002	0.29	0.85	10	16	cardioblast differentiation	BP	1	SRF,NRG1,TBX5,PRICKLE1,TGFB2,RBPJ,TBX2,GATA6,ISL1,NKX2-5	grey	VSMC_M10
GO:0021979	0.29	0.91	5	7	hypothalamus cell differentiation	BP	1	NDNF,SEMA3A,HAP1,UBB,POU3F2	grey	VSMC_M10
GO:0006635	0.29	0.79	37	64	fatty acid beta-oxidation	BP	1	HSD17B4,CPT1B,PPARA,MCAT,ECHDC1,CROT,ETFB,HADHA,ACOX1,AKT2,ACOXL,ACOX2,PEX2,ETFDH,IVD,ECI2,LONP2,IRS1,CPT1A,BDH2,ABCB11,EHHADH,ACADL,TYSND1,ACADVL,HSD17B10,ABCD4,GCDH,ACAA2,DECR2,MLYCD,ABCD3,ACADM,HADHB,AMACR,ECI1,AUH	grey	VSMC_M10
GO:0007389	0.29	0.74	180	329	pattern specification process	BP	1	GLI1,FRS2,TBC1D32,SYNGAP1,SMAD5,LRRC6,PTCH1,MFNG,SMO,DAAM2,MDFI,FOXH1,IFT74,SRF,RFX3,ROR2,MEOX2,SOSTDC1,ANKS6,DYNC2LI1,SIX2,SCMH1,DNAH11,HOXA2,HOXA4,HOXA6,HOXA7,FUZ,OSR1,NTF4,ARMC4,INTU,SPRY1,BBS7,BMI1,SETDB2,DRC1,ABI1,GLI2,MEGF8,PCDH8,GALNT11,XRCC2,ACVR2B,IFT172,FOXJ1,WNT11,TGFBR2,OVOL2,ACVR2A,BHLHE40,MKKS,SEMA3A,PRKDC,HOXC6,TCF15,POFUT1,KIF3B,PAX8,HAND2,EYA1,ROBO1,ROBO2,FAM208A,MEF2C,STC1,NKX3-1,TBX5,IFT52,RPGRIP1L,PKD2,RIPPLY3,PAX2,NKD1,DNAH5,DPCD,LDB1,BMPR1B,FBXL15,SUFU,IRX2,PGAP1,SEMA3F,POGLUT1,SATB2,AXIN2,SNAI1,TTC21B,OFD1,CFAP45,AP1B1,GBX2,BICC1,HES6,MMP21,CHRD,DLX1,GRHL3,WNT3,HOXD8,HOXD4,HOXD3,AIDA,FZD5,BCOR,DNAAF2,CRAMP1,MEOX1,PKD1L1,FKBP8,GORAB,GPR161,NKX3-2,TULP3,TTC25,DNAAF4,MNS1,DVL2,BMPR1A,WDR19,TCAP,RBPJ,ALDH1A2,RNF111,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,ITGAM,TMEM107,CITED1,SMAD3,CCDC151,MKS1,GSC,TBX2,LHX1,YY1,CDX1,MIB1,NLE1,ISL1,C3,GPC3,CFAP53,HSPB11,HES4,SKI,APC2,RNF207,WDR77,ALX3,CELSR2,FOXF1,ENG,MTF2,PSKH1,ADGRG1,OOEP,FOXG1,MAFB,ACVRL1,HOXB3,NOG,LBX1,WNT5A,BASP1,OTX1,SIX1,DDIT3,C2CD3,APC,NKX2-5,FGF1,PIFO,HEY2,WNT2,HOXA3,ZIC1	grey	VSMC_M10
GO:0098926	0.29	0.82	18	30	postsynaptic signal transduction	BP	1	LY6E,CHRNA3,KPNA2,PLCB1,NRG1,CHRM5,CHRM4,CHRM3,GRK2,CRTC1,STAT3,CHRM1,CHRNB2,HRH4,CDK5R1,GNB1,GNA15,PRR7	grey	VSMC_M10
GO:0070431	0.29	0.86	9	14	nucleotide-binding oligomerization domain containing 2 signaling pathway	BP	1	TNFAIP3,HSPA1B,TLR4,LACC1,RIPK2,OTULIN,NOD2,IRGM,INAVA	grey	VSMC_M10
GO:0001682	0.29	0.87	8	12	tRNA 5'-leader removal	BP	1	RPP21,POP4,RPP40,POP5,KIAA0391,POP7,RPP38,RPP30	grey	VSMC_M10
GO:0002712	0.29	0.81	23	39	regulation of B cell mediated immunity	BP	1	CD226,EXOSC3,MSH2,HMCES,NECTIN2,MLH1,FOXJ1,PAXIP1,SHLD1,HPX,NOD2,CD40,CD28,BCL6,PTPN6,FOXP3,SHLD2,TBX21,BTK,C3,SUPT6H,CD46,FCER2	grey	VSMC_M10
GO:0002889	0.29	0.81	23	39	regulation of immunoglobulin mediated immune response	BP	1	CD226,EXOSC3,MSH2,HMCES,NECTIN2,MLH1,FOXJ1,PAXIP1,SHLD1,HPX,NOD2,CD40,CD28,BCL6,PTPN6,FOXP3,SHLD2,TBX21,BTK,C3,SUPT6H,CD46,FCER2	grey	VSMC_M10
GO:1901509	0.29	0.91	5	7	regulation of endothelial tube morphogenesis	BP	1	FOXP1,ADAMTS12,LCN2,MIR21,FGF1	grey	VSMC_M10
GO:0099072	0.29	0.80	25	43	regulation of postsynaptic membrane neurotransmitter receptor levels	BP	1	ADAM22,USP46,EPS15,CTNND1,DAG1,AP2M1,EPS8,DLG1,CALY,DNM3,NSG1,GRIPAP1,RAB8A,DLG4,IQSEC2,GPHN,CPLX1,STX1B,RAB11A,ARHGAP44,AP2B1,PRKCZ,CACNG7,HRAS,CACNG5	grey	VSMC_M10

GO:0002863	0.29	0.91	5	7	positive regulation of inflammatory response to antigenic stimulus	BP	1	CD28,BTK,C3,PARK7,KARS	grey	VSMC_M10
GO:0035418	0.29	0.79	31	54	protein localization to synapse	BP	1	KIF5A,ABHD17B,ADAM22,SHANK1,DLG2,KIF5C,DAG1,BSN,MPP4,DLG1,MAPT,NRXN2,NSG1,GRIPAP1,RAB8A,DLG4,IQSEC2,NLGN2,CPLX1,STX1B,ZDHHC15,RAB11A,ARHGAP44,ASIC2,PRKCZ,MAPK8IP3,ZDHHC12,WNT5A,CACNG7,HRAS,MAP1A	grey	VSMC_M10
GO:0000050	0.29	0.91	5	7	urea cycle	BP	1	SLC25A15,CEBPA,ASL,CPS1,ASS1	grey	VSMC_M10
GO:0061157	0.29	0.78	45	79	mRNA destabilization	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,PNLDC1,AGO2,TNRC6B,TUT7,EXOSC3,PNPT1,TUT4,MLH1,TNRC6C,LSM1,PAN3,CNOT1,CELF1,CNOT6L,FTO,TENT4B,RBM24,DIS3L2,GIGYF2,YTHDF2,YTHDF1,EIF4ENIF1,RC3H1,UPF1,SAMD4A,POLR2G,NT5C3B,DCP1B,TARDBP,TOB1,TNRC6A,CNOT8,PARN,METTL16,PLEKHN1,METTL14,NANOS1,ZFP36L2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0048308	0.30	0.86	9	14	organelle inheritance	BP	1	YWHAZ,PLK3,GBF1,PDCD10,MAPK1,STX5,MAPK3,MAP2K1,PLK5	grey	VSMC_M10
GO:0048313	0.30	0.86	9	14	Golgi inheritance	BP	1	YWHAZ,PLK3,GBF1,PDCD10,MAPK1,STX5,MAPK3,MAP2K1,PLK5	grey	VSMC_M10
GO:0097501	0.30	0.91	5	7	stress response to metal ion	BP	1	SLC30A10,ABCB6,PARK7,HSPA5,MT1X	grey	VSMC_M10
GO:0090136	0.30	0.85	10	16	epithelial cell-cell adhesion	BP	1	SERPINB8,SRF,KIT,BVES,KIFC3,PLEKHA7,DSP,ITGB5,VCL,CAMSAP3	grey	VSMC_M10
GO:0045668	0.30	0.80	24	41	negative regulation of osteoblast differentiation	BP	1	PTCH1,RORB,CDK6,SEMA4D,HOXA2,AREG,TRPM4,SOX9,HAND2,VEGFC,HDAC7,SUFU,AXIN2,HDAC4,CHRDMEN1,RIOX1,TOB1,CITED1,SMAD3,TWSG1,RANBP3L,SKI,NOG	grey	VSMC_M10
GO:1902547	0.30	0.83	14	23	regulation of cellular response to vascular endothelial growth factor stimulus	BP	1	SEMA6A,PTP4A3,ADAMTS3,TSPAN12,SPRY2,DCN,PIK3CB,ROBO1,IL12A,ADAMTS12,DAB2IP,MIR199A1,MIR21,CADM4	grey	VSMC_M10
GO:0006110	0.30	0.81	20	34	regulation of glycolytic process	BP	1	PPARA,PRXL2C,SLC4A4,PRKAG2,GPD1,P2RX7,PRKAG1,ZBTB20,ARNT,ACTN3,HDAC4,MLXIPL,STAT3,PSEN1,OGT,NCOR1,INSR,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:1902600	0.30	0.76	66	115	proton transmembrane transport	BP	1	ATP5MGL,ATP6V1F,MFSD3,ATP6V1E2,ATP6V1C2,UCP1,SPHK2,ATP6V0E2,ATP6V0B,ATP1A3,ATP5F1C,TMCO3,COX7A1,ATP6V1H,COX4I2,CYB5A,ATP5F1A,SLC9A9,HVCN1,SLC33A1,TESC,COX15,FAM173B,ATP6V1B2,PM20D1,COX6B1,SLC4A10,SLC2A10,SLC9B1,SLC9B2,TCIRG1,COX17,SLC9A8,CLCN4,ATP1A2,SLC9A1,DNAJC30,COX6A1,ATP5S,COX8A,SLC9A7,ATP6V0A1,SLC2A9,ATP6V1D,COX6A2,NOX5,COX5A,SLC46A1,SLC9A6,ATP6V0C,ATP6AP1,PARK7,ATP5PB,VPS9D1,SLC9A5,MT-ATP8,MT-ATP6,MT-CO3,MT-CYB,SLC25A3,ATP5ME,SLC36A1,ATP5MF,APOPT1,COX7A2L,PPIF	grey	VSMC_M10
GO:0072655	0.30	0.77	59	103	establishment of protein localization to mitochondrion	BP	1	TIMM21,PRKN,TSPO,HSPA4,TOMM22,RAC2,FBXO7,DNAJA1,MGARP,AGK,DNAJC15,PITRM1,TIMM50,USP36,BAG4,MIPEP,IMMP1L,FBXW7,HTRA2,CSNK2A2,AP3B1,TOMM34,SIRT4,OXA1L,HPS4,ARIH2,BAG3,TOMM40L,FZD5,MAPT,FIS1,NMT1,HK1,GRPEL1,C11orf65,BCS1L,PINK1,TIMM17B,MFN2,NPEPPS,HAX1,CALM1,TIMM29,SREBF1,MAIP1,PAM16,BCAP31,SH3GLB1,MICALL2,BNIP3L,TIMM10B,TIMM23B,DDIT3,RALA,TIMM8B,RHOU,LEPROT,GRPEL2,DNAJC19	grey	VSMC_M10
GO:0006586	0.30	0.91	5	7	indolalkylamine metabolic process	BP	1	IL4I1,AANAT,IDO2,IDO1,GCDH	grey	VSMC_M10
GO:0033080	0.30	0.91	5	7	immature T cell proliferation in thymus	BP	1	BMI1,IL1A,TMEM131L,WNT4,FOXP3	grey	VSMC_M10
GO:0046942	0.30	0.75	96	173	carboxylic acid transport	BP	1	ATP8B1,SLC26A10,SLC16A7,SLC12A2,NTRK2,PLA2G6,ABCC10,APBA1,SLC1A1,SLC25A13,SLC3A1,SLC1A4,SLC7A11,SLC26A5,SLC25A30,LLGL2,SLC22A13,SLC25A38,ABCC4,SLC6A15,SLC25A15,SLC23A2,ARL6IP5,SLC7A1,SLC38A9,SLC5A8,CYP7A1,SLC43A1,SERINC5,SLC38A2,SLC38A1,SLC10A6,ABCC2,PLA2R1,ABCG2,GRM2,SFXN2,SLC38A3,MAP2K6,SLC16A6,SLC7A7,SLCO3A1,ABCB11,AGT,ABCC5,ACE2,ATP1A2,SLCO1A2,SLCO1C1,PER2,NTSR1,SLC16A1,PLA2G4A,SLC11A1,PQLC2,SLC27A1,SLC38A5,MPC2,ARL6IP1,SLC3A2,SLC38A6,PRAF2,SLC25A11,SLC16A13,CLN8,SLC26A1,PSEN1,SLC7A3,AC138894.1,ABCC3,NMUR2,SLC6A7,SLC26A2,LRRC8E,EMB,NOS2,SLC46A1,SLC25A14,PROCA1,ABAT,SLC1A7,TRPV1,SLC16A4,SLC7A5,LRRC8A,ABCD3,STXBP1,SLC7A6,SLC36A1,LRRC8D,PLA2G2C,SLC25A21,SLC25A32,RGS4,SLC25A29,PTGES	grey	VSMC_M10
GO:0031338	0.30	0.83	13	21	regulation of vesicle fusion	BP	1	GRIK5,TBC1D4,AKT2,SYT1,SYT9,ANKRD27,C2CD5,RAB3A,CPLANE2,ANXA2,CPLX1,STXBP1,DOC2B	grey	VSMC_M10
GO:2000121	0.30	0.91	5	7	regulation of removal of superoxide radicals	BP	1	DHFR,FBLN5,NFE2L2,GCH1,MIR21	grey	VSMC_M10
GO:0006883	0.30	0.85	10	16	cellular sodium ion homeostasis	BP	1	NEDD4L,SLC12A2,ATP1A3,IL1A,AGT,ATP1A2,SLC9A1,ATP1B1,ATP1B2,C7	grey	VSMC_M10
GO:0039528	0.30	0.81	18	30	cytoplasmic pattern recognition receptor signaling pathway in response to virus	BP	1	USP15,ANKRD17,PUM2,PHB,SEC14L1,CLPB,NPLOC4,IRF7,OAS3,IFIH1,OASL,NLRX1,BIRC3,TKFC,TSPAN6,RIOK3,RNF135,ZCCHC3	grey	VSMC_M10
GO:1901379	0.30	0.79	32	56	regulation of potassium ion transmembrane transport	BP	1	NEDD4L,WNK2,KEL,KCNRG,OXSR1,PRNP,KCNIP3,ANO6,KCNE2,CASQ2,KCNIP2,KCNJ2,KCNG1,ANK2,KLHL24,NOS1AP,DLG1,ATP1B1,KCNA1,WNK3,ATP1B2,KCNAB3,KCNIP1,DNM2,RNF207,AMIGO1,WWP2,MIR21,KCNH2,NETO2,CRBN,RGS4	grey	VSMC_M10
GO:1901031	0.30	0.82	17	28	regulation of response to reactive oxygen species	BP	1	GPR37,MET,FOXO3,DHFR,SESN3,PAWR,RIPK1,FBLN5,PDE8A,NFE2L2,GCH1,PINK1,STK26,PARK7,MIR21,GPR37L1,TXN	grey	VSMC_M10
GO:0042492	0.30	0.89	6	9	gamma-delta T cell differentiation	BP	1	TCF7,NCKAP1L,SOX13,STAT5B,JAG2,SOX4	grey	VSMC_M10
GO:0032371	0.30	0.79	27	46	regulation of sterol transport	BP	1	LRP1,TSPO,PTCH1,TTC39B,ABCG5,ABCG8,NR1H2,APOC1,NR1H3,PLTP,ABCA5,EGF,OSBPL6,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,NAXE,ABCA3,ABCA7,RXRA,MIR27B,MIR27A,ABCA8,MIR33B,LDLRAP1	grey	VSMC_M10
GO:0032374	0.30	0.79	27	46	regulation of cholesterol transport	BP	1	LRP1,TSPO,PTCH1,TTC39B,ABCG5,ABCG8,NR1H2,APOC1,NR1H3,PLTP,ABCA5,EGF,OSBPL6,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,NAXE,ABCA3,ABCA7,RXRA,MIR27B,MIR27A,ABCA8,MIR33B,LDLRAP1	grey	VSMC_M10

GO:0042471	0.30	0.77	50	89	ear morphogenesis	BP	1	OSR2,FZD6,PTK7,ROR2,DLX5,SIX2,KCNQ4,HOXA2,WHRN,SOBP,OSR1,MYO3A,SOX9,USH1G,GLI2,MYO7A,SPRY2,CEP290,PAX8,EYA1,PLS1,FZD3,USH1C,TFAP2A,PAX2,ALDH1A3,GBX2,MYO3B,GRHL3,STRC,STOX1,PRKRA,NKX3-2,MAPK1,DVL2,WDR19,TCAP,MAPK3,POU3F4,NTN1,GSC,CHRNA10,FOXG1,MAFB,NOG,WNT5A,OTX1,SIX1,INSIG2,ZIC1	grey	VSMC_M10
GO:0014002	0.30	0.81	19	32	astrocyte development	BP	1	LRP1,AGER,SMO,TTBK1,CDK6,ROR2,FPR2,EGFR,TLR4,C5AR1,TSPAN2,KRAS,MAPT,PSEN1,LDLR,S100A8,LAMC3,CNTF,POU3F2	grey	VSMC_M10
GO:0045672	0.30	0.86	9	14	positive regulation of osteoclast differentiation	BP	1	POU4F1,TRAF6,SLC9B2,CREB1,FOS,GPR68,PPARGC1B,ATP6AP1,CA2	grey	VSMC_M10
GO:0051873	0.30	0.90	5	7	killing by host of symbiont cells	BP	1	GAPDH,MYD88,F2RL1,SCNN1B,CXCL6	grey	VSMC_M10
GO:0051883	0.30	0.90	5	7	killing of cells in other organism involved in symbiotic interaction	BP	1	GAPDH,MYD88,F2RL1,SCNN1B,CXCL6	grey	VSMC_M10
GO:0045342	0.30	0.89	6	9	MHC class II biosynthetic process	BP	1	NFX1,TLR4,HDAC2,TAF7,SLC11A1,CIITA	grey	VSMC_M10
GO:0071475	0.30	0.90	5	7	cellular hyperosmotic salinity response	BP	1	XRCC6,AKR1B1,XRCC5,MICU1,SLC25A23	grey	VSMC_M10
GO:0043300	0.30	0.81	19	32	regulation of leukocyte degranulation	BP	1	RAC2,SPHK2,GAB2,UNC13D,NCKAP1L,FER,F2RL1,FGR,SNX4,C12orf4,STX4,ITGAM,IL4R,STXBP2,PRAM1,PDPK1,FOXF1,STXBP1,AP1G1	grey	VSMC_M10
GO:0006570	0.30	0.90	5	7	tyrosine metabolic process	BP	1	IL4I1,HGD,FAH,GSTZ1,PCBD2	grey	VSMC_M10
GO:0030073	0.30	0.75	83	149	insulin secretion	BP	1	LRP1,RIMS2,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,CYB5R4,BMP8A,TRPM4,GIPR,RAF1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,OSBP,ARNTL,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,PER2,STX1A,GLUL,SIDT2,SLC16A1,KLF7,VGF,ENY2,ABCA12,MCU,PPP3CB,CAMK2G,PTPRN,CD38,MPC2,ILDR2,SYT7,NLGN2,CPLX1,TARDBP,STX4,SYTL4,GPR68,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,PARK7,LRRC8A,CHGA,SOX4,DPP4,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:0070942	0.30	0.90	5	7	neutrophil mediated cytotoxicity	BP	1	MYD88,F2RL1,SCNN1B,DNASE1,CXCL6	grey	VSMC_M10
GO:0007035	0.30	0.83	14	23	vacuolar acidification	BP	1	PPT1,ATP6V0E2,TMEM106B,ATP6V1H,TMEM9,TCIRG1,CLIC4,SLC11A1,ATP6V0A1,DMXL2,AC138894.1,CLN6,SNAPIN,TMEM199	grey	VSMC_M10
GO:0042994	0.30	0.86	9	14	cytoplasmic sequestering of transcription factor	BP	1	MDFI,NFKBIE,FAF1,NFKBIB,PKD2,SUFU,KEAP1,PSMD10,PKD1	grey	VSMC_M10
GO:0015808	0.30	0.90	5	7	L-alanine transport	BP	1	SLC1A4,SLC38A3,SLC38A5,SLC3A2,SLC36A1	grey	VSMC_M10
GO:0043268	0.30	0.81	17	29	positive regulation of potassium ion transport	BP	1	WNK2,ANO6,KCNIP2,KCNJ2,ADRA2A,ANK2,NOS1AP,DLG1,ATP1B1,KCNA1,WNK3,ATP1B2,DNM2,RNF207,AMIGO1,MIR21,KCNH2	grey	VSMC_M10
GO:0009185	0.30	0.77	46	81	ribonucleoside diphosphate metabolic process	BP	1	PPARA,PRXL2C,GAPDH,SLC4A4,NT5E,BPGM,CMPK1,DLG2,NUDT5,DHTKD1,PRKAG2,PFKP,NUDT16,GPI,GPD1,P2RX7,PRKAG1,PFKM,ENTPD4,NUDT18,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,MAGI3,DLG1,HK1,CASK,PRKAG3,STAT3,ENO3,CARD11,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,MPP1,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:0046643	0.30	0.88	6	9	regulation of gamma-delta T cell activation	BP	1	TCF7,NCKAP1L,SOX13,NOD2,STAT5B,SOX4	grey	VSMC_M10
GO:0046697	0.30	0.83	14	23	decidualization	BP	1	CYP27B1,PTN,VDR,STC1,SPP1,DEDD,MEN1,CTSV,MAPK1,MAPK3,EPOR,BSG,TCF23,LIF	grey	VSMC_M10
GO:0016101	0.30	0.79	29	50	diterpenoid metabolic process	BP	1	RDH5,RDH16,LRP1,ALDH8A1,AKR1B1,ALDH1A1,ADH5,RDH13,EGFR,NAPEPLD,LIPE,SDR16C5,RETSAT,PRMT3,SRD5A1,ALDH1A3,DHRS9,BCO2,PECR,DHRS3,RDH11,ALDH1A2,SCPEP1,LRP8,PNPLA4,CRH,LRAT,RDH14,ADH4	grey	VSMC_M10
GO:0034397	0.30	0.90	5	7	telomere localization	BP	1	UBE2B,CCDC155,MLH1,SPO11,MAJIN	grey	VSMC_M10
GO:0090220	0.30	0.90	5	7	chromosome localization to nuclear envelope involved in homologous chromosome segregation	BP	1	UBE2B,CCDC155,MLH1,SPO11,MAJIN	grey	VSMC_M10
GO:0040020	0.30	0.83	13	21	regulation of meiotic nuclear division	BP	1	FBXO43,UBE2B,SIRT2,PLCB1,MOS,NPM2,PRKAR1A,GPR3,WNT4,FZR1,OOEP,WNT5A,LIF	grey	VSMC_M10
GO:0007379	0.30	0.85	9	14	segment specification	BP	1	MEOX2,HOXA2,OSR1,BMI1,IRX2,MEOX1,DVL2,MTF2,MAFB	grey	VSMC_M10
GO:0010172	0.31	0.88	6	9	embryonic body morphogenesis	BP	1	FUZ,CLASP2,MAB21L2,DAG1,PHLDB1,GREM2	grey	VSMC_M10
GO:0072528	0.31	0.81	17	28	pyrimidine-containing compound biosynthetic process	BP	1	NME1,TBPL1,CMPK1,NME4,CTPS2,DTYMK,CPS1,NME7,UPRT,NME3,UCK1,DHODH,TPK1,CMPK2,NME6,DCTD,UPP1	grey	VSMC_M10
GO:0060602	0.31	0.85	10	16	branch elongation of an epithelium	BP	1	ESR1,AREG,TNC,SPRY1,SOX9,SPRY2,MED1,WNT5A,SIX1,FGF1	grey	VSMC_M10
GO:0000966	0.31	0.83	13	21	RNA 5'-end processing	BP	1	RPP21,PNPT1,POP4,RPP40,POP5,NOP9,KIAA0391,POP7,HSD17B10,THG1L,RPP38,TRMT10C,RPP30	grey	VSMC_M10
GO:0046838	0.31	0.84	10	16	phosphorylated carbohydrate dephosphorylation	BP	1	SYNJ2,INPP4B,MTMR2,MTMR7,SYNJ1,INPP5A,INPP5J,IMPA2,INPP5K,INPP1	grey	VSMC_M10
GO:0046855	0.31	0.84	10	16	inositol phosphate dephosphorylation	BP	1	SYNJ2,INPP4B,MTMR2,MTMR7,SYNJ1,INPP5A,INPP5J,IMPA2,INPP5K,INPP1	grey	VSMC_M10
GO:0007342	0.31	0.90	5	7	fusion of sperm to egg plasma membrane involved in single fertilization	BP	1	SPACA6,IZUMO1,LYZL6,SPESP1,NOX5	grey	VSMC_M10
GO:0010669	0.31	0.84	10	16	epithelial structure maintenance	BP	1	SRF,KIAA1211,TLR4,SOX9,NOD2,LDB1,PBLD,MKS1,SLC22A5,INAVA	grey	VSMC_M10
GO:1903588	0.31	0.90	5	7	negative regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	IL12A,PDCD10,NGFR,MIR222,MIR24-1	grey	VSMC_M10
GO:0031204	0.31	0.90	5	7	posttranslational protein targeting to membrane, translocation	BP	1	SEC61B,SEC61G,SEC62,HSPA5,SEC61A2	grey	VSMC_M10
GO:0070561	0.31	0.88	6	9	vitamin D receptor signaling pathway	BP	1	CYP27B1,SNW1,PIM1,VDR,MED1,TRIM24	grey	VSMC_M10
GO:0035860	0.31	0.88	6	9	glial cell-derived neurotrophic factor receptor signaling pathway	BP	1	GFRA3,GFRA4,RET,SULF2,GFRA1,GDF15	grey	VSMC_M10
GO:0015721	0.31	0.84	10	16	bile acid and bile salt transport	BP	1	ATP8B1,ABCC4,CYP7A1,SLC10A6,ABCC2,ABCB11,SLCO1A2,SLCO1C1,ABCC3,ABCD3	grey	VSMC_M10
GO:0046051	0.31	0.90	5	7	UTP metabolic process	BP	1	NME1,NME4,NME7,NME3,NME6	grey	VSMC_M10
GO:0044351	0.31	0.88	6	9	macropinocytosis	BP	1	MAPKAPK3,CARMIL1,MAPKAPK2,STX1B,DOCK2,DNM2	grey	VSMC_M10

GO:0090276	0.31	0.75	78	140	regulation of peptide hormone secretion	BP	1	LRP1,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,BMP8A,EGFR,TRPM4,GIPR,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,KCNJ11,NNAT,TIAM1,PFKM,SLC8B1,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,PER2,STX1A,PASK,GLUL,SIDT2,SLC16A1,KLF7,ENY2,ABCA12,MCU,PPP3CB,CD38,MPC2,SYT7,NLGN2,TARDBP,STX4,RAB8B,SYTL4,GPR68,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,LRRC8A,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:1903203	0.31	0.82	14	23	regulation of oxidative stress-induced neuron death	BP	1	PRKN,NCOA7,ATF4,FBXO7,TLR4,SLC7A11,FBXW7,MCL1,NONO,PINK1,PARP1,PARK7,TSC1,TLDC1	grey	VSMC_M10
GO:2000601	0.31	0.88	6	9	positive regulation of Arp2/3 complex-mediated actin nucleation	BP	1	WASF1,FCHSD2,CYFIP1,WASF2,NCKAP1,WAS	grey	VSMC_M10
GO:0060759	0.31	0.75	72	128	regulation of response to cytokine stimulus	BP	1	TNFAIP3,HSPA1B,PRKN,AGPAT1,IL1R2,VRK2,PXDN,NR1H2,TRIM32,TLR4,CD300LF,IRAK2,IKBKB,MAVS,GAS6,HPX,IRF7,TRIM44,OTUD4,TAF9,ROBO1,IL7,NR1H3,OAS3,NLRC5,RIPK2,OTULIN,F2RL1,RIPK1,IFIH1,SPATA2,YTHDF2,PARP9,PARP14,PELI3,PTPN6,MUL1,SPPL2A,PADI2,GPS2,USP18,MED1,PYDC1,DCST1,MAP2K5,STAT2,CD74,CCL5,MAPK7,PTPN2,SOCS1,PIAS4,SPPL2B,TRAF2,AGPAT2,GFI1,MIR21,MIR125B1,MIR27B,MIR24-1,MIR27A,OAS1,NOL3,FADD,CASP8,MIR125A,IRGM,WNT5A,C1QTNF4,CCDC3,TSLP,HIST1H2BJ	grey	VSMC_M10
GO:0006972	0.31	0.82	14	23	hyperosmotic response	BP	1	SLC12A2,XRCC6,AKR1B1,AQP1,HNMT,ICOSLG,TRPV4,YBX3,XRCC5,MICU1,SLC25A23,PDPK1,MT-CYB,CLDN1	grey	VSMC_M10
GO:0001508	0.31	0.76	55	99	action potential	BP	1	NEDD4L,NTRK2,CLDN19,MYH14,CLCN1,TRPM4,SLC8A2,CACNB2,SCN5A,SCN1A,GPD1L,SLMAP,P2RX3,KCNJ3,KCNE2,DSP,KCNIP2,RYR2,PKP2,KCNJ2,SCN2A,KCNB1,SCN7A,ANK2,GPER1,ATP1A2,SLC9A1,NTSR1,SCN4B,NOS1AP,DLG1,CNTNAP1,ATP1B1,KCNA1,SLC4A3,CACNA1G,AC138894.1,CHRNB2,CALM1,DSG2,FMR1,GNA15,P2RX1,RNF207,CACNA1H,DMD,GPR35,KCNH2,SCN2B,GPR88,YWHAH,KCNJ8,GNA14,HCN4,KCNMB4	grey	VSMC_M10
GO:0014870	0.31	0.90	5	7	response to muscle inactivity	BP	1	SCN5A,DAG1,CASQ1,ACTN3,HDAC4	grey	VSMC_M10
GO:0014877	0.31	0.90	5	7	response to muscle inactivity involved in regulation of muscle adaptation	BP	1	SCN5A,DAG1,CASQ1,ACTN3,HDAC4	grey	VSMC_M10
GO:0014894	0.31	0.90	5	7	response to denervation involved in regulation of muscle adaptation	BP	1	SCN5A,DAG1,CASQ1,ACTN3,HDAC4	grey	VSMC_M10
GO:0048839	0.31	0.75	77	139	inner ear development	BP	1	ATP8B1,EYA4,FZD6,PTK7,SLC25A27,ROR2,DLX5,KCNQ4,GSDME,HOXA13,MYCL,BMPER,WHRN,ATG5,MYCN,SOBP,SLC26A5,MYO3A,SOX9,USH1G,GLI2,MYO7A,TSKU,SPRY2,SLC4A7,JAG1,LRTOMT,AP000812.5,LIN7A,FREM2,CEP290,PAX8,CEBPA,EYA1,PLS1,ADGRV1,FZD3,USH1C,OPA1,RPGRIP1L,TFAP2A,PAX2,ALDH1A3,TGFB2,TRIP11,MAPKAPK2,SOX2,GBX2,MYO3B,KCNK2,GRHL3,STRC,CDKN1B,STOX1,CDH23,EPHA4,DVL2,TCAP,RBPJ,ESRRB,POU3F4,NTN1,MKS1,JAG2,IFT20,MCOLN3,KCNK3,PJVK,CHRNA10,FOXG1,MAFB,WNT5A,OTX1,SIX1,INSIG2,HEY2,ZIC1	grey	VSMC_M10
GO:0070585	0.31	0.75	61	107	protein localization to mitochondrion	BP	1	TIMM21,MTCH2,PRKN,TSPO,HSPA4,TOMM22,RAC2,FBXO7,DNAJA1,MGARP,AGK,DNAJC15,PITRM1,TIMM50,USP36,BAG4,MIPEP,IMMP1L,FBXW7,HTRA2,CSNK2A2,AP3B1,TOMM34,SIRT4,DNM1L,OXA1L,HPS4,ARIH2,BAG3,TOMM40L,FZD5,MAPT,FIS1,NMT1,HK1,GRPEL1,C11orf65,BCS1L,PINK1,TIMM17B,MFN2,NPEPPS,HAX1,CALM1,TIMM29,SREBF1,MAIP1,PAM16,BCAP31,SH3GLB1,MICALL2,BNIP3L,TIMM10B,TIMM23B,DDIT3,RALA,TIMM8B,RHOU,LEPROT,GRPEL2,DNAJC19	grey	VSMC_M10
GO:2000351	0.31	0.79	23	39	regulation of endothelial cell apoptotic process	BP	1	TNFAIP3,TEK,FOXO3,FGF21,NDNF,GAS6,ANO6,CD40,TERT,PDCD4,GPER1,NFE2L2,ITGA4,TNIP2,RAMP2,MAPK7,CCL2,PDPK1,MIR24-1,FGA,MIR125A,CD248,RGCC	grey	VSMC_M10
GO:0021520	0.31	0.90	5	7	spinal cord motor neuron cell fate specification	BP	1	GLI2,MNX1,SUFU,ISL1,ISL2	grey	VSMC_M10
GO:0002260	0.31	0.78	29	50	lymphocyte homeostasis	BP	1	TNFAIP3,BAK1,SLC46A2,TRAF3IP2,NCKAP1L,GAPT,ZC3H8,CASP3,MEF2C,DOCK10,GPAM,TCIRG1,PPP2R3C,RC3H1,PPP3CB,STAT5B,FOXP3,LAT,CD74,DNAJA3,BCL10,FADD,CAMLG,TSC22D3,BCL2L11,SH2B2,SLC39A3,TNFSF13B,RC3H2	grey	VSMC_M10
GO:0033762	0.31	0.85	9	14	response to glucagon	BP	1	CRY1,FGF21,CYSLTR2,ABCC2,CREB1,CPS1,SREBF1,ASS1,MT-CYB	grey	VSMC_M10
GO:0042475	0.31	0.77	36	63	odontogenesis of dentin-containing tooth	BP	1	PPARA,TNFRSF11B,SMO,CNNM4,SOSTDC1,KLK4,TNC,HDAC2,SLC4A2,GLI2,SCN5A,ACVR2A,RELT,TRAF6,HAND2,ITGB6,HDAC1,TCIRG1,FAM20A,FAM20C,AMELX,HTRA1,LAMA5,DLX1,BMPR1A,NGFR,DLX3,BCL11B,JAG2,ROGDI,BSG,ANKRD11,LHX8,CA2,BCL2L11,PERP	grey	VSMC_M10
GO:0002274	0.31	0.74	87	156	myeloid leukocyte activation	BP	1	CD226,ENPP3,AGER,RAC2,TTBK1,KIT,PRKCE,FPR2,CXCL8,TLR4,IL15,TRAF3IP2,SPHK2,C5AR1,CST7,CD300LF,NECTIN2,GAB2,UNC13D,MYD88,TGFBR2,NMI,FOXP1,MFHAS1,TRAF6,CAMK4,CEBPA,FER,RASGRP1,NR1H3,DYSF,IFNGR2,F2RL1,ITGB6,CD200,GPR137B,SNAP23,LAT2,FGR,CBL,SNX4,FCER1G,MAPT,PLA2G4A,BATF2,CXCR2,SLC11A1,PTGDR,TNIP2,LTBR,C12orf4,RBPJ,STX4,PSEN1,ITGAM,SYT11,LCP2,DOCK2,BATF,LAT,IL4R,LDLR,S100A13,BTK,SCNN1B,CD74,CCL5,STXBP2,PRAM1,TICAM1,DNASE1,TRPV1,PDPK1,FOXF1,KARS,STXBP1,S100A12,HAVCR1,CHGA,CXCL6,DHRS2,MIR125A,WNT5A,IL33,TSLP,HAVCR2,BATF3	grey	VSMC_M10
GO:0006882	0.31	0.82	14	23	cellular zinc ion homeostasis	BP	1	SLC39A5,SLC39A4,SLC1A1,SLC39A12,SLC39A13,AP3B1,LCK,SLC30A10,SLC30A4,ATP13A2,S100A8,SLC39A6,SLC30A7,MT1X	grey	VSMC_M10
GO:0045581	0.31	0.80	19	32	negative regulation of T cell differentiation	BP	1	FOXJ1,ZC3H8,TMEM131L,HLX,RUNX3,BCL6,RC3H1,TNFSF18,LAG3,FOXP3,TBX21,ZBTB7B,IL4R,CD74,PTPN2,SOCS1,MIR21,FGL2,RC3H2	grey	VSMC_M10

GO:0070286	0.31	0.81	15	25	axonemal dynein complex assembly	BP	1	LRRC6,WDR92,ARMC4,DRC1,CCDC65,DNAH1,DNAH5,ZMYND10,TTC12,DNAAF2,TTC25,DNAAF4,CCDC151,C16orf71,WDR63	grey	VSMC_M10
GO:0046174	0.31	0.81	15	25	polyol catabolic process	BP	1	MIOX,SYNJ2,INPP4B,MTMR2,MTMR7,GK5,SYNJ1,INPP5A,NTSR1,INPP5J,SORD,TKFC,IMPA2,INPP5K,INPP1	grey	VSMC_M10
GO:0046425	0.31	0.78	30	52	regulation of receptor signaling pathway via JAK-STAT	BP	1	IL5,AKR1B1,OCIAD1,KIT,PPP2R1A,PIBF1,RET,PIGU,PTK2B,F2R,MST1,EGF,PARP14,AGT,IL10RA,IL6R,ELP2,CCL5,CDK5R1,SUZ12,GHR,NLK,PTPN2,SOCS1,DAB1,DOT1L,MIR125A,GADD45A,LIF,LEPROT	grey	VSMC_M10
GO:0046514	0.31	0.84	10	16	ceramide catabolic process	BP	1	ACER3,NEU3,ASAH1,GALC,GLA,HEXA,GM2A,CEL,ACER2,NEU2	grey	VSMC_M10
GO:0061436	0.31	0.84	10	16	establishment of skin barrier	BP	1	GRHL1,MET,ELOVL1,LSR,KDF1,SFN,GRHL3,ABCA12,ALOXE3,CLDN1	grey	VSMC_M10
GO:1904953	0.31	0.88	6	9	Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation	BP	1	CSNK1E,FZD1,RYK,WNT3,WNT5A,WNT2	grey	VSMC_M10
GO:2000320	0.31	0.88	6	9	negative regulation of T-helper 17 cell differentiation	BP	1	RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,RC3H2	grey	VSMC_M10
GO:0010452	0.31	0.86	7	11	histone H3-K36 methylation	BP	1	IWS1,PAXIP1,NSD3,SETD2,BCOR,NSD1,SETD3	grey	VSMC_M10
GO:1903715	0.31	0.81	17	28	regulation of aerobic respiration	BP	1	SHMT2,DNAJC15,COX7A1,IDE,TRPV4,ISCU,ACTN3,MLXIPL,PINK1,SLC25A23,PARK7,SLC25A33,RHOA,COX7A2,UQCC2,COX7A2L,PPIF	grey	VSMC_M10
GO:0043436	0.32	0.71	370	677	oxoacid metabolic process	BP	1	ATP8B1,GLS2,HSD17B4,SHMT2,ALDH8A1,MARS,AIG1,LTC4S,GFPT2,TPH2,RIDA,CPT1B,DPYS,SLC27A6,TNXB,QKI,PPARA,ACSL6,PNPLA3,MCAT,HSD17B8,ECHDC1,ACO2,PRXL2C,AKR1B1,ATF4,PYCR3,MAPK14,PSAT1,GPT,HACD4,MTAP,CARNMT1,GNMT,ALDH1A1,CROT,ABCC10,GNPDA2,SLC35B2,KIT,SLC25A13,GAPDH,AASDH,PPAT,LIPT1,HMGCLL1,ADH5,RIMKLA,PRKCE,ETFB,SLC4A4,ME1,BPGM,NR1H2,DDC,IL4I1,LPIN1,MGST2,QRSL1,SLC7A11,DLD,DDO,BCAT2,NANP,PRKAR2B,DHFR,FAAH,HADHA,GAD2,SOX9,ABHD5,AKR1A1,APOC1,HPDL,DHTKD1,ECHDC3,PRKAG2,ACOX1,SLC22A13,XYLB,PIBF1,CYGB,HYI,HNMT,ELOVL1,CSGALNACT1,AKT2,PFKP,IDO2,IDO1,MDH2,HARS,HARS2,BTD,HACL1,SLC23A2,CARS2,PANK2,PDK1,AMDHD1,LARS,SUCLG2,NR1H4,PDHX,APIP,TRIB3,LYPLA1,ACOXL,CSAD,CYP7A1,ELOVL7,ASAH1,CYP7B1,ACOX2,GPI,ABHD6,THNSL2,AHCY,CBR4,OSBP,GSS,MCCC2,HPGD,MSRA,GPD1,PEX2,P2RX7,ETFDH,ACOT12,MTHFD2,PRKAG1,GMPS,NR1H3,SERINC5,ENOPH1,PFKM,SDSL,IVD,LPIN3,HOGA1,NIT2,BPHL,ASNSD1,ECI2,HIBCH,GLS,ABCC2,ERLIN1,PLA2G4B,ACAD8,ADTRP,PRMT3,PRKAB1,WARS2,LONP2,MTRR,PM20D1,SIRT4,GATC,ASL,MCEE,ALDH5A1,AZIN2,IRS1,MTR,YARS2,CBSL,ALDH1A3,CPT1A,TPST1,BDH2,ZBTB20,GPAM,PPA2,ACSL5,NR5A2,SLC7A7,CYP2U1,HGD,MARC2,MARC1,MAPKAPK2,AMT,PFKFB2,ABHD2,MSMO1,MECR,MCCC1,GNPAT,CMAS,ENO4,TARS2,DALRD3,ABCB11,DHRS9,PC,HACD2,ARNT,LPGAT1,CTPS2,PER2,ACTN3,HDAC4,OSBPL2,ACADSB,OAT,THEM5,THEM4,MLXIPL,HMGCL,GLUL,D2HGDH,SCAP,EHHADH,SMS,MDH1B,POR,PDK3,PLA2G4A,OSBPL6,UPB1,ACADL,PLOD3,GGT2,HK1,FAH,BCO2,CPS1,MTHFS,TYMP1,ARG2,OSBPL1A,PRODH,UPP2A,ASGR2,L2HG	grey	VSMC_M10
GO:0006816	0.32	0.73	154	282	calcium ion transport	BP	1	STAC3,CYP27B1,TSPO,SMDT1,BAK1,CATSPER3,MCHR1,PKD2L2,PLA2G6,TRPM6,TSPAN13,PRKCE,IBTK,BSPRY,ATG5,TRPM4,SPHK2,GRIN2D,TRPC3,SLC8A2,PANX1,CACNB2,STAC,SLC24A3,CACNB4,EFHB,RYR1,NALCN,PRNP,DIAPH1,P2RX2,GAS6,RASA3,MICU3,P2RX3,TRPC4AP,RYR3,ORAI1,ASIC1,TMBIM6,P2RX7,PTK2B,TPCN1,SLC8B1,HOMER1,VDR,STC1,OPA1,F2R,ANO6,KCNE2,PKD2,CASQ2,MCUR1,RYR2,TRPM1,CALHM1,DNM1L,LCK,PPP3CA,TRPV4,ADRA2A,MCUB,EGF,EPB41,OPRD1,UBASH3B,ANK2,GPER1,TRPM8,AGT,ATP1A2,SLC9A1,PLPP4,C4orf3,CASQ1,NTSR1,NOS1AP,HOMER2,CATSPER2,TMCO1,IL16,CEMIP,SESTD1,CDH23,CASK,PTPN6,MICU1,MCU,HTT,PKD1L1,CALCRL,RAMP2,CAMK2G,TRPM7,ATP1B1,BHLHA15,SLC3A2,GNB5,HAP1,PSEN2,WNK3,STAC2,CACNB1,ANXA2,FAM155B,PSEN1,CACNA1A,CACNA1G,CHRNB2,ATP2A1,CD19,CALM1,PRKCB,VMP1,BDKRB1,NMUR2,TRPV2,CAMK2A,CCL5,CCL2,SLC25A23,MAIP1,FMR1,INPP5K,ATP2B3,TRPV3,TRPV1,PDPK1,P2RX1,CACNA1B,PKD1,CACNA1H,CYBA,JPH3,ATP2C2,SLC25A25,PKD1L3,MCOLN3,RRAD,MIR21,RHOA,DMD,GPR35,NOL3,CHRNA10,JPH2,THY1,CACNG7,RGS4,DDIT3,CRH,CACNG5,GEM	grey	VSMC_M10
GO:0050691	0.32	0.81	15	25	regulation of defense response to virus by host	BP	1	TNFAIP3,IL15,TRAF3IP2,TMEM173,MAVS,TRIM44,EIF2AK4,PARP9,DTX3L,MUL1,RNF216,SIN3A,ZDHHC1,ZDHHC11,IFNLR1	grey	VSMC_M10
GO:0002396	0.32	0.90	5	7	MHC protein complex assembly	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TAPBPL	grey	VSMC_M10
GO:1904526	0.32	0.88	6	9	regulation of microtubule binding	BP	1	HSF1,MAPRE1,MAPRE3,PPP2CB,TTBK2,MARK2	grey	VSMC_M10
GO:0099003	0.32	0.74	83	151	vesicle-mediated transport in synapse	BP	1	CANX,SYNJ2,RIMS2,BTBD9,CHRNA5,APBA1,USP46,BRSK1,RIMS1,RIMS3,DDC,AMPH,PPFIA3,EPS15,NAPA,CACNB2,GRIK5,NAPB,ACTG1,SYT1,RAB5A,STX2,SYT9,SNPH,ERC2,FCHO2,P2RY1,SYNJ1,AP3B1,VPS18,CYFIP1,DTNBP1,SYT8,DNM1L,ADRA2A,SNAP23,NLGN4Y,BSN,AP2M1,STX1A,BACE1,DNAJC5,CSPG5,CALY,RAP1B,BLOC1S6,CASK,DNM3,PPP3CB,RAB3A,SYN1,SNAP29,NSG1,GRIPAP1,RAB8A,ACTB,SYT7,SLC2A4,NLGN2,DGKQ,GAK,CPLX1,STX1B,STX4,PSEN1,SYT11,NLGN3,RAB11A,CALM1,SNAPIN,PRKCB,DNM2,AP2B1,CDK5R1,FMR1,PIP5K1C,P2RX1,CEL,STXBP1,BTBD8,DENND1A,SNAP47,DOC2B	grey	VSMC_M10
GO:0039530	0.32	0.88	6	9	MDA-5 signaling pathway	BP	1	ANKRD17,IRF7,OAS3,IFIH1,TKFC,RIOK3	grey	VSMC_M10
GO:0021511	0.32	0.88	6	9	spinal cord patterning	BP	1	SMO,INTU,GLI2,SUFU,CHRD,TULP3	grey	VSMC_M10
GO:0042398	0.32	0.79	22	37	cellular modified amino acid biosynthetic process	BP	1	ALDH7A1,CKB,SLC1A1,CHAC2,MGST2,SLC7A11,DHFR,GSS,CHDH,CKMT2,CKMT1B,NFE2L2,PLOD3,MTHFS,GCH1,GGT6,SLC27A1,GAMT,TMLHE,PARK7,ACADM,GGT5	grey	VSMC_M10
GO:0031342	0.32	0.88	6	9	negative regulation of cell killing	BP	1	NCKAP1L,PPP3CB,IL7R,CRK,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0051955	0.32	0.81	15	25	regulation of amino acid transport	BP	1	SLC12A2,ARL6IP5,SLC43A1,GRM2,SLC38A3,AGT,ACE2,ATP1A2,PER2,NTSR1,ARL6IP1,PSEN1,ABAT,STXBP1,RGS4	grey	VSMC_M10

GO:0070316	0.32	0.88	6	9	regulation of G0 to G1 transition	BP	1	PPP2R5B,RHNO1,MED1,SOX15,FOXO4,DAB2IP	grey	VSMC_M10
GO:1901032	0.32	0.85	9	14	negative regulation of response to reactive oxygen species	BP	1	GPR37,MET,PDE8A,NFE2L2,PINK1,PARK7,MIR21,GPR37L1,TXN	grey	VSMC_M10
GO:1903206	0.32	0.85	9	14	negative regulation of hydrogen peroxide-induced cell death	BP	1	GPR37,MET,PDE8A,NFE2L2,PINK1,PARK7,MIR21,GPR37L1,TXN	grey	VSMC_M10
GO:0045833	0.32	0.76	41	72	negative regulation of lipid metabolic process	BP	1	ORMDL2,PIP4K2C,CYP27B1,DKKL1,PIP4K2A,SOX9,APOC1,SLC22A13,PIBF1,ALK,TRIB3,CYP7A1,DKK3,FBXW7,ORMDL1,ERLIN1,PRMT3,SIRT4,GPLD1,LPCAT1,SIK1,ADRA2A,SNAI1,SORL1,GPER1,PPP2R5A,RUBCN,PIK3IP1,SCAP,APOD,ACADL,WNT4,SLC27A1,ACADVL,ASXL3,NCOR1,GFI1,DAB2IP,BSCL2,INSIG2,CCDC3	grey	VSMC_M10
GO:0070528	0.32	0.81	14	23	protein kinase C signaling	BP	1	PLA2G6,PLEK,SPHK2,WNT11,GPD1L,ADGRV1,CD40,DGKD,DGKG,DGKQ,SEZ6,PRKCZ,ADGRG1,WNT5A	grey	VSMC_M10
GO:0051453	0.32	0.77	33	58	regulation of intracellular pH	BP	1	SLC4A4,PPT1,RAB7A,ATP6V0E2,SLC4A2,AQP11,SLC4A7,TMEM106B,ATP6V1H,TM9SF4,SLC9A9,HVCN1,SLC4A10,SLC9B1,TMEM9,TCIRG1,SLC9A8,SLAMF8,SLC9A1,CLIC4,SLC11A1,SLC9A7,ATP6V0A1,DMXL2,SLC4A3,AC138894.1,CLN6,SNAPIN,TMEM199,SLC9A6,SLC9A5,CA2,RAB39A	grey	VSMC_M10
GO:0051709	0.32	0.88	6	9	regulation of killing of cells of other organism	BP	1	P2RX7,F2RL1,NOS2,CXCL6,FCER2,SERPINB9	grey	VSMC_M10
GO:0001959	0.32	0.74	67	119	regulation of cytokine-mediated signaling pathway	BP	1	TNFAIP3,HSPA1B,PRKN,AGPAT1,IL1R2,VRK2,PXDN,NR1H2,TRIM32,CD300LF,IRAK2,IKBKB,MAVS,GAS6,HPX,IRF7,TRIM44,OTUD4,ROBO1,IL7,NR1H3,OAS3,NLRC5,RIPK2,OTULIN,F2RL1,RIPK1,SPATA2,YTHDF2,PARP9,PARP14,PELI3,PTPN6,MUL1,SPPL2A,PADI2,GPS2,USP18,MED1,PYDC1,DCST1,STAT2,CD74,CCL5,PTPN2,SOCS1,PIAS4,SPPL2B,TRAF2,AGPAT2,GFI1,MIR21,MIR125B1,MIR27B,MIR24-1,MIR27A,OAS1,NOL3,FADD,CASP8,MIR125A,IRGM,WNT5A,C1QTNF4,CCDC3,TSLP,HIST1H2BJ	grey	VSMC_M10
GO:0001919	0.32	0.83	11	18	regulation of receptor recycling	BP	1	BVES,EPS15,OPTN,TBC1D16,AP1AR,NSF,ECE1,NSG1,ANXA2,PSEN1,VAMP3	grey	VSMC_M10
GO:0099504	0.32	0.74	76	138	synaptic vesicle cycle	BP	1	CANX,SYNJ2,RIMS2,BTBD9,CHRNA5,APBA1,BRSK1,RIMS1,RIMS3,DDC,AMPH,PPFIA3,NAPA,CACNB2,GRIK5,NAPB,ACTG1,SYT1,RAB5A,STX2,SYT9,SNPH,ERC2,FCHO2,P2RY1,SYNJ1,AP3B1,VPS18,CYFIP1,DTNBP1,SYT8,DNM1L,ADRA2A,SNAP23,NLGN4Y,BSN,AP2M1,STX1A,BACE1,DNAJC5,CSPG5,RAP1B,BLOC1S6,CASK,DNM3,PPP3CB,RAB3A,SYN1,SNAP29,GRIPAP1,ACTB,SYT7,SLC2A4,NLGN2,DGKQ,GAK,CPLX1,STX1B,STX4,PSEN1,SYT11,NLGN3,CALM1,SNAPIN,PRKCB,DNM2,CDK5R1,FMR1,PIP5K1C,P2RX1,CEL,STXBP1,BTBD8,DENND1A,SNAP47,DOC2B	grey	VSMC_M10
GO:0022600	0.32	0.77	32	56	digestive system process	BP	1	KIAA1211,ABCG5,ABCG8,AQP1,NR1H2,TLR4,SOX9,CCKBR,SOAT2,HIP1R,PLS1,CHRM5,LIMA1,NR1H3,VDR,NOD2,CHRM3,ADRA2A,EPB41,COPA,PBLD,LPCAT3,CHRM1,HRH2,LDLR,SLC46A1,TRPV1,CEL,SLC22A5,SNX10,INAVA,CRH	grey	VSMC_M10
GO:0045686	0.32	0.83	11	18	negative regulation of glial cell differentiation	BP	1	DAAM2,MYCN,KDM4A,NKX6-1,DLX1,DUSP10,LDLR,MBD1,DAB1,GPR37L1,NOG	grey	VSMC_M10
GO:0006821	0.32	0.77	34	60	chloride transport	BP	1	ATP8B1,SLC26A10,SLC12A2,TSPO,ABCB1,GABRA1,CLIC5,SLC1A1,CLCN1,SLC26A5,ANO10,CLNS1A,PRNP,CLIC1,ANO4,ANO6,SLC12A5,SLC4A10,SLC12A7,CLCN4,TMEM206,SLC12A8,CLIC4,SLC12A9,ANO8,TTYH3,SLC26A1,SLC26A2,GABRE,GABRA3,CLCN7,LRRC8A,CLCA2,SLC12A4	grey	VSMC_M10
GO:0046929	0.32	0.87	6	9	negative regulation of neurotransmitter secretion	BP	1	PRKN,ASIC1,RAP1B,PNKD,SYT11,FMR1	grey	VSMC_M10
GO:0090335	0.32	0.83	11	18	regulation of brown fat cell differentiation	BP	1	MAPK14,PIM1,NAPEPLD,FTO,RREB1,SOX13,TRPV4,DUSP10,TFE3,ZBTB7B,SIX1	grey	VSMC_M10
GO:0048841	0.32	0.80	17	29	regulation of axon extension involved in axon guidance	BP	1	SEMA6A,PLXNA4,SEMA4D,SEMA4C,MEGF8,SEMA3D,SEMA3A,RYK,SEMA4F,SEMA3G,SEMA4G,SEMA3F,WNT3,SEMA6D,SEMA4A,PLXNA3,WNT5A	grey	VSMC_M10
GO:0071867	0.32	0.76	39	69	response to monoamine	BP	1	PRKN,ATF4,SLC1A1,VPS35,HDAC2,ALK,SIRT2,HTR7,CHRM5,CHRM4,DTNBP1,CHRM3,RYR2,SRDSA1,SLC9A1,CALY,HTR3B,MAPK1,CHRM1,GNB5,NSG1,HRH2,PKLR,HCN3,MAPK3,DNM2,SIN3A,HRH4,GNAL,GNB1,GNA15,PALM,GNAI3,FUK,HTR1D,RGS4,GNA14,GNG2,ARPP19	grey	VSMC_M10
GO:0071869	0.32	0.76	39	69	response to catecholamine	BP	1	PRKN,ATF4,SLC1A1,VPS35,HDAC2,ALK,SIRT2,HTR7,CHRM5,CHRM4,DTNBP1,CHRM3,RYR2,SRDSA1,SLC9A1,CALY,HTR3B,MAPK1,CHRM1,GNB5,NSG1,HRH2,PKLR,HCN3,MAPK3,DNM2,SIN3A,HRH4,GNAL,GNB1,GNA15,PALM,GNAI3,FUK,HTR1D,RGS4,GNA14,GNG2,ARPP19	grey	VSMC_M10
GO:0032429	0.32	0.87	6	9	regulation of phospholipase A2 activity	BP	1	LRP1,PPT1,EGFR,PLA2R1,ANXA8,NMUR2	grey	VSMC_M10

GO:0019752	0.32	0.71	360	659	carboxylic acid metabolic process	BP	1	ATP8B1,GLS2,HSD17B4,SHMT2,ALDH8A1,MARS,AIG1,LTC4S,GFPT2,TPH2,RIDA,CPT1B,DPYS,SLC27A6,TNXB,QKI,PPARA,ACSL6,PNPLA3,MCAT,HSD17B8,ECHDC1,ACO2,PRXL2C,AKR1B1,ATF4,PYCR3,MAPK14,PSAT1,GPT,HACD4,MTAP,CARNMT1,GNMT,ALDH1A1,CROT,ABCC10,GNPDA2,KIT,SLC25A13,GAPDH,AASDH,PPAT,LIPT1,HMGCLL1,ADH5,RIMKLA,PRKCE,ETFB,SLC4A4,ME1,BPGM,NR1H2,DDC,IL4I1,LPIN1,MGST2,QRSL1,SLC7A11,DLD,DDO,BCAT2,NANP,PRKAR2B,DHFR,FAAH,HADHA,GAD2,SOX9,ABHD5,AKR1A1,APOC1,HPDL,DHTKD1,ECHDC3,PRKAG2,ACOX1,SLC22A13,XYLB,PIBF1,CYGB,HYI,HNMT,ELOVL1,CSGALNACT1,AKT2,PFKP,IDO2,IDO1,MDH2,HARS,HARS2,BTD,HACL1,SLC23A2,CARS2,PANK2,PDK1,AMDHD1,LARS,SUCLG2,NR1H4,PDHX,APIP,TRIB3,LYPLA1,ACOXL,CSAD,CYP7A1,ELOVL7,ASAH1,CYP7B1,ACOX2,GPI,ABHD6,THNSL2,AHCY,CBR4,OSBP,GSS,MCCC2,HPGD,MSRA,GPD1,PEX2,P2RX7,ETFDH,ACOT12,MTHFD2,PRKAG1,GMPS,NR1H3,SERINC5,ENOPH1,PFKM,SDSL,IVD,LPIN3,HOGA1,NIT2,BPHL,ASNSD1,ECI2,HIBCH,GLS,ABCC2,ERLIN1,PLA2G4B,ACAD8,ADTRP,PRMT3,PRKAB1,WARS2,LONP2,MTRR,PM20D1,SIRT4,GATC,ASL,MCEE,ALDH5A1,AZIN2,IRS1,MTR,YARS2,CBSL,ALDH1A3,CPT1A,BDH2,ZBTB20,GPAM,ACSL5,NR5A2,SLC7A7,CYP2U1,HGD,MAPKAPK2,AMT,PFKFB2,ABHD2,MSMO1,MECR,MCCC1,GNPAT,CMAS,ENO4,TARS2,DALRD3,ABCB11,DHRS9,PC,HACD2,ARNT,LPGAT1,CTPS2,PER2,ACTN3,HDAC4,OSBPL2,ACADSB,OAT,THEM5,THEM4,MLXIPL,HMGCL,GLUL,D2HGDH,SCAP,EHHADH,SMS,MDH1B,POR,PDK3,PLA2G4A,OSBPL6,UPB1,ACADL,PLOD3,GGT2,HK1,FAH,BCO2,CPS1,MTHFS,TYSND1,LARS2,OSBPL1A,PRODH,ID	grey	VSMC_M10
GO:0005984	0.32	0.87	6	9	disaccharide metabolic process	BP	1	MGAM,BRAF,GANC,TREH,IDUA,FBP2	grey	VSMC_M10
GO:0000012	0.32	0.87	6	9	single strand break repair	BP	1	XRCC1,ERCC6,ERCC8,PARP1,TDP1,TERF2	grey	VSMC_M10
GO:0001779	0.32	0.83	11	18	natural killer cell differentiation	BP	1	NFIL3,IL15,IL15RA,GAS6,TOX,RASGRP1,RABL3,SP3,STAT5B,ZBTB1,KAT7	grey	VSMC_M10
GO:0072178	0.32	0.87	6	9	nephric duct morphogenesis	BP	1	EPHA7,OSR1,PAX2,EPHA4,LHX1,GPC3	grey	VSMC_M10
GO:0098915	0.32	0.87	6	9	membrane repolarization during ventricular cardiac muscle cell action potential	BP	1	KCNJ3,KCNE2,NOS1AP,RNF207,KCNH2,KCNJ8	grey	VSMC_M10
GO:0072577	0.32	0.78	25	43	endothelial cell apoptotic process	BP	1	MAP3K5,TNFAIP3,TEK,FOXO3,FGF21,NDNF,GAS6,ANO6,CD40,TERT,PDCD4,GPER1,NFE2L2,ITGA4,TNIP2,RAMP2,MAPK7,CCL2,PDPK1,DAB2IP,MIR24-1,FGA,MIR125A,CD248,RGCC	grey	VSMC_M10
GO:1903204	0.32	0.83	10	16	negative regulation of oxidative stress-induced neuron death	BP	1	PRKN,NCOA7,ATF4,FBXO7,SLC7A11,NONO,PINK1,PARK7,TSC1,TLDC1	grey	VSMC_M10
GO:0032024	0.32	0.77	32	56	positive regulation of insulin secretion	BP	1	LRP1,PLA2G6,PRKCE,TRPM4,GIPR,SIRT3,OSBP,NNAT,PFKM,NKX6-1,GPLD1,TCF7L2,PFKFB2,GPER1,GLUL,MCU,PPP3CB,CD38,MPC2,NLGN2,TARDBP,STX4,GPR68,ISL1,OXCT1,ABAT,NADK,BAIAP3,LRRC8A,SOX4,CRH,DOC2B	grey	VSMC_M10
GO:0043242	0.32	0.76	39	70	negative regulation of protein-containing complex disassembly	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,ADD2,CLASP2,TRIM54,NAV3,SPEF1,LMOD3,ATXN7,LIMA1,KATNB1,SCAF4,DMTN,CARMIL1,LMOD1,ADD3,TMEM39A,TTBK2,CIB1,SPTBN2,TMOD4,EPS8,RUBCN,CAPZA1,TMOD2,PHF23,SPTB,CAMSAP3,TAOK1,CLEC16A,APC2,CAMSAP1,CARMIL2,APC,MAP6D1	grey	VSMC_M10
GO:0052646	0.33	0.87	6	9	alditol phosphate metabolic process	BP	1	GPD1L,ABHD6,GK5,GPD1,GPAM,ACP6	grey	VSMC_M10
GO:0006335	0.33	0.83	10	16	DNA replication-dependent nucleosome assembly	BP	1	ASF1A,RBBP4,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H3F,HIST1H3H,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0034723	0.33	0.83	10	16	DNA replication-dependent nucleosome organization	BP	1	ASF1A,RBBP4,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H3F,HIST1H3H,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0071545	0.33	0.82	11	18	inositol phosphate catabolic process	BP	1	SYNJ2,INPP4B,MTMR2,MTMR7,SYNJ1,INPP5A,NTSR1,INPP5J,IMPA2,INPP5K,INPP1	grey	VSMC_M10
GO:0072207	0.33	0.82	11	18	metanephric epithelium development	BP	1	POU3F3,OSR1,SOX9,PAX8,PKD2,PAX2,CXCR2,WNT4,PKD1,SOX8,LIF	grey	VSMC_M10
GO:0002483	0.33	0.87	6	9	antigen processing and presentation of endogenous peptide antigen	BP	1	HLA-DRA,TAP1,IDE,ABCB9,ERAP1,ERAP2	grey	VSMC_M10
GO:0030007	0.33	0.86	7	11	cellular potassium ion homeostasis	BP	1	SLC12A2,ATP1A3,KCNJ2,ATP1A2,ATP1B1,KCNMA1,ATP1B2	grey	VSMC_M10
GO:0009584	0.33	0.80	15	25	detection of visible light	BP	1	OPN1SW,PRPH2,CAMKMT,GJA10,CEP250,CCDC66,RRH,SAG,NMT1,GRK4,ROM1,GUCY2D,GNAT2,REEP6,GPR88	grey	VSMC_M10
GO:1901215	0.33	0.73	89	161	negative regulation of neuron death	BP	1	ERBB3,LRP1,AGAP2,PRKN,PPARA,SYNGAP1,NCOA7,ATF4,NTRK2,NRBP2,HSF1,FBXO7,CNTFR,SLC1A1,TFAP2B,MSH2,REL,PPT1,VPS35,SLC7A11,NTF4,FGF21,NDNF,C5AR1,XRCC2,POU4F1,ARRB1,SLC23A2,GPI,GBE1,MEF2C,FAIM2,HTRA2,PTK2B,NR4A2,F2R,PM20D1,BDNF,CD200,HDAC1,TERT,SLC30A10,INPP5A,KRAS,ADNP,SORL1,CBL,HYOU1,NFATC4,DLX1,DNAJC5,FZD9,SNX6,ADAM8,CREB1,NONO,PINK1,STAT3,ATP13A2,TNFRSF1B,PSEN1,AC138894.1,CITED1,ALKBH1,GPRASP2,BHLHB9,AP2B1,CCL2,ISL1,GHR,PDPK1,MECP2,TRAF2,IKBKG,TMEM259,PARK7,TSC1,TLDC1,STXBP1,AARS,RHOA,CHGA,CNTF,PSMC1,TIGAR,SIX1,HRAS,CEBPB,NMNAT1	grey	VSMC_M10
GO:1900016	0.33	0.84	9	14	negative regulation of cytokine production involved in inflammatory response	BP	1	PPARA,IL1R2,CHID1,ADCY7,PDCD4,APOD,MIR222,C5orf30,MIR125A	grey	VSMC_M10
GO:0098974	0.33	0.87	6	9	postsynaptic actin cytoskeleton organization	BP	1	FARP1,ACTG1,INA,WASF2,NOS1AP,ACTB	grey	VSMC_M10
GO:0099188	0.33	0.87	6	9	postsynaptic cytoskeleton organization	BP	1	FARP1,ACTG1,INA,WASF2,NOS1AP,ACTB	grey	VSMC_M10
GO:0042733	0.33	0.77	27	47	embryonic digit morphogenesis	BP	1	OSR2,FZD6,TBC1D32,ROR2,MYCN,OSR1,INTU,HDAC2,GLI2,LMBR1,FREM2,HAND2,IFT52,SALL1,HDAC1,ECE1,TULP3,BMPR1A,TMEM107,MKS1,TBX2,CREBBP,TMEM231,NOG,WNT5A,C2CD3,BCL2L11	grey	VSMC_M10
GO:0055069	0.33	0.80	15	25	zinc ion homeostasis	BP	1	SLC39A5,PRKN,SLC39A4,SLC1A1,SLC39A12,SLC39A13,AP3B1,LCK,SLC30A10,SLC30A4,ATP13A2,S100A8,SLC39A6,SLC30A7,MT1X	grey	VSMC_M10
GO:0002021	0.33	0.82	11	18	response to dietary excess	BP	1	BMP8A,UCP1,ACVR1C,TRPV4,SORL1,VGF,GDF15,NMUR2,SGIP1,TRPV1,SLC25A25	grey	VSMC_M10

GO:0045596	0.33	0.70	265	489	negative regulation of cell differentiation	BP	1	NFATC1,NME1,SEMA6A,FRS2,PPARA,FBLN1,TSPO,FSTL4,SYNGAP1,TRIB1,MYC,TOB2,PTCH1,SOX10,PI16,SMO,DAAM2,FBXO7,RORB,CDK6,SEMA4D,S1PR3,SEMA4C,SOSTDC1,SIX2,RTN4,RUFY3,HOXA2,HOXA7,ANKRD17,AREG,AKIRIN1,EPHA7,NR1H2,PTN,ITGB1BP1,EGFR,FUZ,TLR4,CDK5RAP2,MYCN,TRPM4,OSR1,FOXO3,MKX,SPRY1,FOXE3,SOX9,GLI2,KDM4A,FOXJ1,TSKU,SPRY2,HOOK3,OVOL2,JAG1,SIRT2,RARB,SRA1,SPRED3,LSM1,SEMA3D,SPART,SEMA3A,ULK1,RYK,TCF15,TRIB3,EPHB1,ZC3H8,ASXL1,ZNF536,PIK3R1,HAND2,IL17RD,ARNTL,FBXW7,ADGRV1,TMEM131L,SEMA4F,VEGFC,TLX2,SOX6,PTK2B,RAPGEF2,CCL17,EIF2AK4,NR1H3,RUNX1T1,HDAC7,NKX6-1,TRIO,TBX5,SRSF6,TP53INP1,SEMA3G,SPP1,ZBED6,DMTN,SEMA4G,PRICKLE1,LDB1,IGF2,BDNF,SUFU,RNF10,KIAA0319,PKP2,NEPRO,PPP3CA,SINHCAF,USF3,CCND1,TRPV4,SEMA3F,PDCD4,ABCA5,TGFB2,PTHLH,GPR137B,AXIN2,PIAS3,HLX,KRAS,TCTA,SNAI1,SOX2,AP1AR,YTHDF2,UBASH3B,SORL1,GPER1,CIB1,CERS2,NFATC4,FZD7,DDX6,HDAC4,CHRD,RUNX3,DLX1,ZBTB46,MELTF,EIF4ENIF1,WNT3,NFE2L2,DUSP10,BCL6,SEMA6D,DIXDC1,MMP11,MEN1,WDR61,TNR,RC3H1,GPR137,FBN1,TNFSF18,WNT4,LAG3,COL5A2,RAP1GAP,STAT3,NKX3-2,MAPK1,BHLHA15,STAT5B,LEO1,INHA,FOXP3,BMPR1A,GPS2,RBPJ,CDK12,MED1,TBX21,PSEN1,RIOX1,SEMA4A,HOXB8,TGFB1I1,FOXO4,JDP2,TRIM46,EFNA1,RBPMS2,ZBTB7B,TOB1,ESRRB,CITED1,SMAD3,NTN1,IL4R,LDLR,GPR68,YY1,CD74,MIB1,CDK5R1,ISL1,SUZ12,TWSG1,RANBP3L,MBNL3,ADAMTS12,PTPN2,SOCS1,MBD1,DAB1,RFLNB,TRPV1,SKI,ARHGAP4,MECP2,PLX	grey	VSMC_M10
GO:0009218	0.33	0.81	14	23	pyrimidine ribonucleotide metabolic process	BP	1	NME1,DPYS,CMPK1,ENTPD4,NME4,CTPS2,UPB1,NME7,UPRT,NME3,UCK1,DHODH,NME6,UPP1	grey	VSMC_M10
GO:0042773	0.33	0.75	49	83	ATP synthesis coupled electron transport	BP	1	UQCRQ,NDUFA6,DLD,NDUFB2,NDUFB6,DNAJC15,NDUFC2,NDUFS8,NDUFA12,COX7A1,COX4I2,NDUFS3,DGUOK,UQCRB,COX15,NDUFV3,NDUFB4,ISCU,COA6,NDUFB3,NDUFS2,SDHC,COX6A1,COX8A,PINK1,NDUFA9,COX6A2,NDUFAB1,COX5A,NDUFA7,NDUFV2,NDUFB10,UQCR11,PARK7,MT-ND1,MT-ND2,MT-CO3,MT-ND6,MT-CYB,NDUFA5,NDUFC1,COX7A2,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,COX7A2L	grey	VSMC_M10
GO:0042775	0.33	0.75	49	83	mitochondrial ATP synthesis coupled electron transport	BP	1	UQCRQ,NDUFA6,DLD,NDUFB2,NDUFB6,DNAJC15,NDUFC2,NDUFS8,NDUFA12,COX7A1,COX4I2,NDUFS3,DGUOK,UQCRB,COX15,NDUFV3,NDUFB4,ISCU,COA6,NDUFB3,NDUFS2,SDHC,COX6A1,COX8A,PINK1,NDUFA9,COX6A2,NDUFAB1,COX5A,NDUFA7,NDUFV2,NDUFB10,UQCR11,PARK7,MT-ND1,MT-ND2,MT-CO3,MT-ND6,MT-CYB,NDUFA5,NDUFC1,COX7A2,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,COX7A2L	grey	VSMC_M10
GO:0019882	0.33	0.76	35	61	antigen processing and presentation	BP	1	HLA-DRA,HLA-DOB,PSMB8,TAP1,HLA-DMA,HLA-DPB1,NOD1,ATG5,RAB10,IKBKB,TRAF6,MARCH8,IDE,ABCB9,ERAP1,AP3B1,MFSD6,NOD2,PSME1,RAB4A,YTHDF1,FCER1G,PIKFYVE,CTSH,SLC11A1,CTSV,TAPBPL,WAS,RAB8B,DNM2,CD74,RAB33A,ERAP2,FGL2,RAB32	grey	VSMC_M10
GO:0006073	0.33	0.76	33	58	cellular glucan metabolic process	BP	1	GNMT,MGAM,PYGB,RUBCNL,KHK,EPM2AIP1,PRKAG2,PPP1CB,AKT2,PPP1R3B,GBE1,SORBS1,PFKM,IGF2,NHLRC1,PHKB,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PHKA2,PYGM,PYGL,PRKAG3,PPP1R3F,PHKA1,INSR,LEPR,INPP5K,AGL,ACADM,PPP1R1A	grey	VSMC_M10
GO:0044042	0.33	0.76	33	58	glucan metabolic process	BP	1	GNMT,MGAM,PYGB,RUBCNL,KHK,EPM2AIP1,PRKAG2,PPP1CB,AKT2,PPP1R3B,GBE1,SORBS1,PFKM,IGF2,NHLRC1,PHKB,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PHKA2,PYGM,PYGL,PRKAG3,PPP1R3F,PHKA1,INSR,LEPR,INPP5K,AGL,ACADM,PPP1R1A	grey	VSMC_M10
GO:0006283	0.33	0.87	6	9	transcription-coupled nucleotide-excision repair	BP	1	ERCC2,ERCC3,POLR2I,ERCC6,ERCC8,XAB2	grey	VSMC_M10
GO:0070936	0.33	0.76	33	58	protein K48-linked ubiquitination	BP	1	NEDD4L,TNFAIP3,PRKN,RNF5,SKP1,UBE2B,RNF146,KLHL3,PELI1,TRIM32,HACE1,KBTBD6,UBE2E2,UBE2E1,NMI,TRIM44,AMFR,TTC3,RNF115,DTX3L,ARIH2,SYVN1,RNF4,RNF216,UBE2Q2,FBXO38,RNF126,UBE2G1,RNF8,UBE2G2,UBE2R2,RNF152,UBE2D1	grey	VSMC_M10
GO:0045649	0.33	0.82	11	18	regulation of macrophage differentiation	BP	1	TRIB1,HSF1,ROR2,RIPK1,HCLS1,ZBTB46,INHA,PTPN2,FADD,CASP8,LIF	grey	VSMC_M10
GO:0006868	0.33	0.87	6	9	glutamine transport	BP	1	SLC1A4,SLC38A2,SLC38A1,SLC38A3,SLC38A5,SLC38A6	grey	VSMC_M10
GO:1903299	0.33	0.87	6	9	regulation of hexokinase activity	BP	1	PRKN,GCKR,PFKFB2,DUSP12,COX11,TIGAR	grey	VSMC_M10
GO:0003093	0.33	0.87	6	9	regulation of glomerular filtration	BP	1	GAS6,F2RL1,F2R,PTPRO,CORO2B,CYBA	grey	VSMC_M10
GO:2000650	0.33	0.85	7	11	negative regulation of sodium ion transmembrane transporter activity	BP	1	NEDD4L,PRKCE,HECW1,OSR1,HECW2,ATP1A2,MIR24-1	grey	VSMC_M10
GO:0007213	0.33	0.83	10	16	G protein-coupled acetylcholine receptor signaling pathway	BP	1	PLCB1,CHRM5,CHRM4,CHRM3,GRK2,CHRM1,HRH4,CDK5R1,GNB1,GNA15	grey	VSMC_M10
GO:0016246	0.33	0.85	7	11	RNA interference	BP	1	AGO2,XPO5,CLP1,CELF1,TERT,PRKRA,NRDE2	grey	VSMC_M10
GO:0046629	0.33	0.85	7	11	gamma-delta T cell activation	BP	1	TCF7,NCKAP1L,SOX13,NOD2,STAT5B,JAG2,SOX4	grey	VSMC_M10
GO:0098885	0.33	0.87	6	9	modification of postsynaptic actin cytoskeleton	BP	1	CTTNBP2,WASF1,TIAM1,CYFIP1,MYH10,RHOA	grey	VSMC_M10
GO:0009135	0.33	0.75	44	78	purine nucleoside diphosphate metabolic process	BP	1	PPARA,PRXL2C,GAPDH,SLC4A4,NT5E,BPGM,DLG2,DHTKD1,PRKAG2,PFKP,NUDT16,GPI,GPD1,P2RX7,PRKAG1,PFKM,ENTPD4,NUDT18,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,MAGI3,DLG1,HK1,CASK,PRKAG3,STAT3,ENO3,CARD11,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,MPP1,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:0009179	0.33	0.75	44	78	purine ribonucleoside diphosphate metabolic process	BP	1	PPARA,PRXL2C,GAPDH,SLC4A4,NT5E,BPGM,DLG2,DHTKD1,PRKAG2,PFKP,NUDT16,GPI,GPD1,P2RX7,PRKAG1,PFKM,ENTPD4,NUDT18,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,MAGI3,DLG1,HK1,CASK,PRKAG3,STAT3,ENO3,CARD11,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,MPP1,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:0019226	0.33	0.77	25	44	transmission of nerve impulse	BP	1	NTRK2,CLDN19,MYH14,CLCN1,SCN5A,SCN1A,P2RX3,CHRM5,SCN2A,SCN7A,GPER1,AGT,TNR,CNTNAP1,KCNA1,CACNA1G,OTOA,FMR1,P2RX1,CACNA1H,GPR35,CACNG7,GPR88,CACNG5,KCNMB4	grey	VSMC_M10

GO:0008206	0.33	0.78	21	36	bile acid metabolic process	BP	1	ATP8B1,KIT,PANK2,NR1H4,CYP7A1,CYP7B1,OSBP,NR5A2,ABCB11,OSBPL2,OSBPL6,OSBPL1A,CYP27A1,HSD17B10,FGFR4,OSBPL7,CYP46A1,NPC1,ABCD3,AMACR,STARD4	grey	VSMC_M10
GO:0045945	0.33	0.85	7	11	positive regulation of transcription by RNA polymerase III	BP	1	CHD8,RPTOR,ZC3H8,ZNF143,CEBPA,ELL,ICE2	grey	VSMC_M10
GO:0090208	0.33	0.83	10	16	positive regulation of triglyceride metabolic process	BP	1	NR1H2,FGF21,ABHD5,NR1H3,GPLD1,SLC27A1,DAGLB,LDLR,SREBF1,CNEP1R1	grey	VSMC_M10
GO:0071287	0.33	0.85	7	11	cellular response to manganese ion	BP	1	PRKN,A3GALT2,SLC30A10,BACE1,ATP13A2,SLFN14,HSPA5	grey	VSMC_M10
GO:0036474	0.33	0.80	14	23	cell death in response to hydrogen peroxide	BP	1	GPR37,MET,FOXO3,PAWR,RIPK1,PDE8A,NFE2L2,PDCD10,PINK1,STK26,PARK7,MIR21,GPR37L1,TXN	grey	VSMC_M10
GO:0009110	0.33	0.82	10	16	vitamin biosynthetic process	BP	1	CYP27B1,PSAT1,AKR1A1,CYP2R1,PLTP,SNAI1,CYP27A1,PNPO,GFI1,TPK1	grey	VSMC_M10
GO:0010043	0.34	0.78	19	32	response to zinc ion	BP	1	TSPO,MTF1,KHK,AANAT,HVCN1,SLC39A13,SLC30A10,D2HGDH,CREB1,SLC30A4,CPS1,ATP13A2,PARP1,S100A8,ASS1,KCNK3,MT1X,CA2,BGLAP	grey	VSMC_M10
GO:0033561	0.34	0.82	11	18	regulation of water loss via skin	BP	1	SRF,GRHL1,MET,ELOVL1,LSR,KDF1,SFN,GRHL3,ABCA12,ALOXE3,CLDN1	grey	VSMC_M10
GO:0009301	0.34	0.82	11	18	snRNA transcription	BP	1	RPAP2,SNAPC3,ZC3H8,ZNF143,CDK7,MEPCE,ELL,CC2D1A,ICE2,SNAPC5,SNAPC4	grey	VSMC_M10
GO:0006096	0.34	0.75	34	60	glycolytic process	BP	1	PPARA,PRXL2C,GAPDH,SLC4A4,BPGM,DHTKD1,PRKAG2,PFKP,GPI,GPD1,P2RX7,PRKAG1,PFKM,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,HK1,PRKAG3,STAT3,ENO3,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:0006757	0.34	0.75	34	60	ATP generation from ADP	BP	1	PPARA,PRXL2C,GAPDH,SLC4A4,BPGM,DHTKD1,PRKAG2,PFKP,GPI,GPD1,P2RX7,PRKAG1,PFKM,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,HK1,PRKAG3,STAT3,ENO3,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:0050982	0.34	0.77	23	40	detection of mechanical stimulus	BP	1	PKD2L2,PTK2,PHF24,KIT,WHRN,ASIC3,SCN1A,MKKS,ADGRV1,PKD2,BACE1,STRC,TTN,KCNK4,PKD1L1,KCNA1,TCAP,ASIC2,PKD1,PIEZO1,PKD1L3,PJVK,CHRNA10	grey	VSMC_M10
GO:0090183	0.34	0.79	16	27	regulation of kidney development	BP	1	MYC,SMO,SIX2,OSR1,SOX9,RET,PAX8,PAX2,AGT,WNT4,MAGED1,LHX1,SOX8,NOG,BASP1,SIX1	grey	VSMC_M10
GO:0001886	0.34	0.85	7	11	endothelial cell morphogenesis	BP	1	HOXA13,MET,ARHGEF26,STC1,CLIC4,PLOD3,TNMD	grey	VSMC_M10
GO:0045026	0.34	0.86	6	9	plasma membrane fusion	BP	1	SPACA6,IZUMO1,LYZL6,NSF,SPESP1,NOX5	grey	VSMC_M10
GO:1904292	0.34	0.81	11	18	regulation of ERAD pathway	BP	1	AQP11,USP25,RNFT2,USP13,USP19,RNF185,NFE2L2,BCAP31,SGTA,TMEM259,RNFT1	grey	VSMC_M10
GO:1901620	0.34	0.86	6	9	regulation of smoothened signaling pathway involved in dorsal/ventral neural tube patterning	BP	1	GLI2,SUFU,GORAB,GPR161,TULP3,MKS1	grey	VSMC_M10
GO:0045620	0.34	0.77	21	36	negative regulation of lymphocyte differentiation	BP	1	FBXO7,FOXJ1,ZC3H8,TMEM131L,HLX,RUNX3,BCL6,RC3H1,TNFSF18,LAG3,INHA,FOXP3,TBX21,ZBTB7B,IL4R,CD74,PTPN2,SOCS1,MIR21,FGL2,RC3H2	grey	VSMC_M10
GO:0040018	0.34	0.81	12	20	positive regulation of multicellular organism growth	BP	1	SMO,MKKS,PLS1,CELF1,IGF2,SLC6A3,GPAM,CREB1,STAT5B,GHR,DIO3,POU3F2	grey	VSMC_M10
GO:0061844	0.34	0.83	9	14	antimicrobial humoral immune response mediated by antimicrobial peptide	BP	1	CXCL14,GAPDH,CXCL8,NOD2,S100A12,HIST1H2BK,CXCL6,HIST1H2BF,HIST1H2BJ	grey	VSMC_M10
GO:0003222	0.34	0.83	8	13	ventricular trabecula myocardium morphogenesis	BP	1	FOXH1,NRG1,TGFB2,BMPR1A,RBPJ,MED1,ENG,HEY2	grey	VSMC_M10
GO:0090160	0.34	0.85	7	11	Golgi to lysosome transport	BP	1	RBSN,CCDC91,AP4M1,ANKFY1,GAK,AC138894.1,AP1G1	grey	VSMC_M10
GO:0036475	0.34	0.79	16	27	neuron death in response to oxidative stress	BP	1	PRKN,NCOA7,ATF4,FBXO7,SLC1A1,TLR4,SLC7A11,ARL6IP5,FBXW7,MCL1,NONO,PINK1,PARP1,PARK7,TSC1,TLDC1	grey	VSMC_M10
GO:0042362	0.34	0.86	6	9	fat-soluble vitamin biosynthetic process	BP	1	CYP27B1,CYP2R1,PLTP,SNAI1,CYP27A1,GFI1	grey	VSMC_M10
GO:0061000	0.34	0.85	7	11	negative regulation of dendritic spine development	BP	1	FSTL4,ASAP1,HDAC2,PLK2,SRGAP2C,DNM3,EFNA1	grey	VSMC_M10
GO:0018202	0.34	0.86	6	9	peptidyl-histidine modification	BP	1	DPH2,DPH3,HIF1AN,SETD3,DPH1,METTL18	grey	VSMC_M10
GO:0140115	0.34	0.76	28	49	export across plasma membrane	BP	1	ABCB1,SLC4A4,SLC8A2,ATP7B,ATP1A3,ABCC4,SLC40A1,ANO6,ABCC2,KCNE2,ABCG2,KCNIP2,ABCC5,ATP1A2,SLC9A1,DLG1,ATP1B1,SLC27A1,SLC29A4,ATP1B2,CALM1,RALBP1,ATP2B3,MIR21,SLC22A5,KCNH2,KCNK5,KCNT2	grey	VSMC_M10
GO:0015711	0.34	0.71	125	228	organic anion transport	BP	1	ATP8B1,SLC26A10,SLC16A7,SLC12A2,SLC27A6,NTRK2,PLA2G6,ABCC10,APBA1,SLC35B2,SLC1A1,SLC25A13,SLC3A1,SLC4A4,CYB5R4,SLC35A1,SLC1A4,SLC7A11,SLC26A5,SLC25A30,SLC4A2,ASIC3,LLGL2,SLC22A13,SLC25A38,ABCC4,SLC4A7,SLC6A15,SLC25A15,SLC23A2,ARL6IP5,SLC7A1,SLC38A9,SLC5A8,CYP7A1,SLCO6A1,SLC43A1,SLC33A1,SERINC5,SLC38A2,SLC38A1,SLC10A6,COL4A3BP,ABCC2,PLA2R1,ABCG2,GRM2,SLC4A10,SFXN2,CYB5R1,CALHM1,SLC2A10,SLC38A3,MAP2K6,SLC16A6,SLC7A7,SLCO3A1,ABCB11,AGT,ABCC5,ACE2,ATP1A2,SLCO1A2,SLCO1C1,PER2,NTSR1,SLC16A1,PLA2G4A,SLC25A42,SLC11A1,MFSD10,SLC2A2,PQLC2,SLC27A1,SLC38A5,MPC2,ARL6IP1,SLC3A2,SLC2A9,SLC38A6,SLC35A2,SLC4A3,PRAF2,SLC25A11,SLC16A13,CLN8,SLC26A1,PSEN1,SLC7A3,SLC35B1,AC138894.1,ABCC3,NMUR2,CA4,SLC6A7,SLC26A2,LRRC8E,EMB,NOS2,SLC25A23,SLC25A41,SLC46A1,SLC25A14,PROCA1,ABAT,CYB5RL,SLC1A7,TRPV1,SLC2A6,SLC16A4,SLC7A5,LRRC8A,SLC25A25,ABCD3,STXBP1,SLC7A6,SLC36A1,LRRC8D,PLA2G2C,SLC25A21,SLC25A32,RGS4,CPTP,SLC25A29,PTGES	grey	VSMC_M10
GO:0090317	0.34	0.77	20	34	negative regulation of intracellular protein transport	BP	1	RAB23,ITGB1BP1,UBAC2,FERMT1,BAG4,PKIA,DMTN,SUFU,CABP1,SP100,YOD1,BAG3,APOD,DERL3,C11orf65,INPP5K,PARK7,TXN,UBE2G2,DERL2	grey	VSMC_M10
GO:0051657	0.34	0.85	7	11	maintenance of organelle location	BP	1	ALB,ARHGAP21,TBCCD1,ATP2A1,GPSM2,SPOUT1,POLR2M	grey	VSMC_M10
GO:0070129	0.34	0.80	14	23	regulation of mitochondrial translation	BP	1	SHMT2,TSFM,RMND1,LRPPRC,MRPS27,NSUN3,RPUSD4,RCC1L,MTG2,COA3,ALKBH1,RPUSD3,UQCC2,TRMT10C	grey	VSMC_M10

GO:0030858	0.34	0.76	26	45	positive regulation of epithelial cell differentiation	BP	1	CYP27B1,PTCH1,RFX3,SFRP4,SOX9,PTCH2,FOXJ1,OVOL2,BTG1,PAX8,VDR,NKX6-1,PAX2,KDF1,SFN,H2AFY2,MED1,TMEM100,VEZF1,LHX1,MIR21,MIR125B1,ACVRL1,MIR99B,ZBED2,LIF	grey	VSMC_M10
GO:0006699	0.34	0.79	16	27	bile acid biosynthetic process	BP	1	NR1H4,CYP7A1,CYP7B1,OSBP,ABCB11,OSBPL2,OSBPL6,OSBPL1A,CYP27A1,HSD17B10,FGFR4,OSBPL7,CYP46A1,ABCD3,AMACR,STARD4	grey	VSMC_M10
GO:0090313	0.34	0.78	17	29	regulation of protein targeting to membrane	BP	1	SLC1A1,ITGB1BP1,TCAF2,AKT2,PRNP,DMTN,KCNB1,C2CD5,CIB1,FIS1,CEMIP,ITGAM,MIEF2,CDK5R1,INPP5K,HRAS,MIEF1	grey	VSMC_M10
GO:0009141	0.34	0.73	49	86	nucleoside triphosphate metabolic process	BP	1	NME1,TBPL1,ENPP3,ATP5MGL,PPARA,SMPDL3A,GTPBP1,IMPDH1,SLC25A13,RAB23,SPHK2,CMPK1,NUDT15,PRKAG2,ATP5F1C,NUDT16,ATP5F1A,DGUOK,OPA1,ENTPD4,FAM173B,NME4,MFN1,CTPS2,DNAJC30,DTYMK,EFL1,ATP5S,PINK1,STAT3,NME7,ADK,PARP1,PKLR,ATP6V0C,NME3,ATP5PB,VPS9D1,GNAI3,AK8,UCK1,MT-ATP8,MT-ATP6,RHOA,ATP5ME,ATP5MF,CMPK2,NME6,NUDT2	grey	VSMC_M10
GO:0042447	0.34	0.86	6	9	hormone catabolic process	BP	1	IDE,SPP1,SRD5A1,ECE1,DIO3,DIO2	grey	VSMC_M10
GO:0051588	0.34	0.74	41	73	regulation of neurotransmitter transport	BP	1	SNCAIP,PRKN,CHRNA3,CHRNA5,APBA1,RIMS1,RIMS3,CACNB2,SYT1,RAB5A,MEF2C,ASIC1,P2RY1,VPS18,DTNBP1,DNM1L,ADRA2A,GPER1,ATP1A2,PER2,STX1A,BACE1,CSPG5,RAP1B,CASK,PNKD,RAB3A,SYN1,CPLX1,STX1B,SYT11,CALM1,SNAPIN,PRKCB,CAMK2A,FMR1,P2RX1,BAIAP3,STXBP1,CHRNB4,KCNMB4	grey	VSMC_M10
GO:1905208	0.34	0.84	7	11	negative regulation of cardiocyte differentiation	BP	1	FRS2,EGFR,SOX6,PRICKLE1,FZD7,MIR222,HEY2	grey	VSMC_M10
GO:1905065	0.34	0.86	6	9	positive regulation of vascular associated smooth muscle cell differentiation	BP	1	KIT,GPER1,EFEMP2,ENG,MIR21,MIR125B1	grey	VSMC_M10
GO:0045851	0.34	0.77	22	38	pH reduction	BP	1	PPT1,RAB7A,ATP6V0E2,AQP11,TMEM106B,CCKBR,ATP6V1H,TMEM9,TCIRG1,SLAMF8,CLIC4,SLC11A1,SLC9A7,ATP6V0A1,DMXL2,AC138894.1,CLN6,SNAPIN,TMEM199,ATP6AP1,CA2,RAB39A	grey	VSMC_M10
GO:0002711	0.34	0.78	16	27	positive regulation of T cell mediated immunity	BP	1	STX7,HLA-DRA,RSAD2,NECTIN2,PVR,SLC22A13,TRAF6,DENND1B,FZD5,IL12A,FOXP3,ZBTB1,FBXO38,PRKCZ,TRAF2,FADD	grey	VSMC_M10
GO:0006367	0.35	0.74	37	65	transcription initiation from RNA polymerase II promoter	BP	1	ESR1,MED30,TAF2,TAF8,SRF,ERCC1,ERCC3,GTF2F2,PAXIP1,TAF7,GTF2E2,TAF10,POLR2I,ERCC6,CDK7,TAF9,CCNH,TAF5,GTF2E1,TAF4,E2F2,CREB1,MED14,TAF6,POLR2G,THRA,MED24,MED1,TAF1,MED7,TAF4B,TAF13,MED27,TAF12,NKX2-5,HEY2,GTF2H5	grey	VSMC_M10
GO:0014819	0.35	0.84	7	11	regulation of skeletal muscle contraction	BP	1	NR4A1,KCNJ2,MYH7,CASQ1,ACTN3,ATP2A1,DMD	grey	VSMC_M10
GO:1901616	0.35	0.75	32	56	organic hydroxy compound catabolic process	BP	1	CYP27B1,MIOX,SYNJ2,SRD5A3,INPP4B,MTMR2,LRTOMT,AP000812.5,MTMR7,CYP7A1,GK5,SYNJ1,SLC6A3,INPP5A,ALDH3B2,NTSR1,INPP5J,SORD,FAH,COMT,CYP27A1,TKFC,CYP46A1,IMPA2,INPP5K,ALDH2,CEL,DIO3,INPP1,ADH4,PDXP,DIO2	grey	VSMC_M10
GO:0035510	0.35	0.80	12	20	DNA dealkylation	BP	1	APOBEC3H,STPG4,ASCC3,ALKBH3,TOX,OTUD4,FTO,ALKBH2,MGMT,TET1,ALKBH1,MPG	grey	VSMC_M10
GO:0001976	0.35	0.86	6	9	nervous system process involved in regulation of systemic arterial blood pressure	BP	1	TNNI3,P2RX2,AGT,ACE2,ASIC2,MECP2	grey	VSMC_M10
GO:0003356	0.35	0.84	7	11	regulation of cilium beat frequency	BP	1	DNAH11,ARMC4,MKKS,CFAP20,CFAP43,CFAP45,CCSAP	grey	VSMC_M10
GO:0070050	0.35	0.80	13	22	neuron cellular homeostasis	BP	1	PRKN,SLC8A2,CACNB2,CHMP2B,P2RY1,SLC6A2,NELL2,DNAJB2,FGGY,TAOK1,ATP2B3,P2RX1,MAP1A	grey	VSMC_M10
GO:1902476	0.35	0.77	19	33	chloride transmembrane transport	BP	1	SLC26A10,SLC12A2,GABRA1,SLC1A1,CLCN1,SLC26A5,ANO4,ANO6,SLC12A5,SLC12A7,SLC12A8,SLC12A9,SLC26A1,SLC26A2,GABRE,GABRA3,CLCN7,LRRC8A,SLC12A4	grey	VSMC_M10
GO:0070588	0.35	0.70	115	211	calcium ion transmembrane transport	BP	1	STAC3,SMDT1,CATSPER3,PKD2L2,PLA2G6,TRPM6,TSPAN13,PRKCE,IBTK,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,PANX1,CACNB2,STAC,SLC24A3,CACNB4,RYR1,NALCN,PRNP,DIAPH1,GAS6,RASA3,MICU3,TRPC4AP,RYR3,ORAI1,ASIC1,P2RX7,PTK2B,TPCN1,SLC8B1,OPA1,F2R,ANO6,KCNE2,PKD2,CASQ2,MCUR1,RYR2,TRPM1,CALHM1,LCK,TRPV4,ADRA2A,MCUB,UBASH3B,ANK2,GPER1,TRPM8,ATP1A2,SLC9A1,C4orf3,CASQ1,NTSR1,NOS1AP,CATSPER2,TMCO1,CEMIP,SESTD1,PTPN6,MICU1,MCU,HTT,PKD1L1,TRPM7,ATP1B1,BHLHA15,GNB5,HAP1,PSEN2,STAC2,CACNB1,ANXA2,FAM155B,PSEN1,CACNA1A,CACNA1G,ATP2A1,CD19,CALM1,VMP1,BDKRB1,TRPV2,SLC25A23,MAIP1,FMR1,ATP2B3,TRPV3,TRPV1,PDPK1,P2RX1,CACNA1B,PKD1,CACNA1H,CYBA,JPH3,ATP2C2,SLC25A25,PKD1L3,MCOLN3,RRAD,MIR21,DMD,GPR35,NOL3,CHRNA10,JPH2,THY1,CACNG7,DDIT3,CACNG5,GEM	grey	VSMC_M10
GO:0060231	0.35	0.81	11	18	mesenchymal to epithelial transition	BP	1	SMO,SIX2,TCF15,PAX8,PAX2,SALL1,FZD7,WNT4,CITED1,BASP1,LIF	grey	VSMC_M10

GO:0006839	0.35	0.70	117	210	mitochondrial transport	BP	1	TIMM21,HEBP2,CPT1B,PRKN,TSPO,HSPA4,SMDT1,BAK1,TOMM22,RAC2,FBXO7,SLC25A13,TMEM14A,PNPT1,UCP1,VPS35,MGARP,AGK,SLC25A30,DNAJC15,ATP5F1C,SLC25A38,PITRM1,TIMM50,USP36,SLC25A15,BAG4,MICU3,MIPEP,IMMP1L,HIP1R,ATP5F1A,FBXW7,HTRA2,CSNK2A2,SLC8B1,SLC25A37,OPA1,TOMM34,TMEM14C,MCUR1,FAM173B,SFXN2,SIRT4,CPT1A,OXA1L,MCUB,HPS4,ARIH2,SLC25A20,BAG3,SLC9A1,TOMM40L,THEM4,DNAJC30,STPG1,FZD9,FZD5,SLC25A16,FIS1,KIF1BP,NMT1,GRPEL1,C11orf65,MICU1,MCU,BCS1L,PINK1,MUL1,STAT3,MPC2,TIMM17B,PSEN2,TMEM102,MFN2,NPEPPS,PSEN1,HAX1,TIMM29,CAMK2A,SREBF1,SLC25A23,MAIP1,SLC25A41,SLC25A14,ACAA2,PAM16,BCAP31,SLC25A33,ATP5PB,NAIF1,SH3GLB1,MIR29A,MT-ATP8,MT-ATP6,MICALL2,SLC25A3,ATP5ME,NOL3,ATP5MF,BNIP3L,SLC25A21,SLC25A32,TIMM10B,TIMM23B,BCL2L11,SLC25A29,SLC35F6,BCL2L2,TIMM8B,RHOU,MRPL18,LEPROT,GRPEL2,PPIF,AC140504.1,DNAJC19	grey	VSMC_M10
GO:0150104	0.35	0.74	39	70	transport across blood-brain barrier	BP	1	LRP1,SLC16A7,SLC12A2,AGER,ABCB1,SLC1A1,SLC4A4,SLC1A4,SLC8A2,SLC24A3,ABCC4,SLC7A1,SLC38A2,SLC38A1,ABCC2,ABCG2,SLC2A13,SLC2A10,SLC38A3,SLCO3A1,ABCC5,ATP1A2,SLCO1C1,SLC29A2,SLC16A1,SLC27A1,SLC38A5,SLC4A3,SLC29A4,SLC2A4,ATP1B2,SLC7A3,ABCC3,INSR,LEPR,SLC7A5,FABP5,SLC22A5,KCNJ8	grey	VSMC_M10
GO:0048143	0.35	0.81	11	18	astrocyte activation	BP	1	LRP1,AGER,SMO,TTBK1,FPR2,EGFR,C5AR1,MAPT,PSEN1,LDLR,CNTF	grey	VSMC_M10
GO:0042474	0.35	0.81	11	18	middle ear morphogenesis	BP	1	OSR2,SIX2,HOXA2,OSR1,EYA1,PRKRA,NKX3-2,GSC,NOG,SIX1,INSIG2	grey	VSMC_M10
GO:0010977	0.35	0.72	64	116	negative regulation of neuron projection development	BP	1	LRP1,SEMA6A,FSTL4,SYNGAP1,SEMA4D,SEMA4C,RTN4,RUFY3,ACP4,LPAR1,EPHA7,HDAC2,TSKU,SEMA3D,SPART,SEMA3A,ULK1,DPYSL3,RYK,CBFA2T2,SEMA4F,DGUOK,PAQR3,SEMA3G,SPP1,SEMA4G,MYLIP,KIAA0319,TRPV4,SEMA3F,KREMEN1,CIB1,CERS2,PTPRO,INPP5J,LRIG2,WNT3,SEMA6D,TNR,DNM3,CD38,CRMP1,EPHA4,GAK,STX1B,PSEN1,SEMA4A,TRIM46,EFNA1,NTN1,SNAPIN,RIT2,CDK5R1,THOC2,DAB1,ARHGAP4,PLXNA3,TSC1,GFI1,RHOA,RTN4RL1,THY1,WNT5A,EFNB3	grey	VSMC_M10
GO:1990542	0.35	0.73	48	84	mitochondrial transmembrane transport	BP	1	TIMM21,CPT1B,SMDT1,SLC25A13,PNPT1,UCP1,DNAJC15,ATP5F1C,SLC25A38,TIMM50,SLC25A15,MICU3,ATP5F1A,SLC8B1,SLC25A37,OPA1,MCUR1,FAM173B,SFXN2,CPT1A,MCUB,SLC25A20,TOMM40L,DNAJC30,GRPEL1,MICU1,MCU,MPC2,TIMM17B,PSEN2,SLC25A23,MAIP1,SLC25A41,PAM16,SLC25A33,ATP5PB,MT-ATP8,MT-ATP6,SLC25A3,ATP5ME,ATP5MF,SLC25A21,SLC25A32,TIMM23B,SLC25A29,MRPL18,GRPEL2,DNAJC19	grey	VSMC_M10
GO:0010659	0.35	0.77	21	36	cardiac muscle cell apoptotic process	BP	1	MAP3K5,PPP1R10,RGL2,HSF1,PAX8,HAND2,SIRT5,SIRT4,AGT,NFE2L2,CXCR2,CAMK2A,GNB1,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,TIGAR,NKX2-5,HEY2	grey	VSMC_M10
GO:0032369	0.35	0.79	14	23	negative regulation of lipid transport	BP	1	CRY1,ABCG5,ABCG8,NR1H2,APOC1,AKT2,NR1H3,CRY2,PLA2R1,EGF,FIS1,MIR27B,MIR27A,MIR33B	grey	VSMC_M10
GO:0090103	0.35	0.80	12	20	cochlea morphogenesis	BP	1	PTK7,MYO3A,SOX9,GLI2,EYA1,PAX2,MYO3B,GRHL3,DVL2,POU3F4,WNT5A,SIX1	grey	VSMC_M10
GO:0046488	0.35	0.71	76	138	phosphatidylinositol metabolic process	BP	1	PIP4K2C,SYNJ2,GPAA1,CWH43,INPP4A,TMEM246,PIGF,MBOAT7,PLEK,INPP4B,FIG4,MTMR2,PIP4K2A,ITPKC,PIP4P1,MTMR14,PLCB1,PGAP2,MTMR7,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,CHRM5,MTMR9,SLA2,SYNJ1,CDS1,ITPKA,PIGT,GPLD1,PGAP1,INPP5A,PITPNM1,MTMR11,PIGM,BMX,FAM126B,IP6K2,LPGAT1,PIGV,MTMR3,INPP5J,PIGX,PIGZ,PIKFYVE,SACM1L,PIGC,PLCD4,SOCS4,PI4KA,SLC27A1,PGAP3,PIGH,PI4K2B,SOCS7,DGKE,TTC7B,PIGL,CSF1R,MPPE1,IMPA2,MTMR12,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,PIP5KL1,PYURF,LCLAT1,PIGB,PIGA,INPP1,CDIPT	grey	VSMC_M10
GO:0098789	0.35	0.84	7	11	pre-mRNA cleavage required for polyadenylation	BP	1	CPSF6,CPSF1,CPSF2,NCBP2,CPSF4,AP002990.1,CSTF2	grey	VSMC_M10
GO:0031102	0.35	0.75	28	49	neuron projection regeneration	BP	1	LRP1,TSPO,PTN,TNC,DHFR,PTPRF,CHL1,ULK1,SPP1,KIAA0319,MTR,GAP43,DAG1,KREMEN1,CERS2,LRIG2,APOD,TNR,EPHA4,NDEL1,MAP2K1,ISL1,OMG,MAPK8IP3,MIR222,CNTF,RTN4RL1,THY1	grey	VSMC_M10
GO:0006631	0.35	0.69	149	271	fatty acid metabolic process	BP	1	HSD17B4,AIG1,LTC4S,CPT1B,SLC27A6,TNXB,QKI,PPARA,ACSL6,PNPLA3,MCAT,HSD17B8,ECHDC1,AKR1B1,MAPK14,HACD4,CROT,AASDH,ADH5,ETFB,NR1H2,LPIN1,DLD,PRKAR2B,FAAH,HADHA,SOX9,ABHD5,APOC1,ECHDC3,PRKAG2,ACOX1,SLC22A13,PIBF1,CYGB,ELOVL1,AKT2,HACL1,PANK2,PDK1,TRIB3,LYPLA1,ACOXL,CYP7A1,ELOVL7,ASAH1,ACOX2,ABHD6,THNSL2,CBR4,HPGD,PEX2,ETFDH,ACOT12,PRKAG1,NR1H3,IVD,LPIN3,ECI2,ERLIN1,PLA2G4B,ADTRP,PRKAB1,LONP2,PM20D1,SIRT4,MCEE,IRS1,CPT1A,BDH2,GPAM,ACSL5,CYP2U1,ABHD2,MSMO1,MECR,GNPAT,ABCB11,HACD2,LPGAT1,PER2,ACADSB,THEM5,THEM4,MLXIPL,SCAP,EHHADH,POR,PDK3,PLA2G4A,ACADL,TYSND1,ACSBG1,PECR,PRKAG3,SLC27A1,DAGLB,FADS3,LIAS,ACADVL,EPHX1,TECR,HSD17B10,DEGS1,LIPC,ACOT2,AC005520.1,ABCD4,ALOXE3,GCDH,MAPK3,HACD3,NDUFAB1,ACSM3,ACACA,NCOR1,CD74,ABHD3,SREBF1,LPIN2,C3,ACSBG2,CYP2J2,ACAA2,ACOT11,DECR2,ACSF3,CEL,MLYCD,PTGES2,ABCD3,PLA2G15,CES2,ACADM,PHYH,ACOT4,FABP5,FADS6,ELOVL3,HADHB,AMACR,NUDT19,GGT5,ECI1,AUH,LYPLA2,PTGES,INSIG2,ADH4	grey	VSMC_M10
GO:0061548	0.35	0.84	7	11	ganglion development	BP	1	SEMA3A,FZD3,SEMA3F,TULP3,TUBB3,SIX1,RGS4	grey	VSMC_M10
GO:0070254	0.35	0.86	6	9	mucus secretion	BP	1	PRKCE,EGFR,ATG5,TRAF3IP2,SCNN1B,CYBA	grey	VSMC_M10

GO:0071621	0.35	0.73	43	76	granulocyte chemotaxis	BP	1	PTK2,RAC2,CXCL8,AKIRIN1,C5AR2,C5AR1,NCKAP1L,CCL17,NOD2,GBF1,DNM1L,TRPV4,TGFB2,CMKLR1,MOSPD2,FCER1G,PIKFYVE,MCU,TNFSF18,CXCR2,BST1,MAPK1,DAPK2,MAPK3,S100A14,S100A8,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,VAV1,PIP5K1C,MPP1,BSG,VAV3,CCL16,S100A12,DPP4,CXCL6,CCL22	grey	VSMC_M10
GO:1902644	0.35	0.84	7	11	tertiary alcohol metabolic process	BP	1	AKR1B1,AKR1A1,CBR4,DKK3,WNT4,DGKQ,CACNA1H	grey	VSMC_M10
GO:0090385	0.35	0.84	7	11	phagosome-lysosome fusion	BP	1	RAB7A,RAB7B,SPG11,PIKFYVE,SYT7,AC138894.1,RAB39A	grey	VSMC_M10
GO:0051238	0.35	0.86	6	9	sequestering of metal ion	BP	1	SLC30A4,FTH1,S100A8,SLC30A7,LCN2,FTL	grey	VSMC_M10
GO:0033555	0.35	0.76	24	42	multicellular organismal response to stress	BP	1	MAPK8IP2,TSPO,USP46,SLC1A1,P2RX2,RET,P2RX3,MEF2C,ASIC1,NR4A2,SLC6A2,KIAA0319,PPP3CA,ADRA2A,ATP1A2,COMT,GCH1,ASIC4,NMUR2,VWA1,TRPV1,MECP2,DPP4,CRH	grey	VSMC_M10
GO:0042119	0.35	0.78	15	25	neutrophil activation	BP	1	CXCL8,IL15,TRAF3IP2,MYD88,F2RL1,FCER1G,CXCR2,ITGAM,SCNN1B,CCL5,STXBP2,PRAM1,DNASE1,CXCL6,MIR125A	grey	VSMC_M10
GO:0006896	0.35	0.80	12	20	Golgi to vacuole transport	BP	1	AP3S1,VPS52,RBSN,CCDC91,VTI1A,RNF215,AP4M1,ANKFY1,GAK,AC138894.1,AP1G1,AP3S2	grey	VSMC_M10
GO:0007026	0.35	0.79	14	24	negative regulation of microtubule depolymerization	BP	1	CLASP2,TRIM54,NAV3,SPEF1,ATXN7,KATNB1,TTBK2,CIB1,CAMSAP3,TAOK1,APC2,CAMSAP1,APC,MAP6D1	grey	VSMC_M10
GO:0098792	0.35	0.84	7	11	xenophagy	BP	1	NOD1,OPTN,RIPK2,NOD2,ATG16L1,WIPI2,MAPK3	grey	VSMC_M10
GO:0007288	0.35	0.80	11	18	sperm axoneme assembly	BP	1	UBE2B,CFAP69,ARMC2,DNAH1,NEURL1,CFAP43,TTC12,SPAG16,MNS1,SPEF2,TPGS1	grey	VSMC_M10
GO:0120316	0.35	0.80	11	18	sperm flagellum assembly	BP	1	UBE2B,CFAP69,ARMC2,DNAH1,NEURL1,CFAP43,TTC12,SPAG16,MNS1,SPEF2,TPGS1	grey	VSMC_M10
GO:0036035	0.35	0.82	8	13	osteoclast development	BP	1	FOXP1,FBXW7,LRRK1,SLC9B2,FBN1,ANXA2,GPR68,ATP6AP1	grey	VSMC_M10
GO:0001921	0.35	0.82	8	13	positive regulation of receptor recycling	BP	1	BVES,EPS15,NSF,ECE1,NSG1,ANXA2,PSEN1,VAMP3	grey	VSMC_M10
GO:0098856	0.35	0.84	7	11	intestinal lipid absorption	BP	1	ABCG5,ABCG8,SOAT2,LIMA1,LPCAT3,LDLR,CEL	grey	VSMC_M10
GO:0090140	0.36	0.77	18	31	regulation of mitochondrial fission	BP	1	PRKN,VPS35,DDHD2,DCN,DNM1L,MAPT,FIS1,C11orf65,MCU,DDHD1,PINK1,MUL1,STAT2,MIEF2,RALBP1,DHODH,RALA,MIEF1	grey	VSMC_M10
GO:0086010	0.36	0.77	17	30	membrane depolarization during action potential	BP	1	TRPM4,CACNB2,SCN5A,SCN1A,SLMAP,KCNJ2,SCN2A,SCN7A,ANK2,ATP1A2,SCN4B,CACNA1G,CACNA1H,KCNH2,SCN2B,YWHAH,HCN4	grey	VSMC_M10
GO:0007173	0.36	0.72	50	90	epidermal growth factor receptor signaling pathway	BP	1	PTK2,NCK2,EPGN,AREG,TGFA,EGFR,GAB1,BRAF,RAB7A,SOX9,NEU3,SNX5,HBEGF,PDE6G,FER,HIP1R,PLCE1,FBXW7,PTPRJ,WDR54,PTK2B,NEURL1,ADRA2A,SLC30A10,RNF115,NCF1,EGF,GPER1,DGKD,IFI6,AGT,CBL,REPS2,PDE6H,SNX6,ZFYVE28,SOCS4,HAP1,PSEN1,RPS6KA5,GAREM1,PTPN2,PDPK1,RNF126,MVB12B,DAB2IP,MIR29A,MIR21,GRB2,EREG	grey	VSMC_M10
GO:0009134	0.36	0.84	7	11	nucleoside diphosphate catabolic process	BP	1	NT5E,ENTPD6,NUDT5,NUDT16,ENTPD4,NUDT18,ENTPD5	grey	VSMC_M10
GO:0060761	0.36	0.73	35	61	negative regulation of response to cytokine stimulus	BP	1	IL1R2,PXDN,NR1H2,GAS6,OTUD4,ROBO1,NR1H3,OAS3,NLRC5,F2RL1,YTHDF2,PARP14,PELI3,MUL1,PADI2,GPS2,USP18,PYDC1,DCST1,MAP2K5,STAT2,CCL5,MAPK7,PTPN2,PIAS4,MIR21,MIR125B1,MIR27B,MIR24-1,MIR27A,OAS1,NOL3,MIR125A,CCDC3,HIST1H2BJ	grey	VSMC_M10
GO:0008652	0.36	0.74	32	56	cellular amino acid biosynthetic process	BP	1	GLS2,SHMT2,PYCR3,PSAT1,MTAP,ALDH1A1,BCAT2,DHFR,APIP,SERINC5,ENOPH1,SDSL,ASNSD1,GLS,MTRR,ASL,MTR,CBSL,OAT,GLUL,UPB1,PLOD3,CPS1,AASDHPPT,AC138894.1,SHMT1,ABAT,PARK7,ASS1,MTHFD2L,PHGDH,PCBD2	grey	VSMC_M10
GO:0003382	0.36	0.78	14	24	epithelial cell morphogenesis	BP	1	HOXA13,MET,SPINT2,RILPL1,RILPL2,FLNB,ARHGEF26,STC1,CLIC4,PLOD3,RAB25,TNMD,CCDC88C,BCL11B	grey	VSMC_M10
GO:0039531	0.36	0.79	12	20	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	BP	1	USP15,ANKRD17,PUM2,SEC14L1,NPLOC4,OASL,NLRX1,BIRC3,TKFC,TSPAN6,RIOK3,ZCCHC3	grey	VSMC_M10
GO:0097205	0.36	0.79	13	22	renal filtration	BP	1	XPNPEP3,GAS6,F2RL1,F2R,SULF2,MCAM,PTPRO,ITGA3,TMEM63C,CORO2B,TBC1D8B,CYBA,JCHAIN	grey	VSMC_M10
GO:0007411	0.36	0.70	98	181	axon guidance	BP	1	LRP1,SEMA6A,KIF5A,GFRA3,PTK2,PTCH1,PLXNA4,RAC2,SMO,SEMA4D,DLX5,ETV1,SEMA4C,HOXA2,EPHA7,EPHA1,NRCAM,PLXNA1,GLI2,MEGF8,MYCBP2,KIF5C,FEZ2,SEMA3D,PLXNC1,SEMA3A,CHL1,UNC5D,RYK,EPHB1,RET,ROBO1,ROBO2,FZD3,SEMA4F,DPYSL2,SLIT1,TRIO,SEMA3G,CYFIP1,ALCAM,SEMA4G,SIAH1,BMPR1B,BDNF,LGR6,SEMA3F,GAP43,DAG1,LHX9,GBX2,KALRN,LAMA5,YTHDF1,PTPRO,EPHB3,WNT3,KLF7,MYPN,SEMA6D,EPHB4,TNR,CRMP1,EPHA4,LRTM2,UNC5A,SEMA4A,NGFR,EFNA1,NTN1,RPS6KA5,RNF165,BCL11B,LHX1,LAMA3,CDK5R1,ISL1,EMB,LAMA1,L1CAM,NTN3,PLXNA3,BSG,TUBB3,DPYSL5,EFNA4,CNTN2,VASP,FOXG1,ISL2,NOG,WNT5A,CHN1,ARTN,NRXN3,LYPLA2,EFNB3,ISPD	grey	VSMC_M10
GO:1901016	0.36	0.76	20	35	regulation of potassium ion transmembrane transporter activity	BP	1	NEDD4L,KCNRG,OXSR1,KCNE2,CASQ2,KCNIP2,KCNG1,ANK2,KLHL24,NOS1AP,DLG1,ATP1B1,KCNA1,ATP1B2,DNM2,RNF207,AMIGO1,WWP2,NETO2,CRBN	grey	VSMC_M10
GO:0030318	0.36	0.79	12	20	melanocyte differentiation	BP	1	SOX10,KIT,MITF,MEF2C,ADAMTS20,OCA2,USP13,HPS4,BLOC1S6,MREG,LRMDA,CITED1	grey	VSMC_M10
GO:0045109	0.36	0.84	7	11	intermediate filament organization	BP	1	BFSP1,NEFM,DSP,PKP2,KLHL24,DES,MTM1	grey	VSMC_M10
GO:0006754	0.36	0.75	23	39	ATP biosynthetic process	BP	1	ATP5MGL,PPARA,SLC25A13,SPHK2,PRKAG2,ATP5F1C,ATP5F1A,DGUOK,FAM173B,DNAJC30,ATP5S,PINK1,STAT3,PARP1,PKLR,ATP6V0C,ATP5PB,VPS9D1,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,NUDT2	grey	VSMC_M10
GO:0007625	0.36	0.84	7	11	grooming behavior	BP	1	SLC1A1,PPT1,DDO,DLG4,HOXB8,NMUR2,CNTNAP4	grey	VSMC_M10
GO:0009081	0.36	0.80	11	18	branched-chain amino acid metabolic process	BP	1	BCAT2,SDSL,IVD,HIBCH,ACAD8,ACADSB,HSD17B10,SLC25A44,ALDH6A1,HIBADH,AUH	grey	VSMC_M10

GO:0044281	0.36	0.66	705	1301	small molecule metabolic process	BP	1	NME1,RDH5,KDSR,APOF,ATP8B1,GLS2,RDH16,HSD17B4,SHMT2,TBPL1,ALDH8A1,MARS,PDE7B,PEX7,CYP27B1,AIG1,FUCA2,LTC4S,ENPP3,ATP5MGL,GFPT2,TPH2,RIDA,MIOX,CPT1B,SYNJ2,DPYS,SLC27A6,TNXB,PPT2,PRKN,QKI,PPARA,PDE10A,ACSL6,PNPLA3,MCAT,HSD17B8,SMPDL3A,PMM1,ECHDC1,ACO2,PRXL2C,HSD17B3,AKR1B1,ATF4,PYCR3,APOBEC3H,GTPBP1,MAPK14,PLA2G6,TTC39B,TXN2,PSAT1,OARD1,GUCA1B,GPT,IMPDH1,HACD4,MTAP,NMRK1,CARNMT1,GNMT,ALDH1A1,CRY1,GDA,CROT,ABCC10,GNPDA2,PGM5,GALT,SLC35B2,ENPP4,KIT,PLPP6,CA9,SRD5A3,UXS1,TFAP2B,SPTLC1,SLC25A13,GAPDH,AASDH,PPAT,IPPK,LIPT1,HMGCLL1,INPP4A,ADH5,RAB23,CAT,PPCS,RIMKLA,TMEM86B,PRKCE,RDH13,ETFB,PPP4R3B,SLC4A4,ME1,NT5E,PPT1,ZNF692,BPGM,PLEK,NR1H2,DDC,IL4I1,FAM3C,LPIN1,INPP4B,DKKL1,MGST2,QRSL1,SLC7A11,DLD,DHDH,DDO,APOB,BCAT2,NANP,PRKAR2B,SPHK2,DHFR,CMPK1,ADCY3,MTMR2,NAPEPLD,FAAH,PRTFDC1,HADHA,EBP,GAD2,ENTPD6,SOX9,CDADC1,NUDT15,ABHD5,ESD,RUBCNL,DLG2,AKR1A1,CUBN,MMACHC,LACC1,APOC1,HPDL,GLB1,KHK,EPM2AIP1,NUDT5,LIPE,DHTKD1,ECHDC3,MBD4,PRKAG2,ACOX1,SLC22A13,ATP5F1C,XYLB,PIBF1,ITPKC,CYGB,GCKR,HYI,HNMT,RBKS,ACER3,TSKU,PPP1CB,ELOVL1,TGDS,CSGALNACT1,AKT2,PIP4P1,PFKP,UGGT2,PGM2L1,C1QTNF1,SPTLC3,IDO2,IDO1,ACSS3,MDH2,SIRT7,HARS,HARS2,BTD,HACL1,SLC25A15,SLC23A2,CARS2,NUDT16,PANK2,PDK1,FUT10,AMDHD1,LARS,SUCLG2,PPP1R3B,NR1H4,PDHX,APIP,MTMR7,SLC5A8,TRIB3,LYPLA1,SDR16C5,ACOXL,CSAD,SOAT2,CYP7A1,ELOVL7,ASAH1,PANK1,POFUT1,CYP7B1,ACOX2,GPI,ABHD6,CEBPA,THNSL2,N	grey	VSMC_M10
GO:0098962	0.36	0.82	8	13	regulation of postsynaptic neurotransmitter receptor activity	BP	1	DLGAP3,DLGAP4,HOMER1,CNIH2,NPTX2,BEGAIN,DLGAP1,CACNG5	grey	VSMC_M10
GO:2000831	0.36	0.83	7	11	regulation of steroid hormone secretion	BP	1	GDF9,CRY1,C1QTNF1,NKX3-1,CRY2,AGT,CRH	grey	VSMC_M10
GO:0090336	0.36	0.82	8	13	positive regulation of brown fat cell differentiation	BP	1	MAPK14,PIM1,NAPEPLD,RREB1,SOX13,TFE3,ZBTB7B,SIX1	grey	VSMC_M10
GO:0021510	0.36	0.73	39	70	spinal cord development	BP	1	PTCH1,SMO,DAAM2,PTN,INTU,VSTM5,EED,ERCC2,GLI2,IFT172,MNX1,SOX12,ROBO2,SOX6,PKD2,SOX13,SUFU,SRD5A1,ADARB1,GIGYF2,BAG3,CHRD,MDGA2,SCYL3,TULP3,CLN8,PLXDC1,HOXB8,LHX1,ISL1,SUZ12,DAB1,LRP8,PKD1,SOX4,ISL2,NOG,LBX1,PHGDH	grey	VSMC_M10
GO:0060347	0.36	0.83	7	11	heart trabecula formation	BP	1	ADGRG6,TEK,SRF,FHL2,OVOL2,ADAMTS1,HEY2	grey	VSMC_M10
GO:2000345	0.36	0.83	7	11	regulation of hepatocyte proliferation	BP	1	GLI1,TNFAIP3,PTN,FBXW7,SULF2,MED1,FGF1	grey	VSMC_M10
GO:2000463	0.36	0.78	14	24	positive regulation of excitatory postsynaptic potential	BP	1	RIMS2,RIMS1,SHANK1,CUX2,PTK2B,IGSF11,SSH1,STX1A,DLG4,NLGN2,STX1B,NLGN3,PRKCZ,RGS4	grey	VSMC_M10
GO:1901889	0.36	0.77	15	26	negative regulation of cell junction assembly	BP	1	LRP1,EPHA7,ITGB1BP1,CLASP2,IKBKB,FAM107A,ROBO2,SLIT1,DMTN,ARHGAP6,APOD,BCAS3,ACVRL1,WNT5A,DUSP22	grey	VSMC_M10
GO:0080182	0.36	0.81	9	15	histone H3-K4 trimethylation	BP	1	KMT2D,RTF1,WDR82,ZNF335,WDR61,SETD1A,OGT,ARID4A,BEND3	grey	VSMC_M10
GO:0010658	0.36	0.75	22	38	striated muscle cell apoptotic process	BP	1	MAP3K5,PPP1R10,RGL2,HSF1,PAX8,HAND2,SIRT5,SIRT4,AGT,BAG3,NFE2L2,CXCR2,CAMK2A,GNB1,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,TIGAR,NKX2-5,HEY2	grey	VSMC_M10
GO:0017062	0.36	0.85	6	9	respiratory chain complex III assembly	BP	1	LYRM7,UQCC1,BCS1L,SLC25A33,C12orf73,UQCC2	grey	VSMC_M10
GO:0034551	0.36	0.85	6	9	mitochondrial respiratory chain complex III assembly	BP	1	LYRM7,UQCC1,BCS1L,SLC25A33,C12orf73,UQCC2	grey	VSMC_M10
GO:0070102	0.36	0.79	12	20	interleukin-6-mediated signaling pathway	BP	1	ST18,CEBPA,FER,RIPK1,STAT3,IL6R,JAK1,PTPN2,GFI1,MIR125B1,MIR125A,C1QTNF4	grey	VSMC_M10
GO:1990748	0.36	0.72	45	79	cellular detoxification	BP	1	LTC4S,APOM,PRXL2C,KDM3B,FANCC,PIM1,ALDH1A1,TXNRD1,PRDX1,ADH5,CAT,ALB,PXDN,MGST2,TXNRD3,DHFR,ESD,AKR1A1,GSTK1,PRDX3,CYGB,PXDNL,GLRX,GPX8,TP53INP1,ABCG2,FBLN5,MARC2,MARC1,NFE2L2,DUOX1,GCH1,ABCB6,RDH11,SOD3,GSTZ1,MPO,TXNDC2,PARK7,NQO1,MIR21,HBA2,TXN,PTGES,ADH4	grey	VSMC_M10
GO:0140131	0.36	0.83	7	11	positive regulation of lymphocyte chemotaxis	BP	1	CCL27,OXSR1,PTK2B,TMEM102,CCL5,CCL7,WNT5A	grey	VSMC_M10
GO:0099590	0.36	0.82	8	13	neurotransmitter receptor internalization	BP	1	USP46,EPS15,AP2M1,CALY,DNM3,AP2B1,CACNG7,CACNG5	grey	VSMC_M10
GO:0044764	0.36	0.82	8	13	multi-organism cellular process	BP	1	EPS15,NECTIN2,FCHSD2,FCHSD1,GAS6,TPCN1,PIKFYVE,PI4KA	grey	VSMC_M10
GO:0071625	0.36	0.82	8	13	vocalization behavior	BP	1	SHANK1,MYH14,FOXP2,NLGN4Y,NRXN2,DLG4,NLGN3,NRXN3	grey	VSMC_M10
GO:0051645	0.36	0.82	8	13	Golgi localization	BP	1	YWHAZ,ARHGAP21,COPG1,HOOK3,TBCCD1,PDCD10,DAB1,RIPOR1	grey	VSMC_M10
GO:0071902	0.37	0.69	93	170	positive regulation of protein serine/threonine kinase activity	BP	1	MAP3K5,STK3,MAP3K4,AGER,TAB1,CCND3,KIT,ROR2,EPGN,ETAA1,TGFA,EGFR,ARHGEF5,TLR4,CCNY,SLC8A2,MAPRE3,RALB,SPRY2,NEK10,RPTOR,TCIM,FLT1,TRAF6,ROBO1,PTK2B,RASGRP1,RAPGEF2,TIAM1,PKD2,STK4,NOD2,TAOK3,CD40,IGF2,BMPR1B,CCND1,MAP2K6,ADRA2A,FAM20A,AJUBA,KRAS,EGF,SPATC1L,CIB1,DVL3,SYAP1,STRADA,CDKN1B,MAP3K11,ADAM8,FZD5,CEMIP,DBF4B,MAP4K2,DDX3X,DUSP19,PDCD10,SLC27A1,EPHA4,MAGED1,DVL2,BMPR1A,PSEN1,FGF18,MAP2K1,PIK3R5,MAP2K5,CALM1,PSMD10,INSR,CSF1R,CDK5R1,GHR,TAOK1,MLST8,PKD1,TRAF2,MTCP1,PSRC1,DAB2IP,RHOA,S100A12,IRGM,WNT5A,SPDYA,RGCC,DAZAP2,HRAS,MAP2K7,C3orf58,FGF1,PDGFD	grey	VSMC_M10
GO:0031018	0.37	0.76	18	31	endocrine pancreas development	BP	1	ONECUT2,BAK1,SMO,CDK6,RFX3,SOX9,GIPR,MNX1,ARNTL,NKX6-1,ZBED6,SIDT2,MEN1,IL6R,GATA6,PDPK1,SOX4,WNT5A	grey	VSMC_M10
GO:0030888	0.37	0.74	24	42	regulation of B cell proliferation	BP	1	IL5,TNFRSF13C,TNFRSF21,PELI1,TLR4,BMI1,PAWR,NCKAP1L,CASP3,MEF2C,IL7,CD40,BCL6,RC3H1,CD38,BST1,CARD11,CHRNB2,BTK,CD74,CD320,TICAM1,VAV3,TNFSF13B	grey	VSMC_M10
GO:0015937	0.37	0.83	7	11	coenzyme A biosynthetic process	BP	1	PPCS,PANK2,PANK1,SLC25A16,COASY,PANK3,PANK4	grey	VSMC_M10
GO:0002504	0.37	0.79	11	18	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TRAF6,MARCH8,FCER1G,PIKFYVE,CTSV,DNM2,CD74	grey	VSMC_M10

GO:0001913	0.37	0.79	12	20	T cell mediated cytotoxicity	BP	1	STX7,AGER,HLA-DRA,NECTIN2,PVR,SLC22A13,NCKAP1L,CTSH,IL12A,PPP3CB,IL7R,FADD	grey	VSMC_M10
GO:1901096	0.37	0.82	8	13	regulation of autophagosome maturation	BP	1	TMEM39A,RUBCN,TBC1D25,PHF23,AC138894.1,SMCR8,CLEC16A,IRGM	grey	VSMC_M10
GO:0007185	0.37	0.88	4	6	transmembrane receptor protein tyrosine phosphatase signaling pathway	BP	1	FRS2,PTN,PTPRF,TRIO	grey	VSMC_M10
GO:0032494	0.37	0.83	7	11	response to peptidoglycan	BP	1	IRF5,C5AR1,MYD88,RIPK2,NOD2,DEFB124,INAVA	grey	VSMC_M10
GO:0001502	0.37	0.80	9	15	cartilage condensation	BP	1	MAPK14,ROR2,MYCN,SOX9,SOX6,BMPR1B,THRA,PKD1,OTOR	grey	VSMC_M10
GO:0006399	0.37	0.69	90	162	tRNA metabolic process	BP	1	MARS,ADAT2,RPP21,TRMU,TRMT11,C9orf64,EXOSC3,MTO1,TSEN34,ELP1,PUS10,TRIT1,QRSL1,DUS4L,NSUN6,THUMPD3,DPH3,HARS,HARS2,TRMT6,TRNT1,CARS2,LARS,THUMPD2,TRMT9B,ELP4,POP4,CLP1,ELP3,BCDIN3D,TPRKB,NSUN3,OSGEPL1,RPP40,WARS2,CDKAL1,GATC,POP5,RPUSD4,YARS2,TRMT10A,ZBTB8OS,QTRT2,TYW1B,TYW5,TRUB1,RTRAF,TARS2,DALRD3,LCMT2,METTL8,ELP6,METTL2B,KIAA0391,TRMT1L,LARS2,POP7,DARS2,TRPT1,ALKBH8,TRMT5,FARSB,HSD17B10,MTFMT,ALKBH1,THG1L,QTRT1,EARS2,ELP2,THUMPD1,METTL6,PUSL1,LRRC47,POLR3K,KARS,ADAT1,AARS,DUS2,CTU1,MARS2,RPP38,TRMT10B,DTD1,TP53RK,TRMT61A,DTD2,TRMT10C,RPP30,TRMT61B,TYW3	grey	VSMC_M10
GO:0045050	0.37	0.85	6	9	protein insertion into ER membrane by stop-transfer membrane-anchor sequence	BP	1	EMC2,EMC10,EMC3,EMC4,EMC6,EMC7	grey	VSMC_M10
GO:0031345	0.37	0.69	82	150	negative regulation of cell projection organization	BP	1	LRP1,SEMA6A,TBC1D30,FSTL4,SYNGAP1,SEMA4D,SEMA4C,RTN4,RUFY3,ACP4,LPAR1,EPHA7,HDAC2,TSKU,SPRY2,PRNP,SEMA3D,SPART,SEMA3A,ULK1,DPYSL3,RYK,CBFA2T2,SEMA4F,TLX2,RAPGEF2,DGUOK,PAQR3,ARHGAP24,SEMA3G,SPP1,SEMA4G,MYLIP,SRGAP2C,KIAA0319,PPP3CA,TRPV4,SEMA3F,KREMEN1,CIB1,CERS2,NFATC4,PTPRO,INPP5J,LIMK2,LRIG2,WNT3,SEMA6D,TNR,DNM3,RAP1GAP,CD38,CRMP1,EPHA4,GAK,STX1B,PSEN1,SEMA4A,ITGA3,TRIM46,EFNA1,NTN1,SNAPIN,DNM2,RIT2,ARHGAP44,EVL,CDK5R1,THOC2,DAB1,ARHGAP4,PLXNA3,CDK10,TSC1,GFI1,ODF2L,RHOA,RTN4RL1,THY1,WNT5A,YWHAH,EFNB3	grey	VSMC_M10
GO:0008347	0.37	0.74	23	40	glial cell migration	BP	1	LRP1,TSPO,SUN2,MBOAT7,RTN4,P2RY1,TIAM1,SRGAP2C,TGFB2,DISC1,CERS2,EPHA4,ATP1B2,CCL2,CDK5R1,DAB1,LRP8,DAB2IP,MIR222,ADGRG1,FOXG1,LAMB1,CSPG4	grey	VSMC_M10
GO:0090322	0.37	0.77	16	27	regulation of superoxide metabolic process	BP	1	FPR2,EGFR,DHFR,HVCN1,F2RL1,FBLN5,AGT,NFE2L2,MAPT,GCH1,BST1,ITGAM,GNAI3,CYBA,MIR21,MIR27B	grey	VSMC_M10
GO:0033539	0.37	0.83	7	11	fatty acid beta-oxidation using acyl-CoA dehydrogenase	BP	1	ETFB,ETFDH,IVD,ACADL,ACADVL,GCDH,ACADM	grey	VSMC_M10
GO:1900037	0.37	0.81	8	13	regulation of cellular response to hypoxia	BP	1	TMBIM6,AJUBA,USP19,HYOU1,KCNK2,PINK1,MIR21,NOL3	grey	VSMC_M10
GO:0062125	0.37	0.76	16	27	regulation of mitochondrial gene expression	BP	1	SHMT2,TSFM,RMND1,LRPPRC,C6orf203,MRPS27,NSUN3,RPUSD4,RCC1L,MTG2,COA3,ALKBH1,METTL4,RPUSD3,UQCC2,TRMT10C	grey	VSMC_M10
GO:0001964	0.37	0.81	8	13	startle response	BP	1	PRKN,GRIN2D,CHD8,SLC6A3,BACE1,KCNA1,MECP2,GRID2	grey	VSMC_M10
GO:0070373	0.37	0.73	30	53	negative regulation of ERK1 and ERK2 cascade	BP	1	SEMA6A,FBLN1,WNK2,ITGB1BP1,VRK3,TLR4,SPRY1,PHB,SPRY2,ARRB1,SPRED3,DUSP6,SIRT3,TBC1D10C,GPER1,DLG1,DUSP10,RGS14,SYNJ2BP,TNIP1,PTPN2,DAB2IP,MIR21,CHRNA10,DUSP26,DUSP1,DUSP4,C3orf33,LIF,C1QL4	grey	VSMC_M10
GO:0009650	0.37	0.83	7	11	UV protection	BP	1	CAT,ERCC1,ERCC2,ERCC3,SCARA3,ERCC4,SDF4	grey	VSMC_M10
GO:0072243	0.37	0.80	9	15	metanephric nephron epithelium development	BP	1	POU3F3,OSR1,SOX9,PAX8,PKD2,PAX2,PKD1,SOX8,LIF	grey	VSMC_M10
GO:0044088	0.37	0.74	24	42	regulation of vacuole organization	BP	1	PIP4K2C,RNF5,PIP4K2A,RALB,TMEM106B,RAB5A,FEZ2,ULK1,TBC1D12,SEC22B,TMEM39A,ADPRH,MTMR3,RAB1B,PIKFYVE,TBC1D14,PINK1,PHF23,ANXA2,SMCR8,IFT20,MTM1,KIAA1324,SH3GLB1	grey	VSMC_M10
GO:0014046	0.37	0.78	12	20	dopamine secretion	BP	1	PRKN,SYT1,SYT9,DTNBP1,SYT8,GRM2,RAB3A,PINK1,SYT7,SYT11,CHRNB2,ABAT	grey	VSMC_M10
GO:0014059	0.37	0.78	12	20	regulation of dopamine secretion	BP	1	PRKN,SYT1,SYT9,DTNBP1,SYT8,GRM2,RAB3A,PINK1,SYT7,SYT11,CHRNB2,ABAT	grey	VSMC_M10
GO:0086070	0.37	0.85	5	8	SA node cell to atrial cardiac muscle cell communication	BP	1	SCN5A,RYR2,ANK2,CACNA1G,HCN4	grey	VSMC_M10
GO:0031114	0.37	0.76	16	28	regulation of microtubule depolymerization	BP	1	CLASP2,TRIM54,NAV3,SPEF1,ATXN7,KATNB1,TRPV4,TTBK2,CIB1,CAMSAP3,TAOK1,APC2,CAMSAP1,APC,MAP1A,MAP6D1	grey	VSMC_M10
GO:0097479	0.37	0.73	26	46	synaptic vesicle localization	BP	1	AP3S1,KIF5A,PRKN,BRSK1,AP3M2,KIF5C,LIN7A,TMEM230,SYNJ1,AP3B1,DTNBP1,CNIH2,SPG11,BLOC1S6,RAB3A,PINK1,SYN1,AP3M1,SLC2A4,NLGN2,TRIM46,SNAPIN,DNM2,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0043506	0.37	0.73	26	46	regulation of JUN kinase activity	BP	1	MAP3K5,TNXB,MAP3K4,AGER,ROR2,DNAJA1,ARHGEF5,TRAF6,PTK2B,TIAM1,DTNBP1,TAOK3,PDCD4,DVL3,MAP3K11,AIDA,FZD5,DUSP10,MAP4K2,DUSP19,EPHA4,DVL2,TRAF2,DAB2IP,WNT5A,MAP2K7	grey	VSMC_M10
GO:0050671	0.37	0.71	46	82	positive regulation of lymphocyte proliferation	BP	1	AGER,IL5,HLA-DPB1,TNFRSF13C,NCK2,PELI1,TLR4,IL15,BMI1,MYD88,TGFBR2,NCKAP1L,SLC7A1,TRAF6,IL1A,MEF2C,IL7,RIPK2,ZNF335,CD40,IGF2,ICOSLG,GPAM,CD28,BCL6,IL12A,CD38,BST1,STAT5B,FOXP3,RASAL3,CARD11,CHRNB2,CD74,CCL5,CD320,TICAM1,DNAJA3,VAV3,MIR21,FADD,CD46,CD70,TNFSF9,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0007141	0.37	0.78	12	20	male meiosis I	BP	1	MOV10L1,DMC1,FOXJ3,ING2,HSF2BP,SPO11,RAD51C,MEIOB,UBB,SYCP3,FOXJ2,ZSCAN21	grey	VSMC_M10
GO:0045651	0.37	0.81	8	13	positive regulation of macrophage differentiation	BP	1	TRIB1,HSF1,ROR2,RIPK1,HCLS1,FADD,CASP8,LIF	grey	VSMC_M10

GO:0043269	0.37	0.66	240	444	regulation of ion transport	BP	1	NEDD4L,ATP8B1,STAC3,MAPK8IP2,SLC12A2,KCNV1,PRRT1,PRKN,TSPO,GOPC,BAK1,CATSPER3,MCHR1,KCNJ4,PLA2G6,CHRNA3,ABCB1,CLIC5,WNK2,TSPAN13,PRKCE,KCNQ4,SHANK1,SLC31A2,HECW1,TCAF2,CLCN1,SFRP4,KEL,ATG5,OSR1,SPHK2,KCNJ14,TRPC3,SLC26A5,KCNRG,CACNB2,STAC,OXSR1,SCN5A,SCN1A,GPD1L,SYT1,CACNB4,EFHB,NALCN,PRNP,DIAPH1,P2RX2,CLIC1,ARL6IP5,SYT9,KCNIP3,PXK,SLMAP,SLC43A1,GLRX,P2RX3,ORAI1,MEF2C,TMBIM6,P2RX7,HVCN1,KCNH3,P2RY1,PTK2B,KCNJ11,TPCN1,SLC8B1,HOMER1,IFNGR2,STC1,KCNJ3,F2R,TESC,RIPK1,ANO6,CRY2,KCNK15,ABCC2,KCNE2,PKD2,PLA2R1,CASQ2,KCNJ15,CNTN1,DTNBP1,KCNIP2,CHRM3,RYR2,SYT8,FAM173B,GRM2,PM20D1,CALHM1,PKP2,SIK1,HECW2,KCNJ2,SLC38A3,MAP2K6,ADRA2A,SLC30A10,TCIRG1,COX17,SCN2A,ISCU,KCNB1,EGF,KCNG1,SCN7A,EPB41,OPRD1,UBASH3B,ANK2,GPER1,KLHL24,ABCB11,AGT,ACE2,ATP1A2,SLC9A1,PLPP4,PER2,C4orf3,CASQ1,SNX4,NTSR1,SCN4B,CNIH2,CLIC4,DNAJC30,NOS1AP,HOMER2,CATSPER2,DLG1,KCNK7,PLA2G4A,IL16,CEMIP,SESTD1,CASK,PTPN6,KCNK4,HTT,RAB3A,PINK1,CAMK2G,ATP1B1,KCNA1,ARL6IP1,KCNMA1,CHRM1,KCNH4,GNB5,KCND1,MINK1,HAP1,DLG4,PSEN2,SYT7,NLGN2,CNIH3,WNK3,STAC2,CACNB1,ATP1B2,PSEN1,KCNAB3,CACNA1A,SYT11,KCNIP1,HCN3,NLGN3,CACNA1G,CHRNB2,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,TRPV2,CAMK2A,CCL5,CCL2,ASIC2,KCNJ18,ABAT,FMR1,GABRE,INPP5K,TRPV3,PDPK1,P2RX1,CACNA1B,RNF207,CACNA1H,PARK7,KCNC4,AMIGO1,CYBA,JPH3,ATP2C2,LCN2,STXBP1,WWP2,RRAD,MIR21,MIR24-1,RHOA,DMD,GPR35,JPH2,CA2,KCNH2,FGF11,THY1,S	grey	VSMC_M10
GO:0035137	0.37	0.77	14	24	hindlimb morphogenesis	BP	1	OSR2,PITX1,PTCH1,TFAP2B,OSR1,RARB,FMN1,RPGRIP1L,WNT3,BMPR1A,MED1,TBX4,GPC3,ALX3	grey	VSMC_M10
GO:0050999	0.37	0.75	18	31	regulation of nitric-oxide synthase activity	BP	1	ZDHHC21,NOD1,EGFR,NOSIP,DHFR,ACVR2A,IL1A,PIK3CB,PTK2B,TERT,KRAS,NOS1AP,GCH1,CALM1,GLA,TERF2,MIR27B,FCER2	grey	VSMC_M10
GO:0043507	0.37	0.75	20	35	positive regulation of JUN kinase activity	BP	1	MAP3K5,MAP3K4,AGER,ROR2,ARHGEF5,TRAF6,PTK2B,TIAM1,TAOK3,DVL3,MAP3K11,FZD5,MAP4K2,DUSP19,EPHA4,DVL2,TRAF2,DAB2IP,WNT5A,MAP2K7	grey	VSMC_M10
GO:0035909	0.37	0.76	16	28	aorta morphogenesis	BP	1	LRP1,FOXH1,SRF,TFAP2B,JAG1,EYA1,TGFB2,EFEMP2,BMPR1A,RBPJ,TBX2,ENG,SOX4,ACVRL1,SIX1,HEY2	grey	VSMC_M10
GO:0060045	0.37	0.77	14	24	positive regulation of cardiac muscle cell proliferation	BP	1	GLI1,MAPK14,PIM1,MEF2C,TBX5,MAPK1,BMPR1A,RBPJ,TBX2,GATA6,MIR199A1,MIR222,HEY2,WNT2	grey	VSMC_M10
GO:0045779	0.37	0.83	7	11	negative regulation of bone resorption	BP	1	TNFAIP3,TNFRSF11B,P2RX7,GPR137B,UBASH3B,GPR137,CD38	grey	VSMC_M10
GO:0005977	0.37	0.72	32	57	glycogen metabolic process	BP	1	GNMT,PYGB,RUBCNL,KHK,EPM2AIP1,PRKAG2,PPP1CB,AKT2,PPP1R3B,GBE1,SORBS1,PFKM,IGF2,NHLRC1,PHKB,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PHKA2,PYGM,PYGL,PRKAG3,PPP1R3F,PHKA1,INSR,LEPR,INPP5K,AGL,ACADM,PPP1R1A	grey	VSMC_M10
GO:0007042	0.37	0.83	7	11	lysosomal lumen acidification	BP	1	PPT1,TMEM106B,TMEM9,AC138894.1,CLN6,SNAPIN,TMEM199	grey	VSMC_M10
GO:0033292	0.37	0.87	4	6	T-tubule organization	BP	1	MYOF,DYSF,ANK2,SYPL2	grey	VSMC_M10
GO:0071286	0.37	0.87	4	6	cellular response to magnesium ion	BP	1	RYR3,SLC41A1,KCNA1,SLFN14	grey	VSMC_M10
GO:0010694	0.38	0.87	4	6	positive regulation of alkaline phosphatase activity	BP	1	MEF2C,GPLD1,SMAD3,PPARGC1B	grey	VSMC_M10
GO:0051150	0.38	0.75	18	31	regulation of smooth muscle cell differentiation	BP	1	NFATC1,SRF,KIT,ANKRD17,PDCD4,GPER1,EFEMP2,FOXO4,RBPMS2,MECP2,ENG,NFATC3,MIR21,MIR125B1,MIR22,PRDM6,EREG,HEY2	grey	VSMC_M10
GO:0010661	0.38	0.77	13	22	positive regulation of muscle cell apoptotic process	BP	1	MAP3K5,CDKN2A,ARRB1,STK4,PDCD4,AGT,IL12A,CXCR2,RBM10,MFN2,CAMK2A,MIR24-1,TIGAR	grey	VSMC_M10
GO:0061323	0.38	0.80	9	15	cell proliferation involved in heart morphogenesis	BP	1	PIM1,SOX9,HAND2,EYA1,TBX5,RBPJ,MKS1,ISL1,SIX1	grey	VSMC_M10
GO:2000136	0.38	0.80	9	15	regulation of cell proliferation involved in heart morphogenesis	BP	1	PIM1,SOX9,HAND2,EYA1,TBX5,RBPJ,MKS1,ISL1,SIX1	grey	VSMC_M10
GO:0002544	0.38	0.82	7	11	chronic inflammatory response	BP	1	TNFAIP3,UNC13D,AHCY,FOXP3,S100A8,CCL5,PTGES	grey	VSMC_M10
GO:0062208	0.38	0.75	19	33	positive regulation of pattern recognition receptor signaling pathway	BP	1	USP15,HSPA1B,NINJ1,RTN4,ANKRD17,SLC46A2,PELI1,RSAD2,TLR4,PUM2,MFHAS1,NR1H3,F2RL1,OASL,TLR5,DDX3X,WDFY1,CYBA,ZCCHC3	grey	VSMC_M10
GO:0018149	0.38	0.80	9	15	peptide cross-linking	BP	1	NDNF,EVPL,DCN,DSP,TGM1,FN1,SPOCK2,COL3A1,ABCA7	grey	VSMC_M10
GO:0002793	0.38	0.71	37	66	positive regulation of peptide secretion	BP	1	LRP1,PLA2G6,PRKCE,EGFR,TRPM4,GIPR,AIMP1,SIRT3,OSBP,NNAT,PFKM,NKX6-1,GPLD1,TCF7L2,PFKFB2,GPER1,GLUL,MCU,PPP3CB,CD38,MPC2,NLGN2,TARDBP,STX4,RAB8B,GPR68,S100A8,ISL1,OXCT1,ABAT,NADK,BAIAP3,LRRC8A,FGA,SOX4,CRH,DOC2B	grey	VSMC_M10
GO:0042276	0.38	0.87	4	6	error-prone translesion synthesis	BP	1	POLI,REV1,REV3L,PRIMPOL	grey	VSMC_M10
GO:0032872	0.38	0.68	81	148	regulation of stress-activated MAPK cascade	BP	1	PHLPP1,MAP3K5,STK3,MAPK8IP2,MAP3K4,PRKN,AGER,MYC,GADD45G,KLHL31,PRDX1,SEMA4C,DNAJA1,FKTN,EMC10,MTURN,NOD1,EGFR,TLR4,TRAF1,SDCBP,MYD88,ZMYND11,PLCB1,EIF2AK2,RELL2,SEMA3A,SH3RF2,ARL6IP5,MFHAS1,TRAF6,EPHB1,HAND2,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,TRPV4,PDCD4,TGFB2,NCF1,TRAF5,FZD7,MAP3K3,MAGI3,DLG1,MAP3K11,AIDA,DUSP10,MBIP,MEN1,MAP4K2,DUSP19,PDCD10,PINK1,LTBR,MAPK1,MINK1,GPS2,RELL1,TAOK2,MAPK3,MAP2K1,NCOR1,TRAF3,TAOK1,SERPINF2,MAPK8IP3,TRAF2,MARVELD3,DAB2IP,ZNF622,WNT5A,GADD45A,INAVA,DUSP1,DUSP22,HRAS	grey	VSMC_M10
GO:0060013	0.38	0.87	4	6	righting reflex	BP	1	USP46,SLC1A1,SHANK1,ALDH1A3	grey	VSMC_M10
GO:1901607	0.38	0.72	28	49	alpha-amino acid biosynthetic process	BP	1	GLS2,SHMT2,PYCR3,PSAT1,MTAP,DHFR,APIP,SERINC5,ENOPH1,SDSL,ASNSD1,GLS,MTRR,ASL,MTR,CBSL,OAT,GLUL,PLOD3,CPS1,AASDHPPT,AC138894.1,SHMT1,PARK7,ASS1,MTHFD2L,PHGDH,PCBD2	grey	VSMC_M10
GO:2001223	0.38	0.87	4	6	negative regulation of neuron migration	BP	1	NRG1,COL3A1,STAT3,ADGRG1	grey	VSMC_M10
GO:0034471	0.38	0.78	12	20	ncRNA 5'-end processing	BP	1	RPP21,POP4,RPP40,POP5,NOP9,KIAA0391,POP7,HSD17B10,THG1L,RPP38,TRMT10C,RPP30	grey	VSMC_M10

GO:0032365	0.38	0.74	20	35	intracellular lipid transport	BP	1	CPT1B,SERAC1,PIP4K2A,OSBP,COL4A3BP,CPT1A,SLC25A20,OSBPL2,ABCA12,SYT7,ANXA2,ABCD4,LDLR,NPC1,ABCD3,VPS4A,MIR27B,LDLRAP1,STARD4,SGPP1	grey	VSMC_M10
GO:0008211	0.38	0.81	8	13	glucocorticoid metabolic process	BP	1	CYP21A2,DKK3,WNT4,DGKQ,MECP2,CACNA1H,HSD11B2,YWHAH	grey	VSMC_M10
GO:0007267	0.38	0.64	614	1146	cell-cell signaling	BP	1	NFATC1,LRP1,RPS12,STAC3,GLI1,KIF5A,PDE7B,TNFAIP3,STK3,SNCAIP,MAPK8IP2,SLC12A2,FZD6,RIMS2,PRRT1,PRKN,AGER,GDF9,TCF7,SYNGAP1,UBE2B,RSPO3,RNF146,CXCL14,AKAP7,GRM4,LY6E,GRAP2,EXOC4,ATF4,SYNGR1,MAPK14,NTRK2,CBY1,CSNK1E,PLA2G6,PICK1,SOX10,BTBD9,SMO,DAAM2,MDFI,GUCA1B,CHRNA3,TEK,LRRC4,GRM8,CHRNA5,CRY1,PTK7,SRF,GABRA1,APBA1,CDK14,FZD1,CCL27,PHF24,USP46,RFX3,KIT,SLC1A1,TFAP2B,ROR2,DLX5,WNK2,SOSTDC1,GABBR2,IL11,BRSK1,PRKCE,RIMS1,PPP2R1A,HMGN3,RIMS3,ACP4,SHANK1,CYB5R4,PPT1,AREG,BMP8A,CRHR2,GJA10,SLC1A4,RSPO1,PTN,DGKI,GRB10,TNC,ATP6V1C2,EGFR,HECW1,FUZ,NCDN,GRIK2,DLGAP3,GJB5,AMPH,IL15,SFRP4,CCNY,DKKL1,VPS35,SDCBP,TRPM4,SLC7A11,FOXO3,PPFIA3,LIN7B,NTF4,FGF21,PRKAR2B,WISP3,GRIN2D,MTMR2,NAPA,SLC8A2,PANX1,PTGIR,GAD2,SOX9,GIPR,PPM1N,CACNB2,DLG2,LRRFIP2,GLI2,PCDH8,GRIK5,RAF1,KLF5,SCN5A,NAPB,SCEL,TSKU,PLAT,WNT11,KPNA2,ABCC4,CHRNA6,RBMS3,C1QTNF1,FARP1,CHD8,FCHSD2,SYT1,CACNB4,UBAC2,RAB5A,LIN7A,PLCB1,PLCL2,FERMT1,RAC3,PRNP,ADRA1D,SPEF1,FCHSD1,PCDH1,P2RX2,AIMP1,NRG1,SIRT3,PTPRA,MITF,STX2,CALCOCO1,RYK,SYT9,ADRA2B,SNPH,NR1H4,EPHB1,PLK2,PFDN5,NDUFAF2,FAM3D,HTR7,FAM107A,PAX8,FGFBP3,NR4A1,PXK,ABHD6,OSBP,CLSTN2,CTND1,DKK3,TRABD2A,PCSK1,P2RX3,CHRM5,ARNTL,ERC2,SCG5,FZD3,MEF2C,TMEM131L,ASIC1,SEMA4F,IL7,P2RX7,DLGAP4,CSNK2A2,GUCY1A1,GUCY1B1,CUX2,P2RY1,PTK2B,LMBR1L,MME,RAPGEF2,KCNJ11,CCL17,EIF2AK4,NNAT,TIAM1,FGF5,RAB11FIP5,OTULIN,PFKM,SYNJ1,SLC8B1,HOMER1,NKX3-1,NKX6-	grey	VSMC_M10
GO:0017158	0.38	0.76	15	26	regulation of calcium ion-dependent exocytosis	BP	1	SYT1,SYT9,SYT8,HYAL3,ADRA2A,KCNB1,STX1A,RAP1B,SYT7,SYT11,CACNA1G,SCAMP5,CACNA1H,STXBP1,DOC2B	grey	VSMC_M10
GO:0030514	0.38	0.73	22	39	negative regulation of BMP signaling pathway	BP	1	LEMD2,SOSTDC1,BMPER,SPART,SORL1,HTRA1,CHRD,DLX1,CTDSPL2,HTRA3,FBN1,GREM2,RBPMS2,TOB1,CHRDL1,TWSG1,SKI,FSTL3,LEMD3,NOG,WNT5A,UBE2D1	grey	VSMC_M10
GO:0003211	0.38	0.87	4	6	cardiac ventricle formation	BP	1	HAND2,MEF2C,TBX5,SOX4	grey	VSMC_M10
GO:0021522	0.38	0.77	13	22	spinal cord motor neuron differentiation	BP	1	PTCH1,GLI2,IFT172,MNX1,SUFU,GIGYF2,MDGA2,SCYL3,CLN8,ISL1,SOX4,ISL2,LBX1	grey	VSMC_M10
GO:0045948	0.38	0.77	13	22	positive regulation of translational initiation	BP	1	HABP4,CDC123,EIF2AK4,RPS6KB2,YTHDF2,YTHDF1,UHMK1,DDX3X,POLR2G,LARP1,CCL5,IMPACT,PPP1R15A	grey	VSMC_M10
GO:0035092	0.38	0.87	4	6	sperm chromatin condensation	BP	1	SYCP1,CHD5,SYCP3,RNF8	grey	VSMC_M10
GO:0021602	0.38	0.76	14	24	cranial nerve morphogenesis	BP	1	ATP8B1,PLXNA4,SEMA3A,EPHB1,TFAP2A,PAX2,SEMA3F,ADARB1,CHRNB2,PLXNA3,MAFB,HOXB3,SIX1,HOXA3	grey	VSMC_M10
GO:1900006	0.38	0.79	9	15	positive regulation of dendrite development	BP	1	PTN,ALK,TMEM106B,OPA1,CYFIP1,CRTC1,ZDHHC15,LRP8,DAB2IP	grey	VSMC_M10
GO:0045588	0.38	0.87	4	6	positive regulation of gamma-delta T cell differentiation	BP	1	NCKAP1L,SOX13,STAT5B,SOX4	grey	VSMC_M10
GO:0030593	0.38	0.71	34	60	neutrophil chemotaxis	BP	1	RAC2,CXCL8,C5AR2,C5AR1,NCKAP1L,CCL17,NOD2,GBF1,DNM1L,TGFB2,MOSPD2,FCER1G,PIKFYVE,MCU,CXCR2,BST1,DAPK2,S100A8,CD74,CCL14,CCL5,CCL7,CCL2,CCL25,VAV1,PIP5K1C,MPP1,BSG,VAV3,CCL16,S100A12,DPP4,CXCL6,CCL22	grey	VSMC_M10
GO:0099509	0.38	0.87	4	6	regulation of presynaptic cytosolic calcium ion concentration	BP	1	CACNB2,P2RY1,ATP2B3,P2RX1	grey	VSMC_M10
GO:0001865	0.38	0.87	4	6	NK T cell differentiation	BP	1	TGFBR2,TOX,AP3B1,ZBTB7B	grey	VSMC_M10
GO:0097062	0.38	0.79	9	15	dendritic spine maintenance	BP	1	PICK1,ABHD17B,VPS35,MTMR2,PRNP,HOMER1,ITPKA,ITGA3,INSR	grey	VSMC_M10
GO:0048853	0.38	0.87	4	6	forebrain morphogenesis	BP	1	SMO,SLIT1,WNT5A,OTX1	grey	VSMC_M10
GO:1990264	0.38	0.87	4	6	peptidyl-tyrosine dephosphorylation involved in inactivation of protein kinase activity	BP	1	ACP4,PTPRQ,PTPRO,DUSP10	grey	VSMC_M10
GO:0032927	0.38	0.87	4	6	positive regulation of activin receptor signaling pathway	BP	1	ZC3H3,ACVR2B,ACVR2A,ACVR1B	grey	VSMC_M10
GO:1903779	0.38	0.78	11	19	regulation of cardiac conduction	BP	1	TRPM4,SLC8A2,TBX5,RYR2,ANK2,AGT,ACE2,ATP2A1,ATP2B3,TMEM65,NKX2-5	grey	VSMC_M10
GO:0009209	0.38	0.82	7	11	pyrimidine ribonucleoside triphosphate biosynthetic process	BP	1	NME1,NME4,CTPS2,NME7,NME3,UCK1,NME6	grey	VSMC_M10
GO:0098937	0.38	0.87	4	6	anterograde dendritic transport	BP	1	KIF5A,KIF5C,KIF3B,KIF17	grey	VSMC_M10
GO:0038007	0.38	0.87	4	6	netrin-activated signaling pathway	BP	1	PTK2,UNC5D,UNC5A,TUBB3	grey	VSMC_M10
GO:0007605	0.38	0.69	56	102	sensory perception of sound	BP	1	ATP8B1,MYO1A,EYA4,ALDH7A1,COL11A2,CLIC5,KIT,KCNQ4,GSDME,MYH14,WHRN,SOBP,SLC26A5,MYO3A,MYO7B,EML2,USH1G,MYO7A,SPRY2,MKKS,LRTOMT,AP000812.5,TMTC4,DIAPH1,P2RX2,TUB,CASP3,MARVELD2,EYA1,ADGRV1,USH1C,TFAP2A,PGAP1,MYO3B,COCH,STRC,HOMER2,CDKN1B,LRIG2,CEMIP,CDH23,CHRNB2,POU3F4,OTOA,CRYM,ASIC2,CDC14A,SRRM4,PJVK,CHRNA10,EPS8L2,SIX1,DDIT3,OTOR,TIMM8B,OTOS	grey	VSMC_M10
GO:0036466	0.39	0.87	4	6	synaptic vesicle recycling via endosome	BP	1	AP3B1,DNM1L,GRIPAP1,BTBD8	grey	VSMC_M10
GO:0090493	0.39	0.82	7	11	catecholamine uptake	BP	1	PRKN,MAPK15,SLC6A2,SLC6A3,ACTB,SLC29A4,PARK7	grey	VSMC_M10
GO:0001738	0.39	0.69	46	84	morphogenesis of a polarized epithelium	BP	1	FZD6,RSPO3,PTK7,ROR2,BRSK1,FUZ,INTU,RAB10,WNT11,ACTG1,SPEF1,SYNE4,RYK,TCF15,NPHP1,FZD3,TIAM1,RPGRIP1L,VANGL1,PRICKLE1,NKD1,JHY,ZNRF3,DVL3,FZD7,TRAF3IP1,LAMA5,GRHL3,EXOC5,DAAM1,ARHGEF19,ACTB,DVL2,MKS1,MYO9A,LAMA3,CAMSAP3,LAMA1,IFT20,GPC3,SAPCD2,CELSR2,FOXF1,RHOA,WNT5A,CELSR3	grey	VSMC_M10
GO:0008207	0.39	0.76	13	22	C21-steroid hormone metabolic process	BP	1	TSPO,AKR1B1,DKK3,SRD5A1,DHRS9,WNT4,STAT5B,HSD17B10,DGKQ,SCNN1B,CYP46A1,CACNA1H,DHRS2	grey	VSMC_M10
GO:0033522	0.39	0.75	15	26	histone H2A ubiquitination	BP	1	SKP1,UBE2B,BMI1,RYBP,DDB2,PCGF6,DTX3L,RNF168,BCOR,DDB1,PCGF3,TRIM37,OTUB2,CUL4B,RNF8	grey	VSMC_M10

GO:0045776	0.39	0.76	14	24	negative regulation of blood pressure	BP	1	ADM2,PPARA,SNX5,MKKS,VEGFC,NTSR1,GCH1,SCPEP1,BDKRB1,NOS2,ABAT,TRPV1,GPR37L1,CRH	grey	VSMC_M10
GO:0095500	0.39	0.76	13	22	acetylcholine receptor signaling pathway	BP	1	LY6E,CHRNA3,PLCB1,CHRM5,CHRM4,CHRM3,GRK2,CHRM1,CHRNB2,HRH4,CDK5R1,GNB1,GNA15	grey	VSMC_M10
GO:0032793	0.39	0.78	10	17	positive regulation of CREB transcription factor activity	BP	1	ADGRF1,PRKD2,CD200,OPRD1,TSSK4,CRTC1,CRTC2,RPS6KA5,LRP8,RPS6KA4	grey	VSMC_M10
GO:0033209	0.39	0.70	42	75	tumor necrosis factor-mediated signaling pathway	BP	1	TNFAIP3,HSPA1B,PRKN,TNFRSF13C,TRIM32,TRAF1,FOXO3,TRAF3IP2,IKBKB,GAS6,ST18,TRAF6,PTK2B,OTULIN,F2RL1,RIPK1,PIAS3,SPATA2,TRAF5,PELI3,TNFSF18,BIRC3,SPPL2A,GPS2,TNFRSF1B,PYDC1,TRAF3,PTPN2,PIAS4,CDIP1,SPPL2B,TRAF2,TNFRSF25,MIR27B,MIR24-1,NOL3,CASP8,CD70,COMMD7,CCDC3,TNFSF13B,HIST1H2BJ	grey	VSMC_M10
GO:1904294	0.39	0.80	8	13	positive regulation of ERAD pathway	BP	1	RNFT2,USP13,RNF185,NFE2L2,BCAP31,SGTA,TMEM259,RNFT1	grey	VSMC_M10
GO:1900151	0.39	0.78	10	17	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	BP	1	PABPC1,AGO2,TNRC6B,TNRC6C,CNOT1,TENT4B,RC3H1,TOB1,NANOS1,ZFP36L2	grey	VSMC_M10
GO:0086012	0.39	0.77	11	19	membrane depolarization during cardiac muscle cell action potential	BP	1	TRPM4,CACNB2,SCN5A,SLMAP,KCNJ2,ANK2,ATP1A2,SCN4B,CACNA1G,SCN2B,HCN4	grey	VSMC_M10
GO:0030903	0.39	0.79	9	15	notochord development	BP	1	GLI1,TEAD2,SOX9,GLI2,WNT11,COL13A1,EFNA1,NOG,WNT5A	grey	VSMC_M10
GO:0036158	0.39	0.79	9	15	outer dynein arm assembly	BP	1	LRRC6,ARMC4,DNAH5,ZMYND10,DNAAF2,TTC25,DNAAF4,CCDC151,C16orf71	grey	VSMC_M10
GO:0097485	0.39	0.67	98	182	neuron projection guidance	BP	1	LRP1,SEMA6A,KIF5A,GFRA3,PTK2,PTCH1,PLXNA4,RAC2,SMO,SEMA4D,DLX5,ETV1,SEMA4C,HOXA2,EPHA7,EPHA1,NRCAM,PLXNA1,GLI2,MEGF8,MYCBP2,KIF5C,FEZ2,SEMA3D,PLXNC1,SEMA3A,CHL1,UNC5D,RYK,EPHB1,RET,ROBO1,ROBO2,FZD3,SEMA4F,DPYSL2,SLIT1,TRIO,SEMA3G,CYFIP1,ALCAM,SEMA4G,SIAH1,BMPR1B,BDNF,LGR6,SEMA3F,GAP43,DAG1,LHX9,GBX2,KALRN,LAMA5,YTHDF1,PTPRO,EPHB3,WNT3,KLF7,MYPN,SEMA6D,EPHB4,TNR,CRMP1,EPHA4,LRTM2,UNC5A,SEMA4A,NGFR,EFNA1,NTN1,RPS6KA5,RNF165,BCL11B,LHX1,LAMA3,CDK5R1,ISL1,EMB,LAMA1,L1CAM,NTN3,PLXNA3,BSG,TUBB3,DPYSL5,EFNA4,CNTN2,VASP,FOXG1,ISL2,NOG,WNT5A,CHN1,ARTN,NRXN3,LYPLA2,EFNB3,ISPD	grey	VSMC_M10
GO:0090209	0.39	0.87	4	6	negative regulation of triglyceride metabolic process	BP	1	FBXW7,GPLD1,SIK1,SORL1	grey	VSMC_M10
GO:0003417	0.39	0.79	9	15	growth plate cartilage development	BP	1	COL27A1,SOX9,TSKU,TGFBR2,RARB,STC1,POR,MMP13,THBS3	grey	VSMC_M10
GO:0002790	0.39	0.67	94	172	peptide secretion	BP	1	LRP1,RIMS2,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,CYB5R4,BMP8A,EGFR,TRPM4,GIPR,RAF1,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,PER2,STX1A,PASK,GLUL,SIDT2,SLC16A1,KLF7,VGF,ENY2,ABCA12,MCU,PPP3CB,CAMK2G,PTPRN,CD38,MPC2,ILDR2,SYT7,NLGN2,CPLX1,TARDBP,STX4,RAB8B,UBE2Q1,SYTL4,GPR68,S100A8,CD74,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,TRPV1,BAIAP3,PARK7,LRRC8A,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:0046486	0.39	0.65	172	317	glycerolipid metabolic process	BP	1	PIP4K2C,AVIL,ABHD16A,SYNJ2,SERAC1,TNXB,AGPAT4,AGPAT1,SLC22A4,PNPLA3,PNPLA5,PLA2G6,GPAA1,CWH43,INPP4A,CAT,TMEM246,TMEM86B,PIGF,MBOAT7,PLEK,NR1H2,MBOAT2,DGKI,LPIN1,INPP4B,FIG4,APOB,AGK,FGF21,MTMR2,PIP4K2A,NAPEPLD,FAAH,HADHA,SELENOI,ABHD5,APOC1,LIPE,TAMM41,ITPKC,PIP4P1,MTMR14,PLCB1,PGAP2,CRLS1,CDS2,DDHD2,PANK2,NR1H4,MTMR7,ABHD6,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,GK5,PLCE1,CHRM5,MTMR9,FBXW7,GPD1,SLA2,NR1H3,SERINC5,SYNJ1,LPIN3,CDS1,FITM2,ITPKA,PIGT,PLA2G4B,GPLD1,LPCAT1,SIK1,PGAP1,CPT1A,GPAM,CHKA,PLA1A,ACP6,INPP5A,ABHD4,AJUBA,PITPNM1,ABHD2,MTMR11,SORL1,GNPAT,DGKD,PIGM,BMX,FAM126B,IP6K2,LPGAT1,PIGV,MTMR3,THEM5,PCYT1A,INPP5J,PIGX,PIGZ,PISD,DGKG,PIKFYVE,PLA2G4A,MOGAT3,CPS1,SACM1L,LPCAT3,ABHD12B,GNB3,PIGC,PLCD4,SMPD4,SOCS4,PLA2G16,PI4KA,SLC27A1,ABHD8,DAGLB,PGAP3,PIGH,PI4K2B,LIPC,SOCS7,DGKQ,GDPD3,APOBR,AC138894.1,SEL1L,DGKE,TTC7B,LDLR,GDPD1,PIGL,GDE1,CSF1R,ABHD3,PNPLA6,SREBF1,LPIN2,C3,MPPE1,IMPA2,MTMR12,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,ABCA3,MECP2,AGPAT2,LMF1,PIP5KL1,PLA2G15,FABP5,PNPLA4,PEMT,CNEP1R1,PYURF,LYPLA2,LCLAT1,INSIG2,PIGB,PIGA,INPP1,PTPMT1,DNAJC19,CDIPT	grey	VSMC_M10
GO:0050909	0.39	0.76	13	22	sensory perception of taste	BP	1	ASIC3,P2RX2,P2RX3,ASIC1,CALHM1,RTP4,SCNN1B,ASIC2,GNB1,GNG13,GNAT2,PKD1L3,TAS2R3	grey	VSMC_M10
GO:0099612	0.39	0.87	4	6	protein localization to axon	BP	1	CNTNAP1,TRIM46,EPB41L3,CNTN2	grey	VSMC_M10
GO:0072319	0.39	0.87	4	6	vesicle uncoating	BP	1	SYNJ1,HSPA8,GAK,VPS4A	grey	VSMC_M10
GO:0098532	0.39	0.87	4	6	histone H3-K27 trimethylation	BP	1	SUZ12,CHD5,BEND3,ZNF304	grey	VSMC_M10
GO:0010985	0.39	0.83	6	9	negative regulation of lipoprotein particle clearance	BP	1	APOC1,MYLIP,LRPAP1,MIR199A1,MIR27B,MIR27A	grey	VSMC_M10
GO:1905005	0.39	0.87	4	6	regulation of epithelial to mesenchymal transition involved in endocardial cushion formation	BP	1	TGFBR2,TGFB2,ENG,NOG	grey	VSMC_M10
GO:0086013	0.39	0.79	9	15	membrane repolarization during cardiac muscle cell action potential	BP	1	KCNJ3,KCNE2,KCNIP2,KCNJ2,NOS1AP,ATP1B1,RNF207,KCNH2,KCNJ8	grey	VSMC_M10
GO:0002076	0.39	0.79	9	15	osteoblast development	BP	1	HOXA2,GLI2,PTHLH,SATB2,HDAC4,PTH1R,MEN1,SMAD3,BGLAP	grey	VSMC_M10

GO:0022406	0.39	0.69	42	76	membrane docking	BP	1	STX7,TSNARE1,EXOC4,SCFD2,STX17,PLEK,BVES,PPFIA3,RAB7A,RAB10,SYTL2,RALB,SYT1,CEP290,STX2,SNPH,PEX16,VPS18,KCNB1,PDZD8,STX1A,STX6,NSF,BLOC1S6,MOSPD3,RAB3A,SNAP29,STX5,RAB8A,PSEN2,RAB15,STX1B,STX4,RAB8B,AC138894.1,STX8,RAB3D,CALM1,VMP1,STXBP2,STXBP1,VAMP3	grey	VSMC_M10
GO:0045621	0.39	0.70	40	72	positive regulation of lymphocyte differentiation	BP	1	HLA-DRA,XRCC6,IL4I1,IL15,GLI2,IL15RA,TGFBR2,NCKAP1L,GAS6,PRKDC,SOX12,TOX,IL7,RASGRP1,RIPK2,AP3B1,SOX13,HLX,RUNX3,PPP2R3C,ADAM8,DUSP10,BCL6,VSIR,STAT5B,FOXP3,ZBTB1,ZBTB7B,IL4R,BTK,CD74,NKAP,IL7R,SOCS1,PRKCZ,MIR21,RHOA,SOX4,CD46,TNFSF9	grey	VSMC_M10
GO:0046949	0.39	0.75	14	24	fatty-acyl-CoA biosynthetic process	BP	1	PPT2,ACSL6,PPT1,ELOVL1,ELOVL7,ACSL5,HACD2,ACSBG1,TECR,GCDH,ACACA,ACSBG2,ACSF3,ELOVL3	grey	VSMC_M10
GO:0070327	0.39	0.87	4	6	thyroid hormone transport	BP	1	ABCC2,SLCO1C1,CRYM,SLC7A5	grey	VSMC_M10
GO:0001960	0.39	0.71	33	58	negative regulation of cytokine-mediated signaling pathway	BP	1	IL1R2,PXDN,NR1H2,GAS6,OTUD4,ROBO1,NR1H3,OAS3,NLRC5,F2RL1,YTHDF2,PARP14,PELI3,MUL1,PADI2,GPS2,USP18,PYDC1,DCST1,STAT2,CCL5,PTPN2,PIAS4,MIR21,MIR125B1,MIR27B,MIR24-1,MIR27A,OAS1,NOL3,MIR125A,CCDC3,HIST1H2BJ	grey	VSMC_M10
GO:0006750	0.39	0.80	8	13	glutathione biosynthetic process	BP	1	SLC1A1,CHAC2,MGST2,SLC7A11,GSS,NFE2L2,GGT6,GGT5	grey	VSMC_M10
GO:0032933	0.39	0.79	9	15	SREBP signaling pathway	BP	1	C12orf49,FBXW7,AMFR,ERLIN1,SCAP,LPCAT3,ZBTB7B,SREBF1,INSIG2	grey	VSMC_M10
GO:0071501	0.39	0.79	9	15	cellular response to sterol depletion	BP	1	C12orf49,FBXW7,AMFR,ERLIN1,SCAP,LPCAT3,ZBTB7B,SREBF1,INSIG2	grey	VSMC_M10
GO:0090596	0.39	0.66	107	198	sensory organ morphogenesis	BP	1	FRS2,OSR2,FZD6,BAK1,ATF4,AGTPBP1,NTRK2,RORB,PTK7,SLC1A1,TFAP2B,ROR2,DLX5,TDRD7,SIX2,RDH13,KCNQ4,HOXA2,WHRN,PTN,TSPAN12,SOBP,OSR1,INTU,FOXE3,HDAC2,MYO3A,SOX9,USH1G,GLI2,IFT172,MYO7A,TSKU,SPRY2,DZANK1,JAG1,RARB,FSCN2,CEP290,EPHB1,PAX8,EYA1,PLS1,TENM3,FZD3,USH1C,RPGRIP1L,TFAP2A,PAX2,NKD1,NECTIN3,HDAC1,ALDH1A3,SHROOM2,NRL,GBX2,MYO3B,GRHL3,SP3,STRC,FZD5,STOX1,PRKRA,FBN1,COL5A2,STAT3,NKX3-2,MAPK1,OBSL1,ROM1,MFAP2,DVL2,WDR19,SDK1,TCAP,MFN2,MAPK3,MEGF11,LCTL,POU3F4,NTN1,GSC,TBX2,LHX1,STRA6,YY1,SKI,SOX8,COL5A1,OLFM3,FJX1,CHRNA10,FOXG1,MAFB,CNTF,NOG,THY1,WNT5A,DIO3,OTX1,SIX1,TBC1D20,INSIG2,PITX3,WNT2,COL8A2,ZIC1	grey	VSMC_M10
GO:0007223	0.39	0.86	4	6	Wnt signaling pathway, calcium modulating pathway	BP	1	ROR2,WNT11,NLK,WNT5A	grey	VSMC_M10
GO:0015074	0.39	0.86	4	6	DNA integration	BP	1	GIN1,THAP9,NYNRIN,KRBA2	grey	VSMC_M10
GO:2000300	0.39	0.72	22	39	regulation of synaptic vesicle exocytosis	BP	1	CHRNA5,APBA1,RIMS3,CACNB2,SYT1,RAB5A,P2RY1,VPS18,DTNBP1,DNM1L,ADRA2A,BACE1,CSPG5,RAP1B,CASK,RAB3A,SYN1,CALM1,SNAPIN,PRKCB,FMR1,P2RX1	grey	VSMC_M10
GO:0006651	0.39	0.86	4	6	diacylglycerol biosynthetic process	BP	1	AVIL,PLCE1,GPAM,PLA2G15	grey	VSMC_M10
GO:2000773	0.39	0.79	9	15	negative regulation of cellular senescence	BP	1	CDK6,PRKDC,PLK2,TERT,SLC30A10,MAP3K3,BCL6,TERF2,YBX1	grey	VSMC_M10
GO:1901880	0.39	0.70	34	62	negative regulation of protein depolymerization	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,ADD2,CLASP2,TRIM54,NAV3,SPEF1,LMOD3,ATXN7,LIMA1,KATNB1,DMTN,CARMIL1,LMOD1,ADD3,TTBK2,CIB1,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,CAMSAP3,TAOK1,APC2,CAMSAP1,CARMIL2,APC,MAP6D1	grey	VSMC_M10
GO:0098751	0.39	0.74	17	30	bone cell development	BP	1	MPIG6B,SRF,KIT,PIP4K2A,ABI1,FOXP1,FBXW7,LRRK1,SLC9B2,WASF2,THPO,PTPN6,FBN1,MED1,ANXA2,GPR68,ATP6AP1	grey	VSMC_M10
GO:0060134	0.39	0.86	4	6	prepulse inhibition	BP	1	CHD8,SLC6A3,BACE1,GRID2	grey	VSMC_M10
GO:0006352	0.39	0.68	58	105	DNA-templated transcription, initiation	BP	1	BAZ2A,TBPL1,ESR1,TFB1M,MED30,TAF2,TAF8,SRF,ERCC1,ERCC3,GTF2F2,RSF1,PAXIP1,TAF7,BRF2,GTF2E2,MITF,TAF10,POLR2I,ERCC6,NCOA6,CDK7,TAF9,CCNH,TAF5,CRCP,GTF2E1,TFAM,TAF4,E2F2,CREB1,MED14,TAF6,POLR2G,THRA,MED24,MED1,TAF1,TAF9B,SNAPC5,MED7,TAF4B,RRN3,JUN,TAF13,GTF3C4,MED27,TAF1C,TAF12,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H4D,HIST1H4A,NKX2-5,HIST1H4F,HEY2,GTF2H5	grey	VSMC_M10
GO:0048861	0.39	0.86	4	6	leukemia inhibitory factor signaling pathway	BP	1	CTF1,OSMR,LIFR,LIF	grey	VSMC_M10

GO:1901615	0.39	0.64	207	382	organic hydroxy compound metabolic process	BP	1	RDH5,APOF,ATP8B1,RDH16,CYP27B1,TPH2,SNCAIP,MIOX,SYNJ2,CYP21A2,PRKN,ACO2,HSD17B3,LY6E,AKR1B1,BTBD9,TTC39B,PSAT1,GPR37,ALDH1A1,KIT,SLC1A1,PLPP6,SRD5A3,SPTLC1,IPPK,INPP4A,ADH5,CAT,EPAS1,RDH13,PLEK,DDC,INPP4B,DKKL1,SLC7A11,APOB,SPHK2,DHFR,MTMR2,NAPEPLD,EBP,EBPL,AKR1A1,CUBN,LIPE,PRKAG2,ITPKC,ACER3,TSKU,PIP4P1,SPTLC3,LRTOMT,AP000812.5,PANK2,NR1H4,MTMR7,SDR16C5,SOAT2,CYP7A1,ASAH1,CYP7B1,PAX8,CEBPA,CBR4,OSBP,GK5,RETSAT,DKK3,HAND2,LIMA1,GPD1,EPHX2,CYP2R1,P2RY1,PTK2B,RAPGEF2,SPR,SYNJ1,COQ2,NR4A2,ITPKA,ERLIN1,PLTP,OCA2,SRD5A1,CYB5R1,SLC6A3,ALDH1A3,ABCA5,TGFB2,FMO5,CHKA,ITPK1,INPP5A,NR5A2,ALDH3B2,SNAI1,PFKFB2,MSMO1,THTPA,GPER1,SC5D,ABCB11,DHRS9,IP6K2,DPAGT1,SLCO1C1,PER2,ACTN3,OSBPL2,NTSR1,INPP5J,SCAP,HSD17B7,POR,PTH1R,SORD,DUOX1,PLA2G4A,OSBPL6,ACADL,SOAT1,MOGAT3,TM7SF2,FAH,OSBPL1A,IDH3A,FDX1,COMT,PECR,LPCAT3,PNKD,GNB3,WNT4,CYP27A1,GCH1,HDC,CH25H,LIPA,ACADVL,TKFC,HSD17B10,CLN8,DHRS3,MED1,RDH11,ALDH1A2,FGFR4,LIPC,DGKQ,OSBPL7,PNPO,ITGAM,ERG28,GDPD3,APOBR,CITED1,CHRNB2,CLN6,LDLR,GDPD1,SCNN1B,CRYM,CYP46A1,GDE1,NPC1,SREBF1,LEPR,IMPA2,SLC45A2,ACAA2,ABAT,PIAS4,INPP5K,MECP2,TKTL1,CACNA1H,PARK7,ALDH2,RXRA,CEL,ABCD3,GFI1,NFE2L1,TPK1,PNPLA4,DHDDS,MINPP1,WNT5A,TIGAR,LDLRAP1,DIO3,AMACR,ACER2,LRAT,STARD4,AOC2,INSIG2,RDH14,INPP1,ADH4,PDXP,FGF1,SGPP1,DIO2,PCBD2	grey	VSMC_M10
GO:0051891	0.39	0.86	4	6	positive regulation of cardioblast differentiation	BP	1	TBX5,TGFB2,GATA6,NKX2-5	grey	VSMC_M10
GO:0060232	0.40	0.86	4	6	delamination	BP	1	AKNA,TRPV4,YTHDF2,ABCA12	grey	VSMC_M10
GO:2000197	0.40	0.86	4	6	regulation of ribonucleoprotein complex localization	BP	1	IWS1,SETD2,AKAP8L,SUPT6H	grey	VSMC_M10
GO:0019532	0.40	0.86	4	6	oxalate transport	BP	1	SLC26A10,SLC26A5,SLC26A1,SLC26A2	grey	VSMC_M10
GO:0000245	0.40	0.71	29	51	spliceosomal complex assembly	BP	1	SF3A3,PUF60,YTHDC1,SRSF10,CELF2,CRNKL1,USP39,GCFC2,CELF1,SRSF6,SCAF11,RBM5,ZRSR2,CELF3,GEMIN2,PRPF39,PRPF19,KHDC4,LUC7L3,SLU7,CELF5,LUC7L,RNVU1-6,NOL3,RNU4ATAC,RF00003,SNRPC,RNU2-1,SRSF12	grey	VSMC_M10
GO:0003433	0.40	0.86	4	6	chondrocyte development involved in endochondral bone morphogenesis	BP	1	COL27A1,SOX9,TSKU,TGFBR2	grey	VSMC_M10
GO:0070729	0.40	0.86	4	6	cyclic nucleotide transport	BP	1	ABCC4,ABCC5,LRRC8E,LRRC8A	grey	VSMC_M10
GO:0043376	0.40	0.86	4	6	regulation of CD8-positive, alpha-beta T cell differentiation	BP	1	NCKAP1L,RUNX3,ZBTB7B,SOCS1	grey	VSMC_M10
GO:0010232	0.40	0.69	39	71	vascular transport	BP	1	LRP1,SLC16A7,SLC12A2,AGER,ABCB1,SLC1A1,SLC4A4,SLC1A4,SLC8A2,SLC24A3,ABCC4,SLC7A1,SLC38A2,SLC38A1,ABCC2,ABCG2,SLC2A13,SLC2A10,SLC38A3,SLCO3A1,ABCC5,ATP1A2,SLCO1C1,SLC29A2,SLC16A1,SLC27A1,SLC38A5,SLC4A3,SLC29A4,SLC2A4,ATP1B2,SLC7A3,ABCC3,INSR,LEPR,SLC7A5,FABP5,SLC22A5,KCNJ8	grey	VSMC_M10
GO:0097064	0.40	0.86	4	6	ncRNA export from nucleus	BP	1	PHAX,NOL6,NCBP2,TSC1	grey	VSMC_M10
GO:0008063	0.40	0.86	4	6	Toll signaling pathway	BP	1	PELI1,MYD88,PELI3,TRAF3	grey	VSMC_M10
GO:0051055	0.40	0.71	25	44	negative regulation of lipid biosynthetic process	BP	1	ORMDL2,CYP27B1,DKKL1,APOC1,PIBF1,TRIB3,CYP7A1,DKK3,FBXW7,ORMDL1,ERLIN1,PRMT3,LPCAT1,SIK1,SNAI1,GPER1,SCAP,ACADL,WNT4,SLC27A1,ACADVL,ASXL3,GFI1,INSIG2,CCDC3	grey	VSMC_M10
GO:0097090	0.40	0.83	5	8	presynaptic membrane organization	BP	1	NLGN4Y,NLGN2,NLGN3,CEL,CNTN2	grey	VSMC_M10
GO:0072525	0.40	0.76	13	22	pyridine-containing compound biosynthetic process	BP	1	PSAT1,NMRK1,SLC22A13,IDO2,IDO1,SLC5A8,NUDT12,PARP9,PNPO,NADK,NNMT,NAPRT,NMNAT1	grey	VSMC_M10
GO:0016556	0.40	0.75	14	24	mRNA modification	BP	1	CMTR1,TRMT6,BAG4,WTAP,RPUSD2,TRUB1,METTL8,METTL16,CMTR2,METTL14,TRMT61A,TRMT10C,TRMT61B,CBLL1	grey	VSMC_M10
GO:0051895	0.40	0.77	10	17	negative regulation of focal adhesion assembly	BP	1	LRP1,ITGB1BP1,CLASP2,FAM107A,DMTN,ARHGAP6,APOD,BCAS3,ACVRL1,DUSP22	grey	VSMC_M10
GO:0150118	0.40	0.77	10	17	negative regulation of cell-substrate junction organization	BP	1	LRP1,ITGB1BP1,CLASP2,FAM107A,DMTN,ARHGAP6,APOD,BCAS3,ACVRL1,DUSP22	grey	VSMC_M10
GO:0002707	0.40	0.74	15	26	negative regulation of lymphocyte mediated immunity	BP	1	IL4I1,FOXJ1,NCKAP1L,NOD2,CD96,BCL6,PTPN6,PPP3CB,FOXP3,TBX21,IL7R,CRK,CD46,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0060317	0.40	0.74	16	28	cardiac epithelial to mesenchymal transition	BP	1	RTN4,SPRY1,TGFBR2,JAG1,PDCD4,TGFB2,SNAI1,RBPJ,EFNA1,TMEM100,ENG,MIR21,NOG,HEY2,OLFM1,WNT2	grey	VSMC_M10
GO:0002716	0.40	0.86	4	6	negative regulation of natural killer cell mediated immunity	BP	1	CD96,CRK,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0010719	0.40	0.74	15	26	negative regulation of epithelial to mesenchymal transition	BP	1	FUZ,SPRY1,SPRY2,OVOL2,SPRED3,IL17RD,TBX5,USF3,TGFB2,EFNA1,DAB2IP,NOG,DACT3,SDHAF2,LDLRAD4	grey	VSMC_M10
GO:1903147	0.40	0.86	4	6	negative regulation of autophagy of mitochondrion	BP	1	TSPO,USP30,PINK1,TIGAR	grey	VSMC_M10
GO:0048671	0.40	0.83	5	8	negative regulation of collateral sprouting	BP	1	FSTL4,EPHA7,SPART,ULK1,SPP1	grey	VSMC_M10
GO:0002322	0.40	0.86	4	6	B cell proliferation involved in immune response	BP	1	TLR4,PLCL2,GAPT,CD19	grey	VSMC_M10
GO:0090400	0.40	0.86	4	6	stress-induced premature senescence	BP	1	MAPK14,ARNTL,MAPKAPK5,PLA2R1	grey	VSMC_M10
GO:2000738	0.40	0.77	10	17	positive regulation of stem cell differentiation	BP	1	PTN,SOX9,TCF15,SOX6,TBX5,RBM24,TGFB2,GATA6,SP7,NKX2-5	grey	VSMC_M10
GO:0009208	0.40	0.79	8	13	pyrimidine ribonucleoside triphosphate metabolic process	BP	1	NME1,ENTPD4,NME4,CTPS2,NME7,NME3,UCK1,NME6	grey	VSMC_M10
GO:0072283	0.40	0.78	9	15	metanephric renal vesicle morphogenesis	BP	1	SMO,SIX2,PAX8,FMN1,PAX2,SALL1,CITED1,LHX1,LIF	grey	VSMC_M10
GO:0015015	0.40	0.86	4	6	heparan sulfate proteoglycan biosynthetic process, enzymatic modification	BP	1	HS3ST5,HS6ST2,HS6ST3,HS2ST1	grey	VSMC_M10
GO:0046532	0.40	0.86	4	6	regulation of photoreceptor cell differentiation	BP	1	SOX9,DLX1,SOX8,CNTF	grey	VSMC_M10
GO:0046533	0.40	0.86	4	6	negative regulation of photoreceptor cell differentiation	BP	1	SOX9,DLX1,SOX8,CNTF	grey	VSMC_M10
GO:0038031	0.40	0.86	4	6	non-canonical Wnt signaling pathway via JNK cascade	BP	1	NKD1,DVL3,FZD7,WNT5A	grey	VSMC_M10

GO:0006661	0.40	0.67	63	115	phosphatidylinositol biosynthetic process	BP	1	PIP4K2C,SYNJ2,GPAA1,CWH43,INPP4A,TMEM246,PIGF,MBOAT7,INPP4B,FIG4,MTMR2,PIP4K2A,ITPKC,MTMR14,PGAP2,MTMR7,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,SLA2,SYNJ1,CDS1,ITPKA,PIGT,PGAP1,PITPNM1,PIGM,BMX,FAM126B,IP6K2,PIGV,MTMR3,INPP5J,PIGX,PIGZ,PIKFYVE,SACM1L,PIGC,SOCS4,PI4KA,SLC27A1,PGAP3,PIGH,PI4K2B,SOCS7,DGKE,TTC7B,PIGL,MPPE1,IMPA2,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,PIP5KL1,PYURF,PIGB,PIGA,INPP1,CDIPT	grey	VSMC_M10
GO:0060745	0.40	0.86	4	6	mammary gland branching involved in pregnancy	BP	1	ESR1,VDR,WNT4,MED1	grey	VSMC_M10
GO:0009064	0.40	0.70	33	59	glutamine family amino acid metabolic process	BP	1	GLS2,GFPT2,PYCR3,PPAT,RIMKLA,SLC7A11,GAD2,AMDHD1,NR1H4,GMPS,NIT2,ASNSD1,GLS,SIRT4,ASL,ALDH5A1,SLC7A7,CTPS2,OAT,GLUL,FAH,CPS1,MTHFS,PRODH,ALDH4A1,ASRGL1,AC138894.1,ADSSL1,NOS2,MECP2,ASS1,MIR21,PHGDH	grey	VSMC_M10
GO:0070873	0.40	0.74	15	26	regulation of glycogen metabolic process	BP	1	RUBCNL,KHK,EPM2AIP1,PPP1CB,AKT2,PPP1R3B,SORBS1,IGF2,IRS1,PPP1R3E,PPP1R3D,PASK,PPP1R3F,INSR,INPP5K	grey	VSMC_M10
GO:1903209	0.40	0.78	9	15	positive regulation of oxidative stress-induced cell death	BP	1	TLR4,FOXO3,PAWR,FBXW7,RIPK1,MCL1,MMP3,SFPQ,PARK7	grey	VSMC_M10
GO:0007586	0.40	0.69	35	63	digestion	BP	1	ADM2,KIAA1211,ABCG5,ABCG8,AQP1,NR1H2,TLR4,SOX9,CCKBR,SOAT2,HIP1R,PLS1,CHRM5,LIMA1,NR1H3,VDR,NOD2,CHRM3,ADRA2A,EPB41,UCN2,COPA,PBLD,LPCAT3,CHRM1,CAPN8,HRH2,LDLR,SLC46A1,TRPV1,CEL,SLC22A5,SNX10,INAVA,CRH	grey	VSMC_M10
GO:0033085	0.40	0.86	4	6	negative regulation of T cell differentiation in thymus	BP	1	FOXJ1,ZC3H8,TMEM131L,PTPN2	grey	VSMC_M10
GO:0006112	0.40	0.69	36	65	energy reserve metabolic process	BP	1	GFPT2,MYC,GNMT,PYGB,RUBCNL,KHK,EPM2AIP1,PRKAG2,PPP1CB,AKT2,KL,PPP1R3B,GBE1,SORBS1,PFKM,IGF2,NHLRC1,PHKB,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PHKA2,PYGM,PYGL,PRKAG3,PPP1R3F,PHKA1,INSR,LEPR,INPP5K,AGL,ACADM,PPP1R1A,MRAP2	grey	VSMC_M10
GO:0019530	0.40	0.86	4	6	taurine metabolic process	BP	1	CSAD,STAT5B,GHR,PHGDH	grey	VSMC_M10
GO:0019694	0.40	0.86	4	6	alkanesulfonate metabolic process	BP	1	CSAD,STAT5B,GHR,PHGDH	grey	VSMC_M10
GO:0006605	0.40	0.65	143	262	protein targeting	BP	1	TIMM21,PEX7,PEX3,ZDHHC14,PRKN,TSPO,HSPA4,SIL1,SYNGR1,TOMM22,MICALL1,RAC2,ZDHHC21,PEX6,FBXO7,PEX1,SLC1A1,TRAM2,SEC61B,ITGB1BP1,YWHAZ,SEC61G,TCAF2,VPS41,SDCBP,MGARP,AGK,RAB7A,DNAJC15,AQP11,ZFAND6,SEC62,AKT2,PITRM1,TIMM50,USP36,HACL1,PRNP,BAG4,FUT10,SRP14,NCOA4,MIPEP,ZDHHC20,IMMP1L,FBXW7,PEX2,HTRA2,CSNK2A2,NUP54,KATNB1,SSR3,SPCS1,AP3B1,GOLGA7B,AP4B1,PEX16,TOMM34,DMTN,LONP2,SIRT4,SRPRA,ZDHHC23,MON1A,ZDHHC6,KCNB1,NCF1,HSPA8,HPS4,SORL1,C2CD5,ARIH2,CIB1,BAG3,ZDHHC18,PEX19,ZDHHC24,RNF215,TOMM40L,VPS37D,RPL11,FZD5,YWHAG,PIKFYVE,FIS1,CEMIP,RTP4,GRPEL1,C11orf65,AP4M1,PINK1,ZFAND2B,AP3M1,ARL6IP1,TIMM17B,ZDHHC4,HAP1,PEX26,VPS13D,MFN2,NPEPPS,VPS13C,PEX14,ITGAM,SSR2,RAB8B,TAOK2,HAX1,ZDHHC15,TIMM29,AP1M2,MIEF2,CDK5R1,SREBF1,LAMP2,INPP5K,PAM16,BCAP31,SGTA,PEX10,ZDHHC12,HSPA5,SH3GLB1,VPS4A,ZDHHC1,MICALL2,RASSF9,ZDHHC11,BNIP3L,TIMM10B,TIMM23B,TRAM1L1,SNX16,HRAS,TIMM8B,MIEF1,RHOU,LEPROT,GRPEL2,PEX12,SPCS2,DNAJC19,SEC61A2	grey	VSMC_M10
GO:0032000	0.40	0.86	4	6	positive regulation of fatty acid beta-oxidation	BP	1	PPARA,AKT2,IRS1,CPT1A	grey	VSMC_M10
GO:0043470	0.40	0.71	23	41	regulation of carbohydrate catabolic process	BP	1	PPARA,PRXL2C,SLC4A4,PRKAG2,PPP1CB,PPP1R3B,GPD1,P2RX7,PRKAG1,ZBTB20,ARNT,PPP1R3D,ACTN3,HDAC4,MLXIPL,STAT3,PSEN1,OGT,NCOR1,INSR,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:0009649	0.40	0.74	15	26	entrainment of circadian clock	BP	1	PHLPP1,FBXL6,CRY1,PPP1CB,BHLHE40,CRY2,SIK1,ARNTL2,USP2,PER2,CRTC1,FBXL22,PER3,FBXL8,FBXL12	grey	VSMC_M10
GO:0043570	0.40	0.86	4	6	maintenance of DNA repeat elements	BP	1	MSH2,TCF7L2,AXIN2,RMI2	grey	VSMC_M10
GO:1902803	0.40	0.86	4	6	regulation of synaptic vesicle transport	BP	1	PRKN,CNIH2,PINK1,BORCS5	grey	VSMC_M10
GO:0043501	0.40	0.77	10	17	skeletal muscle adaptation	BP	1	IL15,TNNC1,PPP3CA,TNNI1,MYH7,GTF2IRD1,MYOZ2,ACTN3,MYOZ1,CAMK2G	grey	VSMC_M10
GO:0044805	0.40	0.86	4	6	late nucleophagy	BP	1	ULK1,ATG2A,ATG9A,ATG2B	grey	VSMC_M10
GO:0032534	0.40	0.86	4	6	regulation of microvillus assembly	BP	1	ATP8B1,PODXL,KLF5,RAP1GAP	grey	VSMC_M10
GO:0090150	0.40	0.65	115	210	establishment of protein localization to membrane	BP	1	PEX3,ZDHHC14,EMC2,GOPC,HSPA4,SIL1,TOMM22,MICALL1,ZDHHC21,SLC1A1,TRAM2,SEC61B,SPTBN1,EMC10,ITGB1BP1,SEC61G,EGFR,TCAF2,VPS35,SDCBP,AGK,BRAF,RAB7A,RAB10,OPTN,GOLGA4,AQP11,EMC3,SEC62,AKT2,PRNP,SRP14,LYPLA1,ZDHHC20,RILPL1,RILPL2,VAMP5,EMC4,SSR3,AP3B1,GOLGA7B,PEX16,DMTN,KIF13A,NECTIN3,SRPRA,ZDHHC23,ZDHHC6,OXA1L,GET4,KCNB1,NCF1,C2CD5,CIB1,ZDHHC18,PEX19,ZDHHC24,BBS1,GORASP2,VPS37D,NSF,PIKFYVE,FIS1,CEMIP,NMT1,RTP4,BCS1L,ZFAND2B,ATP1B1,ARL6IP1,NSG1,GRIPAP1,ZDHHC4,RAB8A,CNST,RSC1A1,PEX26,CPLX1,STX1B,ITGAM,SSR2,RAB8B,TAOK2,AC138894.1,ZDHHC15,RAB11A,CALM1,TIMM29,GGA2,ARHGAP44,NPC1,MIEF2,CDK5R1,MAIP1,INPP5K,EMC6,SGTA,RAB26,UBL4A,SEC16A,ZDHHC12,HSPA5,ZDHHC1,C16orf70,ZDHHC11,WDR83OS,TIMM10B,CAMLG,EMC7,TRAM1L1,HRAS,TIMM8B,MIEF1,VAMP3,SEC61A2	grey	VSMC_M10
GO:0060440	0.40	0.86	4	6	trachea formation	BP	1	TGFBR2,MAPK1,MAPK3,MAP2K1	grey	VSMC_M10
GO:0035754	0.40	0.86	4	6	B cell chemotaxis	BP	1	GAS6,CYP7B1,PTK2B,CH25H	grey	VSMC_M10
GO:0023019	0.40	0.78	9	15	signal transduction involved in regulation of gene expression	BP	1	EPCAM,TRAF3IP2,P2RY1,FGF5,TRAF5,PARP1,SMAD3,GSC,TRAF2	grey	VSMC_M10
GO:0016255	0.40	0.86	4	6	attachment of GPI anchor to protein	BP	1	GPAA1,PIGU,PIGT,PGAP1	grey	VSMC_M10
GO:0021885	0.40	0.71	24	43	forebrain cell migration	BP	1	SUN2,SRF,EFHC1,MBOAT7,RTN4,POU3F3,NRG1,ROBO1,SRGAP2C,DISC1,DIXDC1,TNR,PSEN1,NDEL1,CDK5R1,DAB1,LRP8,DAB2IP,RHOA,ADGRG1,CNTN2,FOXG1,LAMB1,POU3F2	grey	VSMC_M10

GO:0006081	0.40	0.70	26	46	cellular aldehyde metabolic process	BP	1	ALDH8A1,ALDH7A1,ALDH1A1,ADH5,RDH13,ESD,AKR1A1,HYI,SDR16C5,DKK3,HOGA1,GLYCTK,ALDH1A3,ALDH3B2,BCO2,PNKD,WNT4,RDH11,ALDH1A2,PNPO,SCNN1B,CACNA1H,PARK7,GLO1,ADH4,PDXP	grey	VSMC_M10
GO:0046543	0.41	0.86	4	6	development of secondary female sexual characteristics	BP	1	AREG,STAT5B,MED1,WNT5A	grey	VSMC_M10
GO:1903358	0.41	0.77	10	17	regulation of Golgi organization	BP	1	RBSN,ARMH3,PDCD10,MAPK1,STX5,STX18,MAPK3,MAP2K1,DNM2,CAMSAP3	grey	VSMC_M10
GO:0042473	0.41	0.86	4	6	outer ear morphogenesis	BP	1	EYA1,PRKRA,MAPK1,MAPK3	grey	VSMC_M10
GO:0032526	0.41	0.68	46	84	response to retinoic acid	BP	1	ADNP2,SNW1,IGF2R,RXRB,PTCH1,RORB,PTK7,HOXA2,AQP1,TNC,TEAD2,OSR1,HDAC2,SOX9,WNT11,RET,ASXL1,HTRA2,PTK2B,SYNJ1,TESC,PAX2,GDAP2,FZD7,RXRG,WNT3,CREB1,ABL2,CTSH,BRINP2,DNAAF2,CD38,ALDH1A2,GATA6,YES1,SREBF1,SUZ12,RXRA,OVCA2,WNT5A,ACER2,DUSP1,LRAT,PTGES,ZNF35,WNT2	grey	VSMC_M10
GO:0035066	0.41	0.74	15	26	positive regulation of histone acetylation	BP	1	SPHK2,PAXIP1,ARRB1,AUTS2,TADA2B,FOXP3,KAT7,MUC1,MAPK3,NAP1L2,RPS6KA5,ISL1,GLYR1,LIF,RPS6KA4	grey	VSMC_M10
GO:0072330	0.41	0.66	79	144	monocarboxylic acid biosynthetic process	BP	1	LTC4S,QKI,MCAT,HSD17B8,HACD4,NR1H2,APOC1,PRKAG2,PIBF1,ELOVL1,NR1H4,TRIB3,CYP7A1,ELOVL7,CYP7B1,THNSL2,CBR4,OSBP,PRKAG1,NR1H3,HOGA1,ERLIN1,PRMT3,PRKAB1,ALDH1A3,ABHD2,MECR,ABCB11,DHRS9,HACD2,LPGAT1,PER2,OSBPL2,MLXIPL,SCAP,PLA2G4A,OSBPL6,ACADL,OSBPL1A,ACSBG1,PECR,CYP27A1,PRKAG3,DAGLB,FADS3,LIAS,ACADVL,TECR,HSD17B10,DEGS1,ALDH1A2,FGFR4,LIPC,OSBPL7,ALOXE3,PKLR,HACD3,NDUFAB1,CYP46A1,ACSM3,ACACA,CD74,ABHD3,ACSBG2,GAMT,PARK7,DECR2,ACSF3,MLYCD,PTGES2,ABCD3,ACOT4,FABP5,FADS6,ELOVL3,AMACR,STARD4,PTGES,INSIG2	grey	VSMC_M10
GO:0046137	0.41	0.86	4	6	negative regulation of vitamin metabolic process	BP	1	CYP27B1,PRMT3,SNAI1,GFI1	grey	VSMC_M10
GO:0042755	0.41	0.78	9	15	eating behavior	BP	1	NAPEPLD,TCF15,P2RY1,CPT1A,TTC21B,OPRD1,GDF15,STAT3,NMUR2	grey	VSMC_M10
GO:0006777	0.41	0.86	4	6	Mo-molybdopterin cofactor biosynthetic process	BP	1	MOCS1,GPHN,MOCOS,MOCS2	grey	VSMC_M10
GO:0019720	0.41	0.86	4	6	Mo-molybdopterin cofactor metabolic process	BP	1	MOCS1,GPHN,MOCOS,MOCS2	grey	VSMC_M10
GO:0043545	0.41	0.86	4	6	molybdopterin cofactor metabolic process	BP	1	MOCS1,GPHN,MOCOS,MOCS2	grey	VSMC_M10
GO:0051189	0.41	0.86	4	6	prosthetic group metabolic process	BP	1	MOCS1,GPHN,MOCOS,MOCS2	grey	VSMC_M10
GO:0015727	0.41	0.86	4	6	lactate transport	BP	1	SLC16A7,SLC5A8,SLC16A1,EMB	grey	VSMC_M10
GO:0035873	0.41	0.86	4	6	lactate transmembrane transport	BP	1	SLC16A7,SLC5A8,SLC16A1,EMB	grey	VSMC_M10
GO:0048741	0.41	0.73	16	28	skeletal muscle fiber development	BP	1	STAC3,SMO,KEL,KLHL40,RYR1,P2RX2,LMOD3,HOMER1,BIN3,PPP3CA,ACTN3,HDAC4,FBXO22,SKI,SIX1,MYORG	grey	VSMC_M10
GO:0046329	0.41	0.73	17	30	negative regulation of JNK cascade	BP	1	PRKN,KLHL31,DNAJA1,FKTN,ZMYND11,SH3RF2,F2RL1,TAOK3,PDCD4,AIDA,DUSP10,MEN1,DUSP19,PINK1,GPS2,NCOR1,MARVELD3	grey	VSMC_M10
GO:0048846	0.41	0.72	19	34	axon extension involved in axon guidance	BP	1	SEMA6A,PLXNA4,SEMA4D,SEMA4C,MEGF8,SEMA3D,SEMA3A,RYK,SEMA4F,SLIT1,SEMA3G,ALCAM,SEMA4G,SEMA3F,WNT3,SEMA6D,SEMA4A,PLXNA3,WNT5A	grey	VSMC_M10
GO:1902284	0.41	0.72	19	34	neuron projection extension involved in neuron projection guidance	BP	1	SEMA6A,PLXNA4,SEMA4D,SEMA4C,MEGF8,SEMA3D,SEMA3A,RYK,SEMA4F,SLIT1,SEMA3G,ALCAM,SEMA4G,SEMA3F,WNT3,SEMA6D,SEMA4A,PLXNA3,WNT5A	grey	VSMC_M10
GO:2000698	0.41	0.86	4	6	positive regulation of epithelial cell differentiation involved in kidney development	BP	1	PAX8,PAX2,LHX1,LIF	grey	VSMC_M10
GO:0002230	0.41	0.76	10	17	positive regulation of defense response to virus by host	BP	1	TRAF3IP2,TMEM173,MAVS,TRIM44,EIF2AK4,PARP9,DTX3L,SIN3A,ZDHHC1,ZDHHC11	grey	VSMC_M10
GO:0062042	0.41	0.83	5	8	regulation of cardiac epithelial to mesenchymal transition	BP	1	TGFBR2,JAG1,TGFB2,ENG,NOG	grey	VSMC_M10
GO:0032892	0.41	0.74	15	26	positive regulation of organic acid transport	BP	1	SLC12A2,PLA2G6,PLA2R1,SLC38A3,MAP2K6,ACSL5,AGT,ACE2,NTSR1,PLA2G4A,ARL6IP1,PSEN1,ABAT,STXBP1,PTGES	grey	VSMC_M10
GO:0060920	0.41	0.83	5	8	cardiac pacemaker cell differentiation	BP	1	MAML1,BVES,TBX5,BMPR1A,ISL1	grey	VSMC_M10
GO:0060926	0.41	0.83	5	8	cardiac pacemaker cell development	BP	1	MAML1,BVES,TBX5,BMPR1A,ISL1	grey	VSMC_M10
GO:0042104	0.41	0.79	8	13	positive regulation of activated T cell proliferation	BP	1	AGER,IGF2,ICOSLG,GPAM,STAT5B,MIR21,FADD,TNFSF9	grey	VSMC_M10
GO:2000323	0.41	0.86	4	6	negative regulation of glucocorticoid receptor signaling pathway	BP	1	CRY1,PHB,ARNTL,CRY2	grey	VSMC_M10
GO:0006090	0.41	0.68	42	76	pyruvate metabolic process	BP	1	PPARA,PRXL2C,GAPDH,SLC4A4,ME1,BPGM,DLD,DHTKD1,PRKAG2,PFKP,PDK1,PDHX,GPI,GPD1,P2RX7,PRKAG1,PFKM,HOGA1,ZBTB20,PFKFB2,ENO4,PC,ARNT,ACTN3,HDAC4,MLXIPL,PDK3,HK1,PRKAG3,STAT3,MPC2,ENO3,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:0031112	0.41	0.72	18	32	positive regulation of microtubule polymerization or depolymerization	BP	1	HSPA1B,SLAIN2,MET,CDK5RAP2,MAPRE1,SLAIN1,NAV3,CLIP1,KATNB1,TRPV4,CDKN1B,MAPT,TOGARAM1,NIN,CDK5R1,MECP2,PSRC1,DRG1	grey	VSMC_M10
GO:1903286	0.41	0.83	5	8	regulation of potassium ion import	BP	1	WNK2,DLG1,ATP1B1,WNK3,ATP1B2	grey	VSMC_M10
GO:0090190	0.41	0.76	10	17	positive regulation of branching involved in ureteric bud morphogenesis	BP	1	SMO,SOX9,PAX8,PAX2,AGT,MAGED1,LHX1,SOX8,NOG,SIX1	grey	VSMC_M10
GO:0006689	0.41	0.86	4	6	ganglioside catabolic process	BP	1	NEU3,HEXA,GM2A,NEU2	grey	VSMC_M10
GO:0050906	0.41	0.69	29	52	detection of stimulus involved in sensory perception	BP	1	PRPH2,PHF24,KIT,GJA10,WHRN,GRIK2,ASIC3,SCN1A,MKKS,EPHB1,CEP250,CCDC66,ADGRV1,NTSR1,BACE1,STRC,RTP4,KCNK4,KCNA1,ROM1,ASIC2,TRPV1,GNAT2,PKD1L3,REEP6,PJVK,CHRNA10,TAS2R3,OR5AN1	grey	VSMC_M10
GO:0014744	0.41	0.86	4	6	positive regulation of muscle adaptation	BP	1	FOXO3,TRPC3,PPP3CA,MIR199A1	grey	VSMC_M10
GO:1990535	0.41	0.83	5	8	neuron projection maintenance	BP	1	ATP1A3,PRNP,PSEN1,INSR,MAP1A	grey	VSMC_M10
GO:0048665	0.41	0.77	9	15	neuron fate specification	BP	1	GLI2,MNX1,POU4F1,EYA1,SUFU,ISL1,ISL2,POU3F2,SIX1	grey	VSMC_M10
GO:0090166	0.41	0.86	4	6	Golgi disassembly	BP	1	PLK3,GBF1,STX5,PLK5	grey	VSMC_M10
GO:1904892	0.41	0.69	33	59	regulation of receptor signaling pathway via STAT	BP	1	IL5,AKR1B1,OCIAD1,KIT,PPP2R1A,PIBF1,RET,PIGU,PTK2B,F2R,MST1,EGF,PARP14,AGT,IL10RA,IL6R,ELP2,CCL5,CDK5R1,SUZ12,GHR,NLK,IL7R,PTPN2,SOCS1,DAB1,DOT1L,MIR125B1,MIR125A,GADD45A,LIF,TSLP,LEPROT	grey	VSMC_M10
GO:0033129	0.41	0.85	4	6	positive regulation of histone phosphorylation	BP	1	MAPK3,RPS6KA5,FMR1,RPS6KA4	grey	VSMC_M10
GO:0015693	0.41	0.76	10	17	magnesium ion transport	BP	1	NIPAL2,SLC41A2,CNNM4,ZDHHC13,NIPA1,SLC41A1,KCNJ2,NIPAL3,NIPAL4,NIPAL1	grey	VSMC_M10

GO:0033084	0.41	0.85	4	6	regulation of immature T cell proliferation in thymus	BP	1	BMI1,IL1A,TMEM131L,FOXP3	grey	VSMC_M10
GO:0062012	0.41	0.64	132	243	regulation of small molecule metabolic process	BP	1	CYP27B1,PRKN,PPARA,PRXL2C,TTC39B,GUCA1B,GPT,GNMT,CRY1,KIT,PRKCE,PPP4R3B,SLC4A4,ZNF692,PLEK,NR1H2,FAM3C,DKKL1,SLC7A11,APOB,SPHK2,SOX9,RUBCNL,LACC1,APOC1,KHK,EPM2AIP1,PRKAG2,SLC22A13,PIBF1,GCKR,PPP1CB,AKT2,C1QTNF1,SIRT7,PANK2,PDK1,PPP1R3B,NR1H4,TRIB3,CYP7A1,NLN,NCOA2,DKK3,SORBS1,GPD1,P2RX7,EPHX2,P2RY1,PTK2B,PRKAG1,NR1H3,ERLIN1,PRMT3,SIRT5,LONP2,FAM173B,IGF2,SIRT4,GPLD1,IRS1,SIK1,CPT1A,ZBTB20,FMO5,SLC7A7,MST1,PPP1R3E,SNAI1,PFKFB2,GPER1,ABCB11,ARNT,LPGAT1,PPP1R3D,ACTN3,HDAC4,NTSR1,PASK,DNAJC30,MLXIPL,DUSP12,SCAP,POR,PDK3,PTH1R,ACADL,TYSND1,COMT,LPCAT3,GNB3,WNT4,PINK1,STAT3,PPP1R3F,ACADVL,IGFBP4,PARP1,DDB1,FGFR4,DGKQ,PSEN1,OGT,AC138894.1,COX11,LCMT1,LDLR,NCOR1,CD74,INSR,SREBF1,LEPR,NOS2,PTPN2,INPP5K,PARK7,SLC2A6,MLYCD,GFI1,ACADM,MIR21,FABP5,ENTPD5,PDZD3,TIGAR,LDLRAP1,NNMT,STARD4,INSIG2,CLYBL,FGF1,ARPP19	grey	VSMC_M10
GO:0043371	0.41	0.76	10	17	negative regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	HLX,RUNX3,BCL6,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,RC3H2	grey	VSMC_M10
GO:0060430	0.41	0.85	4	6	lung saccule development	BP	1	ASXL1,CREB1,STRA6,GATA6	grey	VSMC_M10
GO:0009838	0.41	0.85	4	6	abscission	BP	1	SPART,CHMP4C,ZFYVE19,VPS4A	grey	VSMC_M10
GO:0007638	0.41	0.83	5	8	mechanosensory behavior	BP	1	ETV1,NRXN2,HTT,STRA6,STRBP	grey	VSMC_M10
GO:0043525	0.41	0.70	26	46	positive regulation of neuron apoptotic process	BP	1	ATF4,TFAP2B,EPHA7,FOXO3,GRIK5,PRNP,CASP3,FBXW7,NQO2,TFAP2A,TGFB2,MCL1,HDAC4,BACE1,MAP3K11,FIS1,ITGAM,CDK5R1,JUN,LCN2,NQO1,MIR125B1,RHOA,DDIT3,BCL2L11,PITX3	grey	VSMC_M10
GO:1902525	0.41	0.85	4	6	regulation of protein monoubiquitination	BP	1	WDR48,PEF1,PDCD6,UBB	grey	VSMC_M10
GO:2000369	0.41	0.75	11	19	regulation of clathrin-dependent endocytosis	BP	1	SMAP1,AAK1,NEU3,PIK3CB,HIP1R,BMP2K,DGKD,SH3GL3,SYT11,DNM2,UNC119	grey	VSMC_M10
GO:0038092	0.41	0.82	5	8	nodal signaling pathway	BP	1	FOXH1,ACVR1B,ACVR1C,SMAD3,TGIF2	grey	VSMC_M10
GO:0030856	0.41	0.66	58	106	regulation of epithelial cell differentiation	BP	1	CYP27B1,PTCH1,SMO,ZDHHC21,RFX3,S1PR3,CD109,HOXA7,MYCL,GRHL1,SFRP4,MYCN,OSR1,SPRY1,FOXE3,SOX9,PTCH2,FOXJ1,SPRY2,OVOL2,IKBKB,JAG1,PLCB1,MAFG,SPRED3,BTG1,PAX8,VDR,NKX6-1,SRSF6,PAX2,CCND1,PRKX,KDF1,SFN,APOLD1,CDKN1B,KLF7,H2AFY2,ABCA12,VCL,STAT5B,MED1,CITED1,TMEM100,VEZF1,KEAP1,LHX1,MIR21,MIR125B1,ACVRL1,FOXJ2,MIR99B,ZBED2,LIF,CEBPB,SGPP1,HEY2	grey	VSMC_M10
GO:0006091	0.41	0.63	215	392	generation of precursor metabolites and energy	BP	1	FECH,RDH16,SHMT2,GFPT2,LYRM7,PPARA,P4HA2,UQCRQ,NDUFA6,ACO2,MYC,MCHR1,PRXL2C,AKR1B1,GNMT,CROT,SLC25A13,GAPDH,HMGCLL1,ADH5,CAT,SDHAF4,MSH2,ETFB,PNPT1,SLC4A4,ME1,CYB5R4,BPGM,DLD,NDUFB2,SPHK2,PYGB,GIPR,NDUFB6,RUBCNL,AKR1A1,DNAJC15,KHK,EPM2AIP1,DHTKD1,NDUFC2,PRKAG2,ACOX1,ATP5F1C,XYLB,RBKS,PPP1CB,AKT2,PFKP,IDO1,ACSS3,MDH2,NDUFS8,PANK2,NDUFA12,KL,SIRT3,COX7A1,SUCLG2,PPP1R3B,COX4I2,ASPH,CYB5A,GPI,CEBPA,IDE,GBE1,ATP5F1A,SORBS1,GPD1,P2RX7,NDUFS3,ETFDH,CIAPIN1,DGUOK,PRKAG1,PFKM,LOXL2,NQO2,UQCRB,COX15,FAM173B,IGF2,NHLRC1,COX6B1,PHKB,SRD5A1,IRS1,NDUFV3,GLRX2,TRPV4,ZBTB20,COQ10B,COX17,OXA1L,NDUFB4,ISCU,NCF1,PPP1R3E,COA6,PFKFB2,THTPA,POLG2,ENO4,PDIA5,NDUFB3,ARNT,CISD1,PPP1R3D,NFATC4,PER2,ACTN3,HDAC4,PASK,NDUFS2,PHKA2,DNAJC30,MLXIPL,SDHC,HMGCL,NCF2,MDH1B,POR,COX6A1,RPE,VGF,HK1,IDH3A,FDX1,PYGM,PYGL,COX8A,PRKAG3,PINK1,STAT3,NDUFA9,ALDH4A1,ENO3,SDHB,PPP1R3F,ACADVL,DHRS3,DEGS1,PSEN1,COX6A2,PKLR,OGT,PHKA1,COX11,NDUFAB1,ADPGK,UQCRC2,COX10,COX5A,NCOR1,INSR,TEFM,NDUFA7,OXCT1,LEPR,NOS2,SLC25A23,NDUFV2,ALDOC,SLC25A14,ENOX2,INPP5K,PRDM16,NDUFB10,UQCR11,PARK7,SLC25A33,ATP5PB,ALDH2,SLC2A6,CYBA,AGL,SLC25A25,ACADM,MT-ND1,MT-ND2,MT-ATP8,MT-ATP6,MT-CO3,MT-ND6,MT-CYB,RHOA,ATP5ME,ATP5MF,NDUFA5,ENTPD5,DHRS2,IFNLR1,NDUFC1,COX7A2,TIGAR,FXN,PPP1R1A,ETFRF1,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,AOC2,PHGDH,APOPT1,UQCC2,ADH4,MRAP2,CO	grey	VSMC_M10
GO:0003162	0.41	0.82	5	8	atrioventricular node development	BP	1	MAML1,TBX5,BMPR1A,GATA6,NKX2-5	grey	VSMC_M10
GO:0007585	0.41	0.69	28	50	respiratory gaseous exchange by respiratory system	BP	1	ZFAND5,ADH5,BPGM,YWHAZ,DACH1,HNMT,NEK10,NDUFA12,TCF15,AP3B1,NR4A2,TNNC1,FTO,GLS,COX15,CFAP43,ATP1A2,MTG2,NTSR1,PASK,SPAG16,RAB3A,TTC25,NLGN2,NLGN3,JAG2,MECP2,MAFB	grey	VSMC_M10
GO:1902884	0.41	0.85	4	6	positive regulation of response to oxidative stress	BP	1	FOXO3,PAWR,ACOX2,RIPK1	grey	VSMC_M10
GO:0042148	0.41	0.85	4	6	strand invasion	BP	1	DMC1,XRCC2,WRN,RAD51D	grey	VSMC_M10
GO:2001033	0.41	0.85	4	6	negative regulation of double-strand break repair via nonhomologous end joining	BP	1	HSF1,CYREN,ERCC6,NUDT16L1	grey	VSMC_M10
GO:0034144	0.41	0.85	4	6	negative regulation of toll-like receptor 4 signaling pathway	BP	1	TNFAIP3,MFHAS1,RAB7B,DAB2IP	grey	VSMC_M10
GO:0047496	0.41	0.70	25	45	vesicle transport along microtubule	BP	1	AP3S1,KIF5A,KIF3A,AP3M2,KIF3B,RASGRP1,AP3B1,DTNBP1,KIF13A,BICDL1,CNIH2,BLOC1S6,HTT,AP3M1,KIF1C,HAP1,TRIM46,NDEL1,AC138894.1,SNAPIN,BICDL2,PRKCZ,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0006991	0.41	0.76	10	17	response to sterol depletion	BP	1	PIP4P1,C12orf49,FBXW7,AMFR,ERLIN1,SCAP,LPCAT3,ZBTB7B,SREBF1,INSIG2	grey	VSMC_M10
GO:2000772	0.41	0.71	21	37	regulation of cellular senescence	BP	1	CDKN2A,NUAK1,CDK6,PNPT1,ZNF277,PAWR,PRKDC,PLK2,ING2,ARNTL,TERT,SLC30A10,KRAS,MAP3K3,BCL6,BMPR1A,YPEL3,VASH1,TERF2,MIR22,YBX1	grey	VSMC_M10

GO:0048878	0.41	0.61	446	832	chemical homeostasis	BP	1	ZNF236,NME1,ORMDL2,SLC39A5,NEDD4L,LRP1,CYP27B1,ESR1,APOM,SLC12A2,PRKN,AGER,PNPLA3,PNPLA5,TSPO,SMDT1,BAK1,MYC,KLHL3,MCHR1,GPR20,PTCH1,AKR1B1,PLA2G6,CKB,BTBD9,TMPRSS6,TTC39B,SLC39A4,CRY1,SRF,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,WNK2,CNNM4,ABCG5,ABCG8,PRKCE,TNNI3,EPAS1,RTN4,FPR2,HMGN3,IBTK,SLC4A4,CYB5R4,LPAR1,PPT1,AQP1,SLC31A2,NR1H2,GRHL1,MET,POU3F3,EGFR,SFRP4,KEL,ATG5,TRPM4,SLC7A11,FOXO3,APOB,FGF21,GRIN2D,TRPC3,SESN3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,CNBP,FOXA3,GIPR,ABHD5,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,STEAP3,AQP11,GRIK5,RAF1,ATP1A3,ACOX1,SCN5A,GCKR,TSKU,ELOVL1,ACKR2,SLC24A3,GPD1L,SNX5,C1QTNF1,SLC4A7,NR1D2,TMEM106B,ASPSCR1,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DCN,DIAPH1,P2RX2,KL,CCKBR,GAS6,HPX,RASA3,NCOA4,COMMD9,NR1H4,MICU3,ATP6V1H,USF2,ACOXL,SOAT2,LSR,CYP7A1,TM9SF4,NDUFAF2,IL1A,CYP7B1,ACOX2,GPI,CEBPA,IMMT,OSBP,C19orf12,PIK3R1,SLMAP,P2RX3,PLCE1,SLC9A9,RYR3,FBXW7,LIMA1,TMBIM6,P2RX7,EPHX2,HVCN1,P2RY1,PTK2B,SLC39A13,KCNJ11,NR1H3,TIAM1,RAB11FIP5,PFKM,TPCN1,SLC8B1,HOMER1,VDR,STC1,SLC25A37,OPA1,TBX5,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,FITM2,CRY2,ORMDL1,COL4A3BP,GLS,CUTC,ABCC2,ZBED6,PKD2,PAX2,TWNK,CASQ2,MCUR1,ITGB6,MYLIP,SLC12A5,TENT4B,CD40,RYR2,GRM2,SLC41A1,SLC4A10,RAP1GDS1,GPLD1,TRPM1,IRS1,SPPL3,LPCAT1,LCK,PPP3CA,KCNJ2,TESMIN,SLC9B1,SLC12A7,TRPV4,SLC9B2,ABCA5,BDH2,ZBTB20,TMEM9,ADRA2A,SLC30A10,GPAM,TCIRG1,FAM20A,TCF7L2,GNA13,ABHD4,NR5A2,	grey	VSMC_M10
GO:0097468	0.41	0.78	8	13	programmed cell death in response to reactive oxygen species	BP	1	MET,FOXO3,PAWR,PDCD10,PINK1,PARK7,MIR21,PJVK	grey	VSMC_M10
GO:0071499	0.42	0.85	4	6	cellular response to laminar fluid shear stress	BP	1	NFE2L2,MAP2K5,MAPK7,ASS1	grey	VSMC_M10
GO:2000109	0.42	0.85	4	6	regulation of macrophage apoptotic process	BP	1	CDKN2A,IRF7,MEF2C,NOD2	grey	VSMC_M10
GO:0032930	0.42	0.77	9	15	positive regulation of superoxide anion generation	BP	1	FPR2,EGFR,HVCN1,F2RL1,AGT,MAPT,ITGAM,GNAI3,CYBA	grey	VSMC_M10
GO:0031573	0.42	0.77	9	15	mitotic intra-S DNA damage checkpoint signaling	BP	1	MDC1,MSH2,XPC,NEK11,RAD17,RAD9B,CHEK2,EME1,TIPIN	grey	VSMC_M10
GO:2000425	0.42	0.85	4	6	regulation of apoptotic cell clearance	BP	1	CD300LF,CCL2,C3,ABCA7	grey	VSMC_M10
GO:0051590	0.42	0.76	10	17	positive regulation of neurotransmitter transport	BP	1	PRKN,CACNB2,SYT1,DTNBP1,DNM1L,GPER1,STX1A,STX1B,BAIAP3,STXBP1	grey	VSMC_M10
GO:0099527	0.42	0.82	5	8	postsynapse to nucleus signaling pathway	BP	1	KPNA2,NRG1,CRTC1,STAT3,PRR7	grey	VSMC_M10
GO:0043302	0.42	0.76	10	17	positive regulation of leukocyte degranulation	BP	1	SPHK2,GAB2,F2RL1,FGR,SNX4,STX4,ITGAM,IL4R,STXBP1,AP1G1	grey	VSMC_M10
GO:0030432	0.42	0.85	4	6	peristalsis	BP	1	P2RX2,P2RX3,DLG1,TBX2	grey	VSMC_M10
GO:0090277	0.42	0.68	36	65	positive regulation of peptide hormone secretion	BP	1	LRP1,PLA2G6,PRKCE,EGFR,TRPM4,GIPR,AIMP1,SIRT3,OSBP,NNAT,PFKM,NKX6-1,GPLD1,TCF7L2,PFKFB2,GPER1,GLUL,MCU,PPP3CB,CD38,MPC2,NLGN2,TARDBP,STX4,RAB8B,GPR68,ISL1,OXCT1,ABAT,NADK,BAIAP3,LRRC8A,FGA,SOX4,CRH,DOC2B	grey	VSMC_M10
GO:0045346	0.42	0.82	5	8	regulation of MHC class II biosynthetic process	BP	1	NFX1,TLR4,HDAC2,TAF7,CIITA	grey	VSMC_M10
GO:0090118	0.42	0.85	4	6	receptor-mediated endocytosis involved in cholesterol transport	BP	1	ANXA2,LDLR,MIR27B,LDLRAP1	grey	VSMC_M10
GO:0044003	0.42	0.77	9	15	modulation by symbiont of host process	BP	1	ATG5,ULK1,ANO6,DAG1,TNIP1,INSR,RXRA,IRGM,SERPINB9	grey	VSMC_M10
GO:0045586	0.42	0.82	5	8	regulation of gamma-delta T cell differentiation	BP	1	TCF7,NCKAP1L,SOX13,STAT5B,SOX4	grey	VSMC_M10
GO:0019227	0.42	0.85	4	6	neuronal action potential propagation	BP	1	NTRK2,CLDN19,CLCN1,CNTNAP1	grey	VSMC_M10
GO:0098870	0.42	0.85	4	6	action potential propagation	BP	1	NTRK2,CLDN19,CLCN1,CNTNAP1	grey	VSMC_M10
GO:0009111	0.42	0.85	4	6	vitamin catabolic process	BP	1	CYP27B1,CBR3,MTHFS,PDXP	grey	VSMC_M10
GO:0010226	0.42	0.76	10	17	response to lithium ion	BP	1	TPH2,CEBPA,XRCC4,PTK2B,ADCY7,FABP4,NFATC4,CDKN1B,NFE2L2,PKLR	grey	VSMC_M10
GO:0015838	0.42	0.85	4	6	amino-acid betaine transport	BP	1	SLC22A4,SLC38A2,SLC25A20,SLC22A5	grey	VSMC_M10
GO:0061371	0.42	0.69	26	47	determination of heart left/right asymmetry	BP	1	SMO,FOXH1,SRF,BBS7,SETDB2,MEGF8,IFT172,TGFBR2,OVOL2,MKKS,HAND2,MEF2C,IFT52,PKD2,SUFU,MMP21,PSEN1,SMAD3,TBX2,MIB1,RNF207,ENG,LBX1,WNT5A,C2CD3,NKX2-5	grey	VSMC_M10
GO:0048340	0.42	0.82	5	8	paraxial mesoderm morphogenesis	BP	1	EXOC4,WNT11,BMPR1A,SMAD3,WNT5A	grey	VSMC_M10
GO:0060331	0.42	0.85	4	6	negative regulation of response to interferon-gamma	BP	1	NR1H2,NR1H3,PARP14,PTPN2	grey	VSMC_M10
GO:0060336	0.42	0.85	4	6	negative regulation of interferon-gamma-mediated signaling pathway	BP	1	NR1H2,NR1H3,PARP14,PTPN2	grey	VSMC_M10
GO:0043504	0.42	0.85	4	6	mitochondrial DNA repair	BP	1	MGME1,PRIMPOL,PARP1,LIG3	grey	VSMC_M10
GO:0032946	0.42	0.67	46	83	positive regulation of mononuclear cell proliferation	BP	1	AGER,IL5,HLA-DPB1,TNFRSF13C,NCK2,PELI1,TLR4,IL15,BMI1,MYD88,TGFBR2,NCKAP1L,SLC7A1,TRAF6,IL1A,MEF2C,IL7,RIPK2,ZNF335,CD40,IGF2,ICOSLG,GPAM,CD28,BCL6,IL12A,CD38,BST1,STAT5B,FOXP3,RASAL3,CARD11,CHRNB2,CD74,CCL5,CD320,TICAM1,DNAJA3,VAV3,MIR21,FADD,CD46,CD70,TNFSF9,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0007286	0.42	0.66	55	100	spermatid development	BP	1	TBPL1,YTHDC2,PACRG,QKI,UBE2B,CATSPER3,H3F3C,DMC1,CFAP69,FANCG,SMARCA2,KIT,ARMC2,DLD,TTC26,RSPH6A,TOPAZ1,NECTIN2,TTC21A,CCNB1IP1,MKKS,PANK2,ING2,CELF1,JAM2,CDYL,SYCP1,DNAH1,OCA2,ROPN1L,NECTIN3,NEURL1,DDX25,CFAP43,ABHD2,SPO11,TSSK4,CIB1,OSBP2,CATSPER2,TTC12,SPAG16,ZMYND15,MNS1,SOX30,CCDC42,SPEF2,CATSPERD,CHD5,TPGS1,MFSD14A,STRBP,SYCP3,RNF8,TBC1D20	grey	VSMC_M10
GO:0090383	0.42	0.85	4	6	phagosome acidification	BP	1	RAB7A,TCIRG1,SLAMF8,RAB39A	grey	VSMC_M10

GO:0015833	0.42	0.64	101	186	peptide transport	BP	1	LRP1,RIMS2,PRKN,TAP1,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,CYBSR4,BMP8A,EGFR,TRPM4,SLC7A11,GIPR,RAF1,ABCC4,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ABCB9,ARNTL,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,CDH17,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,ABCC5,PER2,STX1A,PASK,GLUL,SIDT2,SLC16A1,KLF7,VGF,ENY2,ABCA12,MCU,PPP3CB,CAMK2G,PTPRN,CD38,MPC2,ILDR2,SYT7,NLGN2,CPLX1,TARDBP,STX4,RAB8B,UBE2Q1,SYTL4,GPR68,S100A8,CD74,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,TRPV1,BAIAP3,PARK7,LRRC8A,FGA,CHGA,SOX4,DPP4,CA2,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:0002886	0.42	0.70	23	41	regulation of myeloid leukocyte mediated immunity	BP	1	RAC2,SPHK2,GAB2,UNC13D,MAVS,FER,F2RL1,FGR,SNX4,C12orf4,STX4,ITGAM,IL4R,BTK,STXBP2,PRAM1,C3,TICAM1,DNASE1,PDPK1,FOXF1,STXBP1,CXCL6	grey	VSMC_M10
GO:0052651	0.42	0.85	4	6	monoacylglycerol catabolic process	BP	1	ABHD16A,FAAH,ABHD6,ABHD12B	grey	VSMC_M10
GO:0030949	0.42	0.82	5	8	positive regulation of vascular endothelial growth factor receptor signaling pathway	BP	1	GRB10,PRKD2,ARNT,FGF18,PRKCB	grey	VSMC_M10
GO:0097006	0.42	0.68	30	53	regulation of plasma lipoprotein particle levels	BP	1	APOM,NR1H2,APOB,FGF21,APOC1,NR1H4,SOAT2,PLTP,MYLIP,GPLD1,ABCA5,AGT,SOAT1,EHD1,ZDHHC8,LPCAT3,LRPAP1,LIPA,LIPC,ANXA2,MPO,LDLR,ABCA7,MIR199A1,MIR27B,MIR27A,MIR33B,NCEH1,LDLRAP1,PLAGL2	grey	VSMC_M10
GO:0006575	0.42	0.65	75	136	cellular modified amino acid metabolic process	BP	1	SHMT2,CPT1B,ALDH7A1,ABHD16A,SLC22A4,CKB,GNMT,CROT,CLIC5,SLC1A1,CHAC2,MBOAT2,MGST2,SLC7A11,DHFR,MMACHC,GSTK1,GGACT,PANK2,CLIC1,ARL6IP5,PAX8,AHCY,GSS,CHDH,CKMT2,MTHFD2,SERINC5,HOGA1,MTRR,GLRX2,CPT1A,PLA1A,SLCO1C1,CKMT1B,POR,NFE2L2,DUOX1,ACADL,PLOD3,GGT2,MTHFS,PRODH,LPCAT3,ABHD12B,AASDHPPT,GCH1,GGT6,SLC27A1,ALDH4A1,MED1,GSTZ1,CRYM,SHMT1,PCYOX1L,SLC46A1,PIPOX,GAMT,TMLHE,PARK7,SARDH,ASS1,KYAT1,PTGES2,PLA2G15,ACADM,GSTT4,MTHFD2L,PEMT,SLC25A32,GLO1,DIO3,ALDH1L1,GGT5,DIO2	grey	VSMC_M10
GO:0071356	0.42	0.64	89	163	cellular response to tumor necrosis factor	BP	1	MAP3K5,TNFAIP3,HSPA1B,PRKN,TNFRSF13C,MAPK14,TNFRSF21,GSDME,CXCL8,TRIM32,TRAF1,FOXO3,APOB,TRAF3IP2,ZFAND6,IKBKB,BAG4,GAS6,ST18,TRAF6,ASAH1,CEBPA,GPD1,PTK2B,KCNJ11,CCL17,OTULIN,NKX3-1,F2RL1,RIPK1,ABCC2,CD40,HDAC1,HYAL1,HYAL3,PIAS3,FABP4,SPATA2,GPER1,CIB1,TRAF5,HDAC4,PELI3,YBX3,NFE2L2,TNFSF18,SMPD4,BIRC3,SPPL2A,MAPK1,SGMS1,SLC2A4,GPS2,TNFRSF1B,PYDC1,MAPK3,TRAF3,CCL14,CCL5,CCL7,CCL2,CCL25,ADAMTS12,PTPN2,PIAS4,INPP5K,CDIP1,TRPV1,SPPL2B,TRAF2,TNFRSF25,ADAMTS13,CYBA,ASS1,LCN2,DAB2IP,MIR27B,MIR24-1,CCL16,NOL3,CASP8,CLDN1,CD70,COMMD7,CCDC3,ZFP36L2,TNFSF13B,HIST1H2BJ,CCL22	grey	VSMC_M10
GO:0006560	0.42	0.85	4	6	proline metabolic process	BP	1	PYCR3,OAT,PRODH,ALDH4A1	grey	VSMC_M10
GO:0072070	0.42	0.82	5	8	loop of Henle development	BP	1	POU3F3,JAG1,PKD2,IRX2,PKD1	grey	VSMC_M10
GO:0046761	0.42	0.85	4	6	viral budding from plasma membrane	BP	1	VPS4B,CHMP2A,CHMP4C,VPS4A	grey	VSMC_M10
GO:0048148	0.42	0.82	5	8	behavioral response to cocaine	BP	1	HOMER1,HOMER2,SDK1,ABAT,FADD	grey	VSMC_M10
GO:2000678	0.42	0.76	9	15	negative regulation of transcription regulatory region DNA binding	BP	1	FBXW7,PER2,MSX2,PSEN1,TAF1,SIN3A,DDIT3,ZNF593,HEY2	grey	VSMC_M10
GO:0097396	0.42	0.82	5	8	response to interleukin-17	BP	1	TRIM32,TRAF3IP2,TRAF6,TRAF5,TRAF2	grey	VSMC_M10
GO:0097398	0.42	0.82	5	8	cellular response to interleukin-17	BP	1	TRIM32,TRAF3IP2,TRAF6,TRAF5,TRAF2	grey	VSMC_M10
GO:0097400	0.42	0.82	5	8	interleukin-17-mediated signaling pathway	BP	1	TRIM32,TRAF3IP2,TRAF6,TRAF5,TRAF2	grey	VSMC_M10
GO:0006568	0.42	0.85	4	6	tryptophan metabolic process	BP	1	IL4I1,IDO2,IDO1,GCDH	grey	VSMC_M10
GO:0051291	0.42	0.74	11	19	protein heterooligomerization	BP	1	CPSF6,HSD17B8,PRPH2,SYT1,CBR4,TMEM120B,PKD2,CALHM1,ROM1,FARSB,PKD1	grey	VSMC_M10
GO:0098810	0.42	0.75	10	17	neurotransmitter reuptake	BP	1	PRKN,SLC6A2,SLC6A3,ATP1A2,PER2,SLC29A2,SLC29A4,CLN8,SLC1A7,PARK7	grey	VSMC_M10
GO:0050931	0.42	0.72	16	28	pigment cell differentiation	BP	1	SOX10,KIT,MITF,ANKRD27,MEF2C,ADAMTS20,OCA2,USP13,HPS4,BLOC1S6,MREG,LRMDA,CITED1,AP1G1,BLOC1S3,RAB32	grey	VSMC_M10
GO:0035902	0.42	0.75	10	17	response to immobilization stress	BP	1	BRD1,FOXO3,ERCC1,HNMT,GPI,PTK2B,FOXO4,FOS,CRH,PITX3	grey	VSMC_M10
GO:0015936	0.42	0.75	10	17	coenzyme A metabolic process	BP	1	CROT,PPCS,PANK2,PANK1,MCCC2,SLC25A16,COASY,PANK3,PANK4,NUDT19	grey	VSMC_M10
GO:0016081	0.42	0.82	5	8	synaptic vesicle docking	BP	1	PPFIA3,SNPH,STX1A,BLOC1S6,STX1B	grey	VSMC_M10
GO:0070427	0.42	0.85	4	6	nucleotide-binding oligomerization domain containing 1 signaling pathway	BP	1	TNFAIP3,SLC46A2,TLR4,RIPK2	grey	VSMC_M10
GO:1902747	0.42	0.85	4	6	negative regulation of lens fiber cell differentiation	BP	1	SPRY1,FOXE3,SPRY2,SPRED3	grey	VSMC_M10
GO:0033632	0.42	0.82	5	8	regulation of cell-cell adhesion mediated by integrin	BP	1	PODXL,FERMT3,CCL5,PIEZO1,DPP4	grey	VSMC_M10
GO:1904464	0.42	0.85	4	6	regulation of matrix metallopeptidase secretion	BP	1	SLC12A2,TLR4,CD200,MIR199A1	grey	VSMC_M10
GO:1990773	0.42	0.85	4	6	matrix metallopeptidase secretion	BP	1	SLC12A2,TLR4,CD200,MIR199A1	grey	VSMC_M10
GO:0034138	0.42	0.76	9	15	toll-like receptor 3 signaling pathway	BP	1	TNFAIP3,PELI1,F2RL1,UNC93B1,TNIP2,WDFY1,COLEC12,OAS1,HAVCR2	grey	VSMC_M10
GO:0014866	0.42	0.82	5	8	skeletal myofibril assembly	BP	1	LMOD3,ACTC1,TTN,TCAP,MYH11	grey	VSMC_M10
GO:0009948	0.42	0.71	18	32	anterior/posterior axis specification	BP	1	FRS2,SRF,SIX2,FAM208A,LDB1,PGAP1,WNT3,HOXD8,FZD5,LHX1,CDX1,GPC3,SKI,WDR77,WNT5A,BASP1,DDIT3,HEY2	grey	VSMC_M10
GO:0019731	0.42	0.77	8	13	antibacterial humoral response	BP	1	PLA2G6,NOD2,SPON2,FGA,HIST1H2BK,JCHAIN,HIST1H2BF,HIST1H2BJ	grey	VSMC_M10
GO:0033081	0.42	0.74	11	19	regulation of T cell differentiation in thymus	BP	1	CLPTM1,GLI2,FOXJ1,TOX,ZC3H8,CAMK4,TMEM131L,RASGRP1,ADAM8,IL7R,PTPN2	grey	VSMC_M10

GO:0043433	0.42	0.64	69	126	negative regulation of DNA-binding transcription factor activity	BP	1	TNFAIP3,ESR1,FZD6,TRIB1,PTCH1,PIM1,MDFI,FOXH1,LRRC14,CDKN2A,NFKBIE,CAT,MTURN,PELI1,ANXA4,SFRP4,FAF1,HDAC2,TAF3,FOXJ1,PAXIP1,IRAK2,ARRB1,EOMES,BHLHE40,NFKBIB,PURA,PRNP,GAS6,HAND2,SETD6,EIF2AK4,NLRC5,OTULIN,PKD2,NOD2,SUFU,CD200,SIK1,SP100,TCF7L2,CMKLR1,HES6,HDAC4,MEN1,NWD1,FOXP3,PEX14,PYDC1,TAF1,MAP2K5,TRIM37,KEAP1,PSMD10,TRAF3,PIAS4,PKD1,GFI1,WWP2,DAB2IP,MIR199A1,MIR21,MIR27A,MIR125A,RWDD3,COMMD6,DDIT3,COMMD7,HAVCR2	grey	VSMC_M10
GO:0070943	0.42	0.85	4	6	neutrophil-mediated killing of symbiont cell	BP	1	MYD88,F2RL1,SCNN1B,CXCL6	grey	VSMC_M10
GO:0070570	0.42	0.72	16	28	regulation of neuron projection regeneration	BP	1	LRP1,PTN,PTPRF,SPP1,KIAA0319,KREMEN1,CERS2,LRIG2,TNR,EPHA4,NDEL1,MAP2K1,MIR222,CNTF,RTN4RL1,THY1	grey	VSMC_M10
GO:0002823	0.43	0.71	17	30	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	IL4I1,FOXJ1,NCKAP1L,NOD2,BCL6,RC3H1,PTPN6,TNFSF18,PPP3CB,FOXP3,TBX21,ZBTB7B,IL4R,IL7R,CD46,HAVCR2,RC3H2	grey	VSMC_M10
GO:0015810	0.43	0.82	5	8	aspartate transmembrane transport	BP	1	SLC25A13,SLC3A1,LRRC8E,LRRC8A,LRRC8D	grey	VSMC_M10
GO:0061085	0.43	0.82	5	8	regulation of histone H3-K27 methylation	BP	1	PHF1,OGT,SUPT6H,MTF2,ZNF304	grey	VSMC_M10
GO:0002024	0.43	0.82	5	8	diet induced thermogenesis	BP	1	BMP8A,UCP1,TRPV4,SORL1,TRPV1	grey	VSMC_M10
GO:0050680	0.43	0.65	59	108	negative regulation of epithelial cell proliferation	BP	1	RIDA,MTSS1,PTCH1,IFT74,CDK6,CD109,PTN,INTU,SOX9,AQP11,IFT172,AIMP1,FLT1,ATP5F1A,ROBO1,FBXW7,MEF2C,PEX2,VDR,NKX3-1,IFT52,TGFB2,SOX2,KDF1,SFN,RUNX3,CDKN1B,DLG1,DUSP10,MEN1,IL12A,CASK,SAV1,PDCD10,RAP1GAP,WDR13,MAGED1,MED1,SYNJ2BP,NGFR,VASH1,TNMD,CCL2,ISL1,SUZ12,GPC3,WDR77,MARVELD3,DAB2IP,MIR21,MIR222,MIR125B1,MIR22,MIR24-1,ACVRL1,TINF2,WNT5A,RGCC,EREG	grey	VSMC_M10
GO:0023061	0.43	0.62	175	325	signal release	BP	1	LRP1,SNCAIP,RIMS2,PRKN,GDF9,GRM4,PLA2G6,PICK1,CHRNA3,CHRNA5,CRY1,APBA1,RFX3,TFAP2B,IL11,BRSK1,PRKCE,RIMS1,HMGN3,RIMS3,CYB5R4,PPT1,BMP8A,EGFR,TRPM4,PPFIA3,LIN7B,NAPA,GIPR,CACNB2,GRIK5,RAF1,NAPB,ABCC4,C1QTNF1,SYT1,RAB5A,LIN7A,AIMP1,SIRT3,STX2,SYT9,ADRA2B,SNPH,NR1H4,NDUFAF2,FAM3D,PAX8,NR4A1,OSBP,ARNTL,ERC2,SCG5,MEF2C,ASIC1,P2RY1,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SYNJ1,SLC8B1,NKX3-1,NKX6-1,ACVR1C,F2RL1,F2R,CRY2,VPS18,SPP1,ZBED6,DTNBP1,SYT8,GRM2,SIRT4,GPLD1,IRS1,DNM1L,HDAC1,PPP3CA,CPT1A,MAP2K6,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,SNAP23,KCNB1,PFKFB2,GPER1,RAB11FIP2,AGT,PER2,OSM,STX1A,SNX4,PASK,BACE1,DNAJC5,GLUL,CSPG5,SIDT2,SLC16A1,KLF7,CREB1,RAP1B,BLOC1S6,PLA2G4A,VGF,ENY2,ABCA12,NRXN2,CASK,MCU,ADRA2C,PNKD,PPP3CB,RAB3A,PINK1,SYN1,CAMK2G,SNAP29,PTPRN,CD38,MPC2,ILDR2,INHA,SYT7,NLGN2,CPLX1,TARDBP,STX1B,STX4,PSEN1,SYT11,RAB8B,CHRNB2,UBE2Q1,CALM1,SYTL4,SNAPIN,GPR68,PRKCB,BTK,CAMK2A,CCL5,STXBP2,SREBF1,ISL1,OXCT1,NOS2,ABAT,FMR1,PIP5K1C,NADK,P2RX1,BAIAP3,PARK7,LRRC8A,STXBP1,FGA,CHRNB4,CHGA,SOX4,DPP4,SNAP47,PDZD11,CRH,DOC2B,PTGES,LIF,UQCC2,KCNMB4	grey	VSMC_M10
GO:0070544	0.43	0.79	6	10	histone H3-K36 demethylation	BP	1	KDM4C,KDM7A,KDM4A,PHF8,RIOX1,KDM8	grey	VSMC_M10
GO:0046164	0.43	0.69	23	41	alcohol catabolic process	BP	1	MIOX,SYNJ2,SRD5A3,INPP4B,MTMR2,MTMR7,CYP7A1,GK5,SYNJ1,INPP5A,ALDH3B2,NTSR1,INPP5J,SORD,CYP27A1,TKFC,CYP46A1,IMPA2,INPP5K,ALDH2,CEL,INPP1,ADH4	grey	VSMC_M10
GO:1904950	0.43	0.65	55	100	negative regulation of establishment of protein localization	BP	1	PRKN,GOPC,RAB23,DNAJA1,BMP8A,RSAD2,ITGB1BP1,FRMD4A,UBAC2,DPH3,FERMT1,BAG4,LYPLA1,NDUFAF2,FAM3D,PKIA,KCNJ11,NR1H3,RAB11FIP5,ACVR1C,F2R,DMTN,ADTRP,SUFU,SIRT4,IRS1,CABP1,CD200,HDAC1,PPP3CA,SP100,ADRA2A,KCNB1,YOD1,BAG3,APOD,KLF7,MAPT,DERL3,IL12A,ENY2,C11orf65,RSC1A1,SNX12,CORO2B,SYTL4,SREBF1,INPP5K,PARK7,WWP2,MIR199A1,CHGA,TXN,UBE2G2,DERL2	grey	VSMC_M10
GO:0060219	0.43	0.74	11	19	camera-type eye photoreceptor cell differentiation	BP	1	NTRK2,RORB,PTN,SOX9,USH1C,RPGRIP1L,NRL,ROM1,SOX8,THY1,DIO3	grey	VSMC_M10
GO:1903960	0.43	0.81	5	8	negative regulation of anion transmembrane transport	BP	1	GOPC,TCAF2,ARL6IP5,SLC43A1,RGS4	grey	VSMC_M10
GO:1905063	0.43	0.75	10	17	regulation of vascular associated smooth muscle cell differentiation	BP	1	NFATC1,KIT,PDCD4,GPER1,EFEMP2,ENG,NFATC3,MIR21,MIR125B1,HEY2	grey	VSMC_M10
GO:0090189	0.43	0.74	11	19	regulation of branching involved in ureteric bud morphogenesis	BP	1	SMO,SIX2,SOX9,PAX8,PAX2,AGT,MAGED1,LHX1,SOX8,NOG,SIX1	grey	VSMC_M10
GO:0071051	0.43	0.84	4	6	polyadenylation-dependent snoRNA 3'-end processing	BP	1	EXOSC4,EXOSC3,PARN,EXOSC5	grey	VSMC_M10
GO:0070306	0.43	0.71	17	30	lens fiber cell differentiation	BP	1	FRS2,ATF4,TDRD7,TMOD1,SLC7A11,SPRY1,FOXE3,SPRY2,BFSP1,SPRED3,CDKN1B,PLA2G16,SMAD3,FZR1,HSF4,TBC1D20,PITX3	grey	VSMC_M10
GO:0051968	0.43	0.74	11	19	positive regulation of synaptic transmission, glutamatergic	BP	1	ROR2,EGFR,PTK2B,GLUL,TNR,NLGN2,NLGN3,CCL2,STXBP1,CACNG7,CACNG5	grey	VSMC_M10
GO:0006626	0.43	0.66	48	86	protein targeting to mitochondrion	BP	1	TIMM21,PRKN,TSPO,HSPA4,TOMM22,RAC2,FBXO7,MGARP,AGK,DNAJC15,PITRM1,TIMM50,USP36,BAG4,MIPEP,IMMP1L,FBXW7,HTRA2,CSNK2A2,TOMM34,SIRT4,HPS4,ARIH2,BAG3,TOMM40L,FZDS,FIS1,GRPEL1,C11orf65,PINK1,TIMM17B,MFN2,NPEPPS,HAX1,TIMM29,SREBF1,PAM16,BCAP31,SH3GLB1,MICALL2,BNIP3L,TIMM10B,TIMM23B,TIMM8B,RHOU,LEPROT,GRPEL2,DNAJC19	grey	VSMC_M10
GO:1903232	0.43	0.84	4	6	melanosome assembly	BP	1	HPS4,ABCB6,RAB32,TRAPPC6A	grey	VSMC_M10
GO:0033625	0.43	0.81	5	8	positive regulation of integrin activation	BP	1	PLEK,FERMT1,CDH17,RAP1B,PIEZO1	grey	VSMC_M10
GO:0061687	0.43	0.84	4	6	detoxification of inorganic compound	BP	1	ABCC2,ABCB6,PARK7,MT1X	grey	VSMC_M10
GO:0019432	0.43	0.70	18	32	triglyceride biosynthetic process	BP	1	PNPLA3,NR1H2,LPIN1,FBXW7,NR1H3,LPIN3,FITM2,GPLD1,SIK1,GPAM,LPGAT1,MOGAT3,SLC27A1,LDLR,SREBF1,LPIN2,C3,CNEP1R1	grey	VSMC_M10
GO:0089709	0.43	0.84	4	6	L-histidine transmembrane transport	BP	1	SLC7A1,SLC38A3,SLC38A5,SLC25A29	grey	VSMC_M10

GO:0072584	0.43	0.81	5	8	caveolin-mediated endocytosis	BP	1	NEDD4L,MAPK1,MAPK3,AC138894.1,UNC119	grey	VSMC_M10
GO:0006558	0.43	0.84	4	6	L-phenylalanine metabolic process	BP	1	IL4I1,HGD,FAH,GSTZ1	grey	VSMC_M10
GO:1902221	0.43	0.84	4	6	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process	BP	1	IL4I1,HGD,FAH,GSTZ1	grey	VSMC_M10
GO:0036465	0.43	0.67	35	64	synaptic vesicle recycling	BP	1	CANX,SYNJ2,BTBD9,AMPH,ACTG1,SYT1,RAB5A,FCHO2,SYNJ1,AP3B1,CYFIP1,SYT8,DNM1L,NLGN4Y,AP2M1,STX1A,DNM3,PPP3CB,RAB3A,GRIPAP1,ACTB,SYT7,SLC2A4,NLGN2,DGKQ,GAK,STX1B,SYT11,NLGN3,CALM1,DNM2,PIP5K1C,CEL,BTBD8,DENND1A	grey	VSMC_M10
GO:0006564	0.43	0.84	4	6	L-serine biosynthetic process	BP	1	SHMT2,PSAT1,SERINC5,PHGDH	grey	VSMC_M10
GO:0140627	0.43	0.81	5	8	ubiquitin-dependent protein catabolic process via the C-end degron rule pathway	BP	1	FEM1C,KLHDC3,DCAF12,TRPC4AP,KLHDC1	grey	VSMC_M10
GO:0021702	0.43	0.79	6	10	cerebellar Purkinje cell differentiation	BP	1	AGTPBP1,FAIM2,LDB1,TTC21B,LHX1,CEND1	grey	VSMC_M10
GO:0051096	0.43	0.84	4	6	positive regulation of helicase activity	BP	1	POT1,MSH2,SSBP1,CHTOP	grey	VSMC_M10
GO:0061339	0.43	0.72	13	23	establishment or maintenance of monopolar cell polarity	BP	1	PTK7,FOXJ1,SYNE4,TCF15,GBF1,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,CARMIL2,RHOA,WNT5A	grey	VSMC_M10
GO:1904153	0.43	0.81	5	8	negative regulation of retrograde protein transport, ER to cytosol	BP	1	UBAC2,YOD1,DERL3,UBE2G2,DERL2	grey	VSMC_M10
GO:0060392	0.43	0.81	5	8	negative regulation of SMAD protein signal transduction	BP	1	LRP1,VEPH1,SLC2A10,PBLD,CILP	grey	VSMC_M10
GO:0051665	0.43	0.84	4	6	membrane raft localization	BP	1	MAL,NAXE,DOCK2,RALA	grey	VSMC_M10
GO:0070255	0.43	0.84	4	6	regulation of mucus secretion	BP	1	PRKCE,EGFR,ATG5,CYBA	grey	VSMC_M10
GO:2001204	0.43	0.81	5	8	regulation of osteoclast development	BP	1	FBXW7,SLC9B2,FBN1,GPR68,ATP6AP1	grey	VSMC_M10
GO:0003214	0.43	0.79	6	10	cardiac left ventricle morphogenesis	BP	1	TGFBR2,TBX5,RYR2,RBPJ,FOXF1,HEY2	grey	VSMC_M10
GO:1902473	0.43	0.74	11	19	regulation of protein localization to synapse	BP	1	ABHD17B,DAG1,DLG1,MAPT,GRIPAP1,IQSEC2,NLGN2,ARHGAP44,PRKCZ,WNT5A,HRAS	grey	VSMC_M10
GO:0035511	0.43	0.84	4	6	oxidative DNA demethylation	BP	1	ALKBH3,FTO,ALKBH2,ALKBH1	grey	VSMC_M10
GO:0072574	0.43	0.75	10	17	hepatocyte proliferation	BP	1	GLI1,TNFAIP3,TGFA,PTN,FBXW7,SULF2,RPS6KA1,MED1,CEBPB,FGF1	grey	VSMC_M10
GO:0072575	0.43	0.75	10	17	epithelial cell proliferation involved in liver morphogenesis	BP	1	GLI1,TNFAIP3,TGFA,PTN,FBXW7,SULF2,RPS6KA1,MED1,CEBPB,FGF1	grey	VSMC_M10
GO:0034312	0.43	0.75	10	17	diol biosynthetic process	BP	1	SPTLC1,SPHK2,DHFR,ACER3,SPTLC3,ASAH1,SPR,GCH1,ACER2,PCBD2	grey	VSMC_M10
GO:0101023	0.43	0.74	11	19	vascular endothelial cell proliferation	BP	1	FLT1,MEF2C,IGF2,ITGA4,STAT3,CCL2,PDPK1,MIR29A,MIR21,MIR24-1,MIR27A	grey	VSMC_M10
GO:1905562	0.43	0.74	11	19	regulation of vascular endothelial cell proliferation	BP	1	FLT1,MEF2C,IGF2,ITGA4,STAT3,CCL2,PDPK1,MIR29A,MIR21,MIR24-1,MIR27A	grey	VSMC_M10
GO:1990253	0.43	0.79	6	10	cellular response to leucine starvation	BP	1	RRAGD,SESN3,LARS,EIF2AK4,RRAGB,IMPACT	grey	VSMC_M10
GO:0045141	0.43	0.84	4	6	meiotic telomere clustering	BP	1	UBE2B,MLH1,SPO11,MAJIN	grey	VSMC_M10
GO:0032020	0.43	0.84	4	6	ISG15-protein conjugation	BP	1	UBE2E2,UBE2E1,UBE2L6,HERC5	grey	VSMC_M10
GO:0036119	0.43	0.73	12	21	response to platelet-derived growth factor	BP	1	MARS,HAS1,PTN,TLR4,FER,HYAL1,CBL,SYAP1,CREB1,YES1,MTSS1L,PDGFD	grey	VSMC_M10
GO:0002456	0.43	0.67	30	54	T cell mediated immunity	BP	1	STX7,AGER,HLA-DRA,RSAD2,IL4I1,TRPM4,NECTIN2,PVR,SLC22A13,JAG1,NCKAP1L,TRAF6,NOD2,DENND1B,FZD5,CTSH,IL12A,PPP3CB,WAS,FOXP3,ZBTB1,TNFRSF1B,TBX21,FBXO38,IL7R,PRKCZ,TRAF2,FADD,CD46,CD70	grey	VSMC_M10
GO:0009131	0.43	0.84	4	6	pyrimidine nucleoside monophosphate catabolic process	BP	1	DPYS,UPB1,NT5M,UPP1	grey	VSMC_M10
GO:0009178	0.43	0.84	4	6	pyrimidine deoxyribonucleoside monophosphate catabolic process	BP	1	DPYS,UPB1,NT5M,UPP1	grey	VSMC_M10
GO:0046079	0.43	0.84	4	6	dUMP catabolic process	BP	1	DPYS,UPB1,NT5M,UPP1	grey	VSMC_M10
GO:1901299	0.43	0.84	4	6	negative regulation of hydrogen peroxide-mediated programmed cell death	BP	1	MET,PINK1,PARK7,MIR21	grey	VSMC_M10
GO:0098884	0.43	0.79	6	10	postsynaptic neurotransmitter receptor internalization	BP	1	USP46,EPS15,AP2M1,CALY,DNM3,AP2B1	grey	VSMC_M10
GO:0140239	0.43	0.79	6	10	postsynaptic endocytosis	BP	1	USP46,EPS15,AP2M1,CALY,DNM3,AP2B1	grey	VSMC_M10
GO:1902932	0.43	0.74	10	17	positive regulation of alcohol biosynthetic process	BP	1	CYP7A1,P2RY1,GPER1,NTSR1,SCAP,POR,PTH1R,WNT4,SREBF1,FGF1	grey	VSMC_M10
GO:0046394	0.43	0.62	116	213	carboxylic acid biosynthetic process	BP	1	GLS2,SHMT2,LTC4S,QKI,MCAT,HSD17B8,PYCR3,PSAT1,HACD4,MTAP,ALDH1A1,NR1H2,MGST2,BCAT2,NANP,DHFR,AKR1A1,APOC1,PRKAG2,PIBF1,ELOVL1,NR1H4,APIP,TRIB3,CYP7A1,ELOVL7,CYP7B1,THNSL2,CBR4,OSBP,PRKAG1,NR1H3,SERINC5,ENOPH1,SDSL,HOGA1,ASNSD1,GLS,ERLIN1,PRMT3,PRKAB1,MTRR,ASL,MTR,CBSL,ALDH1A3,ABHD2,MECR,ABCB11,DHRS9,HACD2,LPGAT1,PER2,OSBPL2,OAT,MLXIPL,GLUL,SCAP,PLA2G4A,OSBPL6,UPB1,ACADL,PLOD3,GGT2,CPS1,OSBPL1A,ACSBG1,PECR,AASDHPPT,CYP27A1,PRKAG3,GGT6,DAGLB,FADS3,LIAS,ACADVL,TECR,HSD17B10,DEGS1,ALDH1A2,FGFR4,LIPC,OSBPL7,ALOXE3,PKLR,AC138894.1,HACD3,NDUFAB1,CYP46A1,ACSM3,ACACA,CD74,ABHD3,SHMT1,ACSBG2,ABAT,GAMT,PARK7,DECR2,ACSF3,ASS1,MLYCD,PTGES2,ABCD3,ACOT4,FABP5,FADS6,ELOVL3,MTHFD2L,AMACR,GGT5,STARD4,PTGES,INSIG2,PHGDH,PCBD2	grey	VSMC_M10
GO:0001708	0.43	0.66	34	62	cell fate specification	BP	1	PTCH1,SMO,SIX2,HOXA13,SOX9,PTCH2,GLI2,MNX1,POU4F1,WNT11,EOMES,EYA1,TBX5,MGA,PAX2,SUFU,SOX2,FZD7,FKBP8,TBX19,BMPR1A,RBPJ,TBX21,PSEN1,GSC,TBX4,TBX2,ISL1,APC2,ISL2,WNT5A,POU3F2,SIX1,APC	grey	VSMC_M10
GO:1905719	0.43	0.81	5	8	protein localization to perinuclear region of cytoplasm	BP	1	HOOK3,FAM160A2,FAM160A1,RNF26,HOOK2	grey	VSMC_M10
GO:0034316	0.43	0.84	4	6	negative regulation of Arp2/3 complex-mediated actin nucleation	BP	1	PICK1,HIP1R,WDR63,GMFG	grey	VSMC_M10
GO:0010721	0.43	0.63	70	130	negative regulation of cell development	BP	1	SEMA6A,FBLN1,TSPO,FSTL4,SYNGAP1,SOX10,DAAM2,SEMA4D,S1PR3,SEMA4C,RTN4,RUFY3,EPHA7,PTN,ITGB1BP1,MYCN,KDM4A,HOOK3,SIRT2,SEMA3D,SPART,SEMA3A,ULK1,RYK,FBXW7,SEMA4F,TLX2,RAPGEF2,NKX6-1,SEMA3G,SPP1,DMTN,SEMA4G,RNF10,KIAA0319,PPP3CA,SEMA3F,PTHLH,AP1AR,SORL1,CERS2,NFATC4,DLX1,MELTF,WNT3,DUSP10,SEMA6D,TNR,FBN1,BMPR1A,PSEN1,SEMA4A,TRIM46,NTN1,LDLR,CDK5R1,MBD1,DAB1,RFLNB,TRPV1,SKI,ARHGAP4,PLXNA3,GPR37L1,NOG,THY1,WNT5A,YWHAH,EFNB3,PITX3	grey	VSMC_M10

GO:0016575	0.43	0.66	39	71	histone deacetylation	BP	1	BAZ2A,C6orf89,SPHK2,HDAC2,PRKD2,PHB,HDAC11,TADA3,SIRT2,SIRT7,SIRT3,MTA3,SDR16C5,ING2,HDAC7,SUDS3,ELK4,HDAC1,RCOR3,PER2,HDAC4,BCL6,RCOR2,PINK1,TBL1XR1,KDM5A,FOXP3,AKAP8L,AKAP8,JDP2,ZBTB7B,SFPQ,SIN3A,RCOR1,SREBF1,SKI,MIER2,PRMT6,SAP30BP	grey	VSMC_M10
GO:0044346	0.43	0.73	11	19	fibroblast apoptotic process	BP	1	BAK1,MYC,XRCC2,CHD8,BTG1,GAS6,PRDM11,STK17B,CFDP1,MIR24-1,BCL2L11	grey	VSMC_M10
GO:0003413	0.43	0.79	6	10	chondrocyte differentiation involved in endochondral bone morphogenesis	BP	1	COL27A1,SOX9,TSKU,TGFBR2,TRIP11,AXIN2	grey	VSMC_M10
GO:0002087	0.43	0.81	5	8	regulation of respiratory gaseous exchange by nervous system process	BP	1	GLS,ATP1A2,NLGN2,NLGN3,MECP2	grey	VSMC_M10
GO:0009221	0.43	0.84	4	6	pyrimidine deoxyribonucleotide biosynthetic process	BP	1	TBPL1,DTYMK,CMPK2,DCTD	grey	VSMC_M10
GO:0033615	0.43	0.84	4	6	mitochondrial proton-transporting ATP synthase complex assembly	BP	1	ATP23,ATPAF1,OXA1L,ATPAF2	grey	VSMC_M10
GO:0043461	0.43	0.84	4	6	proton-transporting ATP synthase complex assembly	BP	1	ATP23,ATPAF1,OXA1L,ATPAF2	grey	VSMC_M10
GO:0035900	0.44	0.84	4	6	response to isolation stress	BP	1	ACO2,NAPEPLD,KRAS,HRAS	grey	VSMC_M10
GO:0042590	0.44	0.84	4	6	antigen processing and presentation of exogenous peptide antigen via MHC class I	BP	1	TAP1,IKBKB,MFSD6,FCER1G	grey	VSMC_M10
GO:0060027	0.44	0.81	5	8	convergent extension involved in gastrulation	BP	1	WNT11,MKKS,DVL2,WNT5A,LBX2	grey	VSMC_M10
GO:1900542	0.44	0.67	31	56	regulation of purine nucleotide metabolic process	BP	1	PPARA,PRXL2C,GUCA1B,SLC4A4,SPHK2,LACC1,PRKAG2,PDK1,GPD1,P2RX7,PRKAG1,FAM173B,ZBTB20,ARNT,ACTN3,HDAC4,DNAJC30,MLXIPL,PDK3,PINK1,STAT3,PARP1,PSEN1,OGT,NCOR1,INSR,NOS2,SLC2A6,ENTPD5,PDZD3,TIGAR	grey	VSMC_M10
GO:0000455	0.44	0.84	4	6	enzyme-directed rRNA pseudouridine synthesis	BP	1	RPUSD2,RPUSD4,RPUSD1,RPUSD3	grey	VSMC_M10
GO:0043457	0.44	0.69	22	39	regulation of cellular respiration	BP	1	SHMT2,PNPT1,DNAJC15,COX7A1,IDE,TRPV4,ISCU,CISD1,ACTN3,MLXIPL,PINK1,NOS2,SLC25A23,PRDM16,PARK7,SLC25A33,RHOA,IFNLR1,COX7A2,UQCC2,COX7A2L,PPIF	grey	VSMC_M10
GO:0051000	0.44	0.73	11	19	positive regulation of nitric-oxide synthase activity	BP	1	NOD1,DHFR,PIK3CB,PTK2B,TERT,KRAS,NOS1AP,GCH1,CALM1,TERF2,FCER2	grey	VSMC_M10
GO:0019885	0.44	0.81	5	8	antigen processing and presentation of endogenous peptide antigen via MHC class I	BP	1	TAP1,IDE,ABCB9,ERAP1,ERAP2	grey	VSMC_M10
GO:0003094	0.44	0.73	12	21	glomerular filtration	BP	1	XPNPEP3,GAS6,F2RL1,F2R,SULF2,MCAM,PTPRO,TMEM63C,CORO2B,TBC1D8B,CYBA,JCHAIN	grey	VSMC_M10
GO:0043467	0.44	0.64	57	104	regulation of generation of precursor metabolites and energy	BP	1	SHMT2,PPARA,PRXL2C,PNPT1,SLC4A4,SPHK2,RUBCNL,DNAJC15,KHK,EPM2AIP1,PRKAG2,PPP1CB,AKT2,COX7A1,PPP1R3B,IDE,SORBS1,GPD1,P2RX7,PRKAG1,IGF2,IRS1,TRPV4,ZBTB20,COX17,ISCU,PPP1R3E,ARNT,CISD1,PPP1R3D,ACTN3,HDAC4,PASK,MLXIPL,PINK1,STAT3,PPP1R3F,PSEN1,OGT,NCOR1,INSR,NOS2,SLC25A23,INPP5K,PRDM16,PARK7,SLC25A33,SLC2A6,RHOA,ENTPD5,IFNLR1,COX7A2,TIGAR,APOPT1,UQCC2,COX7A2L,PPIF	grey	VSMC_M10
GO:0071600	0.44	0.81	5	8	otic vesicle morphogenesis	BP	1	SOX9,CEP290,EYA1,STOX1,TCAP	grey	VSMC_M10
GO:0006721	0.44	0.67	31	56	terpenoid metabolic process	BP	1	RDH5,RDH16,LRP1,ALDH8A1,AKR1B1,ALDH1A1,ADH5,RDH13,EGFR,NAPEPLD,LIPE,SDR16C5,RETSAT,HTRA2,PRMT3,SRD5A1,ALDH1A3,GGPS1,DHRS9,BCO2,PECR,DHRS3,RDH11,ALDH1A2,SCPEP1,LRP8,PNPLA4,CRH,LRAT,RDH14,ADH4	grey	VSMC_M10
GO:0060379	0.44	0.79	6	10	cardiac muscle cell myoblast differentiation	BP	1	SRF,NRG1,PRICKLE1,RBPJ,TBX2,ISL1	grey	VSMC_M10
GO:1903533	0.44	0.66	38	69	regulation of protein targeting	BP	1	PRKN,RAC2,SLC1A1,ITGB1BP1,TCAF2,AKT2,USP36,PRNP,BAG4,FBXW7,HTRA2,CSNK2A2,DMTN,KCNB1,HPS4,C2CD5,ARIH2,CIB1,BAG3,FZD5,FIS1,CEMIP,C11orf65,PINK1,NPEPPS,ITGAM,HAX1,MIEF2,CDK5R1,SREBF1,INPP5K,SH3GLB1,MICALL2,BNIP3L,HRAS,MIEF1,RHOU,LEPROT	grey	VSMC_M10
GO:0030072	0.44	0.62	91	168	peptide hormone secretion	BP	1	LRP1,RIMS2,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,CYB5R4,BMP8A,EGFR,TRPM4,GIPR,RAF1,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,ACVR1C,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,PER2,STX1A,PASK,GLUL,SIDT2,SLC16A1,KLF7,VGF,ENY2,ABCA12,MCU,PPP3CB,CAMK2G,PTPRN,CD38,MPC2,ILDR2,SYT7,NLGN2,CPLX1,TARDBP,STX4,RAB8B,UBE2Q1,SYTL4,GPR68,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,PARK7,LRRC8A,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,UQCC2	grey	VSMC_M10
GO:0016053	0.44	0.62	117	215	organic acid biosynthetic process	BP	1	GLS2,SHMT2,LTC4S,QKI,MCAT,HSD17B8,PYCR3,PSAT1,HACD4,MTAP,ALDH1A1,NR1H2,MGST2,BCAT2,NANP,DHFR,AKR1A1,APOC1,PRKAG2,PIBF1,ELOVL1,NR1H4,APIP,TRIB3,CSAD,CYP7A1,ELOVL7,CYP7B1,THNSL2,CBR4,OSBP,PRKAG1,NR1H3,SERINC5,ENOPH1,SDSL,HOGA1,ASNSD1,GLS,ERLIN1,PRMT3,PRKAB1,MTRR,ASL,MTR,CBSL,ALDH1A3,ABHD2,MECR,ABCB11,DHRS9,HACD2,LPGAT1,PER2,OSBPL2,OAT,MLXIPL,GLUL,SCAP,PLA2G4A,OSBPL6,UPB1,ACADL,PLOD3,GGT2,CPS1,OSBPL1A,ACSBG1,PECR,AASDHPPT,CYP27A1,PRKAG3,GGT6,DAGLB,FADS3,LIAS,ACADVL,TECR,HSD17B10,DEGS1,ALDH1A2,FGFR4,LIPC,OSBPL7,ALOXE3,PKLR,AC138894.1,HACD3,NDUFAB1,CYP46A1,ACSM3,ACACA,CD74,ABHD3,SHMT1,ACSBG2,ABAT,GAMT,PARK7,DECR2,ACSF3,ASS1,MLYCD,PTGES2,ABCD3,ACOT4,FABP5,FADS6,ELOVL3,MTHFD2L,AMACR,GGT5,STARD4,PTGES,INSIG2,PHGDH,PCBD2	grey	VSMC_M10
GO:1903747	0.44	0.68	24	43	regulation of establishment of protein localization to mitochondrion	BP	1	PRKN,RAC2,DNAJA1,USP36,BAG4,FBXW7,HTRA2,CSNK2A2,HPS4,ARIH2,BAG3,FZD5,MAPT,NMT1,C11orf65,PINK1,NPEPPS,HAX1,SREBF1,SH3GLB1,MICALL2,BNIP3L,RHOU,LEPROT	grey	VSMC_M10
GO:0042415	0.44	0.81	5	8	norepinephrine metabolic process	BP	1	PRKN,LY6E,AKR1B1,EPAS1,HAND2	grey	VSMC_M10
GO:0046639	0.44	0.73	11	19	negative regulation of alpha-beta T cell differentiation	BP	1	HLX,RUNX3,BCL6,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,SOCS1,RC3H2	grey	VSMC_M10
GO:0030656	0.44	0.81	5	8	regulation of vitamin metabolic process	BP	1	CYP27B1,PRMT3,SNAI1,GFI1,CLYBL	grey	VSMC_M10
GO:0099639	0.44	0.78	6	10	neurotransmitter receptor transport, endosome to plasma membrane	BP	1	VPS35,NSG1,GRIPAP1,RAB8A,RAB11A,ARHGAP44	grey	VSMC_M10

GO:0030225	0.44	0.69	18	32	macrophage differentiation	BP	1	TRIB1,L3MBTL3,HSF1,ROR2,IL15,CEBPA,RIPK1,TSPAN2,HCLS1,ZBTB46,INHA,PARP1,CSF1R,PTPN2,FADD,CASP8,NRROS,LIF	grey	VSMC_M10
GO:0010960	0.44	0.77	7	12	magnesium ion homeostasis	BP	1	TFAP2B,CNNM4,EGFR,KEL,SLC41A1,TRPM7,KCNA1	grey	VSMC_M10
GO:0048515	0.44	0.63	58	106	spermatid differentiation	BP	1	TBPL1,YTHDC2,PACRG,QKI,UBE2B,CATSPER3,H3F3C,DMC1,CFAP69,FANCG,SMARCA2,KIT,ARMC2,DLD,TTC26,RSPH6A,TOPAZ1,NECTIN2,TTC21A,CCNB1IP1,MKKS,PANK2,NPHP1,ING2,CELF1,JAM2,CDYL,SYCP1,DNAH1,OCA2,ROPN1L,NECTIN3,RHBDD1,NEURL1,DDX25,CFAP43,ABHD2,SPO11,TSSK4,CIB1,DDX6,OSBP2,CATSPER2,TTC12,SPAG16,ZMYND15,MNS1,SOX30,CCDC42,SPEF2,CATSPERD,CHDS,TPGS1,MFSD14A,STRBP,SYCP3,RNF8,TBC1D20	grey	VSMC_M10
GO:0048635	0.44	0.81	5	8	negative regulation of muscle organ development	BP	1	SIRT2,SFMBT1,USP19,YBX3,SOX15	grey	VSMC_M10
GO:0042402	0.44	0.74	10	17	cellular biogenic amine catabolic process	BP	1	ALDH7A1,IL4I1,HNMT,IDO2,IDO1,LRTOMT,AP000812.5,CHDH,SLC6A3,COMT	grey	VSMC_M10
GO:0007606	0.44	0.67	24	43	sensory perception of chemical stimulus	BP	1	CFAP69,ADCY3,C5AR1,ASIC3,MKKS,P2RX2,P2RX3,ASIC1,NCAM2,CALHM1,SLC6A3,BBS1,RTP4,SCNN1B,PDE4A,ASIC2,GNAL,GNB1,TRPV1,GNG13,GNAT2,PKD1L3,TAS2R3,OR5AN1	grey	VSMC_M10
GO:0031642	0.44	0.80	5	8	negative regulation of myelination	BP	1	TNFRSF21,LPIN1,FIG4,MTMR2,JAM2	grey	VSMC_M10
GO:1902373	0.44	0.67	27	49	negative regulation of mRNA catabolic process	BP	1	PABPC1,MAPK14,TRAF3IP2,DHX34,MYD88,PKP3,TENT5C,TENT4B,RBM24,AXIN2,MAPKAPK2,TRAF5,ANGEL2,EIF4ENIF1,YBX3,SLC11A1,RBM10,TARDBP,TOB1,TENT5D,LARP1,FMR1,METTL16,CIRBP,TRAF2,YBX1,TENT5A	grey	VSMC_M10
GO:0033152	0.44	0.80	5	8	immunoglobulin V(D)J recombination	BP	1	CYREN,PRKDC,XRCC4,YY1,NHEJ1	grey	VSMC_M10
GO:0048675	0.44	0.63	57	106	axon extension	BP	1	LRP1,SEMA6A,RAB21,PLXNA4,SRF,SEMA4D,SEMA4C,RTN4,RUFY3,NRCAM,GOLGA4,MEGF8,SEMA3D,SEMA3A,ULK1,RYK,TTL,SEMA4F,DPYSL2,SLIT1,NKX6-1,ZFYVE27,SEMA3G,CYFIP1,ALCAM,SEMA4G,KIAA0319,SEMA3F,AUTS2,ADNP,DISC1,CDKL5,WNT3,SPG11,MAPT,SEMA6D,TNR,FN1,PPP3CB,VCL,SEMA4A,NLGN3,TRIM46,NDEL1,RAB11A,NTN1,DNM2,SIN3A,TRPV2,CDK5R1,SLC9A6,L1CAM,ARHGAP4,PLXNA3,BARHL2,WNT5A,OLFM1	grey	VSMC_M10
GO:0002934	0.44	0.78	6	10	desmosome organization	BP	1	GRHL1,PKP3,DSP,PKP2,DSG2,PERP	grey	VSMC_M10
GO:0090162	0.44	0.70	15	27	establishment of epithelial cell polarity	BP	1	PTK7,FRMD4A,FBF1,FERMT1,FRMD4B,SYNE4,TCF15,CYTH3,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,WNT5A	grey	VSMC_M10
GO:0045860	0.44	0.60	164	305	positive regulation of protein kinase activity	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,MAP3K4,AGER,XRCC6,PTK2,TAB1,CCND3,CHRNA3,TTBK1,KIT,SLC1A1,ROR2,EPGN,AREG,ETAA1,TNFSF15,TGFA,ITGB1BP1,EGFR,ARHGEF5,TLR4,CCNY,SLC8A2,PHB,ABI1,MAPRE3,RALB,PRKAG2,PIBF1,SPRY2,WNT11,TGFBR2,NEK10,RPTOR,TCIM,HBEGF,PRNP,NRG1,NCKAP1L,GAS6,ERCC6,FLT1,ADRA2B,TRAF6,ZFP91,ROBO1,FBXW7,VEGFC,MADD,PTK2B,RASGRP1,RAPGEF2,PRKAG1,TIAM1,PKD2,STK4,NOD2,TAOK3,CD40,IGF2,BMPR1B,NEURL1,CCND1,MAP2K6,TGFB2,ADRA2A,FAM20A,DAG1,AJUBA,NCF1,KRAS,EGF,ADNP,CASS4,SPATC1L,CACUL1,AGT,CIB1,DVL3,STRADB,SYAP1,STRADA,GPRC5D,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,STOX1,CEMIP,DBF4B,MAP4K2,DDX3X,XRCC5,DUSP19,PDCD10,ADRA2C,DOK7,SLC11A1,MARK2,PINK1,SLC27A1,EPHA4,DLG4,MAGED1,DVL2,BMPR1A,RPLP1,DGKQ,PSEN1,FGF18,LCP2,TAOK2,EFNA1,IL6R,MAP2K1,LAT,PIK3R5,MAP2K5,CALM1,PSMD10,INSR,CCL5,CSF1R,CDK5R1,GHR,UNC119,TAOK1,SOCS1,DAB1,LRP8,PDPK1,CAMKK1,PRKCZ,MLST8,PKD1,TRAF2,MTCP1,PARK7,PSRC1,DAB2IP,MIR21,MIR125B1,RHOA,S100A12,IRGM,WNT5A,MMD,SPDYA,TXN,COPS8,RGCC,DAZAP2,HRAS,EREG,MAP2K7,C3orf58,FGF1,PDGFD	grey	VSMC_M10
GO:0048710	0.44	0.72	12	21	regulation of astrocyte differentiation	BP	1	TTBK1,MYCN,KDM4A,EPHA4,PRPF19,LDLR,MBD1,DAB1,CNTN2,GPR37L1,NOG,LIF	grey	VSMC_M10
GO:0043046	0.44	0.80	5	8	DNA methylation involved in gamete generation	BP	1	MOV10L1,PICK1,DNMT3A,TDRKH,PRMT7	grey	VSMC_M10
GO:0035094	0.44	0.69	18	32	response to nicotine	BP	1	PPARA,CHRNA3,CHRNA5,SLC7A11,HDAC2,CASP3,KCNJ11,NKX6-1,GRM2,SLC6A3,KCNK1,ATP1A2,CREB1,MAPK1,CHRNB1,CHRNB2,ABAT,MT-ND6	grey	VSMC_M10
GO:0043374	0.44	0.78	6	10	CD8-positive, alpha-beta T cell differentiation	BP	1	EOMES,NCKAP1L,TOX,RUNX3,ZBTB7B,SOCS1	grey	VSMC_M10
GO:0140052	0.44	0.80	5	8	cellular response to oxidised low-density lipoprotein particle stimulus	BP	1	TLR4,MYD88,ADTRP,MIA3,TICAM1	grey	VSMC_M10
GO:0016254	0.44	0.80	5	8	preassembly of GPI anchor in ER membrane	BP	1	PIGV,PIGZ,PIGL,PIGB,PIGA	grey	VSMC_M10
GO:0001523	0.44	0.67	25	45	retinoid metabolic process	BP	1	RDH5,RDH16,LRP1,ALDH8A1,AKR1B1,ALDH1A1,ADH5,RDH13,NAPEPLD,LIPE,SDR16C5,RETSAT,PRMT3,ALDH1A3,DHRS9,BCO2,DHRS3,RDH11,ALDH1A2,SCPEP1,LRP8,PNPLA4,LRAT,RDH14,ADH4	grey	VSMC_M10
GO:0071636	0.44	0.73	11	19	positive regulation of transforming growth factor beta production	BP	1	WNT11,FERMT1,LUM,CD200,CREB1,FOXP3,BMPR1A,SMAD3,GATA6,SERPINF2,CD46	grey	VSMC_M10
GO:1901856	0.44	0.80	5	8	negative regulation of cellular respiration	BP	1	DNAJC15,ACTN3,MLXIPL,RHOA,PPIF	grey	VSMC_M10
GO:0002643	0.44	0.78	6	10	regulation of tolerance induction	BP	1	PHLPP1,FOXJ1,TGFBR2,MARCH7,FOXP3,HAVCR2	grey	VSMC_M10
GO:0009435	0.44	0.73	10	17	NAD biosynthetic process	BP	1	NMRK1,SLC22A13,IDO2,IDO1,SLC5A8,NUDT12,PARP9,NNMT,NAPRT,NMNAT1	grey	VSMC_M10
GO:0032092	0.44	0.65	40	73	positive regulation of protein binding	BP	1	LRP1,STK3,PRKN,DERL1,MFNG,HSF1,ADD2,MAPRE1,MAPRE3,RALB,TMEM173,PLCL2,PPP2CB,TRIB3,PLK2,IDE,HIP1R,RAPGEF2,TIAM1,RIPK2,AMFR,STK4,BDNF,SPPL3,CAPRIN2,TERT,TCF7L2,EPB41,DTX3L,RPL11,MEN1,RAMP2,NVL,ANXA2,PSEN1,TAF1,MARK3,TICAM1,PKD1,WNT5A	grey	VSMC_M10

GO:0031056	0.45	0.62	67	124	regulation of histone modification	BP	1	SNW1,PHF1,UBE2B,C6orf89,RNF20,ATG5,SETD7,SPHK2,PRKD2,IWS1,KDM4A,PAXIP1,TADA3,ARRB1,CHTOP,NSD3,TAF7,SDR16C5,DNMT3B,HPF1,ING2,RTF1,ZNF335,JARID2,IGF2,AUTS2,SART3,TET1,BCL6,BCOR,WDR61,TADA2B,NELFA,PINK1,KDM5A,FOXP3,AKAP8L,AKAP8,NSD1,KAT7,MUC1,IDP2,MAPK3,ZBTB7B,OGT,NAP1L2,RPS6KA5,OTUB2,SIN3A,SREBF1,ISL1,SUPT6H,FMR1,GLYR1,SKI,MECP2,PARK7,MTF2,GFI1,CTCF,PRMT6,SAP30BP,ZNF304,NNMT,UBE2N,LIF,RPS6KA4	grey	VSMC_M10
GO:0016056	0.45	0.80	5	8	rhodopsin mediated signaling pathway	BP	1	CAMKMT,SAG,NMT1,GRK4,GUCY2D	grey	VSMC_M10
GO:0003334	0.45	0.76	7	12	keratinocyte development	BP	1	IFT74,FLNB,KDF1,SFN,ABCA12,BCL11B,DNASE1L2	grey	VSMC_M10
GO:0070091	0.45	0.80	5	8	glucagon secretion	BP	1	AIMP1,FAM3D,PASK,SYT7,CRH	grey	VSMC_M10
GO:0070092	0.45	0.80	5	8	regulation of glucagon secretion	BP	1	AIMP1,FAM3D,PASK,SYT7,CRH	grey	VSMC_M10
GO:0035176	0.45	0.69	17	31	social behavior	BP	1	MAPK8IP2,SHANK1,CHD8,MKKS,RPTOR,ATXN1,NLGN4Y,NPAS4,EIF4EBP2,NRXN2,DLG4,CLN8,NLGN3,CHRNB2,MECP2,ATXN1L,NRXN3	grey	VSMC_M10
GO:0006704	0.45	0.78	6	10	glucocorticoid biosynthetic process	BP	1	CYP21A2,DKK3,WNT4,DGKQ,CACNA1H,HSD11B2	grey	VSMC_M10
GO:0051965	0.45	0.67	25	46	positive regulation of synapse assembly	BP	1	NTRK2,LINGO2,SEMA4D,LRRN3,VSTM5,EPHB1,CLSTN2,CUX2,AMIGO2,BDNF,AMIGO3,ADNP,EPHB3,LRTM2,NLGN2,SEMA4A,NLGN3,GPRASP2,BHLHB9,ASIC2,SLITRK2,AMIGO1,ADGRL2,GRID2,LRRTM2	grey	VSMC_M10
GO:0046365	0.45	0.69	17	30	monosaccharide catabolic process	BP	1	GALT,DHDH,GLB1,NUDT5,XYLB,RBKS,PFKP,FUT10,PFKM,GLYCTK,PFKFB2,ACTN3,RPE,HK1,TKTL1,FUT4,TIGAR	grey	VSMC_M10
GO:0009953	0.45	0.65	33	60	dorsal/ventral pattern formation	BP	1	GLI1,TBC1D32,PTCH1,SMO,MDFI,SOSTDC1,HOXA2,INTU,GLI2,IFT172,OVOL2,IFT52,BMPR1B,FBXL15,SUFU,TTC21B,CHRD,WNT3,AIDA,FKBP8,GORAB,GPR161,TULP3,BMPR1A,WDR19,PSEN1,MKS1,GSC,LHX1,FOXG1,ACVRL1,NOG,DDIT3	grey	VSMC_M10
GO:0016926	0.45	0.80	5	8	protein desumoylation	BP	1	SENP1,SENP5,SENP2,SENP7,HINT1	grey	VSMC_M10
GO:0035672	0.45	0.78	6	10	oligopeptide transmembrane transport	BP	1	SLC7A11,ABCC4,ABCB9,CDH17,ABCC5,CA2	grey	VSMC_M10
GO:0009994	0.45	0.68	19	34	oocyte differentiation	BP	1	YTHDC2,GDF9,WASHC5,TUT7,DMC1,TUT4,FOXO3,SIRT2,SOHLH2,PTK2B,KMT2D,NPM2,YTHDF2,WNT4,YBX2,WDR77,AURKC,EREG,ZGLP1	grey	VSMC_M10
GO:0008088	0.45	0.65	37	68	axo-dendritic transport	BP	1	AP3S1,KIF5A,RAB21,KIF3A,AGTPBP1,APBA1,MGARP,WASF1,KLC3,DLG2,AP3M2,KIF5C,PURA,KIF3B,OPA1,AP3B1,DTNBP1,HSPA8,CNIH2,CALY,SPG11,MAPT,BLOC1S6,KIF17,AP3M1,KIF1C,HAP1,TRIM46,NDEL1,SNAPIN,SFPQ,MAPK8IP3,TERF2,BLOC1S3,BORCS5,AP3S2,MAP1A	grey	VSMC_M10
GO:0021860	0.45	0.78	6	10	pyramidal neuron development	BP	1	UQCRQ,DCLK2,SLC4A10,DISC1,PLXNA3,FOXG1	grey	VSMC_M10
GO:1904044	0.45	0.83	4	6	response to aldosterone	BP	1	RPL27,PARP1,SCNN1B,CYBA	grey	VSMC_M10
GO:0072524	0.45	0.69	16	28	pyridine-containing compound metabolic process	BP	1	PSAT1,NMRK1,SLC22A13,IDO2,IDO1,SLC5A8,NUDT12,NUDT17,PARP9,NAXE,PNPO,NADK,NNMT,NAPRT,PDXP,NMNAT1	grey	VSMC_M10
GO:0002699	0.45	0.62	77	142	positive regulation of immune effector process	BP	1	CD226,STX7,ENPP3,HLA-DRA,IL5,RAC2,KIT,EXOSC3,MSH2,ANKRD17,RSAD2,TLR4,SPHK2,HMCES,PHB,LACC1,NECTIN2,PVR,GAB2,MLH1,UNC13D,SLC22A13,PAXIP1,SHLD1,MAVS,HPX,TRAF6,GPI,FER,PTPRJ,RASGRP1,RIPK2,F2RL1,NOD2,CD40,HLX,DENND1B,FGR,SNX4,CD28,CADM1,FZD5,HK1,IL12A,LAG3,C12orf4,STAT5B,FOXP3,ZBTB1,SHLD2,SPON2,TBX21,STX4,ITGAM,IL4R,BTK,CD74,STXBP2,FBXO38,VAV1,C3,NOS2,TICAM1,PDPK1,PRKCZ,TRAF2,SLC7A5,FOXF1,STXBP1,AP1G1,BCL10,MIR21,FADD,CD46,WNT5A,INAVA,FCER2	grey	VSMC_M10
GO:0046135	0.45	0.83	4	6	pyrimidine nucleoside catabolic process	BP	1	APOBEC3H,CDADC1,UPB1,UPP1	grey	VSMC_M10
GO:2000317	0.45	0.78	6	10	negative regulation of T-helper 17 type immune response	BP	1	RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,RC3H2	grey	VSMC_M10
GO:0070932	0.45	0.73	10	17	histone H3 deacetylation	BP	1	HDAC2,HDAC11,SIRT2,SIRT7,HDAC7,ELK4,HDAC1,PER2,HDAC4,SFPQ	grey	VSMC_M10
GO:1901203	0.45	0.78	6	10	positive regulation of extracellular matrix assembly	BP	1	SOX9,CLASP2,DAG1,PHLDB1,SMAD3,RGCC	grey	VSMC_M10
GO:1902410	0.45	0.72	11	19	mitotic cytokinetic process	BP	1	VPS4B,MITD1,CHMP2A,CHMP2B,CHMP4C,CHMP7,KLHDC8B,CNTROB,CHMP1A,VPS4A,RHOA	grey	VSMC_M10
GO:0090312	0.45	0.71	13	23	positive regulation of protein deacetylation	BP	1	C6orf89,PRKD2,SDR16C5,ING2,BCL6,PINK1,AKAP8L,AKAP8,JDP2,ZBTB7B,SREBF1,SAP30BP,NNMT	grey	VSMC_M10
GO:2000786	0.45	0.78	6	10	positive regulation of autophagosome assembly	BP	1	PIP4K2C,PIP4K2A,RALB,ULK1,KIAA1324,SH3GLB1	grey	VSMC_M10
GO:0009065	0.45	0.71	12	21	glutamine family amino acid catabolic process	BP	1	GLS2,PPAT,GAD2,GLS,OAT,GLUL,FAH,PRODH,ALDH4A1,ASRGL1,NOS2,MIR21	grey	VSMC_M10
GO:0021694	0.45	0.76	7	12	cerebellar Purkinje cell layer formation	BP	1	AGTPBP1,WHRN,FAIM2,LDB1,TTC21B,LHX1,CEND1	grey	VSMC_M10
GO:0006312	0.45	0.71	12	21	mitotic recombination	BP	1	DMC1,ERCC1,ERCC2,XRCC1,MLH1,TPRKB,RAD54B,RAD52,RAD51C,RAD51D,ERCC4,TERF2	grey	VSMC_M10
GO:0032755	0.45	0.65	34	62	positive regulation of interleukin-6 production	BP	1	AGER,MAPK13,NOD1,AKIRIN2,TLR4,SPHK2,MYD88,MAVS,TRAF6,IL1A,RIPK2,F2RL1,F2R,NOD2,RAB7B,IFIH1,TRPV4,IL16,STAT3,SPON2,IL6R,CD74,ISL1,NOS2,TICAM1,CYBA,BCL10,WNT5A,INAVA,IL33,C1QTNF4,TSLP,EREG,IL17D	grey	VSMC_M10
GO:0099022	0.45	0.78	6	10	vesicle tethering	BP	1	FAM91A1,EXOC4,STARD3NL,EXOC6B,TRIP11,C17orf75	grey	VSMC_M10
GO:0006573	0.45	0.80	5	8	valine metabolic process	BP	1	BCAT2,HIBCH,ACAD8,ALDH6A1,HIBADH	grey	VSMC_M10
GO:0034142	0.45	0.69	17	30	toll-like receptor 4 signaling pathway	BP	1	TNFAIP3,NINJ1,PRKCE,PELI1,TLR4,NMI,MFHAS1,NR1H4,NR1H3,RIPK2,F2RL1,RAB7B,RAB11FIP2,WDFY1,S100A14,DAB2IP,OAS1	grey	VSMC_M10
GO:0072710	0.45	0.78	6	10	response to hydroxyurea	BP	1	SPIDR,RTF2,DDX11,DDI2,KAT7,FMR1	grey	VSMC_M10
GO:0097152	0.45	0.78	6	10	mesenchymal cell apoptotic process	BP	1	HOXA13,SOX9,PAX8,PAX2,ETV6,POU3F4	grey	VSMC_M10
GO:0043124	0.45	0.68	19	34	negative regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	TNFAIP3,TRIM39,ESR1,PPM1N,OPTN,ZMYND11,NR1H4,RIPK1,MAPKBP1,OTUD7A,HDAC1,OTUD7B,NLRX1,PPM1A,TNIP1,RIOK3,DAB2IP,RHOA,CASP8	grey	VSMC_M10
GO:0072540	0.45	0.80	5	8	T-helper 17 cell lineage commitment	BP	1	TNFSF18,STAT3,TBX21,BATF,IL6R	grey	VSMC_M10
GO:0060253	0.45	0.78	6	10	negative regulation of glial cell proliferation	BP	1	TSPO,SOX10,PTN,RNF10,CERS2,SKI	grey	VSMC_M10
GO:0045606	0.45	0.71	12	21	positive regulation of epidermal cell differentiation	BP	1	CYP27B1,PTCH1,SFRP4,PTCH2,OVOL2,VDR,KDF1,SFN,H2AFY2,MED1,MIR125B1,ZBED2	grey	VSMC_M10
GO:1905666	0.45	0.76	7	12	regulation of protein localization to endosome	BP	1	ABHD17B,ANKRD13A,EGF,SORL1,DTX3L,ABHD17A,ABHD17C	grey	VSMC_M10
GO:0006553	0.45	0.80	5	8	lysine metabolic process	BP	1	AASDHPPT,CRYM,PIPOX,SLC25A21,HYKK	grey	VSMC_M10

GO:0009310	0.45	0.72	11	19	amine catabolic process	BP	1	ALDH7A1,IL4I1,HNMT,IDO2,IDO1,LRTOMT,AP000812.5,CHDH,SLC6A3,COMT,MIR21	grey	VSMC_M10
GO:0060706	0.45	0.71	12	21	cell differentiation involved in embryonic placenta development	BP	1	STK3,MDFI,GJB5,EOMES,SPINT2,STK4,SNAI1,FZD5,SOX15,KRT19,CASP8,LIF	grey	VSMC_M10
GO:0043584	0.45	0.76	7	12	nose development	BP	1	DLX5,RPGRIP1L,ALDH1A3,STRA6,SMCHD1,SKI,SIX1	grey	VSMC_M10
GO:0032147	0.45	0.62	57	105	activation of protein kinase activity	BP	1	AGAP2,CHRNA3,SLC1A1,TNFSF15,ITGB1BP1,PHB,PRKAG2,PIBF1,WNT11,TGFBR2,RPTOR,PRNP,NRG1,NCKAP1L,GAS6,ADRA2B,TRAF6,ZFP91,MADD,PTK2B,TGFB2,ADRA2A,EGF,ADNP,AGT,STRADB,STRADA,GPRC5D,DLG1,PPP2R3C,DBF4B,DUSP19,ADRA2C,SLC11A1,MARK2,PINK1,RPLP1,DGKQ,TAOK2,IL6R,MAP2K1,INSR,CCL5,CDK5R1,GHR,SOCS1,PDPK1,PRKCZ,TRAF2,PARK7,MIR21,WNT5A,SPDYA,TXN,COPS8,RGCC,FGF1	grey	VSMC_M10
GO:0106035	0.45	0.83	4	6	protein maturation by [4Fe-4S] cluster transfer	BP	1	LTO1,CIAO2B,GLRX5,ISCA2	grey	VSMC_M10
GO:0035904	0.45	0.66	27	50	aorta development	BP	1	LRP1,TAB1,FOXH1,SRF,TFAP2B,CNTRL,JAG1,EYA1,ROBO1,ROBO2,NKX3-1,PKD2,PRICKLE1,SUFU,TGFB2,EFEMP2,BMPR1A,RBPJ,NGFR,DCTN5,TBX2,AP2B1,ENG,SOX4,ACVRL1,SIX1,HEY2	grey	VSMC_M10
GO:0032530	0.45	0.77	6	10	regulation of microvillus organization	BP	1	ATP8B1,PODXL,KLF5,PLS1,USH1C,RAP1GAP	grey	VSMC_M10
GO:1902746	0.45	0.80	5	8	regulation of lens fiber cell differentiation	BP	1	SPRY1,FOXE3,SPRY2,SPRED3,CDKN1B	grey	VSMC_M10
GO:0050802	0.45	0.80	5	8	circadian sleep/wake cycle, sleep	BP	1	BTBD9,SRD5A1,CHRNB2,PER3,CRH	grey	VSMC_M10
GO:0033131	0.45	0.80	5	8	regulation of glucokinase activity	BP	1	PRKN,GCKR,PFKFB2,DUSP12,COX11	grey	VSMC_M10
GO:0010817	0.46	0.59	178	331	regulation of hormone levels	BP	1	RDH5,RDH16,HSD17B4,LRP1,ALDH8A1,CYP27B1,ESR1,RIMS2,CYP21A2,PRKN,TSPO,GDF9,HSD17B8,HSD17B3,AKR1B1,PLA2G6,PICK1,ALDH1A1,CRY1,RFX3,SRD5A3,TFAP2B,IL11,PRKCE,RDH13,HMGN3,CYB5R4,BMP8A,IL4I1,EGFR,TRPM4,DDO,BCAT2,GIPR,LIPE,RAF1,AANAT,C1QTNF1,AIMP1,SIRT3,SYT9,NR1H4,SDR16C5,NDUFAF2,FAM3D,PAX8,IDE,OSBP,RETSAT,DKK3,PCSK1,ARNTL,SCG5,P2RY1,MME,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX3-1,NKX6-1,ACVR1C,CRY2,ABCC2,SPP1,ZBED6,PRMT3,SIRT4,GPLD1,SRD5A1,IRS1,HDAC1,ALDH1A3,PPP3CA,CPT1A,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,SNAP23,KCNB1,PFKFB2,ENPEP,GPER1,RAB11FIP2,DHRS9,AGT,ACE2,ARNT,SLCO1C1,PER2,OSM,ECE2,STX1A,SNX4,PASK,GLUL,PCSK7,SIDT2,HSD17B7,SLC16A1,POR,KLF7,CREB1,DUOX1,VGF,BCO2,FDX1,COMT,ENY2,ABCA12,MCU,GNB3,WNT4,PPP3CB,ECE1,CAMK2G,PTPRN,CD38,MPC2,STAT5B,ILDR2,INHA,SYT7,HSD17B10,NLGN2,DHRS3,MED1,RDH11,ALDH1A2,DGKQ,CPLX1,TARDBP,STX4,RAB8B,UBE2Q1,SCPEP1,SYTL4,GPR68,BTK,SCNN1B,CRYM,CYP46A1,DHRS11,SIN3A,CCL5,SREBF1,ISL1,GHR,OXCT1,NOS2,ABAT,NADK,BAIAP3,CACNA1H,SOX8,PARK7,SLC7A5,LRRC8A,GFI1,FGA,CHGA,SOX4,DPP4,DHRS2,PNPLA4,DIO3,CRH,LRAT,DOC2B,LIF,RDH14,UQCC2,ADH4,DIO2	grey	VSMC_M10
GO:0005979	0.46	0.70	13	23	regulation of glycogen biosynthetic process	BP	1	EPM2AIP1,PPP1CB,AKT2,PPP1R3B,SORBS1,IGF2,IRS1,PPP1R3E,PPP1R3D,PASK,PPP1R3F,INSR,INPP5K	grey	VSMC_M10
GO:0010962	0.46	0.70	13	23	regulation of glucan biosynthetic process	BP	1	EPM2AIP1,PPP1CB,AKT2,PPP1R3B,SORBS1,IGF2,IRS1,PPP1R3E,PPP1R3D,PASK,PPP1R3F,INSR,INPP5K	grey	VSMC_M10
GO:1990961	0.46	0.80	5	8	xenobiotic detoxification by transmembrane export across the plasma membrane	BP	1	ABCB1,ATP7B,ABCC2,RALBP1,SLC22A5	grey	VSMC_M10
GO:0045638	0.46	0.64	35	64	negative regulation of myeloid cell differentiation	BP	1	NME1,TRIB1,MYC,TOB2,CDK6,HOXA7,TLR4,PIK3R1,FBXW7,PTK2B,LDB1,GPR137B,PIAS3,TCTA,UBASH3B,CIB1,ZBTB46,WDR61,GPR137,FBN1,STAT5B,LEO1,INHA,HOXB8,GPR68,PTPN2,MIR125B1,FSTL3,MAFB,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0051452	0.46	0.67	20	36	intracellular pH reduction	BP	1	PPT1,RAB7A,ATP6V0E2,AQP11,TMEM106B,ATP6V1H,TMEM9,TCIRG1,SLAMF8,CLIC4,SLC11A1,SLC9A7,ATP6V0A1,DMXL2,AC138894.1,CLN6,SNAPIN,TMEM199,CA2,RAB39A	grey	VSMC_M10
GO:0046883	0.46	0.60	94	174	regulation of hormone secretion	BP	1	LRP1,PRKN,GDF9,PLA2G6,PICK1,CRY1,RFX3,TFAP2B,IL11,PRKCE,HMGN3,BMP8A,EGFR,TRPM4,GIPR,C1QTNF1,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,SCG5,P2RY1,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX3-1,NKX6-1,ACVR1C,CRY2,SPP1,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,AGT,PER2,OSM,STX1A,SNX4,PASK,GLUL,SIDT2,SLC16A1,KLF7,CREB1,ENY2,ABCA12,MCU,PPP3CB,CD38,MPC2,INHA,SYT7,NLGN2,TARDBP,STX4,RAB8B,SYTL4,GPR68,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,LRRC8A,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,LIF,UQCC2	grey	VSMC_M10
GO:0051205	0.46	0.66	25	44	protein insertion into membrane	BP	1	EMC2,HSPA4,TOMM22,TRAM2,EMC10,EGFR,AGK,EMC3,EMC4,OXA1L,GET4,NMT1,RTP4,BCS1L,TIMM29,MAIP1,EMC6,SGTA,UBL4A,WDR83OS,TIMM10B,CAMLG,EMC7,TRAM1L1,TIMM8B	grey	VSMC_M10
GO:0045023	0.46	0.77	6	10	G0 to G1 transition	BP	1	PPP2R5B,RHNO1,MED1,SOX15,FOXO4,DAB2IP	grey	VSMC_M10
GO:0006702	0.46	0.79	5	8	androgen biosynthetic process	BP	1	HSD17B3,SRD5A3,SRD5A1,WNT4,MED1	grey	VSMC_M10
GO:0009593	0.46	0.68	18	32	detection of chemical stimulus	BP	1	CYB5R4,TLR4,ASIC3,SYT1,P2RX2,NKX6-1,CASQ2,NOD2,KCNIP2,RYR2,RTP4,CALM1,TRPV1,GNAT2,PKD1L3,TAS2R3,OR5AN1,KCNMB4	grey	VSMC_M10
GO:0016601	0.46	0.67	20	36	Rac protein signal transduction	BP	1	RAC2,HACE1,WASF1,KBTBD6,PIK3CB,TIAM1,ARHGAP24,CYFIP1,AUTS2,KRAS,WASF2,EPS8,FARP2,NCKAP1,OGT,HACD3,DNM2,ARHGAP44,CRK,CADM4	grey	VSMC_M10
GO:0072376	0.46	0.79	5	8	protein activation cascade	BP	1	FBLN1,FN1,SERPINC1,F12,FGA	grey	VSMC_M10
GO:0014916	0.46	0.83	4	6	regulation of lung blood pressure	BP	1	GCH1,SMAD3,MIR199A1,MIR27B	grey	VSMC_M10
GO:1900087	0.46	0.68	18	32	positive regulation of G1/S transition of mitotic cell cycle	BP	1	CCND3,ANKRD17,LSM10,EGFR,UBE2E2,RPTOR,PLCB1,TFDP1,ADAMTS1,HYAL1,CCND1,TERT,DDX3X,MEPCE,CDK10,MIR29A,MIR222,RGCC	grey	VSMC_M10

GO:0046831	0.46	0.75	7	12	regulation of RNA export from nucleus	BP	1	CPSF6,IWS1,NCBP2,SETD2,AKAP8L,NRDE2,SUPT6H	grey	VSMC_M10
GO:1902188	0.46	0.77	6	10	positive regulation of viral release from host cell	BP	1	CHMP2A,CHMP2B,PC,DDB1,VPS4A,ZNF502	grey	VSMC_M10
GO:0019359	0.46	0.71	11	19	nicotinamide nucleotide biosynthetic process	BP	1	NMRK1,SLC22A13,IDO2,IDO1,SLC5A8,NUDT12,PARP9,NADK,NNMT,NAPRT,NMNAT1	grey	VSMC_M10
GO:0019363	0.46	0.71	11	19	pyridine nucleotide biosynthetic process	BP	1	NMRK1,SLC22A13,IDO2,IDO1,SLC5A8,NUDT12,PARP9,NADK,NNMT,NAPRT,NMNAT1	grey	VSMC_M10
GO:2000243	0.46	0.65	26	47	positive regulation of reproductive process	BP	1	YTHDC2,UBE2B,AGO2,MAPK15,CFAP69,HDAC2,SOX9,TOPAZ1,SIRT2,PLCB1,SEMA3A,DHX37,ACVR1B,P2RY1,NPM2,HYAL3,CIB1,CCDC87,HDAC4,OVOL1,WNT4,SYDE1,CACNA1H,OOEP,WNT5A,LHFPL2	grey	VSMC_M10
GO:0036159	0.46	0.77	6	10	inner dynein arm assembly	BP	1	LRRC6,DNAH1,ZMYND10,DNAAF2,DNAAF4,WDR63	grey	VSMC_M10
GO:0032471	0.46	0.79	5	8	negative regulation of endoplasmic reticulum calcium ion concentration	BP	1	BAK1,RAP1GDS1,FIS1,ATP2A1,BCAP31	grey	VSMC_M10
GO:0098840	0.46	0.75	7	12	protein transport along microtubule	BP	1	KIF5A,DLG2,KIF5C,BAG3,CAMSAP3,MAPK8IP3,MAP1A	grey	VSMC_M10
GO:0099118	0.46	0.75	7	12	microtubule-based protein transport	BP	1	KIF5A,DLG2,KIF5C,BAG3,CAMSAP3,MAPK8IP3,MAP1A	grey	VSMC_M10
GO:0048548	0.46	0.77	6	10	regulation of pinocytosis	BP	1	PPT1,NR1H2,NR1H3,ANKFY1,STX1B,AC138894.1	grey	VSMC_M10
GO:0036065	0.46	0.77	6	10	fucosylation	BP	1	FUT10,POFUT1,FUOM,FUT4,POFUT2,SLC35C1	grey	VSMC_M10
GO:0070189	0.46	0.79	5	8	kynurenine metabolic process	BP	1	ALDH8A1,IDO2,IDO1,KYAT1,KYAT3	grey	VSMC_M10
GO:0033860	0.46	0.79	5	8	regulation of NAD(P)H oxidase activity	BP	1	SLAMF8,AGT,PARK7,GNAI3,CYBA	grey	VSMC_M10
GO:0006616	0.46	0.79	5	8	SRP-dependent cotranslational protein targeting to membrane, translocation	BP	1	TRAM2,SEC61B,ZFAND2B,TRAM1L1,SEC61A2	grey	VSMC_M10
GO:2000781	0.46	0.67	20	36	positive regulation of double-strand break repair	BP	1	MRNIP,WDR48,SHLD1,PRKDC,ERCC6,SLF1,SPIDR,SLF2,PARP9,DTX3L,MGMT,ZCWPW1,WAS,DDX11,PARP1,SHLD2,WRAP53,SMCHD1,SPIRE2,OOEP	grey	VSMC_M10
GO:0042574	0.46	0.75	7	12	retinal metabolic process	BP	1	ALDH8A1,RDH13,SDR16C5,ALDH1A3,BCO2,RDH11,ALDH1A2	grey	VSMC_M10
GO:0051589	0.46	0.77	6	10	negative regulation of neurotransmitter transport	BP	1	PRKN,ASIC1,RAP1B,PNKD,SYT11,FMR1	grey	VSMC_M10
GO:0061384	0.46	0.69	15	27	heart trabecula morphogenesis	BP	1	ADGRG6,FOXH1,TEK,SRF,FHL2,OVOL2,NRG1,ADAMTS1,TGFB2,BMPR1A,RBPJ,MED1,ENG,NOG,HEY2	grey	VSMC_M10
GO:0046512	0.46	0.77	6	10	sphingosine biosynthetic process	BP	1	SPTLC1,SPHK2,ACER3,SPTLC3,ASAH1,ACER2	grey	VSMC_M10
GO:0046520	0.46	0.77	6	10	sphingoid biosynthetic process	BP	1	SPTLC1,SPHK2,ACER3,SPTLC3,ASAH1,ACER2	grey	VSMC_M10
GO:0043153	0.46	0.70	13	23	entrainment of circadian clock by photoperiod	BP	1	FBXL6,CRY1,PPP1CB,BHLHE40,CRY2,SIK1,USP2,PER2,CRTC1,FBXL22,PER3,FBXL8,FBXL12	grey	VSMC_M10
GO:0048066	0.46	0.67	18	32	developmental pigmentation	BP	1	SOX10,KIT,MITF,ANKRD27,MEF2C,ADAMTS20,OCA2,USP13,HPS4,BLOC1S6,MREG,LRMDA,CITED1,SLC45A2,AP1G1,BLOC1S3,RAB32,BCL2L11	grey	VSMC_M10
GO:0046078	0.46	0.79	5	8	dUMP metabolic process	BP	1	DPYS,UPB1,NT5M,DCTD,UPP1	grey	VSMC_M10
GO:0005513	0.46	0.77	6	10	detection of calcium ion	BP	1	SYT1,CASQ2,KCNIP2,RYR2,CALM1,KCNMB4	grey	VSMC_M10
GO:0002224	0.46	0.62	50	92	toll-like receptor signaling pathway	BP	1	TNFAIP3,ESR1,GRAMD4,LRRC14,NINJ1,PRKCE,RTN4,PELI1,RSAD2,TLR4,CD300LF,MYD88,IRAK2,NMI,IRF7,MFHAS1,TRAF6,NR1H4,OTUD4,NR1H3,RIPK2,AP3B1,F2RL1,NOD2,CD40,RAB7B,MAPKAPK3,UNC93B1,TLR5,MAPKAPK2,RAB11FIP2,DDX3X,TNIP2,BIRC3,GPS2,WDFY1,S100A14,BTK,TNIP1,TRAF3,COLEC12,GPR108,TICAM1,PDPK1,CYBA,GFI1,BCL10,DAB2IP,OAS1,HAVCR2	grey	VSMC_M10
GO:0032438	0.46	0.69	13	23	melanosome organization	BP	1	AP3B1,DTNBP1,KIF13A,SHROOM2,HPS4,PIKFYVE,BLOC1S6,ABCB6,SNAPIN,AP1G1,BLOC1S3,RAB32,TRAPPC6A	grey	VSMC_M10
GO:2000273	0.46	0.66	20	36	positive regulation of signaling receptor activity	BP	1	EPGN,AREG,TGFA,HDAC2,HBEGF,ADRA2B,FBXW7,IFNGR2,NEURL1,HDAC1,ADRA2A,NCF1,EGF,ADRA2C,PINK1,NLGN3,TAF1,CCL2,PARK7,EREG	grey	VSMC_M10
GO:0032049	0.46	0.79	5	8	cardiolipin biosynthetic process	BP	1	PLA2G6,TAMM41,CRLS1,SLC27A1,PTPMT1	grey	VSMC_M10
GO:1904646	0.46	0.67	19	34	cellular response to amyloid-beta	BP	1	LRP1,AGER,FPR2,TLR4,FOXO3,ATP1A3,PRNP,BACE1,SNX6,ITGA4,EPHA4,PARP1,CACNB1,PSEN1,CACNA1A,NGFR,LCN2,BCL2L11,BCL2L2	grey	VSMC_M10
GO:0043270	0.46	0.59	98	182	positive regulation of ion transport	BP	1	STAC3,SLC12A2,TSPO,BAK1,MCHR1,PLA2G6,ABCB1,WNK2,SPHK2,TRPC3,CACNB2,STAC,SCN5A,GPD1L,SYT1,P2RX2,GLRX,P2RX3,ORAI1,P2RX7,P2RY1,KCNJ11,HOMER1,IFNGR2,STC1,F2R,TESC,ANO6,KCNE2,PKD2,PLA2R1,CNTN1,KCNIP2,RYR2,FAM173B,PKP2,KCNJ2,SLC38A3,MAP2K6,ADRA2A,COX17,ANK2,GPER1,ABCB11,AGT,ACE2,SLC9A1,CASQ1,SNX4,NTSR1,SCN4B,NOS1AP,DLG1,PLA2G4A,CEMIP,CASK,HTT,PINK1,ATP1B1,KCNA1,ARL6IP1,CHRM1,HAP1,WNK3,STAC2,ATP1B2,PSEN1,NLGN3,CHRNB2,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,TRPV2,CAMK2A,CCL5,CCL2,ABAT,TRPV3,PDPK1,P2RX1,RNF207,AMIGO1,ATP2C2,LCN2,STXBP1,MIR21,DMD,JPH2,KCNH2,THY1,CRH,PTGES,APOPT1,CEBPB,NKX2-5	grey	VSMC_M10
GO:0048147	0.46	0.69	13	23	negative regulation of fibroblast proliferation	BP	1	B4GALT7,MYC,MED25,TRIM32,DACH1,PAWR,PEX2,TP53INP1,MORC3,FTH1,SKI,DAB2IP,C1QL4	grey	VSMC_M10
GO:0090382	0.46	0.69	13	23	phagosome maturation	BP	1	RAB7A,MYO7A,RAB7B,TCIRG1,SLAMF8,SPG11,PIKFYVE,MREG,SYT7,SYT11,AC138894.1,RAB32,RAB39A	grey	VSMC_M10
GO:1902306	0.46	0.75	7	12	negative regulation of sodium ion transmembrane transport	BP	1	NEDD4L,PRKCE,HECW1,OSR1,HECW2,ATP1A2,MIR24-1	grey	VSMC_M10
GO:0031340	0.46	0.77	6	10	positive regulation of vesicle fusion	BP	1	AKT2,SYT1,SYT9,C2CD5,ANXA2,DOC2B	grey	VSMC_M10
GO:0018195	0.46	0.71	11	19	peptidyl-arginine modification	BP	1	PRDM4,NDUFAF7,NR1H4,PRMT9,ART3,PRMT3,PADI2,KRTCAP2,PARK7,PRMT7,PRMT6	grey	VSMC_M10
GO:0032305	0.47	0.77	6	10	positive regulation of icosanoid secretion	BP	1	PLA2G6,PLA2R1,MAP2K6,NTSR1,PLA2G4A,PTGES	grey	VSMC_M10
GO:0010765	0.47	0.68	15	27	positive regulation of sodium ion transport	BP	1	WNK2,SCN5A,GPD1L,GLRX,TESC,CNTN1,PKP2,SLC9A1,SCN4B,ATP1B1,WNK3,ATP1B2,DNM2,DMD,NKX2-5	grey	VSMC_M10
GO:1903313	0.47	0.61	57	105	positive regulation of mRNA metabolic process	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,SNW1,PNLDC1,AGO2,TNRC6B,TUT7,GTPBP1,HSF1,EXOSC3,TRA2A,PNPT1,TUT4,ZC3HAV1,MLH1,TNRC6C,NUP98,LSM1,PAN3,CNOT1,CELF1,CNOT6L,FTO,TENT4B,RBM24,DIS3L2,GIGYF2,HSPA8,YTHDF2,YTHDF1,CELF3,NCBP2,EIF4ENIF1,RC3H1,UPF1,SAMD4A,POLR2G,LEO1,NT5C3B,DCP1B,PRPF19,TARDBP,TOB1,TNRC6A,CNOT8,PARN,METTL16,PLEKHN1,CIRBP,METTL14,NANOS1,ZFP36L2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0021859	0.47	0.75	7	12	pyramidal neuron differentiation	BP	1	UQCRQ,UNC5D,DCLK2,SLC4A10,DISC1,PLXNA3,FOXG1	grey	VSMC_M10

GO:0046834	0.47	0.75	7	12	lipid phosphorylation	BP	1	DGKI,AGK,SPHK2,DGKD,DGKG,DGKQ,DGKE	grey	VSMC_M10
GO:0038203	0.47	0.75	7	12	TORC2 signaling	BP	1	SESN3,NCKAP1L,SYAP1,SIK3,PINK1,OTUD5,MAPKAP1	grey	VSMC_M10
GO:2000651	0.47	0.73	8	14	positive regulation of sodium ion transmembrane transporter activity	BP	1	WNK2,GLRX,TESC,SLC9A1,ATP1B1,WNK3,DNM2,DMD	grey	VSMC_M10
GO:0031116	0.47	0.68	16	29	positive regulation of microtubule polymerization	BP	1	HSPA1B,SLAIN2,MET,CDK5RAP2,MAPRE1,SLAIN1,NAV3,CLIP1,CDKN1B,MAPT,TOGARAM1,NIN,CDK5R1,MECP2,PSRC1,DRG1	grey	VSMC_M10
GO:0038127	0.47	0.61	55	102	ERBB signaling pathway	BP	1	PTK2,NCK2,RTN4,ACP4,EPGN,AREG,TGFA,EGFR,GAB1,BRAF,RAB7A,SOX9,NEU3,SNX5,HBEGF,PDE6G,NRG1,FER,HIP1R,PLCE1,FBXW7,PTPRJ,WDR54,PTK2B,NEURL1,ADRA2A,SLC30A10,RNF115,NCF1,EGF,GPER1,DGKD,IFI6,AGT,CBL,REPS2,PDE6H,SNX6,ZFYVE28,SOCS4,MAPK1,HAP1,RBPJ,PSEN1,RPS6KA5,GAREM1,PTPN2,PDPK1,RNF126,MVB12B,DAB2IP,MIR29A,MIR21,GRB2,EREG	grey	VSMC_M10
GO:0010470	0.47	0.75	7	12	regulation of gastrulation	BP	1	OSR1,CLASP2,POGLUT1,DAG1,PHLDB1,LHX1,TGIF2	grey	VSMC_M10
GO:1903729	0.47	0.73	8	14	regulation of plasma membrane organization	BP	1	ATP8B1,ASAP1,MYH9,RAB3A,NOX5,SYTL4,DNM2,SH3GLB1	grey	VSMC_M10
GO:0071108	0.47	0.67	17	31	protein K48-linked deubiquitination	BP	1	TNFAIP3,USP15,MINDY4,OTUD4,USP25,OTUD7A,USP13,YOD1,USP19,OTUD7B,USP37,OTUD3,OTUD5,MINDY2,OTUB2,PARK7,USP20	grey	VSMC_M10
GO:0072583	0.47	0.65	25	46	clathrin-dependent endocytosis	BP	1	CANX,SMAP1,AAK1,AP2S1,NEU3,FCHSD2,PIK3CB,HIP1R,FCHO2,BMP2K,SLC9B2,DGKD,AP2M1,SH3GL3,ITGA4,GAK,SYT11,DNM2,AP2B1,SGIP1,UNC119,PIP5K1C,GPR107,FNBP1L,BTBD8	grey	VSMC_M10
GO:0010919	0.47	0.76	6	10	regulation of inositol phosphate biosynthetic process	BP	1	PLEK,P2RY1,PTK2B,GPER1,NTSR1,PTH1R	grey	VSMC_M10
GO:0048563	0.47	0.79	5	8	post-embryonic animal organ morphogenesis	BP	1	BAK1,MYO7A,FBN1,MFAP2,BCL2L11	grey	VSMC_M10
GO:0009147	0.47	0.70	11	19	pyrimidine nucleoside triphosphate metabolic process	BP	1	NME1,TBPL1,ENTPD4,NME4,CTPS2,DTYMK,NME7,NME3,UCK1,CMPK2,NME6	grey	VSMC_M10
GO:0000266	0.47	0.65	22	40	mitochondrial fission	BP	1	PRKN,VPS35,DDHD2,DCN,OPA1,AP3B1,DNM1L,MTFP1,MAPT,FIS1,C11orf65,MCU,DDHD1,PINK1,MUL1,STAT2,COX10,MIEF2,RALBP1,DHODH,RALA,MIEF1	grey	VSMC_M10
GO:0071347	0.47	0.62	41	75	cellular response to interleukin-1	BP	1	MAPK13,IL1R2,VRK2,CXCL8,MYLK3,BMI1,SOX9,MYD88,IRAK2,IKBKB,PLCB1,ST18,TRAF6,OTUD4,CCL17,NKX3-1,ABCC2,TOLLIP,CD40,HYAL1,HYAL3,RC3H1,UPF1,TNIP2,MAPK3,RPS6KA5,YY1,CCL14,CCL5,CCL7,CCL2,CCL25,ADAMTS12,LCN2,DAB2IP,MIR21,MIR27A,CCL16,CEBPB,RPS6KA4,CCL22	grey	VSMC_M10
GO:0045725	0.47	0.74	7	12	positive regulation of glycogen biosynthetic process	BP	1	EPM2AIP1,AKT2,SORBS1,IGF2,IRS1,PPP1R3E,INSR	grey	VSMC_M10
GO:0045654	0.47	0.76	6	10	positive regulation of megakaryocyte differentiation	BP	1	ZNF16,MTURN,TESC,RAB7B,THPO,RCOR1	grey	VSMC_M10
GO:0090370	0.47	0.82	4	6	negative regulation of cholesterol efflux	BP	1	EGF,MIR27B,MIR27A,MIR33B	grey	VSMC_M10
GO:1902033	0.47	0.76	6	10	regulation of hematopoietic stem cell proliferation	BP	1	PIM1,EIF2AK2,THPO,KAT7,MIR222,ATXN1L	grey	VSMC_M10
GO:0048339	0.47	0.73	8	14	paraxial mesoderm development	BP	1	EXOC4,TEAD2,WNT11,TCF15,POGLUT1,BMPR1A,SMAD3,WNT5A	grey	VSMC_M10
GO:0006613	0.47	0.70	12	21	cotranslational protein targeting to membrane	BP	1	SIL1,TRAM2,SEC61B,SEC62,SRP14,SSR3,SRPRA,ZFAND2B,ARL6IP1,SSR2,TRAM1L1,SEC61A2	grey	VSMC_M10
GO:0038202	0.47	0.65	22	40	TORC1 signaling	BP	1	RRAGD,MFSD8,KPTN,SESN3,SZT2,PIP4P1,RPTOR,LARS,GPR137B,DYRK3,SIK3,GPR137,OTUD5,CARD11,RRAGB,DGKQ,LARP1,SMCR8,CLEC16A,MLST8,LAMTOR5,RNF152	grey	VSMC_M10
GO:1902622	0.47	0.66	19	34	regulation of neutrophil migration	BP	1	RAC2,CXCL8,C5AR2,C5AR1,MYD88,NCKAP1L,NOD2,DNM1L,CD99,SLAMF8,MOSPD2,ADAM8,MCU,CXCR2,BST1,DAPK2,CD74,MPP1,DPP4	grey	VSMC_M10
GO:0098787	0.47	0.74	7	12	mRNA cleavage involved in mRNA processing	BP	1	CPSF6,CPSF1,CPSF2,NCBP2,CPSF4,AP002990.1,CSTF2	grey	VSMC_M10
GO:0046462	0.47	0.76	6	10	monoacylglycerol metabolic process	BP	1	ABHD16A,FAAH,ABHD6,PLA2G4A,MOGAT3,ABHD12B	grey	VSMC_M10
GO:0035282	0.47	0.62	40	74	segmentation	BP	1	FRS2,ROR2,MEOX2,HOXA2,OSR1,BMI1,ABI1,PCDH8,XRCC2,SEMA3A,PRKDC,TCF15,POFUT1,FAM208A,NKX3-1,NKD1,IRX2,SEMA3F,POGLUT1,AXIN2,HOXD8,FZD5,MEOX1,DVL2,BMPR1A,TCAP,RBPJ,ALDH1A2,PSEN1,SMAD3,LHX1,CDX1,MIB1,NLE1,WDR77,FOXF1,MTF2,MAFB,WNT5A,BASP1	grey	VSMC_M10
GO:0032328	0.47	0.76	6	10	alanine transport	BP	1	SLC1A4,SLC38A2,SLC38A3,SLC38A5,SLC3A2,SLC36A1	grey	VSMC_M10
GO:0033628	0.47	0.65	22	40	regulation of cell adhesion mediated by integrin	BP	1	PTK2,PODXL,IFT74,ITGB1BP1,FERMT1,RAC3,NCKAP1L,RET,LPXN,TESC,TGFB2,CIB1,PTPN6,FERMT3,MUC1,EFNA1,CCL5,CRK,PIEZO1,DPP4,ACER2,LIF	grey	VSMC_M10
GO:2000403	0.47	0.70	12	21	positive regulation of lymphocyte migration	BP	1	CCL27,OXSR1,JAM2,PTK2B,ADAM8,ITGA4,TMEM102,CCL5,CCL7,RHOA,FADD,WNT5A	grey	VSMC_M10
GO:0021895	0.47	0.73	8	14	cerebral cortex neuron differentiation	BP	1	RAC3,TOX,ZNF335,DLX1,PSEN1,SIN3A,CHD5,CNTN2	grey	VSMC_M10
GO:0098703	0.47	0.73	8	14	calcium ion import across plasma membrane	BP	1	SLC8A2,PRNP,TRPV4,FAM155B,TRPV2,TRPV3,TRPV1,P2RX1	grey	VSMC_M10
GO:1902656	0.47	0.73	8	14	calcium ion import into cytosol	BP	1	SLC8A2,PRNP,TRPV4,FAM155B,TRPV2,TRPV3,TRPV1,P2RX1	grey	VSMC_M10
GO:0033006	0.47	0.68	14	25	regulation of mast cell activation involved in immune response	BP	1	ENPP3,RAC2,SPHK2,GAB2,UNC13D,FER,FGR,SNX4,C12orf4,IL4R,STXBP2,PDPK1,FOXF1,STXBP1	grey	VSMC_M10
GO:0045722	0.47	0.74	7	12	positive regulation of gluconeogenesis	BP	1	PPARA,GPT,PPP4R3B,DDB1,PTPN2,NNMT,ARPP19	grey	VSMC_M10
GO:2000659	0.47	0.78	5	8	regulation of interleukin-1-mediated signaling pathway	BP	1	IL1R2,VRK2,OTUD4,MIR21,MIR27A	grey	VSMC_M10
GO:0044090	0.47	0.74	7	12	positive regulation of vacuole organization	BP	1	PIP4K2C,PIP4K2A,RALB,ULK1,ANXA2,KIAA1324,SH3GLB1	grey	VSMC_M10
GO:0070933	0.47	0.76	6	10	histone H4 deacetylation	BP	1	HDAC2,SIRT2,SIRT7,HDAC1,HDAC4,RCOR1	grey	VSMC_M10
GO:0045911	0.47	0.66	20	36	positive regulation of DNA recombination	BP	1	MRNIP,UBE2B,EXOSC3,MSH2,HMCES,ERCC2,MLH1,PAXIP1,WDR48,SHLD1,ERCC6,CD40,CD28,ZCWPW1,WAS,PARP1,SHLD2,TBX21,WRAP53,OOEP	grey	VSMC_M10
GO:0045913	0.47	0.63	31	57	positive regulation of carbohydrate metabolic process	BP	1	PPARA,PRXL2C,GPT,PRKCE,PPP4R3B,SLC4A4,EPM2AIP1,AKT2,SORBS1,GPD1,P2RX7,P2RY1,IGF2,GPLD1,IRS1,ZBTB20,PPP1R3E,EGF,GPER1,ARNT,ACTN3,NTSR1,MLXIPL,PTH1R,DDB1,PSEN1,INSR,PTPN2,ENTPD5,NNMT,ARPP19	grey	VSMC_M10
GO:0030431	0.47	0.76	6	10	sleep	BP	1	BTBD9,SRD5A1,FOS,CHRNB2,PER3,CRH	grey	VSMC_M10

GO:0009648	0.47	0.68	14	25	photoperiodism	BP	1	FBXL6,CRY1,AANAT,PPP1CB,BHLHE40,CRY2,SIK1,USP2,PER2,CRTC1,FBXL22,PER3,FBXL8,FBXL12	grey	VSMC_M10
GO:0072132	0.47	0.64	24	44	mesenchyme morphogenesis	BP	1	MYC,EXOC4,OSR1,SOX9,WNT11,TGFBR2,ROBO1,ROBO2,ACTG2,TGFB2,SNAI1,ACTC1,BMPR1A,RBPJ,TMEM100,SMAD3,TBX2,ISL1,FOXF1,ENG,ACVRL1,NOG,WNT5A,HEY2	grey	VSMC_M10
GO:0070234	0.47	0.76	6	10	positive regulation of T cell apoptotic process	BP	1	IDO1,ZC3H8,PDCD1,ADAM8,CCL5,WNT5A	grey	VSMC_M10
GO:0032543	0.47	0.62	40	72	mitochondrial translation	BP	1	SHMT2,TSFM,RMND1,LRPPRC,MTIF2,QRSL1,MTRF1,MRPS12,HARS,MRPS27,MRPS28,NSUN3,WARS2,MRPS17,GATC,RPUSD4,YARS2,MRPS35,MRPL52,RCC1L,MRPS11,MRPS21,TARS2,MTG2,LARS2,DARS2,COA3,MRPL44,ALKBH1,EARS2,NDUFA7,MRPS34,MRPS2,MRPS6,RPUSD3,MRPL57,MRPL51,UQCC2,TRMT10C,MRPL16	grey	VSMC_M10
GO:0010842	0.47	0.70	10	18	retina layer formation	BP	1	SLC1A1,TFAP2B,RDH13,TSPAN12,TFAP2A,OBSL1,SDK1,MEGF11,LHX1,FJX1	grey	VSMC_M10
GO:0009086	0.47	0.76	6	10	methionine biosynthetic process	BP	1	MTAP,APIP,ENOPH1,MTRR,MTR,MTHFD2L	grey	VSMC_M10
GO:0002710	0.47	0.74	7	12	negative regulation of T cell mediated immunity	BP	1	IL4I1,NCKAP1L,NOD2,PPP3CB,FOXP3,TBX21,IL7R	grey	VSMC_M10
GO:0044068	0.47	0.76	6	10	modulation by symbiont of host cellular process	BP	1	ATG5,ULK1,ANO6,TNIP1,IRGM,SERPINB9	grey	VSMC_M10
GO:0042953	0.47	0.74	7	12	lipoprotein transport	BP	1	LRP1,APOB,CUBN,MIA3,PRKCB,VMP1,UNC119	grey	VSMC_M10
GO:0030149	0.47	0.69	13	23	sphingolipid catabolic process	BP	1	PPT1,SMPD2,ACER3,NEU3,ASAH1,SMPD4,GALC,GLA,HEXA,GM2A,CEL,ACER2,NEU2	grey	VSMC_M10
GO:0045454	0.47	0.66	18	32	cell redox homeostasis	BP	1	TXN2,TXNRD1,PRDX1,ERP44,DLD,TXNRD3,PRDX3,EGLN2,HVCN1,GLRX2,SLC2A10,NFE2L2,SLC11A1,NOS2,TXNDC2,NQO1,DDIT3,TXN	grey	VSMC_M10
GO:0003198	0.48	0.72	8	14	epithelial to mesenchymal transition involved in endocardial cushion formation	BP	1	TGFBR2,TGFB2,SNAI1,RBPJ,TMEM100,ENG,NOG,HEY2	grey	VSMC_M10
GO:0043647	0.48	0.64	23	42	inositol phosphate metabolic process	BP	1	SYNJ2,IPPK,INPP4A,PLEK,INPP4B,MTMR2,ITPKC,MTMR7,P2RY1,PTK2B,SYNJ1,ITPKA,ITPK1,INPP5A,GPER1,IP6K2,NTSR1,INPP5J,PTH1R,IMPA2,INPP5K,MINPP1,INPP1	grey	VSMC_M10
GO:2001032	0.48	0.68	14	25	regulation of double-strand break repair via nonhomologous end joining	BP	1	MRNIP,HSF1,POT1,CYREN,SIRT7,SHLD1,PRKDC,ERCC6,PARP9,DTX3L,SHLD2,WRAP53,SMCHD1,NUDT16L1	grey	VSMC_M10
GO:0072677	0.48	0.76	6	10	eosinophil migration	BP	1	ADAM8,DAPK2,CCL5,CCL7,CCL2,PTGER4	grey	VSMC_M10
GO:0098743	0.48	0.71	9	16	cell aggregation	BP	1	MAPK14,ROR2,MYCN,SOX9,SOX6,BMPR1B,THRA,PKD1,OTOR	grey	VSMC_M10
GO:1900153	0.48	0.72	8	14	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	BP	1	PABPC1,AGO2,TNRC6B,TNRC6C,CNOT1,TOB1,NANOS1,ZFP36L2	grey	VSMC_M10
GO:0042130	0.48	0.65	22	40	negative regulation of T cell proliferation	BP	1	TNFRSF21,PELI1,IL4I1,FOXJ1,PAWR,PRNP,CASP3,TMEM131L,MARCH7,BTN2A2,PRKAR1A,DLG1,VSIR,RC3H1,PTPN6,SCGB1A1,FOXP3,ZBTB7B,TWSG1,GLMN,CEBPB,HAVCR2	grey	VSMC_M10
GO:0051013	0.48	0.74	7	12	microtubule severing	BP	1	VPS4B,KATNA1,KATNAL1,KATNB1,FIGN,TTLL11,FIGNL2	grey	VSMC_M10
GO:0061709	0.48	0.72	8	14	reticulophagy	BP	1	TMEM173,DDRGK1,ULK1,TEX264,UFC1,ATG2A,RETREG3,ATG2B	grey	VSMC_M10
GO:0021953	0.48	0.60	62	116	central nervous system neuron differentiation	BP	1	UQCRQ,PTCH1,AGTPBP1,PLXNA4,NTRK2,SMO,NDNF,GLI2,IFT172,MYCBP2,MNX1,POU4F1,TSKU,SZT2,RAC3,SEMA3A,EPHB1,TOX,ZSWIM6,DCLK2,FAIM2,RAPGEF2,NKX6-1,NR4A2,ZNF335,LDB1,SUFU,SLC4A10,SATB2,ADARB1,GIGYF2,TTC21B,DISC1,GBX2,DLX1,EPHB3,MAPT,MDGA2,NIN,SCYL3,TULP3,EPHA4,CLN8,MPP5,PSEN1,NDEL1,CHRNB2,BCL11B,LHX1,SIN3A,ISL1,CHD5,PLXNA3,LHX8,UBB,CNTN2,FOXG1,SOX4,GRID2,ISL2,LBX1,CEND1	grey	VSMC_M10
GO:0070989	0.48	0.74	7	12	oxidative demethylation	BP	1	ALKBH3,FTO,ALKBH2,TET1,CYP3A43,ALKBH1,ALKBH5	grey	VSMC_M10
GO:0060396	0.48	0.71	9	16	growth hormone receptor signaling pathway	BP	1	PTK2,LEPROTL1,PIK3R1,PXN,GDF15,STAT3,STAT5B,GHR,LEPROT	grey	VSMC_M10
GO:0071378	0.48	0.71	9	16	cellular response to growth hormone stimulus	BP	1	PTK2,LEPROTL1,PIK3R1,PXN,GDF15,STAT3,STAT5B,GHR,LEPROT	grey	VSMC_M10
GO:0000028	0.48	0.72	9	15	ribosomal small subunit assembly	BP	1	RRP7A,RPS14,RPSA,PRKDC,MRPS11,RPS27,XRCC5,ERAL1,RPS27L	grey	VSMC_M10
GO:0043523	0.48	0.58	91	169	regulation of neuron apoptotic process	BP	1	ERBB3,LRP1,AGAP2,PRKN,SYNGAP1,GRM4,ATF4,NTRK2,NRBP2,CNTFR,SLC1A1,TFAP2B,MSH2,PPT1,EPHA7,FOXO3,NTF4,NDNF,C5AR1,GRIK5,XRCC2,EGLN2,POU4F1,ARRB1,PRNP,GPI,CASP3,GBE1,FBXW7,TRIM2,MEF2C,FAIM2,PTK2B,NR4A2,F2R,NQO2,TFAP2A,BDNF,HDAC1,TERT,TGFB2,SLC30A10,KCNB1,KRAS,ADNP,MCL1,HYOU1,NFATC4,HDAC4,DLX1,BACE1,DNAJC5,FZD9,EGLN3,SNX6,MAP3K11,ADAM8,NONO,FIS1,PINK1,PARP1,PSEN1,ITGAM,AC138894.1,CITED1,ALKBH1,GPRASP2,BHLHB9,CCL2,CDK5R1,ISL1,JUN,PDPK1,MECP2,PARK7,LCN2,STXBP1,AARS,NQO1,NAE1,MIR125B1,RHOA,GRID2,CNTF,SIX1,DDIT3,BCL2L11,HRAS,CEBPB,PITX3,NMNAT1	grey	VSMC_M10
GO:0002690	0.48	0.61	39	71	positive regulation of leukocyte chemotaxis	BP	1	GPSM3,PTK2,RAC2,CCL27,FPR2,CXCL8,AKIRIN1,PTN,C5AR1,OXSR1,NCKAP1L,GAS6,VEGFC,PTK2B,F2RL1,ANO6,DNM1L,TRPV4,PRSS56,CMKLR1,MOSPD2,IL12A,MCU,TNFSF18,CXCR2,MAPK1,TMEM102,PGF,DAPK2,MAPK3,IL6R,S100A14,CD74,CCL5,CSF1R,CCL7,DEFB124,ZNF580,WNT5A	grey	VSMC_M10
GO:0098732	0.48	0.60	55	102	macromolecule deacylation	BP	1	BAZ2A,ABHD16A,PPT2,C6orf89,ABHD17B,PPT1,SPHK2,HDAC2,PRKD2,PHB,HDAC11,BEX4,TADA3,SIRT2,SIRT7,SIRT3,MTA3,LYPLA1,SDR16C5,ING2,HDAC7,SIRT5,SUDS3,ELK4,SIRT4,HDAC1,LYPLAL1,RCOR3,PER2,HDAC4,MAPT,BCL6,ABHD12B,RCOR2,PINK1,TBL1XR1,KDM5A,FOXP3,AKAP8L,AKAP8,JDP2,ZBTB7B,SFPQ,SIN3A,RCOR1,SREBF1,SKI,ABHD17A,MIER2,PRMT6,ABHD10,SAP30BP,ABHD17C,NNMT,LYPLA2	grey	VSMC_M10
GO:0043392	0.48	0.64	22	40	negative regulation of DNA binding	BP	1	HABP4,C6orf106,SMO,MDFI,ZNF462,HDAC2,RSF1,HAND2,FBXW7,SP100,PER2,MSX2,PSEN1,TAF1,WFIKKN2,SIN3A,ERCC4,JUN,WFIKKN1,DDIT3,ZNF593,HEY2	grey	VSMC_M10
GO:0016574	0.48	0.64	24	44	histone ubiquitination	BP	1	SKP1,UBE2B,RNF20,BMI1,UBE2E1,RYBP,DDB2,PCGF6,DTX3L,RNF168,PHC1,BCOR,ATXN7L3,LEO1,DDB1,PCGF3,TRIM37,OTUB2,CUL4B,PARK7,RNF8,UBE2N,UBE2U,CBX8	grey	VSMC_M10

GO:0048596	0.48	0.70	10	18	embryonic camera-type eye morphogenesis	BP	1	FRS2,IFT172,TFAP2A,PAX2,ALDH1A3,SP3,FZD5,TBX2,STRA6,WNT5A	grey	VSMC_M10
GO:0050922	0.48	0.64	25	46	negative regulation of chemotaxis	BP	1	SEMA6A,SEMA4D,SEMA4C,C5AR2,SEMA3D,SEMA3A,RYK,ROBO1,ROBO2,SEMA4F,SEMA3G,SEMA4G,SEMA3F,SLAMF8,PTPRO,WNT3,SEMA6D,PADI2,SEMA4A,CCL2,PTPN2,PLXNA3,DPP4,WNT5A,DUSP1	grey	VSMC_M10
GO:0031122	0.48	0.63	28	52	cytoplasmic microtubule organization	BP	1	TUBGCP6,SLAIN2,PLK3,IFT172,SLAIN1,CLIP4,CCDC13,HOOK3,CLIP1,TUBGCP5,SLK,TRPV4,TUBGCP4,CIB1,WDR73,LIMK2,DLG1,MAPT,TUBG1,CEP126,KPNB1,HOOK2,RAB11A,CCDC88C,CAMSAP3,FSD1,CAMSAP1,RHOA	grey	VSMC_M10
GO:0046475	0.48	0.67	14	25	glycerophospholipid catabolic process	BP	1	ABHD16A,PLA2G6,APOC1,PLA2G4B,PLA2G4A,ABHD12B,SMPD4,LIPC,GDPD3,LDLR,GDPD1,GDE1,PNPLA6,PLA2G15	grey	VSMC_M10
GO:0062013	0.48	0.60	52	96	positive regulation of small molecule metabolic process	BP	1	PPARA,PRXL2C,GUCA1B,GPT,PRKCE,PPP4R3B,SLC4A4,NR1H2,EPM2AIP1,AKT2,NR1H4,CYP7A1,SORBS1,GPD1,P2RX7,P2RY1,NR1H3,IGF2,GPLD1,IRS1,CPT1A,ZBTB20,PPP1R3E,GPER1,ARNT,LPGAT1,ACTN3,NTSR1,MLXIPL,SCAP,POR,PTH1R,COMT,WNT4,PINK1,STAT3,DDB1,PSEN1,CD74,INSR,SREBF1,NOS2,PTPN2,PARK7,MLYCD,ENTPD5,LDLRAP1,NNMT,STARD4,CLYBL,FGF1,ARPP19	grey	VSMC_M10
GO:0070302	0.48	0.58	81	151	regulation of stress-activated protein kinase signaling cascade	BP	1	PHLPP1,MAP3K5,STK3,MAPK8IP2,MAP3K4,PRKN,AGER,MYC,GADD45G,KLHL31,PRDX1,SEMA4C,DNAJA1,FKTN,EMC10,MTURN,NOD1,EGFR,TLR4,TRAF1,SDCBP,MYD88,ZMYND11,PLCB1,EIF2AK2,RELL2,SEMA3A,SH3RF2,ARL6IP5,MFHAS1,TRAF6,EPHB1,HAND2,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,TRPV4,PDCD4,TGFB2,NCF1,TRAF5,FZD7,MAP3K3,MAGI3,DLG1,MAP3K11,AIDA,DUSP10,MBIP,MEN1,MAP4K2,DUSP19,PDCD10,PINK1,LTBR,MAPK1,MINK1,GPS2,RELL1,TAOK2,MAPK3,MAP2K1,NCOR1,TRAF3,TAOK1,SERPINF2,MAPK8IP3,TRAF2,MARVELD3,DAB2IP,ZNF622,WNT5A,GADD45A,INAVA,DUSP1,DUSP22,HRAS	grey	VSMC_M10
GO:0019730	0.48	0.67	16	28	antimicrobial humoral response	BP	1	CXCL14,PLA2G6,GAPDH,CXCL8,NOD2,PPP2R3C,SLC11A1,SPON2,GATA6,FGA,S100A12,HIST1H2BK,CXCL6,JCHAIN,HIST1H2BF,HIST1H2BJ	grey	VSMC_M10
GO:0042761	0.48	0.73	7	12	very long-chain fatty acid biosynthetic process	BP	1	HACD4,ELOVL1,ELOVL7,HACD2,TECR,HACD3,ELOVL3	grey	VSMC_M10
GO:0003337	0.48	0.73	7	12	mesenchymal to epithelial transition involved in metanephros morphogenesis	BP	1	SMO,SIX2,PAX8,PAX2,SALL1,CITED1,LIF	grey	VSMC_M10
GO:0003143	0.48	0.63	27	50	embryonic heart tube morphogenesis	BP	1	SMO,FOXH1,SRF,TEAD2,BBS7,SETDB2,MEGF8,IFT172,TGFBR2,OVOL2,MKKS,HAND2,MEF2C,IFT52,PKD2,RYR2,SUFU,PSEN1,SMAD3,TBX2,MIB1,RNF207,ENG,LBX1,WNT5A,C2CD3,NKX2-5	grey	VSMC_M10
GO:1901569	0.48	0.75	6	10	fatty acid derivative catabolic process	BP	1	ABHD16A,HPGD,FITM2,OXCT1,NUDT19,LYPLA2	grey	VSMC_M10
GO:0006929	0.48	0.69	11	20	substrate-dependent cell migration	BP	1	ANKS1A,ITGB1BP1,SDCBP,ROBO1,VEGFC,STK4,ADAM8,FN1,NTN1,ITGA11,CSPG4	grey	VSMC_M10
GO:0001510	0.48	0.61	40	73	RNA methylation	BP	1	RNMT,TFB1M,TRMT11,CMTR1,MTO1,NSUN6,THUMPD3,TRMT6,WTAP,THUMPD2,TRMT9B,TGS1,DIMT1,BCDIN3D,NSUN3,TRMT10A,DALRD3,LCMT2,METTL8,NSUN5,METTL2B,TRMT1L,MEPCE,ALKBH8,TRMT5,HSD17B10,MRM2,ZCCHC4,METTL4,METTL6,MRM3,METTL16,CMTR2,METTL14,TRMT10B,TRMT61A,TRMT10C,TRMT61B,CBLL1,TYW3	grey	VSMC_M10
GO:0048670	0.48	0.71	9	16	regulation of collateral sprouting	BP	1	LRP1,FSTL4,SEMA4D,EPHA7,SPART,ULK1,SPP1,BDNF,WNT3	grey	VSMC_M10
GO:0090494	0.48	0.75	6	10	dopamine uptake	BP	1	PRKN,MAPK15,SLC6A2,SLC6A3,SLC29A4,PARK7	grey	VSMC_M10
GO:0071472	0.48	0.73	7	12	cellular response to salt stress	BP	1	XRCC6,AKR1B1,AQP1,TRPV4,XRCC5,MICU1,SLC25A23	grey	VSMC_M10
GO:0000722	0.48	0.73	7	12	telomere maintenance via recombination	BP	1	ERCC1,XRCC1,TPRKB,RAD51C,RAD51D,ERCC4,TERF2	grey	VSMC_M10
GO:2000402	0.48	0.73	7	12	negative regulation of lymphocyte migration	BP	1	ADTRP,CD200,APOD,MIA3,PADI2,CCL2,GCSAM	grey	VSMC_M10
GO:0034427	0.48	0.75	6	10	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	BP	1	SKIV2L,EXOSC4,EXOSC3,TTC37,DIS3L2,EXOSC5	grey	VSMC_M10
GO:0048246	0.49	0.66	15	27	macrophage chemotaxis	BP	1	PTK2,AKIRIN1,C5AR1,FAM19A4,MTUS1,PTK2B,TRPV4,CMKLR1,SLAMF8,TNFSF18,MAPK1,MAPK3,CCL5,CSF1R,CCL2	grey	VSMC_M10
GO:0045604	0.49	0.63	24	44	regulation of epidermal cell differentiation	BP	1	CYP27B1,PTCH1,CD109,HOXA7,MYCL,GRHL1,SFRP4,MYCN,PTCH2,OVOL2,MAFG,VDR,SRSF6,KDF1,SFN,KLF7,H2AFY2,ABCA12,MED1,KEAP1,MIR125B1,ZBED2,SGPP1,HEY2	grey	VSMC_M10
GO:0033623	0.49	0.72	8	14	regulation of integrin activation	BP	1	PLEK,FERMT1,CDH17,FARP2,RAP1B,FBLIM1,PTGER4,PIEZO1	grey	VSMC_M10
GO:0010867	0.49	0.73	7	12	positive regulation of triglyceride biosynthetic process	BP	1	NR1H2,NR1H3,GPLD1,SLC27A1,LDLR,SREBF1,CNEP1R1	grey	VSMC_M10
GO:1903861	0.49	0.69	10	18	positive regulation of dendrite extension	BP	1	NEDD4L,RIMS2,PRKN,CPNE5,RIMS1,CPNE9,SYT1,SLC23A2,MUL1,CACNG7	grey	VSMC_M10
GO:1901298	0.49	0.75	6	10	regulation of hydrogen peroxide-mediated programmed cell death	BP	1	MET,FOXO3,PAWR,PINK1,PARK7,MIR21	grey	VSMC_M10
GO:0030852	0.49	0.73	7	12	regulation of granulocyte differentiation	BP	1	IL5,TRIB1,TESC,HCLS1,ZBTB46,HAX1,EVI2B	grey	VSMC_M10
GO:0046006	0.49	0.67	14	25	regulation of activated T cell proliferation	BP	1	AGER,PRNP,CASP3,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,RC3H1,STAT5B,FOXP3,MIR21,FADD,TNFSF9	grey	VSMC_M10
GO:0032941	0.49	0.67	14	25	secretion by tissue	BP	1	PRKCE,AQP1,NR1H2,EGFR,ATG5,TRAF3IP2,NR1H3,CHRM3,COPA,CHRM1,SCNN1B,CELSR2,CEL,CYBA	grey	VSMC_M10
GO:0000492	0.49	0.75	6	10	box C/D snoRNP assembly	BP	1	C12orf45,TAF9,ZNHIT3,SNU13,ZNHIT6,PIH1D2	grey	VSMC_M10
GO:0048488	0.49	0.62	28	52	synaptic vesicle endocytosis	BP	1	CANX,SYNJ2,BTBD9,AMPH,ACTG1,SYT1,FCHO2,SYNJ1,SYT8,DNM1L,NLGN4Y,AP2M1,STX1A,DNM3,PPP3CB,ACTB,SLC2A4,NLGN2,DGKQ,GAK,SYT11,NLGN3,CALM1,DNM2,PIP5K1C,CEL,BTBD8,DENND1A	grey	VSMC_M10
GO:0140238	0.49	0.62	28	52	presynaptic endocytosis	BP	1	CANX,SYNJ2,BTBD9,AMPH,ACTG1,SYT1,FCHO2,SYNJ1,SYT8,DNM1L,NLGN4Y,AP2M1,STX1A,DNM3,PPP3CB,ACTB,SLC2A4,NLGN2,DGKQ,GAK,SYT11,NLGN3,CALM1,DNM2,PIP5K1C,CEL,BTBD8,DENND1A	grey	VSMC_M10
GO:0050855	0.49	0.71	8	14	regulation of B cell receptor signaling pathway	BP	1	PLCL2,FOXP1,LPXN,GPS2,CD19,PRKCB,CMTM3,GCSAM	grey	VSMC_M10

GO:0021879	0.49	0.65	16	29	forebrain neuron differentiation	BP	1	UQCRQ,NDNF,SEMA3A,ZSWIM6,DCLK2,RAPGEF2,SLC4A10,SATB2,DISC1,GBX2,DLX1,BCL11B,PLXNA3,LHX8,UBB,FOXG1	grey	VSMC_M10
GO:0003128	0.49	0.70	9	16	heart field specification	BP	1	FOXH1,WNT11,ROBO1,ROBO2,MEF2C,AXIN2,RBPJ,ISL1,WNT5A	grey	VSMC_M10
GO:0008334	0.49	0.70	9	16	histone mRNA metabolic process	BP	1	EXOSC4,LSM10,MTPAP,LSM1,TENT2,TENT4B,CPSF2,UPF1,ZNF473	grey	VSMC_M10
GO:0033151	0.49	0.71	8	14	V(D)J recombination	BP	1	TCF7,CYREN,PRKDC,XRCC4,DCAF1,BCL11B,YY1,NHEJ1	grey	VSMC_M10
GO:0002507	0.49	0.71	8	14	tolerance induction	BP	1	PHLPP1,TNFAIP3,FOXJ1,TGFBR2,MARCH7,FOXP3,HAVCR2,XKR8	grey	VSMC_M10
GO:0001845	0.49	0.71	8	14	phagolysosome assembly	BP	1	RAB7A,MYO7A,RAB7B,SPG11,PIKFYVE,SYT7,AC138894.1,RAB39A	grey	VSMC_M10
GO:0042180	0.49	0.57	81	150	cellular ketone metabolic process	BP	1	KDSR,ALDH8A1,PPARA,HSD17B3,AKR1B1,PRKCE,NR1H2,DKKL1,SLC7A11,SOX9,AKR1A1,APOC1,PRKAG2,SLC22A13,PIBF1,AKT2,IDO2,IDO1,PANK2,PDK1,NR1H4,TRIB3,CYP7A1,CBR4,DKK3,GPD1,NR1H3,COQ2,NQO2,CRYZL1,ERLIN1,CBR3,PRMT3,SIRT5,LONP2,SIRT4,SRD5A1,COQ5,IRS1,CPT1A,COQ10B,SLC7A7,ABCB11,DHRS9,LPGAT1,MLXIPL,SCAP,PDK3,ACADL,NMT1,TYSND1,COMT,PNKD,WNT4,NDUFA9,STAT5B,ACADVL,COQ8A,HSD17B10,FGFR4,DGKQ,AC138894.1,SCNN1B,CYP46A1,NCOR1,CD74,SREBF1,OXCT1,CACNA1H,PARK7,MLYCD,KYAT1,COQ4,KYAT3,MIR21,FABP5,GLO1,PDSS2,STARD4,INSIG2,ADH4	grey	VSMC_M10
GO:0032770	0.49	0.66	15	27	positive regulation of monooxygenase activity	BP	1	CYP27B1,NOD1,DHFR,PIK3CB,PTK2B,VDR,TERT,KRAS,NOS1AP,POR,GCH1,CALM1,PARK7,TERF2,FCER2	grey	VSMC_M10
GO:0030220	0.49	0.70	9	16	platelet formation	BP	1	MPIG6B,MYH9,SRF,PRKDC,CASP3,MEF2C,CIB1,NBEAL2,PTPN6	grey	VSMC_M10
GO:0036344	0.49	0.70	9	16	platelet morphogenesis	BP	1	MPIG6B,MYH9,SRF,PRKDC,CASP3,MEF2C,CIB1,NBEAL2,PTPN6	grey	VSMC_M10
GO:0044788	0.49	0.66	14	25	modulation by host of viral process	BP	1	YTHDC2,IGF2R,PRKN,PHB,FBXL2,EIF2AK4,CFL1,HSPA8,PC,PSMC3,FMR1,MIR222,TBC1D20,ZNF502	grey	VSMC_M10
GO:0086019	0.49	0.67	13	24	cell-cell signaling involved in cardiac conduction	BP	1	TRPM4,CACNB2,SCN5A,KCNJ3,TBX5,CASQ2,RYR2,PKP2,ANK2,SCN4B,CACNA1G,RNF207,HCN4	grey	VSMC_M10
GO:0050770	0.49	0.58	70	132	regulation of axonogenesis	BP	1	LRP1,SEMA6A,TIAM2,FSTL4,SYNGAP1,PLXNA4,NTRK2,SRF,SEMA4D,SEMA4C,BRSK1,RTN4,RUFY3,EPHA7,KEL,PLXNA1,GOLGA4,MEGF8,SEMA3D,SPART,PLXNC1,SEMA3A,ULK1,RYK,RET,ROBO1,ROBO2,SEMA4F,TIAM1,ZFYVE27,SEMA3G,SPP1,CYFIP1,SEMA4G,BDNF,KIAA0319,SEMA3F,ADNP,DISC1,CDKL5,EPHB3,WNT3,MAPT,SEMA6D,TNR,FN1,NIN,MARK2,EPHA4,PSEN1,SEMA4A,TRIM46,EFNA1,NDEL1,RAB11A,MAP2K1,NTN1,TRPV2,CDK5R1,DAB1,L1CAM,ARHGAP4,PLXNA3,AMIGO1,CNTN2,THY1,WNT5A,POU3F2,CHN1,EFNB3	grey	VSMC_M10
GO:0048311	0.49	0.70	9	16	mitochondrion distribution	BP	1	ARMC1,OPA1,DNM1L,MAPT,BHLHA15,HAP1,MSTO1,MTM1,CLUH	grey	VSMC_M10
GO:0009070	0.49	0.72	7	12	serine family amino acid biosynthetic process	BP	1	SHMT2,PSAT1,DHFR,SERINC5,CBSL,SHMT1,PHGDH	grey	VSMC_M10
GO:0090239	0.49	0.72	7	12	regulation of histone H4 acetylation	BP	1	ATG5,IWS1,ARRB1,TAF7,AUTS2,KAT7,MUC1	grey	VSMC_M10
GO:0034638	0.49	0.72	7	12	phosphatidylcholine catabolic process	BP	1	PLA2G6,APOC1,PLA2G4A,LIPC,GDPD3,LDLR,PLA2G15	grey	VSMC_M10
GO:0097028	0.49	0.65	16	29	dendritic cell differentiation	BP	1	AGER,TGFBR2,GAS6,TRAF6,CAMK4,F2RL1,ITGB6,ZBTB46,BATF2,LTBR,RBPJ,PSEN1,BATF,DHRS2,CEBPB,BATF3	grey	VSMC_M10
GO:0051148	0.49	0.61	30	55	negative regulation of muscle cell differentiation	BP	1	NFATC1,FRS2,PPARA,PI16,ANKRD17,SOX6,ZBED6,IGF2,BDNF,PDCD4,FZD7,HDAC4,BHLHA15,BMPR1A,FOXO4,RBPMS2,YY1,MECP2,PLPP7,NFATC3,MIR199A1,MIR21,MIR222,PRDM6,RGS4,TCF23,YBX1,EREG,NKX2-5,HEY2	grey	VSMC_M10
GO:0019362	0.49	0.67	13	23	pyridine nucleotide metabolic process	BP	1	NMRK1,SLC22A13,IDO2,IDO1,SLC5A8,NUDT12,NUDT17,PARP9,NAXE,NADK,NNMT,NAPRT,NMNAT1	grey	VSMC_M10
GO:0046496	0.49	0.67	13	23	nicotinamide nucleotide metabolic process	BP	1	NMRK1,SLC22A13,IDO2,IDO1,SLC5A8,NUDT12,NUDT17,PARP9,NAXE,NADK,NNMT,NAPRT,NMNAT1	grey	VSMC_M10
GO:0033540	0.49	0.72	7	12	fatty acid beta-oxidation using acyl-CoA oxidase	BP	1	CROT,ACOX1,ACOXL,ACOX2,EHHADH,DECR2,AMACR	grey	VSMC_M10
GO:0072189	0.50	0.70	9	16	ureter development	BP	1	OSR1,SOX9,RET,PAX2,ALDH1A2,LHX1,SOX8,FOXF1,SIX1	grey	VSMC_M10
GO:0006140	0.50	0.61	31	57	regulation of nucleotide metabolic process	BP	1	PPARA,PRXL2C,GUCA1B,SLC4A4,SPHK2,LACC1,PRKAG2,PDK1,GPD1,P2RX7,PRKAG1,FAM173B,ZBTB20,ARNT,ACTN3,HDAC4,DNAJC30,MLXIPL,PDK3,PINK1,STAT3,PARP1,PSEN1,OGT,NCOR1,INSR,NOS2,SLC2A6,ENTPD5,PDZD3,TIGAR	grey	VSMC_M10
GO:0090342	0.50	0.63	23	42	regulation of cell aging	BP	1	CDKN2A,NUAK1,CDK6,PNPT1,ZNF277,PAWR,PRKDC,PLK2,ING2,ARNTL,TERT,SLC30A10,KRAS,MAP3K3,BCL6,BMPR1A,YPEL3,VASH1,FZR1,TERF2,MIR21,MIR22,YBX1	grey	VSMC_M10
GO:0031060	0.50	0.61	28	52	regulation of histone methylation	BP	1	SNW1,PHF1,RNF20,SETD7,IWS1,KDM4A,PAXIP1,CHTOP,NSD3,DNMT3B,RTF1,ZNF335,JARID2,AUTS2,TET1,BCOR,WDR61,NELFA,NSD1,OGT,SUPT6H,MECP2,MTF2,GFI1,CTCF,PRMT6,ZNF304,NNMT	grey	VSMC_M10
GO:0060546	0.50	0.71	8	14	negative regulation of necroptotic process	BP	1	PELI1,RIPK1,FZD9,YBX3,BIRC3,MIR22,FADD,CASP8	grey	VSMC_M10
GO:0046676	0.50	0.64	17	31	negative regulation of insulin secretion	BP	1	PRKN,BMP8A,NDUFAF2,FAM3D,KCNJ11,ACVR1C,SIRT4,IRS1,HDAC1,PPP3CA,ADRA2A,KCNB1,KLF7,ENY2,SYTL4,SREBF1,CHGA	grey	VSMC_M10
GO:0043627	0.50	0.61	31	57	response to estrogen	BP	1	CYP27B1,ESR1,TPH2,TNFRSF11B,TEK,TGFBR2,SRA1,ASH2L,ARID5A,NCOA4,ZNF366,KMT2D,ABCC2,RBBP5,SRD5A1,CCND1,DTYMK,COMT,PTPRN,MAPK1,CITED1,IL4R,BCAS3,GATA6,KRT19,TRIM24,CA2,BGLAP,CRH,SERPINB9,SFR1	grey	VSMC_M10
GO:0048535	0.50	0.71	8	14	lymph node development	BP	1	IL15,TRAF3IP2,TOX,RC3H1,IL7R,FADD,CD248,RC3H2	grey	VSMC_M10
GO:0048520	0.50	0.72	7	12	positive regulation of behavior	BP	1	HDAC2,MEF2C,CFAP20,HDAC4,STRA6,SGIP1,CRH	grey	VSMC_M10
GO:0048532	0.50	0.69	9	16	anatomical structure arrangement	BP	1	PLXNA4,SEMA3A,TFAP2A,PAX2,SEMA3F,BMPR1A,DAB1,PLXNA3,HSPA5	grey	VSMC_M10
GO:0046189	0.50	0.65	16	29	phenol-containing compound biosynthetic process	BP	1	TPH2,GPR37,DDC,SLC7A11,HAND2,RAPGEF2,NR4A2,OCA2,SLC6A3,TGFB2,GCH1,HDC,CITED1,SLC45A2,PARK7,WNT5A	grey	VSMC_M10

GO:0034762	0.50	0.54	211	396	regulation of transmembrane transport	BP	1	NEDD4L,STAC3,MAPK8IP2,KCNV1,PRRT1,GOPC,CATSPER3,MAPK14,KCNJ4,PLA2G6,PIM1,ABCB1,CLIC5,SLC25A27,WNK2,TSPAN13,PRKCE,KCNQ4,SHANK1,SLC31A2,GRB10,HECW1,TCAF2,CLCN1,KEL,ATG5,OSR1,FGF21,BRAF,SPHK2,KCNJ14,SLC26A5,KCNRG,CACNB2,STAC,PRKAG2,OXSR1,SCN5A,SCN1A,AKT2,GPD1L,CACNB4,ASPSCR1,NALCN,PRNP,DIAPH1,CLIC1,ARL6IP5,KCNIP3,TRIB3,PIK3R1,SLMAP,SLC43A1,GLRX,SORBS1,MEF2C,P2RX7,HVCN1,KCNH3,PTK2B,KCNJ11,TPCN1,HOMER1,IFNGR2,KCNJ3,F2R,TESC,RIPK1,ANO6,KCNK15,KCNE2,PKD2,CASQ2,KCNJ15,KCNIP2,CHRM3,RYR2,FAM173B,PM20D1,AZIN2,IRS1,CALHM1,HECW2,KCNJ2,TERT,ADRA2A,ACSL5,TCIRG1,COX17,SCN2A,ISCU,KCNB1,KCNG1,SCN7A,UBASH3B,ANK2,C2CD5,GPER1,KLHL24,AGT,ACE2,ATP1A2,SLC9A1,PER2,C4orf3,CASQ1,PEA15,NTSR1,SCN4B,CNIH2,CLIC4,DNAJC30,NOS1AP,CATSPER2,DLG1,KCNK7,NFE2L2,CTTNBP2NL,CEMIP,SESTD1,PTPN6,KCNK4,HTT,CLTCL1,PINK1,ATP1B1,KCNA1,ARL6IP1,KCNMA1,KCNH4,GNB5,KCND1,MINK1,HAP1,DLG4,ACTB,PSEN2,RSC1A1,NLGN2,CNIH3,WNK3,STAC2,CACNB1,ATP1B2,PSEN1,KCNAB3,CACNA1A,KCNIP1,HCN3,NLGN3,CACNA1G,ATP2A1,CD19,CALM1,PRKCB,DNM2,VMP1,BDKRB1,INSR,CCL2,ASIC2,YES1,KCNJ18,C3,GPC3,FMR1,INPP5K,PDPK1,P2RX1,CACNA1B,OAZ1,RNF207,CACNA1H,PARK7,KCNC4,AMIGO1,CYBA,JPH3,LCN2,WWP2,RRAD,MIR21,MIR24-1,DMD,GPR35,FABP5,JPH2,CA2,KCNH2,FGF11,THY1,SCN2B,KCNK5,NETO2,CACNG7,CRBN,RGS4,CRH,KCNA6,APOPT1,YWHAH,TMEM109,SHISA8,KCNJ8,CACNG5,HCN4,GEM,PPIF,KCNG2,KCNJ9,ARPP19	grey	VSMC_M10
GO:0051224	0.50	0.58	52	96	negative regulation of protein transport	BP	1	PRKN,GOPC,RAB23,BMP8A,RSAD2,ITGB1BP1,FRMD4A,UBAC2,DPH3,FERMT1,BAG4,LYPLA1,NDUFAF2,FAM3D,PKIA,KCNJ11,NR1H3,RAB11FIP5,ACVR1C,F2R,DMTN,ADTRP,SUFU,SIRT4,IRS1,CABP1,CD200,HDAC1,PPP3CA,SP100,ADRA2A,KCNB1,YOD1,BAG3,APOD,KLF7,DERL3,IL12A,ENY2,C11orf65,RSC1A1,SNX12,SYTL4,SREBF1,INPP5K,PARK7,WWP2,MIR199A1,CHGA,TXN,UBE2G2,DERL2	grey	VSMC_M10
GO:0071391	0.50	0.71	8	14	cellular response to estrogen stimulus	BP	1	ESR1,SRA1,ARID5A,NCOA4,BCAS3,TRIM24,SERPINB9,SFR1	grey	VSMC_M10
GO:0019370	0.50	0.74	6	10	leukotriene biosynthetic process	BP	1	LTC4S,MGST2,PLA2G4A,GGT2,GGT6,GGT5	grey	VSMC_M10
GO:0086002	0.50	0.62	22	41	cardiac muscle cell action potential involved in contraction	BP	1	NEDD4L,TRPM4,CACNB2,SCN5A,SCN1A,GPD1L,KCNJ3,KCNE2,DSP,RYR2,PKP2,KCNJ2,ANK2,SCN4B,NOS1AP,DLG1,CACNA1G,DSG2,RNF207,KCNH2,SCN2B,KCNJ8	grey	VSMC_M10
GO:0050795	0.50	0.64	18	33	regulation of behavior	BP	1	HDAC2,NAPEPLD,MEF2C,CFAP20,EIF2AK4,TTC21B,HDAC4,STAT3,DLG4,CHRNB2,STRA6,SGIP1,LEPR,PER3,CNTNAP4,ZFHX3,HTR1D,CRH	grey	VSMC_M10
GO:2000010	0.50	0.69	9	16	positive regulation of protein localization to cell surface	BP	1	GPD1L,TM9SF4,LRIG2,ABCA12,STX4,ABCA7,CD247,TMEM35A,MAP1A	grey	VSMC_M10
GO:0002283	0.50	0.72	7	12	neutrophil activation involved in immune response	BP	1	MYD88,FCER1G,ITGAM,SCNN1B,STXBP2,PRAM1,DNASE1	grey	VSMC_M10
GO:0009268	0.50	0.64	17	31	response to pH	BP	1	ASIC3,ASIC1,HVCN1,RAB11FIP5,GPLD1,HYAL1,SLC38A3,SLC9A1,KCNK4,GPR68,ASIC2,TRPV1,CLCN7,PKD1L3,INSRR,CA2,IMPACT	grey	VSMC_M10
GO:0045947	0.50	0.69	9	16	negative regulation of translational initiation	BP	1	EIF3E,AGO2,ATF4,EIF2AK4,PAIP2B,BANK1,EIF4EBP2,LARP1,FMR1	grey	VSMC_M10
GO:0030859	0.50	0.67	11	20	polarized epithelial cell differentiation	BP	1	PTK7,RAB10,SYNE4,TCF15,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,WNT5A	grey	VSMC_M10
GO:0002688	0.50	0.58	50	92	regulation of leukocyte chemotaxis	BP	1	GPSM3,PTK2,RAC2,CCL27,FPR2,CXCL8,AKIRIN1,PTN,C5AR2,C5AR1,OXSR1,NCKAP1L,GAS6,MTUS1,VEGFC,PTK2B,SLC8B1,F2RL1,ANO6,NOD2,DNM1L,TRPV4,PRSS56,CMKLR1,SLAMF8,MOSPD2,IL12A,MCU,TNFSF18,CXCR2,BST1,MAPK1,PADI2,TMEM102,PGF,DAPK2,MAPK3,IL6R,S100A14,CD74,CCL5,CSF1R,CCL7,CCL2,MPP1,DEFB124,DPP4,ZNF580,WNT5A,DUSP1	grey	VSMC_M10
GO:0014904	0.50	0.64	17	31	myotube cell development	BP	1	STAC3,SMO,KEL,KLHL40,RYR1,P2RX2,LMOD3,HOMER1,BIN3,PPP3CA,ACTN3,HDAC4,FBXO22,SKI,SMYD3,SIX1,MYORG	grey	VSMC_M10
GO:0007039	0.50	0.68	10	18	protein catabolic process in the vacuole	BP	1	LRP1,MFSD8,TMEM106B,TCIRG1,ATP13A2,AC138894.1,LDLR,RNF128,LAMP2,TMEM199	grey	VSMC_M10
GO:0090022	0.50	0.65	15	27	regulation of neutrophil chemotaxis	BP	1	RAC2,CXCL8,C5AR2,C5AR1,NCKAP1L,NOD2,DNM1L,MOSPD2,MCU,CXCR2,BST1,DAPK2,CD74,MPP1,DPP4	grey	VSMC_M10
GO:2000269	0.50	0.69	9	16	regulation of fibroblast apoptotic process	BP	1	XRCC2,CHD8,BTG1,GAS6,PRDM11,STK17B,CFDP1,MIR24-1,BCL2L11	grey	VSMC_M10
GO:0033077	0.50	0.60	33	61	T cell differentiation in thymus	BP	1	SRF,ATG5,BMI1,CLPTM1,GLI2,FOXJ1,PRKDC,TOX,ZC3H8,IL1A,CAMK4,TMEM131L,RASGRP1,RABL3,FZD7,CD28,ADAM8,FZD5,WNT4,STAT5B,FOXP3,CARD11,DOCK2,BCL11B,CD74,JAG2,IL7R,PTPN2,DNAJA3,MAFB,FADD,ZFP36L2,PRR7	grey	VSMC_M10
GO:0042472	0.50	0.59	39	73	inner ear morphogenesis	BP	1	FZD6,PTK7,ROR2,DLX5,KCNQ4,WHRN,SOBP,MYO3A,SOX9,USH1G,GLI2,MYO7A,SPRY2,CEP290,PAX8,EYA1,PLS1,FZD3,USH1C,TFAP2A,PAX2,ALDH1A3,GBX2,MYO3B,GRHL3,STRC,STOX1,DVL2,TCAP,POU3F4,NTN1,CHRNA10,FOXG1,MAFB,WNT5A,OTX1,SIX1,INSIG2,ZIC1	grey	VSMC_M10
GO:0021517	0.50	0.64	17	31	ventral spinal cord development	BP	1	PTCH1,VSTM5,GLI2,IFT172,MNX1,SUFU,GIGYF2,MDGA2,SCYL3,CLN8,LHX1,ISL1,DAB1,LRP8,SOX4,ISL2,LBX1	grey	VSMC_M10
GO:0050954	0.50	0.57	64	120	sensory perception of mechanical stimulus	BP	1	ATP8B1,MYO1A,EYA4,ALDH7A1,COL11A2,PHF24,CLIC5,KIT,KCNQ4,GSDME,MYH14,WHRN,SOBP,SLC26A5,MYO3A,MYO7B,EML2,USH1G,ASIC3,SCN1A,MYO7A,SPRY2,MKKS,LRTOMT,AP000812.5,TMTC4,DIAPH1,P2RX2,TUB,CASP3,MARVELD2,EYA1,ADGRV1,USH1C,TFAP2A,PGAP1,MYO3B,COCH,BACE1,STRC,HOMER2,CDKN1B,LRIG2,CEMIP,CDH23,KCNK4,RAB3A,KCNA1,CHRNB2,POU3F4,OTOA,CRYM,ASIC2,TRPV1,CDC14A,SRRM4,PJVK,CHRNA10,EPS8L2,SIX1,DDIT3,OTOR,TIMM8B,OTOS	grey	VSMC_M10
GO:0090344	0.50	0.68	10	18	negative regulation of cell aging	BP	1	CDK6,PRKDC,PLK2,TERT,SLC30A10,MAP3K3,BCL6,FZR1,TERF2,YBX1	grey	VSMC_M10
GO:1903830	0.50	0.69	9	16	magnesium ion transmembrane transport	BP	1	NIPAL2,SLC41A2,CNNM4,ZDHHC13,NIPA1,SLC41A1,NIPAL3,NIPAL4,NIPAL1	grey	VSMC_M10

GO:0048569	0.50	0.70	8	14	post-embryonic animal organ development	BP	1	BAK1,ERCC1,MYO7A,FZD5,FBN1,MFAP2,BCL11B,BCL2L11	grey	VSMC_M10
GO:0042476	0.51	0.58	51	95	odontogenesis	BP	1	OSR2,PPARA,TNFRSF11B,SMO,CNNM4,SOSTDC1,KLK4,ACP4,AQP1,TNC,OSR1,HDAC2,SLC4A2,GLI2,SCN5A,ACVR2A,RELT,TRAF6,HAND2,TFAP2A,ITGB6,HDAC1,TGFB2,TCIRG1,FAM20A,FAM20C,AXIN2,AMELX,HTRA1,LAMA5,DLX1,BCOR,ALPL,BMPR1A,SP6,NGFR,DLX3,BCL11B,JAG2,ROGDI,BSG,ANKRD11,LHX8,RHOA,LAMB1,CA2,BGLAP,ZNF22,SNX10,BCL2L11,PERP	grey	VSMC_M10
GO:0001909	0.51	0.60	33	61	leukocyte mediated cytotoxicity	BP	1	CD226,STX7,AGER,HLA-DRA,PRDX1,NECTIN2,PVR,UNC13D,MYD88,SLC22A13,NCKAP1L,RASGRP1,F2RL1,CADM1,CTSH,IL12A,PTPN6,LAG3,PPP3CB,STAT5B,ITGAM,SCNN1B,STXBP2,VAV1,NOS2,IL7R,CRK,DNASE1,AP1G1,FADD,CXCL6,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0042490	0.51	0.60	28	52	mechanoreceptor differentiation	BP	1	ATP8B1,NTRK2,GSDME,MYCL,WHRN,MYCN,NTF4,USH1G,MYO7A,TSKU,SLC4A7,JAG1,LRTOMT,AP000812.5,PLS1,ADGRV1,USH1C,TRIP11,STRC,CDH23,RBPJ,MKS1,TMEM132E,JAG2,IFT20,MCOLN3,PJVK,HEY2	grey	VSMC_M10
GO:0032722	0.51	0.61	26	48	positive regulation of chemokine production	BP	1	LRP1,AGER,TRIM32,TLR4,MYD88,EIF2AK2,MAVS,IL7,OAS3,RIPK2,F2RL1,NOD2,HDAC1,TRPV4,DDX3X,IL6R,IL4R,CD74,CSF1R,TICAM1,OAS1,DEFB124,WNT5A,IL33,TSLP,HAVCR2	grey	VSMC_M10
GO:0034694	0.51	0.66	12	22	response to prostaglandin	BP	1	PRKCE,TNC,APOB,AANAT,PTGER2,AKAP8,YY1,ACACA,PTGER4,GNB1,PTGFR,GNG2	grey	VSMC_M10
GO:0043267	0.51	0.67	10	18	negative regulation of potassium ion transport	BP	1	NEDD4L,KEL,KCNRG,OXSR1,PTK2B,KCNE2,CASQ2,KCNH2,CRBN,RGS4	grey	VSMC_M10
GO:0009620	0.51	0.64	15	27	response to fungus	BP	1	USP15,BAK1,GAPDH,TLR4,ATG5,MYD88,SPON2,MPO,S100A8,BTK,CRK,BCL10,S100A12,CHGA,COTL1	grey	VSMC_M10
GO:0045010	0.51	0.61	24	44	actin nucleation	BP	1	ARPC3,WASHC5,PICK1,LMOD2,WASF1,FCHSD2,ARFIP2,LMOD3,HIP1R,FMN1,IQGAP2,CYFIP1,MAGEL2,LMOD1,AP1AR,WASF2,WHAMM,NCKAP1,ARPC1A,WAS,EVL,SPIRE2,WDR63,GMFG	grey	VSMC_M10
GO:0042769	0.51	0.71	7	12	DNA damage response, detection of DNA damage	BP	1	MRPS9,DNAJA1,MRPS26,MRPS35,MRPS11,PARP1,SOX4	grey	VSMC_M10
GO:0019395	0.51	0.58	47	87	fatty acid oxidation	BP	1	HSD17B4,CPT1B,PPARA,MCAT,ECHDC1,MAPK14,CROT,ADH5,ETFB,HADHA,SOX9,PRKAG2,ACOX1,CYGB,AKT2,HACL1,ACOXL,ACOX2,PEX2,ETFDH,IVD,ECI2,LONP2,SIRT4,IRS1,CPT1A,BDH2,ABCB11,EHHADH,POR,ACADL,TYSND1,ACADVL,HSD17B10,ABCD4,GCDH,ACAA2,DECR2,MLYCD,ABCD3,ACADM,PHYH,HADHB,AMACR,ECI1,AUH,ADH4	grey	VSMC_M10
GO:0046580	0.51	0.61	23	43	negative regulation of Ras protein signal transduction	BP	1	SYNGAP1,MET,SPRY1,SPRY2,PPP2CB,RASA3,RASA2,ARHGAP24,TGFB2,RASA4,BCL6,ABL2,LZTR1,RASAL3,MFN2,ITGA3,KCTD13,ARHGAP44,TNFAIP1,MAPKAP1,SCAI,DAB2IP,STAMBP	grey	VSMC_M10
GO:0036499	0.51	0.68	9	16	PERK-mediated unfolded protein response	BP	1	ATF4,NCK2,QRICH1,NFE2L2,PTPN2,ABCA7,HSPA5,DDIT3,PPP1R15A	grey	VSMC_M10
GO:0050849	0.51	0.67	10	18	negative regulation of calcium-mediated signaling	BP	1	FHL2,PLEK,PRNP,SLA2,TBC1D10C,MYOZ2,ACTN3,HOMER2,MYOZ1,MAPK7	grey	VSMC_M10
GO:0061162	0.51	0.66	12	22	establishment of monopolar cell polarity	BP	1	PTK7,FOXJ1,SYNE4,TCF15,GBF1,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,WNT5A	grey	VSMC_M10
GO:0035089	0.51	0.66	11	20	establishment of apical/basal cell polarity	BP	1	PTK7,FOXJ1,SYNE4,TCF15,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,WNT5A	grey	VSMC_M10
GO:0046500	0.51	0.69	8	14	S-adenosylmethionine metabolic process	BP	1	GNMT,APIP,AHCY,ENOPH1,MTRR,MAT1A,METTL16,PEMT	grey	VSMC_M10
GO:1903427	0.51	0.69	8	14	negative regulation of reactive oxygen species biosynthetic process	BP	1	PPARA,SLC30A10,STAT3,PARK7,MIR21,RHOA,APOPT1,AC140504.1	grey	VSMC_M10
GO:0046683	0.51	0.57	50	94	response to organophosphorus	BP	1	NME1,TEK,PNPT1,AREG,AQP1,TRPM4,TRPC3,PANX1,AANAT,THBD,CRLS1,P2RX2,P2RX3,RYR3,GPD1,P2RX7,P2RY1,PTK2B,RAPGEF2,KCNJ11,STC1,RAPGEF3,PKD2,DMTN,SRD5A1,SLC6A3,SSH1,RAP1B,DUOX1,VGF,CPS1,FDX1,PTPRN,DGKQ,PKLR,FOS,TAF1,CITED1,PPARGC1B,SREBF1,JUN,INPP5K,TRPV1,P2RX1,BSG,ASS1,HSPA5,DUSP1,HCN4,PDXP	grey	VSMC_M10
GO:0021854	0.51	0.69	8	14	hypothalamus development	BP	1	UQCRQ,NDNF,SEMA3A,SRD5A1,HAP1,UBB,POU3F2,CRH	grey	VSMC_M10
GO:0044273	0.51	0.65	14	25	sulfur compound catabolic process	BP	1	CHAC2,GLB1,CSAD,AHCY,FITM2,MTRR,CBSL,HYAL1,GGT2,MAT1A,IDUA,MLYCD,NUDT19,GGT5	grey	VSMC_M10
GO:0046621	0.51	0.63	16	29	negative regulation of organ growth	BP	1	STK3,PPARA,PI16,TGFBR2,TBX5,STK4,JARID2,KCNK2,SAV1,WWC1,YY1,MIR199A1,MIR25,NOG,FXN,RGS4	grey	VSMC_M10
GO:0035020	0.51	0.67	10	18	regulation of Rac protein signal transduction	BP	1	KBTBD6,PIK3CB,ARHGAP24,AUTS2,KRAS,OGT,DNM2,ARHGAP44,CRK,CADM4	grey	VSMC_M10
GO:0001662	0.51	0.67	10	18	behavioral fear response	BP	1	MAPK8IP2,USP46,SLC1A1,MEF2C,ASIC1,ATP1A2,ASIC4,MECP2,DPP4,CRH	grey	VSMC_M10
GO:0045061	0.51	0.68	9	16	thymic T cell selection	BP	1	SRF,ATG5,TOX,CD28,CARD11,DOCK2,CD74,JAG2,PTPN2	grey	VSMC_M10
GO:0016239	0.51	0.59	30	56	positive regulation of macroautophagy	BP	1	PIP4K2C,EPM2A,SPTLC1,NOD1,SCOC,SESN3,PIP4K2A,OPTN,RALB,TMEM173,DCN,ULK1,RIPK2,NOD2,BAG3,HTT,PINK1,VPS13D,MAPK3,LARP1,SMCR8,IKBKG,GPSM1,GNAI3,KIAA1324,TSC1,SH3GLB1,BNIP3L,IRGM,HSPB8	grey	VSMC_M10
GO:0045058	0.51	0.62	18	33	T cell selection	BP	1	SRF,IL15,ATG5,TOX,CD28,TNFSF18,STAT3,FOXP3,CARD11,TBX21,DOCK2,BATF,IL6R,BCL11B,CD74,JAG2,PTPN2,RHOA	grey	VSMC_M10
GO:0036120	0.51	0.66	11	20	cellular response to platelet-derived growth factor stimulus	BP	1	MARS,HAS1,PTN,TLR4,HYAL1,CBL,SYAP1,CREB1,YES1,MTSS1L,PDGFD	grey	VSMC_M10
GO:0002053	0.51	0.66	11	20	positive regulation of mesenchymal cell proliferation	BP	1	MYC,SMO,MYCN,SOX9,TGFBR2,CHRD,BMPR1A,FOXF1,WNT5A,SIX1,WNT2	grey	VSMC_M10
GO:0006970	0.51	0.58	38	71	response to osmotic stress	BP	1	MAP7,SLC12A2,TSPO,XRCC6,AKR1B1,MAPK13,ABCB1,AQP1,EGFR,PLK3,OXSR1,HNMT,CASP3,PTK2B,PKD2,SLC12A5,ICOSLG,TRPV4,SCN2A,YBX3,SORD,DDX3X,XRCC5,MICU1,KCNMA1,SLC2A4,WNK3,AC138894.1,LRRC8E,SLC25A23,PDPK1,LRRC8A,MARVELD3,MT-CYB,LRRC8D,CLDN1,TSC22D3,MAP2K7	grey	VSMC_M10

GO:0051650	0.51	0.55	76	143	establishment of vesicle localization	BP	1	MYO1A,AP3S1,KIF5A,PRKN,KIF3A,FAM91A1,EXOC4,MAPK15,STARD3NL,BBS7,MYO7B,CLASP2,MYO7A,AP3M2,KIF5C,MKKS,LIN7A,TMEM230,KIF3B,RASGRP1,ARFGAP2,EXOC6B,SYNJ1,AP3B1,DTNBP1,KIF13A,GBF1,BICDL1,KLHL12,TRIP11,PEF1,TCIRG1,PDCD6,SNAP23,SHROOM2,AP1AR,MLPH,RAB17,CNIH2,LIMK2,TANC2,SPG11,BLOC1S6,ITGA4,MAP4K2,MREG,HTT,RAB3A,PINK1,SNAP29,AP3M1,KIF1C,HAP1,SLC2A4,PSEN1,SYT11,TMED10,TRIM46,NDEL1,AC138894.1,RAB11A,SNAPIN,DNM2,AP1M2,MYO1D,C17orf75,PPP6C,MYO1F,MYO5B,BICDL2,PRKCZ,IKBKG,FNBP1L,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0010421	0.51	0.71	7	12	hydrogen peroxide-mediated programmed cell death	BP	1	MET,FOXO3,PAWR,PDCD10,PINK1,PARK7,MIR21	grey	VSMC_M10
GO:0048483	0.51	0.62	20	37	autonomic nervous system development	BP	1	GFRA3,PLXNA4,SOX10,TFAP2B,SEMA3A,RET,HAND2,FZD3,TLX2,TFAP2A,SEMA3F,ADARB1,HLX,GBX2,FN1,RHOXF1,PLXNA3,SOX8,SOX4,SIX1	grey	VSMC_M10
GO:0050871	0.52	0.59	33	61	positive regulation of B cell activation	BP	1	IL5,TNFRSF13C,EXOSC3,MSH2,PELI1,TLR4,HMCES,BMI1,MLH1,PAXIP1,SHLD1,NCKAP1L,MEF2C,IL7,NOD2,CD40,CD28,PPP2R3C,BCL6,TNIP2,CD38,BST1,STAT5B,SHLD2,CARD11,TBX21,CHRNB2,BTK,CD74,CD320,TICAM1,VAV3,TNFSF13B	grey	VSMC_M10
GO:0021680	0.52	0.64	13	24	cerebellar Purkinje cell layer development	BP	1	UQCRQ,AGTPBP1,WHRN,B4GALT2,FAIM2,LDB1,TTC21B,SPTBN2,LHX1,SEZ6,AARS,HSPA5,CEND1	grey	VSMC_M10
GO:1905523	0.52	0.67	10	18	positive regulation of macrophage migration	BP	1	PTK2,AKIRIN1,C5AR1,TRPV4,CMKLR1,TNFSF18,MAPK1,MAPK3,CCL5,CSF1R	grey	VSMC_M10
GO:0032731	0.52	0.62	18	33	positive regulation of interleukin-1 beta production	BP	1	AGER,NOD1,TLR4,PANX1,MYD88,P2RX7,RIPK2,F2RL1,NOD2,FZD5,HK1,STAT3,PYDC1,SMAD3,ISL1,CASP8,WNT5A,INAVA	grey	VSMC_M10
GO:0050864	0.52	0.57	50	93	regulation of B cell activation	BP	1	TNFAIP3,IL5,TNFRSF13C,TNFRSF21,EXOSC3,MSH2,PELI1,IL4I1,TLR4,HMCES,BMI1,MLH1,FOXJ1,PAXIP1,PAWR,SHLD1,NCKAP1L,CASP3,MEF2C,IL7,NOD2,CD40,BANK1,TBC1D10C,SLAMF8,THEMIS2,CD28,PPP2R3C,BCL6,RC3H1,PTPN6,TNIP2,CD38,BST1,STAT5B,INHA,FOXP3,SHLD2,CARD11,TBX21,CHRNB2,CD19,BTK,CD74,CD320,SUPT6H,TICAM1,VAV3,ZFP36L2,TNFSF13B	grey	VSMC_M10
GO:0061952	0.52	0.69	8	14	midbody abscission	BP	1	VPS4B,MITD1,CHMP2A,CHMP2B,CHMP4C,CHMP7,CHMP1A,VPS4A	grey	VSMC_M10
GO:0002792	0.52	0.62	19	35	negative regulation of peptide secretion	BP	1	PRKN,BMP8A,NDUFAF2,FAM3D,KCNJ11,ACVR1C,SIRT4,IRS1,HDAC1,PPP3CA,ADRA2A,KCNB1,KLF7,ENY2,SYTL4,CD74,SREBF1,CHGA,CRH	grey	VSMC_M10
GO:0060547	0.52	0.68	9	16	negative regulation of necrotic cell death	BP	1	PELI1,RIPK1,FZD9,YBX3,BIRC3,MIR22,NOL3,FADD,CASP8	grey	VSMC_M10
GO:0032780	0.52	0.70	7	12	negative regulation of ATPase activity	BP	1	TNNI3,PXK,OXA1L,VCPKMT,PAM16,TSC1,PPIF	grey	VSMC_M10
GO:0032259	0.52	0.53	155	290	methylation	BP	1	BAZ2A,RNMT,ARMT1,SNW1,TFB1M,MOV10L1,PHF1,TRMT11,MYC,PICK1,CMTR1,MTAP,CARNMT1,GNMT,PRDM4,CAMKMT,RNF20,STPG4,MTO1,SETD7,DNMT3A,BMI1,SETDB2,NSUN6,EED,IWS1,SUV39H2,KDM4A,PAXIP1,METTL23,HNMT,METTL17,THUMPD3,DPY30,LRTOMT,AP000812.5,SIRT7,METTL25,CHTOP,TRMT6,NSD3,NDUFAF7,ASH2L,BTG1,WTAP,TEX15,THUMPD2,TRMT9B,NR1H4,SETD9,TGS1,DIMT1,EEF1AKMT1,DNMT3B,SMYD1,PRMT9,BCDIN3D,SETD6,KMT2D,NSUN3,PRDM11,RTF1,PRMT3,WDR82,ZNF335,JARID2,RBBP5,FAM173B,MTRR,TPMT,PRDM15,HEMK1,COQ5,MTR,TRMT10A,AUTS2,DALRD3,LCMT2,ECE2,METTL8,EEF1AKMT2,TDRKH,NSUN5,MGMT,METTL2B,SETD2,TRMT1L,TET1,SNRPD3,BCOR,MEN1,WDR61,VCPKMT,COMT,MEPCE,ALKBH8,NELFA,TRMT5,DYDC1,NSUN7,PARP1,HSD17B10,PRDM2,MRM2,ZCCHC4,NSD1,SETD1A,PAGR1,FOS,OGT,RAB3D,LCMT1,SETD3,METTL4,SUZ12,METTL6,SUPT6H,CXXC1,MBD1,MRM3,SMYD4,CREBBP,METTL16,DOT1L,MECP2,PRDM16,GAMT,CHD5,SPOUT1,MTF2,GFI1,CMTR2,PRMT7,CTCF,MIR29A,PRMT6,METTL18,SETDB1,PRDM6,ARID4A,METTL14,TRMT10B,PEMT,BEND3,SMYD3,METTL21A,TRMT61A,ZNF304,NNMT,N6AMT1,TRMT10C,TRMT61B,CBLL1,TYW3,METTL7A	grey	VSMC_M10
GO:0046037	0.52	0.67	9	16	GMP metabolic process	BP	1	IMPDH1,GDA,DLG2,GMPS,MAGI3,DLG1,CASK,CARD11,MPP1	grey	VSMC_M10
GO:0006066	0.52	0.53	138	258	alcohol metabolic process	BP	1	RDH5,APOF,RDH16,CYP27B1,MIOX,SYNJ2,ACO2,AKR1B1,TTC39B,ALDH1A1,PLPP6,SRD5A3,SPTLC1,IPPK,INPP4A,ADH5,CAT,RDH13,PLEK,INPP4B,APOB,SPHK2,DHFR,MTMR2,NAPEPLD,EBP,AKR1A1,CUBN,LIPE,ITPKC,ACER3,TSKU,PIP4P1,SPTLC3,NR1H4,MTMR7,SDR16C5,SOAT2,CYP7A1,ASAH1,CYP7B1,CEBPA,CBR4,GK5,RETSAT,DKK3,LIMA1,GPD1,EPHX2,CYP2R1,P2RY1,PTK2B,SPR,SYNJ1,COQ2,ITPKA,ERLIN1,ALDH1A3,ABCA5,FMO5,CHKA,ITPK1,INPP5A,ALDH3B2,MSMO1,THTPA,GPER1,SC5D,DHRS9,IP6K2,DPAGT1,NTSR1,INPP5J,SCAP,HSD17B7,POR,PTH1R,SORD,PLA2G4A,ACADL,SOAT1,MOGAT3,TM7SF2,OSBPL1A,IDH3A,FDX1,PECR,LPCAT3,GNB3,WNT4,CYP27A1,GCH1,CH25H,ACADVL,TKFC,CLN8,DHRS3,RDH11,ALDH1A2,LIPC,DGKQ,GDPD3,APOBR,CLN6,LDLR,GDPD1,SCNN1B,CYP46A1,GDE1,NPC1,SREBF1,LEPR,IMPA2,ACAA2,INPP5K,MECP2,TKTL1,CACNA1H,PARK7,ALDH2,RXRA,CEL,GFI1,NFE2L1,TPK1,PNPLA4,DHDDS,MINPP1,LDLRAP1,ACER2,LRAT,INSIG2,RDH14,INPP1,ADH4,FGF1,SGPP1,PCBD2	grey	VSMC_M10
GO:0002360	0.52	0.66	10	18	T cell lineage commitment	BP	1	PRKDC,TOX,IL7,TNFSF18,STAT3,FOXP3,TBX21,BATF,IL6R,RHOA	grey	VSMC_M10
GO:0071305	0.52	0.65	11	20	cellular response to vitamin D	BP	1	CYP27B1,SNW1,PIM1,PTN,TNC,IL15,VDR,MED1,MIR125B1,TRIM24,BGLAP	grey	VSMC_M10
GO:0045494	0.52	0.63	14	26	photoreceptor cell maintenance	BP	1	USP45,USH1G,MKKS,ERCC6,TUB,ADGRV1,USH1C,BBS1,CDH23,CLN8,ATP1B2,ESRRB,DRAM2,BBS10	grey	VSMC_M10
GO:0097502	0.52	0.62	17	31	mannosylation	BP	1	RXYLT1,ALG12,LARGE1,ALG2,FKTN,ALG11,TMTC4,PIGM,PIGV,ALG3,PIGZ,ALG9,POMT2,ALG1,POMGNT2,PIGB,ISPD	grey	VSMC_M10

GO:0050858	0.52	0.66	10	18	negative regulation of antigen receptor-mediated signaling pathway	BP	1	PAWR,PLCL2,PRNP,LPXN,PTPRJ,SLA2,PTPN6,GPS2,PTPN2,THY1	grey	VSMC_M10
GO:0031644	0.52	0.56	53	100	regulation of nervous system process	BP	1	RIMS2,SOX10,TNFRSF21,RIMS1,SHANK1,DLGAP3,LPIN1,FIG4,GRIN2D,MTMR2,SLC8A2,CST7,FAM19A4,P2RX3,JAM2,DLGAP4,CUX2,PTK2B,HOMER1,F2R,FAM173B,RNF10,IGSF11,DAG1,SSH1,ZFHX2,OPRD1,AGT,SLC9A1,STX1A,TMEM25,NTSR1,CNIH2,COMT,TNR,ADRA2C,NPTX2,DLG4,NLGN2,TNFRSF1B,STX1B,NLGN3,TMEM100,NMUR2,BEGAIN,DLGAP1,ABAT,FMR1,PRKCZ,GPR35,FABP5,RGS4,CACNG5	grey	VSMC_M10
GO:0140374	0.52	0.68	8	14	antiviral innate immune response	BP	1	PHB,CLPB,AKAP1,RNF135,ATAD3A,ZDHHC1,OAS1,ZDHHC11	grey	VSMC_M10
GO:1903038	0.52	0.56	47	87	negative regulation of leukocyte cell-cell adhesion	BP	1	PPARA,TNFRSF21,PELI1,IL4I1,FOXJ1,PAWR,PRNP,NCKAP1L,ZC3H8,CASP3,TMEM131L,PAG1,MARCH7,ADTRP,BTN2A2,PRKAR1A,HLX,RUNX3,DLG1,MIA3,BCL6,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,SCGB1A1,FOXP3,TBX21,ZBTB7B,IL4R,CD74,CCL25,TWSG1,PTPN2,SOCS1,ASS1,GLMN,MIR21,MIR222,MIR27A,MIR125A,FGL2,LAX1,CEBPB,HAVCR2,RC3H2	grey	VSMC_M10
GO:0048265	0.52	0.65	11	20	response to pain	BP	1	TSPO,P2RX2,RET,P2RX3,SLC6A2,COMT,GCH1,NMUR2,VWA1,TRPV1,CRH	grey	VSMC_M10
GO:0051703	0.52	0.62	17	32	biological process involved in intraspecies interaction between organisms	BP	1	MAPK8IP2,SHANK1,CHD8,MKKS,RPTOR,ATXN1,NLGN4Y,NPAS4,EIF4EBP2,NRXN2,DLG4,CLN8,NLGN3,CHRNB2,MECP2,ATXN1L,NRXN3	grey	VSMC_M10
GO:0042596	0.52	0.65	11	20	fear response	BP	1	MAPK8IP2,USP46,SLC1A1,MEF2C,ASIC1,ADRA2A,ATP1A2,ASIC4,MECP2,DPP4,CRH	grey	VSMC_M10
GO:0010822	0.52	0.58	32	59	positive regulation of mitochondrion organization	BP	1	PRKN,BAK1,PLA2G6,FBXO7,VPS35,MGARP,DDHD2,DCN,HIP1R,HTRA2,OPA1,DNM1L,ZDHHC6,GPER1,CIDEB,FIS1,NMT1,MCU,HTT,DDHD1,PINK1,MUL1,VPS13D,ADCK1,MIEF2,RALBP1,PARK7,MLLT11,BCL2L11,RALA,MIEF1,PPIF	grey	VSMC_M10
GO:0060972	0.52	0.65	11	20	left/right pattern formation	BP	1	SMO,SETDB2,MEGF8,IFT172,FOXJ1,DPCD,SNAI1,PKD1L1,MNS1,HSPB11,PIFO	grey	VSMC_M10
GO:0001736	0.52	0.58	34	64	establishment of planar polarity	BP	1	FZD6,RSPO3,PTK7,ROR2,BRSK1,FUZ,INTU,WNT11,SPEF1,RYK,NPHP1,FZD3,TIAM1,RPGRIP1L,VANGL1,PRICKLE1,NKD1,JHY,ZNRF3,DVL3,FZD7,GRHL3,EXOC5,DAAM1,ARHGEF19,DVL2,MKS1,IFT20,GPC3,SAPCD2,CELSR2,RHOA,WNT5A,CELSR3	grey	VSMC_M10
GO:0007164	0.52	0.58	34	64	establishment of tissue polarity	BP	1	FZD6,RSPO3,PTK7,ROR2,BRSK1,FUZ,INTU,WNT11,SPEF1,RYK,NPHP1,FZD3,TIAM1,RPGRIP1L,VANGL1,PRICKLE1,NKD1,JHY,ZNRF3,DVL3,FZD7,GRHL3,EXOC5,DAAM1,ARHGEF19,DVL2,MKS1,IFT20,GPC3,SAPCD2,CELSR2,RHOA,WNT5A,CELSR3	grey	VSMC_M10
GO:0042886	0.52	0.53	112	210	amide transport	BP	1	LRP1,RIMS2,PRKN,TAP1,PLA2G6,PICK1,ABCB1,RFX3,TFAP2B,PRKCE,HMGN3,CYB5R4,BMP8A,EGFR,TRPM4,SLC7A11,GIPR,RAF1,ABCC4,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ABCB9,ARNTL,KCNJ11,SLC33A1,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,CDH17,NKX6-1,ACVR1C,COL4A3BP,ZBED6,ABCG2,PLTP,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,ABCC5,PER2,STX1A,PASK,GLUL,SIDT2,SLC16A1,KLF7,VGF,ENY2,ABCA12,MCU,PPP3CB,CAMK2G,PTPRN,CD38,SLC27A1,SLC38A5,MPC2,ILDR2,SYT7,NLGN2,CPLX1,TARDBP,STX4,RAB8B,UBE2Q1,SYTL4,GPR68,S100A8,CD74,CCL5,SREBF1,ISL1,OXCT1,NOS2,SLC46A1,ABAT,NADK,TRPV1,BAIAP3,PARK7,LRRC8A,FGA,CHGA,SOX4,DPP4,CA2,SLC25A32,CRH,CPTP,DOC2B,UQCC2,SGPP1	grey	VSMC_M10
GO:0043032	0.53	0.66	10	18	positive regulation of macrophage activation	BP	1	TTBK1,TLR4,CEBPA,PLA2G4A,TNIP2,IL4R,KARS,WNT5A,IL33,HAVCR2	grey	VSMC_M10
GO:1902254	0.53	0.66	10	18	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	PRKN,ARMC10,TAF9,ING2,MARCH7,MUC1,TAF9B,CD74,MIR21,PTTG1IP	grey	VSMC_M10
GO:0031016	0.53	0.59	27	50	pancreas development	BP	1	ONECUT2,BAK1,SMO,CDK6,RFX3,MET,SOX9,GIPR,MNX1,ARNTL,NKX6-1,ZBED6,IGF2,TCF7L2,NR5A2,SIDT2,MEN1,NKX3-2,ILDR2,ALDH1A2,IL6R,GATA6,ISL1,PDPK1,FOXF1,SOX4,WNT5A	grey	VSMC_M10
GO:0034612	0.53	0.53	97	181	response to tumor necrosis factor	BP	1	YTHDC2,MAP3K5,TNFAIP3,HSPA1B,PRKN,TNFRSF13C,MAPK14,TNFRSF21,GSDME,CXCL8,TRIM32,TRAF1,FOXO3,APOB,TRAF3IP2,ZFAND6,IKBKB,BAG4,GAS6,ST18,TRAF6,ASAH1,CEBPA,GSS,CASP3,GPD1,PTK2B,KCNJ11,CCL17,OTULIN,NKX3-1,F2RL1,RIPK1,ABCC2,CD40,HDAC1,HYAL1,HYAL3,PIAS3,FABP4,SPATA2,GPER1,CIB1,TRAF5,HDAC4,PELI3,YBX3,NFE2L2,GGT2,TNFSF18,GCH1,SMPD4,BIRC3,SPPL2A,MAPK1,SGMS1,CXCL16,SLC2A4,GPS2,TNFRSF1B,PYDC1,MAPK3,TRAF3,CCL14,CCL5,CCL7,CCL2,CCL25,ADAMTS12,PTPN2,PIAS4,INPP5K,CDIP1,TRPV1,SPPL2B,TRAF2,TNFRSF25,ADAMTS13,CYBA,ASS1,LCN2,DAB2IP,MIR27B,MIR24-1,CCL16,NOL3,CASP8,CLDN1,GGT5,CD70,COMMD7,CCDC3,ZFP36L2,MAP2K7,TNFSF13B,HIST1H2BJ,CCL22	grey	VSMC_M10
GO:1901028	0.53	0.67	9	16	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	BP	1	TMEM14A,HIP1R,FZD9,NMT1,MUL1,TMEM102,ACAA2,SLC35F6,AC140504.1	grey	VSMC_M10
GO:0042059	0.53	0.63	13	24	negative regulation of epidermal growth factor receptor signaling pathway	BP	1	EGFR,RAB7A,SNX5,PTPRJ,RNF115,CBL,SNX6,ZFYVE28,SOCS4,PSEN1,PTPN2,RNF126,DAB2IP	grey	VSMC_M10
GO:0002474	0.53	0.67	9	16	antigen processing and presentation of peptide antigen via MHC class I	BP	1	TAP1,IKBKB,IDE,ABCB9,ERAP1,MFSD6,FCER1G,TAPBPL,ERAP2	grey	VSMC_M10
GO:0032740	0.53	0.68	8	14	positive regulation of interleukin-17 production	BP	1	IL15,PHB,MYD88,NR1H4,NOD2,OSM,ZBTB7B,SLC7A5	grey	VSMC_M10
GO:0007156	0.53	0.56	46	88	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	PCDH10,FAT4,NECTIN2,PVR,PCDH8,PCDHGC5,PCDH1,RET,CLSTN2,ROBO1,ROBO2,TENM3,CDH17,AMIGO2,NECTIN3,IGSF11,CDH24,NECTIN4,CADM1,MYPN,HMCN1,CDH23,OBSL1,SDK1,PCDH7,PCDH11X,PCDH19,DSG2,DSC3,EMB,CDH6,CDH10,L1CAM,PKD1,BSG,AMIGO1,CELSR2,CDH15,CDH16,PCDHAC2,PCDHA6,CNTN2,CDHR4,CELSR3,PCDHGA2,PCDHB15	grey	VSMC_M10

GO:0060416	0.53	0.63	13	24	response to growth hormone	BP	1	PTK2,PNPT1,LEPROTL1,PIK3R1,PXN,SRD5A1,CPS1,GDF15,STAT3,STAT5B,GHR,ASS1,LEPROT	grey	VSMC_M10
GO:0030104	0.53	0.60	21	39	water homeostasis	BP	1	NEDD4L,AKR1B1,SRF,TFAP2B,AQP1,GRHL1,MET,AQP11,ELOVL1,LSR,TRPV4,KDF1,SFN,GRHL3,ABCA12,ALOXE3,AC138894.1,SCNN1B,MYO5B,INPP5K,CLDN1	grey	VSMC_M10
GO:0086091	0.53	0.62	16	30	regulation of heart rate by cardiac conduction	BP	1	TRPM4,CACNB2,SCN5A,KCNJ3,KCNE2,DSP,PKP2,KCNJ2,ANK2,SCN4B,CACNA1G,DSG2,ISL1,KCNH2,SCN2B,HCN4	grey	VSMC_M10
GO:1904377	0.53	0.58	31	58	positive regulation of protein localization to cell periphery	BP	1	LRP1,STAC3,EPB41L2,PRKCE,SPTBN1,EGFR,STAC,PRNP,PIK3R1,PLS1,SORBS1,KCNJ11,EPB41,GPER1,RAB11FIP2,CIB1,DLG1,ZDHHC8,CNPY4,CNST,WNK3,STAC2,STX4,ITGA3,AC138894.1,RAB11A,EFCAB7,PDPK1,RER1,ARHGEF16,GPSM2	grey	VSMC_M10
GO:0022898	0.53	0.53	99	186	regulation of transmembrane transporter activity	BP	1	NEDD4L,STAC3,MAPK8IP2,PRRT1,GOPC,PLA2G6,PIM1,ABCB1,WNK2,PRKCE,SHANK1,HECW1,TCAF2,OSR1,SPHK2,KCNRG,CACNB2,STAC,OXSR1,GPD1L,CACNB4,PRNP,SLMAP,GLRX,MEF2C,PTK2B,KCNJ11,HOMER1,IFNGR2,TESC,RIPK1,KCNE2,PKD2,CASQ2,KCNIP2,CHRM3,RYR2,FAM173B,PM20D1,HECW2,ADRA2A,COX17,KCNG1,ANK2,KLHL24,ACE2,ATP1A2,SLC9A1,C4orf3,CASQ1,NTSR1,SCN4B,CNIH2,NOS1AP,DLG1,HTT,PINK1,ATP1B1,KCNA1,GNB5,MINK1,HAP1,DLG4,ACTB,NLGN2,CNIH3,WNK3,STAC2,CACNB1,ATP1B2,NLGN3,ATP2A1,CALM1,DNM2,VMP1,CCL2,FMR1,RNF207,PARK7,AMIGO1,JPH3,WWP2,RRAD,MIR24-1,DMD,GPR35,JPH2,FGF11,SCN2B,NETO2,CACNG7,CRBN,CRH,APOPT1,YWHAH,SHISA8,CACNG5,GEM,PPIF	grey	VSMC_M10
GO:0003401	0.53	0.63	13	24	axis elongation	BP	1	ESR1,PTK7,AREG,TNC,SPRY1,SOX9,SPRY2,WNT11,NKD1,MED1,WNT5A,SIX1,FGF1	grey	VSMC_M10
GO:0044262	0.53	0.52	122	229	cellular carbohydrate metabolic process	BP	1	MIOX,SYNJ2,PRKN,PPARA,AKR1B1,GPT,GNMT,CRY1,IPPK,PRKCE,HAS1,PPP4R3B,ZNF692,PLEK,FAM3C,INPP4B,MGAM,BRAF,MTMR2,PYGB,RUBCNL,GLB1,KHK,EPM2AIP1,PRKAG2,XYLB,GCKR,RBKS,PPP1CB,CSGALNACT1,AKT2,C1QTNF1,SIRT7,PDK1,PPP1R3B,MTMR7,NLN,GK5,NCOA2,GBE1,B3GNT4,SORBS1,P2RY1,PTK2B,PFKM,SYNJ1,COQ2,ITPKA,IGF2,GANC,NHLRC1,PHKB,GPLD1,IRS1,SIK1,ITPK1,INPP5A,MST1,PPP1R3E,PFKFB2,GPER1,PPP1R3D,PER2,TREH,PFKFB4,ACTN3,HDAC4,NTSR1,PASK,PHKA2,INPP5J,DUSP12,GAL3ST3,PDK3,PTH1R,SORD,PLA2G4A,RPE,MOGAT3,HK1,PYGM,PYGL,GNB3,PRKAG3,AC022400.6,STAT3,PPP1R3F,IGFBP4,TKFC,DDB1,IDUA,DGKQ,OGT,PHKA1,COX11,LCMT1,NCOR1,INSR,ENOSF1,LEPR,IMPA2,PTPN2,FGGY,INPP5K,MECP2,GNPTG,MLYCD,AGL,FUK,HAS3,ACADM,FBP2,ABHD10,TIGAR,PPP1R1A,IDNK,POMK,NNMT,NEU2,INPP1,HS2ST1,ARPP19	grey	VSMC_M10
GO:0044827	0.53	0.67	9	16	modulation by host of viral genome replication	BP	1	YTHDC2,PRKN,PHB,FBXL2,EIF2AK4,HSPA8,FMR1,MIR222,TBC1D20	grey	VSMC_M10
GO:0006123	0.53	0.66	10	17	mitochondrial electron transport, cytochrome c to oxygen	BP	1	COX7A1,COX4I2,COX15,COX6A1,COX8A,COX6A2,COX5A,MT-CO3,COX7A2,COX7A2L	grey	VSMC_M10
GO:0045577	0.53	0.65	11	20	regulation of B cell differentiation	BP	1	IL4I1,NCKAP1L,IL7,SLAMF8,PPP2R3C,PTPN6,STAT5B,INHA,CARD11,BTK,ZFP36L2	grey	VSMC_M10
GO:0044264	0.53	0.56	40	75	cellular polysaccharide metabolic process	BP	1	GNMT,HAS1,MGAM,PYGB,RUBCNL,KHK,EPM2AIP1,PRKAG2,PPP1CB,CSGALNACT1,AKT2,PPP1R3B,GBE1,B3GNT4,SORBS1,PFKM,IGF2,NHLRC1,PHKB,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PHKA2,GAL3ST3,PYGM,PYGL,PRKAG3,AC022400.6,PPP1R3F,PHKA1,INSR,LEPR,INPP5K,AGL,HAS3,ACADM,PPP1R1A,HS2ST1	grey	VSMC_M10
GO:0060425	0.53	0.60	21	39	lung morphogenesis	BP	1	SRF,TNC,SPRY1,SOX9,SPRY2,TGFBR2,AP3B1,SRSF6,DAG1,KRAS,PLOD3,CTSH,MAPK1,MAPK3,MAP2K1,LAMA1,FOXF1,ESRP2,NOG,LIF,WNT2	grey	VSMC_M10
GO:0051928	0.53	0.56	46	86	positive regulation of calcium ion transport	BP	1	STAC3,TSPO,BAK1,MCHR1,SPHK2,TRPC3,CACNB2,STAC,P2RX2,P2RX3,ORAI1,P2RX7,HOMER1,STC1,F2R,KCNE2,PKD2,RYR2,ANK2,GPER1,SLC9A1,CASQ1,NTSR1,CEMIP,CASK,HTT,ATP1B1,HAP1,WNK3,STAC2,ATP2A1,CD19,CALM1,VMP1,BDKRB1,TRPV2,CAMK2A,CCL5,CCL2,TRPV3,PDPK1,P2RX1,ATP2C2,JPH2,THY1,CRH	grey	VSMC_M10
GO:0044060	0.53	0.65	11	20	regulation of endocrine process	BP	1	GDF9,CRY1,C1QTNF1,NKX3-1,F2RL1,F2R,CRY2,AGT,INHA,RAB8B,CRH	grey	VSMC_M10
GO:1900078	0.53	0.64	12	22	positive regulation of cellular response to insulin stimulus	BP	1	GKAP1,ECHDC3,SNX5,SORBS1,OPA1,IGF2,IRS1,SORL1,AGT,ESRRA,ZBTB7B,PRKCZ	grey	VSMC_M10
GO:0006730	0.53	0.61	17	31	one-carbon metabolic process	BP	1	SHMT2,GNMT,CA9,DHFR,AHCY,MTHFD2,CA14,MTHFS,MAT1A,CA4,SHMT1,CA2,CA5B,MTHFD2L,ALDH1L1,CA13,CA10	grey	VSMC_M10
GO:0060261	0.53	0.64	11	20	positive regulation of transcription initiation from RNA polymerase II promoter	BP	1	ESR1,MED30,SRF,ERCC1,PAXIP1,ERCC6,CREB1,MED14,MED24,MED1,NKX2-5	grey	VSMC_M10
GO:0001947	0.53	0.59	24	45	heart looping	BP	1	SMO,FOXH1,SRF,BBS7,SETDB2,IFT172,TGFBR2,OVOL2,MKKS,HAND2,MEF2C,IFT52,PKD2,SUFU,PSEN1,SMAD3,TBX2,MIB1,RNF207,ENG,LBX1,WNT5A,C2CD3,NKX2-5	grey	VSMC_M10
GO:0034122	0.53	0.63	13	24	negative regulation of toll-like receptor signaling pathway	BP	1	TNFAIP3,GRAMD4,LRRC14,CD300LF,MFHAS1,OTUD4,F2RL1,NOD2,RAB7B,GPS2,GPR108,PDPK1,DAB2IP	grey	VSMC_M10
GO:0070423	0.53	0.64	12	22	nucleotide-binding oligomerization domain containing signaling pathway	BP	1	TNFAIP3,HSPA1B,SLC46A2,TLR4,LACC1,RIPK2,OTULIN,NOD2,MAP2K6,BIRC3,IRGM,INAVA	grey	VSMC_M10
GO:0043586	0.53	0.65	10	18	tongue development	BP	1	BNC2,KIT,EGFR,NTF4,INTU,HDAC2,HAND2,KCNE2,HDAC1,SIX1	grey	VSMC_M10
GO:0097530	0.53	0.55	49	91	granulocyte migration	BP	1	PTK2,RAC2,CXCL8,AKIRIN1,C5AR2,C5AR1,MYD88,NCKAP1L,CCL17,NOD2,GBF1,DNM1L,TRPV4,TGFB2,CD99,CMKLR1,SLAMF8,MOSPD2,FCER1G,ADAM8,PIKFYVE,MCU,TNFSF18,CXCR2,BST1,MAPK1,DAPK2,MAPK3,S100A14,S100A8,UMOD,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,VAV1,PTGER4,PIP5K1C,MPP1,BSG,VAV3,CCL16,S100A12,DPP4,CXCL6,CCL22	grey	VSMC_M10
GO:0097503	0.53	0.65	10	18	sialylation	BP	1	ST6GAL2,ST6GALNAC2,ST8SIA4,ST3GAL6,ST8SIA2,ST8SIA5,ST6GALNAC4,ST3GAL2,ST6GALNAC5,ST8SIA6	grey	VSMC_M10

GO:0006220	0.53	0.59	23	42	pyrimidine nucleotide metabolic process	BP	1	NME1,TBPL1,ENPP3,DPYS,CMPK1,MBD4,ENTPD4,NME4,CTPS2,DTYMK,UPB1,NME7,UPRT,NEIL1,NT5M,NTHL1,NME3,UCK1,DHODH,CMPK2,NME6,DCTD,UPP1	grey	VSMC_M10
GO:2000515	0.53	0.63	12	22	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	HLX,RUNX3,BCL6,VSIR,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,TWSG1,RC3H2	grey	VSMC_M10
GO:0072576	0.53	0.65	10	18	liver morphogenesis	BP	1	GLI1,TNFAIP3,TGFA,PTN,FBXW7,SULF2,RPS6KA1,MED1,CEBPB,FGF1	grey	VSMC_M10
GO:0008344	0.53	0.57	30	56	adult locomotory behavior	BP	1	PRKN,AGTPBP1,BTBD9,ADAM22,TMOD1,PPT1,NTF4,GRIN2D,LGI4,PREX2,HTRA2,NR4A2,GIGYF2,OPRD1,ATP1A2,NTSR1,EPS8,EPHA4,CLN8,HOXB8,NPC1,SEZ6,DAB1,MECP2,PARK7,TSC1,CNTN2,CEND1,FXN,EFNB3	grey	VSMC_M10
GO:0070665	0.53	0.55	50	93	positive regulation of leukocyte proliferation	BP	1	AGER,IL5,HLA-DPB1,TNFRSF13C,PTK2,NCK2,PELI1,TLR4,IL15,BMI1,MYD88,TGFBR2,NCKAP1L,SLC7A1,TRAF6,IL1A,MEF2C,IL7,RIPK2,ZNF335,CD40,IGF2,ICOSLG,GPAM,CD28,BCL6,IL12A,CD38,BST1,MAPK1,STAT5B,FOXP3,RASAL3,CARD11,MAPK3,CHRNB2,CD74,CCL5,CSF1R,CD320,TICAM1,DNAJA3,VAV3,MIR21,FADD,CD46,CD70,TNFSF9,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0048255	0.53	0.59	23	43	mRNA stabilization	BP	1	PABPC1,MAPK14,TRAF3IP2,MYD88,TENT5C,TENT4B,RBM24,AXIN2,MAPKAPK2,TRAF5,ANGEL2,EIF4ENIF1,YBX3,SLC11A1,RBM10,TARDBP,TENT5D,LARP1,METTL16,CIRBP,TRAF2,YBX1,TENT5A	grey	VSMC_M10
GO:0006198	0.53	0.75	4	7	cAMP catabolic process	BP	1	PDE7B,PDE10A,PDE8A,PDE4A	grey	VSMC_M10
GO:0035337	0.53	0.60	19	35	fatty-acyl-CoA metabolic process	BP	1	HSD17B4,PPT2,ACSL6,PPT1,ELOVL1,ELOVL7,FITM2,FAR2,ACSL5,HACD2,THEM5,ACSBG1,TECR,GCDH,ACACA,ACSBG2,ACSF3,ELOVL3,NUDT19	grey	VSMC_M10
GO:0000291	0.54	0.65	10	18	nuclear-transcribed mRNA catabolic process, exonucleolytic	BP	1	CNOT6,SKIV2L,EXOSC4,EXOSC3,TTC37,DIS3L2,POLR2G,NT5C3B,CNOT8,EXOSC5	grey	VSMC_M10
GO:0072386	0.54	0.75	4	7	plus-end-directed organelle transport along microtubule	BP	1	KIF3A,KIF3B,KIF13A,MAPT	grey	VSMC_M10
GO:0006379	0.54	0.64	11	20	mRNA cleavage	BP	1	CPSF6,AGO2,CPSF1,PCF11,POLR2I,CSTF3,CPSF2,NCBP2,CPSF4,AP002990.1,CSTF2	grey	VSMC_M10
GO:0014888	0.54	0.59	20	37	striated muscle adaptation	BP	1	IL15,TRPC3,KDM4A,TNNC1,PPP3CA,TNNI1,MYH7,GTF2IRD1,MYOZ2,ACTN3,HDAC4,MYOZ1,CAMK2G,CAMTA2,TCAP,SMAD3,GATA6,MIR199A1,MIR25,HEY2	grey	VSMC_M10
GO:0140467	0.54	0.64	11	20	integrated stress response signaling	BP	1	ATF4,NCK2,EIF2AK4,QRICH1,NFE2L2,PTPN2,ABCA7,HSPA5,IMPACT,DDIT3,PPP1R15A	grey	VSMC_M10
GO:0140331	0.54	0.74	4	7	aminophospholipid translocation	BP	1	ATP8B1,TMEM30A,TMEM30B,ATP11C	grey	VSMC_M10
GO:1903051	0.54	0.58	27	50	negative regulation of proteolysis involved in cellular protein catabolic process	BP	1	TRIM39,PDCL3,SDCBP,AQP11,KLHL40,DDRGK1,RYBP,PSMF1,TAF9,USP25,CSNK2A2,FAM192A,MARCH7,SUFU,RPL23,USP19,RPL11,EPHA4,PSEN1,EFNA1,TAF1,OGT,SGTA,PARK7,CAMLG,STYX,MAP1A	grey	VSMC_M10
GO:0061462	0.54	0.59	22	41	protein localization to lysosome	BP	1	RTN4,KPTN,RAB7A,SZT2,NCOA4,AP3B1,GPR137B,HSPA8,SORL1,SH3BP4,MFSD1,AP4M1,AP3M1,ATP13A2,RNF128,LAMP2,LAMTOR5,TLDC1,VPS4A,CACNG7,SNX16,CACNG5	grey	VSMC_M10
GO:0097105	0.54	0.74	4	7	presynaptic membrane assembly	BP	1	NLGN4Y,NLGN2,NLGN3,CEL	grey	VSMC_M10
GO:0062043	0.54	0.74	4	7	positive regulation of cardiac epithelial to mesenchymal transition	BP	1	TGFBR2,JAG1,TGFB2,ENG	grey	VSMC_M10
GO:0010524	0.54	0.59	20	37	positive regulation of calcium ion transport into cytosol	BP	1	BAK1,TRPC3,P2RX2,P2RX3,P2RX7,F2R,PKD2,GPER1,CASQ1,NTSR1,CEMIP,HTT,HAP1,CD19,CALM1,BDKRB1,PDPK1,P2RX1,JPH2,THY1	grey	VSMC_M10
GO:0048814	0.54	0.57	30	57	regulation of dendrite morphogenesis	BP	1	NEDD4L,RAB21,CHRNA3,SEMA4D,HECW1,SS18L2,ANKRD27,TLX2,CUX2,RAPGEF2,TIAM1,OPA1,ITPKA,LZTS1,DNM1L,PPP3CA,HECW2,CAPRIN2,NFATC4,SS18L1,CDKL5,OBSL1,EPHA4,CHRNB2,PARP6,GPRASP2,BHLHB9,LRP8,FBXO31,YWHAH	grey	VSMC_M10
GO:0009068	0.54	0.66	9	16	aspartate family amino acid catabolic process	BP	1	RIDA,DDO,SDSL,MAT1A,ASRGL1,CRYM,PIPOX,SLC25A21,HYKK	grey	VSMC_M10
GO:0097428	0.54	0.67	8	14	protein maturation by iron-sulfur cluster transfer	BP	1	ISCA1,CIAO1,LTO1,HSCB,CIAO2B,GLRX5,CISD3,ISCA2	grey	VSMC_M10
GO:2001222	0.54	0.60	17	32	regulation of neuron migration	BP	1	SEMA6A,SEMA3A,UNC5D,NRG1,IGSF10,RAPGEF2,NKX6-1,SRGAP2C,LRIG2,COL3A1,STAT3,ZNF609,CAMK2A,NTNG2,FBXO31,DAB2IP,ADGRG1	grey	VSMC_M10
GO:0040036	0.54	0.62	13	24	regulation of fibroblast growth factor receptor signaling pathway	BP	1	FUZ,SPRY1,PRKD2,SPRY2,FGFBP3,DSTYK,SULF2,LRIT3,WNT4,NGFR,NOG,WNT5A,SHISA2	grey	VSMC_M10
GO:0007423	0.54	0.50	219	415	sensory organ development	BP	1	SLC39A5,ATP8B1,EYA4,MDM1,FRS2,OSR2,FZD6,TBC1D32,BAK1,ATF4,AGTPBP1,NTRK2,BNC2,PRPH2,RORB,PTK7,SRF,SLC25A27,KIT,SLC1A1,TFAP2B,ROR2,DLX5,TDRD7,TMOD1,SIX2,RDH13,ABCB5,KCNQ4,GSDME,HOXA2,HOXA13,MYCL,BMPER,WHRN,PTN,EGFR,TSPAN12,USP45,ATG5,MYCN,SOBP,SLC7A11,OSR1,NTF4,INTU,SPRY1,FOXE3,HDAC2,BBS7,SLC26A5,MYO3A,SOX9,MYO7B,USH1G,GLI2,CRYGN,ZNF513,ACVR2B,IFT172,MYO7A,TSKU,SPRY2,DZANK1,TGFBR2,BFSP1,SLC4A7,JAG1,RARB,FSCN2,LRTOMT,AP000812.5,LIN7A,SPRED3,FREM2,CEP290,KERA,MAB21L1,MITF,FLT1,TUB,TCF15,EPHB1,PFDN5,NPHP1,RET,PAX8,CEBPA,FOXL2,HAND2,EYA1,PLS1,MAB21L2,TENM3,ADGRV1,FZD3,USH1C,TENT2,OPA1,RPGRIP1L,KCNE2,TFAP2A,PAX2,NKD1,BMPR1B,MYH15,NECTIN3,LPCAT1,PKNOX1,SLC6A3,HDAC1,ALDH1A3,TGFB2,TRIP11,TCIRG1,PRSS56,SHROOM2,MAPKAPK2,SOX2,CRYBA4,NRL,GBX2,MYO3B,KCNK2,CLIC4,DLX1,GRHL3,LIMK2,SP3,STRC,CDKN1B,DLG1,FZD5,STOX1,PRKRA,CDH23,FBN1,FKBP8,COL5A2,ECE1,PLA2G16,STAT3,NKX3-2,MAPK1,TULP3,OBSL1,RHOJ,ROM1,MFAP2,EPHA4,DVL2,WDR19,SDK1,MAX,CLN8,TCAP,RBPJ,MED1,ALDH1A2,MFN2,PSEN1,TTLL5,MAPK3,ESRRB,MEGF11,LCTL,POU3F4,SMAD3,NTN1,MKS1,GSC,TBX2,BCL11B,LHX1,STRA6,YY1,CHRDL1,UNC45B,TMEM132E,JAG2,SMCHD1,LAMA1,IFT20,TWSG1,GNB1,FZR1,SKI,SOX8,COL5A1,LAMC3,OLFM3,TMEM231,SLC25A25,MCOLN3,HSF4,KCNK3,BLOC1S3,FJX1,PJVK,CHRNA10,FOXG1,MAFB,CNTF,ACVRL1,NOG,THY1,WNT5A,DIO3,OTX1,SIX1,BCL2L11,TGIF2,TBC1D20,INSIG2,PITX3,HEY2,WNT2,COL8A2,ZIC1	grey	VSMC_M10
GO:1903288	0.54	0.74	4	7	positive regulation of potassium ion import across plasma membrane	BP	1	WNK2,ATP1B1,WNK3,ATP1B2	grey	VSMC_M10

GO:0022904	0.54	0.54	55	99	respiratory electron transport chain	BP	1	UQCRQ,NDUFA6,SLC25A13,DLD,NDUFB2,NDUFB6,DNAJC15,NDUFC2,NDUFS8,NDUFA12,COX7A1,COX4I2,GPD1,NDUFS3,ETFDH,DGUOK,UQCRB,COX15,NDUFV3,NDUFB4,ISCU,COA6,POLG2,NDUFB3,NDUFS2,SDHC,COX6A1,COX8A,PINK1,NDUFA9,SDHB,COX6A2,NDUFAB1,COX5A,NDUFA7,NDUFV2,NDUFB10,UQCR11,PARK7,MT-ND1,MT-ND2,MT-CO3,MT-ND6,MT-CYB,NDUFA5,NDUFC1,COX7A2,ETFRF1,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,COX7A2L	grey	VSMC_M10
GO:0090175	0.54	0.57	27	51	regulation of establishment of planar polarity	BP	1	FZD6,RSPO3,PTK7,ROR2,WNT11,SPEF1,RYK,FZD3,TIAM1,VANGL1,PRICKLE1,NKD1,JHY,ZNRF3,DVL3,FZD7,GRHL3,DAAM1,ARHGEF19,DVL2,MKS1,GPC3,SAPCD2,CELSR2,RHOA,WNT5A,CELSR3	grey	VSMC_M10
GO:0050974	0.54	0.61	14	26	detection of mechanical stimulus involved in sensory perception	BP	1	PHF24,KIT,WHRN,ASIC3,SCN1A,MKKS,ADGRV1,BACE1,STRC,KCNK4,KCNA1,ASIC2,PJVK,CHRNA10	grey	VSMC_M10
GO:0006536	0.54	0.63	12	22	glutamate metabolic process	BP	1	GLS2,SLC7A11,GAD2,AMDHD1,NR1H4,GLS,ALDH5A1,OAT,GLUL,MTHFS,PRODH,ALDH4A1	grey	VSMC_M10
GO:0046653	0.54	0.65	9	16	tetrahydrofolate metabolic process	BP	1	SHMT2,DHFR,MTHFD2,MTHFS,GCH1,SHMT1,PIPOX,MTHFD2L,ALDH1L1	grey	VSMC_M10
GO:0006171	0.54	0.71	5	9	cAMP biosynthetic process	BP	1	ADCY3,ADCY7,ADCY2,ADCY4,ADCY10	grey	VSMC_M10
GO:0042730	0.54	0.65	9	16	fibrinolysis	BP	1	SERPINB2,THBD,PLAT,FAP,USF1,F12,ANXA2,SERPINF2,FGA	grey	VSMC_M10
GO:0003081	0.54	0.65	9	16	regulation of systemic arterial blood pressure by renin-angiotensin	BP	1	MME,F2RL1,F2R,ENPEP,AGT,ACE2,SERPINF2,CYBA,RHOA	grey	VSMC_M10
GO:0070371	0.54	0.51	121	227	ERK1 and ERK2 cascade	BP	1	LRP1,SEMA6A,FRS2,AGER,FBLN1,ROS1,MYC,PRXL2C,TEK,WNK2,FPR2,MTURN,NOD1,BMPER,EPHA7,ITGB1BP1,VRK3,GRB10,YWHAZ,EGFR,TLR4,FGF21,BRAF,SPRY1,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,SOX9,SPRY2,ARRB1,NEK10,SPRED3,DUSP6,NRG1,GAS6,SIRT3,MFHAS1,APIP,ST5,EPHB1,HAND2,FBXW7,P2RY1,PTK2B,RASGRP1,RAPGEF2,CCL17,TIAM1,RIPK2,F2RL1,F2R,NQO2,GCNT2,NOD2,DSTYK,TRPV4,SLC30A10,EGF,TBC1D10C,GPER1,AGT,CIB1,THPO,PDE8A,DLG1,DUSP10,RAP1B,CTSH,FN1,PTPN6,GPBAR1,FGFR3,MAPK1,RGS14,FGFR4,SYNJ2BP,FGF18,MAPK3,MAP2K1,TNIP1,GAREM1,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,PTGER4,PTPN2,SERPINF2,PRKCZ,ATP6AP1,ABCA7,KARS,DAB2IP,MIR21,MIR222,MIR23A,MIR27B,MIR24-1,MIR27A,FGA,CCL16,CHRNA10,DUSP26,DUSP1,DUSP4,C3orf33,LIF,HRAS,ZFP36L2,STYX,MAP2K7,FGF1,C1QL4,HAVCR2,CCL22,PDGFD	grey	VSMC_M10
GO:1902369	0.54	0.56	32	60	negative regulation of RNA catabolic process	BP	1	PABPC1,PHAX,MAPK14,LRPPRC,TRAF3IP2,DHX34,MYD88,PKP3,TENT2,TENT5C,TENT4B,RBM24,AXIN2,MAPKAPK2,TRAF5,ANGEL2,EIF4ENIF1,YBX3,SLC11A1,RBM10,TARDBP,TOB1,TENT5D,NRDE2,LARP1,PARN,FMR1,METTL16,CIRBP,TRAF2,YBX1,TENT5A	grey	VSMC_M10
GO:0045661	0.54	0.58	21	39	regulation of myoblast differentiation	BP	1	MAPK14,SOSTDC1,AKIRIN1,SOX9,SRA1,PLCB1,BTG1,SMYD1,MEF2C,CCL17,HIF1AN,PRICKLE1,RBM24,CDON,RANBP3L,MBNL3,SOX8,LRRC8A,MIR199A1,DDIT3,XKR8	grey	VSMC_M10
GO:0006829	0.54	0.62	13	24	zinc ion transport	BP	1	SLC39A5,SLC39A4,SLC1A1,SLC39A12,TMEM163,SLC39A13,SLC30A10,SLC30A4,SLC39A9,SLC39A6,SLC30A7,SLC39A11,SLC39A3	grey	VSMC_M10
GO:2000649	0.54	0.58	23	43	regulation of sodium ion transmembrane transporter activity	BP	1	NEDD4L,WNK2,PRKCE,HECW1,OSR1,GPD1L,SLMAP,GLRX,TESC,HECW2,KLHL24,ATP1A2,SLC9A1,SCN4B,ATP1B1,WNK3,DNM2,MIR24-1,DMD,FGF11,SCN2B,NETO2,YWHAH	grey	VSMC_M10
GO:0051693	0.54	0.59	18	34	actin filament capping	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,SPTBN1,ADD2,LMOD3,DMTN,CARMIL1,LMOD1,ADD3,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,CARMIL2	grey	VSMC_M10
GO:0044773	0.54	0.55	38	71	mitotic DNA damage checkpoint signaling	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,BRSK1,MSH2,XPC,PLK3,NEK11,PRKDC,STK33,PLK2,RAD17,RAD9B,NBN,ABRAXAS1,DONSON,PIDD1,TAOK3,CCND1,GIGYF2,CHEK2,SYF2,CDKN1B,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,FOXN3,TAOK1,FZR1,FBXO31,RPS27L,SOX4,BRCC3,CRADD	grey	VSMC_M10
GO:0043618	0.54	0.58	23	43	regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	ATF4,HSF1,NCK2,EPAS1,SIRT2,TMBIM6,BACH1,HIF1AN,ARNT,BAG3,NFE2L2,STOX1,DNAJB1,RBPJ,MUC1,SIN3A,MAPK7,JUN,CREB3L3,HSPA5,IMPACT,DDIT3,CEBPB	grey	VSMC_M10
GO:0045582	0.54	0.56	32	60	positive regulation of T cell differentiation	BP	1	HLA-DRA,IL4I1,GLI2,TGFBR2,NCKAP1L,SOX12,IL7,RASGRP1,RIPK2,AP3B1,SOX13,HLX,RUNX3,ADAM8,DUSP10,BCL6,VSIR,STAT5B,FOXP3,ZBTB1,ZBTB7B,IL4R,CD74,NKAP,IL7R,SOCS1,PRKCZ,MIR21,RHOA,SOX4,CD46,TNFSF9	grey	VSMC_M10
GO:0042100	0.54	0.56	30	56	B cell proliferation	BP	1	IL5,TNFRSF13C,TNFRSF21,PELI1,TLR4,BMI1,PAWR,PLCL2,NCKAP1L,GAPT,CASP3,MEF2C,IL7,RASGRP1,CD40,BCL6,RC3H1,CD38,BST1,CARD11,CHRNB2,CD19,BTK,CD74,CD320,IL7R,TICAM1,VAV3,CD70,TNFSF13B	grey	VSMC_M10
GO:0043304	0.55	0.62	13	24	regulation of mast cell degranulation	BP	1	RAC2,SPHK2,GAB2,UNC13D,FER,FGR,SNX4,C12orf4,IL4R,STXBP2,PDPK1,FOXF1,STXBP1	grey	VSMC_M10
GO:0050820	0.55	0.64	10	18	positive regulation of coagulation	BP	1	ENPP4,THBD,F2R,ANO6,DMTN,USF1,NFE2L2,F12,PSEN1,SERPINF2	grey	VSMC_M10
GO:0045940	0.55	0.64	10	18	positive regulation of steroid metabolic process	BP	1	APOC1,CYP7A1,AGT,SCAP,POR,WNT4,SREBF1,LDLRAP1,STARD4,FGF1	grey	VSMC_M10

GO:0072507	0.55	0.50	171	323	divalent inorganic cation homeostasis	BP	1	SLC39A5,LRP1,CYP27B1,ESR1,PRKN,SMDT1,BAK1,MCHR1,GPR20,PLA2G6,SLC39A4,SLC25A27,SLC1A1,TFAP2B,S1PR3,CNNM4,PRKCE,TNNI3,FPR2,IBTK,LPAR1,EGFR,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ACKR2,SLC24A3,C1QTNF1,TMTC4,RYR1,PRNP,ADRA1D,DIAPH1,P2RX2,KL,CCKBR,RASA3,MICU3,IMMT,C19orf12,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,AP3B1,RMDN3,F2RL1,F2R,PKD2,CASQ2,MCUR1,CD40,RYR2,SLC41A1,RAP1GDS1,TRPM1,SPPL3,LCK,TRPV4,SLC30A10,TCIRG1,FAM20A,GNA13,CMKLR1,MCUB,UBASH3B,DISC1,ANK2,GPER1,TRPM8,PDZD8,AGT,ATP1A2,CASQ1,NTSR1,FZD9,TMCO1,PTH1R,SLC30A4,FIS1,CEMIP,ABL2,CDH23,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,TRPM7,ATP1B1,KCNA1,CD38,ATP13A2,HAP1,DLG4,FAM155B,PSEN1,CACNA1A,AC138894.1,ATP2A1,CD19,SMAD3,CALM1,S100A14,S100A8,PRKCB,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,PTGER4,SLC25A23,MAIP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,GPR157,SYPL2,CYBA,JPH3,ATP2C2,SLC30A7,MCOLN3,PTGFR,MIR199A1,KCNK3,DMD,MT1X,GPR35,NOL3,CHRNA10,TRIM24,CCR10,JPH2,SNX10,THY1,WNT5A,DDIT3	grey	VSMC_M10
GO:0072348	0.55	0.58	22	41	sulfur compound transport	BP	1	SLC26A10,SLC35B2,SLC1A1,SLC3A1,SLC1A4,SLC13A4,SLC7A11,SLC26A5,SLC25A30,ABCC4,SLC25A26,SLC33A1,ABCG2,ABCC5,SLC27A1,SLC25A11,SLC26A1,SLC26A2,SLC25A14,LRRC8A,SLC36A1,LRRC8D	grey	VSMC_M10
GO:0001840	0.55	0.74	4	7	neural plate development	BP	1	PTCH1,DVL2,NOG,C2CD3	grey	VSMC_M10
GO:1901570	0.55	0.58	21	39	fatty acid derivative biosynthetic process	BP	1	PPT2,ACSL6,HMGCLL1,PPT1,ELOVL1,ACSS3,ELOVL7,FAR2,ACSL5,HACD2,HMGCL,GGT2,ACSBG1,GGT6,TECR,GCDH,ACACA,ACSBG2,ACSF3,ELOVL3,GGT5	grey	VSMC_M10
GO:0048753	0.55	0.61	13	24	pigment granule organization	BP	1	AP3B1,DTNBP1,KIF13A,SHROOM2,HPS4,PIKFYVE,BLOC1S6,ABCB6,SNAPIN,AP1G1,BLOC1S3,RAB32,TRAPPC6A	grey	VSMC_M10
GO:1903214	0.55	0.58	21	39	regulation of protein targeting to mitochondrion	BP	1	PRKN,RAC2,USP36,BAG4,FBXW7,HTRA2,CSNK2A2,HPS4,ARIH2,BAG3,FZD5,C11orf65,PINK1,NPEPPS,HAX1,SREBF1,SH3GLB1,MICALL2,BNIP3L,RHOU,LEPROT	grey	VSMC_M10
GO:2000677	0.55	0.58	20	37	regulation of transcription regulatory region DNA binding	BP	1	POU4F1,DDRGK1,TRAF6,HAND2,FBXW7,PER2,PARP1,NSD1,MSX2,PSEN1,TAF1,SIN3A,ZBTB7C,DOT1L,PARK7,LAMTOR5,DDIT3,ZNF593,LIF,HEY2	grey	VSMC_M10
GO:0032056	0.55	0.74	4	7	positive regulation of translation in response to stress	BP	1	NCK2,EIF2AK4,DDX3X,IMPACT	grey	VSMC_M10
GO:0008306	0.55	0.56	28	53	associative learning	BP	1	SYNGAP1,SRF,KIT,SLC1A1,BRSK1,SHANK1,PPT1,SLC7A11,ADCY3,B4GALT2,DDHD2,ASIC1,KRAS,AGT,ATP1A2,CREB1,TNR,NPTX2,CLN8,RGS14,FOS,AC138894.1,CHRNB2,IFT20,MECP2,ABCA7,CRH,MAP1A	grey	VSMC_M10
GO:0003299	0.55	0.62	12	22	muscle hypertrophy in response to stress	BP	1	TRPC3,KDM4A,PPP3CA,MYH7,HDAC4,CAMTA2,TCAP,SMAD3,GATA6,MIR199A1,MIR25,HEY2	grey	VSMC_M10
GO:0014887	0.55	0.62	12	22	cardiac muscle adaptation	BP	1	TRPC3,KDM4A,PPP3CA,MYH7,HDAC4,CAMTA2,TCAP,SMAD3,GATA6,MIR199A1,MIR25,HEY2	grey	VSMC_M10
GO:0014898	0.55	0.62	12	22	cardiac muscle hypertrophy in response to stress	BP	1	TRPC3,KDM4A,PPP3CA,MYH7,HDAC4,CAMTA2,TCAP,SMAD3,GATA6,MIR199A1,MIR25,HEY2	grey	VSMC_M10
GO:0030835	0.55	0.58	20	38	negative regulation of actin filament depolymerization	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,ADD2,LMOD3,LIMA1,DMTN,CARMIL1,LMOD1,ADD3,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,CARMIL2	grey	VSMC_M10
GO:0007129	0.55	0.58	21	39	homologous chromosome pairing at meiosis	BP	1	UBE2B,DMC1,CCDC155,MLH1,CCNB1IP1,SIRT7,TEX15,SYCP1,CCDC36,SPO11,TEX12,MAJIN,ZCWPW1,STAG3,P3H4,SYCE2,MEIOB,MSH4,RNF212B,AGO4,SYCE1L	grey	VSMC_M10
GO:0019430	0.55	0.64	10	18	removal of superoxide radicals	BP	1	FANCC,PRDX1,DHFR,FBLN5,NFE2L2,GCH1,SOD3,MPO,NQO1,MIR21	grey	VSMC_M10
GO:0032906	0.55	0.70	5	9	transforming growth factor beta2 production	BP	1	WNT11,TGFB2,BMPR1A,SMAD3,GATA6	grey	VSMC_M10
GO:0032909	0.55	0.70	5	9	regulation of transforming growth factor beta2 production	BP	1	WNT11,TGFB2,BMPR1A,SMAD3,GATA6	grey	VSMC_M10
GO:0045622	0.55	0.61	13	24	regulation of T-helper cell differentiation	BP	1	HLA-DRA,RIPK2,HLX,BCL6,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0045922	0.55	0.62	12	22	negative regulation of fatty acid metabolic process	BP	1	SOX9,APOC1,SLC22A13,PIBF1,TRIB3,CYP7A1,ERLIN1,SIRT4,ACADL,ACADVL,NCOR1,INSIG2	grey	VSMC_M10
GO:0051481	0.55	0.70	5	9	negative regulation of cytosolic calcium ion concentration	BP	1	LRP1,RYR3,ATP1A2,SMAD3,KCNK3	grey	VSMC_M10
GO:0008053	0.55	0.61	13	24	mitochondrial fusion	BP	1	PRKN,BAK1,OPA1,DNM1L,ZDHHC6,USP30,MFN1,FIS1,MUL1,MFN2,ADCK1,THG1L,MIGA2	grey	VSMC_M10
GO:0098693	0.55	0.73	4	7	regulation of synaptic vesicle cycle	BP	1	BSN,DNAJC5,SYN1,CDK5R1	grey	VSMC_M10
GO:1902883	0.55	0.63	10	18	negative regulation of response to oxidative stress	BP	1	NCOA7,GPR37,MET,PDE8A,NFE2L2,PINK1,PARK7,MIR21,GPR37L1,TXN	grey	VSMC_M10
GO:1901568	0.55	0.56	29	54	fatty acid derivative metabolic process	BP	1	HSD17B4,ABHD16A,PPT2,ACSL6,HMGCLL1,PPT1,ELOVL1,ACSS3,ELOVL7,HPGD,FITM2,FAR2,ACSL5,HACD2,THEM5,HMGCL,GGT2,ACSBG1,GGT6,TECR,GCDH,ACACA,OXCT1,ACSBG2,ACSF3,ELOVL3,NUDT19,GGT5,LYPLA2	grey	VSMC_M10
GO:0035050	0.55	0.56	29	55	embryonic heart tube development	BP	1	SMO,FOXH1,SRF,TEAD2,BBS7,SETDB2,MEGF8,IFT172,TGFBR2,OVOL2,MKKS,HAND2,MEF2C,IFT52,PKD2,RYR2,SUFU,MED1,PSEN1,SMAD3,TBX2,MIB1,RNF207,ENG,LBX1,WNT5A,C2CD3,NKX2-5,PIFO	grey	VSMC_M10
GO:0090314	0.55	0.60	14	26	positive regulation of protein targeting to membrane	BP	1	ITGB1BP1,TCAF2,AKT2,PRNP,KCNB1,C2CD5,CIB1,FIS1,CEMIP,ITGAM,MIEF2,CDK5R1,HRAS,MIEF1	grey	VSMC_M10

GO:0048592	0.55	0.52	62	118	eye morphogenesis	BP	1	FRS2,BAK1,ATF4,AGTPBP1,NTRK2,RORB,SLC1A1,TFAP2B,TDRD7,RDH13,PTN,TSPAN12,FOXE3,SOX9,IFT172,MYO7A,TSKU,DZANK1,JAG1,RARB,FSCN2,CEP290,EPHB1,TENM3,USH1C,RPGRIP1L,TFAP2A,PAX2,NKD1,NECTIN3,ALDH1A3,SHROOM2,NRL,SP3,FZD5,FBN1,COL5A2,STAT3,OBSL1,ROM1,MFAP2,SDK1,MFN2,MEGF11,LCTL,TBX2,LHX1,STRA6,YY1,SKI,SOX8,COL5A1,OLFM3,FJX1,CNTF,THY1,WNT5A,DIO3,TBC1D20,PITX3,WNT2,COL8A2	grey	VSMC_M10
GO:0003418	0.55	0.73	4	7	growth plate cartilage chondrocyte differentiation	BP	1	COL27A1,SOX9,TSKU,TGFBR2	grey	VSMC_M10
GO:0046548	0.55	0.73	4	7	retinal rod cell development	BP	1	NTRK2,RORB,RPGRIP1L,NRL	grey	VSMC_M10
GO:0031128	0.55	0.60	15	28	developmental induction	BP	1	FRS2,SPRY1,SOX9,WNT11,ROBO1,ROBO2,SALL1,WNT3,FZD5,WNT4,SOX8,WNT5A,SIX1,FGF1,WNT2	grey	VSMC_M10
GO:0099532	0.55	0.70	5	9	synaptic vesicle endosomal processing	BP	1	AP3B1,DNM1L,STX6,GRIPAP1,BTBD8	grey	VSMC_M10
GO:0034650	0.55	0.73	4	7	cortisol metabolic process	BP	1	DKK3,WNT4,DGKQ,CACNA1H	grey	VSMC_M10
GO:0034651	0.55	0.73	4	7	cortisol biosynthetic process	BP	1	DKK3,WNT4,DGKQ,CACNA1H	grey	VSMC_M10
GO:1902645	0.55	0.73	4	7	tertiary alcohol biosynthetic process	BP	1	DKK3,WNT4,DGKQ,CACNA1H	grey	VSMC_M10
GO:0050854	0.55	0.57	23	43	regulation of antigen receptor-mediated signaling pathway	BP	1	CD226,PRKD2,NECTIN2,PAWR,PLCL2,PRNP,FOXP1,LPXN,PTPRJ,SLA2,LCK,RC3H1,PTPN6,GPS2,CARD11,CD19,PRKCB,PTPN2,IKBKG,BCL10,CMTM3,THY1,GCSAM	grey	VSMC_M10
GO:0060947	0.55	0.73	4	7	cardiac vascular smooth muscle cell differentiation	BP	1	SRF,GPER1,GATA6,HEY2	grey	VSMC_M10
GO:0006688	0.55	0.61	13	24	glycosphingolipid biosynthetic process	BP	1	B4GALNT1,A4GALT,LARGE1,ST8SIA4,A3GALT2,ST8SIA2,B3GALT1,ST8SIA5,ST6GALNAC4,ST3GAL2,ST6GALNAC5,B4GALT3,ST8SIA6	grey	VSMC_M10
GO:0034454	0.55	0.68	6	11	microtubule anchoring at centrosome	BP	1	CCDC68,KIF3A,NINL,HOOK3,NIN,CCDC120	grey	VSMC_M10
GO:0030174	0.55	0.73	4	7	regulation of DNA-dependent DNA replication initiation	BP	1	NBN,WRNIP1,KAT7,WDR18	grey	VSMC_M10
GO:0030224	0.56	0.59	15	28	monocyte differentiation	BP	1	MYC,MYH9,CDK6,HOXA7,FOXP1,IRF7,ACIN1,ZBTB46,SP3,MED1,GPR68,CD74,CSF1R,JUN,MIR125B1	grey	VSMC_M10
GO:1905144	0.56	0.61	13	24	response to acetylcholine	BP	1	LY6E,CHRNA3,PLCB1,CHRM5,CHRM4,CHRM3,GRK2,CHRM1,CHRNB2,HRH4,CDK5R1,GNB1,GNA15	grey	VSMC_M10
GO:1905145	0.56	0.61	13	24	cellular response to acetylcholine	BP	1	LY6E,CHRNA3,PLCB1,CHRM5,CHRM4,CHRM3,GRK2,CHRM1,CHRNB2,HRH4,CDK5R1,GNB1,GNA15	grey	VSMC_M10
GO:1990456	0.56	0.73	4	7	mitochondrion-endoplasmic reticulum membrane tethering	BP	1	PDZD8,PSEN2,CALM1,VMP1	grey	VSMC_M10
GO:0061724	0.56	0.73	4	7	lipophagy	BP	1	SPTLC1,RAB7A,AUP1,HTT	grey	VSMC_M10
GO:1904645	0.56	0.57	22	41	response to amyloid-beta	BP	1	LRP1,AGER,FPR2,TLR4,FOXO3,ATP1A3,PRNP,BACE1,SNX6,ITGA4,MMP13,MMP3,EPHA4,PARP1,CACNB1,PSEN1,CACNA1A,NGFR,CACNA1B,LCN2,BCL2L11,BCL2L2	grey	VSMC_M10
GO:1990700	0.56	0.70	5	9	nucleolar chromatin organization	BP	1	BAZ2A,SIRT2,DDX11,PHF8,BEND3	grey	VSMC_M10
GO:0072393	0.56	0.66	7	13	microtubule anchoring at microtubule organizing center	BP	1	CCDC68,KIF3A,BICD2,NINL,HOOK3,NIN,CCDC120	grey	VSMC_M10
GO:1901725	0.56	0.70	5	9	regulation of histone deacetylase activity	BP	1	C6orf89,SPHK2,PRKD2,PINK1,KDM5A	grey	VSMC_M10
GO:0097104	0.56	0.70	5	9	postsynaptic membrane assembly	BP	1	NLGN4Y,NRXN2,NLGN2,NLGN3,CEL	grey	VSMC_M10
GO:0046427	0.56	0.60	13	24	positive regulation of receptor signaling pathway via JAK-STAT	BP	1	IL5,AKR1B1,OCIAD1,KIT,PIBF1,PTK2B,F2R,AGT,IL10RA,IL6R,CCL5,GHR,SOCS1	grey	VSMC_M10
GO:0003207	0.56	0.70	5	9	cardiac chamber formation	BP	1	HAND2,MEF2C,TBX5,TBX2,SOX4	grey	VSMC_M10
GO:0060700	0.56	0.73	4	7	regulation of ribonuclease activity	BP	1	TMBIM6,OAS3,OASL,OAS1	grey	VSMC_M10
GO:0039529	0.56	0.60	13	24	RIG-I signaling pathway	BP	1	USP15,ANKRD17,PUM2,PHB,SEC14L1,CLPB,NPLOC4,OAS3,OASL,NLRX1,BIRC3,RNF135,ZCCHC3	grey	VSMC_M10
GO:2000401	0.56	0.57	22	41	regulation of lymphocyte migration	BP	1	CCL27,OXSR1,JAM2,PTK2B,SLC8B1,ADTRP,CD200,APOD,ADAM8,MIA3,ITGA4,PADI2,TMEM102,STK10,CCL5,CCL7,CCL2,CRK,RHOA,FADD,WNT5A,GCSAM	grey	VSMC_M10
GO:0071389	0.56	0.73	4	7	cellular response to mineralocorticoid stimulus	BP	1	FOXO3,GPER1,NPAS4,SCNN1B	grey	VSMC_M10
GO:0070562	0.56	0.73	4	7	regulation of vitamin D receptor signaling pathway	BP	1	CYP27B1,SNW1,MED1,TRIM24	grey	VSMC_M10
GO:0045619	0.56	0.52	62	117	regulation of lymphocyte differentiation	BP	1	HLA-DRA,TCF7,XRCC6,FBXO7,SLC46A2,IL4I1,IL15,CLPTM1,GLI2,FOXJ1,IL15RA,TGFBR2,NCKAP1L,GAS6,PRKDC,SOX12,TOX,ZC3H8,CAMK4,TMEM131L,IL7,RASGRP1,RIPK2,AP3B1,SOX13,HLX,SLAMF8,CD28,RUNX3,PPP2R3C,ADAM8,DUSP10,BCL6,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,STAT5B,INHA,FOXP3,ZBTB1,CARD11,TBX21,ZBTB7B,IL4R,BTK,CD74,NKAP,IL7R,PTPN2,SOCS1,DROSHA,PRKCZ,MIR21,RHOA,SOX4,CD46,FGL2,TNFSF9,ZFP36L2,RC3H2	grey	VSMC_M10
GO:1903897	0.56	0.70	5	9	regulation of PERK-mediated unfolded protein response	BP	1	NCK2,PTPN2,ABCA7,HSPA5,PPP1R15A	grey	VSMC_M10
GO:0045876	0.56	0.73	4	7	positive regulation of sister chromatid cohesion	BP	1	SLF1,SLF2,DDX11,SFPQ	grey	VSMC_M10
GO:0021515	0.56	0.59	16	30	cell differentiation in spinal cord	BP	1	PTCH1,GLI2,IFT172,MNX1,SOX6,SOX13,SUFU,GIGYF2,MDGA2,SCYL3,CLN8,LHX1,ISL1,SOX4,ISL2,LBX1	grey	VSMC_M10
GO:0030002	0.56	0.70	5	9	cellular anion homeostasis	BP	1	SLC12A2,CKB,ABCC2,SLC12A5,XPR1	grey	VSMC_M10
GO:0043406	0.56	0.52	49	93	positive regulation of MAP kinase activity	BP	1	MAP3K5,MAP3K4,AGER,TAB1,KIT,ROR2,EPGN,TGFA,EGFR,ARHGEF5,TLR4,NEK10,FLT1,TRAF6,ROBO1,PTK2B,RASGRP1,TIAM1,NOD2,TAOK3,CD40,ADRA2A,AJUBA,KRAS,EGF,DVL3,MAP3K11,ADAM8,FZD5,MAP4K2,DUSP19,PDCD10,EPHA4,MAGED1,DVL2,PSEN1,FGF18,PIK3R5,MAP2K5,INSR,GHR,TRAF2,DAB2IP,S100A12,WNT5A,HRAS,MAP2K7,FGF1,PDGFD	grey	VSMC_M10
GO:0002832	0.56	0.53	41	77	negative regulation of response to biotic stimulus	BP	1	TNFAIP3,USP15,TRIB1,C6orf106,NR1H2,IL4I1,SEC14L1,SIRT2,NMI,NPLOC4,PCBP2,NR1H3,TRAFD1,OAS3,NLRC5,MAPKBP1,CD96,YTHDF2,SLAMF8,PARP14,RNF26,NLRX1,TRAF3IP1,HTRA1,DUSP10,MUL1,FOXP3,TKFC,USP18,DCST1,TSPAN6,STAT2,RIOK3,PTPN2,CRK,MIR21,OAS1,A2M,FGL2,SERPINB9,HAVCR2	grey	VSMC_M10

GO:0016579	0.56	0.52	57	108	protein deubiquitination	BP	1	SHMT2,TNFAIP3,USP15,PRKN,JOSD1,USP49,SUPT3H,USP46,MINDY4,USP45,USP38,OTUD1,USP35,WDR48,USP36,USP44,TAF10,ATXN7,ASXL1,OTUD4,USP39,USP25,USP16,OTULIN,ABRAXAS1,OTUD7A,USP30,SART3,USP13,SPATA2,YOD1,USP19,OTUD7B,USP2,ABRAXAS2,USP21,ENY2,ATXN7L3,USP37,USP48,OTUD3,OTUD5,STAMBPL1,USP18,UIMC1,MINDY2,EPOP,OTUB2,USP31,TNIP1,USP24,PARK7,USP20,STAMBP,UCHL3,USP40,BRCC3	grey	VSMC_M10
GO:0001953	0.56	0.58	17	32	negative regulation of cell-matrix adhesion	BP	1	LRP1,CDKN2A,HOXA7,ITGB1BP1,CLASP2,JAG1,FAM107A,PIK3R1,DMTN,ARHGAP6,APOD,BCL6,CASK,BCAS3,ACVRL1,ACER2,DUSP22	grey	VSMC_M10
GO:0030836	0.56	0.67	6	11	positive regulation of actin filament depolymerization	BP	1	KIAA1211,PLEK,F2RL1,CARMIL1,CARMIL2,PDXP	grey	VSMC_M10
GO:0035735	0.56	0.73	4	7	intraciliary transport involved in cilium assembly	BP	1	IFT74,DYNC2LI1,TTC26,IFT81	grey	VSMC_M10
GO:0071772	0.56	0.51	66	126	response to BMP	BP	1	SLC39A5,USP15,GDF9,SMAD5,LEMD2,KCP,TFAP2B,ROR2,DLX5,SOSTDC1,HOXA13,BMP8A,BMPER,SFRP4,SOX9,MEGF8,ACVR2B,UBE2O,ACVR2A,SPINT2,SPART,SLC33A1,SPINT1,HIVEP1,ZNF423,BMPR1B,FBXL15,PDCD4,TGFB2,HJV,SORL1,HTRA1,CHRD,DLX1,CTDSPL2,HTRA3,FBN1,FKBP8,GDF15,GREM2,BMPR1A,RBPJ,ITGA3,RBPMS2,MAPK3,TOB1,TMEM100,SMAD3,TNMD,RNF165,CHRDL1,GATA6,FAM83G,TWSG1,ADAMTS12,GPC3,SKI,ENG,MIR21,FSTL3,LEMD3,ACVRL1,NOG,WNT5A,RGMB,UBE2D1	grey	VSMC_M10
GO:0071773	0.56	0.51	66	126	cellular response to BMP stimulus	BP	1	SLC39A5,USP15,GDF9,SMAD5,LEMD2,KCP,TFAP2B,ROR2,DLX5,SOSTDC1,HOXA13,BMP8A,BMPER,SFRP4,SOX9,MEGF8,ACVR2B,UBE2O,ACVR2A,SPINT2,SPART,SLC33A1,SPINT1,HIVEP1,ZNF423,BMPR1B,FBXL15,PDCD4,TGFB2,HJV,SORL1,HTRA1,CHRD,DLX1,CTDSPL2,HTRA3,FBN1,FKBP8,GDF15,GREM2,BMPR1A,RBPJ,ITGA3,RBPMS2,MAPK3,TOB1,TMEM100,SMAD3,TNMD,RNF165,CHRDL1,GATA6,FAM83G,TWSG1,ADAMTS12,GPC3,SKI,ENG,MIR21,FSTL3,LEMD3,ACVRL1,NOG,WNT5A,RGMB,UBE2D1	grey	VSMC_M10
GO:0006686	0.56	0.73	4	7	sphingomyelin biosynthetic process	BP	1	SGMS2,SGMS1,ABCA8,PEMT	grey	VSMC_M10
GO:1900115	0.56	0.70	5	9	extracellular regulation of signal transduction	BP	1	FBN1,LRPAP1,GREM2,CD46,NRROS	grey	VSMC_M10
GO:1900116	0.56	0.70	5	9	extracellular negative regulation of signal transduction	BP	1	FBN1,LRPAP1,GREM2,CD46,NRROS	grey	VSMC_M10
GO:0021535	0.56	0.66	7	13	cell migration in hindbrain	BP	1	RBFOX2,SEMA4C,POU4F1,TTBK2,ATP1B2,DAB1,CEND1	grey	VSMC_M10
GO:0090308	0.56	0.67	6	11	regulation of DNA methylation-dependent heterochromatin assembly	BP	1	SETDB2,FAM208A,PPHLN1,TET1,SETDB1,ZNF304	grey	VSMC_M10
GO:0045089	0.56	0.53	44	83	positive regulation of innate immune response	BP	1	CD226,XRCC6,FPR2,AKIRIN2,TLR4,NECTIN2,PVR,IKBKB,NMI,TMEM173,MAVS,HPX,PRKDC,IRF7,TRAF6,HCK,RASGRP1,NLRC5,POLR3D,NOD2,POLR3C,PARP9,COCH,ADAM8,CADM1,NONO,IL12A,XRCC5,LAG3,STAT5B,MED1,SFPQ,SIN3A,CCL5,RIOK3,VAV1,CREBBP,AP1G1,FADD,ZCCHC3,IRGM,WNT5A,EREG,HAVCR2	grey	VSMC_M10
GO:0042074	0.56	0.70	5	9	cell migration involved in gastrulation	BP	1	MEGF8,WNT11,AMOT,GPC3,WNT5A	grey	VSMC_M10
GO:0030101	0.56	0.56	23	43	natural killer cell activation	BP	1	NFIL3,PRDX1,IL15,UNC13D,PIBF1,IL15RA,GAS6,TOX,RASGRP1,RABL3,FGR,SNX27,SP3,BLOC1S6,IL12A,STAT5B,ZBTB1,KAT7,TICAM1,AP1G1,BLOC1S3,CASP8,HAVCR2	grey	VSMC_M10
GO:0048477	0.56	0.54	33	62	oogenesis	BP	1	YTHDC2,GDF9,WASHC5,H3F3C,TUT7,DMC1,YTHDC1,PTN,NOBOX,CCDC155,TUT4,FOXO3,PANX1,ERCC1,MLH1,SIRT2,SOHLH2,PTK2B,KMT2D,NPM2,BMPR1B,CCDC36,YTHDF2,SPO11,WNT4,YBX2,PAQR5,TAF4B,WDR77,AURKC,NANOS1,EREG,ZGLP1	grey	VSMC_M10
GO:0035315	0.56	0.58	18	34	hair cell differentiation	BP	1	MYCL,WHRN,MYCN,ERCC2,ERCC3,MYO7A,SLC4A7,JAG1,LRTOMT,AP000812.5,PLS1,USH1C,STRC,RBPJ,TMEM132E,JAG2,MCOLN3,HEY2	grey	VSMC_M10
GO:0032757	0.56	0.56	22	41	positive regulation of interleukin-8 production	BP	1	HSPA1B,NOD1,TLR4,PRKD2,MYD88,MAVS,F2RL1,F2R,RIPK1,NOD2,TLR5,STAT3,CD74,NOS2,PARK7,LAMTOR5,BCL10,FADD,ZNF580,WNT5A,DDIT3,IL17D	grey	VSMC_M10
GO:0150003	0.56	0.73	4	7	regulation of spontaneous synaptic transmission	BP	1	SLC12A2,PRKN,AGER,STX1B	grey	VSMC_M10
GO:0032536	0.56	0.72	4	7	regulation of cell projection size	BP	1	KEL,PLS1,USH1C,CNTN2	grey	VSMC_M10
GO:1905383	0.56	0.69	5	9	protein localization to presynapse	BP	1	KIF5A,DLG2,KIF5C,MAPK8IP3,MAP1A	grey	VSMC_M10
GO:0043410	0.56	0.48	189	356	positive regulation of MAPK cascade	BP	1	LRP1,MAP3K5,FRS2,STK3,MAPK8IP2,MAP3K4,AGER,PRXL2C,GRM4,TAB1,NTRK2,TEK,GPR37,KIT,ROR2,GADD45G,SEMA4C,IL11,PRKCE,FPR2,GSDME,EMC10,LPAR1,MTURN,EPGN,NOD1,BMPER,TGFA,EGFR,ARHGEF5,TLR4,TRAF1,SDCBP,FGF21,BRAF,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,RAF1,MYD88,SPRY2,ALK,ARRB1,C1QTNF1,NEK10,PDE6G,PLCB1,EIF2AK2,ADRA1D,RELL2,SEMA3A,KL,NRG1,SH3RF2,GAS6,ARL6IP5,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,ST5,MOS,RET,HAND2,ROBO1,PLCE1,FBXW7,PTPRJ,P2RY1,MADD,PTK2B,RASGRP1,RAPGEF2,CCL17,TIAM1,RIPK2,F2RL1,F2R,NQO2,RIPK1,GCNT2,NOD2,TAOK3,CD40,DSTYK,IGF2,BANK1,MAP2K6,TRPV4,TGFB2,ADRA2A,SLC30A10,AJUBA,NCF1,KRAS,EGF,SOX2,GPER1,DOK5,CIB1,TRAF5,DVL3,FZD7,OSM,THPO,PDE6H,MAP3K3,PDE8A,MAP3K11,ADAM8,FZD5,MBIP,RAP1B,MAP4K2,DUSP19,PDCD10,ADRA2C,GPBAR1,GDF15,FGFR3,LTBR,MINK1,EPHA4,MAGED1,DVL2,IGFBP4,RELL1,FGFR4,PSEN1,FGF18,TAOK2,EFNA1,WWC1,MAPK3,MAP2K1,PIK3R5,MAP2K5,RIT2,GAREM1,TRAF3,CD74,CCL14,INSR,CCL5,CSF1R,CCL7,CCL2,CCL25,GHR,KSR1,TAOK1,SERPINF2,PRKCZ,MAPK8IP3,TRAF2,ATP6AP1,ABCA7,CDK10,DAB2IP,MIR21,MIR222,MIR23A,MIR27B,MIR24-1,MIR27A,FGA,CCL16,S100A12,ZNF622,GPR37L1,AVPI1,DOK4,WNT5A,GADD45A,LAMTOR2,INAVA,CSPG4,LIF,DUSP22,HRAS,MAP2K7,FGF1,HAVCR2,NMNAT1,CCL22,PDGFD	grey	VSMC_M10

GO:0032635	0.56	0.52	51	96	interleukin-6 production	BP	1	TNFAIP3,AGER,MAPK13,NOD1,AKIRIN2,TLR4,SPHK2,C5AR2,MYD88,FOXJ1,ARRB1,MAVS,NCKAP1L,GAS6,TRAF6,IL1A,IL37,RIPK2,F2RL1,F2R,NOD2,RAB7B,IFIH1,CD200,BANK1,TRPV4,MAPKAPK2,NLRX1,IL16,PTPN6,STAT3,FOXP3,SPON2,SYT11,IL6R,CD74,ISL1,NOS2,TICAM1,CYBA,BCL10,MIR125A,WNT5A,INAVA,IL33,C1QTNF4,TSLP,CEBPB,EREG,HAVCR2,IL17D	grey	VSMC_M10
GO:0032675	0.56	0.52	51	96	regulation of interleukin-6 production	BP	1	TNFAIP3,AGER,MAPK13,NOD1,AKIRIN2,TLR4,SPHK2,C5AR2,MYD88,FOXJ1,ARRB1,MAVS,NCKAP1L,GAS6,TRAF6,IL1A,IL37,RIPK2,F2RL1,F2R,NOD2,RAB7B,IFIH1,CD200,BANK1,TRPV4,MAPKAPK2,NLRX1,IL16,PTPN6,STAT3,FOXP3,SPON2,SYT11,IL6R,CD74,ISL1,NOS2,TICAM1,CYBA,BCL10,MIR125A,WNT5A,INAVA,IL33,C1QTNF4,TSLP,CEBPB,EREG,HAVCR2,IL17D	grey	VSMC_M10
GO:0030595	0.56	0.50	80	150	leukocyte chemotaxis	BP	1	SLC12A2,GPSM3,PTK2,RAC2,CCL27,KIT,NINJ1,FPR2,CXCL8,AKIRIN1,PTN,TRPM4,C5AR2,C5AR1,OXSR1,NCKAP1L,GAS6,FAM19A4,FLT1,MTUS1,CYP7B1,VEGFC,PTK2B,CCL17,SLC8B1,F2RL1,ANO6,NOD2,GBF1,DNM1L,TRPV4,SBDS,TGFB2,PRSS56,CMKLR1,SLAMF8,MOSPD2,PTPRO,FCER1G,ADAM8,PIKFYVE,IL16,IL12A,MCU,TNFSF18,CXCR2,BST1,MAPK1,CH25H,PADI2,CXCL16,TMEM102,PGF,DAPK2,MAPK3,IL6R,S100A14,S100A8,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,VAV1,PIP5K1C,MPP1,BSG,VAV3,CCL16,S100A12,CHGA,DEFB124,DPP4,CXCL6,ZNF580,WNT5A,DUSP1,CCL22	grey	VSMC_M10
GO:0021819	0.56	0.69	5	9	layer formation in cerebral cortex	BP	1	MBOAT7,CDK5R1,LRP8,DAB2IP,ADGRG1	grey	VSMC_M10
GO:0098887	0.56	0.69	5	9	neurotransmitter receptor transport, endosome to postsynaptic membrane	BP	1	NSG1,GRIPAP1,RAB8A,RAB11A,ARHGAP44	grey	VSMC_M10
GO:0043620	0.56	0.55	26	49	regulation of DNA-templated transcription in response to stress	BP	1	ATF4,HSF1,NCK2,EPAS1,SIRT2,TCIM,TMBIM6,BACH1,HIF1AN,ARNT,BAG3,RPS6KA1,NFE2L2,STOX1,DNAJB1,RBPJ,RGS14,MUC1,SIN3A,MAPK7,JUN,CREB3L3,HSPA5,IMPACT,DDIT3,CEBPB	grey	VSMC_M10
GO:0001408	0.56	0.72	4	7	guanine nucleotide transport	BP	1	ABCC4,ABCC5,LRRC8E,LRRC8A	grey	VSMC_M10
GO:2000758	0.56	0.58	16	30	positive regulation of peptidyl-lysine acetylation	BP	1	SPHK2,PAXIP1,ARRB1,AUTS2,TADA2B,FOXP3,KAT7,MUC1,MAPK3,NAP1L2,RPS6KA5,ISL1,GLYR1,SOX4,LIF,RPS6KA4	grey	VSMC_M10
GO:0099558	0.56	0.65	7	13	maintenance of synapse structure	BP	1	SYNGAP1,ERC2,BSN,DLG1,C1QL1,RAB3A,SDF4	grey	VSMC_M10
GO:0032689	0.56	0.60	13	24	negative regulation of interferon-gamma production	BP	1	TLR4,PRNP,GAS6,NR1H4,NOD2,CD96,VSIR,INHA,SCGB1A1,FOXP3,MIR24-1,DDIT3,HAVCR2	grey	VSMC_M10
GO:1903201	0.56	0.54	30	56	regulation of oxidative stress-induced cell death	BP	1	PRKN,NCOA7,ATF4,GPR37,FBXO7,MET,TLR4,SLC7A11,FOXO3,PAWR,FBXW7,HTRA2,RIPK1,MCL1,PDE8A,NFE2L2,NONO,PINK1,MMP3,PARP1,SFPQ,MAPK7,STK26,PARK7,TSC1,TLDC1,MIR21,NOL3,GPR37L1,TXN	grey	VSMC_M10
GO:0007320	0.56	0.72	4	7	insemination	BP	1	KLK14,DDO,ACVR2A,P2RX1	grey	VSMC_M10
GO:0002696	0.56	0.49	116	218	positive regulation of leukocyte activation	BP	1	CD226,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TNFRSF13C,XRCC6,TTBK1,NCK2,EXOSC3,MSH2,PELI1,IL4I1,TLR4,IL15,SPHK2,HMCES,BMI1,NECTIN2,GAB2,MLH1,GLI2,MYD88,PAXIP1,IL15RA,TGFBR2,SHLD1,NCKAP1L,GAS6,PRKDC,SLC7A1,TRAF6,SOX12,TOX,IL1A,CEBPA,MEF2C,IL7,RASGRP1,RIPK2,AP3B1,F2RL1,SOX13,NOD2,ZNF335,CD40,IGF2,LCK,ICOSLG,GPAM,HLX,FGR,SNX4,CD28,RUNX3,PPP2R3C,ADAM8,DUSP10,BLOC1S6,PLA2G4A,BCL6,IL12A,VSIR,PTPN6,TNIP2,CD38,BST1,STAT5B,FOXP3,RASAL3,ZBTB1,SHLD2,CARD11,TBX21,STX4,ITGAM,ZBTB7B,CHRNB2,IL4R,BTK,CD74,CCL5,CCL2,YES1,NKAP,CD320,VAV1,IL7R,SOCS1,TICAM1,DNAJA3,PRKCZ,VAV3,KARS,STXBP1,AP1G1,BCL10,MIR21,RHOA,HAVCR1,BLOC1S3,SOX4,FADD,DPP4,CD46,THY1,WNT5A,IL33,CD70,TNFSF9,TSLP,EFNB3,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0016240	0.56	0.72	4	7	autophagosome membrane docking	BP	1	STX17,SNAP29,CALM1,VMP1	grey	VSMC_M10
GO:0051969	0.56	0.72	4	7	regulation of transmission of nerve impulse	BP	1	AGT,TNR,FMR1,GPR35	grey	VSMC_M10
GO:2001054	0.56	0.72	4	7	negative regulation of mesenchymal cell apoptotic process	BP	1	SOX9,PAX8,PAX2,POU3F4	grey	VSMC_M10
GO:0018022	0.56	0.51	57	108	peptidyl-lysine methylation	BP	1	SNW1,PHF1,CAMKMT,SETD7,SETDB2,EED,IWS1,SUV39H2,KDM4A,PAXIP1,DPY30,NSD3,ASH2L,EEF1AKMT1,DNMT3B,SMYD1,SETD6,KMT2D,RTF1,WDR82,ZNF335,JARID2,RBBP5,FAM173B,AUTS2,EEF1AKMT2,SETD2,BCOR,MEN1,WDR61,VCPKMT,NELFA,DYDC1,NSD1,SETD1A,PAGR1,OGT,SETD3,SUZ12,SUPT6H,CXXC1,DOT1L,MECP2,PRDM16,CHD5,MTF2,GFI1,PRMT6,METTL18,SETDB1,ARID4A,BEND3,SMYD3,METTL21A,ZNF304,NNMT,N6AMT1	grey	VSMC_M10
GO:0034440	0.56	0.52	48	90	lipid oxidation	BP	1	HSD17B4,CPT1B,PPARA,MCAT,ECHDC1,MAPK14,CROT,ADH5,ETFB,HADHA,SOX9,PRKAG2,ACOX1,CYGB,AKT2,HACL1,ACOXL,ACOX2,PEX2,ETFDH,IVD,ECI2,LONP2,SIRT4,IRS1,CPT1A,BDH2,ABCB11,EHHADH,APOD,POR,ACADL,TYSND1,ACADVL,HSD17B10,ABCD4,GCDH,ACAA2,DECR2,MLYCD,ABCD3,ACADM,PHYH,HADHB,AMACR,ECI1,AUH,ADH4	grey	VSMC_M10
GO:0033089	0.56	0.72	4	7	positive regulation of T cell differentiation in thymus	BP	1	GLI2,RASGRP1,ADAM8,IL7R	grey	VSMC_M10
GO:0051956	0.56	0.72	4	7	negative regulation of amino acid transport	BP	1	ARL6IP5,SLC43A1,ABAT,RGS4	grey	VSMC_M10
GO:1905331	0.56	0.72	4	7	negative regulation of morphogenesis of an epithelium	BP	1	NKD1,TBX2,MIR21,WNT5A	grey	VSMC_M10
GO:0032768	0.56	0.56	23	43	regulation of monooxygenase activity	BP	1	CYP27B1,ZDHHC21,NOD1,EGFR,NOSIP,DHFR,ACVR2A,IL1A,PIK3CB,PTK2B,VDR,TERT,KRAS,NOS1AP,POR,GCH1,CALM1,GLA,PARK7,GFI1,TERF2,MIR27B,FCER2	grey	VSMC_M10
GO:1905668	0.56	0.67	6	11	positive regulation of protein localization to endosome	BP	1	ABHD17B,EGF,SORL1,DTX3L,ABHD17A,ABHD17C	grey	VSMC_M10
GO:0071450	0.56	0.61	11	20	cellular response to oxygen radical	BP	1	FANCC,PRDX1,DHFR,GLRX2,FBLN5,NFE2L2,GCH1,SOD3,MPO,NQO1,MIR21	grey	VSMC_M10
GO:0071451	0.56	0.61	11	20	cellular response to superoxide	BP	1	FANCC,PRDX1,DHFR,GLRX2,FBLN5,NFE2L2,GCH1,SOD3,MPO,NQO1,MIR21	grey	VSMC_M10

GO:0045806	0.56	0.56	22	41	negative regulation of endocytosis	BP	1	NR1H2,SDCBP,MTMR2,APOC1,NEU3,WDR54,NR1H3,ANKRD13A,ANKRD13D,RUBCN,SH3GL3,LRPAP1,DLG4,STX1B,SYT11,SCAMP5,UNC119,ABCA7,MIR199A1,MIR27B,MIR27A,LRRTM2	grey	VSMC_M10
GO:0046031	0.57	0.53	35	66	ADP metabolic process	BP	1	PPARA,PRXL2C,GAPDH,SLC4A4,NT5E,BPGM,DHTKD1,PRKAG2,PFKP,GPI,GPD1,P2RX7,PRKAG1,PFKM,ZBTB20,PFKFB2,ENO4,ARNT,ACTN3,HDAC4,MLXIPL,HK1,PRKAG3,STAT3,ENO3,PSEN1,PKLR,OGT,ADPGK,NCOR1,INSR,ALDOC,SLC2A6,ENTPD5,TIGAR	grey	VSMC_M10
GO:1900038	0.57	0.72	4	7	negative regulation of cellular response to hypoxia	BP	1	TMBIM6,HYOU1,PINK1,NOL3	grey	VSMC_M10
GO:1901214	0.57	0.49	133	251	regulation of neuron death	BP	1	ERBB3,LRP1,MAP3K5,AGAP2,PRKN,PPARA,SYNGAP1,NCOA7,GRM4,ATF4,NTRK2,NRBP2,HSF1,FBXO7,CNTFR,SLC1A1,TFAP2B,MSH2,REL,PPT1,EPHA7,TLR4,VPS35,SLC7A11,FOXO3,NTF4,FGF21,NDNF,C5AR1,ZNF746,GRIK5,XRCC2,EGLN2,POU4F1,ARRB1,SLC23A2,PRNP,EPHB1,GPI,RILPL1,CASP3,GBE1,FBXW7,TRIM2,MEF2C,FAIM2,HTRA2,PTK2B,NR4A2,F2R,NQO2,TFAP2A,PM20D1,BDNF,CD200,HDAC1,TERT,TGFB2,SLC30A10,INPP5A,SSH1,KCNB1,KRAS,ADNP,SORL1,MCL1,CBL,HYOU1,NFATC4,HDAC4,DLX1,BACE1,DNAJC5,FZD9,EGLN3,SNX6,MAP3K11,ADAM8,CREB1,MAPT,NONO,FIS1,PINK1,STAT3,ATP13A2,PARP1,TNFRSF1B,PSEN1,ITGAM,FOS,AC138894.1,CITED1,ALKBH1,GPRASP2,BHLHB9,CCL5,AP2B1,PPP1R13B,CCL2,CDK5R1,ISL1,GHR,JUN,PDPK1,MECP2,TRAF2,IKBKG,TMEM259,PARK7,TSC1,TLDC1,LCN2,STXBP1,AARS,NQO1,NAE1,MIR125B1,RHOA,UBB,CHGA,GRID2,CNTF,CASP8,PSMC1,WNT5A,TIGAR,SIX1,DDIT3,BCL2L11,HRAS,CEBPB,PITX3,NMNAT1	grey	VSMC_M10
GO:0006760	0.57	0.60	12	22	folic acid-containing compound metabolic process	BP	1	SHMT2,DHFR,MTHFD2,MTRR,MTHFS,GCH1,SHMT1,SLC46A1,PIPOX,MTHFD2L,SLC25A32,ALDH1L1	grey	VSMC_M10
GO:0048385	0.57	0.69	5	9	regulation of retinoic acid receptor signaling pathway	BP	1	SNW1,ASXL1,ZNF536,CNOT1,DHRS3	grey	VSMC_M10
GO:0060856	0.57	0.72	4	7	establishment of blood-brain barrier	BP	1	LSR,FOXP3,MXRA8,TRPV1	grey	VSMC_M10
GO:0060433	0.57	0.72	4	7	bronchus development	BP	1	SRF,SOX9,TGFBR2,TULP3	grey	VSMC_M10
GO:0034154	0.57	0.72	4	7	toll-like receptor 7 signaling pathway	BP	1	RSAD2,UNC93B1,DDX3X,HAVCR2	grey	VSMC_M10
GO:2000826	0.57	0.69	5	9	regulation of heart morphogenesis	BP	1	SMO,WNT11,ROBO1,ROBO2,WNT5A	grey	VSMC_M10
GO:0062237	0.57	0.58	16	30	protein localization to postsynapse	BP	1	ADAM22,DAG1,DLG1,NSG1,GRIPAP1,RAB8A,DLG4,IQSEC2,CPLX1,STX1B,ZDHHC15,RAB11A,ARHGAP44,PRKCZ,CACNG7,HRAS	grey	VSMC_M10
GO:0090288	0.57	0.52	41	78	negative regulation of cellular response to growth factor stimulus	BP	1	SEMA6A,LEMD2,SOSTDC1,BMPER,FUZ,SPRY1,SPRY2,DCN,SPART,PIK3CB,SULF2,PDCD6,SORL1,AGT,HTRA1,CHRD,DLX1,CTDSPL2,IL12A,CASK,HTRA3,FBN1,WNT4,GREM2,NGFR,RBPMS2,TOB1,TNMD,CHRDL1,TWSG1,ADAMTS12,SKI,DAB2IP,MIR199A1,FSTL3,LEMD3,NOG,WNT5A,SHISA2,CADM4,UBE2D1	grey	VSMC_M10
GO:0046321	0.57	0.69	5	9	positive regulation of fatty acid oxidation	BP	1	PPARA,AKT2,IRS1,CPT1A,MLYCD	grey	VSMC_M10
GO:0071044	0.57	0.67	6	11	histone mRNA catabolic process	BP	1	EXOSC4,MTPAP,LSM1,TENT2,TENT4B,UPF1	grey	VSMC_M10
GO:0061004	0.57	0.72	4	7	pattern specification involved in kidney development	BP	1	OSR1,PAX8,PAX2,IRX2	grey	VSMC_M10
GO:0072048	0.57	0.72	4	7	renal system pattern specification	BP	1	OSR1,PAX8,PAX2,IRX2	grey	VSMC_M10
GO:0048368	0.57	0.69	5	9	lateral mesoderm development	BP	1	SMO,FOXH1,TEAD2,BMPR1A,FOXF1	grey	VSMC_M10
GO:0034163	0.57	0.72	4	7	regulation of toll-like receptor 9 signaling pathway	BP	1	GRAMD4,RTN4,RSAD2,RAB7B	grey	VSMC_M10
GO:0002697	0.57	0.49	109	206	regulation of immune effector process	BP	1	CD226,STX7,ENPP3,AGER,HLA-DRA,IL5,RAC2,KIT,EXOSC3,MSH2,ANKRD17,RSAD2,IL4I1,TLR4,ATG5,TRPM4,SPHK2,HMCES,PHB,LACC1,NECTIN2,PVR,GAB2,MLH1,UNC13D,SLC22A13,FOXJ1,PAXIP1,SHLD1,MAVS,NCKAP1L,HPX,PRKDC,TRAF6,GPI,FER,PTPRJ,TMBIM6,RASGRP1,RIPK2,F2RL1,NOD2,CD40,CD96,TGFB2,HLX,DENND1B,NCF1,SLAMF8,FGR,SNX4,CD28,CADM1,FZD5,DUSP10,BCL6,HK1,IL12A,RC3H1,PTPN6,TNFSF18,LAG3,PPP3CB,C12orf4,STAT5B,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,SPON2,TBX21,STX4,ITGAM,ZBTB7B,IL4R,BTK,CD74,STXBP2,FBXO38,PRAM1,VAV1,C3,NOS2,IL7R,SUPT6H,TICAM1,CRK,DNASE1,PDPK1,PRKCZ,TRAF2,SLC7A5,FOXF1,STXBP1,AP1G1,BCL10,MIR21,FADD,CXCL6,CD46,A2M,WNT5A,INAVA,FGL2,FCER2,SERPINB9,HAVCR2,RC3H2	grey	VSMC_M10
GO:0051402	0.57	0.49	105	198	neuron apoptotic process	BP	1	ERBB3,LRP1,AGAP2,PRKN,SYNGAP1,GRM4,ATF4,NTRK2,NRBP2,CNTFR,SLC1A1,TNFRSF21,TFAP2B,GAPDH,MSH2,PPT1,EPHA7,FOXO3,NTF4,NDNF,C5AR1,GRIK5,XRCC2,EGLN2,POU4F1,AKT2,ARRB1,TMTC4,PRNP,GPI,CASP3,GBE1,DIABLO,FBXW7,TRIM2,MEF2C,FAIM2,PTK2B,NR4A2,F2R,NQO2,TFAP2A,PIGT,SIAH1,BDNF,HDAC1,TERT,TGFB2,SLC30A10,ADARB1,SCN2A,KCNB1,KRAS,ADNP,MCL1,HYOU1,NFATC4,HDAC4,DLX1,BACE1,DNAJC5,FZD9,EGLN3,SNX6,MAP3K11,ADAM8,NONO,FIS1,PINK1,PARP1,MAX,PSEN1,ITGAM,NGFR,AC138894.1,CITED1,ALKBH1,GPRASP2,BHLHB9,CCL2,CDK5R1,ISL1,JUN,PDPK1,MECP2,PARK7,LCN2,STXBP1,AARS,HSPA5,NQO1,NAE1,MIR125B1,RHOA,FADD,GRID2,CNTF,DIO3,SIX1,DDIT3,BCL2L11,HRAS,CEBPB,PITX3,NMNAT1	grey	VSMC_M10
GO:0016553	0.57	0.72	4	7	base conversion or substitution editing	BP	1	ADAT2,APOBEC3H,NUDT16,ADARB1	grey	VSMC_M10
GO:0048663	0.57	0.57	18	34	neuron fate commitment	BP	1	GLI2,MNX1,POU4F1,NRG1,EYA1,SUFU,SATB2,DLX1,RBPJ,EPOP,BCL11B,JAG2,ISL1,FOXG1,ISL2,LBX1,POU3F2,SIX1	grey	VSMC_M10
GO:0007614	0.57	0.69	5	9	short-term memory	BP	1	CUX2,ADNP,NPAS4,COMT,SLC2A4	grey	VSMC_M10

GO:0070646	0.57	0.50	66	125	protein modification by small protein removal	BP	1	SHMT2,TNFAIP3,USP15,PRKN,JOSD1,USP49,SUPT3H,USP46,MINDY4,USP45,USP38,OTUD1,USP35,WDR48,USP36,GPS1,USP44,TAF10,ATXN7,ASXL1,OTUD4,USP39,USP25,USP16,OTULIN,SENP1,ABRAXAS1,OTUD7A,COPS7B,USP30,SART3,USP13,SPATA2,YOD1,USP19,OTUD7B,USP2,ABRAXAS2,USP21,SENP5,SENP2,ENY2,ATXN7L3,COPS7A,USP37,USP48,OTUD3,OTUD5,STAMBPL1,USP18,UIMC1,MINDY2,EPOP,OTUB2,USP31,TNIP1,USP24,PARK7,USP20,STAMBP,UCHL3,SENP7,COPS8,USP40,BRCC3,HINT1	grey	VSMC_M10
GO:1901879	0.57	0.52	39	75	regulation of protein depolymerization	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,PLEK,ADD2,CLASP2,TRIM54,NAV3,SPEF1,LMOD3,ATXN7,LIMA1,KATNB1,F2RL1,DMTN,CARMIL1,LMOD1,ADD3,TRPV4,TTBK2,CIB1,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,CAMSAP3,TAOK1,APC2,CAMSAP1,CARMIL2,APC,PDXP,MAP1A,MAP6D1	grey	VSMC_M10
GO:0032412	0.57	0.49	94	178	regulation of ion transmembrane transporter activity	BP	1	NEDD4L,STAC3,MAPK8IP2,PRRT1,GOPC,PLA2G6,ABCB1,WNK2,PRKCE,SHANK1,HECW1,TCAF2,OSR1,SPHK2,KCNRG,CACNB2,STAC,OXSR1,GPD1L,CACNB4,PRNP,SLMAP,GLRX,MEF2C,PTK2B,KCNJ11,HOMER1,IFNGR2,TESC,RIPK1,KCNE2,PKD2,CASQ2,KCNIP2,CHRM3,RYR2,FAM173B,HECW2,ADRA2A,COX17,KCNG1,ANK2,KLHL24,ATP1A2,SLC9A1,C4orf3,CASQ1,NTSR1,SCN4B,CNIH2,NOS1AP,DLG1,HTT,PINK1,ATP1B1,KCNA1,GNB5,MINK1,HAP1,DLG4,NLGN2,CNIH3,WNK3,STAC2,CACNB1,ATP1B2,NLGN3,ATP2A1,CALM1,DNM2,VMP1,CCL2,FMR1,RNF207,AMIGO1,JPH3,WWP2,RRAD,MIR24-1,DMD,GPR35,JPH2,FGF11,SCN2B,NETO2,CACNG7,CRBN,CRH,APOPT1,YWHAH,SHISA8,CACNG5,GEM,PPIF	grey	VSMC_M10
GO:0019614	0.57	0.72	4	7	catechol-containing compound catabolic process	BP	1	LRTOMT,AP000812.5,SLC6A3,COMT	grey	VSMC_M10
GO:0042424	0.57	0.72	4	7	catecholamine catabolic process	BP	1	LRTOMT,AP000812.5,SLC6A3,COMT	grey	VSMC_M10
GO:0048599	0.57	0.57	17	32	oocyte development	BP	1	YTHDC2,GDF9,WASHC5,TUT7,DMC1,TUT4,FOXO3,SIRT2,PTK2B,KMT2D,YTHDF2,WNT4,YBX2,WDR77,AURKC,EREG,ZGLP1	grey	VSMC_M10
GO:0072522	0.57	0.49	84	157	purine-containing compound biosynthetic process	BP	1	NME1,SHMT2,ATP5MGL,PPT2,PPARA,ACSL6,GUCA1B,IMPDH1,MTAP,SLC35B2,SLC25A13,PPAT,PPCS,NT5E,PPT1,DLD,SPHK2,ADCY3,PRTFDC1,PRKAG2,ATP5F1C,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,AMPD3,ATP5F1A,GUCY1A1,GUCY1B1,DGUOK,GMPS,AMPD1,ADCY7,FAM173B,ADCY2,NME4,ACSL5,PRPS2,HACD2,ADCY4,DNAJC30,PDK3,SLC25A16,ACSBG1,ATP5S,COASY,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,PARP1,TECR,SLC26A1,GUCY2D,PKLR,PANK3,GCDH,ACACA,SLC26A2,PRPSAP2,SHMT1,ADSSL1,NOS2,ACSBG2,ATP6V0C,PANK4,NME3,ATP5PB,VPS9D1,ACSF3,MLYCD,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,PDZD3,ELOVL3,MTHFD2L,NME6,NUDT2	grey	VSMC_M10
GO:0090179	0.57	0.69	5	9	planar cell polarity pathway involved in neural tube closure	BP	1	PTK7,DVL3,GRHL3,DVL2,WNT5A	grey	VSMC_M10
GO:0031098	0.57	0.49	104	197	stress-activated protein kinase signaling cascade	BP	1	PHLPP1,MAP3K5,STK3,MAPK8IP2,MAP3K4,PRKN,AGER,TRIB1,MYC,AKR1B1,MAPK14,MAPK13,ROR2,GADD45G,KLHL31,PRDX1,SEMA4C,DNAJA1,FKTN,EMC10,MTURN,NOD1,EGFR,TLR4,TRAF1,SDCBP,MYD88,IKBKB,ZMYND11,PLCB1,MAP4K1,GPS1,EIF2AK2,RELL2,SEMA3A,SH3RF2,ARL6IP5,ERCC6,MFHAS1,TRAF6,EPHB1,HAND2,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,MAP2K6,TRPV4,PDCD4,TGFB2,NCF1,MAPKAPK2,AGT,TRAF5,STRADB,FZD7,MAP3K3,MAGI3,DLG1,MAP3K11,AIDA,DUSP10,MBIP,MEN1,MAP4K2,DUSP19,PDCD10,PINK1,LTBR,MAPK1,MINK1,GPS2,RELL1,KAT7,TAOK2,MAPK3,HACD3,MAP2K1,SMAD3,CCDC88C,NCOR1,TRAF3,ADORA2B,SH2D3A,PTGER4,TAOK1,ARHGEF6,SERPINF2,MAPK8IP3,TRAF2,MARVELD3,DAB2IP,RHOA,ZNF622,WNT5A,GADD45A,INAVA,DUSP1,DUSP22,HRAS,MAP2K7	grey	VSMC_M10
GO:0008038	0.57	0.55	22	42	neuron recognition	BP	1	TNFRSF21,RTN4,YWHAZ,NRCAM,MEGF8,SEMA3A,CASP3,ROBO1,ROBO2,NCAM2,CRTAC1,GAP43,EPHB3,MYPN,EPHA4,CDK5R1,EMB,BSG,AMIGO1,CNTN2,FOXG1,EFNB3	grey	VSMC_M10
GO:1902950	0.57	0.72	4	7	regulation of dendritic spine maintenance	BP	1	ABHD17B,VPS35,PRNP,HOMER1	grey	VSMC_M10
GO:0006072	0.57	0.72	4	7	glycerol-3-phosphate metabolic process	BP	1	GPD1L,GK5,GPD1,GPAM	grey	VSMC_M10
GO:0140289	0.57	0.66	6	11	protein mono-ADP-ribosylation	BP	1	PARP4,PARP9,PARP15,PARP14,PARP11,PARP6	grey	VSMC_M10
GO:0043471	0.57	0.72	4	7	regulation of cellular carbohydrate catabolic process	BP	1	PPP1CB,PPP1R3B,PPP1R3D,TIGAR	grey	VSMC_M10
GO:0061053	0.57	0.53	33	63	somite development	BP	1	PTCH1,SMO,ROR2,MEOX2,ABI1,PCDH8,XRCC2,WNT11,PRKDC,TCF15,POFUT1,NKX3-1,NKD1,POGLUT1,AXIN2,MEOX1,WNT4,BMPR1A,WDR19,TCAP,RBPJ,ALDH1A2,RAD51B,PSEN1,SMAD3,LHX1,CDX1,MIB1,NLE1,FOXF1,NOG,WNT5A,SIX1	grey	VSMC_M10
GO:0072210	0.57	0.57	18	34	metanephric nephron development	BP	1	SMO,TFAP2B,SIX2,OSR1,SOX9,RET,PAX8,FMN1,PKD2,PAX2,SALL1,IRX2,WNT4,CITED1,LHX1,PKD1,SOX8,LIF	grey	VSMC_M10
GO:1904894	0.57	0.58	15	28	positive regulation of receptor signaling pathway via STAT	BP	1	IL5,AKR1B1,OCIAD1,KIT,PIBF1,PTK2B,F2R,AGT,IL10RA,IL6R,CCL5,GHR,IL7R,SOCS1,TSLP	grey	VSMC_M10
GO:1903579	0.57	0.59	13	24	negative regulation of ATP metabolic process	BP	1	PPARA,TSPO,DNAJC15,ACTN3,HDAC4,MLXIPL,FIS1,STAT3,PARP1,NCOR1,RHOA,TIGAR,PPIF	grey	VSMC_M10
GO:0055022	0.57	0.60	12	22	negative regulation of cardiac muscle tissue growth	BP	1	PPARA,PI16,TGFBR2,TBX5,JARID2,KCNK2,SAV1,YY1,MIR199A1,MIR25,NOG,RGS4	grey	VSMC_M10
GO:0061117	0.57	0.60	12	22	negative regulation of heart growth	BP	1	PPARA,PI16,TGFBR2,TBX5,JARID2,KCNK2,SAV1,YY1,MIR199A1,MIR25,NOG,RGS4	grey	VSMC_M10
GO:0010831	0.57	0.66	6	11	positive regulation of myotube differentiation	BP	1	MAML1,MAPK14,MAMSTR,SMYD1,RBM24,PIEZO1	grey	VSMC_M10

GO:0043648	0.57	0.52	39	73	dicarboxylic acid metabolic process	BP	1	GLS2,SHMT2,ME1,SLC7A11,DLD,DDO,DHFR,GAD2,MDH2,AMDHD1,SUCLG2,NR1H4,MTHFD2,HOGA1,NIT2,GLS,MTRR,ALDH5A1,OAT,GLUL,D2HGDH,MDH1B,MTHFS,PRODH,L2HGDH,MRPS36,ALDH4A1,SDHB,SHMT1,ADSSL1,SLC46A1,ACSF3,ASS1,KYAT3,PHYH,ACOT4,MTHFD2L,SLC25A32,ALDH1L1	grey	VSMC_M10
GO:1905064	0.57	0.69	5	9	negative regulation of vascular associated smooth muscle cell differentiation	BP	1	NFATC1,PDCD4,NFATC3,MIR21,HEY2	grey	VSMC_M10
GO:0071361	0.57	0.66	6	11	cellular response to ethanol	BP	1	PRKCE,DNMT3A,SLC23A2,TP53INP1,ADCY7,CCL7	grey	VSMC_M10
GO:0002138	0.57	0.72	4	7	retinoic acid biosynthetic process	BP	1	PRMT3,ALDH1A3,DHRS9,ALDH1A2	grey	VSMC_M10
GO:0016102	0.57	0.72	4	7	diterpenoid biosynthetic process	BP	1	PRMT3,ALDH1A3,DHRS9,ALDH1A2	grey	VSMC_M10
GO:0071605	0.57	0.66	6	11	monocyte chemotactic protein-1 production	BP	1	AGER,OAS3,NOD2,TRPV4,APOD,OAS1	grey	VSMC_M10
GO:0071637	0.57	0.66	6	11	regulation of monocyte chemotactic protein-1 production	BP	1	AGER,OAS3,NOD2,TRPV4,APOD,OAS1	grey	VSMC_M10
GO:0030150	0.57	0.61	10	18	protein import into mitochondrial matrix	BP	1	TIMM21,DNAJC15,TIMM50,TOMM40L,GRPEL1,TIMM17B,PAM16,TIMM23B,GRPEL2,DNAJC19	grey	VSMC_M10
GO:0072160	0.57	0.64	7	13	nephron tubule epithelial cell differentiation	BP	1	MTSS1,OSR1,PAX8,MEF2C,PAX2,LHX1,LIF	grey	VSMC_M10
GO:0046058	0.57	0.61	10	19	cAMP metabolic process	BP	1	PDE7B,PDE10A,ADCY3,ADCY7,ADCY2,PTHLH,ADCY4,PDE8A,ADCY10,PDE4A	grey	VSMC_M10
GO:0061515	0.57	0.53	31	59	myeloid cell development	BP	1	MPIG6B,BRD1,L3MBTL3,SRF,KIT,PTBP3,BPGM,PIP4K2A,ABI1,ERCC2,NCKAP1L,FOXP1,FBXW7,TSPAN2,DMTN,ALAS1,LRRK1,SLC9B2,WASF2,THPO,BCL6,PTPN6,FBN1,MED1,ANXA2,GPR68,EVI2B,ATP6AP1,ARID4A,NROS,FAM210B	grey	VSMC_M10
GO:0060439	0.57	0.72	4	7	trachea morphogenesis	BP	1	TGFBR2,MAPK1,MAPK3,MAP2K1	grey	VSMC_M10
GO:0060020	0.57	0.72	4	7	Bergmann glial cell differentiation	BP	1	TTC21B,MAPK1,MAPK3,MAP2K1	grey	VSMC_M10
GO:0000303	0.57	0.60	12	22	response to superoxide	BP	1	FANCC,PRDX1,DHFR,ERCC6,GLRX2,FBLN5,NFE2L2,GCH1,SOD3,MPO,NQO1,MIR21	grey	VSMC_M10
GO:0046415	0.57	0.72	4	7	urate metabolic process	BP	1	GCKR,ABCG2,CARMIL1,SLC2A9	grey	VSMC_M10
GO:0050913	0.57	0.72	4	7	sensory perception of bitter taste	BP	1	CALHM1,RTP4,GNAT2,TAS2R3	grey	VSMC_M10
GO:0070862	0.57	0.68	5	9	negative regulation of protein exit from endoplasmic reticulum	BP	1	UBAC2,YOD1,DERL3,UBE2G2,DERL2	grey	VSMC_M10
GO:0032612	0.57	0.53	33	62	interleukin-1 production	BP	1	TNFAIP3,AGER,IL1R2,S1PR3,NOD1,TLR4,HDAC2,PANX1,MYD88,GAS6,FOXP1,P2RX7,RIPK2,SERPINB1,F2RL1,F2R,NOD2,HDAC1,FZD5,IL16,HK1,STAT3,PYDC1,TMED10,SMAD3,S100A13,ISL1,MIR27B,CASP8,WNT5A,INAVA,CPTP,HAVCR2	grey	VSMC_M10
GO:0032652	0.57	0.53	33	62	regulation of interleukin-1 production	BP	1	TNFAIP3,AGER,IL1R2,S1PR3,NOD1,TLR4,HDAC2,PANX1,MYD88,GAS6,FOXP1,P2RX7,RIPK2,SERPINB1,F2RL1,F2R,NOD2,HDAC1,FZD5,IL16,HK1,STAT3,PYDC1,TMED10,SMAD3,S100A13,ISL1,MIR27B,CASP8,WNT5A,INAVA,CPTP,HAVCR2	grey	VSMC_M10
GO:0060296	0.57	0.72	4	7	regulation of cilium beat frequency involved in ciliary motility	BP	1	MKKS,CFAP20,CFAP45,CCSAP	grey	VSMC_M10
GO:0010826	0.57	0.66	6	11	negative regulation of centrosome duplication	BP	1	MDM1,CDK5RAP2,TMEM67,CCDC84,TRIM37,NUBP1	grey	VSMC_M10
GO:0046606	0.57	0.66	6	11	negative regulation of centrosome cycle	BP	1	MDM1,CDK5RAP2,TMEM67,CCDC84,TRIM37,NUBP1	grey	VSMC_M10
GO:0046950	0.57	0.71	4	7	cellular ketone body metabolic process	BP	1	HMGCLL1,ACSS3,HMGCL,OXCT1	grey	VSMC_M10
GO:1902224	0.57	0.71	4	7	ketone body metabolic process	BP	1	HMGCLL1,ACSS3,HMGCL,OXCT1	grey	VSMC_M10
GO:0071872	0.57	0.68	5	9	cellular response to epinephrine stimulus	BP	1	SIRT2,RYR2,SRD5A1,SLC9A1,PKLR	grey	VSMC_M10
GO:0021554	0.57	0.68	5	9	optic nerve development	BP	1	EPHB1,PAX2,TCIRG1,CHRNB2,TMEM126A	grey	VSMC_M10
GO:1901881	0.57	0.63	8	15	positive regulation of protein depolymerization	BP	1	KIAA1211,PLEK,KATNB1,F2RL1,CARMIL1,TRPV4,CARMIL2,PDXP	grey	VSMC_M10
GO:0046466	0.57	0.58	14	26	membrane lipid catabolic process	BP	1	PPT1,MGST2,SMPD2,ACER3,NEU3,ASAH1,SMPD4,GALC,GLA,HEXA,GM2A,CEL,ACER2,NEU2	grey	VSMC_M10
GO:0033700	0.57	0.71	4	7	phospholipid efflux	BP	1	APOC1,ABCA12,ABCA3,ABCA7	grey	VSMC_M10
GO:1990144	0.57	0.71	4	7	intrinsic apoptotic signaling pathway in response to hypoxia	BP	1	TMBIM6,HYOU1,PINK1,NOL3	grey	VSMC_M10
GO:0022400	0.57	0.71	4	7	regulation of rhodopsin mediated signaling pathway	BP	1	CAMKMT,NMT1,GRK4,GUCY2D	grey	VSMC_M10
GO:0051132	0.57	0.71	4	7	NK T cell activation	BP	1	IL15,IL12A,RASAL3,ZBTB7B	grey	VSMC_M10
GO:0032988	0.57	0.71	4	7	ribonucleoprotein complex disassembly	BP	1	ZFAND1,DYRK3,DHX8,KLC1	grey	VSMC_M10
GO:0072711	0.57	0.68	5	9	cellular response to hydroxyurea	BP	1	SPIDR,RTF2,DDX11,DDI2,FMR1	grey	VSMC_M10
GO:0045059	0.57	0.68	5	9	positive thymic T cell selection	BP	1	SRF,TOX,DOCK2,CD74,PTPN2	grey	VSMC_M10
GO:0045869	0.57	0.71	4	7	negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	BP	1	APOBEC3H,FAM208A,INPP5K,SETDB1	grey	VSMC_M10
GO:0006975	0.57	0.71	4	7	DNA damage induced protein phosphorylation	BP	1	CRY1,MAP2K6,CHEK2,MAPK3	grey	VSMC_M10
GO:0015791	0.57	0.71	4	7	polyol transport	BP	1	AQP1,AQP11,SLC2A13,SLC5A11	grey	VSMC_M10
GO:0070857	0.57	0.71	4	7	regulation of bile acid biosynthetic process	BP	1	NR1H4,CYP7A1,FGFR4,STARD4	grey	VSMC_M10
GO:0043252	0.57	0.68	5	9	sodium-independent organic anion transport	BP	1	SLCO6A1,SLCO3A1,SLCO1A2,SLCO1C1,MFSD10	grey	VSMC_M10
GO:0010454	0.57	0.71	4	7	negative regulation of cell fate commitment	BP	1	SOSTDC1,FZD7,TNFSF18,TBX21	grey	VSMC_M10
GO:2001053	0.57	0.68	5	9	regulation of mesenchymal cell apoptotic process	BP	1	HOXA13,SOX9,PAX8,PAX2,POU3F4	grey	VSMC_M10
GO:0033353	0.58	0.71	4	7	S-adenosylmethionine cycle	BP	1	APIP,AHCY,ENOPH1,MTRR	grey	VSMC_M10
GO:0018904	0.58	0.59	13	24	ether metabolic process	BP	1	PEX7,PLA2G6,TXN2,TMEM86B,LIPE,EPHX2,GNPAT,PLA2G4A,PLA2G16,EPHX1,NCEH1,EPHX3,TXN	grey	VSMC_M10
GO:0032370	0.58	0.53	29	55	positive regulation of lipid transport	BP	1	LRP1,PTCH1,PLA2G6,TMEM30A,NR1H2,C1QTNF1,NR1H3,NKX3-1,SPP1,PLA2R1,PLTP,MAP2K6,ABCA5,ACSL5,NTSR1,PLA2G4A,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,ABCA3,ABCA7,RXRA,ABCA8,LDLRAP1,CRH,LRAT,PTGES	grey	VSMC_M10
GO:0070828	0.58	0.55	21	40	heterochromatin organization	BP	1	BAZ2A,H3F3C,SETD7,DNMT3A,SETDB2,SIRT2,FAM208A,BAHD1,LOXL2,PPHLN1,HDAC1,ZNFX1,SNAI1,TET1,PHF8,NRDE2,SMCHD1,PRDM16,SETDB1,BEND3,ZNF304	grey	VSMC_M10
GO:0008209	0.58	0.59	12	22	androgen metabolic process	BP	1	HSD17B4,ESR1,HSD17B8,HSD17B3,SRD5A3,SPP1,SRD5A1,DHRS9,HSD17B7,WNT4,HSD17B10,MED1	grey	VSMC_M10
GO:0006013	0.58	0.71	4	7	mannose metabolic process	BP	1	PMM1,HK1,MPI,PMM2	grey	VSMC_M10
GO:0046719	0.58	0.71	4	7	regulation by virus of viral protein levels in host cell	BP	1	STAU1,DDB1,HACD3,TBC1D20	grey	VSMC_M10
GO:0071380	0.58	0.64	7	13	cellular response to prostaglandin E stimulus	BP	1	PRKCE,PTGER2,AKAP8,ACACA,PTGER4,GNB1,GNG2	grey	VSMC_M10
GO:0046007	0.58	0.66	6	11	negative regulation of activated T cell proliferation	BP	1	PRNP,CASP3,BTN2A2,PRKAR1A,RC3H1,FOXP3	grey	VSMC_M10
GO:0099638	0.58	0.64	7	13	endosome to plasma membrane protein transport	BP	1	VPS35,RAB7A,NSG1,GRIPAP1,RAB8A,RAB11A,ARHGAP44	grey	VSMC_M10

GO:0044819	0.58	0.58	14	26	mitotic G1/S transition checkpoint signaling	BP	1	PLK3,PRKDC,PLK2,PIDD1,CCND1,GIGYF2,CHEK2,CDKN1B,MUC1,FBXO31,PLK5,RPS27L,SOX4,CRADD	grey	VSMC_M10
GO:0061951	0.58	0.53	29	55	establishment of protein localization to plasma membrane	BP	1	GOPC,SPTBN1,VPS35,RAB7A,RAB10,OPTN,GOLGA4,LYPLA1,RILPL1,RILPL2,VAMP5,KIF13A,NECTIN3,BBS1,GORASP2,NSF,NSG1,GRIPAP1,RAB8A,CNST,RSC1A1,AC138894.1,RAB11A,GGA2,ARHGAP44,RAB26,SEC16A,C16orf70,VAMP3	grey	VSMC_M10
GO:0015816	0.58	0.71	4	7	glycine transport	BP	1	SLC25A38,SLC38A5,SLC36A1,RGS4	grey	VSMC_M10
GO:0017121	0.58	0.66	6	11	plasma membrane phospholipid scrambling	BP	1	ANO4,XKR6,PLSCR4,P2RX7,ANO6,XKR8	grey	VSMC_M10
GO:0006805	0.58	0.55	22	41	xenobiotic metabolic process	BP	1	NUDT15,CYP2R1,BPHL,ABCC2,CBR3,CMBL,TPMT,FMO5,CYP2U1,ABCB11,POR,EPHX1,CYP46A1,CYP2J2,NQO1,CRYZ,S100A12,SULT1C3,AHRR,NCEH1,AOC2,N6AMT1	grey	VSMC_M10
GO:0002704	0.58	0.57	16	30	negative regulation of leukocyte mediated immunity	BP	1	IL4I1,FOXJ1,NCKAP1L,NOD2,CD96,BCL6,PTPN6,PPP3CB,FOXP3,TBX21,IL7R,CRK,FOXF1,CD46,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0048103	0.58	0.68	5	9	somatic stem cell division	BP	1	KIT,BMI1,TGFB2,FZD7,ZFP36L2	grey	VSMC_M10
GO:0032873	0.58	0.55	20	38	negative regulation of stress-activated MAPK cascade	BP	1	PRKN,MYC,KLHL31,DNAJA1,FKTN,ZMYND11,SH3RF2,F2RL1,TAOK3,PDCD4,DLG1,AIDA,DUSP10,MEN1,DUSP19,PINK1,GPS2,NCOR1,MARVELD3,DUSP1	grey	VSMC_M10
GO:0070303	0.58	0.55	20	38	negative regulation of stress-activated protein kinase signaling cascade	BP	1	PRKN,MYC,KLHL31,DNAJA1,FKTN,ZMYND11,SH3RF2,F2RL1,TAOK3,PDCD4,DLG1,AIDA,DUSP10,MEN1,DUSP19,PINK1,GPS2,NCOR1,MARVELD3,DUSP1	grey	VSMC_M10
GO:0072384	0.58	0.51	41	78	organelle transport along microtubule	BP	1	AP3S1,KIF5A,KIF3A,AGTPBP1,SUN2,COPG2,BICD2,LRPPRC,MGARP,WASF1,KIF3C,ARHGAP21,COPG1,AP3M2,KIF3B,RASGRP1,OPA1,AP3B1,DTNBP1,KIF13A,BICDL1,CNIH2,MAPT,BLOC1S6,MREG,HTT,UXT,AP3M1,KIF1C,HAP1,PEX14,TRIM46,NDEL1,AC138894.1,SNAPIN,BICDL2,PRKCZ,UBB,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:1902259	0.58	0.68	5	9	regulation of delayed rectifier potassium channel activity	BP	1	KCNRG,KCNE2,KCNG1,NOS1AP,RNF207	grey	VSMC_M10
GO:0086069	0.58	0.66	6	11	bundle of His cell to Purkinje myocyte communication	BP	1	TRPM4,SCN5A,TBX5,DSP,PKP2,DSG2	grey	VSMC_M10
GO:0042448	0.58	0.68	5	9	progesterone metabolic process	BP	1	SRD5A1,DHRS9,STAT5B,DGKQ,CYP46A1	grey	VSMC_M10
GO:0009798	0.58	0.53	31	59	axis specification	BP	1	FRS2,PTCH1,SMO,MDFI,SRF,SIX2,SETDB2,IFT172,FAM208A,STC1,LDB1,PGAP1,WNT3,HOXD8,FZD5,BCOR,PKD1L1,MNS1,BMPR1A,CITED1,LHX1,CDX1,GPC3,HSPB11,SKI,WDR77,WNT5A,BASP1,DDIT3,C2CD3,HEY2	grey	VSMC_M10
GO:0040015	0.58	0.68	5	9	negative regulation of multicellular organism growth	BP	1	PTCH1,GDF15,RAI1,FXN,PLAC8	grey	VSMC_M10
GO:0060042	0.58	0.54	22	42	retina morphogenesis in camera-type eye	BP	1	NTRK2,RORB,SLC1A1,TFAP2B,RDH13,PTN,TSPAN12,SOX9,USH1C,RPGRIP1L,TFAP2A,NECTIN3,NRL,OBSL1,ROM1,SDK1,MEGF11,LHX1,SOX8,FJX1,THY1,DIO3	grey	VSMC_M10
GO:0008212	0.58	0.68	5	9	mineralocorticoid metabolic process	BP	1	CYP21A2,DKK3,WNT4,SCNN1B,CACNA1H	grey	VSMC_M10
GO:0051085	0.58	0.58	14	26	chaperone cofactor-dependent protein refolding	BP	1	HSPA1B,BAG1,HSPE1,DNAJC18,HSPA8,DNAJB12,SDF2L1,DNAJB1,GAK,CD74,TOR1B,TOR2A,HSPA5,SDF2	grey	VSMC_M10
GO:0042632	0.58	0.52	33	62	cholesterol homeostasis	BP	1	APOM,TTC39B,ABCG5,ABCG8,NR1H2,APOB,CNBP,TSKU,COMMD9,SOAT2,CYP7A1,CYP7B1,LIMA1,EPHX2,NR1H3,MYLIP,ABCA5,NR5A2,FABP4,GRAMD1B,ABCB11,ABCG4,SOAT1,EHD1,FGFR4,LIPC,LDLR,ACSM3,NPC1,TMEM97,MIR27B,MIR33B,LDLRAP1	grey	VSMC_M10
GO:0009914	0.58	0.48	112	212	hormone transport	BP	1	LRP1,RIMS2,PRKN,GDF9,PLA2G6,PICK1,CRY1,RFX3,TFAP2B,IL11,PRKCE,HMGN3,CYB5R4,BMP8A,EGFR,TRPM4,GIPR,RAF1,C1QTNF1,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,SCG5,P2RY1,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX3-1,NKX6-1,ACVR1C,CRY2,ABCC2,SPP1,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,SNAP23,KCNB1,PFKFB2,GPER1,RAB11FIP2,AGT,SLCO1C1,PER2,OSM,STX1A,SNX4,PASK,GLUL,SIDT2,SLC16A1,KLF7,CREB1,VGF,ENY2,ABCA12,MCU,PPP3CB,CAMK2G,PTPRN,CD38,MPC2,ILDR2,INHA,SYT7,NLGN2,CPLX1,TARDBP,STX4,RAB8B,UBE2Q1,SYTL4,GPR68,BTK,CRYM,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,PARK7,SLC7A5,LRRC8A,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,LIF,UQCC2	grey	VSMC_M10
GO:0150093	0.58	0.71	4	7	amyloid-beta clearance by transcytosis	BP	1	LRP1,RAB5A,LRPAP1,RAB11A	grey	VSMC_M10
GO:0045824	0.58	0.54	25	47	negative regulation of innate immune response	BP	1	TNFAIP3,USP15,NR1H2,NMI,NR1H3,TRAFD1,OAS3,NLRC5,CD96,YTHDF2,SLAMF8,PARP14,NLRX1,DUSP10,MUL1,USP18,DCST1,STAT2,PTPN2,CRK,MIR21,OAS1,A2M,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0007620	0.58	0.66	6	11	copulation	BP	1	KLK14,DDO,ACVR2A,P2RY1,ABAT,P2RX1	grey	VSMC_M10
GO:2001214	0.58	0.68	5	9	positive regulation of vasculogenesis	BP	1	RIN2,RAPGEF2,HIF1AN,RAMP2,TMEM100	grey	VSMC_M10
GO:0042670	0.58	0.71	4	7	retinal cone cell differentiation	BP	1	RORB,USH1C,THY1,DIO3	grey	VSMC_M10
GO:0046549	0.58	0.71	4	7	retinal cone cell development	BP	1	RORB,USH1C,THY1,DIO3	grey	VSMC_M10
GO:0000096	0.58	0.57	15	28	sulfur amino acid metabolic process	BP	1	MTAP,GNMT,SLC7A11,APIP,CSAD,MSRA,ENOPH1,MTRR,MTR,CBSL,SMS,CPS1,COMT,MAT1A,MTHFD2L	grey	VSMC_M10
GO:0071677	0.58	0.55	22	41	positive regulation of mononuclear cell migration	BP	1	AGER,CCL27,FPR2,OXSR1,GAS6,JAM2,PTK2B,ANO6,MOSPD2,ADAM8,ITGA4,IL12A,TNFSF18,TMEM102,S100A14,CCL5,CCL7,RHOA,DEFB124,FADD,WNT5A,PDGFD	grey	VSMC_M10
GO:0090278	0.58	0.56	18	34	negative regulation of peptide hormone secretion	BP	1	PRKN,BMP8A,NDUFAF2,FAM3D,KCNJ11,ACVR1C,SIRT4,IRS1,HDAC1,PPP3CA,ADRA2A,KCNB1,KLF7,ENY2,SYTL4,SREBF1,CHGA,CRH	grey	VSMC_M10
GO:0002444	0.58	0.52	37	70	myeloid leukocyte mediated immunity	BP	1	RAC2,KIT,TRAF3IP2,SPHK2,GAB2,UNC13D,MYD88,MAVS,FER,RASGRP1,F2RL1,SNAP23,LAT2,FGR,CBL,SNX4,PTGDR,C12orf4,SPON2,STX4,ITGAM,LAT,IL4R,S100A13,BTK,SCNN1B,STXBP2,PRAM1,C3,TICAM1,DNASE1,PDPK1,FOXF1,STXBP1,CHGA,CXCL6,SERPINB9	grey	VSMC_M10
GO:0010766	0.58	0.61	9	17	negative regulation of sodium ion transport	BP	1	NEDD4L,WNK2,PRKCE,HECW1,OSR1,HECW2,ATP1A2,WNK3,MIR24-1	grey	VSMC_M10

GO:0042554	0.58	0.57	16	30	superoxide anion generation	BP	1	FPR2,EGFR,FAM19A4,HVCN1,F2RL1,SH3PXD2A,NCF1,AGT,NCF2,MAPT,DUOX1,ITGAM,NOX5,NOXA1,GNAI3,CYBA	grey	VSMC_M10
GO:0051898	0.58	0.57	16	30	negative regulation of protein kinase B signaling	BP	1	PHLPP1,PPARA,LEMD2,PIK3CB,PTPRJ,BANK1,PDCD6,DAG1,GPER1,CIB1,DLG1,MUL1,OTUD3,INPP5K,MIR29A,DDIT3	grey	VSMC_M10
GO:1902774	0.58	0.71	4	7	late endosome to lysosome transport	BP	1	VPS41,VPS35,VPS39,SNAPIN	grey	VSMC_M10
GO:0097720	0.58	0.55	21	40	calcineurin-mediated signaling	BP	1	NFATC1,FHL2,SLC8A2,EFHB,PRNP,NRG1,SPPL3,PPP3CA,NR5A2,TBC1D10C,CIB1,SLC9A1,NFATC4,MYO2,ACTN3,HOMER2,PPP3CB,MYOZ1,MAPK7,CAMTA1,NFATC3	grey	VSMC_M10
GO:0070914	0.58	0.68	5	9	UV-damage excision repair	BP	1	ERCC1,XPC,DDB2,DDB1,CUL4B	grey	VSMC_M10
GO:0006957	0.58	0.71	4	7	complement activation, alternative pathway	BP	1	CFP,C7,C3,CFD	grey	VSMC_M10
GO:0045843	0.58	0.71	4	7	negative regulation of striated muscle tissue development	BP	1	SIRT2,USP19,YBX3,SOX15	grey	VSMC_M10
GO:0090713	0.58	0.68	5	9	immunological memory process	BP	1	HLA-DRA,BCL6,TSC1,CD46,FGL2	grey	VSMC_M10
GO:0071340	0.58	0.68	5	9	skeletal muscle acetylcholine-gated channel clustering	BP	1	PTN,FZD9,DNAJA3,RER1,MESD	grey	VSMC_M10
GO:1902959	0.58	0.68	5	9	regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process	BP	1	AGER,SORL1,EPHA4,TMED10,EFNA1	grey	VSMC_M10
GO:0010992	0.58	0.68	5	9	ubiquitin recycling	BP	1	PRKN,IDE,FBXW7,PINK1,RNF135	grey	VSMC_M10
GO:0045054	0.58	0.71	4	7	constitutive secretory pathway	BP	1	TRAPPC11,RAB3A,TMEM167A,TMEM167B	grey	VSMC_M10
GO:1905146	0.58	0.62	8	15	lysosomal protein catabolic process	BP	1	LRP1,MFSD8,TMEM106B,ATP13A2,AC138894.1,LDLR,LAMP2,TMEM199	grey	VSMC_M10
GO:1902514	0.58	0.68	5	9	regulation of calcium ion transmembrane transport via high voltage-gated calcium channel	BP	1	CACNB2,NOS1AP,SESTD1,CACNB1,MIR21	grey	VSMC_M10
GO:1901385	0.58	0.57	15	28	regulation of voltage-gated calcium channel activity	BP	1	STAC3,CACNB2,STAC,CACNB4,KCNE2,NOS1AP,GNB5,STAC2,CACNB1,CALM1,FMR1,RRAD,DMD,GPR35,GEM	grey	VSMC_M10
GO:0090084	0.58	0.68	5	9	negative regulation of inclusion body assembly	BP	1	HSPA1B,HSF1,SORL1,DNAJB2,DNAJB1	grey	VSMC_M10
GO:0032351	0.58	0.68	5	9	negative regulation of hormone metabolic process	BP	1	CYP27B1,DKK3,PRMT3,WNT4,GFI1	grey	VSMC_M10
GO:0009222	0.58	0.71	4	7	pyrimidine ribonucleotide catabolic process	BP	1	DPYS,ENTPD4,UPB1,UPP1	grey	VSMC_M10
GO:0071599	0.58	0.64	7	13	otic vesicle development	BP	1	SOX9,CEP290,PAX8,EYA1,STOX1,TCAP,SIX1	grey	VSMC_M10
GO:2000271	0.58	0.71	4	7	positive regulation of fibroblast apoptotic process	BP	1	BTG1,PRDM11,STK17B,BCL2L11	grey	VSMC_M10
GO:0021772	0.58	0.60	10	19	olfactory bulb development	BP	1	AGTPBP1,SRF,DLX5,SEMA3A,ROBO1,ROBO2,RPGRIP1L,SALL1,SKI,WNT5A	grey	VSMC_M10
GO:0033004	0.58	0.71	4	7	negative regulation of mast cell activation	BP	1	ENPP3,CD300LF,FER,FOXF1	grey	VSMC_M10
GO:1903432	0.58	0.56	17	32	regulation of TORC1 signaling	BP	1	RRAGD,KPTN,SESN3,SZT2,PIP4P1,LARS,GPR137B,DYRK3,SIK3,GPR137,OTUD5,RRAGB,DGKQ,SMCR8,CLEC16A,LAMTOR5,RNF152	grey	VSMC_M10
GO:0021545	0.58	0.55	20	38	cranial nerve development	BP	1	ERBB3,ATP8B1,PLXNA4,POU4F1,SEMA3A,EPHB1,TFAP2A,PAX2,SALL1,SEMA3F,TCIRG1,ADARB1,CHRNB2,ISL1,PLXNA3,MAFB,HOXB3,SIX1,TMEM126A,HOXA3	grey	VSMC_M10
GO:1903409	0.58	0.53	25	47	reactive oxygen species biosynthetic process	BP	1	PPARA,TLR4,UCP1,FOXO3,SPHK2,WISP3,ACOX1,GBF1,SLC30A10,NCF1,HDAC4,PIKFYVE,DUOX1,STAT3,MPO,PARK7,SLC25A33,CYBA,LCN2,MIR21,MIR24-1,RHOA,INAVA,APOPT1,AC140504.1	grey	VSMC_M10
GO:1902416	0.58	0.71	4	7	positive regulation of mRNA binding	BP	1	EIF3E,EIF3C,LARP6,FMR1	grey	VSMC_M10
GO:0051290	0.58	0.65	6	11	protein heterotetramerization	BP	1	CPSF6,HSD17B8,CBR4,PKD2,FARSB,PKD1	grey	VSMC_M10
GO:0060155	0.58	0.71	4	7	platelet dense granule organization	BP	1	AP3B1,F2R,DTNBP1,BLOC1S3	grey	VSMC_M10
GO:0042364	0.58	0.71	4	7	water-soluble vitamin biosynthetic process	BP	1	PSAT1,AKR1A1,PNPO,TPK1	grey	VSMC_M10
GO:0032790	0.58	0.71	4	7	ribosome disassembly	BP	1	MTIF2,EIF2D,MCTS1,MRRF	grey	VSMC_M10
GO:0031998	0.58	0.62	8	15	regulation of fatty acid beta-oxidation	BP	1	PPARA,AKT2,LONP2,IRS1,CPT1A,ABCB11,TYSND1,MLYCD	grey	VSMC_M10
GO:0071675	0.58	0.50	43	81	regulation of mononuclear cell migration	BP	1	AGER,PTK2,CCL27,FPR2,AKIRIN1,C5AR1,OXSR1,PLCB1,GAS6,JAM2,PTK2B,SLC8B1,ANO6,ADTRP,CD200,TRPV4,CMKLR1,SLAMF8,MOSPD2,APOD,ADAM8,MIA3,ITGA4,IL12A,TNFSF18,MAPK1,PADI2,TMEM102,STK10,MAPK3,S100A14,CCL5,CSF1R,CCL7,CCL2,CRK,RHOA,DEFB124,FADD,WNT5A,DUSP1,GCSAM,PDGFD	grey	VSMC_M10
GO:0046753	0.58	0.71	4	7	non-lytic viral release	BP	1	VPS4B,CHMP2A,CHMP4C,VPS4A	grey	VSMC_M10
GO:0021988	0.58	0.59	11	21	olfactory lobe development	BP	1	AGTPBP1,SRF,DLX5,SEMA3A,ROBO1,ROBO2,RPGRIP1L,SALL1,ATP1A2,SKI,WNT5A	grey	VSMC_M10
GO:0046339	0.58	0.60	10	19	diacylglycerol metabolic process	BP	1	AVIL,DGKI,LIPE,PLCE1,GPAM,DGKD,DGKG,DGKQ,DGKE,PLA2G15	grey	VSMC_M10
GO:1904948	0.58	0.63	7	13	midbrain dopaminergic neuron differentiation	BP	1	CSNK1E,FZD1,RYK,NR4A2,WNT3,WNT5A,WNT2	grey	VSMC_M10
GO:0070839	0.58	0.54	21	40	metal ion export	BP	1	SLC4A4,SLC8A2,ATP7B,ATP1A3,SLC8B1,SLC40A1,ANO6,KCNE2,KCNIP2,ATP1A2,SLC9A1,DLG1,SLC11A1,ATP1B1,ATP1B2,CALM1,ATP2B3,MIR21,KCNH2,KCNK5,KCNT2	grey	VSMC_M10
GO:0032196	0.58	0.63	7	13	transposition	BP	1	TUT7,APOBEC3H,TUT4,SIRT7,TEX15,THAP9,PGBD5	grey	VSMC_M10
GO:1902307	0.58	0.61	9	17	positive regulation of sodium ion transmembrane transport	BP	1	WNK2,GLRX,TESC,SLC9A1,ATP1B1,WNK3,ATP1B2,DNM2,DMD	grey	VSMC_M10
GO:0150079	0.58	0.67	5	9	negative regulation of neuroinflammatory response	BP	1	CST7,CD200,TNFRSF1B,SYT11,LDLR	grey	VSMC_M10
GO:0043383	0.59	0.70	4	7	negative T cell selection	BP	1	ATG5,CD28,DOCK2,CD74	grey	VSMC_M10
GO:0045060	0.59	0.70	4	7	negative thymic T cell selection	BP	1	ATG5,CD28,DOCK2,CD74	grey	VSMC_M10
GO:0098696	0.59	0.70	4	7	regulation of neurotransmitter receptor localization to postsynaptic specialization membrane	BP	1	DAG1,IQSEC2,PRKCZ,HRAS	grey	VSMC_M10
GO:0060159	0.59	0.67	5	9	regulation of dopamine receptor signaling pathway	BP	1	VPS35,ALK,DTNBP1,PALM,RGS4	grey	VSMC_M10

GO:0051403	0.59	0.47	100	190	stress-activated MAPK cascade	BP	1	PHLPP1,MAP3K5,STK3,MAPK8IP2,MAP3K4,PRKN,AGER,TRIB1,MYC,MAPK14,MAPK13,ROR2,GADD45G,KLHL31,PRDX1,SEMA4C,DNAJA1,FKTN,EMC10,MTURN,NOD1,EGFR,TLR4,TRAF1,SDCBP,MYD88,IKBKB,ZMYND11,PLCB1,MAP4K1,GPS1,EIF2AK2,RELL2,SEMA3A,SH3RF2,ARL6IP5,ERCC6,MFHAS1,TRAF6,EPHB1,HAND2,PTK2B,RASGRP1,RIPK2,F2RL1,RIPK1,NOD2,TAOK3,MAP2K6,TRPV4,PDCD4,TGFB2,NCF1,MAPKAPK2,AGT,TRAF5,STRADB,FZD7,MAP3K3,MAGI3,DLG1,MAP3K11,AIDA,DUSP10,MBIP,MEN1,MAP4K2,DUSP19,PDCD10,PINK1,LTBR,MAPK1,MINK1,GPS2,RELL1,TAOK2,MAPK3,HACD3,MAP2K1,SMAD3,NCOR1,TRAF3,ADORA2B,SH2D3A,PTGER4,TAOK1,ARHGEF6,SERPINF2,MAPK8IP3,TRAF2,MARVELD3,DAB2IP,ZNF622,WNT5A,GADD45A,INAVA,DUSP1,DUSP22,HRAS,MAP2K7	grey	VSMC_M10
GO:0010764	0.59	0.67	5	9	negative regulation of fibroblast migration	BP	1	HAS1,ITGB1BP1,CYGB,ARHGAP4,C5orf30	grey	VSMC_M10
GO:0033008	0.59	0.65	6	11	positive regulation of mast cell activation involved in immune response	BP	1	SPHK2,GAB2,FGR,SNX4,IL4R,STXBP1	grey	VSMC_M10
GO:0043306	0.59	0.65	6	11	positive regulation of mast cell degranulation	BP	1	SPHK2,GAB2,FGR,SNX4,IL4R,STXBP1	grey	VSMC_M10
GO:0009119	0.59	0.58	12	22	ribonucleoside metabolic process	BP	1	APOBEC3H,MTAP,GNMT,ENPP4,NT5E,PRTFDC1,CDADC1,AHCY,DGUOK,ADK,PEMT,UPP1	grey	VSMC_M10
GO:0035627	0.59	0.65	6	11	ceramide transport	BP	1	ABCB1,COL4A3BP,PLTP,ABCA12,CPTP,SGPP1	grey	VSMC_M10
GO:0034162	0.59	0.63	7	13	toll-like receptor 9 signaling pathway	BP	1	GRAMD4,RTN4,RSAD2,RAB7B,UNC93B1,TNIP2,HAVCR2	grey	VSMC_M10
GO:0036152	0.59	0.70	4	7	phosphatidylethanolamine acyl-chain remodeling	BP	1	MBOAT2,ABHD4,LPCAT3,PLA2G16	grey	VSMC_M10
GO:0006020	0.59	0.65	6	11	inositol metabolic process	BP	1	MIOX,IPPK,ITPKA,ITPK1,IMPA2,MECP2	grey	VSMC_M10
GO:0035855	0.59	0.61	9	17	megakaryocyte development	BP	1	MPIG6B,SRF,KIT,PIP4K2A,ABI1,WASF2,THPO,PTPN6,MED1	grey	VSMC_M10
GO:0070734	0.59	0.60	9	17	histone H3-K27 methylation	BP	1	PHF1,EED,OGT,SUZ12,SUPT6H,CHD5,MTF2,BEND3,ZNF304	grey	VSMC_M10
GO:1905461	0.59	0.70	4	7	positive regulation of vascular associated smooth muscle cell apoptotic process	BP	1	STK4,PDCD4,MFN2,MIR24-1	grey	VSMC_M10
GO:0002250	0.59	0.46	129	244	adaptive immune response	BP	1	CD226,STX7,TNFAIP3,AGER,HLA-DRA,HLA-DOB,TAP1,HLA-DMA,HLA-DPB1,TNFRSF13C,TFEB,TEC,TNFRSF21,EXOSC3,MSH2,LAIR1,BACH2,RSAD2,IL4I1,TLR4,TRPM4,TRAF3IP2,HMCES,PRKD2,PHB,ERCC1,NECTIN2,PVR,MLH1,UNC13D,MYD88,SLC22A13,FOXJ1,PAXIP1,EOMES,JAG1,SHLD1,NCKAP1L,HPX,IRF7,TRAF6,MARCH8,GAPT,CAMK4,ERAP1,ORAI1,MEF2C,PAG1,SLA2,PTK2B,EIF2AK4,RIPK2,NBN,RAPGEF3,ALCAM,NOD2,ADCY7,CD40,NFKB2,ICOSLG,TCIRG1,UNC93B1,HLX,DENND1B,OTUD7B,LAT2,BMX,CD28,FCER1G,RNF168,PDCD1,FZD5,DUSP10,PLA2G4A,BCL6,CTSH,IL12A,RC3H1,PTPN6,TNFSF18,SLC11A1,LAG3,PPP3CB,RAP1GAP,STAT3,WAS,TFE3,FOXP3,ZBTB1,SHLD2,TNFRSF1B,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,CD19,LAT,IL4R,PRKCB,BTK,CD74,FBXO38,C7,C3,IL7R,SUPT6H,RAP1GAP2,PRKCZ,TRAF2,TSC1,BCL10,MIR21,FGA,ERAP2,FADD,CD46,JCHAIN,CD247,TRDV3,FCER2,RNF8,CD70,HRAS,LAX1,PRR7,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0070233	0.59	0.63	7	13	negative regulation of T cell apoptotic process	BP	1	SLC46A2,GPAM,EFNA1,CCL5,IL7R,FADD,TSC22D3	grey	VSMC_M10
GO:0048484	0.59	0.65	6	11	enteric nervous system development	BP	1	SOX10,RET,TLX2,HLX,RHOXF1,SOX8	grey	VSMC_M10
GO:0010820	0.59	0.67	5	9	positive regulation of T cell chemotaxis	BP	1	CCL27,OXSR1,TMEM102,CCL5,WNT5A	grey	VSMC_M10
GO:0070988	0.59	0.52	27	52	demethylation	BP	1	UBE2B,KDM3B,APOBEC3H,KDM4C,STPG4,KDM7A,MMACHC,KDM4A,PPME1,ALKBH3,TOX,OTUD4,FTO,JARID2,ALKBH2,POR,TET1,CYP3A43,KDM5A,KDM5C,PHF8,KDM6B,RIOX1,ALKBH1,KDM8,ALKBH5,HSF4	grey	VSMC_M10
GO:0002713	0.59	0.67	5	9	negative regulation of B cell mediated immunity	BP	1	FOXJ1,BCL6,PTPN6,FOXP3,CD46	grey	VSMC_M10
GO:0002890	0.59	0.67	5	9	negative regulation of immunoglobulin mediated immune response	BP	1	FOXJ1,BCL6,PTPN6,FOXP3,CD46	grey	VSMC_M10
GO:0033299	0.59	0.70	4	7	secretion of lysosomal enzymes	BP	1	NR1H2,NR1H3,BLOC1S6,BLOC1S3	grey	VSMC_M10
GO:0060037	0.59	0.58	11	21	pharyngeal system development	BP	1	PTCH1,EYA1,NKX3-1,RIPPLY3,TGFB2,ECE1,BMPR1A,ISL1,NOG,SIX1,NKX2-5	grey	VSMC_M10
GO:0031000	0.59	0.62	8	15	response to caffeine	BP	1	HDAC2,RYR1,DNMT3B,RYR3,CASQ2,RYR2,HDAC1,DHODH	grey	VSMC_M10
GO:0006554	0.59	0.70	4	7	lysine catabolic process	BP	1	CRYM,PIPOX,SLC25A21,HYKK	grey	VSMC_M10
GO:0045989	0.59	0.67	5	9	positive regulation of striated muscle contraction	BP	1	TRPV4,ACE2,ACTN3,ATP2A1,CHGA	grey	VSMC_M10
GO:0106074	0.59	0.65	6	11	aminoacyl-tRNA metabolism involved in translational fidelity	BP	1	LARS,TARS2,LARS2,AARS,DTD1,DTD2	grey	VSMC_M10
GO:0003339	0.59	0.70	4	7	regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis	BP	1	PAX8,PAX2,CITED1,LIF	grey	VSMC_M10
GO:0009152	0.59	0.48	73	137	purine ribonucleotide biosynthetic process	BP	1	NME1,ATP5MGL,PPT2,PPARA,ACSL6,IMPDH1,SLC35B2,SLC25A13,PPAT,PPCS,PPT1,DLD,SPHK2,ADCY3,PRKAG2,ATP5F1C,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,AMPD3,ATP5F1A,GUCY1A1,GUCY1B1,DGUOK,GMPS,AMPD1,ADCY7,FAM173B,ADCY2,NME4,ACSL5,HACD2,ADCY4,DNAJC30,PDK3,SLC25A16,ACSBG1,ATP5S,COASY,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,PARP1,TECR,SLC26A1,GUCY2D,PKLR,PANK3,GCDH,ACACA,SLC26A2,ADSSL1,ACSBG2,ATP6V0C,PANK4,NME3,ATP5PB,VPS9D1,ACSF3,MLYCD,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,ELOVL3,NME6,NUDT2	grey	VSMC_M10
GO:0001756	0.59	0.53	25	48	somitogenesis	BP	1	ROR2,MEOX2,ABI1,PCDH8,XRCC2,PRKDC,TCF15,POFUT1,NKX3-1,NKD1,POGLUT1,AXIN2,MEOX1,BMPR1A,TCAP,RBPJ,ALDH1A2,PSEN1,SMAD3,LHX1,CDX1,MIB1,NLE1,FOXF1,WNT5A	grey	VSMC_M10
GO:0071397	0.59	0.61	8	15	cellular response to cholesterol	BP	1	PTCH1,SMO,CYP7A1,GPLD1,DAG1,GRAMD1B,OSBPL7,LRP8	grey	VSMC_M10
GO:0042149	0.59	0.53	23	44	cellular response to glucose starvation	BP	1	ATF4,PICK1,NUAK1,BRSK1,FOXO3,KPTN,SESN3,PRKAG2,SZT2,PRKAG1,NUAK2,SIK1,MTMR3,TBL2,NFE2L2,SIK2,PRKAG3,BHLHA15,NIM1K,HSPA5,SH3GLB1,IMPACT,UPP1	grey	VSMC_M10

GO:0098877	0.59	0.60	9	17	neurotransmitter receptor transport to plasma membrane	BP	1	SLC1A1,VPS35,NSG1,GRIPAP1,RAB8A,CPLX1,STX1B,RAB11A,ARHGAP44	grey	VSMC_M10
GO:0021546	0.59	0.70	4	7	rhombomere development	BP	1	HOXA2,GBX2,MAFB,HOXB3	grey	VSMC_M10
GO:2000347	0.59	0.70	4	7	positive regulation of hepatocyte proliferation	BP	1	TNFAIP3,PTN,MED1,FGF1	grey	VSMC_M10
GO:0035930	0.59	0.67	5	9	corticosteroid hormone secretion	BP	1	CRY1,C1QTNF1,CRY2,AGT,CRH	grey	VSMC_M10
GO:2000846	0.59	0.67	5	9	regulation of corticosteroid hormone secretion	BP	1	CRY1,C1QTNF1,CRY2,AGT,CRH	grey	VSMC_M10
GO:0021952	0.59	0.58	12	23	central nervous system projection neuron axonogenesis	BP	1	PLXNA4,GLI2,MYCBP2,TSKU,SZT2,EPHB1,NR4A2,ADARB1,EPHB3,NIN,EPHA4,CHRNB2	grey	VSMC_M10
GO:0009313	0.59	0.67	5	9	oligosaccharide catabolic process	BP	1	NEU3,TREH,GM2A,CTBS,NEU2	grey	VSMC_M10
GO:0035601	0.59	0.49	52	99	protein deacylation	BP	1	BAZ2A,C6orf89,ABHD17B,PPT1,SPHK2,HDAC2,PRKD2,PHB,HDAC11,BEX4,TADA3,SIRT2,SIRT7,SIRT3,MTA3,LYPLA1,SDR16C5,ING2,HDAC7,SIRT5,SUDS3,ELK4,SIRT4,HDAC1,LYPLAL1,RCOR3,PER2,HDAC4,MAPT,BCL6,RCOR2,PINK1,TBL1XR1,KDM5A,FOXP3,AKAP8L,AKAP8,JDP2,ZBTB7B,SFPQ,SIN3A,RCOR1,SREBF1,SKI,ABHD17A,MIER2,PRMT6,ABHD10,SAP30BP,ABHD17C,NNMT,LYPLA2	grey	VSMC_M10
GO:0045603	0.59	0.65	6	11	positive regulation of endothelial cell differentiation	BP	1	BTG1,TMEM100,VEZF1,MIR21,ACVRL1,MIR99B	grey	VSMC_M10
GO:2000018	0.59	0.70	4	7	regulation of male gonad development	BP	1	SOX9,SEMA3A,DHX37,WNT4	grey	VSMC_M10
GO:1903799	0.59	0.63	7	13	negative regulation of production of miRNAs involved in gene silencing by miRNA	BP	1	ZC3H10,ESR1,BCDIN3D,PPP3CA,TERT,STAT3,NCOR1	grey	VSMC_M10
GO:0043476	0.59	0.65	6	11	pigment accumulation	BP	1	ANKRD27,SHROOM2,BLOC1S6,AP1G1,BLOC1S3,RAB32	grey	VSMC_M10
GO:0043482	0.59	0.65	6	11	cellular pigment accumulation	BP	1	ANKRD27,SHROOM2,BLOC1S6,AP1G1,BLOC1S3,RAB32	grey	VSMC_M10
GO:0098779	0.59	0.67	5	9	positive regulation of mitophagy in response to mitochondrial depolarization	BP	1	PRKN,OPTN,PINK1,MFN2,VPS13C	grey	VSMC_M10
GO:0044794	0.59	0.63	7	13	positive regulation by host of viral process	BP	1	YTHDC2,IGF2R,CFL1,HSPA8,PC,TBC1D20,ZNF502	grey	VSMC_M10
GO:0090102	0.59	0.54	21	40	cochlea development	BP	1	PTK7,SOBP,SLC26A5,MYO3A,SOX9,GLI2,EYA1,OPA1,RPGRIP1L,PAX2,MYO3B,KCNK2,GRHL3,EPHA4,DVL2,POU3F4,IFT20,KCNK3,WNT5A,SIX1,HEY2	grey	VSMC_M10
GO:0009309	0.59	0.56	14	26	amine biosynthetic process	BP	1	GPR37,DDC,AANAT,HAND2,NR4A2,AZIN2,SLC6A3,TGFB2,SMS,GCH1,HDC,OAZ1,PARK7,NNMT	grey	VSMC_M10
GO:0042401	0.59	0.56	14	26	cellular biogenic amine biosynthetic process	BP	1	GPR37,DDC,AANAT,HAND2,NR4A2,AZIN2,SLC6A3,TGFB2,SMS,GCH1,HDC,OAZ1,PARK7,NNMT	grey	VSMC_M10
GO:0050709	0.59	0.52	27	51	negative regulation of protein secretion	BP	1	PRKN,BMP8A,RSAD2,FRMD4A,DPH3,NDUFAF2,FAM3D,KCNJ11,NR1H3,RAB11FIP5,ACVR1C,F2R,ADTRP,SIRT4,IRS1,CD200,HDAC1,PPP3CA,ADRA2A,KCNB1,KLF7,IL12A,ENY2,SYTL4,SREBF1,MIR199A1,CHGA	grey	VSMC_M10
GO:0006729	0.59	0.70	4	7	tetrahydrobiopterin biosynthetic process	BP	1	DHFR,SPR,GCH1,PCBD2	grey	VSMC_M10
GO:0046146	0.59	0.70	4	7	tetrahydrobiopterin metabolic process	BP	1	DHFR,SPR,GCH1,PCBD2	grey	VSMC_M10
GO:0090240	0.59	0.70	4	7	positive regulation of histone H4 acetylation	BP	1	ARRB1,AUTS2,KAT7,MUC1	grey	VSMC_M10
GO:0035646	0.59	0.67	5	9	endosome to melanosome transport	BP	1	ANKRD27,BLOC1S6,AP1G1,BLOC1S3,RAB32	grey	VSMC_M10
GO:0043485	0.59	0.67	5	9	endosome to pigment granule transport	BP	1	ANKRD27,BLOC1S6,AP1G1,BLOC1S3,RAB32	grey	VSMC_M10
GO:0048757	0.59	0.67	5	9	pigment granule maturation	BP	1	ANKRD27,BLOC1S6,AP1G1,BLOC1S3,RAB32	grey	VSMC_M10
GO:0035088	0.59	0.53	22	42	establishment or maintenance of apical/basal cell polarity	BP	1	PTK7,LIN7B,DLG2,FOXJ1,WNT11,ANK1,LIN7A,SYNE4,TCF15,CLIC4,DLG1,MARK2,SYNJ2BP,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,OOEP,PDZD11,WNT5A	grey	VSMC_M10
GO:0061245	0.59	0.53	22	42	establishment or maintenance of bipolar cell polarity	BP	1	PTK7,LIN7B,DLG2,FOXJ1,WNT11,ANK1,LIN7A,SYNE4,TCF15,CLIC4,DLG1,MARK2,SYNJ2BP,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,OOEP,PDZD11,WNT5A	grey	VSMC_M10
GO:0035376	0.59	0.70	4	7	sterol import	BP	1	LRP1,STARD5,LDLR,STARD4	grey	VSMC_M10
GO:0070508	0.59	0.70	4	7	cholesterol import	BP	1	LRP1,STARD5,LDLR,STARD4	grey	VSMC_M10
GO:0046688	0.59	0.56	14	26	response to copper ion	BP	1	HSF1,AQP1,ATP7B,AANAT,PRNP,IL1A,LOXL2,BACE1,NFE2L2,SORD,SOD3,PARK7,MT-CYB,MT1X	grey	VSMC_M10
GO:0045017	0.59	0.46	113	214	glycerolipid biosynthetic process	BP	1	PIP4K2C,AVIL,SYNJ2,AGPAT4,AGPAT1,PNPLA3,PLA2G6,GPAA1,CWH43,INPP4A,TMEM246,PIGF,MBOAT7,NR1H2,LPIN1,INPP4B,FIG4,MTMR2,PIP4K2A,SELENOI,ABHD5,TAMM41,ITPKC,MTMR14,PGAP2,CRLS1,CDS2,NR1H4,MTMR7,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,PLCE1,FBXW7,SLA2,NR1H3,SYNJ1,LPIN3,CDS1,FITM2,ITPKA,PIGT,GPLD1,LPCAT1,SIK1,PGAP1,GPAM,CHKA,ACP6,ABHD4,AJUBA,PITPNM1,GNPAT,DGKD,PIGM,BMX,FAM126B,IP6K2,LPGAT1,PIGV,MTMR3,PCYT1A,INPP5J,PIGX,PIGZ,PISD,DGKG,PIKFYVE,PLA2G4A,MOGAT3,SACM1L,LPCAT3,PIGC,SOCS4,PI4KA,SLC27A1,ABHD8,PGAP3,PIGH,PI4K2B,SOCS7,DGKQ,AC138894.1,DGKE,TTC7B,LDLR,PIGL,ABHD3,SREBF1,LPIN2,C3,MPPE1,IMPA2,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,AGPAT2,PIP5KL1,PLA2G15,FABP5,PEMT,CNEP1R1,PYURF,LCLAT1,PIGB,PIGA,INPP1,PTPMT1,CDIPT	grey	VSMC_M10
GO:0060071	0.59	0.52	25	48	Wnt signaling pathway, planar cell polarity pathway	BP	1	FZD6,RSPO3,PTK7,ROR2,WNT11,SPEF1,RYK,FZD3,TIAM1,VANGL1,PRICKLE1,NKD1,ZNRF3,DVL3,FZD7,GRHL3,DAAM1,ARHGEF19,DVL2,MKS1,GPC3,CELSR2,RHOA,WNT5A,CELSR3	grey	VSMC_M10
GO:0007588	0.59	0.54	19	36	excretion	BP	1	NEDD4L,CHRNA3,ABCG5,ABCG8,POU3F3,SNX5,NPHP1,STC1,ABCG2,AGT,COMT,KCNMA1,AC138894.1,CHRNB2,SCNN1B,ADORA2B,TRPV1,CHRNB4,KCNK5	grey	VSMC_M10
GO:0097494	0.59	0.64	6	11	regulation of vesicle size	BP	1	WASHC5,RAB5A,RAB22A,AP2M1,RAB11A,RILP	grey	VSMC_M10
GO:0009215	0.59	0.70	4	7	purine deoxyribonucleoside triphosphate metabolic process	BP	1	NUDT15,NUDT16,DGUOK,ADK	grey	VSMC_M10
GO:0060026	0.59	0.62	7	13	convergent extension	BP	1	PTK7,WNT11,MKKS,NKD1,DVL2,WNT5A,LBX2	grey	VSMC_M10

GO:0033674	0.59	0.45	196	373	positive regulation of kinase activity	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,MAP3K4,AGER,ROS1,XRCC6,PTK2,TAB1,NTRK2,CCND3,ZNF16,CHRNA3,TEK,TTBK1,KIT,SLC1A1,ROR2,FPR2,MOB1B,EPGN,AREG,ETAA1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,EGFR,ARHGEF5,TLR4,EPHA1,CCNY,SLC8A2,PHB,ABI1,MAPRE3,RALB,PRKAG2,PIBF1,SPRY2,WNT11,ALK,TGFBR2,NEK10,RPTOR,TCIM,HBEGF,PRNP,NRG1,NCKAP1L,GAS6,ERCC6,FLT1,RYK,ADRA2B,TRAF6,EPHB1,RET,ZFP91,ROBO1,FBXW7,VEGFC,MADD,PTK2B,RASGRP1,RAPGEF2,PRKAG1,TIAM1,NBN,PKD2,STK4,NOD2,TAOK3,CD40,DSTYK,IGF2,BMPR1B,IRS1,NEURL1,CCND1,MAP2K6,TGFB2,ADRA2A,FAM20A,DAG1,AJUBA,NCF1,KRAS,EGF,PFKFB2,ADNP,CASS4,SPATC1L,CACUL1,AGT,FGR,CIB1,DVL3,STRADB,SYAP1,STRADA,EPHB3,DUSP12,GPRC5D,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,MAPT,STOX1,CEMIP,DBF4B,EPHB4,MAP4K2,DDX3X,XRCC5,DUSP19,PDCD10,ADRA2C,DOK7,SLC11A1,MARK2,FGFR3,PINK1,SLC27A1,EPHA4,DLG4,MAGED1,DVL2,BMPR1A,FGFR4,RPLP1,DGKQ,PSEN1,FGF18,LCP2,TAOK2,EFNA1,IL6R,MAP2K1,CD19,LAT,PIK3R5,MAP2K5,CALM1,PSMD10,CD74,INSR,CCL5,CSF1R,CDK5R1,GHR,UNC119,TAOK1,SOCS1,DAB1,LRP8,PDPK1,CAMKK1,PRKCZ,MLST8,PKD1,TRAF2,MTCP1,PARK7,PSRC1,VAV3,BCL10,DAB2IP,MIR21,MIR125B1,RHOA,S100A12,ZNF622,INSRR,IRGM,WNT5A,TIGAR,MMD,SPDYA,TXN,COPS8,RGCC,DAZAP2,HRAS,EREG,MAP2K7,C3orf58,FGF1,PIFO,PDGFD	grey	VSMC_M10
GO:0042762	0.59	0.64	6	11	regulation of sulfur metabolic process	BP	1	SLC7A11,PDK1,PDK3,NFE2L2,COMT,MIR21	grey	VSMC_M10
GO:0005978	0.59	0.54	19	36	glycogen biosynthetic process	BP	1	EPM2AIP1,PPP1CB,AKT2,PPP1R3B,GBE1,SORBS1,IGF2,NHLRC1,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PRKAG3,PPP1R3F,INSR,INPP5K,AGL,ACADM	grey	VSMC_M10
GO:0009250	0.59	0.54	19	36	glucan biosynthetic process	BP	1	EPM2AIP1,PPP1CB,AKT2,PPP1R3B,GBE1,SORBS1,IGF2,NHLRC1,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PRKAG3,PPP1R3F,INSR,INPP5K,AGL,ACADM	grey	VSMC_M10
GO:0070875	0.59	0.62	7	13	positive regulation of glycogen metabolic process	BP	1	EPM2AIP1,AKT2,SORBS1,IGF2,IRS1,PPP1R3E,INSR	grey	VSMC_M10
GO:0034356	0.59	0.67	5	9	NAD biosynthesis via nicotinamide riboside salvage pathway	BP	1	SLC22A13,SLC5A8,NUDT12,PARP9,NNMT	grey	VSMC_M10
GO:0034116	0.59	0.67	5	9	positive regulation of heterotypic cell-cell adhesion	BP	1	AGER,GCNT2,LCK,FGA,THY1	grey	VSMC_M10
GO:0032715	0.59	0.55	16	30	negative regulation of interleukin-6 production	BP	1	TNFAIP3,TLR4,C5AR2,FOXJ1,ARRB1,NCKAP1L,GAS6,IL37,CD200,BANK1,NLRX1,PTPN6,FOXP3,SYT11,MIR125A,HAVCR2	grey	VSMC_M10
GO:0071732	0.59	0.62	7	13	cellular response to nitric oxide	BP	1	AQP1,GUCY1B1,MTR,MMP3,DNM2,CRK,TRAF2	grey	VSMC_M10
GO:0010675	0.59	0.48	60	114	regulation of cellular carbohydrate metabolic process	BP	1	PRKN,PPARA,GPT,GNMT,CRY1,PRKCE,PPP4R3B,ZNF692,PLEK,FAM3C,RUBCNL,KHK,EPM2AIP1,GCKR,PPP1CB,AKT2,C1QTNF1,SIRT7,PDK1,PPP1R3B,NLN,NCOA2,SORBS1,P2RY1,PTK2B,IGF2,GPLD1,IRS1,SIK1,MST1,PPP1R3E,PFKFB2,GPER1,PPP1R3D,ACTN3,HDAC4,NTSR1,PASK,DUSP12,PDK3,PTH1R,GNB3,STAT3,PPP1R3F,IGFBP4,DDB1,DGKQ,OGT,COX11,LCMT1,NCOR1,INSR,LEPR,PTPN2,INPP5K,MLYCD,ACADM,TIGAR,NNMT,ARPP19	grey	VSMC_M10
GO:0035563	0.59	0.62	7	13	positive regulation of chromatin binding	BP	1	ZNF618,MED25,HMBOX1,EBF2,PARP9,DTX3L,DDX11	grey	VSMC_M10
GO:0036010	0.59	0.57	12	23	protein localization to endosome	BP	1	MICALL1,ABHD17B,TMEM30A,VPS35,WASHC2A,TOLLIP,ANKRD13A,EGF,SORL1,DTX3L,ABHD17A,ABHD17C	grey	VSMC_M10
GO:0039532	0.59	0.64	6	11	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	BP	1	SEC14L1,NPLOC4,NLRX1,TKFC,TSPAN6,RIOK3	grey	VSMC_M10
GO:0090659	0.59	0.58	11	21	walking behavior	BP	1	AGTPBP1,HTRA2,SPG11,EPHA4,CLN8,NPC1,DAB1,CNTN2,CEND1,FXN,EFNB3	grey	VSMC_M10
GO:0006549	0.59	0.70	4	7	isoleucine metabolic process	BP	1	BCAT2,SDSL,ACADSB,HSD17B10	grey	VSMC_M10
GO:0006359	0.59	0.60	9	17	regulation of transcription by RNA polymerase III	BP	1	CHD8,RPTOR,BRF2,ZC3H8,ZNF143,CEBPA,POLR3C,ELL,ICE2	grey	VSMC_M10
GO:0070741	0.59	0.54	18	34	response to interleukin-6	BP	1	PHB,ST18,CEBPA,FER,ST3GAL6,RIPK1,ABCC2,SELPLG,STAT3,CITED1,IL6R,JAK1,PTPN2,LCN2,GFI1,MIR125B1,MIR125A,C1QTNF4	grey	VSMC_M10
GO:0034379	0.59	0.66	5	9	very-low-density lipoprotein particle assembly	BP	1	APOB,APOC1,SOAT2,SOAT1,LPCAT3	grey	VSMC_M10
GO:0043373	0.59	0.62	7	13	CD4-positive, alpha-beta T cell lineage commitment	BP	1	TOX,TNFSF18,STAT3,FOXP3,TBX21,BATF,IL6R	grey	VSMC_M10
GO:0021561	0.59	0.64	6	11	facial nerve development	BP	1	PLXNA4,SEMA3A,SEMA3F,ADARB1,PLXNA3,SIX1	grey	VSMC_M10
GO:0021610	0.59	0.64	6	11	facial nerve morphogenesis	BP	1	PLXNA4,SEMA3A,SEMA3F,ADARB1,PLXNA3,SIX1	grey	VSMC_M10
GO:0044872	0.59	0.62	7	13	lipoprotein localization	BP	1	LRP1,APOB,CUBN,MIA3,PRKCB,VMP1,UNC119	grey	VSMC_M10
GO:0003272	0.59	0.57	12	23	endocardial cushion formation	BP	1	TGFBR2,ROBO1,ROBO2,TGFB2,SNAI1,BMPR1A,RBPJ,TMEM100,TBX2,ENG,NOG,HEY2	grey	VSMC_M10
GO:0050766	0.59	0.53	20	38	positive regulation of phagocytosis	BP	1	LRP1,FPR2,IL15,CD300LF,IL15RA,NCKAP1L,GAS6,TUB,PTPRJ,F2RL1,ANO6,NOD2,FCER1G,SLC11A1,DOCK2,DNM2,CCL2,C3,ABCA7,CYBA	grey	VSMC_M10
GO:0060438	0.60	0.61	8	15	trachea development	BP	1	SRF,SOX9,TGFBR2,MAPK1,MAPK3,MAP2K1,FOXF1,HYDIN	grey	VSMC_M10
GO:0032273	0.60	0.48	61	116	positive regulation of protein polymerization	BP	1	ARPC3,HSPA1B,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,TTBK1,SLAIN2,NCK2,KIAA1211,PRKCE,MET,CDK5RAP2,MAPRE1,WASF1,SLAIN1,FCHSD2,NAV3,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,CLIP1,FMN1,PTK2B,IQGAP2,CYFIP1,MAGEL2,CARMIL1,LMOD1,AP1AR,WASF2,WHAMM,CDKN1B,DLG1,CDC42EP2,MAPT,TOGARAM1,NCKAP1,NIN,PINK1,ARPC1A,WAS,EVL,CDK5R1,MLST8,MECP2,SPIRE2,PSRC1,WDR63,CARMIL2,RHOA,VASP,GMFG,GRB2,DRG1	grey	VSMC_M10
GO:0008090	0.60	0.59	10	19	retrograde axonal transport	BP	1	KIF5A,AGTPBP1,MGARP,DLG2,CALY,KIF1C,HAP1,NDEL1,SNAPIN,MAP1A	grey	VSMC_M10

GO:0007018	0.60	0.45	149	283	microtubule-based movement	BP	1	AP3S1,KIF5A,RAB21,KIF3A,UBE2B,CATSPER3,LRRC6,AGTPBP1,SUN2,COPG2,IFT74,CFAP69,APBA1,RFX3,BICD2,DYNC2LI1,LRPPRC,DNAJA1,DNAH11,CABS1,MGARP,ARMC2,WASF1,ARMC4,APOB,TCTE3,ADCY3,TTC26,KIF3C,ARHGAP21,COPG1,DRC1,RSPH6A,KLC3,DLG2,TCTEX1D4,IFT172,TTC21A,WDR60,CFAP61,TTLL3,DYNC1LI1,AP3M2,KIF5C,MKKS,NEK10,PURA,SPEF1,TUB,DNAH10,KIF3B,ING2,DNAH6,WDR66,IFT81,CFAP20,KIFC3,KATNB1,RASGRP1,CCDC65,OPA1,AP3B1,IFT52,DNAH1,PLTP,DNAH5,DTNBP1,DPCD,ROPN1L,KIF13A,BICDL1,KIF21A,NEURL1,CFAP43,ZMYND10,SLC9B1,SLC9B2,CFAP46,INTS13,TTC21B,HSPA8,JHY,OFD1,CFAP45,ENO4,TSSK4,BAG3,TRAF3IP1,CELF3,CNIH2,CATSPER2,KIF9,CALY,TTC30A,SPG11,MAPT,SORD,BLOC1S6,TTC12,DNAAF2,SPAG16,MREG,HTT,CFAP70,STK36,KIF17,UXT,AP3M1,ADCY10,KIF1C,TTC25,HAP1,DNAAF4,MNS1,WDR19,KPNB1,DNAH2,PEX14,TRIM46,NDEL1,AC138894.1,CCDC151,SNAPIN,SFPQ,DNAH3,TEKT3,CAMSAP3,IFT20,SPEF2,CATSPERD,CFAP53,HSPB11,BICDL2,PRKCZ,MAPK8IP3,TPGS1,CELSR2,HYDIN,TERF2,WDR63,DYNC1LI2,UBB,BLOC1S3,KIF21B,BORCS5,CCSAP,AP3S2,MAP1A,SPA17	grey	VSMC_M10
GO:0042558	0.60	0.55	15	28	pteridine-containing compound metabolic process	BP	1	SHMT2,DHFR,MTHFD2,SPR,MTRR,MTR,MTHFS,GCH1,SHMT1,SLC46A1,PIPOX,MTHFD2L,SLC25A32,ALDH1L1,PCBD2	grey	VSMC_M10
GO:0080111	0.60	0.60	9	17	DNA demethylation	BP	1	APOBEC3H,STPG4,ALKBH3,TOX,OTUD4,FTO,ALKBH2,TET1,ALKBH1	grey	VSMC_M10
GO:2000479	0.60	0.61	8	15	regulation of cAMP-dependent protein kinase activity	BP	1	PRKAR2B,PRKAG2,PKIA,RAPGEF2,PRKAR1A,MST1,SPATC1L,HTT	grey	VSMC_M10
GO:0048538	0.60	0.53	20	38	thymus development	BP	1	SRF,SLC46A2,RAF1,PRKDC,ASXL1,HAND2,JARID2,EPHB3,MAPK1,ZBTB1,PSEN1,CTC1,MAPK3,MAP2K1,BCL11B,MAFB,FADD,SIX1,BCL2L11,HOXA3	grey	VSMC_M10
GO:0007200	0.60	0.51	28	53	phospholipase C-activating G protein-coupled receptor signaling pathway	BP	1	ESR1,GPR20,FPR2,LPAR1,C5AR2,C5AR1,ADRA1D,CCKBR,PLCE1,P2RY1,HOMER1,F2RL1,F2R,ADRA2A,CMKLR1,OPRD1,AGT,PTH1R,CXCR2,CHRM1,NMUR2,GNB1,GNA15,GNG13,GPR157,GPR35,CHGA,GNA14	grey	VSMC_M10
GO:1902166	0.60	0.64	6	11	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	BP	1	TAF9,ING2,MARCH7,MUC1,TAF9B,CD74	grey	VSMC_M10
GO:0006109	0.60	0.47	73	139	regulation of carbohydrate metabolic process	BP	1	PRKN,PPARA,PRXL2C,GPT,GNMT,CRY1,PRKCE,PPP4R3B,SLC4A4,ZNF692,PLEK,FAM3C,RUBCNL,KHK,EPM2AIP1,PRKAG2,GCKR,PPP1CB,AKT2,C1QTNF1,SIRT7,PDK1,PPP1R3B,NLN,NCOA2,SORBS1,GPD1,P2RX7,P2RY1,PTK2B,PRKAG1,IGF2,GPLD1,IRS1,SIK1,ZBTB20,MST1,PPP1R3E,EGF,PFKFB2,GPER1,ARNT,PPP1R3D,ACTN3,HDAC4,NTSR1,PASK,MLXIPL,DUSP12,PDK3,PTH1R,GNB3,STAT3,PPP1R3F,IGFBP4,DDB1,DGKQ,PSEN1,OGT,COX11,LCMT1,NCOR1,INSR,LEPR,PTPN2,INPP5K,SLC2A6,MLYCD,ACADM,ENTPD5,TIGAR,NNMT,ARPP19	grey	VSMC_M10
GO:0072079	0.60	0.61	8	15	nephron tubule formation	BP	1	OSR1,SOX9,PAX8,PAX2,IRX2,SOX8,NOG,SIX1	grey	VSMC_M10
GO:0035929	0.60	0.62	7	13	steroid hormone secretion	BP	1	GDF9,CRY1,C1QTNF1,NKX3-1,CRY2,AGT,CRH	grey	VSMC_M10
GO:0032488	0.60	0.64	6	11	Cdc42 protein signal transduction	BP	1	WAS,RHOJ,NTN1,RIT2,RALBP1,RHOU	grey	VSMC_M10
GO:0022410	0.60	0.66	5	9	circadian sleep/wake cycle process	BP	1	BTBD9,SRD5A1,CHRNB2,PER3,CRH	grey	VSMC_M10
GO:0086001	0.60	0.51	30	58	cardiac muscle cell action potential	BP	1	NEDD4L,TRPM4,CACNB2,SCN5A,SCN1A,GPD1L,SLMAP,KCNJ3,KCNE2,DSP,KCNIP2,RYR2,PKP2,KCNJ2,ANK2,ATP1A2,SCN4B,NOS1AP,DLG1,ATP1B1,SLC4A3,CACNA1G,CALM1,DSG2,RNF207,DMD,KCNH2,SCN2B,KCNJ8,HCN4	grey	VSMC_M10
GO:0070885	0.60	0.61	8	15	negative regulation of calcineurin-NFAT signaling cascade	BP	1	FHL2,PRNP,TBC1D10C,MYOZ2,ACTN3,HOMER2,MYOZ1,MAPK7	grey	VSMC_M10
GO:0106057	0.60	0.61	8	15	negative regulation of calcineurin-mediated signaling	BP	1	FHL2,PRNP,TBC1D10C,MYOZ2,ACTN3,HOMER2,MYOZ1,MAPK7	grey	VSMC_M10
GO:0048048	0.60	0.56	13	25	embryonic eye morphogenesis	BP	1	FRS2,IFT172,RARB,TFAP2A,PAX2,ALDH1A3,SP3,FZD5,FBN1,MFAP2,TBX2,STRA6,WNT5A	grey	VSMC_M10
GO:0044774	0.60	0.49	39	74	mitotic DNA integrity checkpoint signaling	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,BRSK1,MSH2,XPC,PLK3,NEK11,PRKDC,STK33,PLK2,RAD17,RAD9B,NBN,ABRAXAS1,DONSON,PIDD1,TAOK3,CCND1,GIGYF2,CHEK2,SYF2,CDKN1B,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,FOXN3,TAOK1,FZR1,FBXO31,NAE1,RPS27L,SOX4,BRCC3,CRADD	grey	VSMC_M10
GO:1900272	0.60	0.66	5	9	negative regulation of long-term synaptic potentiation	BP	1	AGER,PTN,PRNP,FAM107A,EPHA4	grey	VSMC_M10
GO:0010890	0.60	0.69	4	7	positive regulation of sequestering of triglyceride	BP	1	PLIN2,FITM2,FITM1,PLIN3	grey	VSMC_M10
GO:0033864	0.60	0.69	4	7	positive regulation of NAD(P)H oxidase activity	BP	1	AGT,PARK7,GNAI3,CYBA	grey	VSMC_M10
GO:0048485	0.60	0.61	8	15	sympathetic nervous system development	BP	1	GFRA3,PLXNA4,TFAP2B,SEMA3A,HAND2,FZD3,SEMA3F,SOX4	grey	VSMC_M10
GO:1905477	0.60	0.49	46	88	positive regulation of protein localization to membrane	BP	1	LRP1,STAC3,PRKN,PRKCE,SPTBN1,PTN,ITGB1BP1,EGFR,TCAF2,STAC,AKT2,PRNP,PIK3R1,PLS1,SORBS1,KCNJ11,SSH1,KCNB1,C2CD5,GPER1,RAB11FIP2,CIB1,DLG1,FIS1,CEMIP,NMT1,ZDHHC8,CNPY4,CNST,WNK3,STAC2,STX4,ITGAM,ITGA3,AC138894.1,RAB11A,AP2B1,MIEF2,CDK5R1,EFCAB7,PDPK1,RER1,ARHGEF16,HRAS,MIEF1,MESD	grey	VSMC_M10
GO:0031146	0.60	0.52	23	44	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	BP	1	SKP1,FBXL6,FBXO48,FBXL13,FBXL2,DMAC2,FBXO17,FBXW7,FBXW4,FBXL15,AMN1,FBXO33,FBXL14,FBXL18,FBXO2,FBXL22,FBXO38,CUL4B,FBXL16,FBXO31,FBXL8,FBXL12,STYX	grey	VSMC_M10
GO:0007021	0.60	0.69	4	7	tubulin complex assembly	BP	1	TBCE,TBCEL,VBP1,TBCA	grey	VSMC_M10
GO:0048854	0.60	0.55	14	27	brain morphogenesis	BP	1	FZD6,FANCC,SMO,FOXO3,MKKS,FZD3,SLIT1,PAX2,ZNF335,SLC4A10,PSEN1,SPEF2,WNT5A,OTX1	grey	VSMC_M10
GO:0031050	0.60	0.52	24	46	dsRNA processing	BP	1	ZC3H10,ESR1,AGO2,TUT7,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,BCDIN3D,RIPK1,PPP3CA,TERT,PRKRA,DDX3X,STAT3,MAP2K1,SMAD3,NCOR1,DROSHA,SPOUT1,AGO4	grey	VSMC_M10
GO:0035196	0.60	0.52	24	46	production of miRNAs involved in gene silencing by miRNA	BP	1	ZC3H10,ESR1,AGO2,TUT7,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,BCDIN3D,RIPK1,PPP3CA,TERT,PRKRA,DDX3X,STAT3,MAP2K1,SMAD3,NCOR1,DROSHA,SPOUT1,AGO4	grey	VSMC_M10

GO:0070918	0.60	0.52	24	46	production of small RNA involved in gene silencing by RNA	BP	1	ZC3H10,ESR1,AGO2,TUT7,PUS10,SNIP1,AGO1,EGFR,MYCN,TUT4,PUM2,BCDIN3D,RIPK1,PPP3CA,TERT,PRKRA,DDX3X,STAT3,MAP2K1,SMAD3,NCOR1,DROSHA,SPOUT1,AGO4	grey	VSMC_M10
GO:0007009	0.60	0.48	49	94	plasma membrane organization	BP	1	ATP8B1,A4GALT,FER1L6,MTSS1,ASAP1,BAIAP2L2,MICALL1,MYH9,SPTBN1,SPACA6,IZUMO1,PRX,AKT2,STX2,ANO4,MYOF,XKR6,PLSCR4,P2RX7,DYSF,BIN3,ANO6,TGFB2,ANK2,OSBPL2,WHAMM,LYZL6,NSF,RAB3A,SYT7,MPP5,DEGS1,STX4,SYT11,AC138894.1,SPESP1,NOX5,SYTL4,DNM2,EPB41L3,ABCA7,SYPL2,COL5A1,FNBP1L,MTSS1L,SH3GLB1,TLCD1,XKR8,CAVIN2	grey	VSMC_M10
GO:0016338	0.60	0.66	5	9	calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	BP	1	CLDN12,CLDN19,CLDN7,CLDN15,CLDN1	grey	VSMC_M10
GO:0001892	0.60	0.50	35	67	embryonic placenta development	BP	1	STK3,RSPO3,MDFI,TFEB,EPAS1,GJB5,OVOL2,EOMES,SPINT2,CEBPA,SPINT1,PKD2,STK4,IGF2,SNAI1,ARNT,VASH2,SP3,SETD2,FZD5,MAPK1,RBPJ,MED1,SOX15,VASH1,CITED1,MAP2K1,PKD1,KRT19,CASP8,GRB2,LIF,CEBPB,HEY2,WNT2	grey	VSMC_M10
GO:0032332	0.60	0.59	9	17	positive regulation of chondrocyte differentiation	BP	1	SOX9,ZNF219,SOX6,LOXL2,BMPR1B,POR,FGF18,SMAD3,ACVRL1	grey	VSMC_M10
GO:0006303	0.60	0.50	31	59	double-strand break repair via nonhomologous end joining	BP	1	ATP23,MRNIP,XRCC6,HSF1,POT1,CYREN,HMCES,ERCC1,XRCC1,MLH1,SIRT7,SHLD1,PRKDC,ERCC6,ERCC8,XRCC4,POLL,PARP9,DTX3L,XRCC5,IFFO1,SHLD2,PRPF19,WRAP53,LIG3,SMCHD1,ERCC4,NUDT16L1,PAXX,RNF8,NHEJ1	grey	VSMC_M10
GO:1901380	0.60	0.59	9	17	negative regulation of potassium ion transmembrane transport	BP	1	NEDD4L,KEL,KCNRG,OXSR1,KCNE2,CASQ2,KCNH2,CRBN,RGS4	grey	VSMC_M10
GO:0099637	0.60	0.57	11	21	neurotransmitter receptor transport	BP	1	SLC1A1,VPS35,NSG1,GRIPAP1,RAB8A,CPLX1,STX1B,RAB11A,ARHGAP44,CACNG7,CACNG5	grey	VSMC_M10
GO:1902237	0.60	0.69	4	7	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	BP	1	NCK2,PTPN2,DDIT3,BCL2L11	grey	VSMC_M10
GO:0030497	0.60	0.62	7	13	fatty acid elongation	BP	1	HACD4,ELOVL1,ELOVL7,HACD2,TECR,HACD3,ELOVL3	grey	VSMC_M10
GO:0018026	0.60	0.64	6	11	peptidyl-lysine monomethylation	BP	1	SETD7,SETD6,EEF1AKMT2,SETD2,SETD3,METTL18	grey	VSMC_M10
GO:0046716	0.60	0.62	7	13	muscle cell cellular homeostasis	BP	1	LARGE1,SRF,TRIM32,PFKM,BAG3,MTM1,DMD	grey	VSMC_M10
GO:0042780	0.60	0.69	4	7	tRNA 3'-end processing	BP	1	TRNT1,HSD17B10,POLR3K,TRMT10C	grey	VSMC_M10
GO:0010676	0.60	0.52	21	40	positive regulation of cellular carbohydrate metabolic process	BP	1	PPARA,GPT,PRKCE,PPP4R3B,EPM2AIP1,AKT2,SORBS1,P2RY1,IGF2,GPLD1,IRS1,PPP1R3E,GPER1,ACTN3,NTSR1,PTH1R,DDB1,INSR,PTPN2,NNMT,ARPP19	grey	VSMC_M10
GO:0040037	0.60	0.60	8	15	negative regulation of fibroblast growth factor receptor signaling pathway	BP	1	FUZ,SPRY1,SPRY2,SULF2,WNT4,NGFR,WNT5A,SHISA2	grey	VSMC_M10
GO:0061052	0.60	0.66	5	9	negative regulation of cell growth involved in cardiac muscle cell development	BP	1	PPARA,PI16,YY1,MIR199A1,RGS4	grey	VSMC_M10
GO:0002363	0.60	0.60	8	15	alpha-beta T cell lineage commitment	BP	1	TOX,TNFSF18,STAT3,FOXP3,TBX21,BATF,IL6R,RHOA	grey	VSMC_M10
GO:0046348	0.60	0.66	5	9	amino sugar catabolic process	BP	1	ALDH1A1,GNPDA2,MGAT1,OVGP1,CTBS	grey	VSMC_M10
GO:0010893	0.60	0.62	7	13	positive regulation of steroid biosynthetic process	BP	1	CYP7A1,SCAP,POR,WNT4,SREBF1,STARD4,FGF1	grey	VSMC_M10
GO:0002720	0.60	0.52	22	42	positive regulation of cytokine production involved in immune response	BP	1	CD226,KIT,RSAD2,TLR4,SPHK2,LACC1,MAVS,TRAF6,F2RL1,NOD2,DENND1B,FZD5,HK1,SPON2,CD74,TICAM1,PRKCZ,TRAF2,SLC7A5,BCL10,WNT5A,INAVA	grey	VSMC_M10
GO:0007130	0.60	0.59	9	17	synaptonemal complex assembly	BP	1	TEX15,SYCP1,SPO11,TEX12,STAG3,P3H4,SYCE2,AGO4,SYCE1L	grey	VSMC_M10
GO:0070314	0.60	0.66	5	9	G1 to G0 transition	BP	1	SLC39A5,CYP27B1,RIDA,CDK5R1,PHGDH	grey	VSMC_M10
GO:0002209	0.60	0.58	10	19	behavioral defense response	BP	1	MAPK8IP2,USP46,SLC1A1,MEF2C,ASIC1,ATP1A2,ASIC4,MECP2,DPP4,CRH	grey	VSMC_M10
GO:0032769	0.60	0.66	5	9	negative regulation of monooxygenase activity	BP	1	CYP27B1,NOSIP,GLA,GFI1,MIR27B	grey	VSMC_M10
GO:0071801	0.60	0.63	6	11	regulation of podosome assembly	BP	1	IL5,ASAP1,LCP1,HCK,KIF9,RHOA	grey	VSMC_M10
GO:1902902	0.60	0.61	7	13	negative regulation of autophagosome assembly	BP	1	FEZ2,SEC22B,TMEM39A,PINK1,PHF23,SMCR8,MTM1	grey	VSMC_M10
GO:0002407	0.60	0.60	8	15	dendritic cell chemotaxis	BP	1	TRPM4,GAS6,ANO6,SLAMF8,IL12A,TNFSF18,CXCR2,CCL5	grey	VSMC_M10
GO:0022011	0.60	0.56	13	25	myelination in peripheral nervous system	BP	1	ADGRG6,NTRK2,ADAM22,PRX,AKT2,SIRT2,NRG1,LGI4,DAG1,CNTNAP1,MPP5,SKI,POU3F2	grey	VSMC_M10
GO:0032292	0.60	0.56	13	25	peripheral nervous system axon ensheathment	BP	1	ADGRG6,NTRK2,ADAM22,PRX,AKT2,SIRT2,NRG1,LGI4,DAG1,CNTNAP1,MPP5,SKI,POU3F2	grey	VSMC_M10
GO:0033866	0.60	0.50	30	57	nucleoside bisphosphate biosynthetic process	BP	1	PPT2,ACSL6,SLC35B2,PPCS,PPT1,DLD,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,ACSL5,HACD2,PDK3,SLC25A16,ACSBG1,COASY,MPC2,TECR,SLC26A1,PANK3,GCDH,ACACA,SLC26A2,ACSBG2,PANK4,ACSF3,MLYCD,ELOVL3	grey	VSMC_M10
GO:0034030	0.60	0.50	30	57	ribonucleoside bisphosphate biosynthetic process	BP	1	PPT2,ACSL6,SLC35B2,PPCS,PPT1,DLD,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,ACSL5,HACD2,PDK3,SLC25A16,ACSBG1,COASY,MPC2,TECR,SLC26A1,PANK3,GCDH,ACACA,SLC26A2,ACSBG2,PANK4,ACSF3,MLYCD,ELOVL3	grey	VSMC_M10
GO:0034033	0.60	0.50	30	57	purine nucleoside bisphosphate biosynthetic process	BP	1	PPT2,ACSL6,SLC35B2,PPCS,PPT1,DLD,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,ACSL5,HACD2,PDK3,SLC25A16,ACSBG1,COASY,MPC2,TECR,SLC26A1,PANK3,GCDH,ACACA,SLC26A2,ACSBG2,PANK4,ACSF3,MLYCD,ELOVL3	grey	VSMC_M10
GO:0032042	0.60	0.61	7	13	mitochondrial DNA metabolic process	BP	1	MGME1,PRIMPOL,POLG2,STOX1,PARP1,LIG3,LONP1	grey	VSMC_M10
GO:0030325	0.60	0.59	9	17	adrenal gland development	BP	1	TSPO,LY6E,WNT11,DKK3,SALL1,WNT4,SMAD3,STRA6,FSTL3	grey	VSMC_M10

GO:0005996	0.60	0.45	105	199	monosaccharide metabolic process	BP	1	FUCA2,PRKN,PPARA,PMM1,AKR1B1,ATF4,MAPK14,GPT,GNMT,CRY1,PGM5,GALT,UXS1,TFAP2B,SLC25A13,GAPDH,PPP4R3B,ZNF692,FAM3C,DHDH,RUBCNL,AKR1A1,GLB1,KHK,EPM2AIP1,NUDT5,XYLB,GCKR,RBKS,PPP1CB,AKT2,PFKP,PGM2L1,C1QTNF1,SIRT7,SLC23A2,PDK1,FUT10,PPP1R3B,POFUT1,GPI,NLN,NCOA2,SORBS1,GPD1,KCNJ11,PFKM,CHST1,GLYCTK,IGF2,GPLD1,IRS1,SIK1,CPT1A,MST1,PPP1R3E,PFKFB2,PC,PPP1R3D,SLC37A4,PER2,PFKFB4,ACTN3,USF1,PASK,DUSP12,GAL3ST3,APOD,FUOM,PDK3,SORD,RPE,HK1,GNB3,SLC35A2,PPP1R3F,IGFBP4,DDB1,DGKQ,OGT,COX11,CRTC2,LCMT1,ADPGK,MPI,INSR,LEPR,ALDOC,PTPN2,FGGY,PMM2,INPP5K,TKTL1,MLYCD,ACADM,FBP2,OAS1,FABP5,FUT4,FPGT,POFUT2,TIGAR,NNMT,ARPP19,RPIA	grey	VSMC_M10
GO:1901386	0.60	0.63	6	11	negative regulation of voltage-gated calcium channel activity	BP	1	GNB5,CALM1,FMR1,RRAD,GPR35,GEM	grey	VSMC_M10
GO:0043687	0.60	0.54	16	30	post-translational protein modification	BP	1	ATG12,AGTPBP1,ATG5,CRTAP,TTL,RNF7,GPLD1,RHBDD1,FAM20C,ATG16L1,WIPI2,VIPAS39,LCMT1,FOLH1,IRGM,UCHL3	grey	VSMC_M10
GO:0002830	0.60	0.63	6	11	positive regulation of type 2 immune response	BP	1	RSAD2,NOD2,DENND1B,IL4R,CD74,PRKCZ	grey	VSMC_M10
GO:1901673	0.60	0.60	8	15	regulation of mitotic spindle assembly	BP	1	VPS4B,HSPA1B,CHMP2A,CHMP2B,CHMP4C,CHMP1A,CCSAP,DRG1	grey	VSMC_M10
GO:0045646	0.60	0.52	22	42	regulation of erythrocyte differentiation	BP	1	HSPA1B,BRD1,MAPK14,ZNF16,RBFOX2,CDK6,SMAP1,FOXO3,ACVR2A,NCKAP1L,PRKDC,ACVR1B,LDB1,ARNT,STAT3,STAT5B,MED1,KAT7,MIR222,ANKRD54,MAFB,FAM210B	grey	VSMC_M10
GO:0046628	0.60	0.58	10	19	positive regulation of insulin receptor signaling pathway	BP	1	GKAP1,SNX5,SORBS1,OPA1,IGF2,IRS1,SORL1,AGT,ZBTB7B,PRKCZ	grey	VSMC_M10
GO:0048680	0.60	0.65	5	9	positive regulation of axon regeneration	BP	1	LRP1,PTN,NDEL1,MIR222,CNTF	grey	VSMC_M10
GO:1905939	0.61	0.65	5	9	regulation of gonad development	BP	1	GDF9,SOX9,SEMA3A,DHX37,WNT4	grey	VSMC_M10
GO:0002831	0.61	0.45	118	224	regulation of response to biotic stimulus	BP	1	CD226,TNFAIP3,USP15,XRCC6,TRIB1,C6orf106,FPR2,ANKRD17,NOD1,AKIRIN2,NR1H2,IL4I1,TLR4,IL15,PUM2,TRAF3IP2,NECTIN2,PVR,OPTN,SLC22A13,SEC14L1,IKBKB,SIRT2,NMI,TMEM173,NPLOC4,MAVS,HPX,FOXP1,PRKDC,IRF7,TRAF6,PCBP2,TRIM44,HCK,ERAP1,RASGRP1,EIF2AK4,NR1H3,TRAFD1,OAS3,NLRC5,RIPK2,F2RL1,POLR3D,MAPKBP1,HERC5,NOD2,CD96,OASL,POLR3C,NCF1,YTHDF2,SLAMF8,PARP9,DTX3L,PARP14,RNF26,FGR,NLRX1,TRAF3IP1,HTRA1,COCH,PPP2R3C,ADAM8,CADM1,DUSP10,NONO,IL12A,XRCC5,PTPN6,LAG3,MUL1,BIRC3,STAT5B,FOXP3,RNF216,TKFC,USP18,MED1,SYT11,MAPK3,DCST1,TSPAN6,SFPQ,STAT2,SIN3A,TRAF3,CCL5,RIOK3,GATA6,FBXO38,RNF135,VAV1,PTPN2,SOCS1,LRP8,CRK,CREBBP,CYBA,AP1G1,ZDHHC1,MIR21,OAS1,ZDHHC11,FADD,CXCL6,CASP8,ZCCHC3,A2M,IFNLR1,IRGM,WNT5A,TIGAR,FGL2,SERPINB9,EREG,HAVCR2	grey	VSMC_M10
GO:0007416	0.61	0.46	68	132	synapse assembly	BP	1	NTRK2,LRRC4,LINGO2,GABRA1,FZD1,ADGRF1,SEMA4D,ADGRL3,GJA10,LRRN3,EPHA7,ADD2,VPS35,SDCBP,NRCAM,VSTM5,POU4F1,SLITRK5,LRFN1,FARP1,NRG1,LRFN3,RYK,EPHB1,CLSTN2,ROBO2,MEF2C,CUX2,SLIT1,AMIGO2,BDNF,GAP43,AMIGO3,NLGN4Y,BSN,ADNP,GNPAT,RAB17,SPTBN2,NPAS4,EPHB3,FZD5,NRXN2,SPOCK2,DNM3,OBSL1,LRTM2,SDK1,NLGN2,LGI2,SEMA4A,NLGN3,CHRNB2,NTN1,GPRASP2,BHLHB9,ASIC2,SLITRK2,MECP2,AMIGO1,CEL,NTNG2,ZDHHC12,ADGRL2,GRID2,WNT5A,SIX1,LRRTM2	grey	VSMC_M10
GO:0009176	0.61	0.65	5	9	pyrimidine deoxyribonucleoside monophosphate metabolic process	BP	1	DPYS,UPB1,NT5M,DCTD,UPP1	grey	VSMC_M10
GO:0009642	0.61	0.65	5	9	response to light intensity	BP	1	CAT,RDH13,AKT2,TENT2,GNB5	grey	VSMC_M10
GO:0042745	0.61	0.63	6	11	circadian sleep/wake cycle	BP	1	BTBD9,AHCY,SRD5A1,CHRNB2,PER3,CRH	grey	VSMC_M10
GO:0006222	0.61	0.65	5	9	UMP biosynthetic process	BP	1	CMPK1,UPRT,UCK1,DHODH,UPP1	grey	VSMC_M10
GO:0009174	0.61	0.65	5	9	pyrimidine ribonucleoside monophosphate biosynthetic process	BP	1	CMPK1,UPRT,UCK1,DHODH,UPP1	grey	VSMC_M10
GO:0051702	0.61	0.49	32	61	biological process involved in interaction with symbiont	BP	1	YTHDC2,SNW1,IGF2R,PRKN,GAPDH,NAPEPLD,PHB,FBXL2,MYD88,SAP30,EIF2AK4,F2RL1,HDAC1,ZNF639,CFL1,HSPA8,POU2F3,PC,FN1,DDB1,PSMC3,TARDBP,SCN1B,CCL5,JUN,FMR1,INPP5K,MIR222,CXCL6,SAP30BP,TBC1D20,ZNF502	grey	VSMC_M10
GO:0010447	0.61	0.58	9	17	response to acidic pH	BP	1	ASIC3,ASIC1,RAB11FIP5,SLC38A3,SLC9A1,ASIC2,TRPV1,PKD1L3,IMPACT	grey	VSMC_M10
GO:0060512	0.61	0.57	11	21	prostate gland morphogenesis	BP	1	ESR1,FRS2,HOXA13,TNC,SOX9,GLI2,CYP7B1,NKX3-1,SERPINB5,NOG,WNT5A	grey	VSMC_M10
GO:0060351	0.61	0.55	13	25	cartilage development involved in endochondral bone morphogenesis	BP	1	COL27A1,SOX9,TSKU,TGFBR2,RARB,STC1,TRPV4,TRIP11,AXIN2,POR,MMP13,THBS3,GHR	grey	VSMC_M10
GO:0050773	0.61	0.48	45	87	regulation of dendrite development	BP	1	NEDD4L,RAB21,CHRNA3,SEMA4D,PTN,HECW1,RTN4IP1,SS18L2,ALK,TMEM106B,ANKRD27,TLX2,CUX2,RAPGEF2,TIAM1,OPA1,ITPKA,CYFIP1,LZTS1,KIAA0319,DNM1L,PPP3CA,HECW2,CAPRIN2,MARK1,RAB17,NFATC4,SS18L1,CDKL5,DGKG,CRTC1,OBSL1,EPHA4,CHRNB2,ZDHHC15,PARP6,GPRASP2,BHLHB9,SEZ6,LRP8,CRK,FBXO31,DAB2IP,RHOA,YWHAH	grey	VSMC_M10
GO:0046717	0.61	0.56	11	21	acid secretion	BP	1	APBA1,CCKBR,HIP1R,CHRM5,ABCC2,ABCB11,NTSR1,HRH2,ABAT,TRPV1,SNX10	grey	VSMC_M10
GO:0060113	0.61	0.51	25	48	inner ear receptor cell differentiation	BP	1	ATP8B1,GSDME,MYCL,WHRN,MYCN,USH1G,MYO7A,TSKU,SLC4A7,JAG1,LRTOMT,AP000812.5,PLS1,ADGRV1,USH1C,TRIP11,STRC,CDH23,RBPJ,MKS1,JAG2,IFT20,MCOLN3,PJVK,HEY2	grey	VSMC_M10
GO:0071300	0.61	0.50	27	52	cellular response to retinoic acid	BP	1	ADNP2,SNW1,RORB,PTK7,HOXA2,AQP1,TNC,TEAD2,OSR1,HDAC2,SOX9,WNT11,RET,HTRA2,PTK2B,TESC,PAX2,FZD7,WNT3,CREB1,ABL2,BRINP2,ALDH1A2,YES1,WNT5A,ZNF35,WNT2	grey	VSMC_M10
GO:0035116	0.61	0.57	10	19	embryonic hindlimb morphogenesis	BP	1	OSR2,PITX1,OSR1,RARB,RPGRIP1L,WNT3,MED1,TBX4,GPC3,ALX3	grey	VSMC_M10
GO:0046851	0.61	0.61	7	13	negative regulation of bone remodeling	BP	1	TNFAIP3,TNFRSF11B,P2RX7,GPR137B,UBASH3B,GPR137,CD38	grey	VSMC_M10
GO:0051917	0.61	0.65	5	9	regulation of fibrinolysis	BP	1	THBD,FAP,USF1,F12,SERPINF2	grey	VSMC_M10

GO:0035493	0.61	0.61	7	13	SNARE complex assembly	BP	1	SEPT8,ANKRD27,STX1A,VAMP1,STX4,STXBP1,VAMP3	grey	VSMC_M10
GO:0035999	0.61	0.65	5	9	tetrahydrofolate interconversion	BP	1	SHMT2,MTHFD2,MTHFS,SHMT1,MTHFD2L	grey	VSMC_M10
GO:0034384	0.61	0.68	4	7	high-density lipoprotein particle clearance	BP	1	APOM,GPLD1,LDLR,MIR33B	grey	VSMC_M10
GO:0035090	0.61	0.65	5	9	maintenance of apical/basal cell polarity	BP	1	LIN7B,WNT11,ANK1,LIN7A,PDZD11	grey	VSMC_M10
GO:0045199	0.61	0.65	5	9	maintenance of epithelial cell apical/basal polarity	BP	1	LIN7B,WNT11,ANK1,LIN7A,PDZD11	grey	VSMC_M10
GO:0006620	0.61	0.63	6	11	posttranslational protein targeting to endoplasmic reticulum membrane	BP	1	SEC61B,SEC61G,SEC62,SGTA,HSPA5,SEC61A2	grey	VSMC_M10
GO:1902683	0.61	0.59	8	15	regulation of receptor localization to synapse	BP	1	STX7,DAG1,CNIH2,GRIPAP1,IQSEC2,ARHGAP44,PRKCZ,HRAS	grey	VSMC_M10
GO:0050868	0.61	0.48	40	76	negative regulation of T cell activation	BP	1	TNFRSF21,PELI1,IL4I1,FOXJ1,PAWR,PRNP,NCKAP1L,ZC3H8,CASP3,TMEM131L,PAG1,MARCH7,BTN2A2,PRKAR1A,HLX,RUNX3,DLG1,BCL6,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,SCGB1A1,FOXP3,TBX21,ZBTB7B,IL4R,CD74,TWSG1,PTPN2,SOCS1,GLMN,MIR21,MIR27A,FGL2,LAX1,CEBPB,HAVCR2,RC3H2	grey	VSMC_M10
GO:0030099	0.61	0.44	154	293	myeloid cell differentiation	BP	1	NME1,MPIG6B,HSPA1B,BRD1,IL5,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,MAPK14,HSF1,MYH9,ZNF16,RBFOX2,SRF,CDK6,KIT,ROR2,RPS14,IL11,SMAP1,EPAS1,CD109,HOXA7,PTBP3,MTURN,BPGM,CNOT4,TLR4,IL15,OSTM1,FOXO3,PIP4K2A,ABI1,ERCC2,GAB2,PRDX3,SLC25A38,POU4F1,TGFBR2,ACVR2A,JAG1,RASGRP4,NCKAP1L,FOXP1,MITF,PRKDC,IRF7,MFHAS1,TRAF6,ACVR1B,CAMK4,CEBPA,NCOA6,PIK3R1,CASP3,FBXW7,MEF2C,PTK2B,AP3B1,F2RL1,TESC,RIPK1,TMEM14C,TSPAN2,DMTN,ITGB6,ALAS1,LDB1,RAB7B,SH3PXD2A,PKNOX1,LRRK1,SLC9B2,TCIRG1,GPR137B,PRKX,PIAS3,ACIN1,DYRK3,TCTA,HCLS1,UBASH3B,CIB1,WASF2,ARNT,THPO,FARP2,ZBTB46,SP3,CREB1,NBEAL2,BCL6,BATF2,WDR61,ESRRA,PTPN6,GPR137,FBN1,LTBR,STAT3,STAT5B,LEO1,INHA,TFE3,PARP1,THRA,RBPJ,MED1,ANXA2,PSEN1,HOXB8,AHSP,KAT7,FOS,BATF,DNASE2,HAX1,GPR68,RCOR1,CD74,CSF1R,PPARGC1B,EVI2B,PTPN2,GPC3,JUN,ATP6AP1,MIR222,MIR125B1,PRMT6,FSTL3,ANKRD54,ARID4A,MAFB,FADD,CASP8,CA2,DHRS2,BGLAP,SNX10,HIST1H4B,HIST2H4A,HIST1H4H,GLO1,NRROS,HIST1H4D,FAM210B,LIF,CEBPB,HIST1H4A,BATF3,HIST1H4F	grey	VSMC_M10
GO:0030520	0.61	0.51	24	46	intracellular estrogen receptor signaling pathway	BP	1	ESR1,CNOT2,FOXH1,RBFOX2,EGLN2,TADA3,TAF7,DDRGK1,NCOA4,CYP7B1,UFSP2,ZNF366,CNOT1,KMT2D,DDX54,VPS18,ARID1A,PADI2,DNAAF4,PARP1,MED1,PAGR1,PPARGC1B,ISL1	grey	VSMC_M10
GO:1905168	0.61	0.61	7	13	positive regulation of double-strand break repair via homologous recombination	BP	1	MRNIP,WDR48,ERCC6,WAS,PARP1,WRAP53,OOEP	grey	VSMC_M10
GO:0062099	0.61	0.59	8	15	negative regulation of programmed necrotic cell death	BP	1	PELI1,RIPK1,FZD9,YBX3,BIRC3,MIR22,FADD,CASP8	grey	VSMC_M10
GO:0032205	0.61	0.53	16	31	negative regulation of telomere maintenance	BP	1	POT1,ERCC1,XRCC1,NBN,TENT4B,STN1,RTEL1,PARP1,GNL3L,CTC1,PIF1,ERCC4,SLX4,TERF2,TINF2,TEN1	grey	VSMC_M10
GO:0000097	0.61	0.61	7	13	sulfur amino acid biosynthetic process	BP	1	MTAP,APIP,ENOPH1,MTRR,MTR,CBSL,MTHFD2L	grey	VSMC_M10
GO:0051646	0.61	0.51	24	46	mitochondrion localization	BP	1	AGTPBP1,LRPPRC,ALB,MGARP,WASF1,NECTIN2,ARMC1,OPA1,DNM1L,MARK1,MFN1,MAPT,MARK2,MUL1,UXT,BHLHA15,HAP1,MFN2,MSTO1,ATP2A1,MTM1,TLE6,CLUH,UBB	grey	VSMC_M10
GO:0018216	0.61	0.61	7	13	peptidyl-arginine methylation	BP	1	PRDM4,NDUFAF7,NR1H4,PRMT9,PRMT3,PRMT7,PRMT6	grey	VSMC_M10
GO:0010660	0.61	0.49	30	57	regulation of muscle cell apoptotic process	BP	1	MAP3K5,PPP1R10,RGL2,HSF1,CDKN2A,ARRB1,PAX8,HAND2,PTK2B,STK4,SIRT5,SIRT4,PDCD4,AGT,BAG3,NFE2L2,IL12A,CXCR2,RBM10,MFN2,CAMK2A,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,TIGAR,C3orf58,NKX2-5,HEY2	grey	VSMC_M10
GO:0090169	0.61	0.56	11	21	regulation of spindle assembly	BP	1	VPS4B,HSPA1B,MAPK15,CHMP2A,CHMP2B,CHMP4C,RNF4,CHMP1A,GPSM2,CCSAP,DRG1	grey	VSMC_M10
GO:0016074	0.61	0.61	7	13	sno(s)RNA metabolic process	BP	1	EXOSC4,EXOSC3,NUDT16,TENT4B,RNF113B,PARN,EXOSC5	grey	VSMC_M10
GO:0039535	0.61	0.58	9	17	regulation of RIG-I signaling pathway	BP	1	USP15,ANKRD17,PUM2,SEC14L1,NPLOC4,OASL,NLRX1,BIRC3,ZCCHC3	grey	VSMC_M10
GO:0043144	0.61	0.62	6	11	sno(s)RNA processing	BP	1	EXOSC4,EXOSC3,TENT4B,RNF113B,PARN,EXOSC5	grey	VSMC_M10
GO:0042532	0.61	0.61	7	13	negative regulation of tyrosine phosphorylation of STAT protein	BP	1	PPP2R1A,PIBF1,PARP14,SUZ12,PTPN2,SOCS1,MIR125A	grey	VSMC_M10
GO:0032480	0.61	0.56	11	21	negative regulation of type I interferon production	BP	1	C6orf106,REL,NMI,NPLOC4,NLRX1,TRAF3IP1,OTUD5,RNF216,YY1,MIR21,HAVCR2	grey	VSMC_M10
GO:0007616	0.61	0.54	14	27	long-term memory	BP	1	BTBD9,SRF,SHANK1,NTF4,PRNP,CAMK4,EIF2AK4,NFATC4,NPAS4,SLC2A4,RGS14,LDLR,PRKCZ,MECP2	grey	VSMC_M10
GO:0001881	0.61	0.54	14	27	receptor recycling	BP	1	BVES,EPS15,OPTN,TBC1D16,AP1AR,SORL1,NSF,ECE1,NSG1,ANXA2,PSEN1,PHETA1,VAMP3,PLEKHJ1	grey	VSMC_M10
GO:1900543	0.61	0.59	8	15	negative regulation of purine nucleotide metabolic process	BP	1	PPARA,ACTN3,HDAC4,STAT3,PARP1,NCOR1,PDZD3,TIGAR	grey	VSMC_M10
GO:0036462	0.61	0.68	4	7	TRAIL-activated apoptotic signaling pathway	BP	1	PARK7,MIR222,FADD,CASP8	grey	VSMC_M10
GO:0035338	0.61	0.57	10	19	long-chain fatty-acyl-CoA biosynthetic process	BP	1	ACSL6,ELOVL1,ELOVL7,ACSL5,HACD2,ACSBG1,TECR,ACSBG2,ACSF3,ELOVL3	grey	VSMC_M10
GO:1990138	0.61	0.45	76	147	neuron projection extension	BP	1	NEDD4L,LRP1,SEMA6A,RAB21,RIMS2,PRKN,PLXNA4,CPNE5,SRF,SEMA4D,SEMA4C,RIMS1,RTN4,RUFY3,NRCAM,WASF1,PLXNA1,GOLGA4,MEGF8,CPNE9,SYT1,SLC23A2,SEMA3D,SEMA3A,ULK1,RYK,TTL,SEMA4F,DPYSL2,EIF2AK4,TIAM1,SLIT1,NKX6-1,ZFYVE27,SEMA3G,CYFIP1,ALCAM,SEMA4G,KIAA0319,SEMA3F,AUTS2,ADNP,DISC1,CDKL5,WNT3,SPG11,MAPT,SEMA6D,ITGA4,TNR,FN1,FLRT1,PPP3CB,MUL1,VCL,SEMA4A,NLGN3,TRIM46,NDEL1,RAB11A,NTN1,DNM2,SIN3A,TRPV2,CDK5R1,SLC9A6,L1CAM,PRKCZ,ARHGAP4,PLXNA3,BARHL2,IMPACT,WNT5A,CACNG7,LLPH,OLFM1	grey	VSMC_M10

GO:0050808	0.61	0.43	171	329	synapse organization	BP	1	PRRT1,SYNGAP1,MAPK14,NTRK2,PICK1,LRRC4,LINGO2,ABHD17B,GABRA1,FZD1,SLC1A1,ADGRF1,SEMA4D,ADGRL3,SHANK1,GJA10,LRRN3,EPHA7,PTN,ADD2,TNC,CTTNBP2,YWHAZ,DLGAP3,VPS35,SDCBP,NRCAM,SLC7A11,PPFIA3,WASF1,MTMR2,SLC8A2,C5AR1,VSTM5,CACNB2,PCDH8,PTPRF,POU4F1,SLITRK5,LRFN1,FARP1,ACTG1,CACNB4,PRNP,PCDHGC5,P2RX2,NRG1,LRFN3,RYK,EPHB1,CLSTN2,CHMP2B,ROBO2,ERC2,MEF2C,CUX2,SEPT11,TIAM1,SLIT1,HOMER1,OPA1,AMIGO2,F2R,SPARCL1,ITPKA,CYFIP1,TUBA1A,BDNF,DOCK10,PPFIA4,INA,NEURL1,DNM1L,PPFIA1,CAPRIN2,SEMA3F,GAP43,PPFIBP1,CAMKV,DAG1,AMIGO3,NLGN4Y,SSH1,CFL1,STAU1,BSN,ADNP,HSPA8,DISC1,GNPAT,WASF2,RAB17,SPTBN2,NFATC4,NPAS4,PTPRO,CDKL5,IL10RA,EPHB3,TANC2,NOS1AP,FZD9,DLG1,FZD5,MAPT,SRGN,C1QL1,TNR,NRXN2,SPOCK2,DOK7,DNM3,RAB3A,SYN1,OBSL1,GRIPAP1,EPHA4,LRTM2,DLG4,ACTB,SDK1,NLGN2,GPHN,CHRNB1,LGI2,CACNB1,PSEN1,SEMA4A,ITGAM,ITGA3,NLGN3,EFNA1,AC138894.1,CHRNB2,ZDHHC15,MYH10,NTN1,SNAPIN,DRP2,GPRASP2,BHLHB9,ARHGAP44,INSR,ASIC2,CDK5R1,C3,SEZ6,SLITRK2,LRP8,DNAJA3,SDF4,L1CAM,RER1,MECP2,ABHD17A,PALM,AMIGO1,CEL,TSC1,NTNG2,ZDHHC12,DAB2IP,ADGRL2,RHOA,CNTN2,GRID2,ABHD17C,WNT5A,SIX1,MESD,LRRTM2	grey	VSMC_M10
GO:0050776	0.61	0.42	284	538	regulation of immune response	BP	1	CD226,STX7,TNFAIP3,USP15,ENPP3,ESR1,HSPA1B,GRAMD4,AGER,HLA-DRA,HLA-DPB1,XRCC6,PTK2,C6orf106,MAPK14,PLA2G6,RAC2,LRRC14,TEC,KIT,TNFRSF21,NINJ1,EXOSC3,PRKCE,MSH2,RTN4,FPR2,ANKRD17,SLC46A2,NOD1,AKIRIN2,PELI1,RSAD2,NR1H2,IL4I1,TLR4,IL15,TRPM4,PUM2,TRAF3IP2,SPHK2,HMCES,C5AR2,C5AR1,PRKD2,PHB,CD300LF,LACC1,NECTIN2,PVR,EIF2B3,GAB2,MLH1,UNC13D,MYD88,SLC22A13,FOXJ1,PAXIP1,IRAK2,SEC14L1,IKBKB,SIRT2,NMI,TMEM173,CLPB,NPLOC4,PAWR,PLCL2,SHLD1,PRNP,MAVS,NCKAP1L,HPX,FOXP1,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,PLK2,HCK,FER,OTUD4,LPXN,ERAP1,PTPRJ,MEF2C,SLA2,RASGRP1,EIF2AK4,NR1H3,TRAFD1,OAS3,NLRC5,RIPK2,OTULIN,AP3B1,F2RL1,POLR3D,MAPKBP1,HERC5,NOD2,ADCY7,CD40,RAB7B,MAPKAPK3,GPLD1,CD96,IFIH1,CD200,SPPL3,OASL,LCK,BANK1,ICOSLG,MAP2K6,TGFB2,BTN2A2,UNC93B1,POLR3C,HLX,DENND1B,TLR5,CMKLR1,NCF1,MAPKAPK2,TIFA,ALPK1,YTHDF2,SLAMF8,PARP9,DTX3L,PARP14,RAB11FIP2,THEMIS2,LAT2,BMX,RNF26,FGR,NLRX1,PLPP4,TRAF3IP1,HTRA1,SNX4,COCH,CD28,FCER1G,PDCD1,PPP2R3C,ADAM8,CADM1,FZD5,DUSP10,NONO,PLA2G4A,BCL6,CTSH,IL12A,DDX3X,VSIR,XRCC5,RC3H1,PTPN6,TNFSF18,SLC11A1,LAG3,COL3A1,PPP3CB,TNIP2,MUL1,BIRC3,CFP,CD38,SPPL2A,C12orf4,MAPK1,STAT5B,WAS,FOXP3,RNF216,ZBTB1,SHLD2,GPS2,TKFC,WDFY1,USP18,CARD11,TNFRSF1B,MED1,TBX21,STX4,PSEN1,ITGAM,SYT11,LCP2,DCST1,DNASE2,ZBTB7B,CD19,SMAD3,IL4R,TSPAN6,S100A14,SFPQ,PRKCB,BTK,STAT2,TNIP1,SIN3A,TRAF3,CD74,CCL5,RIOK3,GATA6,STXBP2,COLEC12,FBXO38,YES1,RNF13	grey	VSMC_M10
GO:0032409	0.61	0.44	104	198	regulation of transporter activity	BP	1	NEDD4L,STAC3,MAPKBIP2,PRRT1,GOPC,PLA2G6,PIM1,ABCB1,WNK2,PRKCE,SHANK1,HECW1,TCAF2,OSR1,SPHK2,KCNRG,CACNB2,STAC,OXSR1,GPD1L,CACNB4,PRNP,SLMAP,GLRX,MEF2C,PTK2B,KCNJ11,NR1H3,HOMER1,IFNGR2,TESC,RIPK1,KCNE2,PKD2,CASQ2,KCNIP2,CHRM3,RYR2,FAM173B,PM20D1,HECW2,ADRA2A,COX17,KCNG1,ANK2,KLHL24,ACE2,ATP1A2,SLC9A1,C4orf3,CASQ1,NTSR1,SCN4B,CNIH2,NOS1AP,DLG1,CTTNBP2NL,HTT,PINK1,ATP1B1,KCNA1,GNB5,MINK1,HAP1,DLG4,ACTB,NLGN2,CNIH3,WNK3,STAC2,CACNB1,ATP1B2,NLGN3,ATP2A1,SLC5A11,CALM1,DNM2,VMP1,CCL2,FMR1,RNF207,PARK7,AMIGO1,RXRA,JPH3,WWP2,RRAD,MIR24-1,DMD,GPR35,JPH2,MIR33B,FGF11,SCN2B,NETO2,CACNG7,CRBN,CRH,APOPT1,YWHAH,SHISA8,CACNG5,GEM,PPIF	grey	VSMC_M10
GO:0034446	0.61	0.47	46	89	substrate adhesion-dependent cell spreading	BP	1	FBLN1,PARVG,PTK2,TEK,ITGB1BP1,EPHA1,BVES,UNC13D,RAC3,ARHGEF7,AKIP1,FER,PIK3R1,LPXN,PARVA,DOCK5,RREB1,DMTN,PXN,CARMIL1,AP1AR,LAMB3,CASS4,CIB1,FZD7,LAMA5,EPHB3,DOCK1,MELTF,CSPG5,LAMC1,ITGA4,FN1,FERMT3,RADIL,EFNA1,DNM2,CRK,NTNG2,LAMC3,MICALL2,RHOA,FGA,LAMB1,PEAK1,VAMP3	grey	VSMC_M10
GO:0043368	0.61	0.55	12	23	positive T cell selection	BP	1	SRF,TOX,TNFSF18,STAT3,FOXP3,TBX21,DOCK2,BATF,IL6R,BCL11B,CD74,PTPN2	grey	VSMC_M10
GO:1902036	0.61	0.60	7	13	regulation of hematopoietic stem cell differentiation	BP	1	EIF2AK2,PRKDC,TCF15,YTHDF2,OSM,NFE2L2,SETD1A	grey	VSMC_M10
GO:0043173	0.61	0.60	7	13	nucleotide salvage	BP	1	AMPD3,AMPD1,ADK,UCK1,FUK,NAPRT,UPP1	grey	VSMC_M10
GO:0006164	0.61	0.45	79	149	purine nucleotide biosynthetic process	BP	1	NME1,ATP5MGL,PPT2,PPARA,ACSL6,GUCA1B,IMPDH1,SLC35B2,SLC25A13,PPAT,PPCS,PPT1,DLD,SPHK2,ADCY3,PRKAG2,ATP5F1C,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,AMPD3,ATP5F1A,GUCY1A1,GUCY1B1,DGUOK,GMPS,AMPD1,ADCY7,FAM173B,ADCY2,NME4,ACSL5,PRPS2,HACD2,ADCY4,DNAJC30,PDK3,SLC25A16,ACSBG1,ATP5S,COASY,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,PARP1,TECR,SLC26A1,GUCY2D,PKLR,PANK3,GCDH,ACACA,SLC26A2,PRPSAP2,ADSSL1,NOS2,ACSBG2,ATP6V0C,PANK4,NME3,ATP5PB,VPS9D1,ACSF3,MLYCD,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,PDZD3,ELOVL3,MTHFD2L,NME6,NUDT2	grey	VSMC_M10
GO:0000462	0.61	0.52	18	34	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	1	HELB,UTP23,TSR1,RPS14,UTP3,ERCC2,RPS8,DHX37,BMS1,RPP40,HEATR1,FAM207A,MRPS11,NOP9,TSR2,KRI1,UTP6,GTF2H5	grey	VSMC_M10

GO:0030838	0.61	0.47	43	82	positive regulation of actin filament polymerization	BP	1	ARPC3,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,NCK2,KIAA1211,PRKCE,WASF1,FCHSD2,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,FMN1,PTK2B,IQGAP2,CYFIP1,MAGEL2,CARMIL1,LMOD1,AP1AR,WASF2,WHAMM,DLG1,CDC42EP2,NCKAP1,ARPC1A,WAS,EVL,MLST8,SPIRE2,WDR63,CARMIL2,RHOA,VASP,GMFG,GRB2	grey	VSMC_M10
GO:0030509	0.62	0.46	60	116	BMP signaling pathway	BP	1	SLC39A5,USP15,GDF9,SMAD5,LEMD2,KCP,TFAP2B,ROR2,DLX5,SOSTDC1,HOXA13,BMP8A,BMPER,SFRP4,MEGF8,ACVR2B,UBE2O,ACVR2A,SPART,SLC33A1,HIVEP1,ZNF423,BMPR1B,FBXL15,PDCD4,TGFB2,HJV,SORL1,HTRA1,CHRD,DLX1,CTDSPL2,HTRA3,FBN1,FKBP8,GDF15,GREM2,BMPR1A,RBPJ,ITGA3,RBPMS2,MAPK3,TOB1,TMEM100,SMAD3,RNF165,CHRDL1,FAM83G,TWSG1,GPC3,SKI,ENG,MIR21,FSTL3,LEMD3,ACVRL1,NOG,WNT5A,RGMB,UBE2D1	grey	VSMC_M10
GO:0009260	0.62	0.45	79	149	ribonucleotide biosynthetic process	BP	1	NME1,ATP5MGL,PPT2,PPARA,ACSL6,IMPDH1,SLC35B2,SLC25A13,PPAT,PPCS,PPT1,DLD,SPHK2,CMPK1,ADCY3,PRKAG2,ATP5F1C,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,AMPD3,ATP5F1A,GUCY1A1,GUCY1B1,DGUOK,GMPS,AMPD1,ADCY7,FAM173B,ADCY2,NME4,ACSL5,HACD2,ADCY4,CTPS2,DNAJC30,PDK3,SLC25A16,ACSBG1,ATP5S,COASY,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,PARP1,TECR,SLC26A1,GUCY2D,PKLR,PANK3,GCDH,UPRT,ACACA,SLC26A2,ADSSL1,ACSBG2,ATP6V0C,PANK4,NME3,ATP5PB,VPS9D1,ACSF3,UCK1,MLYCD,DHODH,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,ELOVL3,NME6,NUDT2,UPP1	grey	VSMC_M10
GO:0019915	0.62	0.48	34	65	lipid storage	BP	1	B4GALNT1,PPARA,MEST,TTC39B,PLIN2,CRY1,NR1H2,LDAH,APOB,ABHD5,CDS2,ASXL1,FBXW7,AUP1,NR1H3,CDS1,ACVR1C,FITM2,CRY2,FTO,CPT1A,FITM1,SOAT1,EHD1,STAT5B,ZFYVE1,TMEM159,GM2A,SREBF1,C3,PTPN2,PLIN3,BSCL2,STARD4	grey	VSMC_M10
GO:0050775	0.62	0.52	18	35	positive regulation of dendrite morphogenesis	BP	1	RAB21,SS18L2,ANKRD27,CUX2,TIAM1,OPA1,ITPKA,DNM1L,CAPRIN2,SS18L1,CDKL5,OBSL1,EPHA4,PARP6,GPRASP2,BHLHB9,LRP8,FBXO31	grey	VSMC_M10
GO:1903078	0.62	0.49	27	52	positive regulation of protein localization to plasma membrane	BP	1	LRP1,STAC3,PRKCE,SPTBN1,EGFR,STAC,PRNP,PIK3R1,PLS1,SORBS1,KCNJ11,GPER1,RAB11FIP2,CIB1,DLG1,ZDHHC8,CNPY4,CNST,WNK3,STAC2,STX4,ITGA3,AC138894.1,RAB11A,PDPK1,RER1,ARHGEF16	grey	VSMC_M10
GO:1903008	0.62	0.46	53	101	organelle disassembly	BP	1	ATG12,PRKN,TSPO,FBXO7,MTIF2,ATG5,PLK3,OPTN,USP36,TMEM173,DDRGK1,ULK1,FBXW7,HTRA2,ZFAND1,CSNK2A2,TEX264,GBF1,EIF2D,DNM1L,CISD2,USP30,DYRK3,UFC1,KIF9,FZD5,FIS1,ATG2A,FUNDC1,HTT,RETREG3,MARK2,PINK1,MUL1,ATG9A,PLA2G16,STX5,ATP13A2,WIPI2,VPS13D,MFN2,VPS13C,HAX1,ATG2B,KLC1,SREBF1,MCTS1,FUNDC2,PARK7,PLK5,BNIP3L,TIGAR,MRRF	grey	VSMC_M10
GO:0042491	0.62	0.53	15	29	inner ear auditory receptor cell differentiation	BP	1	MYCL,WHRN,MYCN,MYO7A,SLC4A7,JAG1,LRTOMT,AP000812.5,PLS1,USH1C,STRC,RBPJ,JAG2,MCOLN3,HEY2	grey	VSMC_M10
GO:0060263	0.62	0.60	7	13	regulation of respiratory burst	BP	1	RAC2,NCF1,SLAMF8,DUSP10,INSR,NOXA1,JCHAIN	grey	VSMC_M10
GO:0032924	0.62	0.52	16	31	activin receptor signaling pathway	BP	1	ZC3H3,FOXH1,ACVR2B,TGFBR2,ACVR2A,AMHR2,ACVR1B,ACVR1C,HJV,MEN1,SMAD3,SKI,FSTL3,LEMD3,ACVRL1,TGIF2	grey	VSMC_M10
GO:0001906	0.62	0.47	41	78	cell killing	BP	1	CD226,STX7,AGER,HLA-DRA,GAPDH,PRDX1,NECTIN2,PVR,UNC13D,MYD88,SLC22A13,NCKAP1L,P2RX7,RASGRP1,F2RL1,CADM1,CTSH,IL12A,PTPN6,LAG3,PPP3CB,STAT5B,ITGAM,SCNN1B,STXBP2,VAV1,C3,NOS2,IL7R,CRK,DNASE1,AP1G1,S100A12,HIST1H2BK,CHGA,FADD,CXCL6,FCER2,SERPINB9,HIST1H2BJ,HAVCR2	grey	VSMC_M10
GO:0002534	0.62	0.51	21	40	cytokine production involved in inflammatory response	BP	1	PPARA,GPSM3,MAPK14,IL1R2,TLR4,MYD88,CHID1,NOD2,ADCY7,PDCD4,APOD,STAT3,PLD4,NOS2,TICAM1,MIR21,MIR222,C5orf30,MIR125A,IL17D,IL17B	grey	VSMC_M10
GO:1900015	0.62	0.51	21	40	regulation of cytokine production involved in inflammatory response	BP	1	PPARA,GPSM3,MAPK14,IL1R2,TLR4,MYD88,CHID1,NOD2,ADCY7,PDCD4,APOD,STAT3,PLD4,NOS2,TICAM1,MIR21,MIR222,C5orf30,MIR125A,IL17D,IL17B	grey	VSMC_M10
GO:0030003	0.62	0.42	228	434	cellular cation homeostasis	BP	1	SLC39A5,NEDD4L,LRP1,ESR1,SLC12A2,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,TMPRSS6,SLC39A4,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,PRKCE,TNNI3,FPR2,IBTK,SLC4A4,LPAR1,PPT1,SLC31A2,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,AQP11,ATP1A3,ACKR2,SLC24A3,C1QTNF1,SLC4A7,TMEM106B,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,HPX,RASA3,NCOA4,MICU3,ATP6V1H,TM9SF4,IL1A,IMMT,C19orf12,P2RX3,PLCE1,SLC9A9,RYR3,TMBIM6,P2RX7,HVCN1,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,PKD2,CASQ2,MCUR1,CD40,RYR2,SLC41A1,SLC4A10,RAP1GDS1,TRPM1,SPPL3,LCK,KCNJ2,TESMIN,SLC9B1,TRPV4,TMEM9,SLC30A10,TCIRG1,GNA13,ISCU,CMKLR1,MCUB,HJV,SLC9A8,UBASH3B,DISC1,ANK2,GPER1,SLAMF8,TRPM8,PDZD8,AGT,ATP1A2,SLC9A1,CASQ1,NTSR1,CLIC4,FZD9,TMCO1,PTH1R,SLC30A4,FIS1,CEMIP,ABL2,CDH23,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,SLC9A7,ATP6V0A1,ABCB6,TRPM7,ATP1B1,CD38,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP13A2,FTH1,HAP1,DLG4,CYB561A3,ATP1B2,FAM155B,PSEN1,CACNA1A,MAPK3,AC138894.1,ATP2A1,CD19,SMAD3,CLN6,NOX5,CALM1,SNAPIN,S100A8,PRKCB,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,C7,PTGER4,SLC25A23,MAIP1,TMEM199,SLC46A1,SLC9A6,NUBP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,ATP6AP1,GPR157,SYPL2,CYBA,JPH3,ATP2C2,SLC30A7,FRRS1,LCN2,MCOLN3,PTGFR,SLC9A5,MIR199A1,KCNK3,DMD,MT1X,GPR35,NOL3,	grey	VSMC_M10

GO:2000108	0.62	0.56	10	19	positive regulation of leukocyte apoptotic process	BP	1	CDKN2A,IDO1,ZC3H8,PIK3CB,MEF2C,RAPGEF2,PDCD1,ADAM8,CCL5,WNT5A	grey	VSMC_M10
GO:0035872	0.62	0.55	12	23	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	BP	1	TNFAIP3,HSPA1B,SLC46A2,TLR4,LACC1,RIPK2,OTULIN,NOD2,MAP2K6,BIRC3,IRGM,INAVA	grey	VSMC_M10
GO:0007219	0.62	0.45	72	138	Notch signaling pathway	BP	1	MAML1,PTP4A3,MFNG,IFT74,DLK2,KIT,S1PR3,BEND6,AAK1,ANXA4,ITGB1BP1,MAML2,SOX9,LLGL2,GALNT11,TIMP4,IFT172,ARRB1,TGFBR2,JAG1,TCIM,POFUT1,CEBPA,CBFA2T2,DTX4,ROBO1,ROBO2,FBXW7,BMP2K,HIF1AN,NOD2,CNTN1,ZNF423,GAS2,NEURL1,NEPRO,TGFB2,POGLUT1,SNAI1,YTHDF2,DTX3L,WDR12,DLX1,CDKN1B,HOXD3,BCL6,PDCD10,STAT3,PSEN2,SPEN,RBPJ,SYNJ2BP,PSEN1,NEURL1B,SEL1L,TMEM100,TBX2,MIB1,NLE1,JAG2,NKAP,CDH6,MIB2,ARRDC1,WWP2,KRT19,CD46,CFD,PERP,APH1B,SLC35C1,HEY2	grey	VSMC_M10
GO:0051251	0.62	0.44	98	186	positive regulation of lymphocyte activation	BP	1	AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TNFRSF13C,XRCC6,NCK2,EXOSC3,MSH2,PELI1,IL4I1,TLR4,IL15,HMCES,BMI1,MLH1,GLI2,MYD88,PAXIP1,IL15RA,TGFBR2,SHLD1,NCKAP1L,GAS6,PRKDC,SLC7A1,TRAF6,SOX12,TOX,IL1A,MEF2C,IL7,RASGRP1,RIPK2,AP3B1,SOX13,NOD2,ZNF335,CD40,IGF2,LCK,ICOSLG,GPAM,HLX,CD28,RUNX3,PPP2R3C,ADAM8,DUSP10,BLOC1S6,BCL6,IL12A,VSIR,PTPN6,TNIP2,CD38,BST1,STAT5B,FOXP3,RASAL3,ZBTB1,SHLD2,CARD11,TBX21,ZBTB7B,CHRNB2,IL4R,BTK,CD74,CCL5,CCL2,YES1,NKAP,CD320,VAV1,IL7R,SOCS1,TICAM1,DNAJA3,PRKCZ,VAV3,AP1G1,BCL10,MIR21,RHOA,BLOC1S3,SOX4,FADD,DPP4,CD46,THY1,CD70,TNFSF9,EFNB3,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0031507	0.62	0.52	17	33	heterochromatin assembly	BP	1	BAZ2A,H3F3C,DNMT3A,SETDB2,SIRT2,FAM208A,BAHD1,PPHLN1,HDAC1,ZNFX1,TET1,PHF8,NRDE2,SMCHD1,SETDB1,BEND3,ZNF304	grey	VSMC_M10
GO:0043649	0.62	0.60	7	13	dicarboxylic acid catabolic process	BP	1	DDO,GAD2,GLUL,MTHFS,ACSF3,ACOT4,ALDH1L1	grey	VSMC_M10
GO:0060044	0.62	0.60	7	13	negative regulation of cardiac muscle cell proliferation	BP	1	TGFBR2,TBX5,JARID2,KCNK2,SAV1,MIR199A1,NOG	grey	VSMC_M10
GO:0051152	0.62	0.60	7	13	positive regulation of smooth muscle cell differentiation	BP	1	KIT,GPER1,EFEMP2,ENG,MIR21,MIR125B1,MIR22	grey	VSMC_M10
GO:0034983	0.62	0.67	4	7	peptidyl-lysine deacetylation	BP	1	SIRT2,SIRT3,SIRT4,HDAC4	grey	VSMC_M10
GO:0051875	0.62	0.56	10	19	pigment granule localization	BP	1	BBS7,MYO7A,MKKS,SHROOM2,MLPH,RAB17,BLOC1S6,MREG,RAB11A,BLOC1S3	grey	VSMC_M10
GO:0051905	0.62	0.56	10	19	establishment of pigment granule localization	BP	1	BBS7,MYO7A,MKKS,SHROOM2,MLPH,RAB17,BLOC1S6,MREG,RAB11A,BLOC1S3	grey	VSMC_M10
GO:1902305	0.62	0.49	26	50	regulation of sodium ion transmembrane transport	BP	1	NEDD4L,WNK2,PRKCE,HECW1,OSR1,SCN5A,GPD1L,SLMAP,GLRX,TESC,HECW2,KLHL24,ATP1A2,SLC9A1,SCN4B,DLG1,ATP1B1,WNK3,ATP1B2,DNM2,MIR24-1,DMD,FGF11,SCN2B,NETO2,YWHAH	grey	VSMC_M10
GO:0006953	0.62	0.55	11	21	acute-phase response	BP	1	IL1A,CD163,FN1,STAT3,IL6R,SERPINF2,TRPV1,ASS1,LCN2,PTGES,CEBPB	grey	VSMC_M10
GO:0031268	0.62	0.60	7	13	pseudopodium organization	BP	1	CDC42EP1,KIT,F2RL1,SRGAP2C,CDC42EP2,RAB25,APC	grey	VSMC_M10
GO:0051220	0.62	0.55	11	21	cytoplasmic sequestering of protein	BP	1	GOPC,MDFI,NFKBIE,FAF1,NFKBIB,PKD2,SUFU,GET4,KEAP1,PSMD10,PKD1	grey	VSMC_M10
GO:0002764	0.62	0.43	146	278	immune response-regulating signaling pathway	BP	1	CD226,TNFAIP3,USP15,ESR1,HSPA1B,GRAMD4,HLA-DPB1,PTK2,PLA2G6,LRRC14,TEC,KIT,TNFRSF21,NINJ1,PRKCE,RTN4,FPR2,ANKRD17,SLC46A2,NOD1,PELI1,RSAD2,TLR4,PUM2,C5AR2,C5AR1,PRKD2,PHB,CD300LF,LACC1,NECTIN2,EIF2B3,MYD88,IRAK2,SEC14L1,IKBKB,NMI,CLPB,NPLOC4,PAWR,PLCL2,PRNP,NCKAP1L,FOXP1,IRF7,MFHAS1,TRAF6,NR1H4,HCK,FER,OTUD4,LPXN,PTPRJ,MEF2C,SLA2,NR1H3,OAS3,RIPK2,OTULIN,AP3B1,F2RL1,NOD2,CD40,RAB7B,MAPKAPK3,GPLD1,IFIH1,SPPL3,OASL,LCK,BANK1,ICOSLG,MAP2K6,BTN2A2,UNC93B1,DENND1B,TLR5,CMKLR1,MAPKAPK2,TIFA,ALPK1,RAB11FIP2,THEMIS2,LAT2,BMX,FGR,NLRX1,PLPP4,CD28,FCER1G,CTSH,DDX3X,RC3H1,PTPN6,TNIP2,BIRC3,CD38,MAPK1,FOXP3,GPS2,TKFC,WDFY1,CARD11,PSEN1,LCP2,CD19,TSPAN6,S100A14,PRKCB,BTK,TNIP1,TRAF3,RIOK3,COLEC12,YES1,RNF135,PRAM1,VAV1,GPR108,PTPN2,TICAM1,CREBBP,PDPK1,IKBKG,CYBA,VAV3,GFI1,BCL10,DAB2IP,CMTM3,FYB1,OAS1,BTN1A1,ZCCHC3,IRGM,CD247,THY1,INAVA,UBE2N,GCSAM,HRAS,LAX1,SH2B2,MAP2K7,HAVCR2,RC3H2	grey	VSMC_M10
GO:0015980	0.62	0.43	139	259	energy derivation by oxidation of organic compounds	BP	1	SHMT2,GFPT2,LYRM7,UQCRQ,NDUFA6,ACO2,MYC,GNMT,SLC25A13,CAT,SDHAF4,MSH2,PNPT1,DLD,NDUFB2,PYGB,NDUFB6,RUBCNL,DNAJC15,KHK,EPM2AIP1,DHTKD1,NDUFC2,PRKAG2,ATP5F1C,PPP1CB,AKT2,MDH2,NDUFS8,PANK2,NDUFA12,KL,SIRT3,COX7A1,SUCLG2,PPP1R3B,COX4I2,IDE,GBE1,ATP5F1A,SORBS1,GPD1,NDUFS3,ETFDH,DGUOK,PFKM,UQCRB,COX15,FAM173B,IGF2,NHLRC1,COX6B1,PHKB,IRS1,NDUFV3,TRPV4,COQ10B,OXA1L,NDUFB4,ISCU,PPP1R3E,COA6,POLG2,NDUFB3,CISD1,PPP1R3D,NFATC4,PER2,ACTN3,PASK,NDUFS2,PHKA2,DNAJC30,MLXIPL,SDHC,MDH1B,COX6A1,IDH3A,PYGM,PYGL,COX8A,PRKAG3,PINK1,NDUFA9,SDHB,PPP1R3F,ACADVL,COX6A2,PHKA1,NDUFAB1,UQCRC2,COX10,COX5A,INSR,TEFM,NDUFA7,LEPR,NOS2,SLC25A23,NDUFV2,SLC25A14,INPP5K,PRDM16,NDUFB10,UQCR11,PARK7,SLC25A33,ATP5PB,AGL,SLC25A25,ACADM,MT-ND1,MT-ND2,MT-ATP8,MT-ATP6,MT-CO3,MT-ND6,MT-CYB,RHOA,ATP5ME,ATP5MF,NDUFA5,IFNLR1,NDUFC1,COX7A2,TIGAR,FXN,PPP1R1A,ETFRF1,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,UQCC2,MRAP2,COX7A2L,PPIF	grey	VSMC_M10
GO:0009265	0.62	0.62	6	11	2'-deoxyribonucleotide biosynthetic process	BP	1	TBPL1,DGUOK,DTYMK,ADK,CMPK2,DCTD	grey	VSMC_M10
GO:0046385	0.62	0.62	6	11	deoxyribose phosphate biosynthetic process	BP	1	TBPL1,DGUOK,DTYMK,ADK,CMPK2,DCTD	grey	VSMC_M10

GO:0042102	0.62	0.49	29	55	positive regulation of T cell proliferation	BP	1	AGER,HLA-DPB1,TNFRSF13C,NCK2,IL15,BMI1,TGFBR2,NCKAP1L,SLC7A1,TRAF6,IL1A,RIPK2,IGF2,ICOSLG,GPAM,CD28,STAT5B,FOXP3,RASAL3,CARD11,CCL5,DNAJA3,MIR21,FADD,CD46,CD70,TNFSF9,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0046888	0.62	0.49	25	48	negative regulation of hormone secretion	BP	1	PRKN,CRY1,IL11,BMP8A,NDUFAF2,FAM3D,KCNJ11,RAB11FIP5,ACVR1C,CRY2,SIRT4,IRS1,HDAC1,PPP3CA,ADRA2A,KCNB1,OSM,KLF7,ENY2,INHA,SYTL4,SREBF1,CHGA,CRH,LIF	grey	VSMC_M10
GO:0001706	0.62	0.50	22	43	endoderm formation	BP	1	ITGA7,EOMES,MMP15,RTF1,SOX2,LAMB3,COL7A1,ITGB5,SETD2,ITGA4,FN1,COL5A2,LEO1,LHX1,LAMA3,GATA6,COL5A1,DUSP2,LAMB1,NOG,DUSP1,DUSP4	grey	VSMC_M10
GO:0021587	0.62	0.52	17	33	cerebellum morphogenesis	BP	1	GLI1,AGTPBP1,SMO,WHRN,XRCC1,GLI2,FAIM2,LDB1,TTC21B,GNPAT,SPTBN2,MAP2K1,LHX1,DAB1,HSPA5,GRID2,CEND1	grey	VSMC_M10
GO:0060339	0.62	0.56	10	19	negative regulation of type I interferon-mediated signaling pathway	BP	1	OAS3,NLRC5,YTHDF2,MUL1,USP18,DCST1,STAT2,PTPN2,MIR21,OAS1	grey	VSMC_M10
GO:0042537	0.62	0.60	7	13	benzene-containing compound metabolic process	BP	1	ALDH8A1,IDO2,IDO1,EPHX2,FAH,KYAT1,KYAT3	grey	VSMC_M10
GO:0009165	0.62	0.43	105	198	nucleotide biosynthetic process	BP	1	NME1,TBPL1,ATP5MGL,PPT2,PPARA,ACSL6,GUCA1B,IMPDH1,NMRK1,SLC35B2,SLC25A13,PPAT,PPCS,ME1,PPT1,DLD,SPHK2,CMPK1,ADCY3,PRKAG2,SLC22A13,ATP5F1C,ELOVL1,IDO2,IDO1,PANK2,PDK1,PDHX,SLC5A8,ELOVL7,PANK1,NUDT12,AMPD3,ATP5F1A,GUCY1A1,GUCY1B1,DGUOK,GMPS,AMPD1,ADCY7,FAM173B,ADCY2,NME4,ACSL5,PRPS2,PARP9,HACD2,ADCY4,CTPS2,DNAJC30,DTYMK,PDK3,SLC25A16,ACSBG1,ATP5S,COASY,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,MAPK1,PARP1,TECR,SLC26A1,GUCY2D,PKLR,PANK3,GCDH,UPRT,ACACA,SLC26A2,PRPSAP2,ADSSL1,NOS2,ACSBG2,NADK,ATP6V0C,PANK4,NME3,ATP5PB,VPS9D1,ACSF3,AK8,UCK1,MLYCD,KARS,FUK,DHODH,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,PDZD3,ELOVL3,MTHFD2L,CMPK2,NNMT,NME6,DCTD,NUDT2,NAPRT,UPP1,NMNAT1	grey	VSMC_M10
GO:2000144	0.62	0.54	13	25	positive regulation of DNA-templated transcription, initiation	BP	1	ESR1,MED30,SRF,ERCC1,PAXIP1,MITF,ERCC6,CREB1,MED14,MED24,MED1,JUN,NKX2-5	grey	VSMC_M10
GO:1903202	0.62	0.51	20	38	negative regulation of oxidative stress-induced cell death	BP	1	PRKN,NCOA7,ATF4,GPR37,FBXO7,MET,SLC7A11,HTRA2,PDE8A,NFE2L2,NONO,PINK1,MAPK7,PARK7,TSC1,TLDC1,MIR21,NOL3,GPR37L1,TXN	grey	VSMC_M10
GO:0048009	0.62	0.53	14	27	insulin-like growth factor receptor signaling pathway	BP	1	IGF2R,PHIP,GRB10,PLCB1,PIK3R1,NKX3-1,IRS1,GIGYF2,GIGYF1,ZFAND2B,IGFBP4,CILP,GHR,MYORG	grey	VSMC_M10
GO:0005975	0.62	0.41	242	458	carbohydrate metabolic process	BP	1	B4GALT7,B4GALNT1,FUCA2,MIOX,SYNJ2,PRKN,PPARA,PMM1,PRXL2C,AKR1B1,ATF4,MAPK14,GPT,GNMT,CRY1,GNPDA2,PGM5,GALT,ST6GAL2,UXS1,TFAP2B,SLC25A13,GAPDH,CHST10,IPPK,SLC3A1,PRKCE,HAS1,PPP4R3B,SLC4A4,ME1,SLC35A1,ZNF692,BPGM,PLEK,LANCL2,FAM3C,INPP4B,MGAM,DHDH,BRAF,NANP,MTMR2,PYGB,RUBCNL,AKR1A1,GLB1,KHK,EPM2AIP1,NUDT5,DHTKD1,B4GALT2,PRKAG2,XYLB,LCT,GCKR,RBKS,PPP1CB,CSGALNACT1,AKT2,GPD1L,NEU3,PFKP,PGM2L1,C1QTNF1,MDH2,SIRT7,SLC23A2,PDK1,KL,FUT10,PPP1R3B,MTMR7,POFUT1,GPI,NLN,ST8SIA4,GK5,NCOA2,GBE1,B3GNT4,SORBS1,GPD1,P2RX7,MOGS,P2RY1,PTK2B,KCNJ11,PRKAG1,PFKM,SYNJ1,COQ2,ST3GAL6,CHST1,ITPKA,CHID1,GLYCTK,IGF2,GANC,NHLRC1,PHKB,GPLD1,A3GALT2,IRS1,MLEC,SIK1,HYAL1,HYAL3,CPT1A,ZBTB20,ITPK1,INPP5A,ST8SIA2,MST1,PPP1R3E,EGF,PFKFB2,B3GALT1,GPER1,ENO4,PC,ARNT,PPP1R3D,SLC37A4,PER2,TREH,PFKFB4,ACTN3,HDAC4,USF1,NTSR1,MAN1C1,PASK,PHKA2,INPP5J,MLXIPL,DUSP12,GAL3ST3,APOD,FUOM,MDH1B,PDK3,EDEM3,PTH1R,SORD,OVGP1,PLA2G4A,RPE,LANCL3,MOGAT3,HK1,IDH3A,MGAT2,PYGM,B3GALNT1,CHST3,GAL3ST4,PYGL,GNB3,CHST7,PRKAG3,SLC2A2,AC022400.6,GLB1L,STAT3,YDJC,SLC3A2,SLC35A2,ENO3,PPP1R3F,IGFBP4,SLC2A4,TKFC,DDB1,CHST12,IDUA,DGKQ,PSEN1,SLC5A2,PKLR,OGT,PHKA1,LCTL,COX11,CRTC2,LCMT1,ST8SIA5,GLA,HEXA,ADPGK,GM2A,MPI,NCOR1,INSR,ENOSF1,LEPR,ALDOC,IMPA2,PTPN2,FGGY,PMM2,INPP5K,MECP2,TKTL1,GNPTG,ABO,ALDH2,SLC2A6,GBGT1,MLYCD,AGL,CHST5,ST6GALNAC4,ST3GAL2,FUK,HAS3,CTBS,ST6GALNAC5,ACADM,FBP2,OAS1,FABP5,FUT4,ENTPD	grey	VSMC_M10
GO:0055010	0.62	0.50	20	39	ventricular cardiac muscle tissue morphogenesis	BP	1	LY6E,FOXH1,TNNI3,POU4F1,NRG1,TNNC1,DSP,RYR2,PKP2,TNNI1,TGFB2,MYH7,BMPR1A,RBPJ,MED1,ISL1,ENG,NOG,NKX2-5,HEY2	grey	VSMC_M10
GO:0003309	0.62	0.55	11	21	type B pancreatic cell differentiation	BP	1	SMO,CDK6,RFX3,ARNTL,NKX6-1,ZBED6,SIDT2,MEN1,GATA6,PDPK1,WNT5A	grey	VSMC_M10
GO:0035883	0.62	0.55	11	21	enteroendocrine cell differentiation	BP	1	SMO,CDK6,RFX3,ARNTL,NKX6-1,ZBED6,SIDT2,MEN1,GATA6,PDPK1,WNT5A	grey	VSMC_M10
GO:0071676	0.62	0.56	10	19	negative regulation of mononuclear cell migration	BP	1	PLCB1,ADTRP,CD200,SLAMF8,APOD,MIA3,PADI2,CCL2,DUSP1,GCSAM	grey	VSMC_M10
GO:0031579	0.62	0.57	9	17	membrane raft organization	BP	1	PPT1,MAL,DLG1,ANXA2,NAXE,DOCK2,AC138894.1,NPC1,ABCA7	grey	VSMC_M10
GO:0032366	0.62	0.54	12	23	intracellular sterol transport	BP	1	SERAC1,PIP4K2A,OSBP,OSBPL2,SYT7,ANXA2,LDLR,NPC1,VPS4A,MIR27B,LDLRAP1,STARD4	grey	VSMC_M10
GO:0032367	0.62	0.54	12	23	intracellular cholesterol transport	BP	1	SERAC1,PIP4K2A,OSBP,OSBPL2,SYT7,ANXA2,LDLR,NPC1,VPS4A,MIR27B,LDLRAP1,STARD4	grey	VSMC_M10
GO:0051339	0.62	0.52	15	29	regulation of lyase activity	BP	1	GUCA1B,GABBR2,ADGRV1,ORAI1,CAP2,GRM2,MTRR,ISCU,NOS2,PARK7,PALM,GNAI3,CAP1,PDZD3,FXN	grey	VSMC_M10
GO:0071577	0.62	0.55	11	21	zinc ion transmembrane transport	BP	1	SLC39A5,SLC39A4,SLC1A1,SLC39A12,TMEM163,SLC39A13,SLC30A10,SLC30A4,SLC39A6,SLC39A11,SLC39A3	grey	VSMC_M10
GO:1990266	0.62	0.47	39	74	neutrophil migration	BP	1	RAC2,CXCL8,C5AR2,C5AR1,MYD88,NCKAP1L,CCL17,NOD2,GBF1,DNM1L,TGFB2,CD99,SLAMF8,MOSPD2,FCER1G,ADAM8,PIKFYVE,MCU,CXCR2,BST1,DAPK2,S100A8,UMOD,CD74,CCL14,CCL5,CCL7,CCL2,CCL25,VAV1,PIP5K1C,MPP1,BSG,VAV3,CCL16,S100A12,DPP4,CXCL6,CCL22	grey	VSMC_M10
GO:1901185	0.63	0.53	14	27	negative regulation of ERBB signaling pathway	BP	1	ACP4,EGFR,RAB7A,SNX5,PTPRJ,RNF115,CBL,SNX6,ZFYVE28,SOCS4,PSEN1,PTPN2,RNF126,DAB2IP	grey	VSMC_M10

GO:0050867	0.63	0.43	119	226	positive regulation of cell activation	BP	1	CD226,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TNFRSF13C,XRCC6,TTBK1,NCK2,EXOSC3,MSH2,PELI1,PLEK,IL4I1,TLR4,IL15,SPHK2,HMCES,BMI1,NECTIN2,GAB2,MLH1,GLI2,MYD88,PAXIP1,IL15RA,TGFBR2,SHLD1,NCKAP1L,GAS6,PRKDC,SLC7A1,TRAF6,SOX12,TOX,IL1A,CEBPA,MEF2C,IL7,RASGRP1,RIPK2,AP3B1,F2RL1,SOX13,NOD2,ZNF335,CD40,IGF2,LCK,ICOSLG,GPAM,HLX,FGR,RPS6KA1,SNX4,CD28,RUNX3,PPP2R3C,ADAM8,DUSP10,BLOC1S6,PLA2G4A,BCL6,IL12A,VSIR,PTPN6,TNIP2,CD38,BST1,STAT5B,FOXP3,RASAL3,ZBTB1,SHLD2,CARD11,SOX15,TBX21,STX4,ITGAM,ZBTB7B,CHRNB2,IL4R,BTK,CD74,CCL5,CCL2,YES1,NKAP,CD320,VAV1,IL7R,SOCS1,TICAM1,DNAJA3,PRKCZ,VAV3,KARS,STXBP1,AP1G1,BCL10,MIR21,RHOA,HAVCR1,BLOC1S3,SOX4,FADD,DPP4,CD46,THY1,WNT5A,IL33,CD70,TNFSF9,TSLP,EFNB3,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0001504	0.63	0.55	11	21	neurotransmitter uptake	BP	1	PRKN,SLC38A1,SLC6A2,SLC6A3,ATP1A2,PER2,SLC29A2,SLC29A4,CLN8,SLC1A7,PARK7	grey	VSMC_M10
GO:0046879	0.63	0.43	108	206	hormone secretion	BP	1	LRP1,RIMS2,PRKN,GDF9,PLA2G6,PICK1,CRY1,RFX3,TFAP2B,IL11,PRKCE,HMGN3,CYB5R4,BMP8A,EGFR,TRPM4,GIPR,RAF1,C1QTNF1,AIMP1,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,PAX8,OSBP,ARNTL,SCG5,P2RY1,KCNJ11,NNAT,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX3-1,NKX6-1,ACVR1C,CRY2,SPP1,ZBED6,SIRT4,GPLD1,IRS1,HDAC1,PPP3CA,CPT1A,TRPV4,SLC9B2,ADRA2A,TCIRG1,TCF7L2,SNAP23,KCNB1,PFKFB2,GPER1,RAB11FIP2,AGT,PER2,OSM,STX1A,SNX4,PASK,GLUL,SIDT2,SLC16A1,KLF7,CREB1,VGF,ENY2,ABCA12,MCU,PPP3CB,CAMK2G,PTPRN,CD38,MPC2,ILDR2,INHA,SYT7,NLGN2,CPLX1,TARDBP,STX4,RAB8B,UBE2Q1,SYTL4,GPR68,BTK,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,NADK,BAIAP3,PARK7,LRRC8A,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,LIF,UQCC2	grey	VSMC_M10
GO:0070098	0.63	0.50	21	40	chemokine-mediated signaling pathway	BP	1	CXCL8,OXSR1,ACKR2,ROBO1,PTK2B,CCL17,CMKLR1,CIB1,THPO,CXCR2,PADI2,CCL14,CCL5,CCL7,CCL2,CCL25,CCL16,GPR35,CCR10,CXCL6,CCL22	grey	VSMC_M10
GO:0009173	0.63	0.59	7	13	pyrimidine ribonucleoside monophosphate metabolic process	BP	1	DPYS,CMPK1,UPB1,UPRT,UCK1,DHODH,UPP1	grey	VSMC_M10
GO:0046049	0.63	0.59	7	13	UMP metabolic process	BP	1	DPYS,CMPK1,UPB1,UPRT,UCK1,DHODH,UPP1	grey	VSMC_M10
GO:0034104	0.63	0.58	8	15	negative regulation of tissue remodeling	BP	1	TNFAIP3,TNFRSF11B,P2RX7,GPR137B,UBASH3B,AGT,GPR137,CD38	grey	VSMC_M10
GO:0070372	0.63	0.43	111	211	regulation of ERK1 and ERK2 cascade	BP	1	LRP1,SEMA6A,FRS2,AGER,FBLN1,ROS1,PRXL2C,TEK,WNK2,FPR2,MTURN,NOD1,BMPER,EPHA7,ITGB1BP1,VRK3,YWHAZ,EGFR,TLR4,FGF21,BRAF,SPRY1,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,SPRY2,ARRB1,NEK10,SPRED3,DUSP6,NRG1,GAS6,SIRT3,MFHAS1,APIP,ST5,EPHB1,HAND2,FBXW7,P2RY1,PTK2B,RASGRP1,RAPGEF2,CCL17,TIAM1,RIPK2,F2RL1,F2R,NQO2,GCNT2,NOD2,DSTYK,TRPV4,SLC30A10,TBC1D10C,GPER1,CIB1,THPO,PDE8A,DLG1,DUSP10,RAP1B,FN1,PTPN6,GPBAR1,FGFR3,RGS14,FGFR4,SYNJ2BP,FGF18,MAPK3,MAP2K1,TNIP1,GAREM1,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,PTPN2,SERPINF2,PRKCZ,ATP6AP1,ABCA7,DAB2IP,MIR21,MIR222,MIR23A,MIR27B,MIR24-1,MIR27A,FGA,CCL16,CHRNA10,DUSP26,DUSP1,DUSP4,C3orf33,LIF,HRAS,STYX,MAP2K7,FGF1,C1QL4,HAVCR2,CCL22,PDGFD	grey	VSMC_M10
GO:0098900	0.63	0.50	20	39	regulation of action potential	BP	1	TRPM4,SLC8A2,SCN5A,DSP,RYR2,PKP2,KCNJ2,KCNB1,ANK2,SLC9A1,NTSR1,NOS1AP,DLG1,CHRNB2,CALM1,DSG2,FMR1,RNF207,GPR35,HCN4	grey	VSMC_M10
GO:0006873	0.63	0.41	233	444	cellular ion homeostasis	BP	1	SLC39A5,NEDD4L,LRP1,ESR1,SLC12A2,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,CKB,TMPRSS6,SLC39A4,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,PRKCE,TNNI3,FPR2,IBTK,SLC4A4,LPAR1,PPT1,SLC31A2,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,AQP11,ATP1A3,ACKR2,SLC24A3,C1QTNF1,SLC4A7,TMEM106B,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,HPX,RASA3,NCOA4,MICU3,ATP6V1H,TM9SF4,IL1A,IMMT,C19orf12,P2RX3,PLCE1,SLC9A9,RYR3,TMBIM6,P2RX7,HVCN1,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,ABCC2,PKD2,CASQ2,MCUR1,SLC12A5,CD40,RYR2,SLC41A1,SLC4A10,RAP1GDS1,TRPM1,SPPL3,LCK,KCNJ2,TESMIN,SLC9B1,TRPV4,TMEM9,SLC30A10,TCIRG1,GNA13,ISCU,CMKLR1,MCUB,HJV,SLC9A8,UBASH3B,DISC1,ANK2,GPER1,SLAMF8,RHCG,TRPM8,PDZD8,AGT,ATP1A2,SLC9A1,CASQ1,NTSR1,XPR1,CLIC4,FZD9,TMCO1,PTH1R,SLC30A4,FIS1,CEMIP,ABL2,CDH23,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,SLC9A7,ATP6V0A1,ABCB6,TRPM7,ATP1B1,CD38,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP13A2,FTH1,HAP1,DLG4,CYB561A3,ATP1B2,FAM155B,PSEN1,CACNA1A,MAPK3,AC138894.1,ATP2A1,CD19,SMAD3,CLN6,NOX5,CALM1,SNAPIN,S100A8,PRKCB,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,C7,PTGER4,SLC25A23,MAIP1,TMEM199,SLC46A1,SLC9A6,NUBP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,ATP6AP1,GPR157,SYPL2,CYBA,JPH3,ATP2C2,SLC30A7,FRRS1,LCN2,MCOLN3,PTGFR,SLC9A5,MIR199	grey	VSMC_M10
GO:0043248	0.63	0.61	6	11	proteasome assembly	BP	1	PSMD5,ECPAS,POMP,PSMD10,PSMG2,PSMG4	grey	VSMC_M10
GO:0019751	0.63	0.46	46	88	polyol metabolic process	BP	1	CYP27B1,MIOX,SYNJ2,AKR1B1,SPTLC1,IPPK,INPP4A,PLEK,INPP4B,SPHK2,DHFR,MTMR2,ITPKC,ACER3,SPTLC3,MTMR7,ASAH1,GK5,CYP2R1,P2RY1,PTK2B,SPR,SYNJ1,COQ2,ITPKA,ITPK1,INPP5A,GPER1,IP6K2,NTSR1,INPP5J,PTH1R,SORD,PLA2G4A,MOGAT3,CYP27A1,GCH1,TKFC,IMPA2,INPP5K,MECP2,MINPP1,ACER2,INPP1,SGPP1,PCBD2	grey	VSMC_M10
GO:0019674	0.63	0.54	11	21	NAD metabolic process	BP	1	NMRK1,GPD1L,PFKP,GPD1,PFKM,ACTN3,HK1,CD38,NADK,NQO1,TIGAR	grey	VSMC_M10

GO:0060271	0.63	0.42	139	266	cilium assembly	BP	1	ONECUT2,AVIL,TBC1D30,ATAT1,KIF3A,TBC1D32,UBE2B,ASAP1,LRRC6,MAPK15,IFT74,CFAP69,RFX3,PTPDC1,RAB23,DYNC2LI1,CEP162,TMEM17,WDR92,FUZ,IQUB,ATG5,ARMC2,MAPRE1,ARMC4,INTU,SPATA6,TTC26,BBS7,DRC1,RSPH6A,GALNT11,FBF1,PIBF1,IFT172,FOXJ1,WDR60,TTLL3,CCDC13,ABCC4,MKKS,CEP290,SPEF1,TMEM80,KIF3B,RILPL1,RILPL2,CEP70,PARVA,CEP250,CCDC66,TCTN3,IFT81,CCDC113,CFAP20,CCDC65,TMEM67,IFT52,RPGRIP1L,DNAH1,DNAH5,ZNF423,GBF1,NEURL1,CFAP43,ZMYND10,ARMC9,CFAP46,TTBK2,CLCN4,ALPK1,JHY,DISC1,OFD1,RAB17,TMEM237,TRAF3IP1,BBS1,LAMA5,CDKL5,SEPT2,LIMK2,CFAP161,TTC12,TOGARAM1,EHD1,DNAAF2,SPAG16,FAM149B1,HTT,CFAP70,STK36,GORAB,CEP126,SNAP29,EXOC5,TTC25,RAB8A,SDCCAG8,HAP1,DNAAF4,CPLANE2,MNS1,WDR19,TMEM138,ATP6V1D,BBOF1,CNTROB,TMEM107,CCDC151,DYNLL2,MKS1,DNM2,TEKT3,IFT20,SPEF2,CFAP53,C16orf71,RILP,CLUAP1,WRAP73,TPGS1,CDK10,CELSR2,CDC14A,TMEM231,FNBP1L,HYDIN,ODF2L,WDR63,C5orf30,TCTN2,HYLS1,SNX10,C2CD3,CC2D2B,C7orf43,ATXN10,BBS10	grey	VSMC_M10
GO:0051648	0.63	0.43	80	154	vesicle localization	BP	1	MYO1A,AP3S1,KIF5A,PRKN,KIF3A,FAM91A1,EXOC4,MAPK15,BRSK1,STARD3NL,BBS7,MYO7B,CLASP2,MYO7A,AP3M2,KIF5C,MKKS,LIN7A,TMEM230,KIF3B,RASGRP1,ARFGAP2,EXOC6B,SYNJ1,AP3B1,DTNBP1,KIF13A,GBF1,BICDL1,KLHL12,TRIP11,PEF1,TCIRG1,PDCD6,SNAP23,SHROOM2,AP1AR,MLPH,RAB17,CNIH2,LIMK2,TANC2,SPG11,BLOC1S6,ITGA4,MAP4K2,MREG,HTT,RAB3A,PINK1,SYN1,SNAP29,AP3M1,KIF1C,HAP1,SLC2A4,NLGN2,PSEN1,SYT11,TMED10,TRIM46,NDEL1,AC138894.1,RAB11A,SNAPIN,DNM2,AP1M2,MYO1D,C17orf75,PPP6C,MYO1F,MYO5B,BICDL2,PRKCZ,IKBKG,TPGS1,FNBP1L,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0070266	0.63	0.52	15	29	necroptotic process	BP	1	PELI1,RIPK1,DNM1L,ITPK1,SPATA2,FZD9,YBX3,PYGL,BIRC3,TRPM7,OGT,MIR22,FADD,CASP8,PPIF	grey	VSMC_M10
GO:1905048	0.63	0.57	8	15	regulation of metallopeptidase activity	BP	1	LRP1,SVBP,DDRGK1,SORL1,STAT3,MIR199A1,MIR21,MIR24-1	grey	VSMC_M10
GO:0043551	0.63	0.49	24	47	regulation of phosphatidylinositol 3-kinase activity	BP	1	AGAP2,PTK2,TEK,KIT,FPR2,WDR91,CCKBR,FLT1,PIK3R1,SLA2,PTK2B,NOD2,IRS1,FGR,RUBCN,PIK3IP1,FGFR3,SOCS4,SOCS7,CD19,PIK3R5,SOCS1,VAV3,DAB2IP	grey	VSMC_M10
GO:0010906	0.63	0.45	50	96	regulation of glucose metabolic process	BP	1	PRKN,PPARA,GPT,GNMT,CRY1,PPP4R3B,ZNF692,FAM3C,RUBCNL,KHK,EPM2AIP1,GCKR,PPP1CB,AKT2,C1QTNF1,SIRT7,PDK1,PPP1R3B,NLN,NCOA2,SORBS1,IGF2,GPLD1,IRS1,SIK1,MST1,PPP1R3E,PFKFB2,PPP1R3D,ACTN3,PASK,DUSP12,PDK3,GNB3,PPP1R3F,IGFBP4,DDB1,DGKQ,OGT,COX11,LCMT1,INSR,LEPR,PTPN2,INPP5K,MLYCD,ACADM,TIGAR,NNMT,ARPP19	grey	VSMC_M10
GO:0051591	0.63	0.46	35	68	response to cAMP	BP	1	NME1,TEK,PNPT1,AREG,AQP1,AANAT,THBD,GPD1,PTK2B,RAPGEF2,STC1,RAPGEF3,PKD2,DMTN,SRD5A1,SLC6A3,RAP1B,DUOX1,VGF,CPS1,FDX1,PTPRN,DGKQ,PKLR,FOS,CITED1,PPARGC1B,SREBF1,JUN,INPP5K,BSG,ASS1,HSPA5,DUSP1,HCN4	grey	VSMC_M10
GO:0015695	0.63	0.54	11	21	organic cation transport	BP	1	SLC22A4,CHRNA3,SEC14L1,SLC25A26,SLC38A2,SLC25A20,SLC25A42,SLC29A4,PSEN1,RALBP1,SLC22A5	grey	VSMC_M10
GO:0055092	0.63	0.47	33	63	sterol homeostasis	BP	1	APOM,TTC39B,ABCG5,ABCG8,NR1H2,APOB,CNBP,TSKU,COMMD9,SOAT2,CYP7A1,CYP7B1,LIMA1,EPHX2,NR1H3,MYLIP,ABCA5,NR5A2,FABP4,GRAMD1B,ABCB11,ABCG4,SOAT1,EHD1,FGFR4,LIPC,LDLR,ACSM3,NPC1,TMEM97,MIR27B,MIR33B,LDLRAP1	grey	VSMC_M10
GO:0031365	0.63	0.53	13	25	N-terminal protein amino acid modification	BP	1	AANAT,HHAT,METAP1D,NMT1,NAA40,NAA30,PPM1A,CREBBP,NAA60,NAA10,SOX4,PDF,MAP6D1	grey	VSMC_M10
GO:0021695	0.63	0.49	20	39	cerebellar cortex development	BP	1	GLI1,UQCRQ,AGTPBP1,SMO,WHRN,GLI2,B4GALT2,CLP1,FAIM2,LDB1,TTBK2,TTC21B,SPTBN2,MAP2K1,LHX1,SEZ6,AARS,HSPA5,GRID2,CEND1	grey	VSMC_M10
GO:1903539	0.63	0.51	15	29	protein localization to postsynaptic membrane	BP	1	ADAM22,DAG1,DLG1,NSG1,GRIPAP1,RAB8A,DLG4,IQSEC2,CPLX1,STX1B,RAB11A,ARHGAP44,PRKCZ,CACNG7,HRAS	grey	VSMC_M10
GO:0010714	0.63	0.54	11	21	positive regulation of collagen metabolic process	BP	1	HDAC2,F2R,AMELX,VSIR,WNT4,SUCO,LARP6,SERPINF2,ENG,RGCC,CBX8	grey	VSMC_M10
GO:0035567	0.63	0.46	35	68	non-canonical Wnt signaling pathway	BP	1	FZD6,RSPO3,CSNK1E,DAAM2,PTK7,FZD1,ROR2,SFRP4,WNT11,SPEF1,RYK,FZD3,TIAM1,VANGL1,PRICKLE1,NKD1,ZNRF3,DVL3,FZD7,GRHL3,FZD9,FZD5,WNT4,DAAM1,ARHGEF19,DVL2,MKS1,CCDC88C,NLK,GPC3,CELSR2,RHOA,WNT5A,LBX2,CELSR3	grey	VSMC_M10
GO:0006633	0.63	0.44	56	107	fatty acid biosynthetic process	BP	1	LTC4S,QKI,MCAT,HSD17B8,HACD4,NR1H2,APOC1,PRKAG2,PIBF1,ELOVL1,TRIB3,CYP7A1,ELOVL7,THNSL2,CBR4,PRKAG1,NR1H3,ERLIN1,PRKAB1,ABHD2,MECR,HACD2,LPGAT1,MLXIPL,SCAP,PLA2G4A,ACADL,ACSBG1,PECR,PRKAG3,DAGLB,FADS3,LIAS,ACADVL,TECR,DEGS1,LIPC,ALOXE3,HACD3,NDUFAB1,ACSM3,ACACA,CD74,ABHD3,ACSBG2,DECR2,ACSF3,MLYCD,PTGES2,ABCD3,ACOT4,FABP5,FADS6,ELOVL3,PTGES,INSIG2	grey	VSMC_M10

GO:0006650	0.63	0.42	135	257	glycerophospholipid metabolic process	BP	1	PIP4K2C,ABHD16A,SYNJ2,SERAC1,AGPAT4,AGPAT1,PNPLA3,PLA2G6,GPAA1,CWH43,INPP4A,TMEM246,TMEM86B,PIGF,MBOAT7,PLEK,NR1H2,MBOAT2,LPIN1,INPP4B,FIG4,MTMR2,PIP4K2A,NAPEPLD,HADHA,SELENOI,ABHD5,APOC1,TAMM41,ITPKC,PIP4P1,MTMR14,PLCB1,PGAP2,CRLS1,CDS2,NR1H4,MTMR7,ABHD6,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,CHRM5,MTMR9,SLA2,NR1H3,SERINC5,SYNJ1,CDS1,ITPKA,PIGT,PLA2G4B,GPLD1,LPCAT1,PGAP1,GPAM,CHKA,PLA1A,ACP6,INPP5A,ABHD4,AJUBA,PITPNM1,MTMR11,GNPAT,DGKD,PIGM,BMX,FAM126B,IP6K2,LPGAT1,PIGV,MTMR3,THEM5,PCYT1A,INPP5J,PIGX,PIGZ,PISD,DGKG,PIKFYVE,PLA2G4A,SACM1L,LPCAT3,ABHD12B,PIGC,PLCD4,SMPD4,SOCS4,PLA2G16,PI4KA,SLC27A1,ABHD8,PGAP3,PIGH,PI4K2B,LIPC,SOCS7,DGKQ,GDPD3,AC138894.1,DGKE,TTC7B,LDLR,GDPD1,PIGL,GDE1,CSF1R,ABHD3,PNPLA6,MPPE1,IMPA2,MTMR12,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,ABCA3,MECP2,AGPAT2,PIP5KL1,PLA2G15,FABP5,PEMT,PYURF,LCLAT1,PIGB,PIGA,INPP1,PTPMT1,DNAJC19,CDIPT	grey	VSMC_M10
GO:0045580	0.63	0.45	51	98	regulation of T cell differentiation	BP	1	HLA-DRA,TCF7,SLC46A2,IL4I1,IL15,CLPTM1,GLI2,FOXJ1,TGFBR2,NCKAP1L,SOX12,TOX,ZC3H8,CAMK4,TMEM131L,IL7,RASGRP1,RIPK2,AP3B1,SOX13,HLX,CD28,RUNX3,ADAM8,DUSP10,BCL6,VSIR,RC3H1,TNFSF18,LAG3,STAT5B,FOXP3,ZBTB1,CARD11,TBX21,ZBTB7B,IL4R,CD74,NKAP,IL7R,PTPN2,SOCS1,DROSHA,PRKCZ,MIR21,RHOA,SOX4,CD46,FGL2,TNFSF9,RC3H2	grey	VSMC_M10
GO:0033144	0.63	0.51	16	31	negative regulation of intracellular steroid hormone receptor signaling pathway	BP	1	CNOT2,FOXH1,CRY1,PHB,FOXP1,CYP7B1,ZNF366,ARNTL,CNOT1,CRY2,VPS18,HDAC1,PIAS2,NCOR1,ISL1,RHOA	grey	VSMC_M10
GO:0005976	0.63	0.45	43	83	polysaccharide metabolic process	BP	1	GNMT,HAS1,MGAM,PYGB,RUBCNL,KHK,EPM2AIP1,PRKAG2,PPP1CB,CSGALNACT1,AKT2,PPP1R3B,GBE1,B3GNT4,SORBS1,PFKM,CHST1,IGF2,NHLRC1,PHKB,IRS1,PPP1R3E,EGF,PPP1R3D,PER2,PASK,PHKA2,GAL3ST3,PYGM,PYGL,CHST7,PRKAG3,AC022400.6,PPP1R3F,PHKA1,INSR,LEPR,INPP5K,AGL,HAS3,ACADM,PPP1R1A,HS2ST1	grey	VSMC_M10
GO:0034377	0.63	0.55	10	19	plasma lipoprotein particle assembly	BP	1	APOM,NR1H2,APOB,APOC1,SOAT2,SOAT1,ZDHHC8,LPCAT3,ABCA7,PLAGL2	grey	VSMC_M10
GO:0070131	0.63	0.57	8	15	positive regulation of mitochondrial translation	BP	1	RMND1,MRPS27,RPUSD4,RCC1L,COA3,RPUSD3,UQCC2,TRMT10C	grey	VSMC_M10
GO:0045981	0.63	0.51	15	29	positive regulation of nucleotide metabolic process	BP	1	PPARA,PRXL2C,GUCA1B,SLC4A4,GPD1,P2RX7,ZBTB20,ARNT,MLXIPL,PINK1,STAT3,PSEN1,INSR,NOS2,ENTPD5	grey	VSMC_M10
GO:1900544	0.63	0.51	15	29	positive regulation of purine nucleotide metabolic process	BP	1	PPARA,PRXL2C,GUCA1B,SLC4A4,GPD1,P2RX7,ZBTB20,ARNT,MLXIPL,PINK1,STAT3,PSEN1,INSR,NOS2,ENTPD5	grey	VSMC_M10
GO:0007212	0.63	0.51	16	31	dopamine receptor signaling pathway	BP	1	SLC1A1,VPS35,ALK,DTNBP1,CALY,GNB5,NSG1,GNAL,GNB1,GNA15,PALM,GNAI3,RGS4,GNA14,GNG2,ARPP19	grey	VSMC_M10
GO:0045453	0.63	0.48	26	50	bone resorption	BP	1	TNFAIP3,TNFRSF11B,RAC2,EGFR,NCDN,TRAF6,IL7,P2RX7,PTK2B,SPP1,LRRK1,TCIRG1,GPR137B,UBASH3B,ADAM8,PTH1R,GPR137,CD38,RAB3D,CSF1R,PPARGC1B,ATP6AP1,DEF8,CA2,BGLAP,SNX10	grey	VSMC_M10
GO:0010989	0.63	0.66	4	7	negative regulation of low-density lipoprotein particle clearance	BP	1	MYLIP,MIR199A1,MIR27B,MIR27A	grey	VSMC_M10
GO:1903580	0.63	0.51	15	29	positive regulation of ATP metabolic process	BP	1	PPARA,PRXL2C,SLC4A4,GPD1,P2RX7,ZBTB20,ARNT,ACTN3,MLXIPL,PINK1,STAT3,PSEN1,INSR,ENTPD5,BEND3	grey	VSMC_M10
GO:0035774	0.63	0.52	13	25	positive regulation of insulin secretion involved in cellular response to glucose stimulus	BP	1	LRP1,PLA2G6,TRPM4,OSBP,GPLD1,PPP3CB,MPC2,STX4,GPR68,OXCT1,NADK,BAIAP3,CRH	grey	VSMC_M10
GO:0034367	0.63	0.54	11	21	protein-containing complex remodeling	BP	1	APOM,TAF8,APOB,APOC1,NR1H4,PLTP,ABCA5,GTF2E1,AGT,LIPC,MPO	grey	VSMC_M10
GO:0030194	0.64	0.55	9	17	positive regulation of blood coagulation	BP	1	ENPP4,THBD,F2R,ANO6,DMTN,USF1,NFE2L2,F12,SERPINF2	grey	VSMC_M10
GO:1900048	0.64	0.55	9	17	positive regulation of hemostasis	BP	1	ENPP4,THBD,F2R,ANO6,DMTN,USF1,NFE2L2,F12,SERPINF2	grey	VSMC_M10
GO:0007205	0.64	0.54	11	21	protein kinase C-activating G protein-coupled receptor signaling pathway	BP	1	LRP1,PICK1,DGKI,F2R,GAP43,DGKD,DGKG,CHRM1,DGKQ,DGKE,BDKRB1	grey	VSMC_M10
GO:0001893	0.64	0.51	15	29	maternal placenta development	BP	1	CYP27B1,PTN,PRDX3,VDR,STC1,SPP1,DEDD,MEN1,CTSV,MAPK1,MAPK3,EPOR,BSG,TCF23,LIF	grey	VSMC_M10
GO:0062207	0.64	0.45	40	77	regulation of pattern recognition receptor signaling pathway	BP	1	TNFAIP3,USP15,ESR1,HSPA1B,GRAMD4,LRRC14,NINJ1,RTN4,ANKRD17,SLC46A2,PELI1,RSAD2,TLR4,PUM2,CD300LF,SEC14L1,NPLOC4,IRF7,MFHAS1,OTUD4,NR1H3,F2RL1,NOD2,RAB7B,OASL,TLR5,NLRX1,DDX3X,BIRC3,GPS2,TKFC,WDFY1,TSPAN6,RIOK3,GPR108,PDPK1,CYBA,GFI1,DAB2IP,ZCCHC3	grey	VSMC_M10
GO:0061013	0.64	0.43	75	144	regulation of mRNA catabolic process	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,PNLDC1,CSDC2,AGO2,TNRC6B,TUT7,GTPBP1,MAPK14,EXOSC3,PNPT1,TUT4,PUM2,TRAF3IP2,ZC3HAV1,DHX34,FASTK,MLH1,MYD88,TNRC6C,LSM1,PKP3,PAN3,CNOT1,CELF1,CNOT6L,FTO,TENT5C,TENT4B,RBM24,DIS3L2,AXIN2,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,EIF4ENIF1,YBX3,RC3H1,UPF1,SLC11A1,RBM10,SAMD4A,POLR2G,SCGB1A1,NT5C3B,DCP1B,FXR2,TARDBP,TOB1,TENT5D,TNRC6A,CNOT8,LARP1,ALKBH5,PARN,FMR1,METTL16,PLEKHN1,CIRBP,TRAF2,METTL14,NANOS1,CACNG7,YBX1,ZFP36L2,TENT5A,RC3H2,EXOSC5	grey	VSMC_M10
GO:0002381	0.64	0.48	25	48	immunoglobulin production involved in immunoglobulin-mediated immune response	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,EXOSC3,MSH2,TRAF3IP2,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,GAPT,NBN,CD40,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,BTK,SUPT6H,RNF8	grey	VSMC_M10
GO:0048566	0.64	0.52	13	25	embryonic digestive tract development	BP	1	VPS52,SIX2,CXCL8,GLI2,OVOL2,RARB,SALL1,TGFB2,HLX,ALDH1A2,RBPMS2,STRA6,FOXF1	grey	VSMC_M10
GO:0045197	0.64	0.49	19	37	establishment or maintenance of epithelial cell apical/basal polarity	BP	1	PTK7,LIN7B,DLG2,WNT11,ANK1,LIN7A,SYNE4,TCF15,DLG1,MARK2,SYNJ2BP,MYO9A,CAMSAP3,LAMA1,IFT20,FOXF1,RHOA,PDZD11,WNT5A	grey	VSMC_M10

GO:0060291	0.64	0.46	32	62	long-term synaptic potentiation	BP	1	PRRT1,AGER,NTRK2,SLC1A1,CRHR2,PTN,GRIN2D,SLC8A2,PRNP,PLK2,FAM107A,PTK2B,MME,EIF2AK4,IGSF11,STAU1,NFATC4,YTHDF1,CREB1,TNR,MPP2,CRTC1,MAPK1,NSG1,EPHA4,RGS14,STX4,CYP46A1,PRKCZ,MECP2,CRH,LRRTM2	grey	VSMC_M10
GO:0032088	0.64	0.46	35	67	negative regulation of NF-kappaB transcription factor activity	BP	1	TNFAIP3,LRRC14,CDKN2A,CAT,MTURN,PELI1,ANXA4,FAF1,FOXJ1,IRAK2,ARRB1,NFKBIB,SETD6,NLRC5,OTULIN,NOD2,CD200,CMKLR1,NWD1,FOXP3,PYDC1,MAP2K5,TRIM37,PSMD10,TRAF3,PIAS4,GFI1,DAB2IP,MIR21,MIR27A,RWDD3,COMMD6,DDIT3,COMMD7,HAVCR2	grey	VSMC_M10
GO:1905521	0.64	0.51	15	29	regulation of macrophage migration	BP	1	PTK2,AKIRIN1,C5AR1,MTUS1,PTK2B,CD200,TRPV4,CMKLR1,SLAMF8,TNFSF18,MAPK1,MAPK3,CCL5,CSF1R,MIR24-1	grey	VSMC_M10
GO:0090026	0.64	0.58	7	13	positive regulation of monocyte chemotaxis	BP	1	FPR2,ANO6,MOSPD2,TNFSF18,S100A14,CCL5,DEFB124	grey	VSMC_M10
GO:0071398	0.64	0.51	15	29	cellular response to fatty acid	BP	1	NME1,UCP1,NR1H4,SMARCD1,IRS1,CPT1A,PDK3,CREB1,CPS1,XRCC5,KCNK4,LDLR,SREBF1,ASS1,CLDN1	grey	VSMC_M10
GO:0009913	0.64	0.43	62	120	epidermal cell differentiation	BP	1	GLI1,CYP27B1,PTCH1,IFT74,CD109,HOXA7,MYCL,WHRN,GRHL1,SFRP4,MYCN,INTU,HDAC2,ERCC2,ERCC3,PTCH2,EVPL,MYO7A,SCEL,OVOL2,SLC4A7,JAG1,LRTOMT,AP000812.5,MAFG,ASAH1,FLNB,CASP3,PLS1,USH1C,VDR,SRSF6,DSP,STK4,PPHLN1,HDAC1,TGM1,KDF1,SFN,CLIC4,STRC,OVOL1,KLF7,H2AFY2,ABCA12,SAV1,RBPJ,MED1,MAP2K1,KEAP1,BCL11B,GATA6,TMEM132E,JAG2,MCOLN3,MIR125B1,WNT5A,DNASE1L2,ZBED2,EREG,SGPP1,HEY2	grey	VSMC_M10
GO:0048512	0.64	0.51	14	27	circadian behavior	BP	1	BTBD9,NR1D2,AHCY,NCOA2,SRD5A1,CIART,USP2,C3orf70,CHRNB2,NCOR1,PER3,GPR157,ZFHX3,CRH	grey	VSMC_M10
GO:0010592	0.64	0.52	12	23	positive regulation of lamellipodium assembly	BP	1	AVIL,RAC2,AKIRIN1,PIK3R1,PLCE1,CYFIP1,AUTS2,WASF2,HDAC4,NCKAP1,DNM2,CARMIL2	grey	VSMC_M10
GO:0072503	0.64	0.40	160	306	cellular divalent inorganic cation homeostasis	BP	1	SLC39A5,LRP1,ESR1,SMDT1,BAK1,MCHR1,GPR20,PLA2G6,SLC39A4,SLC25A27,SLC1A1,S1PR3,PRKCE,TNNI3,FPR2,IBTK,LPAR1,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ACKR2,SLC24A3,C1QTNF1,TMTC4,RYR1,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,RASA3,MICU3,IMMT,C19orf12,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,AP3B1,RMDN3,F2RL1,F2R,PKD2,CASQ2,MCUR1,CD40,RYR2,SLC41A1,RAP1GDS1,TRPM1,SPPL3,LCK,TRPV4,SLC30A10,TCIRG1,GNA13,CMKLR1,MCUB,UBASH3B,DISC1,ANK2,GPER1,TRPM8,PDZD8,AGT,ATP1A2,CASQ1,NTSR1,FZD9,TMCO1,PTH1R,SLC30A4,FIS1,CEMIP,ABL2,CDH23,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,TRPM7,ATP1B1,CD38,ATP13A2,HAP1,DLG4,FAM155B,PSEN1,CACNA1A,AC138894.1,ATP2A1,CD19,SMAD3,CALM1,S100A8,PRKCB,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,PTGER4,SLC25A23,MAIP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,GPR157,SYPL2,CYBA,JPH3,ATP2C2,SLC30A7,MCOLN3,PTGFR,MIR199A1,KCNK3,DMD,MT1X,GPR35,NOL3,CHRNA10,CCR10,JPH2,THY1,WNT5A,DDIT3	grey	VSMC_M10
GO:0009129	0.64	0.55	9	17	pyrimidine nucleoside monophosphate metabolic process	BP	1	DPYS,CMPK1,UPB1,UPRT,NT5M,UCK1,DHODH,DCTD,UPP1	grey	VSMC_M10
GO:0071624	0.64	0.53	11	21	positive regulation of granulocyte chemotaxis	BP	1	RAC2,CXCL8,C5AR1,NCKAP1L,DNM1L,MOSPD2,MCU,CXCR2,DAPK2,S100A14,CD74	grey	VSMC_M10
GO:0007204	0.64	0.41	101	194	positive regulation of cytosolic calcium ion concentration	BP	1	LRP1,ESR1,BAK1,MCHR1,GPR20,PLA2G6,S1PR3,PRKCE,FPR2,IBTK,LPAR1,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,PTGIR,GIPR,CACNB2,ACKR2,C1QTNF1,RYR1,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,RASA3,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,TPCN1,SLC8B1,F2RL1,F2R,PKD2,CASQ2,RYR2,TRPM1,SPPL3,LCK,TRPV4,GNA13,CMKLR1,UBASH3B,ANK2,GPER1,AGT,ATP1A2,CASQ1,NTSR1,PTH1R,FIS1,CEMIP,ABL2,PTPN6,CXCR2,GNG3,HTT,PTGDR,PTGER2,CD38,HAP1,DLG4,FAM155B,CACNA1A,CD19,CALM1,BDKRB1,NMUR2,TRPV2,HRH4,PTGER4,GNB1,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,GPR157,CYBA,JPH3,MCOLN3,PTGFR,MIR199A1,DMD,GPR35,NOL3,CHRNA10,CCR10,JPH2,THY1,DDIT3	grey	VSMC_M10
GO:0006479	0.64	0.42	77	148	protein methylation	BP	1	ARMT1,SNW1,PHF1,PRDM4,CAMKMT,RNF20,SETD7,SETDB2,EED,IWS1,SUV39H2,KDM4A,PAXIP1,DPY30,SIRT7,CHTOP,NSD3,NDUFAF7,ASH2L,BTG1,NR1H4,EEF1AKMT1,DNMT3B,SMYD1,PRMT9,SETD6,KMT2D,RTF1,PRMT3,WDR82,ZNF335,JARID2,RBBP5,FAM173B,HEMK1,AUTS2,EEF1AKMT2,SETD2,TET1,SNRPD3,BCOR,MEN1,WDR61,VCPKMT,NELFA,DYDC1,PRDM2,NSD1,SETD1A,PAGR1,OGT,RAB3D,LCMT1,SETD3,SUZ12,SUPT6H,CXXC1,CREBBP,DOT1L,MECP2,PRDM16,CHD5,MTF2,GFI1,PRMT7,CTCF,PRMT6,METTL18,SETDB1,PRDM6,ARID4A,BEND3,SMYD3,METTL21A,ZNF304,NNMT,N6AMT1	grey	VSMC_M10
GO:0008213	0.64	0.42	77	148	protein alkylation	BP	1	ARMT1,SNW1,PHF1,PRDM4,CAMKMT,RNF20,SETD7,SETDB2,EED,IWS1,SUV39H2,KDM4A,PAXIP1,DPY30,SIRT7,CHTOP,NSD3,NDUFAF7,ASH2L,BTG1,NR1H4,EEF1AKMT1,DNMT3B,SMYD1,PRMT9,SETD6,KMT2D,RTF1,PRMT3,WDR82,ZNF335,JARID2,RBBP5,FAM173B,HEMK1,AUTS2,EEF1AKMT2,SETD2,TET1,SNRPD3,BCOR,MEN1,WDR61,VCPKMT,NELFA,DYDC1,PRDM2,NSD1,SETD1A,PAGR1,OGT,RAB3D,LCMT1,SETD3,SUZ12,SUPT6H,CXXC1,CREBBP,DOT1L,MECP2,PRDM16,CHD5,MTF2,GFI1,PRMT7,CTCF,PRMT6,METTL18,SETDB1,PRDM6,ARID4A,BEND3,SMYD3,METTL21A,ZNF304,NNMT,N6AMT1	grey	VSMC_M10

GO:0010830	0.64	0.49	17	33	regulation of myotube differentiation	BP	1	MAML1,MAPK14,MAMSTR,LMOD3,SMYD1,NLN,RBM24,BDNF,SIK1,ACTN3,HDAC4,BHLHA15,FBXO22,PIEZO1,PLPP7,NKX2-5,RBM38	grey	VSMC_M10
GO:0034656	0.64	0.54	10	19	nucleobase-containing small molecule catabolic process	BP	1	APOBEC3H,GDA,GALT,ENPP4,CDADC1,AHCY,ENTPD4,MGAT1,UPB1,UPP1	grey	VSMC_M10
GO:0001835	0.64	0.52	12	23	blastocyst hatching	BP	1	CCDC62,ZBED6,PLPP4,BCOR,AKAP3,ARHGDIG,SLC25A34,PPP4R4,CMTM3,PEMT,C6orf141,ST8SIA6	grey	VSMC_M10
GO:0035188	0.64	0.52	12	23	hatching	BP	1	CCDC62,ZBED6,PLPP4,BCOR,AKAP3,ARHGDIG,SLC25A34,PPP4R4,CMTM3,PEMT,C6orf141,ST8SIA6	grey	VSMC_M10
GO:0071684	0.64	0.52	12	23	organism emergence from protective structure	BP	1	CCDC62,ZBED6,PLPP4,BCOR,AKAP3,ARHGDIG,SLC25A34,PPP4R4,CMTM3,PEMT,C6orf141,ST8SIA6	grey	VSMC_M10
GO:0035821	0.64	0.45	39	75	modulation of process of other organism	BP	1	YTHDC2,SNW1,IGF2R,PRKN,ATG5,NAPEPLD,PHB,FBXL2,ULK1,SAP30,P2RX7,EIF2AK4,F2RL1,ANO6,HDAC1,DAG1,ZNF639,CFL1,HSPA8,POU2F3,PC,PSMC3,TARDBP,TNIP1,INSR,CCL5,NOS2,JUN,FMR1,INPP5K,RXRA,MIR222,CXCL6,IRGM,SAP30BP,FCER2,SERPINB9,TBC1D20,ZNF502	grey	VSMC_M10
GO:0010970	0.64	0.42	72	139	transport along microtubule	BP	1	AP3S1,KIF5A,RAB21,KIF3A,AGTPBP1,SUN2,COPG2,IFT74,APBA1,BICD2,DYNC2LI1,LRPPRC,MGARP,WASF1,TTC26,KIF3C,ARHGAP21,COPG1,KLC3,DLG2,IFT172,TTC21A,WDR60,AP3M2,KIF5C,PURA,TUB,KIF3B,IFT81,RASGRP1,OPA1,AP3B1,IFT52,DTNBP1,KIF13A,BICDL1,TTC21B,HSPA8,BAG3,TRAF3IP1,CNIH2,CALY,TTC30A,SPG11,MAPT,BLOC1S6,MREG,HTT,KIF17,UXT,AP3M1,KIF1C,HAP1,WDR19,PEX14,TRIM46,NDEL1,AC138894.1,SNAPIN,SFPQ,CAMSAP3,IFT20,HSPB11,BICDL2,PRKCZ,MAPK8IP3,TERF2,UBB,BLOC1S3,BORCS5,AP3S2,MAP1A	grey	VSMC_M10
GO:0003407	0.64	0.47	25	49	neural retina development	BP	1	NTRK2,RORB,SLC1A1,TFAP2B,RDH13,PTN,TSPAN12,USP45,SOX9,USH1C,RPGRIP1L,TFAP2A,TGFB2,NRL,DLX1,OBSL1,ROM1,SDK1,PSEN1,MEGF11,LHX1,SOX8,FJX1,THY1,DIO3	grey	VSMC_M10
GO:0006691	0.64	0.55	9	17	leukotriene metabolic process	BP	1	LTC4S,ABCC10,MGST2,MAPKAPK2,PLA2G4A,GGT2,GGT6,DPEP2,GGT5	grey	VSMC_M10
GO:0055074	0.64	0.40	152	291	calcium ion homeostasis	BP	1	LRP1,CYP27B1,ESR1,SMDT1,BAK1,MCHR1,GPR20,PLA2G6,SLC25A27,TFAP2B,S1PR3,PRKCE,TNNI3,FPR2,IBTK,LPAR1,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,ATP7B,PTGIR,GIPR,CACNB2,ACKR2,SLC24A3,C1QTNF1,TMTC4,RYR1,PRNP,ADRA1D,DIAPH1,P2RX2,KL,CCKBR,RASA3,MICU3,IMMT,C19orf12,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,TPCN1,SLC8B1,VDR,STC1,RMDN3,F2RL1,F2R,PKD2,CASQ2,MCUR1,CD40,RYR2,RAP1GDS1,TRPM1,SPPL3,LCK,TRPV4,TCIRG1,FAM20A,GNA13,CMKLR1,MCUB,UBASH3B,DISC1,ANK2,GPER1,TRPM8,PDZD8,AGT,ATP1A2,CASQ1,NTSR1,FZD9,TMCO1,PTH1R,FIS1,CEMIP,ABL2,CDH23,PTPN6,MICU1,MCU,CXCR2,GNG3,HTT,PTGDR,PTGER2,ATP1B1,CD38,ATP13A2,HAP1,DLG4,FAM155B,PSEN1,CACNA1A,AC138894.1,ATP2A1,CD19,SMAD3,CALM1,S100A14,PRKCB,BDKRB1,NMUR2,TRPV2,HRH4,CCL14,CCL5,CCL7,PTGER4,SLC25A23,MAIP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,GPR157,SYPL2,CYBA,JPH3,ATP2C2,MCOLN3,PTGFR,MIR199A1,KCNK3,DMD,GPR35,NOL3,CHRNA10,TRIM24,CCR10,JPH2,SNX10,THY1,WNT5A,DDIT3	grey	VSMC_M10
GO:1901985	0.64	0.48	20	39	positive regulation of protein acetylation	BP	1	SPHK2,PAXIP1,ARRB1,ARNTL,RAPGEF3,AUTS2,DDX3X,TADA2B,FOXP3,KAT7,MUC1,MAPK3,NAP1L2,RPS6KA5,ISL1,TAOK1,GLYR1,SOX4,LIF,RPS6KA4	grey	VSMC_M10
GO:0042744	0.64	0.56	8	15	hydrogen peroxide catabolic process	BP	1	PRDX1,CAT,PXDN,PRDX3,PXDNL,DUOX1,MPO,HBA2	grey	VSMC_M10
GO:0008202	0.65	0.41	114	217	steroid metabolic process	BP	1	RDH5,APOF,ATP8B1,RDH16,HSD17B4,CYP27B1,ESR1,CYP21A2,SULT4A1,TSPO,HSD17B8,HSD17B3,AKR1B1,TTC39B,KIT,PLPP6,SRD5A3,HINT2,CAT,DKKL1,APOB,HSD17B14,EBP,EBPL,CUBN,APOC1,LIPE,PRKAG2,TSKU,PIP4P1,PANK2,NR1H4,SOAT2,CYP7A1,ASAH1,CYP7B1,CEBPA,OSBP,DKK3,LIMA1,EPHX2,CYP2R1,SPP1,ERLIN1,SRD5A1,CYB5R1,ABCA5,FMO5,NR5A2,SNAI1,MSMO1,SC5D,HSD11B1,ABCB11,DHRS9,AGT,OSBPL2,SCAP,HSD17B7,POR,OSBPL6,ACADL,SOAT1,TM7SF2,OSBPL1A,FDX1,COMT,LPCAT3,GNB3,WNT4,CYP3A43,CYP27A1,STAT5B,CH25H,LIPA,ACADVL,HSD17B10,CLN8,MED1,FGFR4,LIPC,DGKQ,OSBPL7,ERG28,APOBR,CLN6,LDLR,SCNN1B,CYP46A1,DHRS11,NPC1,SREBF1,LEPR,ACAA2,PIAS4,MECP2,CACNA1H,RXRA,CEL,ABCD3,GFI1,HSD11B2,MIR27B,MIR27A,NFE2L1,DHRS2,SDR42E1,LDLRAP1,AMACR,CRH,STARD4,INSIG2,YWHAH,FGF1	grey	VSMC_M10
GO:0045730	0.65	0.52	12	23	respiratory burst	BP	1	RAC2,HCK,NCF1,SLAMF8,NCF2,DUSP10,SLC11A1,MPO,INSR,NOXA1,CYBA,JCHAIN	grey	VSMC_M10
GO:0016571	0.65	0.42	61	118	histone methylation	BP	1	SNW1,PHF1,PRDM4,RNF20,SETD7,SETDB2,EED,IWS1,SUV39H2,KDM4A,PAXIP1,DPY30,SIRT7,CHTOP,NSD3,ASH2L,NR1H4,DNMT3B,SMYD1,SETD6,KMT2D,RTF1,WDR82,ZNF335,JARID2,RBBP5,AUTS2,SETD2,TET1,BCOR,MEN1,WDR61,NELFA,DYDC1,PRDM2,NSD1,SETD1A,PAGR1,OGT,SETD3,SUZ12,SUPT6H,CXXC1,CREBBP,DOT1L,MECP2,PRDM16,CHD5,MTF2,GFI1,PRMT7,CTCF,PRMT6,SETDB1,PRDM6,ARID4A,BEND3,SMYD3,ZNF304,NNMT,N6AMT1	grey	VSMC_M10

GO:0019725	0.65	0.38	335	638	cellular homeostasis	BP	1	ZNF236,NME1,ORMDL2,SLC39A5,NEDD4L,LRP1,ESR1,SLC12A2,PRKN,AGER,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,CKB,TMPRSS6,TXN2,SLC39A4,LARGE1,SRF,STEAP2,TXNRD1,SLC25A27,SLC1A1,TFAP2B,S1PR3,PRDX1,ERP44,PRKCE,TNNI3,RTN4,FPR2,HMGN3,IBTK,SLC4A4,LPAR1,PPT1,AQP1,SLC31A2,TRIM32,KEL,ATG5,TRPM4,FOXO3,DLD,TXNRD3,FGF21,GRIN2D,TRPC3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,FOXA3,GIPR,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,DEDD2,CLNS1A,AQP11,GRIK5,RAF1,ATP1A3,PRDX3,EGLN2,ACKR2,SLC24A3,C1QTNF1,SLC4A7,TMEM106B,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,GAS6,HPX,RASA3,NCOA4,NR1H4,MICU3,ATP6V1H,CYP7A1,TM9SF4,NDUFAF2,IL1A,IDE,IMMT,OSBP,C19orf12,PIK3R1,CHMP2B,P2RX3,PLCE1,SLC9A9,RYR3,FBXW7,TMBIM6,P2RX7,HVCN1,P2RY1,PTK2B,SLC39A13,KCNJ11,TIAM1,RAB11FIP5,PFKM,TPCN1,SLC8B1,VDR,STC1,OPA1,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,ANO6,FITM2,ORMDL1,SLC6A2,ABCC2,ZBED6,NELL2,PKD2,PAX2,TWNK,CASQ2,MCUR1,SLC12A5,CD40,RYR2,SLC41A1,SLC4A10,RAP1GDS1,GPLD1,TRPM1,SPPL3,GLRX2,LCK,SLC2A10,PPP3CA,KCNJ2,TESMIN,SLC9B1,SLC12A7,TRPV4,SLC9B2,ZBTB20,TMEM9,ADRA2A,SLC30A10,TCIRG1,GNA13,ISCU,KCNB1,CMKLR1,MCUB,HJV,SLC9A8,UBASH3B,DISC1,POLG,ANK2,GPER1,SLAMF8,RHCG,TRPM8,PDZD8,RAB11FIP2,MCL1,AGT,ATP1A2,BAG3,SLC9A1,CASQ1,SLC12A8,NTSR1,XPR1,CLIC4,MLXIPL,FZD9,SIDT2,TMCO1,PDK3,KLF7,NFE2L2,PTH1R,SLC30A4,FIS1,CEMIP,HK1,ABL2,SLC12A9,MEN1,CDH23,ENY2,ABCA12,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,GNB3,HTT,PTGDR,PTGER2,SLC9A	grey	VSMC_M10
GO:0043616	0.65	0.48	18	35	keratinocyte proliferation	BP	1	PTCH1,CD109,AREG,INTU,OVOL2,FERMT1,SDR16C5,VDR,SRSF6,TGM1,KDF1,SFN,CASK,MED1,BCL11B,MIR21,MIR125B1,EREG	grey	VSMC_M10
GO:0051607	0.65	0.41	91	174	defense response to virus	BP	1	TNFAIP3,USP15,C6orf106,APOBEC3H,EXOSC4,IRF5,ANKRD17,RSAD2,IL15,PUM2,TRAF3IP2,ZC3HAV1,PHB,UNC13D,MYD88,SEC14L1,ZMYND11,TMEM173,CLPB,NPLOC4,EIF2AK2,MAVS,AIMP1,IRF7,PCBP2,TRIM44,IRF2,EIF2AK4,SERINC5,OAS3,NLRC5,IFNGR2,F2RL1,POLR3D,IFIT2,HERC5,CD40,MX2,IFIH1,OASL,CRCP,GPAM,ADARB1,UNC93B1,POLR3C,PARP9,DTX3L,IRF9,IFI6,RNF26,NLRX1,ABCF3,TRAF3IP1,HTRA1,TRIM52,SETD2,RTP4,MUL1,BIRC3,POLR3A,FOXP3,RNF216,TKFC,SPON2,AKAP1,TSPAN6,STAT2,POLR3E,G3BP1,SIN3A,TRAF3,RIOK3,RNF135,TICAM1,TTC4,ATAD3A,NCBP3,POLR3K,IFI44L,ZDHHC1,OAS1,ZDHHC11,FADD,TRIM34,BNIP3L,ZCCHC3,IFNLR1,FGL2,KCNJ8,IFIT3,EXOSC5	grey	VSMC_M10
GO:0140546	0.65	0.41	91	174	defense response to symbiont	BP	1	TNFAIP3,USP15,C6orf106,APOBEC3H,EXOSC4,IRF5,ANKRD17,RSAD2,IL15,PUM2,TRAF3IP2,ZC3HAV1,PHB,UNC13D,MYD88,SEC14L1,ZMYND11,TMEM173,CLPB,NPLOC4,EIF2AK2,MAVS,AIMP1,IRF7,PCBP2,TRIM44,IRF2,EIF2AK4,SERINC5,OAS3,NLRC5,IFNGR2,F2RL1,POLR3D,IFIT2,HERC5,CD40,MX2,IFIH1,OASL,CRCP,GPAM,ADARB1,UNC93B1,POLR3C,PARP9,DTX3L,IRF9,IFI6,RNF26,NLRX1,ABCF3,TRAF3IP1,HTRA1,TRIM52,SETD2,RTP4,MUL1,BIRC3,POLR3A,FOXP3,RNF216,TKFC,SPON2,AKAP1,TSPAN6,STAT2,POLR3E,G3BP1,SIN3A,TRAF3,RIOK3,RNF135,TICAM1,TTC4,ATAD3A,NCBP3,POLR3K,IFI44L,ZDHHC1,OAS1,ZDHHC11,FADD,TRIM34,BNIP3L,ZCCHC3,IFNLR1,FGL2,KCNJ8,IFIT3,EXOSC5	grey	VSMC_M10
GO:1904037	0.65	0.50	15	29	positive regulation of epithelial cell apoptotic process	BP	1	SFRP4,FOXO3,ANO6,PLA2R1,CD40,HDAC1,PDCD4,GPER1,ITGA4,CCL2,PIAS4,MIR24-1,MIR125A,CD248,RGCC	grey	VSMC_M10
GO:0060043	0.65	0.48	19	37	regulation of cardiac muscle cell proliferation	BP	1	GLI1,MAPK14,PIM1,TGFBR2,MEF2C,TBX5,JARID2,KCNK2,SAV1,MAPK1,BMPR1A,RBPJ,TBX2,GATA6,MIR199A1,MIR222,NOG,HEY2,WNT2	grey	VSMC_M10
GO:0031571	0.65	0.51	13	25	mitotic G1 DNA damage checkpoint signaling	BP	1	PLK3,PRKDC,PLK2,PIDD1,CCND1,GIGYF2,CHEK2,CDKN1B,MUC1,FBXO31,RPS27L,SOX4,CRADD	grey	VSMC_M10
GO:0086014	0.65	0.58	6	12	atrial cardiac muscle cell action potential	BP	1	TRPM4,CACNB2,SCN5A,KCNJ3,RYR2,ANK2	grey	VSMC_M10
GO:0086026	0.65	0.58	6	12	atrial cardiac muscle cell to AV node cell signaling	BP	1	TRPM4,CACNB2,SCN5A,KCNJ3,RYR2,ANK2	grey	VSMC_M10
GO:0086066	0.65	0.58	6	12	atrial cardiac muscle cell to AV node cell communication	BP	1	TRPM4,CACNB2,SCN5A,KCNJ3,RYR2,ANK2	grey	VSMC_M10
GO:0050798	0.65	0.50	14	27	activated T cell proliferation	BP	1	AGER,PRNP,CASP3,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,RC3H1,STAT5B,FOXP3,MIR21,FADD,TNFSF9	grey	VSMC_M10
GO:0006720	0.65	0.44	38	73	isoprenoid metabolic process	BP	1	RDH5,RDH16,LRP1,ALDH8A1,AKR1B1,ALDH1A1,SRD5A3,ADH5,RDH13,EGFR,NAPEPLD,LIPE,SDR16C5,RETSAT,HTRA2,COQ2,PRMT3,SRD5A1,ALDH1A3,GGPS1,DHRS9,DPAGT1,BCO2,PECR,DHRS3,RDH11,ALDH1A2,SCPEP1,LRP8,PHYH,PNPLA4,DHDDS,PDSS2,CRH,LRAT,RDH14,ADH4,ISPD	grey	VSMC_M10
GO:0016226	0.65	0.51	12	23	iron-sulfur cluster assembly	BP	1	ISCA1,CIAO1,CIAPIN1,ISCU,HSCB,NUBPL,NUBP1,CIAO3,CIAO2B,GLRX5,FXN,ISCA2	grey	VSMC_M10
GO:0031163	0.65	0.51	12	23	metallo-sulfur cluster assembly	BP	1	ISCA1,CIAO1,CIAPIN1,ISCU,HSCB,NUBPL,NUBP1,CIAO3,CIAO2B,GLRX5,FXN,ISCA2	grey	VSMC_M10
GO:1901293	0.65	0.40	105	199	nucleoside phosphate biosynthetic process	BP	1	NME1,TBPL1,ATP5MGL,PPT2,PPARA,ACSL6,GUCA1B,IMPDH1,NMRK1,SLC35B2,SLC25A13,PPAT,PPCS,ME1,PPT1,DLD,SPHK2,CMPK1,ADCY3,PRKAG2,SLC22A13,ATP5F1C,ELOVL1,IDO2,IDO1,PANK2,PDK1,PDHX,SLC5A8,ELOVL7,PANK1,NUDT12,AMPD3,ATP5F1A,GUCY1A1,GUCY1B1,DGUOK,GMPS,AMPD1,ADCY7,FAM173B,ADCY2,NME4,ACSL5,PRPS2,PARP9,HACD2,ADCY4,CTPS2,DNAJC30,DTYMK,PDK3,SLC25A16,ACSBG1,ATP5S,COASY,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,MAPK1,PARP1,TECR,SLC26A1,GUCY2D,PKLR,PANK3,GCDH,UPRT,ACACA,SLC26A2,PRPSAP2,ADSSL1,NOS2,ACSBG2,NADK,ATP6V0C,PANK4,NME3,ATP5PB,VPS9D1,ACSF3,AK8,UCK1,MLYCD,KARS,FUK,DHODH,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,PDZD3,ELOVL3,MTHFD2L,CMPK2,NNMT,NME6,DCTD,NUDT2,NAPRT,UPP1,NMNAT1	grey	VSMC_M10

GO:0006471	0.65	0.49	16	31	protein ADP-ribosylation	BP	1	XRCC1,SIRT2,SIRT3,PARP4,HPF1,ART3,SIRT5,SIRT4,ADNP,PARP9,PARP15,PARP14,PARP11,PARP1,PARP6,TINF2	grey	VSMC_M10
GO:0034661	0.65	0.48	18	35	ncRNA catabolic process	BP	1	EXOSC4,EXOSC3,PNPT1,TUT4,DEDD2,NUDT16,ZCCHC8,TENT2,TENT4B,DIS3L2,RBM7,DDX49,ZSWIM8,MRPL44,SLFN14,PARN,DROSHA,EXOSC5	grey	VSMC_M10
GO:0014074	0.65	0.42	56	109	response to purine-containing compound	BP	1	NME1,TEK,PNPT1,AREG,AQP1,TRPM4,HDAC2,TRPC3,PANX1,AANAT,THBD,RYR1,P2RX2,DNMT3B,P2RX3,RYR3,GPD1,P2RX7,P2RY1,PTK2B,RAPGEF2,KCNJ11,STC1,RAPGEF3,PKD2,DMTN,CASQ2,RYR2,SRD5A1,SLC6A3,HDAC1,SSH1,RAP1B,DUOX1,VGF,CPS1,FDX1,PTPRN,DGKQ,PKLR,FOS,TAF1,CITED1,PPARGC1B,SREBF1,JUN,INPP5K,TRPV1,P2RX1,BSG,ASS1,HSPA5,DHODH,DUSP1,HCN4,PDXP	grey	VSMC_M10
GO:0002820	0.65	0.48	17	33	negative regulation of adaptive immune response	BP	1	IL4I1,FOXJ1,NCKAP1L,NOD2,BCL6,RC3H1,PTPN6,TNFSF18,PPP3CB,FOXP3,TBX21,ZBTB7B,IL4R,IL7R,CD46,HAVCR2,RC3H2	grey	VSMC_M10
GO:1902175	0.65	0.51	12	23	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	BP	1	PRKN,FBXW7,HTRA2,MCL1,NFE2L2,NONO,PINK1,PARP1,SFPQ,MAPK7,PARK7,NOL3	grey	VSMC_M10
GO:0071354	0.65	0.48	17	33	cellular response to interleukin-6	BP	1	PHB,ST18,CEBPA,FER,ST3GAL6,RIPK1,ABCC2,SELPLG,STAT3,IL6R,JAK1,PTPN2,LCN2,GFI1,MIR125B1,MIR125A,C1QTNF4	grey	VSMC_M10
GO:1905898	0.65	0.49	15	29	positive regulation of response to endoplasmic reticulum stress	BP	1	BAK1,NCK2,PIK3R1,RNFT2,USP13,RNF185,NFE2L2,PTPN2,BCAP31,SGTA,TMEM259,DAB2IP,RNFT1,DDIT3,BCL2L11	grey	VSMC_M10
GO:0097352	0.65	0.47	19	37	autophagosome maturation	BP	1	STX17,SNX14,MFSD8,RUBCNL,VPS16,LIX1,TMEM39A,RUBCN,SNAP29,TBC1D25,PHF23,AC138894.1,CALM1,SNAPIN,VMP1,SMCR8,LAMP2,CLEC16A,IRGM	grey	VSMC_M10
GO:0070374	0.65	0.41	76	145	positive regulation of ERK1 and ERK2 cascade	BP	1	LRP1,AGER,PRXL2C,TEK,FPR2,MTURN,NOD1,BMPER,EGFR,TLR4,FGF21,BRAF,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,SPRY2,ARRB1,NRG1,GAS6,MFHAS1,ST5,HAND2,FBXW7,P2RY1,PTK2B,RASGRP1,RAPGEF2,CCL17,RIPK2,F2RL1,F2R,NQO2,GCNT2,NOD2,DSTYK,TRPV4,SLC30A10,GPER1,CIB1,THPO,PDE8A,RAP1B,GPBAR1,FGFR3,FGFR4,FGF18,MAPK3,MAP2K1,GAREM1,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,SERPINF2,PRKCZ,ATP6AP1,ABCA7,MIR21,MIR222,MIR23A,MIR27B,MIR24-1,MIR27A,FGA,CCL16,HRAS,MAP2K7,FGF1,HAVCR2,CCL22,PDGFD	grey	VSMC_M10
GO:1902930	0.65	0.47	19	37	regulation of alcohol biosynthetic process	BP	1	CYP27B1,PLEK,APOB,CYP7A1,DKK3,P2RY1,PTK2B,ERLIN1,GPER1,NTSR1,SCAP,POR,PTH1R,LPCAT3,WNT4,DGKQ,SREBF1,GFI1,FGF1	grey	VSMC_M10
GO:0007140	0.65	0.48	18	35	male meiotic nuclear division	BP	1	MOV10L1,DMC1,FOXJ3,MLH1,TEX15,ING2,M1AP,HSF2BP,SPO11,TDRKH,RAD51C,MEIOB,UBB,SYCP3,AGO4,FOXJ2,ZSCAN21,SPDYA	grey	VSMC_M10
GO:0030970	0.65	0.49	14	27	retrograde protein transport, ER to cytosol	BP	1	DERL1,SEC61B,NPLOC4,UBAC2,AUP1,RHBDD1,YOD1,SYVN1,DERL3,TMEM129,SEL1L,BCAP31,UBE2G2,DERL2	grey	VSMC_M10
GO:1903513	0.65	0.49	14	27	endoplasmic reticulum to cytosol transport	BP	1	DERL1,SEC61B,NPLOC4,UBAC2,AUP1,RHBDD1,YOD1,SYVN1,DERL3,TMEM129,SEL1L,BCAP31,UBE2G2,DERL2	grey	VSMC_M10
GO:0042304	0.66	0.49	15	29	regulation of fatty acid biosynthetic process	BP	1	NR1H2,APOC1,PIBF1,TRIB3,CYP7A1,NR1H3,ERLIN1,LPGAT1,MLXIPL,SCAP,ACADL,ACADVL,CD74,FABP5,INSIG2	grey	VSMC_M10
GO:0007189	0.66	0.43	41	80	adenylate cyclase-activating G protein-coupled receptor signaling pathway	BP	1	ADGRG6,ADM2,ADGRF1,S1PR3,ADGRL3,LPAR1,ADCY3,PTGIR,GIPR,ADRA1D,ADRA2B,ADGRG5,RAPGEF2,ADCY7,ADCY2,ADRA2A,PTHLH,GNA13,GPER1,GPR3,ADCY4,UCN2,PTH1R,ADRA2C,PTGER2,CALCRL,RAMP2,GPR161,ADGRE5,RIT2,PTGER4,GNAL,ADGRG4,GNB1,ADGRL2,PTGFR,ADGRE3,ADGRG1,CHGA,GNG2,MRAP2	grey	VSMC_M10
GO:0044782	0.66	0.39	150	288	cilium organization	BP	1	ONECUT2,AVIL,TBC1D30,ATAT1,KIF3A,TBC1D32,UBE2B,ASAP1,LRRC6,MAPK15,IFT74,CFAP69,RFX3,PTPDC1,RAB23,DYNC2LI1,CEP162,TMEM17,WDR92,FUZ,IQUB,ATG5,ARMC2,MAPRE1,ARMC4,INTU,SPATA6,TTC26,BBS7,DRC1,RSPH6A,NECTIN2,GALNT11,FBF1,PIBF1,IFT172,FOXJ1,TTC21A,WDR60,CFAP61,TTLL3,CCDC13,ABCC4,MKKS,CEP290,SPEF1,TMEM80,TTC17,TUB,KIF3B,RILPL1,RILPL2,CEP70,PARVA,CEP250,CCDC66,TCTN3,IFT81,CCDC113,CFAP20,CCDC65,TMEM67,IFT52,RPGRIP1L,PKD2,DNAH1,DNAH5,ZNF423,GBF1,NEURL1,CFAP43,ZMYND10,ARMC9,CFAP46,TTBK2,CLCN4,TTC21B,ALPK1,JHY,DISC1,OFD1,ENO4,RAB17,TMEM237,TRAF3IP1,BBS1,LAMA5,CDKL5,SEPT2,LIMK2,TTC30A,CFAP161,TTC12,TOGARAM1,EHD1,DNAAF2,SPAG16,FAM149B1,HTT,CFAP70,STK36,GORAB,CEP126,SNAP29,EXOC5,TTC25,RAB8A,SDCCAG8,HAP1,DNAAF4,CPLANE2,MNS1,WDR19,TMEM138,ATP6V1D,BBOF1,CNTROB,TMEM107,CCDC151,DYNLL2,MKS1,DNM2,TEKT3,IFT20,SPEF2,CFAP53,HSPB11,C16orf71,RILP,CLUAP1,WRAP73,TPGS1,CDK10,CELSR2,CDC14A,TMEM231,FNBP1L,HYDIN,ODF2L,WDR63,C5orf30,TCTN2,HYLS1,SNX10,C2CD3,CC2D2B,C7orf43,ATXN10,BBS10,PIFO	grey	VSMC_M10
GO:0010155	0.66	0.52	10	19	regulation of proton transport	BP	1	SPHK2,TESC,FAM173B,PM20D1,TCIRG1,COX17,DNAJC30,PARK7,APOPT1,PPIF	grey	VSMC_M10
GO:0000305	0.66	0.51	12	23	response to oxygen radical	BP	1	FANCC,PRDX1,DHFR,ERCC6,GLRX2,FBLN5,NFE2L2,GCH1,SOD3,MPO,NQO1,MIR21	grey	VSMC_M10
GO:0085029	0.66	0.47	20	39	extracellular matrix assembly	BP	1	TNXB,HAS1,PXDN,SOX9,CLASP2,GAS6,FBLN5,DAG1,LAMB3,AGT,PHLDB1,EFEMP2,PLOD3,RAMP2,SMAD3,MYH11,NTNG2,HAS3,LAMB1,RGCC	grey	VSMC_M10
GO:0021872	0.66	0.47	18	35	forebrain generation of neurons	BP	1	UQCRQ,NDNF,SEMA3A,ZSWIM6,DCLK2,RAPGEF2,SLC4A10,SATB2,DISC1,GBX2,DLX1,BCL11B,PLXNA3,LHX8,RHOA,UBB,FOXG1,METTL14	grey	VSMC_M10
GO:0035313	0.66	0.54	8	16	wound healing, spreading of epidermal cells	BP	1	CLASP2,HBEGF,FERMT1,ARHGAP24,RREB1,AJUBA,COL5A1,ACVRL1	grey	VSMC_M10

GO:0050801	0.66	0.37	284	542	ion homeostasis	BP	1	SLC39A5,NEDD4L,LRP1,CYP27B1,ESR1,SLC12A2,PRKN,TSPO,SMDT1,BAK1,MYC,KLHL3,MCHR1,GPR20,PLA2G6,CKB,BTBD9,TMPRSS6,SLC39A4,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,WNK2,CNNM4,PRKCE,TNNI3,EPAS1,FPR2,IBTK,SLC4A4,LPAR1,PPT1,SLC31A2,EGFR,SFRP4,KEL,ATG5,TRPM4,SLC7A11,GRIN2D,TRPC3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,STEAP3,AQP11,ATP1A3,SCN5A,ACKR2,SLC24A3,GPD1L,SNX5,C1QTNF1,SLC4A7,TMEM106B,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DCN,DIAPH1,P2RX2,KL,CCKBR,HPX,RASA3,NCOA4,MICU3,ATP6V1H,TM9SF4,IL1A,IMMT,C19orf12,SLMAP,P2RX3,PLCE1,SLC9A9,RYR3,TMBIM6,P2RX7,HVCN1,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,SLC25A37,TBX5,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,GLS,CUTC,ABCC2,PKD2,CASQ2,MCUR1,SLC12A5,CD40,RYR2,GRM2,SLC41A1,SLC4A10,RAP1GDS1,TRPM1,SPPL3,LCK,KCNJ2,TESMIN,SLC9B1,SLC12A7,TRPV4,BDH2,TMEM9,SLC30A10,TCIRG1,FAM20A,GNA13,ISCU,CMKLR1,MCUB,HJV,SLC9A8,SCN7A,UBASH3B,DISC1,ANK2,GPER1,SLAMF8,RHCG,TRPM8,PDZD8,IFI6,AGT,ATP1A2,SLC9A1,CASQ1,SLC12A8,NTSR1,XPR1,CLIC4,MELTF,FZD9,PPP2R3C,TMCO1,PTH1R,SLC30A4,UNC80,FIS1,CEMIP,ABL2,CPS1,SLC12A9,CDH23,COMT,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,SLC9A7,ATP6V0A1,ABCB6,TRPM7,ATP1B1,KCNA1,CD38,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP13A2,FTH1,HAP1,DLG4,PARP1,CYB561A3,WNK3,FGFR4,ATP1B2,FAM155B,PSEN1,CACNA1A,MAPK3,CACNA1G,AC138894.1,ATP2A1,CD19,COX11,SMAD3,CLN6,NOX5,CALM1,SNAPIN,S100A14,S100A8	grey	VSMC_M10
GO:0016241	0.66	0.41	66	128	regulation of macroautophagy	BP	1	PIP4K2C,EPM2A,EXOC4,NRBP2,SPTLC1,GAPDH,ATP6V1E2,NOD1,ATP6V1C2,VPS35,SCOC,SESN3,PIP4K2A,ATP6V0E2,OPTN,RALB,ATP6V0B,SNX5,USP36,TMEM173,FEZ2,DCN,ULK1,ATP6V1H,CASP3,RIPK2,NOD2,LZTS1,ATP6V1B2,SEC22B,TMEM39A,USP30,BAG3,RUBCN,SNX6,SNX32,VPS26A,HTT,ATP6V0A1,PINK1,TBC1D25,ATP13A2,PHF23,ATP6V1D,VPS13D,VPS13C,MAPK3,AC138894.1,LARP1,NPC1,SMCR8,CDK5R1,CLEC16A,MTM1,ATP6V0C,IKBKG,GPSM1,GNAI3,KIAA1324,TSC1,SH3GLB1,BNIP3L,IRGM,TIGAR,HSPB8,CAPNS1	grey	VSMC_M10
GO:0051963	0.66	0.43	40	79	regulation of synapse assembly	BP	1	NTRK2,LINGO2,SEMA4D,LRRN3,EPHA7,VPS35,VSTM5,SLITRK5,LRFN1,FARP1,LRFN3,EPHB1,CLSTN2,ROBO2,MEF2C,CUX2,SLIT1,AMIGO2,BDNF,AMIGO3,ADNP,RAB17,EPHB3,LRTM2,NLGN2,SEMA4A,NLGN3,CHRNB2,NTN1,GPRASP2,BHLHB9,ASIC2,SLITRK2,AMIGO1,NTNG2,ADGRL2,GRID2,WNT5A,SIX1,LRRTM2	grey	VSMC_M10
GO:0043488	0.66	0.41	71	137	regulation of mRNA stability	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,PNLDC1,CSDC2,AGO2,TNRC6B,TUT7,MAPK14,EXOSC3,PNPT1,TUT4,PUM2,TRAF3IP2,FASTK,MLH1,MYD88,TNRC6C,LSM1,PAN3,CNOT1,CELF1,CNOT6L,FTO,TENT5C,TENT4B,RBM24,DIS3L2,AXIN2,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,EIF4ENIF1,YBX3,RC3H1,UPF1,SLC11A1,RBM10,SAMD4A,POLR2G,SCGB1A1,NT5C3B,DCP1B,FXR2,TARDBP,TOB1,TENT5D,TNRC6A,CNOT8,LARP1,ALKBH5,PARN,FMR1,METTL16,PLEKHN1,CIRBP,TRAF2,METTL14,NANOS1,CACNG7,YBX1,ZFP36L2,TENT5A,RC3H2,EXOSC5	grey	VSMC_M10
GO:0019217	0.66	0.44	32	62	regulation of fatty acid metabolic process	BP	1	PPARA,NR1H2,SOX9,APOC1,PRKAG2,SLC22A13,PIBF1,AKT2,PANK2,PDK1,TRIB3,CYP7A1,NR1H3,ERLIN1,LONP2,SIRT4,IRS1,CPT1A,ABCB11,LPGAT1,MLXIPL,SCAP,PDK3,ACADL,TYSND1,ACADVL,NCOR1,CD74,SREBF1,MLYCD,FABP5,INSIG2	grey	VSMC_M10
GO:0035987	0.66	0.47	17	34	endodermal cell differentiation	BP	1	ITGA7,EOMES,MMP15,RTF1,SOX2,LAMB3,COL7A1,ITGB5,SETD2,ITGA4,FN1,COL5A2,LEO1,LAMA3,GATA6,COL5A1,LAMB1	grey	VSMC_M10
GO:0070972	0.66	0.44	31	60	protein localization to endoplasmic reticulum	BP	1	GPAA1,TRAM2,SEC61B,RTN4,SEC61G,BCAP29,RAB10,GRIK5,SEC62,UBAC2,DDRGK1,SRP14,SSR3,SPCS1,RYR2,GBF1,SRPRA,ANK2,MIA3,SEC16B,ZFAND2B,BCAP31,SGTA,RER1,SEC16A,HSPA5,TRAM1L1,PPP1R15A,INSIG2,SPCS2,SEC61A2	grey	VSMC_M10
GO:0033962	0.66	0.52	9	18	P-body assembly	BP	1	PAN2,CNOT2,CNOT6,PAN3,CNOT1,CNOT6L,DDX6,EIF4ENIF1,RC3H1	grey	VSMC_M10
GO:0050853	0.66	0.46	21	41	B cell receptor signaling pathway	BP	1	TEC,PLCL2,NCKAP1L,FOXP1,LPXN,MEF2C,LCK,BANK1,LAT2,BMX,PTPN6,CD38,MAPK1,GPS2,CD19,PRKCB,BTK,VAV3,CMTM3,GCSAM,SH2B2	grey	VSMC_M10
GO:0046390	0.66	0.40	82	156	ribose phosphate biosynthetic process	BP	1	NME1,ATP5MGL,PPT2,PPARA,ACSL6,IMPDH1,SLC35B2,SLC25A13,PPAT,PPCS,PPT1,DLD,SPHK2,CMPK1,ADCY3,PRKAG2,ATP5F1C,ELOVL1,PANK2,PDK1,PDHX,ELOVL7,PANK1,AMPD3,ATP5F1A,GUCY1A1,GUCY1B1,DGUOK,GMPS,AMPD1,ADCY7,FAM173B,ADCY2,NME4,ACSL5,PRPS2,HACD2,ADCY4,CTPS2,DNAJC30,PDK3,SLC25A16,ACSBG1,ATP5S,PYGL,COASY,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,PARP1,TECR,SLC26A1,GUCY2D,PKLR,PANK3,GCDH,UPRT,ACACA,SLC26A2,PRPSAP2,ADSSL1,ACSBG2,ATP6V0C,PANK4,NME3,ATP5PB,VPS9D1,ACSF3,UCK1,MLYCD,DHODH,MT-ATP8,MT-ATP6,ATP5ME,ATP5MF,ELOVL3,NME6,NUDT2,UPP1	grey	VSMC_M10
GO:1903363	0.66	0.44	31	60	negative regulation of cellular protein catabolic process	BP	1	TRIM39,RGP1,PDCL3,SDCBP,AQP11,KLHL40,DDRGK1,RYBP,PSMF1,TAF9,USP25,CSNK2A2,FAM192A,MARCH7,SUFU,RPL23,USP19,RPL11,ATP13A2,EPHA4,ANXA2,PSEN1,EFNA1,TAF1,OGT,SGTA,PARK7,DAB2IP,CAMLG,STYX,MAP1A	grey	VSMC_M10

GO:0002683	0.66	0.38	152	290	negative regulation of immune system process	BP	1	NME1,TNFAIP3,USP15,ENPP3,HLA-DOB,TRIB1,MYC,TOB2,C6orf106,MAPK14,FBXO7,CDK6,TNFRSF21,HOXA7,PELI1,NR1H2,IL4I1,TLR4,C5AR2,CST7,SOX9,CD300LF,PIBF1,FOXJ1,SEC14L1,SIRT2,NMI,NPLOC4,PAWR,PLCB1,PLCL2,PRNP,NCKAP1L,PRKDC,PCBP2,PLK2,HCK,ZC3H8,FER,PIK3R1,LPXN,CASP3,FBXW7,PTPRJ,TMEM131L,TMBIM6,PAG1,SLA2,NR1H3,TRAFD1,OAS3,NLRC5,MARCH7,MAPKBP1,ADTRP,NOD2,CD96,CD200,BANK1,TGFB2,BTN2A2,GPAM,PRKAR1A,GPR137B,PIAS3,HLX,TCTA,TBC1D10C,YTHDF2,UBASH3B,GPER1,SLAMF8,PARP14,RNF26,FGR,NLRX1,TRAF3IP1,HTRA1,RUNX3,ZBTB46,PDCD1,DLG1,APOD,MIA3,DUSP10,BCL6,VSIR,RC3H1,PTPN6,GPR137,FBN1,TNFSF18,LAG3,COL3A1,PPP3CB,MUL1,TAPBPL,INHA,PADI2,SCGB1A1,FOXP3,GPS2,TKFC,USP18,TBX21,SYT11,DCST1,ZBTB7B,IL4R,TSPAN6,LDLR,GPR68,BTK,STAT2,CD74,RIOK3,CCL2,CCL25,YES1,PTGER4,TWSG1,IL7R,PTPN2,SOCS1,CRK,FOXF1,GLMN,MIR21,MIR222,MIR125B1,MIR24-1,MIR27A,FSTL3,OAS1,LST1,MAFB,FADD,DPP4,CD46,A2M,MIR125A,THY1,DUSP1,TSC22D3,FGL2,SERPINB9,GCSAM,LAX1,CEBPB,HAVCR2,IL17D,RC3H2	grey	VSMC_M10
GO:0051568	0.66	0.45	26	51	histone H3-K4 methylation	BP	1	SNW1,PAXIP1,DPY30,ASH2L,DNMT3B,KMT2D,RTF1,WDR82,ZNF335,RBBP5,AUTS2,BCOR,MEN1,WDR61,NELFA,DYDC1,SETD1A,PAGR1,OGT,SETD3,CXXC1,GFI1,PRMT6,ARID4A,BEND3,NNMT	grey	VSMC_M10
GO:0009219	0.66	0.51	11	21	pyrimidine deoxyribonucleotide metabolic process	BP	1	TBPL1,DPYS,MBD4,DTYMK,UPB1,NEIL1,NT5M,NTHL1,CMPK2,DCTD,UPP1	grey	VSMC_M10
GO:0019229	0.66	0.45	24	47	regulation of vasoconstriction	BP	1	ZDHHC21,EGFR,TRPM4,ADRA1D,ADRA2B,DOCK5,F2R,CHRM3,ADRA2A,AGT,ACE2,ATP1A2,PER2,ADRA2C,ECE1,SMTNL2,CD38,HRH2,ASIC2,P2RX1,MIR21,RHOA,FGA,KCNMB4	grey	VSMC_M10
GO:0021954	0.66	0.44	31	61	central nervous system neuron development	BP	1	UQCRQ,AGTPBP1,PLXNA4,NTRK2,NDNF,GLI2,MYCBP2,TSKU,SZT2,RAC3,SEMA3A,EPHB1,DCLK2,RAPGEF2,NR4A2,SLC4A10,ADARB1,DISC1,GBX2,EPHB3,MAPT,NIN,EPHA4,MPP5,NDEL1,CHRNB2,PLXNA3,LHX8,UBB,CNTN2,FOXG1	grey	VSMC_M10
GO:0046677	0.66	0.46	21	41	response to antibiotic	BP	1	CYB5R4,PPP2CB,ZC3H8,CASP3,MEF2C,SRD5A1,RPL23,HYAL1,HYAL3,CPT1A,CBL,SLC9A1,CDKN1B,PLA2G4A,ALPL,KDM6B,KAT7,JAK1,CIITA,HSPA5,CASP8	grey	VSMC_M10
GO:0032211	0.66	0.52	9	18	negative regulation of telomere maintenance via telomerase	BP	1	POT1,TENT4B,STN1,GNL3L,CTC1,PIF1,TERF2,TINF2,TEN1	grey	VSMC_M10
GO:0003223	0.66	0.61	4	8	ventricular compact myocardium morphogenesis	BP	1	POU4F1,DSP,BMPR1A,NOG	grey	VSMC_M10
GO:0051445	0.66	0.47	18	35	regulation of meiotic cell cycle	BP	1	YTHDC2,FBXO43,UBE2B,MAPK15,TOPAZ1,SIRT2,PLCB1,MOS,NPM2,PRKAR1A,GPR3,OVOL1,WNT4,FZR1,OOEP,WNT5A,DUSP1,LIF	grey	VSMC_M10
GO:0006968	0.66	0.48	14	27	cellular defense response	BP	1	RAB23,C5AR1,PTK2B,TCIRG1,NCF1,FCMR,NCF2,CXCR2,VEZF1,UMOD,ADORA2B,BCL10,KLRG1,IL33	grey	VSMC_M10
GO:0099518	0.66	0.43	33	65	vesicle cytoskeletal trafficking	BP	1	MYO1A,AP3S1,KIF5A,KIF3A,MYO7B,MYO7A,AP3M2,KIF3B,RASGRP1,AP3B1,DTNBP1,KIF13A,BICDL1,CNIH2,TANC2,BLOC1S6,HTT,AP3M1,KIF1C,HAP1,TRIM46,NDEL1,AC138894.1,SNAPIN,MYO1D,MYO1F,MYO5B,BICDL2,PRKCZ,FNBP1L,BLOC1S3,BORCS5,AP3S2	grey	VSMC_M10
GO:0045602	0.67	0.61	4	8	negative regulation of endothelial cell differentiation	BP	1	S1PR3,JAG1,ACVRL1,FOXJ2	grey	VSMC_M10
GO:0050994	0.67	0.46	20	39	regulation of lipid catabolic process	BP	1	PPARA,PRKCE,FGF21,ABHD5,APOC1,ALK,AKT2,LONP2,GPLD1,IRS1,CPT1A,ADRA2A,SORL1,ABCB11,TYSND1,DAGLB,THRA,LDLR,MLYCD,BSCL2	grey	VSMC_M10
GO:0034314	0.67	0.47	17	33	Arp2/3 complex-mediated actin nucleation	BP	1	ARPC3,PICK1,WASF1,FCHSD2,ARFIP2,HIP1R,IQGAP2,CYFIP1,MAGEL2,AP1AR,WASF2,WHAMM,NCKAP1,ARPC1A,WAS,WDR63,GMFG	grey	VSMC_M10
GO:1903859	0.67	0.51	10	20	regulation of dendrite extension	BP	1	NEDD4L,RIMS2,PRKN,CPNE5,RIMS1,CPNE9,SYT1,SLC23A2,MUL1,CACNG7	grey	VSMC_M10
GO:0010657	0.67	0.43	31	60	muscle cell apoptotic process	BP	1	MAP3K5,PPP1R10,RGL2,HSF1,CDKN2A,ARRB1,PAX8,HAND2,PTK2B,STK4,SIRT5,SIRT4,PDCD4,AGT,BAG3,NFE2L2,IL12A,CXCR2,RBM10,MFN2,CAMK2A,GNB1,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,TIGAR,C3orf58,NKX2-5,HEY2	grey	VSMC_M10
GO:0007626	0.67	0.40	68	132	locomotory behavior	BP	1	PRKN,AGTPBP1,BTBD9,CHRNA3,GPR37,ADAM22,APBA1,SLC1A1,TMOD1,PRKCE,PPT1,SOBP,NTF4,FIG4,GRIN2D,B4GALT2,ALK,DDHD2,NRG1,LGI4,PREX2,NCOA2,HTRA2,NR4A2,SLC4A10,SLC6A3,ALDH1A3,GIGYF2,OPRD1,CIART,USP2,ATP1A2,NTSR1,EPS8,SPG11,C1QL1,ZDHHC8,CDH23,ANKH,TNR,PPP3CB,EPHA4,DLG4,NLGN2,CLN8,HOXB8,CHRNB2,CLN6,NCOR1,NPC1,SEZ6,DAB1,ABAT,MECP2,PARK7,TSC1,ZFHX3,MCOLN3,CNTN2,DPP4,CEND1,FXN,CRBN,GPR88,APH1B,EFNB3,PITX3,RASD2	grey	VSMC_M10

GO:0007005	0.67	0.37	232	436	mitochondrion organization	BP	1	TIMM21,ATG12,HEBP2,ATP23,LYRM7,PRKN,TSPO,HSPA4,NDUFA6,BAK1,AGTPBP1,TOMM22,PLA2G6,RAC2,FBXO7,FANCG,TMEM14A,COA5,CAMKMT,SDHAF4,EPAS1,PNPT1,GGCT,MYH14,VPS35,ATG5,MGARP,WASF1,SSBP1,AGK,CHCHD6,NDUFB2,HIGD1A,ATPAF1,PHB,NDUFB6,TMEM126B,NECTIN2,DNAJC15,OPTN,NDUFC2,DMAC2,PRDX3,PITRM1,TIMM50,MGME1,USP36,SIRT7,NDUFS8,NDUFAF7,DDHD2,BAG4,DCN,PANK2,NDUFA12,ULK1,PPP2CB,COX7A1,MIPEP,NDUFAF2,ARMC1,CEBPA,IMMP1L,IMMT,PRIMPOL,HIP1R,UQCC1,FBXW7,HTRA2,NDUFS3,CSNK2A2,MTX3,OPA1,AP3B1,NDUFAF6,COL4A3BP,TOMM34,IFIT2,SIRT5,SIRT4,FOXRED1,DNM1L,TERT,CISD2,ZDHHC6,COX17,OXA1L,USP30,NDUFB4,MFN1,RCC1L,POLG2,HPS4,GPER1,ARIH2,IFI6,NDUFB3,BAG3,SLC9A1,CIDEB,SFN,TFAM,MTFP1,NDUFS2,TOMM40L,THEM4,STPG1,HMGCL,NUBPL,FZD9,PISD,FZD5,MAPT,STOX1,FIS1,SUPV3L1,NMT1,ATG2A,GRPEL1,C11orf65,FUNDC1,MCU,HTT,COA3,NDUFB11,DDHD1,BCS1L,RAB3A,MARK2,PINK1,MUL1,ATG9A,STAT3,NDUFA9,BHLHA15,TIMM17B,ATP13A2,HAP1,WIPI2,PARP1,HSD17B10,TMEM102,CLN8,VPS13D,MFN2,NPEPPS,VPS13C,MSTO1,PIF1,HAX1,ADCK1,ATP2A1,THG1L,CALM1,TIMM29,NDUFAB1,STAT2,ATG2B,COX10,PSMD10,CAMK2A,MIEF2,LIG3,ATPAF2,SREBF1,MAIP1,RALBP1,LONP1,C19orf70,JUN,ACAA2,MTM1,DNAJA3,PAM16,BCAP31,ATAD3A,CLUH,NDUFB10,FUNDC2,PARK7,SLC25A33,MIGA2,MFSD14A,NAIF1,DHODH,SH3GLB1,MIR29A,MT-ND1,MT-ND2,MT-ND6,MICALL2,PRMT6,MLLT11,NOL3,MINOS1,BNIP3L,NDUFA5,NDUFC1,COX16,NDUFAF8,COX7A2,TIGAR,TIMM10B,TIMM23B,DMAC1,FXN,NDUFA3,NDUFB5,N	grey	VSMC_M10
GO:0007193	0.67	0.45	23	45	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	BP	1	MCHR1,GRM4,GRM8,GPR37,S1PR3,OXER1,FPR2,LPAR1,CHRM5,P2RY1,NPY1R,CHRM4,CHRM3,GRM2,RGS1,ADRA2A,OPRD1,CHRM1,HRH4,PALM,GNAI3,HTR1D,GPR37L1	grey	VSMC_M10
GO:0021692	0.67	0.53	8	16	cerebellar Purkinje cell layer morphogenesis	BP	1	AGTPBP1,WHRN,FAIM2,LDB1,TTC21B,SPTBN2,LHX1,CEND1	grey	VSMC_M10
GO:2000378	0.67	0.46	19	37	negative regulation of reactive oxygen species metabolic process	BP	1	PRKN,PPARA,ATG5,MYCN,SIRT2,SIRT3,TFAP2A,PAX2,SIRT5,SLC30A10,PINK1,MMP3,STAT3,PARK7,MIR21,RHOA,TIGAR,APOPT1,AC140504.1	grey	VSMC_M10
GO:0051341	0.67	0.42	41	79	regulation of oxidoreductase activity	BP	1	CYP27B1,PRKN,ZDHHC21,SDHAF4,NOD1,EGFR,NOSIP,SPHK2,DHFR,SZT2,ACVR2A,SIRT3,IL1A,PIK3CB,PTK2B,VDR,NOD2,SIRT4,TERT,COX17,OXA1L,KRAS,SLAMF8,AGT,NOS1AP,POR,ABL2,GCH1,ECSIT,CALM1,GLA,PARK7,GNAI3,CYBA,GFI1,TERF2,MIR21,MIR27B,FXN,FCER2,APOPT1	grey	VSMC_M10
GO:0006888	0.67	0.40	55	106	endoplasmic reticulum to Golgi vesicle-mediated transport	BP	1	GOPC,MAPK15,NRBP2,COPG2,STX17,TRAPPC12,TRAPPC3,BCAP29,COPG1,SEC22C,ANK1,YIPF4,TRAPPC11,SEC31A,SEC31B,GBF1,KLHL12,SEC22B,PGAP1,ERGIC2,TRIP11,PEF1,VTI1A,PDCD6,SORL1,TRAPPC2,SEC22A,HYOU1,SEC23IP,TRAPPC4,COPA,RAB1B,WHAMM,SCAP,MIA3,TRAPPC6B,CTAGE9,SEC16B,SEC24C,STX5,STX18,CNIH4,TMED10,LMAN1L,CXorf56,PPP6C,MPPE1,BCAP31,SEC16A,TMED5,YIF1A,TBC1D20,TMED3,TRAPPC6A,TRAPPC3L	grey	VSMC_M10
GO:0006895	0.67	0.52	8	16	Golgi to endosome transport	BP	1	EPS15,DOP1B,GBF1,AP1AR,KLHL20,AP4M1,VPS13C,CORO7	grey	VSMC_M10
GO:0035372	0.67	0.51	9	18	protein localization to microtubule	BP	1	ABHD17B,MAPRE1,MAPRE3,DIAPH1,CHAMP1,TTBK2,ABHD17A,ABHD17C,MAP1A	grey	VSMC_M10
GO:0031646	0.67	0.48	13	26	positive regulation of nervous system process	BP	1	RIMS2,SOX10,RIMS1,CST7,P2RX3,FAM173B,RNF10,DAG1,NTSR1,TNR,NLGN2,TNFRSF1B,ABAT	grey	VSMC_M10
GO:0048644	0.67	0.43	31	61	muscle organ morphogenesis	BP	1	LY6E,FOXH1,TNNI3,POU4F1,NRG1,TCF15,TNNC1,DSP,RYR2,PKP2,TNNI1,TGFB2,ADARB1,MYH7,ACTC1,EFEMP2,TTN,BMPR1A,TCAP,RBPJ,MED1,GSC,ISL1,ENG,CNTF,NOG,WNT5A,LIF,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0010770	0.67	0.42	33	65	positive regulation of cell morphogenesis involved in differentiation	BP	1	RAB21,UNC13D,SS18L2,RAC3,ARHGEF7,PRKDC,ANKRD27,CUX2,TIAM1,DOCK5,OPA1,RREB1,ITPKA,DMTN,DNM1L,CARMIL1,CAPRIN2,CASS4,CIB1,SS18L1,CDKL5,DOCK1,CSPG5,OBSL1,EPHA4,DNM2,PARP6,GPRASP2,BHLHB9,LRP8,CRK,FBXO31,FGA	grey	VSMC_M10
GO:1904357	0.67	0.49	12	24	negative regulation of telomere maintenance via telomere lengthening	BP	1	POT1,TENT4B,STN1,PARP1,GNL3L,CTC1,PIF1,ERCC4,SLX4,TERF2,TINF2,TEN1	grey	VSMC_M10
GO:0051639	0.67	0.55	6	12	actin filament network formation	BP	1	LCP1,PLS1,CARMIL1,SPIRE2,CARMIL2,FHOD1	grey	VSMC_M10
GO:0061097	0.67	0.42	38	74	regulation of protein tyrosine kinase activity	BP	1	ERBB3,NCK2,IBTK,EPGN,AREG,TGFA,ABI1,HBEGF,PRNP,NRG1,GAS6,ERCC6,FBXW7,NEURL1,ADRA2A,NCF1,EGF,CASS4,AGT,CBL,SNX6,DOK7,ZFYVE28,SOCS4,EPHA4,DLG4,DVL2,PSEN1,EFNA1,CCL5,CSF1R,UNC119,PTPN2,LRP8,THY1,DUSP22,EREG,RAP2B	grey	VSMC_M10
GO:0030326	0.67	0.40	49	96	embryonic limb morphogenesis	BP	1	OSR2,FZD6,TBC1D32,PITX1,PTCH1,ROR2,DLX5,HOXA13,MYCN,OSR1,INTU,HDAC2,GLI2,MEGF8,LMBR1,RARB,FREM2,HAND2,FRAS1,TBX5,IFT52,RPGRIP1L,TFAP2A,SALL1,FBXW4,HDAC1,TGFB2,SP9,WNT3,ECE1,TULP3,BMPR1A,WDR19,MED1,ALDH1A2,PSEN1,TMEM107,MKS1,TBX4,TBX2,GPC3,CREBBP,SKI,ALX3,TMEM231,NOG,WNT5A,C2CD3,BCL2L11	grey	VSMC_M10
GO:0035113	0.67	0.40	49	96	embryonic appendage morphogenesis	BP	1	OSR2,FZD6,TBC1D32,PITX1,PTCH1,ROR2,DLX5,HOXA13,MYCN,OSR1,INTU,HDAC2,GLI2,MEGF8,LMBR1,RARB,FREM2,HAND2,FRAS1,TBX5,IFT52,RPGRIP1L,TFAP2A,SALL1,FBXW4,HDAC1,TGFB2,SP9,WNT3,ECE1,TULP3,BMPR1A,WDR19,MED1,ALDH1A2,PSEN1,TMEM107,MKS1,TBX4,TBX2,GPC3,CREBBP,SKI,ALX3,TMEM231,NOG,WNT5A,C2CD3,BCL2L11	grey	VSMC_M10

GO:0002460	0.67	0.38	90	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	CD226,STX7,TNFAIP3,AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,EXOSC3,MSH2,BACH2,RSAD2,IL4I1,TLR4,TRPM4,TRAF3IP2,HMCES,PHB,ERCC1,NECTIN2,PVR,MLH1,UNC13D,MYD88,SLC22A13,FOXJ1,PAXIP1,JAG1,SHLD1,NCKAP1L,HPX,IRF7,TRAF6,GAPT,MEF2C,SLA2,RIPK2,NBN,NOD2,CD40,NFKB2,TCIRG1,HLX,DENND1B,CD28,FCER1G,RNF168,FZD5,PLA2G4A,BCL6,CTSH,IL12A,RC3H1,PTPN6,TNFSF18,SLC11A1,PPP3CB,STAT3,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,CD19,IL4R,BTK,CD74,FBXO38,C7,C3,IL7R,SUPT6H,PRKCZ,TRAF2,BCL10,MIR21,FADD,CD46,FCER2,RNF8,CD70,HRAS,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0002377	0.67	0.41	42	81	immunoglobulin production	BP	1	HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,EXOSC3,MSH2,CYREN,TRAF3IP2,HMCES,PHB,ERCC1,MLH1,PAXIP1,SHLD1,HPX,PRKDC,TRAF6,GAPT,GPI,TMBIM6,XRCC4,NBN,POLL,CD40,CD28,RNF168,BCL6,PMS2,FOXP3,SHLD2,TBX21,STX4,BATF,IL4R,BTK,YY1,SUPT6H,TRAF2,TRDV3,RNF8,NHEJ1	grey	VSMC_M10
GO:0031445	0.67	0.53	7	14	regulation of heterochromatin assembly	BP	1	SETDB2,FAM208A,PPHLN1,TET1,PHF8,SETDB1,ZNF304	grey	VSMC_M10
GO:0120261	0.67	0.53	7	14	regulation of heterochromatin organization	BP	1	SETDB2,FAM208A,PPHLN1,TET1,PHF8,SETDB1,ZNF304	grey	VSMC_M10
GO:0042445	0.67	0.39	69	133	hormone metabolic process	BP	1	RDH5,RDH16,HSD17B4,ALDH8A1,CYP27B1,ESR1,CYP21A2,TSPO,HSD17B8,HSD17B3,AKR1B1,ALDH1A1,SRD5A3,RDH13,IL4I1,DDO,LIPE,AANAT,SDR16C5,PAX8,IDE,RETSAT,DKK3,PCSK1,SCG5,MME,SPP1,PRMT3,SRD5A1,ALDH1A3,TCF7L2,ENPEP,DHRS9,ACE2,ARNT,SLCO1C1,ECE2,PCSK7,HSD17B7,POR,DUOX1,BCO2,FDX1,COMT,GNB3,WNT4,ECE1,STAT5B,HSD17B10,DHRS3,MED1,RDH11,ALDH1A2,DGKQ,SCPEP1,SCNN1B,CRYM,CYP46A1,DHRS11,GHR,CACNA1H,GFI1,DHRS2,PNPLA4,DIO3,LRAT,RDH14,ADH4,DIO2	grey	VSMC_M10
GO:0045739	0.68	0.42	34	66	positive regulation of DNA repair	BP	1	EYA4,MRNIP,EGFR,XRCC1,WDR48,FAM168A,SHLD1,PRKDC,ERCC6,EYA1,SLF1,ABRAXAS1,SPIDR,SLF2,EYA3,PARP9,DTX3L,RNF168,MGMT,ZCWPW1,WAS,DDX11,PARP1,SHLD2,UIMC1,WRAP53,SMCHD1,SPIRE2,OOEP,TIGAR,RNF8,UBE2N,BRCC3,CBX8	grey	VSMC_M10
GO:0021675	0.68	0.42	30	59	nerve development	BP	1	ERBB3,ATP8B1,PLXNA4,NTF4,POU4F1,SEMA3A,EPHB1,RET,TFAP2A,PAX2,SALL1,BDNF,SEMA3F,SULF2,TCIRG1,ADARB1,DAG1,LRIG2,ITGA4,CTSV,NGFR,CHRNB2,RNF165,ISL1,PLXNA3,MAFB,HOXB3,SIX1,TMEM126A,HOXA3	grey	VSMC_M10
GO:0002327	0.68	0.60	4	8	immature B cell differentiation	BP	1	KIT,TRAF3IP2,SYVN1,LRRC8A	grey	VSMC_M10
GO:1901524	0.68	0.60	4	8	regulation of mitophagy	BP	1	USP30,VPS13D,VPS13C,TIGAR	grey	VSMC_M10
GO:0060384	0.68	0.50	10	20	innervation	BP	1	NTF4,POU4F1,SEMA3A,RET,SULF2,ADARB1,LRIG2,ITGA4,RNF165,ISL1	grey	VSMC_M10
GO:0009267	0.68	0.39	67	130	cellular response to starvation	BP	1	MARS,MAP3K5,PPARA,ATF4,PICK1,TFEB,SLC39A4,NUAK1,BRSK1,ALB,RRAGD,VPS41,ATG5,FOXO3,KPTN,SESN3,FOXA3,DNAJC15,RALB,PRKAG2,SZT2,RPTOR,EIF2AK2,WRN,GAS6,LARS,PRKAG1,EIF2AK4,SLC38A2,NUAK2,NUPR2,SRD5A1,SIK1,SLC38A3,HSPA8,MTMR3,XPR1,TBL2,GLUL,NFE2L2,SIK2,COMT,WNT4,PRKAG3,CTSV,MAPK1,BHLHA15,WIPI2,MAX,RRAGB,ZFYVE1,MAPK3,TNRC6A,SREBF1,LAMP2,NIM1K,STK26,JUN,CLEC16A,KIAA1324,WDR59,HSPA5,SH3GLB1,RIPOR1,IMPACT,UPP1,RNF152	grey	VSMC_M10
GO:0098911	0.68	0.55	6	12	regulation of ventricular cardiac muscle cell action potential	BP	1	TRPM4,DSP,RYR2,PKP2,DLG1,DSG2	grey	VSMC_M10
GO:0006346	0.68	0.52	8	16	DNA methylation-dependent heterochromatin assembly	BP	1	DNMT3A,SETDB2,FAM208A,PPHLN1,HDAC1,TET1,SETDB1,ZNF304	grey	VSMC_M10
GO:0042634	0.68	0.49	10	20	regulation of hair cycle	BP	1	SMO,TSKU,FERMT1,ARNTL,TERT,TGFB2,NGFR,TRPV3,EPS8L3,WNT5A	grey	VSMC_M10
GO:2000737	0.68	0.50	9	18	negative regulation of stem cell differentiation	BP	1	JAG1,TCF15,PRICKLE1,YTHDF2,NFE2L2,STAT3,CDK12,ESRRB,ZFP36L2	grey	VSMC_M10
GO:0072396	0.68	0.59	4	8	response to cell cycle checkpoint signaling	BP	1	FBH1,EME1,SLX4,TIGAR	grey	VSMC_M10
GO:0072402	0.68	0.59	4	8	response to DNA integrity checkpoint signaling	BP	1	FBH1,EME1,SLX4,TIGAR	grey	VSMC_M10
GO:0072423	0.68	0.59	4	8	response to DNA damage checkpoint signaling	BP	1	FBH1,EME1,SLX4,TIGAR	grey	VSMC_M10
GO:0003163	0.68	0.59	4	8	sinoatrial node development	BP	1	BVES,CACNA1G,ISL1,HCN4	grey	VSMC_M10
GO:0007019	0.68	0.44	20	40	microtubule depolymerization	BP	1	CLASP2,TRIM54,NCKAP5,NAV3,SPEF1,ATXN7,NCKAP5L,KATNB1,STMND1,TRPV4,TTBK2,CIB1,CAMSAP3,TAOK1,APC2,CAMSAP1,CCSAP,APC,MAP1A,MAP6D1	grey	VSMC_M10
GO:0098815	0.68	0.45	17	34	modulation of excitatory postsynaptic potential	BP	1	RIMS2,RIMS1,SHANK1,MTMR2,SLC8A2,CUX2,PTK2B,IGSF11,SSH1,STX1A,TMEM25,DLG4,NLGN2,STX1B,NLGN3,PRKCZ,RGS4	grey	VSMC_M10
GO:0021756	0.68	0.53	7	14	striatum development	BP	1	FOXP2,SLC7A11,MKKS,RARB,ZSWIM6,ALDH1A3,BCL11B	grey	VSMC_M10
GO:0036289	0.68	0.59	4	8	peptidyl-serine autophosphorylation	BP	1	RIPK1,PIKFYVE,PINK1,MARK3	grey	VSMC_M10
GO:0007628	0.68	0.49	10	20	adult walking behavior	BP	1	AGTPBP1,HTRA2,EPHA4,CLN8,NPC1,DAB1,CNTN2,CEND1,FXN,EFNB3	grey	VSMC_M10
GO:0031280	0.68	0.54	6	12	negative regulation of cyclase activity	BP	1	GABBR2,ADGRV1,GRM2,PALM,GNAI3,PDZD3	grey	VSMC_M10
GO:0061912	0.68	0.42	32	63	selective autophagy	BP	1	PRKN,KLHL3,SPTLC1,NOD1,ATG5,RAB7A,OPTN,TMEM173,DDRGK1,ULK1,HTRA2,AUP1,RIPK2,NOD2,TEX264,USP30,ATG16L1,BAG3,UFC1,ATG2A,HTT,RETREG3,PINK1,WIPI2,VPS13D,MFN2,VPS13C,MAPK3,ATG2B,PJVK,TIGAR,HSPB8	grey	VSMC_M10
GO:0071313	0.68	0.59	4	8	cellular response to caffeine	BP	1	RYR1,RYR3,CASQ2,RYR2	grey	VSMC_M10
GO:0007398	0.68	0.51	8	16	ectoderm development	BP	1	VPS52,STX2,FZD7,GRHL3,BMPR1A,ITGAM,ZBTB7B,LHX1	grey	VSMC_M10
GO:0071498	0.68	0.50	9	18	cellular response to fluid shear stress	BP	1	MTSS1,MEF2C,PTK2B,PKD2,NFE2L2,MAP2K5,MAPK7,ASS1,CA2	grey	VSMC_M10
GO:0051785	0.68	0.44	21	41	positive regulation of nuclear division	BP	1	UBE2B,PHIP,HOXA13,EPGN,TGFA,SIRT2,PLCB1,IL1A,ANAPC5,ANAPC7,NPM2,IGF2,EGF,CD28,WNT4,ANAPC4,INSR,OOEP,WNT5A,RGCC,EREG	grey	VSMC_M10
GO:0060788	0.68	0.56	5	10	ectodermal placode formation	BP	1	FRS2,HDAC2,HDAC1,TBX2,SIX1	grey	VSMC_M10
GO:0071697	0.68	0.56	5	10	ectodermal placode morphogenesis	BP	1	FRS2,HDAC2,HDAC1,TBX2,SIX1	grey	VSMC_M10
GO:0010501	0.68	0.59	4	8	RNA secondary structure unwinding	BP	1	AGO2,AGO1,DDX3X,AGO4	grey	VSMC_M10

GO:0006383	0.68	0.44	20	39	transcription by RNA polymerase III	BP	1	SNAPC3,GTF3C6,CHD8,RPTOR,BRF2,ZC3H8,ZNF143,CEBPA,POLR3D,GTF3C3,CRCP,POLR3C,IVNS1ABP,ELL,ICE2,SNAPC5,SNAPC4,POLR3K,GTF3C4,POLR2K	grey	VSMC_M10
GO:0032026	0.68	0.52	7	14	response to magnesium ion	BP	1	TNFRSF11B,ENTPD6,RYR3,SLC41A1,CCND1,KCNA1,SLFN14	grey	VSMC_M10
GO:0030834	0.68	0.43	23	46	regulation of actin filament depolymerization	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,PLEK,ADD2,LMOD3,LIMA1,F2RL1,DMTN,CARMIL1,LMOD1,ADD3,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,CARMIL2,PDXP	grey	VSMC_M10
GO:1903426	0.68	0.44	19	37	regulation of reactive oxygen species biosynthetic process	BP	1	PPARA,TLR4,UCP1,FOXO3,SPHK2,WISP3,SLC30A10,HDAC4,PIKFYVE,STAT3,PARK7,SLC25A33,CYBA,LCN2,MIR21,MIR24-1,RHOA,APOPT1,AC140504.1	grey	VSMC_M10
GO:0003215	0.68	0.50	9	18	cardiac right ventricle morphogenesis	BP	1	FOXH1,JAG1,HAND2,TGFB2,BMPR1A,ISL1,SOX4,NKX2-5,HEY2	grey	VSMC_M10
GO:0051350	0.68	0.52	7	14	negative regulation of lyase activity	BP	1	GABBR2,ADGRV1,GRM2,MTRR,PALM,GNAI3,PDZD3	grey	VSMC_M10
GO:0090309	0.68	0.56	5	10	positive regulation of DNA methylation-dependent heterochromatin assembly	BP	1	SETDB2,FAM208A,PPHLN1,SETDB1,ZNF304	grey	VSMC_M10
GO:2000310	0.68	0.50	9	18	regulation of NMDA receptor activity	BP	1	MAPK8IP2,MEF2C,PTK2B,IFNGR2,CNIH2,PINK1,DLG4,CCL2,CRH	grey	VSMC_M10
GO:1902287	0.68	0.54	6	12	semaphorin-plexin signaling pathway involved in axon guidance	BP	1	PLXNA4,PLXNA1,PLXNC1,SEMA3A,SEMA3F,PLXNA3	grey	VSMC_M10
GO:0097484	0.68	0.46	15	30	dendrite extension	BP	1	NEDD4L,RIMS2,PRKN,CPNE5,RIMS1,WASF1,CPNE9,SYT1,SLC23A2,CYFIP1,AUTS2,MUL1,SLC9A6,CACNG7,LPH	grey	VSMC_M10
GO:0055080	0.68	0.35	258	494	cation homeostasis	BP	1	SLC39A5,NEDD4L,LRP1,CYP27B1,ESR1,SLC12A2,PRKN,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,BTBD9,TMPRSS6,SLC39A4,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,CNNM4,PRKCE,TNNI3,EPAS1,FPR2,IBTK,SLC4A4,LPAR1,PPT1,SLC31A2,EGFR,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,STEAP3,AQP11,ATP1A3,ACKR2,SLC24A3,SNX5,C1QTNF1,SLC4A7,TMEM106B,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,KL,CCKBR,HPX,RASA3,NCOA4,MICU3,ATP6V1H,TM9SF4,IL1A,IMMT,C19orf12,P2RX3,PLCE1,SLC9A9,RYR3,TMBIM6,P2RX7,HVCN1,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,SLC25A37,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,CUTC,PKD2,CASQ2,MCUR1,SLC12A5,CD40,RYR2,SLC41A1,SLC4A10,RAP1GDS1,TRPM1,SPPL3,LCK,KCNJ2,TESMIN,SLC9B1,SLC12A7,TRPV4,BDH2,TMEM9,SLC30A10,TCIRG1,FAM20A,GNA13,ISCU,CMKLR1,MCUB,HJV,SLC9A8,SCN7A,UBASH3B,DISC1,ANK2,GPER1,SLAMF8,RHCG,TRPM8,PDZD8,AGT,ATP1A2,SLC9A1,CASQ1,SLC12A8,NTSR1,CLIC4,MELTF,FZD9,TMCO1,PTH1R,SLC30A4,UNC80,FIS1,CEMIP,ABL2,SLC12A9,CDH23,COMT,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,SLC9A7,ATP6V0A1,ABCB6,TRPM7,ATP1B1,KCNA1,CD38,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP13A2,FTH1,HAP1,DLG4,CYB561A3,ATP1B2,FAM155B,PSEN1,CACNA1A,MAPK3,AC138894.1,ATP2A1,CD19,COX11,SMAD3,CLN6,NOX5,CALM1,SNAPIN,S100A14,S100A8,PRKCB,SCNN1B,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,C7,PTGER4,SLC25A23,MAIP1,TMEM199,SLC46A1,SLC9A6,NUBP1,GNB1,AT	grey	VSMC_M10
GO:0036376	0.68	0.54	6	12	sodium ion export across plasma membrane	BP	1	SLC4A4,ATP1A3,ATP1A2,SLC9A1,ATP1B1,ATP1B2	grey	VSMC_M10
GO:0006687	0.68	0.43	24	47	glycosphingolipid metabolic process	BP	1	B4GALNT1,A4GALT,LARGE1,KIT,GLB1,NEU3,ST8SIA4,A3GALT2,ST8SIA2,B3GALT1,B3GALNT1,GALC,CLN6,ST8SIA5,GLA,HEXA,GM2A,ST6GALNAC4,ST3GAL2,ST6GALNAC5,CPTP,NEU2,B4GALT3,ST8SIA6	grey	VSMC_M10
GO:0035973	0.68	0.59	4	8	aggrephagy	BP	1	ATG5,BAG3,HTT,HSPB8	grey	VSMC_M10
GO:0031111	0.68	0.44	18	36	negative regulation of microtubule polymerization or depolymerization	BP	1	MAPRE1,EML2,CLASP2,TRIM54,NAV3,ARHGEF7,SPEF1,ATXN7,KATNB1,TTBK2,CIB1,INPP5J,CAMSAP3,TAOK1,APC2,CAMSAP1,APC,MAP6D1	grey	VSMC_M10
GO:0002833	0.68	0.39	52	101	positive regulation of response to biotic stimulus	BP	1	CD226,USP15,XRCC6,FPR2,ANKRD17,AKIRIN2,TLR4,PUM2,NECTIN2,PVR,SLC22A13,IKBKB,NMI,TMEM173,MAVS,HPX,PRKDC,IRF7,TRAF6,HCK,RASGRP1,NLRC5,F2RL1,POLR3D,NOD2,OASL,POLR3C,PARP9,COCH,ADAM8,CADM1,NONO,IL12A,XRCC5,LAG3,STAT5B,MED1,SFPQ,SIN3A,CCL5,RIOK3,FBXO38,VAV1,CREBBP,CYBA,AP1G1,FADD,ZCCHC3,IRGM,WNT5A,EREG,HAVCR2	grey	VSMC_M10
GO:0034968	0.68	0.39	50	98	histone lysine methylation	BP	1	SNW1,PHF1,SETD7,SETDB2,EED,IWS1,SUV39H2,KDM4A,PAXIP1,DPY30,NSD3,ASH2L,DNMT3B,SMYD1,SETD6,KMT2D,RTF1,WDR82,ZNF335,JARID2,RBBP5,AUTS2,SETD2,BCOR,MEN1,WDR61,NELFA,DYDC1,NSD1,SETD1A,PAGR1,OGT,SETD3,SUZ12,SUPT6H,CXXC1,DOT1L,MECP2,PRDM16,CHD5,MTF2,GFI1,PRMT6,SETDB1,ARID4A,BEND3,SMYD3,ZNF304,NNMT,N6AMT1	grey	VSMC_M10
GO:0014032	0.68	0.41	35	69	neural crest cell development	BP	1	SEMA6A,SOX10,SMO,SEMA4D,SEMA4C,SOX9,OVOL2,JAG1,ALX1,SEMA3D,SEMA3A,NRG1,KBTBD8,RET,HAND2,SEMA4F,SEMA3G,SEMA4G,KLHL12,SEMA3F,PEF1,PDCD6,GBX2,LAMA5,SEMA6D,FN1,MAPK1,BMPR1A,RADIL,ALDH1A2,SEMA4A,MAPK3,TCOF1,ISL1,SOX8	grey	VSMC_M10
GO:0099625	0.68	0.50	9	18	ventricular cardiac muscle cell membrane repolarization	BP	1	SCN5A,KCNJ3,KCNE2,ANK2,SCN4B,NOS1AP,RNF207,KCNH2,KCNJ8	grey	VSMC_M10
GO:1900407	0.68	0.41	34	66	regulation of cellular response to oxidative stress	BP	1	PRKN,NCOA7,ATF4,GPR37,FBXO7,MET,TLR4,SLC7A11,FOXO3,DHFR,PAWR,FBXW7,HTRA2,RIPK1,FBLN5,MCL1,PDE8A,NFE2L2,NONO,GCH1,PINK1,MMP3,PARP1,SFPQ,MAPK7,STK26,PARK7,TSC1,TLDC1,MAPKAP1,MIR21,NOL3,GPR37L1,TXN	grey	VSMC_M10
GO:0021762	0.68	0.44	18	35	substantia nigra development	BP	1	CKB,TTBK1,SIRT2,NDUFS3,SUDS3,COX6B1,INA,PADI2,ACTB,CALM1,SEC16A,ATP5PB,SYPL2,MAPKAP1,HSPA5,RHOA,BASP1,YWHAH	grey	VSMC_M10

GO:0050803	0.68	0.37	87	170	regulation of synapse structure or activity	BP	1	SYNGAP1,MAPK14,NTRK2,LINGO2,ABHD17B,SEMA4D,PPT1,LRRN3,EPHA7,PTN,CTTNBP2,YWHAZ,VPS35,SLC7A11,VSTM5,PCDH8,SLITRK5,LRFN1,FARP1,PRNP,LRFN3,EPHB1,CLSTN2,CHMP2B,ROBO2,MEF2C,CUX2,SEPT11,TIAM1,SLIT1,HOMER1,OPA1,AMIGO2,ITPKA,CYFIP1,TUBA1A,BDNF,NEURL1,DNM1L,CAPRIN2,SEMA3F,CAMKV,DAG1,AMIGO3,CFL1,ADNP,HSPA8,DISC1,RAB17,NFATC4,PTPRO,CDKL5,IL10RA,EPHB3,TANC2,SRGN,DNM3,GRIPAP1,EPHA4,LRTM2,NLGN2,STX1B,SEMA4A,NLGN3,EFNA1,AC138894.1,CHRNB2,ZDHHC15,NTN1,GPRASP2,BHLHB9,ARHGAP44,ASIC2,CDK5R1,SLITRK2,LRP8,ABHD17A,AMIGO1,NTNG2,DAB2IP,ADGRL2,RHOA,GRID2,ABHD17C,WNT5A,SIX1,LRRTM2	grey	VSMC_M10
GO:0007289	0.68	0.52	7	14	spermatid nucleus differentiation	BP	1	TBPL1,NECTIN2,SYCP1,CHD5,MFSD14A,SYCP3,RNF8	grey	VSMC_M10
GO:0021575	0.68	0.45	17	34	hindbrain morphogenesis	BP	1	GLI1,AGTPBP1,SMO,WHRN,XRCC1,GLI2,FAIM2,LDB1,TTC21B,GNPAT,SPTBN2,MAP2K1,LHX1,DAB1,HSPA5,GRID2,CEND1	grey	VSMC_M10
GO:1902808	0.68	0.43	21	41	positive regulation of cell cycle G1/S phase transition	BP	1	GLI1,CCND3,ANKRD17,LSM10,EGFR,UBE2E2,RPTOR,PLCB1,TFDP1,DDRGK1,ADAMTS1,HYAL1,CCND1,TERT,DDX3X,MEPCE,PAGR1,CDK10,MIR29A,MIR222,RGCC	grey	VSMC_M10
GO:0035581	0.68	0.59	4	8	sequestering of extracellular ligand from receptor	BP	1	FBN1,GREM2,CD46,NRROS	grey	VSMC_M10
GO:0032890	0.68	0.43	24	47	regulation of organic acid transport	BP	1	SLC12A2,PPARA,PLA2G6,AKT2,ARL6IP5,SLC43A1,PLA2R1,GRM2,SLC38A3,MAP2K6,ACSL5,AGT,ACE2,ATP1A2,PER2,NTSR1,PLA2G4A,FIS1,ARL6IP1,PSEN1,ABAT,STXBP1,RGS4,PTGES	grey	VSMC_M10
GO:0048820	0.68	0.54	6	12	hair follicle maturation	BP	1	ERCC2,FERMT1,TRPC4AP,TGFB2,RBPJ,WNT5A	grey	VSMC_M10
GO:0019724	0.68	0.40	45	87	B cell mediated immunity	BP	1	CD226,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,EXOSC3,MSH2,TRAF3IP2,HMCES,ERCC1,NECTIN2,MLH1,MYD88,FOXJ1,PAXIP1,SHLD1,HPX,IRF7,GAPT,SLA2,NBN,NOD2,CD40,TCIRG1,CD28,FCER1G,RNF168,BCL6,PTPN6,FOXP3,SHLD2,TBX21,BATF,CD19,IL4R,BTK,CD74,C7,C3,SUPT6H,BCL10,CD46,FCER2,RNF8,CD70	grey	VSMC_M10
GO:0002682	0.68	0.34	482	915	regulation of immune system process	BP	1	CD226,NME1,PHLPP1,STX7,TNFAIP3,USP15,ENPP3,ESR1,HSPA1B,BRD1,GRAMD4,AGER,GPSM3,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,XRCC6,TRIB1,MYC,TOB2,PTK2,C6orf106,MAPK14,PLA2G6,RAC2,HSF1,LRRC14,ZNF16,RBFOX2,FBXO7,TTBK1,TEC,CCL27,CDK6,KIT,TNFRSF21,NCK2,ROR2,NINJ1,EXOSC3,PRKCE,SMAP1,MSH2,RTN4,FPR2,HOXA7,ANKRD17,CXCL8,SLC46A2,MTURN,NOD1,AKIRIN2,PELI1,AKIRIN1,CNOT4,RSAD2,NR1H2,PTN,IL4I1,TLR4,IL15,ATG5,TRPM4,SLC7A11,FOXO3,PUM2,TRAF3IP2,SPHK2,HMCES,BMI1,C5AR2,C5AR1,PRKD2,CST7,PHB,SOX9,CD300LF,LACC1,CLPTM1,NECTIN2,PVR,EIF2B3,GAB2,MLH1,GLI2,UNC13D,MYD88,OXSR1,SLC22A13,PIBF1,FOXJ1,PAXIP1,IRAK2,SEC14L1,POU4F1,IL15RA,TGFBR2,ACVR2A,IKBKB,JAG1,SIRT2,NMI,TMEM173,CLPB,NPLOC4,PAWR,PLCB1,PLCL2,SHLD1,PRNP,MAVS,NCKAP1L,GAS6,HPX,FOXP1,MITF,PRKDC,IRF7,SLC7A1,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,SOX12,PLK2,MTUS1,HCK,TOX,ZC3H8,IL1A,GPI,ACVR1B,CAMK4,CEBPA,FER,PIK3CB,PIK3R1,OTUD4,LPXN,CASP3,ERAP1,FBXW7,PTPRJ,MEF2C,TMEM131L,IL7,TMBIM6,VEGFC,PAG1,JAM2,SLA2,PTK2B,RASGRP1,EIF2AK4,NR1H3,TRAFD1,OAS3,NLRC5,RIPK2,OTULIN,SLC8B1,AP3B1,F2RL1,TESC,RIPK1,ANO6,POLR3D,MARCH7,SOX13,MAPKBP1,ADTRP,HERC5,NOD2,ZNF335,ADCY7,CD40,LDB1,IGF2,RAB7B,MAPKAPK3,GPLD1,CD96,IFIH1,CD200,SPPL3,OASL,DNM1L,LCK,BANK1,ICOSLG,MAP2K6,TRPV4,SLC9B2,TGFB2,BTN2A2,GPAM,PRKAR1A,CD99,GPR137B,UNC93B1,PRSS56,POLR3C,PIAS3,HLX,DENND1B,TLR5,CMKLR1,NCF1,ACIN1,MAPKAPK2,TCTA,HCLS1,TBC1D10C,TIFA,ALPK1,YTHDF2,UBAS	grey	VSMC_M10
GO:0016242	0.68	0.45	16	32	negative regulation of macroautophagy	BP	1	NRBP2,USP36,FEZ2,LZTS1,SEC22B,TMEM39A,USP30,RUBCN,PINK1,PHF23,NPC1,SMCR8,CLEC16A,MTM1,TSC1,TIGAR	grey	VSMC_M10
GO:0072539	0.68	0.49	10	20	T-helper 17 cell differentiation	BP	1	RC3H1,TNFSF18,STAT3,FOXP3,TBX21,BATF,ZBTB7B,IL6R,MIR21,RC3H2	grey	VSMC_M10
GO:0010996	0.69	0.51	8	16	response to auditory stimulus	BP	1	PTN,SLC26A5,XPC,KIAA0319,ATP1A2,NRXN2,HTT,STRA6	grey	VSMC_M10
GO:0003283	0.69	0.49	10	20	atrial septum development	BP	1	SMO,WNT11,TBX5,TGFB2,ANK2,ISL1,SOX4,WNT5A,NKX2-5,HEY2	grey	VSMC_M10
GO:0050731	0.69	0.38	70	136	positive regulation of peptidyl-tyrosine phosphorylation	BP	1	ERBB3,IL5,HSF1,TEC,KIT,SEMA4D,IL11,EPGN,AREG,TGFA,IL15,HDAC2,ABI1,PIBF1,HBEGF,PRNP,NRG1,GAS6,HPX,ERCC6,OSBP,FBXW7,PTPRJ,PTK2B,ARL2BP,RIPK2,NOD2,CNTN1,CD40,IGF2,NEURL1,LRRK1,HDAC1,BANK1,ADRA2A,NCF1,EGF,HCLS1,ADNP,CASS4,PARP9,PARP14,AGT,OSM,IL12A,TNFSF18,DOK7,FGFR3,EPHA4,DLG4,DVL2,DGKQ,CTF1,EFNA1,IL6R,HAX1,CD74,CCL5,CSF1R,YES1,ISL1,GHR,UNC119,LRP8,MLST8,CNTF,CSPG4,LIF,TSLP,EREG	grey	VSMC_M10
GO:0060766	0.69	0.54	6	12	negative regulation of androgen receptor signaling pathway	BP	1	FOXH1,PHB,FOXP1,HDAC1,PIAS2,NCOR1	grey	VSMC_M10
GO:0006611	0.69	0.42	25	49	protein export from nucleus	BP	1	XPO5,XPO1,DNAJC27,SIRT7,GAS6,RAPGEF3,XPO7,SP100,TCF7L2,BAG3,STRADB,SFN,STRADA,UHMK1,DUSP16,CTDSPL2,RANBP17,XPO6,RANBP3L,PKD1,PARK7,NUP214,NUPL2,TXN,STYX	grey	VSMC_M10
GO:0060740	0.69	0.49	10	20	prostate gland epithelium morphogenesis	BP	1	ESR1,FRS2,HOXA13,TNC,SOX9,GLI2,CYP7B1,NKX3-1,NOG,WNT5A	grey	VSMC_M10
GO:0032094	0.69	0.48	11	22	response to food	BP	1	PPARA,MKKS,SLC16A1,CPS1,MPO,SCNN1B,SREBF1,GHR,SLC25A25,BCL10,HSD11B2	grey	VSMC_M10
GO:0010823	0.69	0.43	22	43	negative regulation of mitochondrion organization	BP	1	PRKN,TSPO,TMEM14A,OPA1,DNM1L,USP30,FZD9,MAPT,C11orf65,PINK1,MUL1,ADCK1,PSMD10,ACAA2,PAM16,NOL3,TIGAR,FXN,SLC35F6,BCL2L2,PPIF,AC140504.1	grey	VSMC_M10
GO:1902337	0.69	0.56	5	10	regulation of apoptotic process involved in morphogenesis	BP	1	PAX8,VDR,PAX2,TGFB2,TNFRSF1B	grey	VSMC_M10
GO:1904748	0.69	0.56	5	10	regulation of apoptotic process involved in development	BP	1	PAX8,VDR,PAX2,TGFB2,TNFRSF1B	grey	VSMC_M10

GO:0046474	0.69	0.37	96	185	glycerophospholipid biosynthetic process	BP	1	PIP4K2C,SYNJ2,AGPAT4,AGPAT1,PNPLA3,PLA2G6,GPAA1,CWH43,INPP4A,TMEM246,PIGF,MBOAT7,LPIN1,INPP4B,FIG4,MTMR2,PIP4K2A,SELENOI,ABHD5,TAMM41,ITPKC,MTMR14,PGAP2,CRLS1,CDS2,NR1H4,MTMR7,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,SLA2,SYNJ1,CDS1,ITPKA,PIGT,LPCAT1,PGAP1,GPAM,CHKA,ACP6,ABHD4,AJUBA,PITPNM1,GNPAT,DGKD,PIGM,BMX,FAM126B,IP6K2,PIGV,MTMR3,PCYT1A,INPP5J,PIGX,PIGZ,PISD,DGKG,PIKFYVE,PLA2G4A,SACM1L,LPCAT3,PIGC,SOCS4,PI4KA,SLC27A1,ABHD8,PGAP3,PIGH,PI4K2B,SOCS7,DGKQ,AC138894.1,DGKE,TTC7B,PIGL,ABHD3,MPPE1,IMPA2,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,AGPAT2,PIP5KL1,FABP5,PEMT,PYURF,LCLAT1,PIGB,PIGA,INPP1,PTPMT1,CDIPT	grey	VSMC_M10
GO:0031649	0.69	0.56	5	10	heat generation	BP	1	IL1A,SLC27A1,ABAT,TRPV1,PTGES	grey	VSMC_M10
GO:2000270	0.69	0.58	4	8	negative regulation of fibroblast apoptotic process	BP	1	CHD8,GAS6,CFDP1,MIR24-1	grey	VSMC_M10
GO:0046173	0.69	0.42	25	49	polyol biosynthetic process	BP	1	CYP27B1,AKR1B1,SPTLC1,IPPK,PLEK,SPHK2,DHFR,ITPKC,ACER3,SPTLC3,ASAH1,CYP2R1,P2RY1,PTK2B,SPR,ITPKA,GPER1,IP6K2,NTSR1,PTH1R,CYP27A1,GCH1,IMPA2,ACER2,PCBD2	grey	VSMC_M10
GO:0042921	0.69	0.53	6	12	glucocorticoid receptor signaling pathway	BP	1	CRY1,PHB,ARNTL,CRY2,ARID1A,YWHAH	grey	VSMC_M10
GO:0036315	0.69	0.49	9	18	cellular response to sterol	BP	1	PTCH1,SMO,CYP7A1,GPLD1,DAG1,GRAMD1B,OSBPL7,LRP8,INSIG2	grey	VSMC_M10
GO:0050892	0.69	0.47	12	24	intestinal absorption	BP	1	ABCG5,ABCG8,SOAT2,PLS1,LIMA1,VDR,ADRA2A,EPB41,LPCAT3,LDLR,SLC46A1,CEL	grey	VSMC_M10
GO:0000183	0.69	0.58	4	8	rDNA heterochromatin assembly	BP	1	BAZ2A,SIRT2,PHF8,BEND3	grey	VSMC_M10
GO:0035584	0.69	0.50	8	16	calcium-mediated signaling using intracellular calcium source	BP	1	PRNP,PTPRJ,DMTN,RYR2,HOMER2,FIS1,BCAP31,PTGFR	grey	VSMC_M10
GO:0098771	0.69	0.35	262	502	inorganic ion homeostasis	BP	1	SLC39A5,NEDD4L,LRP1,CYP27B1,ESR1,SLC12A2,PRKN,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,CKB,BTBD9,TMPRSS6,SLC39A4,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,CNNM4,PRKCE,TNNI3,EPAS1,FPR2,IBTK,SLC4A4,LPAR1,PPT1,SLC31A2,EGFR,SFRP4,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,STEAP3,AQP11,ATP1A3,ACKR2,SLC24A3,SNX5,C1QTNF1,SLC4A7,TMEM106B,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,KL,CCKBR,HPX,RASA3,NCOA4,MICU3,ATP6V1H,TM9SF4,IL1A,IMMT,C19orf12,P2RX3,PLCE1,SLC9A9,RYR3,TMBIM6,P2RX7,HVCN1,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,SLC25A37,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,CUTC,ABCC2,PKD2,CASQ2,MCUR1,SLC12A5,CD40,RYR2,SLC41A1,SLC4A10,RAP1GDS1,TRPM1,SPPL3,LCK,KCNJ2,TESMIN,SLC9B1,SLC12A7,TRPV4,BDH2,TMEM9,SLC30A10,TCIRG1,FAM20A,GNA13,ISCU,CMKLR1,MCUB,HJV,SLC9A8,SCN7A,UBASH3B,DISC1,ANK2,GPER1,SLAMF8,RHCG,TRPM8,PDZD8,AGT,ATP1A2,SLC9A1,CASQ1,SLC12A8,NTSR1,XPR1,CLIC4,MELTF,FZD9,TMCO1,PTH1R,SLC30A4,FIS1,CEMIP,ABL2,SLC12A9,CDH23,COMT,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,SLC9A7,ATP6V0A1,ABCB6,TRPM7,ATP1B1,KCNA1,CD38,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP13A2,FTH1,HAP1,DLG4,CYB561A3,FGFR4,ATP1B2,FAM155B,PSEN1,CACNA1A,MAPK3,AC138894.1,ATP2A1,CD19,COX11,SMAD3,CLN6,NOX5,CALM1,SNAPIN,S100A14,S100A8,PRKCB,SCNN1B,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,C7,PTGER4,SLC25A23,MAIP1,TMEM199,SLC46A	grey	VSMC_M10
GO:0033523	0.69	0.56	5	10	histone H2B ubiquitination	BP	1	RNF20,UBE2E1,DTX3L,LEO1,RNF8	grey	VSMC_M10
GO:0090178	0.69	0.56	5	10	regulation of establishment of planar polarity involved in neural tube closure	BP	1	PTK7,DVL3,GRHL3,DVL2,WNT5A	grey	VSMC_M10
GO:0090657	0.69	0.55	5	10	telomeric loop disassembly	BP	1	POT1,WRN,RTEL1,SLX4,TERF2	grey	VSMC_M10
GO:0030032	0.69	0.41	31	61	lamellipodium assembly	BP	1	AVIL,RAC2,KIT,NCK2,AKIRIN1,ARHGEF4,ARHGEF7,SPEF1,ARFIP2,AL359736.1,FER,PIK3R1,PLCE1,BIN3,CYFIP1,DMTN,CARMIL1,AUTS2,AJUBA,WASF2,HDAC4,PTPRO,WHAMM,NCKAP1,ABLIM2,VCL,WAS,DNM2,ARHGEF6,VAV3,CARMIL2	grey	VSMC_M10
GO:0046320	0.69	0.46	13	26	regulation of fatty acid oxidation	BP	1	PPARA,SOX9,PRKAG2,AKT2,LONP2,SIRT4,IRS1,CPT1A,ABCB11,ACADL,TYSND1,ACADVL,MLYCD	grey	VSMC_M10
GO:1904350	0.69	0.55	5	10	regulation of protein catabolic process in the vacuole	BP	1	LRP1,MFSD8,ATP13A2,LDLR,RNF128	grey	VSMC_M10
GO:0061383	0.69	0.43	20	40	trabecula morphogenesis	BP	1	ADGRG6,FOXH1,TEK,SRF,FHL2,SEMA4D,OVOL2,NRG1,ADAMTS1,TGFB2,BMPR1A,RBPJ,MED1,THBS3,CHAD,PPARGC1B,ENG,RHOA,NOG,HEY2	grey	VSMC_M10
GO:1905165	0.69	0.58	4	8	regulation of lysosomal protein catabolic process	BP	1	LRP1,MFSD8,ATP13A2,LDLR	grey	VSMC_M10
GO:1904754	0.69	0.50	8	16	positive regulation of vascular associated smooth muscle cell migration	BP	1	LRP1,ADAMTS1,DOCK5,TERT,SSH1,AGT,DOCK7,MIR221	grey	VSMC_M10
GO:0002755	0.69	0.49	9	18	MyD88-dependent toll-like receptor signaling pathway	BP	1	TLR4,CD300LF,MYD88,IRAK2,IRF7,TRAF6,TLR5,BTK,TNIP1	grey	VSMC_M10
GO:0072520	0.69	0.53	6	12	seminiferous tubule development	BP	1	WDR48,ING2,SPATA2,UBB,ADGRG1,TBC1D20	grey	VSMC_M10
GO:0044546	0.69	0.53	6	12	NLRP3 inflammasome complex assembly	BP	1	ATAT1,TLR4,MYD88,EIF2AK2,DDX3X,CPTP	grey	VSMC_M10
GO:0140632	0.69	0.53	6	12	inflammasome complex assembly	BP	1	ATAT1,TLR4,MYD88,EIF2AK2,DDX3X,CPTP	grey	VSMC_M10
GO:1900225	0.69	0.53	6	12	regulation of NLRP3 inflammasome complex assembly	BP	1	ATAT1,TLR4,MYD88,EIF2AK2,DDX3X,CPTP	grey	VSMC_M10
GO:0044804	0.69	0.52	7	14	autophagy of nucleus	BP	1	ATG12,ATG5,ULK1,ATG2A,ATG9A,WIPI2,ATG2B	grey	VSMC_M10
GO:0045780	0.69	0.52	7	14	positive regulation of bone resorption	BP	1	EGFR,SPP1,ADAM8,PPARGC1B,ATP6AP1,DEF8,CA2	grey	VSMC_M10
GO:0032528	0.69	0.48	10	20	microvillus organization	BP	1	ATP8B1,MYO1A,PODXL,KLF5,PLS1,RAPGEF2,USH1C,RAP1GAP,GLDN,STK26	grey	VSMC_M10
GO:0060717	0.69	0.58	4	8	chorion development	BP	1	MAP3K4,PAXIP1,HTRA1,FZD5	grey	VSMC_M10
GO:0000712	0.69	0.52	7	14	resolution of meiotic recombination intermediates	BP	1	MLH1,EME1,ERCC4,SLX4,MEIOB,MSH4,CENPX	grey	VSMC_M10
GO:0060998	0.69	0.41	27	54	regulation of dendritic spine development	BP	1	FSTL4,ASAP1,SHANK1,HDAC2,PLK2,MEF2C,CUX2,TIAM1,OPA1,ITPKA,SRGAP2C,NEURL1,DNM1L,CAPRIN2,DISC1,CDKL5,TANC2,DNM3,SDK1,PSEN1,EFNA1,GPRASP2,BHLHB9,FMR1,LRP8,LLPH,FOXO6	grey	VSMC_M10

GO:0090630	0.69	0.39	47	93	activation of GTPase activity	BP	1	TBC1D30,TBC1D9B,TIAM2,TBC1D22B,TBC1D8,ARHGEF5,EPHA1,TBC1D9,TBC1D4,FOXJ1,AKT2,TBC1D16,TBC1D12,ARHGEF26,PTK2B,RASGRP1,TIAM1,ARHGAP24,TBCK,ADPRH,TBC1D10C,TBC1D2B,GMIP,TBC1D14,RABGAP1L,RUNDC1,RAP1GAP,TBC1D25,ARHGEF19,SYDE1,TBC1D1,TBC1D10B,NDEL1,BCAS3,TBC1D8B,DOCK7,ABR,CRK,RAP1GAP2,TAX1BP3,ARHGEF16,APC2,ARHGAP45,TSC1,MTSS1L,RABGAP1,WNT5A	grey	VSMC_M10
GO:0098868	0.69	0.47	12	24	bone growth	BP	1	BNC2,COL27A1,SOX9,TSKU,TGFBR2,RARB,STC1,POR,FGFR3,MMP13,THBS3,LEPR	grey	VSMC_M10
GO:0060343	0.69	0.48	10	20	trabecula formation	BP	1	ADGRG6,TEK,SRF,FHL2,OVOL2,ADAMTS1,THBS3,CHAD,PPARGC1B,HEY2	grey	VSMC_M10
GO:0070997	0.69	0.35	150	288	neuron death	BP	1	ERBB3,LRP1,MAP3K5,AGAP2,PRKN,PPARA,SYNGAP1,NCOA7,GRM4,ATF4,NTRK2,NRBP2,HSF1,FBXO7,CNTFR,SLC25A27,SLC1A1,TNFRSF21,TFAP2B,GAPDH,MSH2,REL,PPT1,EPHA7,TLR4,VPS35,SLC7A11,FOXO3,NTF4,FGF21,NDNF,C5AR1,ZNF746,GRIK5,XRCC2,EGLN2,POU4F1,AKT2,ARRB1,TMTC4,SLC23A2,PRNP,ARL6IP5,EPHB1,GPI,RILPL1,CASP3,GBE1,DIABLO,FBXW7,TRIM2,MEF2C,FAIM2,HTRA2,PTK2B,NR4A2,F2R,NQO2,TFAP2A,PIGT,SIAH1,PM20D1,BDNF,CD200,HDAC1,TERT,TGFB2,SLC30A10,ADARB1,SCN2A,INPP5A,SSH1,KCNB1,KRAS,ADNP,SORL1,MCL1,CBL,HYOU1,SLC9A1,NFATC4,HDAC4,DLX1,BACE1,DNAJC5,FZD9,EGLN3,SNX6,MAP3K11,ADAM8,CREB1,MAPT,NONO,FIS1,PINK1,STAT3,ATP13A2,PARP1,MAX,TNFRSF1B,PSEN1,ITGAM,NGFR,FOS,AC138894.1,CITED1,ALKBH1,GPRASP2,BHLHB9,CCL5,AP2B1,PPP1R13B,CCL2,CDK5R1,ISL1,GHR,JUN,PDPK1,MECP2,TRAF2,IKBKG,TMEM259,PARK7,TSC1,TLDC1,LCN2,STXBP1,AARS,HSPA5,NQO1,NAE1,MIR125B1,RHOA,UBB,CHGA,FADD,GRID2,CNTF,CASP8,PSMC1,WNT5A,TIGAR,DIO3,SIX1,DDIT3,BCL2L11,HRAS,CEBPB,PITX3,NMNAT1	grey	VSMC_M10
GO:0010225	0.69	0.53	6	12	response to UV-C	BP	1	MAP3K4,BAK1,WRN,DCUN1D3,YY1,IMPACT	grey	VSMC_M10
GO:2000319	0.69	0.51	7	14	regulation of T-helper 17 cell differentiation	BP	1	RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,MIR21,RC3H2	grey	VSMC_M10
GO:0061820	0.69	0.58	4	8	telomeric D-loop disassembly	BP	1	POT1,WRN,SLX4,TERF2	grey	VSMC_M10
GO:0003416	0.69	0.47	11	22	endochondral bone growth	BP	1	BNC2,COL27A1,SOX9,TSKU,TGFBR2,RARB,STC1,POR,FGFR3,MMP13,THBS3	grey	VSMC_M10
GO:0016188	0.69	0.55	5	10	synaptic vesicle maturation	BP	1	RAB3A,DLG4,ZDHHC15,SNAPIN,STXBP1	grey	VSMC_M10
GO:0017085	0.69	0.58	4	8	response to insecticide	BP	1	FECH,DDC,UBA52,SCN2B	grey	VSMC_M10
GO:0014047	0.69	0.53	6	12	glutamate secretion	BP	1	NTRK2,APBA1,GRM2,NTSR1,TRPV1,STXBP1	grey	VSMC_M10
GO:0015732	0.69	0.51	7	14	prostaglandin transport	BP	1	ABCC4,ABCC2,MAP2K6,SLCO3A1,PLA2G4A,NOS2,PTGES	grey	VSMC_M10
GO:0016070	0.69	0.32	1852	3480	RNA metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,RNMT,TBPL1,GLI1,MARS,CLK4,MAP3K5,TNFAIP3,TSFM,HIVEP2,ADAT2,PLAGL1,MAML1,HELB,RPP21,ZBTB2,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,ZFC3H1,CNOT6,RIDA,STK3,OSR2,PABPC1,SNW1,TFB1M,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,PRKN,QKI,AGER,TRMU,PPARA,PDE10A,UTP23,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,RRP7A,HSF2,TCF7,PHF1,XRCC6,NCOA7,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,HABP4,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,ATF4,TUT7,RPAP2,CBX7,APOBEC3H,GTPBP1,MAPK14,CBY1,PUF60,C9orf64,KDM4C,SOX10,PIM1,CMTR1,NRF1,TMPRSS6,EXOSC4,SMO,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,FOXH1,LRRC14,RBM28,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,ZNF318,NFX1,NOL6,XPO5,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TSR1,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,CNOT11,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,MTO1,SP4,TSEN34,PRPF31,IGF2BP3,PPP2R1A,ZNF462,TRA2A,PHIP,HMGN3,ELP1,YTHDC1,NFYC,NFE2L3,PNPT1,UTP3,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,PUS10,ZNF483,JAZF1,CREB5,PTBP3,MYCL,TRIT1,XPO1,MTURN,NOD1,AKIRIN2,RNGTT,SRSF10,MDN1,CASP8AP2,BACH2,ZN	grey	VSMC_M10
GO:0001709	0.69	0.45	15	30	cell fate determination	BP	1	PTCH1,HOXA2,NTF4,PTCH2,JAG1,MEF2C,EBF2,PAX2,MCL1,TBX2,GATA6,ISL1,BARHL2,FOXG1,LBX1	grey	VSMC_M10
GO:0061517	0.69	0.55	5	10	macrophage proliferation	BP	1	PTK2,MAPK1,MAPK3,CSF1R,IL33	grey	VSMC_M10
GO:0070229	0.69	0.47	11	22	negative regulation of lymphocyte apoptotic process	BP	1	SLC46A2,FOXP1,GPAM,BCL6,EFNA1,CD74,CCL5,IL7R,BCL10,FADD,TSC22D3	grey	VSMC_M10

GO:0007283	0.69	0.35	187	357	spermatogenesis	BP	1	TBPL1,GLI1,YTHDC2,B4GALNT1,ATAT1,TSPAN8,IGF2R,MOV10L1,PACRG,QKI,BRD2,ROS1,HSF2,UBE2B,CATSPER3,H3F3C,DMC1,SPATA31D3,CFAP69,FANCG,SMARCA2,TDRD6,KIT,CCIN,TSGA10,TDRD7,DNAJA1,FOXJ3,SCMH1,RAD23B,YTHDC1,CABS1,HERPUD2,GMCL1,CCDC155,CREM,ARMC2,DLD,TXNRD3,APOB,SPATA6,SPATA5,TTC26,DNMT3A,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,MLH1,ACOX1,FOXJ1,WDR48,TTC21A,CCNB1IP1,ACVR2A,MKKS,SPATA24,ADAM18,GOLGA3,PANK2,BTG1,SOHLH2,TEX15,KATNAL1,NPHP1,ING2,SPATA9,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,PRKAG1,SFMBT1,AP3B1,CDYL,SYCP1,DNAH1,DPCD,OCA2,ROPN1L,SIAH1,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,TESMIN,SPATA2,RNF114,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,TSSK4,CIB1,CCDC87,DDX6,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,SEPT2,LIMK2,PATZ1,CATSPER2,OVOL1,YBX3,CADM1,SPATA32,GGT2,TTC12,BCL6,RPL10L,SPAG16,ZCWPW1,CTSV,BIRC3,ADCY10,PARP11,CALR3,KDM5A,ZMYND15,MNS1,YBX2,MYCBPAP,VIPAS39,SOX30,CCDC42,CREB3L4,RAD51C,DNM2,YY1,TAF4B,ALKBH5,JAG2,IFT20,ACSBG2,TXNDC2,SPEF2,CATSPERD,ZNF449,HSPB11,BCAP31,RNF151,TMEM203,GAMT,CHD5,SOX8,TPGS1,MFSD14A,LRRC8A,STRBP,TSNAXIP1,MSH4,FSTL3,AURKC,SYCP3,ARID4A,TCFL5,NKAPL,METTL14,FOXJ2,TDRP,ZSCAN21,ZFP41,GGT5,RNF8,BCL2L11,TBC1D20,ZNF35,BCL2L2,ZGLP1,SPA17,ZNF628	grey	VSMC_M10
GO:0090311	0.69	0.42	21	42	regulation of protein deacetylation	BP	1	C6orf89,SPHK2,PRKD2,BEX4,TADA3,SDR16C5,ING2,MAPT,BCL6,PINK1,KDM5A,FOXP3,AKAP8L,AKAP8,JDP2,ZBTB7B,SREBF1,SKI,PRMT6,SAP30BP,NNMT	grey	VSMC_M10
GO:2001014	0.69	0.49	9	18	regulation of skeletal muscle cell differentiation	BP	1	AKIRIN1,NR1D2,EPHB1,NLN,ARNTL,MEF2C,RBM24,SIX1,UQCC2	grey	VSMC_M10
GO:0010800	0.69	0.47	11	22	positive regulation of peptidyl-threonine phosphorylation	BP	1	PRKAG2,RPTOR,RIPK2,EGF,STOX1,CEMIP,MAPK1,WNK3,CALM1,IRGM,WNT5A	grey	VSMC_M10
GO:0001771	0.69	0.55	5	10	immunological synapse formation	BP	1	NCK2,EPHB1,DLG1,DOCK2,HAVCR2	grey	VSMC_M10
GO:0043369	0.69	0.51	7	14	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	BP	1	TOX,TNFSF18,STAT3,FOXP3,TBX21,BATF,IL6R	grey	VSMC_M10
GO:0150012	0.69	0.58	4	8	positive regulation of neuron projection arborization	BP	1	DVL3,DLG4,DVL2,WNT5A	grey	VSMC_M10
GO:0048096	0.69	0.55	5	10	chromatin-mediated maintenance of transcription	BP	1	ARID1B,SMARCD1,ARID1A,PADI2,SERTAD2	grey	VSMC_M10
GO:0061314	0.69	0.55	5	10	Notch signaling involved in heart development	BP	1	GALNT11,JAG1,SNAI1,RBPJ,HEY2	grey	VSMC_M10
GO:0021549	0.69	0.39	39	77	cerebellum development	BP	1	GLI1,UQCRQ,AGTPBP1,CKB,SMO,SEMA4C,WHRN,PTN,XRCC1,GLI2,B4GALT2,SCN5A,CLP1,FAIM2,RPGRIP1L,CNTN1,LDB1,TTBK2,TTC21B,GNPAT,GBX2,SPTBN2,HAP1,PSEN1,MAP2K1,LHX1,CDK5R1,SEZ6,DAB1,ABAT,CRK,SDF4,MECP2,AARS,HSPA5,GRID2,NANOS1,CEND1,PDSS2	grey	VSMC_M10
GO:0043508	0.69	0.55	5	10	negative regulation of JUN kinase activity	BP	1	DNAJA1,PDCD4,AIDA,DUSP10,DUSP19	grey	VSMC_M10
GO:0040019	0.69	0.50	8	16	positive regulation of embryonic development	BP	1	NLRP5,OSR1,PLCB1,CFL1,WNT4,LHX1,AMOT,TLE6	grey	VSMC_M10
GO:0014829	0.69	0.46	12	24	vascular associated smooth muscle contraction	BP	1	ZDHHC21,MKKS,ADRA2B,DOCK5,CHRM3,RAP1GDS1,AGT,CD38,SCNN1B,P2RX1,MIR21,RHOA	grey	VSMC_M10
GO:0034309	0.69	0.55	5	10	primary alcohol biosynthetic process	BP	1	DKK3,WNT4,DGKQ,CACNA1H,PARK7	grey	VSMC_M10
GO:0086011	0.69	0.49	9	18	membrane repolarization during action potential	BP	1	KCNJ3,KCNE2,KCNIP2,KCNJ2,NOS1AP,ATP1B1,RNF207,KCNH2,KCNJ8	grey	VSMC_M10
GO:0050714	0.69	0.38	51	100	positive regulation of protein secretion	BP	1	LRP1,PLA2G6,PRKCE,NR1H2,EGFR,TLR4,TRPM4,GIPR,FRMD4A,APBB3,SIRT3,IL1A,OSBP,VEGFC,NNAT,PFKM,NKX6-1,F2RL1,GPLD1,DNM1L,TGFB2,TCF7L2,PFKFB2,GPER1,GLUL,ADAM8,TTN,MCU,PPP3CB,CD38,MPC2,ATP13A2,NLGN2,TARDBP,STX4,TMED10,MYH10,SYTL4,GPR68,ISL1,OXCT1,ABAT,RPH3AL,NADK,BAIAP3,LRRC8A,FGA,SOX4,CRH,DOC2B,PARD6A	grey	VSMC_M10
GO:0072075	0.69	0.51	7	14	metanephric mesenchyme development	BP	1	MYC,OSR1,PKD2,PAX2,WNT4,BASP1,SIX1	grey	VSMC_M10
GO:0001711	0.69	0.55	5	10	endodermal cell fate commitment	BP	1	EOMES,RTF1,SOX2,LEO1,GATA6	grey	VSMC_M10
GO:0006378	0.69	0.43	20	40	mRNA polyadenylation	BP	1	CPSF6,PABPC1,ZC3H3,HSF1,CPSF1,RNF20,YTHDC1,PNPT1,MTPAP,SYMPK,PCF11,CSTF3,CLP1,TENT2,TENT4B,CPSF2,LEO1,AP002990.1,CSTF2,PAPOLA	grey	VSMC_M10
GO:0043619	0.69	0.55	5	10	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	BP	1	ATF4,EPAS1,ARNT,NFE2L2,SIN3A	grey	VSMC_M10
GO:0070664	0.69	0.41	27	53	negative regulation of leukocyte proliferation	BP	1	TNFAIP3,ENPP3,TNFRSF21,PELI1,IL4I1,FOXJ1,PAWR,PRNP,CASP3,TMEM131L,MARCH7,BTN2A2,PRKAR1A,DLG1,VSIR,RC3H1,PTPN6,SCGB1A1,FOXP3,ZBTB7B,BTK,TWSG1,GLMN,LST1,IL33,CEBPB,HAVCR2	grey	VSMC_M10
GO:0035994	0.69	0.48	10	20	response to muscle stretch	BP	1	PTK2,MAPK14,RAF1,GPI,RYR2,SLC9A1,TTN,TCAP,FOS,DMD	grey	VSMC_M10
GO:0060544	0.69	0.48	10	20	regulation of necroptotic process	BP	1	PELI1,RIPK1,SPATA2,FZD9,YBX3,BIRC3,OGT,MIR22,FADD,CASP8	grey	VSMC_M10
GO:1901894	0.69	0.58	4	8	regulation of ATPase-coupled calcium transmembrane transporter activity	BP	1	RYR2,C4orf3,ATP2A1,VMP1	grey	VSMC_M10
GO:0032957	0.69	0.58	4	8	inositol trisphosphate metabolic process	BP	1	P2RY1,PTK2B,ITPK1,GPER1	grey	VSMC_M10
GO:0036336	0.69	0.49	9	18	dendritic cell migration	BP	1	TRPM4,GAS6,ANO6,SLAMF8,EPS8,IL12A,TNFSF18,CXCR2,CCL5	grey	VSMC_M10
GO:1904683	0.69	0.58	4	8	regulation of metalloendopeptidase activity	BP	1	SORL1,STAT3,MIR21,MIR24-1	grey	VSMC_M10
GO:0010663	0.69	0.55	5	10	positive regulation of striated muscle cell apoptotic process	BP	1	MAP3K5,AGT,CXCR2,CAMK2A,TIGAR	grey	VSMC_M10
GO:0010666	0.69	0.55	5	10	positive regulation of cardiac muscle cell apoptotic process	BP	1	MAP3K5,AGT,CXCR2,CAMK2A,TIGAR	grey	VSMC_M10
GO:0055062	0.69	0.58	4	8	phosphate ion homeostasis	BP	1	TFAP2B,SFRP4,XPR1,FGFR4	grey	VSMC_M10
GO:0072506	0.69	0.58	4	8	trivalent inorganic anion homeostasis	BP	1	TFAP2B,SFRP4,XPR1,FGFR4	grey	VSMC_M10

GO:0042592	0.69	0.33	681	1295	homeostatic process	BP	1	ZNF236,NME1,ORMDL2,SLC39A5,NEDD4L,LRP1,TNFAIP3,CYP27B1,ESR1,APOM,MPIG6B,SLC12A2,HSPA1B,BRD1,PRKN,AGER,TNFRSF11B,PNPLA3,PNPLA5,TSPO,SMDT1,BAK1,MYC,SMAD5,L3MBTL3,KLHL3,MCHR1,GPR20,PTCH1,FANCC,AKR1B1,ATF4,MAPK14,PLA2G6,CKB,BTBD9,RAC2,TMPRSS6,SMO,TTC39B,TXN2,HSF1,SLC39A4,ZNF16,RBFOX2,LARGE1,ALDH1A1,CRY1,SRF,STEAP2,CLDN12,TXNRD1,OCIAD1,CDK6,SLC25A27,KIT,SLC1A1,TFAP2B,GADD45G,KIAA1211,S1PR3,WNK2,PRDX1,RPS14,CNNM4,ABCG5,ABCG8,ERP44,PRKCE,SMAP1,TNNI3,EPAS1,RTN4,FPR2,HMGN3,IBTK,SLC4A4,CYB5R4,HOXA13,LPAR1,PPT1,PTBP3,ALB,SLC46A2,BMP8A,AQP1,BPGM,SLC31A2,MTF1,NR1H2,WHRN,GRHL1,MET,GRB10,POU3F3,EGFR,USP45,TRIM32,TLR4,NCDN,LPIN1,IL15,SFRP4,KEL,UCP1,ATG5,TRPM4,SLC7A11,FOXO3,DLD,TXNRD3,APOB,FGF21,TRAF3IP2,GRIN2D,LAMA4,TRPC3,SESN3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,NAPEPLD,ATP7B,PTGIR,CNBP,FOXA3,SOX9,GIPR,ABHD5,CACNB2,ERCC2,SLC39A12,ATP6V0E2,CUBN,LACC1,SLC4A2,USH1G,DEDD2,CLNS1A,STEAP3,AQP11,GRIK5,RAF1,ATP1A3,ACOX1,PRDX3,ACVR2B,SCN5A,WDR48,EGLN2,SLC25A38,GCKR,TSKU,ELOVL1,ALK,ACKR2,SLC24A3,GPD1L,SNX5,ACVR2A,C1QTNF1,SLC4A7,MKKS,ACTG1,NR1D2,TMEM106B,ASPSCR1,PLCL2,TMTC4,MAFG,RYR1,RAC3,LETM2,PRNP,ADRA1D,DCN,DIAPH1,P2RX2,KL,CCKBR,NCKAP1L,GAS6,HPX,RASA3,PRKDC,ERCC6,MFHAS1,NCOA4,TRAF6,COMMD9,NR1H4,MICU3,TUB,ATP6V1H,GAPT,USF2,ACOXL,SOAT2,LSR,CYP7A1,TM9SF4,ZC3H8,NDUFAF2,ASXL1,IL1A,CYP7B1,ACOX2,GPI,ACVR1B,ABHD6,CEBPA,IDE,IMMT,PIK3CB,OSBP,C19orf12,PIK3R1,SLMAP,CASP3,CH	grey	VSMC_M10
GO:0002888	0.69	0.51	7	14	positive regulation of myeloid leukocyte mediated immunity	BP	1	MAVS,F2RL1,STX4,ITGAM,BTK,C3,TICAM1	grey	VSMC_M10
GO:0070193	0.69	0.47	10	20	synaptonemal complex organization	BP	1	UBE2B,TEX15,SYCP1,SPO11,TEX12,STAG3,P3H4,SYCE2,AGO4,SYCE1L	grey	VSMC_M10
GO:0060677	0.69	0.58	4	8	ureteric bud elongation	BP	1	FMN1,SALL1,SIX1,FGF1	grey	VSMC_M10
GO:1903524	0.69	0.45	13	26	positive regulation of blood circulation	BP	1	SLC1A1,TRPM4,ADRA1D,RYR2,TGFB2,ACE2,ATP1A2,PTGER2,GCH1,CHGA,RGS4,NKX2-5,HEY2	grey	VSMC_M10
GO:1905564	0.69	0.51	7	14	positive regulation of vascular endothelial cell proliferation	BP	1	IGF2,ITGA4,STAT3,PDPK1,MIR29A,MIR21,MIR27A	grey	VSMC_M10
GO:0010635	0.69	0.53	6	12	regulation of mitochondrial fusion	BP	1	PRKN,OPA1,DNM1L,ZDHHC6,MUL1,ADCK1	grey	VSMC_M10
GO:0043524	0.69	0.37	59	115	negative regulation of neuron apoptotic process	BP	1	ERBB3,LRP1,AGAP2,PRKN,SYNGAP1,NTRK2,NRBP2,CNTFR,SLC1A1,TFAP2B,MSH2,PPT1,NTF4,NDNF,C5AR1,XRCC2,POU4F1,ARRB1,GPI,GBE1,MEF2C,FAIM2,PTK2B,NR4A2,F2R,BDNF,HDAC1,TERT,SLC30A10,KRAS,ADNP,HYOU1,NFATC4,DLX1,DNAJC5,FZD9,SNX6,ADAM8,NONO,PINK1,PSEN1,AC138894.1,CITED1,ALKBH1,GPRASP2,BHLHB9,CCL2,ISL1,PDPK1,MECP2,PARK7,STXBP1,AARS,RHOA,CNTF,SIX1,HRAS,CEBPB,NMNAT1	grey	VSMC_M10
GO:1900017	0.70	0.48	9	18	positive regulation of cytokine production involved in inflammatory response	BP	1	GPSM3,TLR4,MYD88,NOD2,STAT3,TICAM1,MIR21,IL17D,IL17B	grey	VSMC_M10
GO:1904353	0.70	0.46	12	24	regulation of telomere capping	BP	1	MAP3K4,MAPK15,ERCC1,XRCC1,MAPKAPK5,NBN,RTEL1,MAPK1,MAPK3,ERCC4,TERF2,MAP2K7	grey	VSMC_M10
GO:0016322	0.70	0.55	5	10	neuron remodeling	BP	1	ANKS1A,RND1,FARP2,C1QL1,C3	grey	VSMC_M10
GO:0021783	0.70	0.51	7	14	preganglionic parasympathetic fiber development	BP	1	PLXNA4,SEMA3A,TFAP2A,SEMA3F,ADARB1,PLXNA3,SIX1	grey	VSMC_M10
GO:0010464	0.70	0.45	13	26	regulation of mesenchymal cell proliferation	BP	1	MYC,SMO,PTN,MYCN,SOX9,WNT11,TGFBR2,CHRD,BMPR1A,FOXF1,WNT5A,SIX1,WNT2	grey	VSMC_M10
GO:0010829	0.70	0.52	6	12	negative regulation of glucose transmembrane transport	BP	1	GRB10,PEA15,RSC1A1,PRKCB,INPP5K,FABP5	grey	VSMC_M10
GO:0006857	0.70	0.52	6	12	oligopeptide transport	BP	1	SLC7A11,ABCC4,ABCB9,CDH17,ABCC5,CA2	grey	VSMC_M10
GO:0043414	0.70	0.35	132	254	macromolecule methylation	BP	1	BAZ2A,RNMT,ARMT1,SNW1,TFB1M,MOV10L1,PHF1,TRMT11,MYC,PICK1,CMTR1,PRDM4,CAMKMT,RNF20,STPG4,MTO1,SETD7,DNMT3A,BMI1,SETDB2,NSUN6,EED,IWS1,SUV39H2,KDM4A,PAXIP1,THUMPD3,DPY30,SIRT7,CHTOP,TRMT6,NSD3,NDUFAF7,ASH2L,BTG1,WTAP,TEX15,THUMPD2,TRMT9B,NR1H4,TGS1,DIMT1,EEF1AKMT1,DNMT3B,SMYD1,PRMT9,BCDIN3D,SETD6,KMT2D,NSUN3,RTF1,PRMT3,WDR82,ZNF335,JARID2,RBBP5,FAM173B,MTRR,HEMK1,TRMT10A,AUTS2,DALRD3,LCMT2,METTL8,EEF1AKMT2,TDRKH,NSUN5,MGMT,METTL2B,SETD2,TRMT1L,TET1,SNRPD3,BCOR,MEN1,WDR61,VCPKMT,MEPCE,ALKBH8,NELFA,TRMT5,DYDC1,PARP1,HSD17B10,PRDM2,MRM2,ZCCHC4,NSD1,SETD1A,PAGR1,FOS,OGT,RAB3D,LCMT1,SETD3,METTL4,SUZ12,METTL6,SUPT6H,CXXC1,MBD1,MRM3,CREBBP,METTL16,DOT1L,MECP2,PRDM16,CHD5,MTF2,GFI1,CMTR2,PRMT7,CTCF,MIR29A,PRMT6,METTL18,SETDB1,PRDM6,ARID4A,METTL14,TRMT10B,BEND3,SMYD3,METTL21A,TRMT61A,ZNF304,NNMT,N6AMT1,TRMT10C,TRMT61B,CBLL1,TYW3	grey	VSMC_M10
GO:0043249	0.70	0.55	5	10	erythrocyte maturation	BP	1	BRD1,L3MBTL3,PTBP3,ERCC2,FAM210B	grey	VSMC_M10
GO:0003129	0.70	0.57	4	8	heart induction	BP	1	WNT11,ROBO1,ROBO2,WNT5A	grey	VSMC_M10

GO:1904062	0.70	0.35	125	241	regulation of cation transmembrane transport	BP	1	NEDD4L,STAC3,MAPK8IP2,PRRT1,PLA2G6,WNK2,TSPAN13,PRKCE,SHANK1,SLC31A2,HECW1,KEL,ATG5,OSR1,SPHK2,KCNRG,CACNB2,STAC,OXSR1,SCN5A,GPD1L,CACNB4,PRNP,DIAPH1,KCNIP3,SLMAP,SLC43A1,GLRX,MEF2C,PTK2B,KCNJ11,HOMER1,IFNGR2,F2R,TESC,ANO6,KCNE2,PKD2,CASQ2,KCNIP2,RYR2,FAM173B,PM20D1,HECW2,KCNJ2,ADRA2A,TCIRG1,COX17,ISCU,KCNG1,UBASH3B,ANK2,GPER1,KLHL24,AGT,ACE2,ATP1A2,SLC9A1,C4orf3,CASQ1,NTSR1,SCN4B,CNIH2,DNAJC30,NOS1AP,DLG1,CEMIP,SESTD1,PTPN6,HTT,PINK1,ATP1B1,KCNA1,GNB5,MINK1,HAP1,DLG4,PSEN2,NLGN2,CNIH3,WNK3,STAC2,CACNB1,ATP1B2,KCNAB3,KCNIP1,NLGN3,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,CCL2,FMR1,PDPK1,P2RX1,RNF207,PARK7,AMIGO1,CYBA,JPH3,LCN2,WWP2,RRAD,MIR21,MIR24-1,DMD,GPR35,JPH2,KCNH2,FGF11,THY1,SCN2B,NETO2,CACNG7,CRBN,RGS4,CRH,APOPT1,YWHAH,SHISA8,CACNG5,GEM,PPIF	grey	VSMC_M10
GO:0007188	0.70	0.37	66	129	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	BP	1	ADGRG6,ADM2,MCHR1,GRM4,GRM8,GPR37,ADGRF1,S1PR3,ADGRL3,OXER1,FPR2,LPAR1,CRHR2,ADCY3,PTGIR,GIPR,ADRA1D,ADRA2B,CHRM5,P2RY1,ADGRG5,RAPGEF2,NPY1R,CHRM4,ADCY7,CHRM3,GRM2,ADCY2,RGS1,ADRA2A,PTHLH,GNA13,OPRD1,GPER1,WASF2,GPR3,ADCY4,UCN2,PTH1R,ADRA2C,PTGER2,CALCRL,RAMP2,GPR161,CHRM1,ADGRE5,RIT2,HRH4,PTGER4,GNAL,ADGRG4,GNB1,GNA15,PALM,GNAT2,GNAI3,ADGRL2,PTGFR,HTR1D,ADGRE3,ADGRG1,CHGA,GPR37L1,GNA14,GNG2,MRAP2	grey	VSMC_M10
GO:0007618	0.70	0.46	11	22	mating	BP	1	MAPK8IP2,KLK14,DDO,HDAC2,ACVR2A,P2RY1,HDAC4,THRA,UBE2Q1,ABAT,P2RX1	grey	VSMC_M10
GO:0033173	0.70	0.42	19	38	calcineurin-NFAT signaling cascade	BP	1	NFATC1,FHL2,EFHB,PRNP,NRG1,SPPL3,PPP3CA,TBC1D10C,CIB1,SLC9A1,NFATC4,MYOZ2,ACTN3,HOMER2,PPP3CB,MYOZ1,MAPK7,CAMTA1,NFATC3	grey	VSMC_M10
GO:0006089	0.70	0.52	6	12	lactate metabolic process	BP	1	PFKFB2,PER2,ACTN3,PNKD,PARK7,TIGAR	grey	VSMC_M10
GO:0033147	0.70	0.51	7	14	negative regulation of intracellular estrogen receptor signaling pathway	BP	1	CNOT2,FOXH1,CYP7B1,ZNF366,CNOT1,VPS18,ISL1	grey	VSMC_M10
GO:0045540	0.70	0.49	8	16	regulation of cholesterol biosynthetic process	BP	1	APOB,CYP7A1,ERLIN1,SCAP,POR,LPCAT3,SREBF1,FGF1	grey	VSMC_M10
GO:0106118	0.70	0.49	8	16	regulation of sterol biosynthetic process	BP	1	APOB,CYP7A1,ERLIN1,SCAP,POR,LPCAT3,SREBF1,FGF1	grey	VSMC_M10
GO:1905953	0.70	0.43	19	37	negative regulation of lipid localization	BP	1	PPARA,TTC39B,CRY1,ABCG5,ABCG8,NR1H2,ABHD5,APOC1,AKT2,ASXL1,NR1H3,CRY2,PLA2R1,EGF,FIS1,PTPN2,MIR27B,MIR27A,MIR33B	grey	VSMC_M10
GO:0007512	0.70	0.57	4	8	adult heart development	BP	1	HAND2,MYH7,TCAP,NKX2-5	grey	VSMC_M10
GO:0045161	0.70	0.54	5	10	neuronal ion channel clustering	BP	1	PICK1,NRCAM,KCNIP2,GLDN,CNTN2	grey	VSMC_M10
GO:2001034	0.70	0.51	7	14	positive regulation of double-strand break repair via nonhomologous end joining	BP	1	SHLD1,PRKDC,PARP9,DTX3L,SHLD2,WRAP53,SMCHD1	grey	VSMC_M10
GO:0047484	0.70	0.52	6	12	regulation of response to osmotic stress	BP	1	ABCB1,TRPV4,YBX3,MICU1,AC138894.1,SLC25A23	grey	VSMC_M10
GO:0042359	0.70	0.52	6	12	vitamin D metabolic process	BP	1	CYP27B1,CYP2R1,SNAI1,CYP27A1,PIAS4,GFI1	grey	VSMC_M10
GO:1903599	0.70	0.54	5	10	positive regulation of autophagy of mitochondrion	BP	1	PRKN,FBXO7,HTT,VPS13D,PARK7	grey	VSMC_M10
GO:0001573	0.70	0.46	12	24	ganglioside metabolic process	BP	1	B4GALNT1,NEU3,ST8SIA4,ST8SIA2,CLN6,HEXA,GM2A,ST6GALNAC4,ST3GAL2,ST6GALNAC5,NEU2,ST8SIA6	grey	VSMC_M10
GO:0045091	0.70	0.54	5	10	regulation of single stranded viral RNA replication via double stranded DNA intermediate	BP	1	APOBEC3H,CXCL8,FAM208A,INPP5K,SETDB1	grey	VSMC_M10
GO:0042403	0.70	0.51	7	14	thyroid hormone metabolic process	BP	1	PAX8,SLCO1C1,DUOX1,MED1,CRYM,DIO3,DIO2	grey	VSMC_M10
GO:0045820	0.70	0.52	6	12	negative regulation of glycolytic process	BP	1	PPARA,ACTN3,HDAC4,STAT3,NCOR1,TIGAR	grey	VSMC_M10
GO:0006590	0.70	0.54	5	10	thyroid hormone generation	BP	1	PAX8,SLCO1C1,DUOX1,MED1,DIO2	grey	VSMC_M10
GO:0072697	0.70	0.54	5	10	protein localization to cell cortex	BP	1	EPB41L2,EPB41,NUBP1,SAPCD2,GPSM2	grey	VSMC_M10
GO:0060707	0.70	0.54	5	10	trophoblast giant cell differentiation	BP	1	MDFI,GJB5,SNAI1,SOX15,LIF	grey	VSMC_M10
GO:2000696	0.70	0.51	7	14	regulation of epithelial cell differentiation involved in kidney development	BP	1	OSR1,PAX8,PAX2,PRKX,CITED1,LHX1,LIF	grey	VSMC_M10
GO:1904152	0.70	0.52	6	12	regulation of retrograde protein transport, ER to cytosol	BP	1	UBAC2,YOD1,DERL3,BCAP31,UBE2G2,DERL2	grey	VSMC_M10
GO:0046519	0.70	0.49	8	16	sphingoid metabolic process	BP	1	KDSR,SPTLC1,SPHK2,ACER3,SPTLC3,ASAH1,ACER2,SGPP1	grey	VSMC_M10
GO:0030213	0.70	0.52	6	12	hyaluronan biosynthetic process	BP	1	HAS1,HYAL1,EGF,ABCC5,CEMIP,HAS3	grey	VSMC_M10
GO:0030157	0.70	0.54	5	10	pancreatic juice secretion	BP	1	AQP1,NR1H2,NR1H3,COPA,CEL	grey	VSMC_M10
GO:0070920	0.70	0.46	11	22	regulation of production of small RNA involved in gene silencing by RNA	BP	1	ZC3H10,ESR1,EGFR,MYCN,BCDIN3D,RIPK1,PPP3CA,TERT,STAT3,MAP2K1,NCOR1	grey	VSMC_M10
GO:1903798	0.70	0.46	11	22	regulation of production of miRNAs involved in gene silencing by miRNA	BP	1	ZC3H10,ESR1,EGFR,MYCN,BCDIN3D,RIPK1,PPP3CA,TERT,STAT3,MAP2K1,NCOR1	grey	VSMC_M10
GO:0046479	0.70	0.52	6	12	glycosphingolipid catabolic process	BP	1	NEU3,GALC,GLA,HEXA,GM2A,NEU2	grey	VSMC_M10
GO:0006684	0.70	0.52	6	12	sphingomyelin metabolic process	BP	1	SMPD2,SGMS2,SMPD4,SGMS1,ABCA8,PEMT	grey	VSMC_M10
GO:0006670	0.70	0.50	7	14	sphingosine metabolic process	BP	1	SPTLC1,SPHK2,ACER3,SPTLC3,ASAH1,ACER2,SGPP1	grey	VSMC_M10
GO:2001256	0.70	0.54	5	10	regulation of store-operated calcium entry	BP	1	EFHB,SLC8B1,HOMER1,CASQ1,HOMER2	grey	VSMC_M10
GO:0060122	0.70	0.45	13	26	inner ear receptor cell stereocilium organization	BP	1	WHRN,USH1G,MYO7A,TSKU,PLS1,ADGRV1,USH1C,TRIP11,STRC,CDH23,MKS1,IFT20,PJVK	grey	VSMC_M10
GO:0002228	0.70	0.43	17	34	natural killer cell mediated immunity	BP	1	CD226,PRDX1,NECTIN2,PVR,UNC13D,RASGRP1,CD96,CADM1,IL12A,PTPN6,LAG3,STAT5B,VAV1,CRK,AP1G1,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0032225	0.70	0.57	4	8	regulation of synaptic transmission, dopaminergic	BP	1	PNKD,PINK1,CHRNB2,CNTNAP4	grey	VSMC_M10
GO:0031645	0.70	0.52	6	12	negative regulation of nervous system process	BP	1	TNFRSF21,LPIN1,FIG4,MTMR2,JAM2,GPR35	grey	VSMC_M10
GO:0071236	0.70	0.52	6	12	cellular response to antibiotic	BP	1	MEF2C,RPL23,SLC9A1,CDKN1B,PLA2G4A,HSPA5	grey	VSMC_M10
GO:0036473	0.70	0.38	39	76	cell death in response to oxidative stress	BP	1	MAP3K5,PRKN,NCOA7,ATF4,GPR37,FBXO7,SLC1A1,MET,TLR4,SLC7A11,FOXO3,PAWR,PDK1,ARL6IP5,DIABLO,FBXW7,HTRA2,RIPK1,MCL1,PDE8A,NFE2L2,NONO,PRODH,PDCD10,PINK1,MMP3,PARP1,SFPQ,MAPK7,STK26,PARK7,TSC1,TLDC1,MIR21,ZNF622,PJVK,NOL3,GPR37L1,TXN	grey	VSMC_M10
GO:0009312	0.70	0.49	8	16	oligosaccharide biosynthetic process	BP	1	ST3GAL6,B3GALT1,MGAT2,B3GALNT1,ST3GAL2,ST6GALNAC5,FBP2,FUT4	grey	VSMC_M10
GO:2000726	0.70	0.57	4	8	negative regulation of cardiac muscle cell differentiation	BP	1	FRS2,SOX6,FZD7,MIR222	grey	VSMC_M10

GO:1904749	0.70	0.57	4	8	regulation of protein localization to nucleolus	BP	1	POLR1A,TERT,GLUL,NVL	grey	VSMC_M10
GO:0007501	0.70	0.57	4	8	mesodermal cell fate specification	BP	1	SIX2,EYA1,PAX2,BMPR1A	grey	VSMC_M10
GO:0055008	0.70	0.40	25	50	cardiac muscle tissue morphogenesis	BP	1	LY6E,FOXH1,TNNI3,POU4F1,NRG1,TNNC1,DSP,RYR2,PKP2,TNNI1,TGFB2,MYH7,ACTC1,TTN,BMPR1A,TCAP,RBPJ,MED1,ISL1,ENG,NOG,WNT5A,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:1904776	0.70	0.57	4	8	regulation of protein localization to cell cortex	BP	1	EPB41L2,EPB41,SAPCD2,GPSM2	grey	VSMC_M10
GO:0019221	0.70	0.34	160	306	cytokine-mediated signaling pathway	BP	1	TNFAIP3,HSPA1B,PRKN,AGPAT1,IL5,TNFRSF13C,IRF5,CNTFR,KIT,SLC1A1,IL1R2,VRK2,CXCL8,PXDN,NR1H2,TRIM32,TRAF1,IL15,FOXO3,TRAF3IP2,CD300LF,MYD88,OXSR1,NUMBL,IRAK2,IL15RA,IL17RE,ACKR2,IKBKB,MKKS,NMI,PLCB1,MAVS,GAS6,HPX,IRF7,ST18,TRAF6,TRIM44,HCK,IL1A,IL37,CEBPA,FER,OTUD4,ROBO1,IL17RD,IL17RB,PTPRJ,IL7,PTK2B,CCL17,NR1H3,OAS3,NLRC5,RIPK2,OTULIN,IFNGR2,F2RL1,RIPK1,TOLLIP,OASL,SP100,PIAS3,CMKLR1,KRAS,SPATA2,YTHDF2,PARP9,PARP14,CIB1,CBL,TRAF5,OSM,PELI3,THPO,IL10RA,FCER1G,DUOX1,PTPN6,TNFSF18,CXCR2,TNIP2,MUL1,BIRC3,STAT3,PTPRN,SPPL2A,SLC27A1,STAT5B,GREM2,PADI2,GPS2,USP18,TNFRSF1B,MED1,PYDC1,MAPK3,DCST1,IL6R,EPOR,IL4R,RPS6KA5,STAT2,TYK2,TRAF3,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,GHR,LEPR,JAK1,OSMR,LIFR,IL7R,PTPN2,SOCS1,LRP8,PIAS4,CDIP1,SPPL2B,TRAF2,AGPAT2,TNFRSF25,GFI1,MIR21,MIR125B1,MIR27B,MIR24-1,MIR27A,CCL16,OAS1,GPR35,NOL3,CCR10,FADD,CXCL6,CNTF,CASP8,MIR125A,IFNLR1,IRGM,IL36G,WNT5A,IL33,CD70,COMMD7,C1QTNF4,CCDC3,TSLP,SH2B2,EREG,TNFSF13B,RPS6KA4,HIST1H2BJ,CCL22	grey	VSMC_M10
GO:0021781	0.70	0.57	4	8	glial cell fate commitment	BP	1	SOX9,NRG1,SOX2,SOX8	grey	VSMC_M10
GO:0036124	0.70	0.52	6	12	histone H3-K9 trimethylation	BP	1	SUV39H2,KDM4A,MECP2,ARID4A,BEND3,ZNF304	grey	VSMC_M10
GO:0042573	0.70	0.50	7	14	retinoic acid metabolic process	BP	1	ALDH8A1,PRMT3,ALDH1A3,DHRS9,BCO2,ALDH1A2,SCPEP1	grey	VSMC_M10
GO:0071731	0.70	0.49	8	16	response to nitric oxide	BP	1	AQP1,GUCY1B1,MTR,MMP3,DNM2,CRK,TRAF2,TXN	grey	VSMC_M10
GO:2000193	0.70	0.50	7	14	positive regulation of fatty acid transport	BP	1	PLA2G6,PLA2R1,MAP2K6,ACSL5,NTSR1,PLA2G4A,PTGES	grey	VSMC_M10
GO:0001325	0.70	0.50	7	14	formation of extrachromosomal circular DNA	BP	1	ERCC1,WRN,NBN,RTEL1,XRCC5,SLX4,TERF2	grey	VSMC_M10
GO:0090656	0.70	0.50	7	14	t-circle formation	BP	1	ERCC1,WRN,NBN,RTEL1,XRCC5,SLX4,TERF2	grey	VSMC_M10
GO:0090737	0.70	0.50	7	14	telomere maintenance via telomere trimming	BP	1	ERCC1,WRN,NBN,RTEL1,XRCC5,SLX4,TERF2	grey	VSMC_M10
GO:0051457	0.70	0.47	10	20	maintenance of protein location in nucleus	BP	1	SKP1,SUN2,TAF8,TAF3,ARL2BP,MORC3,SP100,PARK7,SUPT7L,TXN	grey	VSMC_M10
GO:0045907	0.70	0.46	11	22	positive regulation of vasoconstriction	BP	1	EGFR,TRPM4,ADRA1D,F2R,ADRA2C,SMTNL2,CD38,HRH2,MIR21,RHOA,FGA	grey	VSMC_M10
GO:0014821	0.70	0.52	6	12	phasic smooth muscle contraction	BP	1	KIT,P2RX2,P2RX3,DLG1,TBX2,HTR1D	grey	VSMC_M10
GO:0045830	0.70	0.47	10	20	positive regulation of isotype switching	BP	1	EXOSC3,MSH2,HMCES,MLH1,PAXIP1,SHLD1,CD40,CD28,SHLD2,TBX21	grey	VSMC_M10
GO:0002921	0.70	0.57	4	8	negative regulation of humoral immune response	BP	1	FOXJ1,PTPN6,CD46,A2M	grey	VSMC_M10
GO:0003254	0.70	0.43	17	34	regulation of membrane depolarization	BP	1	NEDD4L,TSPO,TRPM4,SCN5A,GPD1L,DCN,SLMAP,TBX5,IFI6,NTSR1,FZD9,PPP2R3C,PARP1,CACNA1G,MLLT11,SCN2B,HCN4	grey	VSMC_M10
GO:0070863	0.70	0.52	6	12	positive regulation of protein exit from endoplasmic reticulum	BP	1	TMEM30A,TM9SF4,SORL1,SEC16B,TMEM30B,BCAP31	grey	VSMC_M10
GO:2000008	0.70	0.43	17	34	regulation of protein localization to cell surface	BP	1	NEDD4L,GOPC,GPD1L,TM9SF4,RAB11FIP5,GBF1,BDNF,EGF,LRIG2,ABCA12,STX4,TAX1BP3,ABCA7,CD247,TMEM35A,LEPROT,MAP1A	grey	VSMC_M10
GO:0060148	0.70	0.44	14	28	positive regulation of posttranscriptional gene silencing	BP	1	AGO2,TNRC6B,XPO5,EGFR,MYCN,PUM2,EIF4E2,RIPK1,AJUBA,DDX6,EIF4ENIF1,STAT3,MAP2K1,FMR1	grey	VSMC_M10
GO:0070424	0.70	0.54	5	10	regulation of nucleotide-binding oligomerization domain containing signaling pathway	BP	1	TNFAIP3,HSPA1B,SLC46A2,TLR4,BIRC3	grey	VSMC_M10
GO:0072530	0.70	0.50	7	14	purine-containing compound transmembrane transport	BP	1	SLC35B2,ABCC4,SLC29A2,SLC25A42,LRRC8E,SLC25A41,LRRC8A	grey	VSMC_M10
GO:0010907	0.70	0.43	16	32	positive regulation of glucose metabolic process	BP	1	PPARA,GPT,PPP4R3B,EPM2AIP1,AKT2,SORBS1,IGF2,GPLD1,IRS1,PPP1R3E,ACTN3,DDB1,INSR,PTPN2,NNMT,ARPP19	grey	VSMC_M10
GO:1905245	0.70	0.54	5	10	regulation of aspartic-type peptidase activity	BP	1	AGER,SORL1,EPHA4,TMED10,EFNA1	grey	VSMC_M10
GO:0032341	0.70	0.57	4	8	aldosterone metabolic process	BP	1	DKK3,WNT4,SCNN1B,CACNA1H	grey	VSMC_M10
GO:0060502	0.70	0.57	4	8	epithelial cell proliferation involved in lung morphogenesis	BP	1	SOX9,SRSF6,MAP2K1,WNT2	grey	VSMC_M10
GO:0046850	0.70	0.42	19	38	regulation of bone remodeling	BP	1	TNFAIP3,TNFRSF11B,EGFR,P2RX7,SPP1,GPR137B,UBASH3B,ADAM8,GPR137,SUCO,CD38,SYT7,CSF1R,PPARGC1B,LEPR,ATP6AP1,DEF8,CA2,BGLAP	grey	VSMC_M10
GO:0034114	0.70	0.50	7	14	regulation of heterotypic cell-cell adhesion	BP	1	AGER,GCNT2,LCK,MAP2K5,MAPK7,FGA,THY1	grey	VSMC_M10
GO:0000002	0.70	0.46	10	20	mitochondrial genome maintenance	BP	1	MGME1,PRIMPOL,OPA1,POLG2,STOX1,PARP1,PIF1,LIG3,LONP1,SLC25A33	grey	VSMC_M10
GO:0002675	0.70	0.50	7	14	positive regulation of acute inflammatory response	BP	1	OSM,ADAM8,BTK,C3,OSMR,CREB3L3,PARK7	grey	VSMC_M10
GO:0048478	0.70	0.57	4	8	replication fork protection	BP	1	ZRANB3,FBH1,DONSON,TIPIN	grey	VSMC_M10
GO:0034390	0.70	0.46	10	20	smooth muscle cell apoptotic process	BP	1	CDKN2A,ARRB1,STK4,PDCD4,IL12A,RBM10,MFN2,MIR21,MIR24-1,C3orf58	grey	VSMC_M10
GO:0034391	0.70	0.46	10	20	regulation of smooth muscle cell apoptotic process	BP	1	CDKN2A,ARRB1,STK4,PDCD4,IL12A,RBM10,MFN2,MIR21,MIR24-1,C3orf58	grey	VSMC_M10
GO:0006705	0.70	0.57	4	8	mineralocorticoid biosynthetic process	BP	1	CYP21A2,DKK3,WNT4,CACNA1H	grey	VSMC_M10
GO:0032329	0.70	0.54	5	10	serine transport	BP	1	SLC1A4,SERINC5,SLC38A2,SFXN2,SLC38A5	grey	VSMC_M10
GO:0010092	0.70	0.43	16	32	specification of animal organ identity	BP	1	FRS2,FOXH1,SPRY1,WNT11,PAX8,ROBO1,ROBO2,MEF2C,PAX2,AXIN2,RBPJ,ISL1,WNT5A,SIX1,FGF1,WNT2	grey	VSMC_M10
GO:0019062	0.70	0.57	4	8	virion attachment to host cell	BP	1	NECTIN2,GAS6,ACE2,LRRC15	grey	VSMC_M10
GO:0007603	0.70	0.54	5	10	phototransduction, visible light	BP	1	CAMKMT,SAG,NMT1,GRK4,GUCY2D	grey	VSMC_M10
GO:0035886	0.70	0.44	13	26	vascular associated smooth muscle cell differentiation	BP	1	NFATC1,SRF,KIT,PDCD4,GPER1,EFEMP2,RAMP2,GATA6,ENG,NFATC3,MIR21,MIR125B1,HEY2	grey	VSMC_M10
GO:0070243	0.70	0.56	4	8	regulation of thymocyte apoptotic process	BP	1	ZC3H8,ADAM8,EFNA1,WNT5A	grey	VSMC_M10
GO:0015865	0.70	0.46	11	22	purine nucleotide transport	BP	1	SLC35B2,ABCC4,SLC33A1,CALHM1,ABCC5,SLC25A42,LRRC8E,SLC25A23,SLC25A41,LRRC8A,SLC25A25	grey	VSMC_M10

GO:0015868	0.70	0.46	11	22	purine ribonucleotide transport	BP	1	SLC35B2,ABCC4,SLC33A1,CALHM1,ABCC5,SLC25A42,LRRC8E,SLC25A23,SLC25A41,LRRC8A,SLC25A25	grey	VSMC_M10
GO:0051503	0.70	0.46	11	22	adenine nucleotide transport	BP	1	SLC35B2,ABCC4,SLC33A1,CALHM1,ABCC5,SLC25A42,LRRC8E,SLC25A23,SLC25A41,LRRC8A,SLC25A25	grey	VSMC_M10
GO:0030214	0.70	0.56	4	8	hyaluronan catabolic process	BP	1	CEMIP2,HYAL1,HYAL3,CEMIP	grey	VSMC_M10
GO:0050869	0.70	0.45	12	24	negative regulation of B cell activation	BP	1	TNFAIP3,TNFRSF21,FOXJ1,PAWR,CASP3,BANK1,TBC1D10C,BCL6,RC3H1,INHA,FOXP3,BTK	grey	VSMC_M10
GO:0071425	0.70	0.45	12	24	hematopoietic stem cell proliferation	BP	1	PIM1,EIF2AK2,SART3,YTHDF2,ARIH2,THPO,ETV6,KAT7,CTC1,MIR222,ATXN1L,WNT5A	grey	VSMC_M10
GO:2000169	0.70	0.56	4	8	regulation of peptidyl-cysteine S-nitrosylation	BP	1	NCOA7,NOS1AP,DMD,TXN	grey	VSMC_M10
GO:0070206	0.70	0.54	5	10	protein trimerization	BP	1	PNPT1,P2RX3,ASIC1,CD74,CLYBL	grey	VSMC_M10
GO:0070232	0.70	0.45	12	24	regulation of T cell apoptotic process	BP	1	SLC46A2,IDO1,ZC3H8,GPAM,PDCD1,ADAM8,EFNA1,CCL5,IL7R,FADD,WNT5A,TSC22D3	grey	VSMC_M10
GO:0003330	0.70	0.56	4	8	regulation of extracellular matrix constituent secretion	BP	1	ADTRP,AGT,TNFRSF1B,RGCC	grey	VSMC_M10
GO:0051047	0.71	0.34	109	211	positive regulation of secretion	BP	1	VPS4B,LRP1,SLC12A2,PLA2G6,CHMP2A,PRKCE,AQP1,NR1H2,EGFR,TLR4,ATG5,SDCBP,TRPM4,SPHK2,RAB7A,GIPR,CACNB2,CLASP2,FRMD4A,GAB2,UNC13D,SNX5,C1QTNF1,SYT1,RAB5A,APBB3,AIMP1,SIRT3,SYT9,IL1A,OSBP,VEGFC,P2RY1,NNAT,PFKM,NKX3-1,NKX6-1,F2RL1,SPP1,PLA2R1,DTNBP1,GPLD1,DNM1L,HYAL3,MAP2K6,TGFB2,TCF7L2,KCNB1,PFKFB2,GRK2,GPER1,ABCB11,AGT,FGR,STX1A,SNX4,NTSR1,GLUL,ADAM8,CREB1,PLA2G4A,TTN,MCU,PPP3CB,RAB3A,PINK1,CD38,MPC2,INHA,ATP13A2,SYT7,RAB15,NLGN2,TARDBP,STX1B,STX4,ITGAM,RAB8B,TMED10,CACNA1G,CHRNB2,MYH10,RAB3D,IL4R,SYTL4,GPR68,S100A8,SCAMP5,ISL1,OXCT1,ABAT,RPH3AL,NADK,TRPV1,ATP6AP1,BAIAP3,CACNA1H,CYBA,LRRC8A,STXBP1,AP1G1,VPS4A,FGA,SOX4,CRH,RGCC,DOC2B,PTGES,PARD6A	grey	VSMC_M10
GO:0006067	0.71	0.56	4	8	ethanol metabolic process	BP	1	ADH5,ALDH3B2,ALDH2,ADH4	grey	VSMC_M10
GO:0010837	0.71	0.44	14	28	regulation of keratinocyte proliferation	BP	1	CD109,AREG,INTU,OVOL2,VDR,SRSF6,TGM1,KDF1,SFN,CASK,MED1,BCL11B,MIR21,MIR125B1	grey	VSMC_M10
GO:0043372	0.71	0.46	10	20	positive regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	HLA-DRA,NCKAP1L,RIPK2,HLX,FOXP3,ZBTB7B,IL4R,SOCS1,PRKCZ,MIR21	grey	VSMC_M10
GO:0006901	0.71	0.48	8	16	vesicle coating	BP	1	MAPK15,ARFGAP2,GBF1,KLHL12,PEF1,PDCD6,TMED10,PPP6C	grey	VSMC_M10
GO:2000757	0.71	0.48	8	16	negative regulation of peptidyl-lysine acetylation	BP	1	HINT2,ATG5,HDAC2,TAF7,SDR16C5,HDAC1,FOXP3,SIN3A	grey	VSMC_M10
GO:1902931	0.71	0.51	6	12	negative regulation of alcohol biosynthetic process	BP	1	CYP27B1,PLEK,DKK3,ERLIN1,SCAP,GFI1	grey	VSMC_M10
GO:0051904	0.71	0.47	9	18	pigment granule transport	BP	1	BBS7,MYO7A,MKKS,MLPH,RAB17,BLOC1S6,MREG,RAB11A,BLOC1S3	grey	VSMC_M10
GO:0061418	0.71	0.51	6	12	regulation of transcription from RNA polymerase II promoter in response to hypoxia	BP	1	SIRT2,BACH1,HIF1AN,NFE2L2,STOX1,RBPJ	grey	VSMC_M10
GO:0050807	0.71	0.35	84	165	regulation of synapse organization	BP	1	MAPK14,NTRK2,LINGO2,ABHD17B,SEMA4D,LRRN3,EPHA7,PTN,CTTNBP2,YWHAZ,VPS35,SLC7A11,VSTM5,PCDH8,SLITRK5,LRFN1,FARP1,PRNP,LRFN3,EPHB1,CLSTN2,CHMP2B,ROBO2,MEF2C,CUX2,SEPT11,TIAM1,SLIT1,HOMER1,OPA1,AMIGO2,ITPKA,CYFIP1,TUBA1A,BDNF,NEURL1,DNM1L,CAPRIN2,SEMA3F,CAMKV,DAG1,AMIGO3,CFL1,ADNP,HSPA8,DISC1,RAB17,NFATC4,PTPRO,CDKL5,IL10RA,EPHB3,TANC2,SRGN,DNM3,GRIPAP1,EPHA4,LRTM2,NLGN2,SEMA4A,NLGN3,EFNA1,AC138894.1,CHRNB2,ZDHHC15,NTN1,GPRASP2,BHLHB9,ARHGAP44,ASIC2,CDK5R1,SLITRK2,LRP8,ABHD17A,AMIGO1,NTNG2,DAB2IP,ADGRL2,RHOA,GRID2,ABHD17C,WNT5A,SIX1,LRRTM2	grey	VSMC_M10
GO:1902745	0.71	0.43	15	30	positive regulation of lamellipodium organization	BP	1	AVIL,RAC2,AKIRIN1,ARHGEF7,PIK3R1,PLCE1,RREB1,CYFIP1,CARMIL1,AUTS2,WASF2,HDAC4,NCKAP1,DNM2,CARMIL2	grey	VSMC_M10
GO:0002523	0.71	0.53	5	10	leukocyte migration involved in inflammatory response	BP	1	NINJ1,PTN,SLAMF8,ADAM8,S100A8	grey	VSMC_M10
GO:2000322	0.71	0.56	4	8	regulation of glucocorticoid receptor signaling pathway	BP	1	CRY1,PHB,ARNTL,CRY2	grey	VSMC_M10
GO:0048240	0.71	0.51	6	12	sperm capacitation	BP	1	CATSPER3,DLD,ROPN1L,ABHD2,CATSPER2,CATSPERD	grey	VSMC_M10
GO:0032891	0.71	0.50	7	14	negative regulation of organic acid transport	BP	1	AKT2,ARL6IP5,SLC43A1,PLA2R1,FIS1,ABAT,RGS4	grey	VSMC_M10
GO:0001562	0.71	0.50	7	14	response to protozoan	BP	1	MYD88,CD40,BATF2,SLC11A1,BATF,IL4R,HRAS	grey	VSMC_M10
GO:0042832	0.71	0.50	7	14	defense response to protozoan	BP	1	MYD88,CD40,BATF2,SLC11A1,BATF,IL4R,HRAS	grey	VSMC_M10
GO:1903532	0.71	0.35	101	196	positive regulation of secretion by cell	BP	1	VPS4B,LRP1,SLC12A2,PLA2G6,CHMP2A,PRKCE,NR1H2,EGFR,TLR4,SDCBP,TRPM4,SPHK2,RAB7A,GIPR,CACNB2,CLASP2,FRMD4A,GAB2,UNC13D,C1QTNF1,SYT1,RAB5A,APBB3,AIMP1,SIRT3,SYT9,IL1A,OSBP,VEGFC,P2RY1,NNAT,PFKM,NKX3-1,NKX6-1,F2RL1,SPP1,DTNBP1,GPLD1,DNM1L,HYAL3,MAP2K6,TGFB2,TCF7L2,KCNB1,PFKFB2,GRK2,GPER1,AGT,FGR,STX1A,SNX4,NTSR1,GLUL,ADAM8,CREB1,PLA2G4A,TTN,MCU,PPP3CB,RAB3A,PINK1,CD38,MPC2,INHA,ATP13A2,SYT7,RAB15,NLGN2,TARDBP,STX1B,STX4,ITGAM,RAB8B,TMED10,CACNA1G,CHRNB2,MYH10,RAB3D,IL4R,SYTL4,GPR68,SCAMP5,ISL1,OXCT1,ABAT,RPH3AL,NADK,ATP6AP1,BAIAP3,CACNA1H,LRRC8A,STXBP1,AP1G1,VPS4A,FGA,SOX4,CRH,RGCC,DOC2B,PTGES,PARD6A	grey	VSMC_M10
GO:0010878	0.71	0.48	8	16	cholesterol storage	BP	1	PPARA,TTC39B,NR1H2,APOB,NR1H3,SOAT1,EHD1,STARD4	grey	VSMC_M10
GO:0032400	0.71	0.47	9	18	melanosome localization	BP	1	BBS7,MKKS,SHROOM2,MLPH,RAB17,BLOC1S6,MREG,RAB11A,BLOC1S3	grey	VSMC_M10
GO:0032401	0.71	0.47	9	18	establishment of melanosome localization	BP	1	BBS7,MKKS,SHROOM2,MLPH,RAB17,BLOC1S6,MREG,RAB11A,BLOC1S3	grey	VSMC_M10
GO:0032303	0.71	0.51	6	12	regulation of icosanoid secretion	BP	1	PLA2G6,PLA2R1,MAP2K6,NTSR1,PLA2G4A,PTGES	grey	VSMC_M10
GO:0043518	0.71	0.51	6	12	negative regulation of DNA damage response, signal transduction by p53 class mediator	BP	1	MARCH7,DYRK3,SNAI1,PSMD10,CD74,PTTG1IP	grey	VSMC_M10

GO:0045124	0.71	0.42	16	32	regulation of bone resorption	BP	1	TNFAIP3,TNFRSF11B,EGFR,P2RX7,SPP1,GPR137B,UBASH3B,ADAM8,GPR137,CD38,CSF1R,PPARGC1B,ATP6AP1,DEF8,CA2,BGLAP	grey	VSMC_M10
GO:1902916	0.71	0.50	7	14	positive regulation of protein polyubiquitination	BP	1	PRKN,NMI,SPSB4,MARCH7,NOD2,DDX3X,UBE2D1	grey	VSMC_M10
GO:0050891	0.71	0.42	18	36	multicellular organismal water homeostasis	BP	1	AKR1B1,SRF,TFAP2B,AQP1,GRHL1,MET,ELOVL1,LSR,TRPV4,KDF1,SFN,GRHL3,ABCA12,ALOXE3,SCNN1B,MYO5B,INPP5K,CLDN1	grey	VSMC_M10
GO:1904491	0.71	0.56	4	8	protein localization to ciliary transition zone	BP	1	MAPK15,TMEM107,TCTN2,CC2D2B	grey	VSMC_M10
GO:2000343	0.71	0.56	4	8	positive regulation of chemokine (C-X-C motif) ligand 2 production	BP	1	LRP1,TLR4,HDAC1,CD74	grey	VSMC_M10
GO:1903265	0.71	0.56	4	8	positive regulation of tumor necrosis factor-mediated signaling pathway	BP	1	HSPA1B,PRKN,TRIM32,TRAF2	grey	VSMC_M10
GO:0034143	0.71	0.47	9	18	regulation of toll-like receptor 4 signaling pathway	BP	1	TNFAIP3,NINJ1,PELI1,MFHAS1,NR1H3,F2RL1,RAB7B,WDFY1,DAB2IP	grey	VSMC_M10
GO:0032353	0.71	0.56	4	8	negative regulation of hormone biosynthetic process	BP	1	CYP27B1,DKK3,WNT4,GFI1	grey	VSMC_M10
GO:0019856	0.71	0.56	4	8	pyrimidine nucleobase biosynthetic process	BP	1	CMPK1,CTPS2,CPS1,DHODH	grey	VSMC_M10
GO:0045445	0.71	0.38	34	67	myoblast differentiation	BP	1	MAML1,PITX1,MAPK14,SRF,SOSTDC1,EPAS1,AKIRIN1,SOX9,JAG1,SRA1,PLCB1,BTG1,NRG1,SMYD1,MEF2C,CCL17,HIF1AN,PRICKLE1,RBM24,CDON,TCF7L2,DTYMK,PLEKHM3,RBPJ,SOX15,TBX2,ISL1,RANBP3L,MBNL3,SOX8,LRRC8A,MIR199A1,DDIT3,XKR8	grey	VSMC_M10
GO:0021604	0.71	0.53	5	10	cranial nerve structural organization	BP	1	PLXNA4,SEMA3A,PAX2,SEMA3F,PLXNA3	grey	VSMC_M10
GO:0007271	0.71	0.47	9	18	synaptic transmission, cholinergic	BP	1	CHRNA3,CHRNA5,CHRNA6,CHRNB1,CHRNB2,NQO1,CHRNB4,CHRNA10,CHRNG	grey	VSMC_M10
GO:0034113	0.71	0.42	18	36	heterotypic cell-cell adhesion	BP	1	ITGA7,AGER,NINJ1,IZUMO1,PARVA,DSP,GCNT2,CD200,PKP2,LCK,ITGA4,GLDN,MAP2K5,DSG2,MAPK7,FGA,THY1,PERP	grey	VSMC_M10
GO:0002347	0.71	0.45	11	22	response to tumor cell	BP	1	CD226,IL4I1,NECTIN2,PVR,SLC22A13,HNMT,RBMS3,IL12A,FBXO38,PLK5,HAVCR2	grey	VSMC_M10
GO:0050857	0.71	0.46	10	20	positive regulation of antigen receptor-mediated signaling pathway	BP	1	CD226,PRKD2,NECTIN2,FOXP1,LCK,CARD11,PRKCB,IKBKG,BCL10,CMTM3	grey	VSMC_M10
GO:0060600	0.71	0.56	4	8	dichotomous subdivision of an epithelial terminal unit	BP	1	AREG,PLXNA1,SEMA3A,CTSH	grey	VSMC_M10
GO:0045136	0.71	0.56	4	8	development of secondary sexual characteristics	BP	1	AREG,STAT5B,MED1,WNT5A	grey	VSMC_M10
GO:0043487	0.71	0.35	76	148	regulation of RNA stability	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,PHAX,DXO,PNLDC1,CSDC2,AGO2,TNRC6B,TUT7,MAPK14,EXOSC3,PNPT1,TUT4,PUM2,TRAF3IP2,FASTK,MLH1,MYD88,TNRC6C,LSM1,PAN3,CNOT1,CELF1,CNOT6L,TENT2,FTO,TENT5C,TENT4B,RBM24,DIS3L2,AXIN2,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,EIF4ENIF1,YBX3,RC3H1,DDX49,UPF1,SLC11A1,RBM10,SAMD4A,POLR2G,SCGB1A1,NT5C3B,DCP1B,TNFRSF1B,FXR2,TARDBP,TOB1,TENT5D,TNRC6A,CNOT8,LARP1,ALKBH5,PARN,FMR1,METTL16,PLEKHN1,CIRBP,TRAF2,METTL14,NANOS1,CACNG7,YBX1,ZFP36L2,TENT5A,RC3H2,EXOSC5	grey	VSMC_M10
GO:0120009	0.71	0.41	19	38	intermembrane lipid transfer	BP	1	TSPO,ABCG5,ABCG8,APOB,OSBP,PITPNM2,COL4A3BP,PLTP,PITPNM1,PITPNC1,GRAMD1B,OSBPL2,STARD5,ATG2B,PRELID3A,PITPNA,ABCA3,CPTP,STARD4	grey	VSMC_M10
GO:0007622	0.71	0.43	14	28	rhythmic behavior	BP	1	BTBD9,NR1D2,AHCY,NCOA2,SRD5A1,CIART,USP2,C3orf70,CHRNB2,NCOR1,PER3,GPR157,ZFHX3,CRH	grey	VSMC_M10
GO:0042743	0.71	0.42	18	35	hydrogen peroxide metabolic process	BP	1	RAC2,PRDX1,CAT,PXDN,EGFR,ACOX1,PRDX3,PXDNL,DUOX1,PINK1,MMP3,STAT3,MPO,NOXA1,PARK7,CYBA,HBA2,AC140504.1	grey	VSMC_M10
GO:0045664	0.71	0.35	74	145	regulation of neuron differentiation	BP	1	TCF4,CSNK1E,KDM4C,BEND6,HOXA2,MYCL,TRIM32,CDK5RAP2,MYCN,NRCAM,FOXO3,NTF4,SOX9,GLI2,KDM4A,ALK,JAG1,RAC3,LSM1,ADRA2B,RET,DNMT3B,ZNF536,EYA1,MEF2C,DPYSL2,EIF2AK4,TIAM1,OPA1,NKX6-1,BDNF,CDON,NEPRO,SOX2,ZFHX2,DDX6,DLX1,EIF4ENIF1,SH3GL3,HOXD3,YWHAG,BCL6,DIXDC1,BRINP2,ADRA2C,RAP1GAP,CYB5D2,PRPF19,MED1,CASZ1,NAP1L2,MOSMO,BCL11B,SIN3A,MIB1,CDK5R1,ISL1,DAB1,SOX8,ZFHX3,RHOA,CNTN2,FOXG1,CNTF,GPR37L1,ISL2,IMPACT,LBX1,MMD,SIX1,TGIF2,YWHAH,NKX2-5,HEY2	grey	VSMC_M10
GO:0061307	0.71	0.56	4	8	cardiac neural crest cell differentiation involved in heart development	BP	1	JAG1,HAND2,MAPK1,MAPK3	grey	VSMC_M10
GO:0061308	0.71	0.56	4	8	cardiac neural crest cell development involved in heart development	BP	1	JAG1,HAND2,MAPK1,MAPK3	grey	VSMC_M10
GO:0070486	0.71	0.53	5	10	leukocyte aggregation	BP	1	RAC2,SEMA4D,JAM2,STK10,S100A8	grey	VSMC_M10
GO:1903955	0.71	0.43	14	28	positive regulation of protein targeting to mitochondrion	BP	1	RAC2,USP36,FBXW7,HTRA2,CSNK2A2,HPS4,ARIH2,FZD5,PINK1,NPEPPS,SH3GLB1,MICALL2,RHOU,LEPROT	grey	VSMC_M10
GO:0071715	0.71	0.43	15	30	icosanoid transport	BP	1	PLA2G6,ABCC10,ABCC4,ABCC2,PLA2R1,MAP2K6,SLCO3A1,NTSR1,PLA2G4A,ABCC3,NMUR2,NOS2,PROCA1,PLA2G2C,PTGES	grey	VSMC_M10
GO:0010835	0.71	0.56	4	8	regulation of protein ADP-ribosylation	BP	1	XRCC1,HPF1,ADNP,TINF2	grey	VSMC_M10
GO:1900745	0.71	0.44	13	26	positive regulation of p38MAPK cascade	BP	1	MAP3K5,MAP3K4,AGER,GADD45G,EMC10,RELL2,MFHAS1,HAND2,NCF1,MAP3K3,MINK1,RELL1,GADD45A	grey	VSMC_M10
GO:0034134	0.71	0.49	7	14	toll-like receptor 2 signaling pathway	BP	1	TNFAIP3,MFHAS1,RIPK2,F2RL1,NOD2,TNIP2,CYBA	grey	VSMC_M10
GO:0032688	0.71	0.56	4	8	negative regulation of interferon-beta production	BP	1	REL,NMI,NLRX1,YY1	grey	VSMC_M10

GO:0046777	0.71	0.34	104	204	protein autophosphorylation	BP	1	CLK4,PTK2,MAPK15,NTRK2,PIM1,TEK,TEC,KIT,WNK2,MOB1B,VRK2,AAK1,EPHA7,EGFR,EPHA1,MKNK1,PRKD2,MYO3A,OXSR1,ALK,DYRK1B,NEK10,AATK,MAP4K1,EIF2AK2,ULK1,FLT1,STK33,EPHB1,MOS,HCK,ACVR1B,CAMK4,FER,ATR,VEGFC,PTK2B,MAPKAPK5,EIF2AK4,NBN,RIPK1,STK4,TAOK3,MAPKAPK3,SLK,SIK1,STK17B,PRKX,MAPKAPK2,MAP3K21,CHEK2,BMX,FGR,TSSK4,CDKL5,PASK,MAP3K3,EPHB3,UHMK1,MAP3K11,PIKFYVE,PPP2R5B,EPHB4,SIK2,DDX3X,MARK2,FGFR3,PINK1,STK16,TRPM7,PIM2,MINK1,ATP13A2,EPHA4,TNK1,CDK12,WNK3,FGFR4,MAP3K9,STK10,DAPK2,TAOK2,TAF1,MAPK3,CALM1,BTK,CLK3,CAMK2A,INSR,CSF1R,MARK3,YES1,NLK,STK26,TAOK1,PDPK1,ENG,INSRR,TRIM24,PEAK1,IMPACT,THY1,RAP2B,PDGFD	grey	VSMC_M10
GO:1904923	0.71	0.49	7	14	regulation of autophagy of mitochondrion in response to mitochondrial depolarization	BP	1	PRKN,OPTN,HTRA2,PINK1,MUL1,MFN2,VPS13C	grey	VSMC_M10
GO:0048207	0.71	0.51	6	12	vesicle targeting, rough ER to cis-Golgi	BP	1	MAPK15,KLHL12,PEF1,PDCD6,TMED10,PPP6C	grey	VSMC_M10
GO:0048208	0.71	0.51	6	12	COPII vesicle coating	BP	1	MAPK15,KLHL12,PEF1,PDCD6,TMED10,PPP6C	grey	VSMC_M10
GO:0015825	0.71	0.56	4	8	L-serine transport	BP	1	SLC1A4,SERINC5,SLC38A2,SLC38A5	grey	VSMC_M10
GO:0071474	0.71	0.49	7	14	cellular hyperosmotic response	BP	1	XRCC6,AKR1B1,AQP1,YBX3,XRCC5,MICU1,SLC25A23	grey	VSMC_M10
GO:0009060	0.71	0.35	86	161	aerobic respiration	BP	1	SHMT2,UQCRQ,NDUFA6,ACO2,CAT,MSH2,DLD,NDUFB2,NDUFB6,DNAJC15,DHTKD1,NDUFC2,ATP5F1C,MDH2,NDUFS8,PANK2,NDUFA12,SIRT3,COX7A1,SUCLG2,COX4I2,IDE,ATP5F1A,NDUFS3,DGUOK,UQCRB,COX15,FAM173B,COX6B1,NDUFV3,TRPV4,OXA1L,NDUFB4,ISCU,COA6,NDUFB3,ACTN3,NDUFS2,DNAJC30,MLXIPL,SDHC,MDH1B,COX6A1,IDH3A,COX8A,PINK1,NDUFA9,SDHB,COX6A2,NDUFAB1,UQCRC2,COX10,COX5A,TEFM,NDUFA7,SLC25A23,NDUFV2,SLC25A14,NDUFB10,UQCR11,PARK7,SLC25A33,ATP5PB,MT-ND1,MT-ND2,MT-ATP8,MT-ATP6,MT-CO3,MT-ND6,MT-CYB,RHOA,ATP5ME,ATP5MF,NDUFA5,NDUFC1,COX7A2,FXN,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,UQCC2,COX7A2L,PPIF	grey	VSMC_M10
GO:0048672	0.71	0.56	4	8	positive regulation of collateral sprouting	BP	1	LRP1,SEMA4D,BDNF,WNT3	grey	VSMC_M10
GO:0090407	0.71	0.32	237	452	organophosphate biosynthetic process	BP	1	NME1,TBPL1,PIP4K2C,ATP5MGL,SYNJ2,SERAC1,AGPAT4,PPT2,AGPAT1,PPARA,ACSL6,PNPLA3,PLA2G6,CKB,GPAA1,MOCS1,GUCA1B,IMPDH1,NMRK1,SLC35B2,CWH43,SRD5A3,SLC25A13,PPAT,IPPK,INPP4A,PPCS,TMEM246,PIGF,MBOAT7,ME1,PPT1,PLEK,MBOAT2,LPIN1,INPP4B,DLD,FIG4,SPHK2,CMPK1,ADCY3,MTMR2,PIP4K2A,SELENOI,ABHD5,AKR1A1,PRKAG2,TAMM41,SLC22A13,ATP5F1C,XYLB,ITPKC,ELOVL1,MTMR14,IDO2,IDO1,PGAP2,CRLS1,CDS2,PANK2,PDK1,NR1H4,PDHX,MTMR7,SLC5A8,ELOVL7,PANK1,NUDT12,AMPD3,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,GK5,ATP5F1A,GUCY1A1,GUCY1B1,SLA2,P2RY1,PTK2B,CKMT2,DGUOK,GMPS,SERINC5,SYNJ1,CDS1,FITM2,AMPD1,ITPKA,PIGT,ADCY7,FAM173B,ADCY2,NME4,LPCAT1,PGAP1,GPAM,ACSL5,CHKA,ACP6,ABHD4,SGMS2,AJUBA,GGPS1,PITPNM1,PRPS2,GPER1,GNPAT,DGKD,PIGM,FITM1,PARP9,BMX,HACD2,FAM126B,IP6K2,LPGAT1,ADCY4,PIGV,DPAGT1,CTPS2,MTMR3,NTSR1,DNAJC30,PCYT1A,INPP5J,PIGX,DTYMK,PIGZ,CKMT1B,PISD,PDK3,DGKG,PTH1R,PIKFYVE,SLC25A16,PLA2G4A,CPS1,SACM1L,ACSBG1,ATP5S,LPCAT3,PYGL,PIGC,COASY,GCH1,SOCS4,PINK1,PLA2G16,STAT3,PI4KA,NME7,SLC27A1,ADK,MPC2,ADCY10,MAPK1,ABHD8,SGMS1,PARP1,TECR,GPHN,PGAP3,PIGH,PI4K2B,SOCS7,SLC26A1,DGKQ,PNPO,GUCY2D,PKLR,PANK3,GCDH,AC138894.1,UPRT,DGKE,TTC7B,MOCOS,ACACA,PIGL,SLC26A2,ABHD3,PRPSAP2,ADSSL1,MOCS2,NOS2,ACSBG2,MPPE1,IMPA2,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,NADK,ATP6V0C,PANK4,NME3,AGPAT2,ATP5PB,VPS9D1,ACSF3,AK8,UCK1,MLYCD,KARS,PIP5KL1,FUK,DHODH,MT-ATP8,MT-	grey	VSMC_M10
GO:1901862	0.71	0.56	4	8	negative regulation of muscle tissue development	BP	1	SIRT2,USP19,YBX3,SOX15	grey	VSMC_M10
GO:0061635	0.71	0.53	5	10	regulation of protein complex stability	BP	1	SCOC,TRAPPC11,HSPA8,ECSIT,IRGM	grey	VSMC_M10
GO:0070230	0.71	0.51	6	12	positive regulation of lymphocyte apoptotic process	BP	1	IDO1,ZC3H8,PDCD1,ADAM8,CCL5,WNT5A	grey	VSMC_M10
GO:0032967	0.71	0.46	10	20	positive regulation of collagen biosynthetic process	BP	1	HDAC2,F2R,AMELX,WNT4,SUCO,LARP6,SERPINF2,ENG,RGCC,CBX8	grey	VSMC_M10
GO:1903749	0.71	0.42	15	30	positive regulation of establishment of protein localization to mitochondrion	BP	1	RAC2,USP36,FBXW7,HTRA2,CSNK2A2,HPS4,ARIH2,FZD5,NMT1,PINK1,NPEPPS,SH3GLB1,MICALL2,RHOU,LEPROT	grey	VSMC_M10
GO:0045980	0.71	0.48	8	16	negative regulation of nucleotide metabolic process	BP	1	PPARA,ACTN3,HDAC4,STAT3,PARP1,NCOR1,PDZD3,TIGAR	grey	VSMC_M10
GO:1901984	0.71	0.47	9	18	negative regulation of protein acetylation	BP	1	HINT2,ATG5,HDAC2,TAF7,SDR16C5,HDAC1,FOXP3,SIN3A,PARK7	grey	VSMC_M10
GO:0070207	0.71	0.56	4	8	protein homotrimerization	BP	1	PNPT1,P2RX3,ASIC1,CLYBL	grey	VSMC_M10
GO:0000381	0.71	0.39	26	52	regulation of alternative mRNA splicing, via spliceosome	BP	1	ZC3H10,PUF60,RBFOX2,SMU1,YTHDC1,CELF2,WTAP,CELF1,SRSF6,RBM24,RBM5,CELF3,RBM7,RBM10,FXR2,RBM25,RAVER2,MBNL3,NSRP1,FMR1,CELF5,SRRM4,NOVA1,RBM11,SRSF12,SAP18	grey	VSMC_M10
GO:0045628	0.71	0.56	4	8	regulation of T-helper 2 cell differentiation	BP	1	HLX,BCL6,IL4R,PRKCZ	grey	VSMC_M10
GO:2000508	0.71	0.56	4	8	regulation of dendritic cell chemotaxis	BP	1	GAS6,SLAMF8,IL12A,TNFSF18	grey	VSMC_M10
GO:0071260	0.71	0.38	35	69	cellular response to mechanical stimulus	BP	1	BAK1,HABP4,AQP1,CASP8AP2,EGFR,TLR4,MKX,SOX9,MYD88,WNT11,CNN2,TMEM150C,SLC38A2,CD40,KCNJ2,DAG1,TLR5,AGT,ATP1A2,BAG3,SLC9A1,HDAC4,KCNK4,LTBR,TNFRSF8,MAPK3,PTGER4,PIEZO1,CYBA,ENG,BCL10,FADD,CASP8,GADD45A,CRADD	grey	VSMC_M10
GO:0002638	0.71	0.56	4	8	negative regulation of immunoglobulin production	BP	1	PRKDC,TMBIM6,BCL6,FOXP3	grey	VSMC_M10
GO:0051180	0.71	0.43	13	26	vitamin transport	BP	1	CUBN,SLC23A2,ABCG2,SLC2A10,ABCC5,SLC2A2,SLC27A1,ABCD4,STRA6,CD320,SLC46A1,SLC2A6,SLC25A32	grey	VSMC_M10
GO:0030449	0.71	0.56	4	8	regulation of complement activation	BP	1	PHB,C3,CD46,A2M	grey	VSMC_M10
GO:0006924	0.71	0.56	4	8	activation-induced cell death of T cells	BP	1	GPAM,DNAJA3,FADD,TSC22D3	grey	VSMC_M10

GO:0008643	0.71	0.36	57	112	carbohydrate transport	BP	1	SLC2A12,SLC45A4,MAPK14,SLC25A27,SLC35A1,AQP1,GRB10,FGF21,BRAF,MFSD4B,MFSD2B,SLC26A5,AQP11,PRKAG2,AKT2,ASPSCR1,SLC23A2,TRIB3,SLC35A4,PIK3R1,PLS1,SORBS1,TMEM144,IRS1,SLC37A1,SLC35A5,SLC2A10,TERT,SLC37A2,C2CD5,SLC37A4,PEA15,NFE2L2,CLTCL1,SLC2A2,SLC27A1,SLC2A9,SLC35A2,SLC2A4,RSC1A1,SLC5A2,SLC35B1,SLC50A1,SLC5A11,PRKCB,INSR,YES1,C3,SLC45A2,GPC3,INPP5K,SLC45A1,SLC2A6,TSC1,FABP5,SLC35C1,ARPP19	grey	VSMC_M10
GO:0006977	0.71	0.48	8	16	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	BP	1	PLK3,PLK2,PIDD1,CHEK2,CDKN1B,MUC1,SOX4,CRADD	grey	VSMC_M10
GO:2000272	0.71	0.42	16	32	negative regulation of signaling receptor activity	BP	1	PPARA,LY6E,DKKL1,DKK3,DKK2,CBL,ACE2,SNX6,LRPAP1,ZFYVE28,SOCS4,PSEN1,WFIKKN2,WFIKKN1,MIR125A,CNRIP1	grey	VSMC_M10
GO:0003352	0.71	0.45	10	20	regulation of cilium movement	BP	1	CFAP69,DNAH11,ARMC4,DRC1,MKKS,CFAP20,CCDC65,CFAP43,CFAP45,CCSAP	grey	VSMC_M10
GO:2000232	0.71	0.48	8	16	regulation of rRNA processing	BP	1	USP36,SIRT7,NUDT16,DIMT1,RIOK1,HEATR1,YTHDF2,METTL18	grey	VSMC_M10
GO:0009067	0.71	0.46	9	18	aspartate family amino acid biosynthetic process	BP	1	MTAP,APIP,ENOPH1,ASNSD1,MTRR,MTR,PLOD3,AASDHPPT,MTHFD2L	grey	VSMC_M10
GO:0044342	0.71	0.48	8	16	type B pancreatic cell proliferation	BP	1	NR4A1,NKX6-1,SERPINB1,SIDT2,MEN1,PTPRN,WDR13,IGFBP4	grey	VSMC_M10
GO:0036353	0.71	0.56	4	8	histone H2A-K119 monoubiquitination	BP	1	BMI1,PCGF6,PCGF3,TRIM37	grey	VSMC_M10
GO:0032928	0.71	0.46	9	18	regulation of superoxide anion generation	BP	1	FPR2,EGFR,HVCN1,F2RL1,AGT,MAPT,ITGAM,GNAI3,CYBA	grey	VSMC_M10
GO:0034311	0.71	0.45	11	22	diol metabolic process	BP	1	SPTLC1,SPHK2,DHFR,ACER3,SPTLC3,ASAH1,SPR,GCH1,ACER2,SGPP1,PCBD2	grey	VSMC_M10
GO:0035751	0.71	0.49	7	14	regulation of lysosomal lumen pH	BP	1	PPT1,TMEM106B,TMEM9,AC138894.1,CLN6,SNAPIN,TMEM199	grey	VSMC_M10
GO:0071578	0.71	0.56	4	8	zinc ion import across plasma membrane	BP	1	SLC39A5,SLC39A4,SLC39A12,SLC39A6	grey	VSMC_M10
GO:0042996	0.71	0.53	5	10	regulation of Golgi to plasma membrane protein transport	BP	1	GOPC,LYPLA1,CNST,RSC1A1,AC138894.1	grey	VSMC_M10
GO:0034135	0.71	0.53	5	10	regulation of toll-like receptor 2 signaling pathway	BP	1	TNFAIP3,MFHAS1,F2RL1,NOD2,CYBA	grey	VSMC_M10
GO:0015780	0.71	0.50	6	12	nucleotide-sugar transmembrane transport	BP	1	SLC35A1,SLC35A4,SLC35A5,SLC35A2,SLC35B1,SLC35C1	grey	VSMC_M10
GO:0014824	0.71	0.55	4	8	artery smooth muscle contraction	BP	1	MKKS,AGT,CD38,SCNN1B	grey	VSMC_M10
GO:0006487	0.71	0.38	28	55	protein N-linked glycosylation	BP	1	B4GALT7,GFPT2,ALG12,PMM1,SRD5A3,ALG2,ALG11,MGAT5B,UGGT2,MOGS,RPN2,ALG10,DAD1,DPAGT1,ALG3,MAN1C1,MGAT1,DERL3,ALG9,MGAT2,DDOST,KRTCAP2,ALG6,PMM2,ALG1,ENTPD5,DHDDS,TMEM258	grey	VSMC_M10
GO:0046847	0.71	0.38	28	56	filopodium assembly	BP	1	SRF,FGD3,VSTM5,ARHGEF4,RAB5A,SPEF1,FGD6,DPYSL3,AL359736.1,PIK3R1,DMTN,SRGAP2C,NEURL1,FGD4,GAP43,RAB17,DNM3,MIEN1,FGD1,FXR2,TENM2,AC138894.1,BCAS3,ARHGAP44,FMR1,PALM,FNBP1L,RALA	grey	VSMC_M10
GO:0071800	0.71	0.49	7	14	podosome assembly	BP	1	IL5,ASAP1,LCP1,HCK,FARP2,KIF9,RHOA	grey	VSMC_M10
GO:0034145	0.71	0.53	5	10	positive regulation of toll-like receptor 4 signaling pathway	BP	1	NINJ1,PELI1,NR1H3,F2RL1,WDFY1	grey	VSMC_M10
GO:1905288	0.71	0.53	5	10	vascular associated smooth muscle cell apoptotic process	BP	1	STK4,PDCD4,MFN2,MIR21,MIR24-1	grey	VSMC_M10
GO:1905459	0.71	0.53	5	10	regulation of vascular associated smooth muscle cell apoptotic process	BP	1	STK4,PDCD4,MFN2,MIR21,MIR24-1	grey	VSMC_M10
GO:0001991	0.71	0.53	5	10	regulation of systemic arterial blood pressure by circulatory renin-angiotensin	BP	1	MME,F2RL1,F2R,ENPEP,ACE2	grey	VSMC_M10
GO:0010224	0.71	0.49	7	14	response to UV-B	BP	1	MSH2,XPC,ERCC6,MME,HYAL1,HYAL3,IL12A	grey	VSMC_M10
GO:0050862	0.71	0.49	7	14	positive regulation of T cell receptor signaling pathway	BP	1	CD226,PRKD2,NECTIN2,LCK,CARD11,IKBKG,BCL10	grey	VSMC_M10
GO:2000352	0.71	0.44	12	24	negative regulation of endothelial cell apoptotic process	BP	1	TNFAIP3,TEK,FGF21,NDNF,GAS6,TERT,NFE2L2,TNIP2,RAMP2,MAPK7,PDPK1,FGA	grey	VSMC_M10
GO:0035246	0.71	0.52	5	10	peptidyl-arginine N-methylation	BP	1	NDUFAF7,PRMT9,PRMT3,PRMT7,PRMT6	grey	VSMC_M10
GO:1902074	0.71	0.49	7	14	response to salt	BP	1	RIDA,MAPK13,HSF1,ZNF16,SLC26A5,HSPA5,PITX3	grey	VSMC_M10
GO:0090023	0.71	0.45	10	20	positive regulation of neutrophil chemotaxis	BP	1	RAC2,CXCL8,C5AR1,NCKAP1L,DNM1L,MOSPD2,MCU,CXCR2,DAPK2,CD74	grey	VSMC_M10
GO:0010819	0.71	0.52	5	10	regulation of T cell chemotaxis	BP	1	CCL27,OXSR1,TMEM102,CCL5,WNT5A	grey	VSMC_M10
GO:1902165	0.71	0.50	6	12	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	BP	1	TAF9,ING2,MARCH7,MUC1,TAF9B,CD74	grey	VSMC_M10
GO:0010677	0.71	0.41	17	34	negative regulation of cellular carbohydrate metabolic process	BP	1	PRKN,PPARA,CRY1,PLEK,FAM3C,GCKR,SIK1,MST1,ACTN3,HDAC4,PASK,STAT3,COX11,NCOR1,LEPR,INPP5K,TIGAR	grey	VSMC_M10
GO:0090650	0.71	0.55	4	8	cellular response to oxygen-glucose deprivation	BP	1	DNM1L,CBL,TSC1,LCN2	grey	VSMC_M10
GO:0071888	0.71	0.55	4	8	macrophage apoptotic process	BP	1	CDKN2A,IRF7,MEF2C,NOD2	grey	VSMC_M10
GO:2000406	0.71	0.46	9	18	positive regulation of T cell migration	BP	1	CCL27,OXSR1,ADAM8,ITGA4,TMEM102,CCL5,RHOA,FADD,WNT5A	grey	VSMC_M10
GO:0006903	0.71	0.40	21	42	vesicle targeting	BP	1	FAM91A1,EXOC4,MAPK15,STARD3NL,CLASP2,ARFGAP2,EXOC6B,GBF1,KLHL12,TRIP11,PEF1,PDCD6,SNAP23,AP1AR,MAP4K2,SNAP29,PSEN1,TMED10,AP1M2,C17orf75,PPP6C	grey	VSMC_M10
GO:0051817	0.71	0.37	34	67	modulation of process of other organism involved in symbiotic interaction	BP	1	YTHDC2,SNW1,IGF2R,PRKN,ATG5,NAPEPLD,PHB,FBXL2,ULK1,SAP30,EIF2AK4,ANO6,HDAC1,DAG1,ZNF639,CFL1,HSPA8,POU2F3,PC,PSMC3,TARDBP,TNIP1,INSR,CCL5,JUN,FMR1,INPP5K,RXRA,MIR222,IRGM,SAP30BP,SERPINB9,TBC1D20,ZNF502	grey	VSMC_M10
GO:0072161	0.72	0.55	4	8	mesenchymal cell differentiation involved in kidney development	BP	1	SIX2,OSR1,PAX2,WNT4	grey	VSMC_M10
GO:2001012	0.72	0.55	4	8	mesenchymal cell differentiation involved in renal system development	BP	1	SIX2,OSR1,PAX2,WNT4	grey	VSMC_M10
GO:0016137	0.72	0.50	6	12	glycoside metabolic process	BP	1	FUCA2,AKR1B1,AKR1A1,CBR4,GLA,ABHD10	grey	VSMC_M10
GO:0045292	0.72	0.44	12	24	mRNA cis splicing, via spliceosome	BP	1	WBP4,CLNS1A,CWC15,PRPF4B,WBP11,NCBP2,PRPF39,RNVU1-6,RNU4ATAC,RF00003,SNRPC,SRSF12	grey	VSMC_M10
GO:1905216	0.72	0.55	4	8	positive regulation of RNA binding	BP	1	EIF3E,EIF3C,LARP6,FMR1	grey	VSMC_M10
GO:0045737	0.72	0.43	13	26	positive regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	CCND3,EGFR,CCNY,MAPRE3,PKD2,CCND1,CDKN1B,PSMD10,CDK5R1,PKD1,PSRC1,SPDYA,RGCC	grey	VSMC_M10
GO:0001963	0.72	0.46	9	18	synaptic transmission, dopaminergic	BP	1	PRKN,SLC6A2,SLC6A3,PNKD,PINK1,CHRNB2,PARK7,CNTNAP4,CRH	grey	VSMC_M10

GO:0051354	0.72	0.47	8	16	negative regulation of oxidoreductase activity	BP	1	CYP27B1,PRKN,NOSIP,OXA1L,GLA,GFI1,MIR21,MIR27B	grey	VSMC_M10
GO:0010944	0.72	0.52	5	10	negative regulation of transcription by competitive promoter binding	BP	1	PHB,DACH1,TFAP2A,CREB1,MUC1	grey	VSMC_M10
GO:0000463	0.72	0.48	7	14	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	1	URB1,WDR12,RPL7L1,ZNHIT3,NOL9,RPL35,ZNHIT6	grey	VSMC_M10
GO:0032703	0.72	0.45	10	20	negative regulation of interleukin-2 production	BP	1	TNFAIP3,NAV3,PRNP,HDAC7,NOD2,HOMER2,LAG3,FOXP3,TBX21,HAVCR2	grey	VSMC_M10
GO:0051775	0.72	0.48	7	14	response to redox state	BP	1	ADH5,SLC7A11,SIRT2,RNF7,ARNTL,RYR2,GLRX2	grey	VSMC_M10
GO:0045088	0.72	0.34	76	148	regulation of innate immune response	BP	1	CD226,TNFAIP3,USP15,XRCC6,FPR2,AKIRIN2,NR1H2,TLR4,NECTIN2,PVR,IKBKB,NMI,TMEM173,MAVS,HPX,PRKDC,IRF7,TRAF6,HCK,ERAP1,RASGRP1,NR1H3,TRAFD1,OAS3,NLRC5,POLR3D,NOD2,CD96,POLR3C,NCF1,YTHDF2,SLAMF8,PARP9,PARP14,FGR,NLRX1,COCH,ADAM8,CADM1,DUSP10,NONO,IL12A,XRCC5,PTPN6,LAG3,MUL1,BIRC3,STAT5B,TKFC,USP18,MED1,DCST1,SFPQ,STAT2,SIN3A,CCL5,RIOK3,RNF135,VAV1,PTPN2,SOCS1,LRP8,CRK,CREBBP,AP1G1,MIR21,OAS1,FADD,CASP8,ZCCHC3,A2M,IRGM,WNT5A,SERPINB9,EREG,HAVCR2	grey	VSMC_M10
GO:0031397	0.72	0.37	37	72	negative regulation of protein ubiquitination	BP	1	TNFAIP3,HSPA1B,TSPO,CRY1,SVBP,DNAJA1,PRKCE,ATG5,SPOPL,SPRY2,KLHL40,ARRB1,SIRT7,USP44,SH3RF2,TRIM44,MARCH7,PRMT3,RPL23,DTX3L,PER2,RPL11,SENP2,IVNS1ABP,GPS2,GNL3L,PSEN1,TAF1,OGT,OTUB2,PARK7,GLMN,SOX4,BAG2,CAMLG,PRR7,RASD2	grey	VSMC_M10
GO:0048070	0.72	0.55	4	8	regulation of developmental pigmentation	BP	1	ADAMTS20,HPS4,BLOC1S6,BCL2L11	grey	VSMC_M10
GO:0120305	0.72	0.55	4	8	regulation of pigmentation	BP	1	ADAMTS20,HPS4,BLOC1S6,BCL2L11	grey	VSMC_M10
GO:1901099	0.72	0.43	13	26	negative regulation of signal transduction in absence of ligand	BP	1	EYA4,HSPA1B,ZC3HC1,IL1A,EYA1,IL7,TERT,EYA3,IFI6,MCL1,STRADB,MAP2K5,MAPK7	grey	VSMC_M10
GO:2001240	0.72	0.43	13	26	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	BP	1	EYA4,HSPA1B,ZC3HC1,IL1A,EYA1,IL7,TERT,EYA3,IFI6,MCL1,STRADB,MAP2K5,MAPK7	grey	VSMC_M10
GO:0060401	0.72	0.35	64	126	cytosolic calcium ion transport	BP	1	SMDT1,BAK1,PRKCE,IBTK,ATG5,GRIN2D,TRPC3,SLC8A2,RYR1,PRNP,DIAPH1,P2RX2,RASA3,MICU3,P2RX3,RYR3,TMBIM6,P2RX7,PTK2B,TPCN1,SLC8B1,OPA1,F2R,PKD2,CASQ2,MCUR1,RYR2,TRPM1,LCK,TRPV4,MCUB,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,MICU1,MCU,HTT,HAP1,PSEN2,FAM155B,CD19,CALM1,BDKRB1,TRPV2,SLC25A23,MAIP1,ATP2B3,TRPV3,TRPV1,PDPK1,P2RX1,CYBA,JPH3,MCOLN3,DMD,NOL3,JPH2,THY1,DDIT3	grey	VSMC_M10
GO:1904181	0.72	0.52	5	10	positive regulation of membrane depolarization	BP	1	TSPO,TRPM4,DCN,PARP1,MLLT11	grey	VSMC_M10
GO:0017185	0.72	0.55	4	8	peptidyl-lysine hydroxylation	BP	1	PLOD3,P3H4,VIPAS39,P3H3	grey	VSMC_M10
GO:0031269	0.72	0.50	6	12	pseudopodium assembly	BP	1	CDC42EP1,KIT,F2RL1,SRGAP2C,CDC42EP2,APC	grey	VSMC_M10
GO:0048742	0.72	0.55	4	8	regulation of skeletal muscle fiber development	BP	1	LMOD3,ACTN3,HDAC4,FBXO22	grey	VSMC_M10
GO:0051899	0.72	0.37	33	66	membrane depolarization	BP	1	NEDD4L,TSPO,TRPM4,CACNB2,SCN5A,SCN1A,GPD1L,DCN,SLMAP,P2RX7,TBX5,KCNJ2,SCN2A,SCN7A,ANK2,IFI6,ATP1A2,NTSR1,SCN4B,FZD9,PPP2R3C,PARP1,CACNA1G,CHRNB2,JUN,PRKCZ,CACNA1H,PARK7,MLLT11,KCNH2,SCN2B,YWHAH,HCN4	grey	VSMC_M10
GO:0000098	0.72	0.55	4	8	sulfur amino acid catabolic process	BP	1	CSAD,MTRR,CBSL,MAT1A	grey	VSMC_M10
GO:0045665	0.72	0.38	26	52	negative regulation of neuron differentiation	BP	1	HOXA2,CDK5RAP2,FOXO3,SOX9,JAG1,LSM1,ZNF536,EIF2AK4,NEPRO,SOX2,DDX6,DLX1,EIF4ENIF1,DIXDC1,RAP1GAP,MED1,MIB1,ISL1,SOX8,RHOA,CNTN2,FOXG1,CNTF,GPR37L1,ISL2,LBX1	grey	VSMC_M10
GO:0070076	0.72	0.43	12	25	histone lysine demethylation	BP	1	UBE2B,KDM3B,KDM4C,KDM7A,KDM4A,KDM5A,KDM5C,PHF8,KDM6B,RIOX1,KDM8,HSF4	grey	VSMC_M10
GO:0061469	0.72	0.55	4	8	regulation of type B pancreatic cell proliferation	BP	1	NR4A1,MEN1,PTPRN,WDR13	grey	VSMC_M10
GO:0060732	0.72	0.55	4	8	positive regulation of inositol phosphate biosynthetic process	BP	1	P2RY1,GPER1,NTSR1,PTH1R	grey	VSMC_M10
GO:0071803	0.72	0.55	4	8	positive regulation of podosome assembly	BP	1	IL5,ASAP1,LCP1,RHOA	grey	VSMC_M10
GO:0051385	0.72	0.43	13	26	response to mineralocorticoid	BP	1	FOXO3,AANAT,CCND1,KRAS,GPER1,NPAS4,RPL27,PARP1,FOS,CALM1,SCNN1B,CYBA,CRH	grey	VSMC_M10
GO:0032964	0.72	0.40	19	38	collagen biosynthetic process	BP	1	TRAM2,ADAMTS3,HDAC2,CYGB,CYP7A1,F2R,AMELX,WNT4,SUCO,P3H4,LARP6,CIITA,SERPINF2,COL5A1,ENG,MIR29A,RGCC,P3H3,CBX8	grey	VSMC_M10
GO:0032608	0.72	0.39	22	44	interferon-beta production	BP	1	IRF5,REL,TLR4,NMI,TMEM173,MAVS,IRF7,OAS3,RIPK2,POLR3D,IFIH1,POLR3C,NLRX1,DDX3X,POLR3A,RNF216,YY1,TRAF3,RIOK3,RNF135,TICAM1,OAS1	grey	VSMC_M10
GO:0032648	0.72	0.39	22	44	regulation of interferon-beta production	BP	1	IRF5,REL,TLR4,NMI,TMEM173,MAVS,IRF7,OAS3,RIPK2,POLR3D,IFIH1,POLR3C,NLRX1,DDX3X,POLR3A,RNF216,YY1,TRAF3,RIOK3,RNF135,TICAM1,OAS1	grey	VSMC_M10
GO:1905517	0.72	0.40	18	36	macrophage migration	BP	1	PTK2,ROR2,AKIRIN1,C5AR1,FAM19A4,MTUS1,PTK2B,CD200,TRPV4,CMKLR1,SLAMF8,TNFSF18,MAPK1,MAPK3,CCL5,CSF1R,CCL2,MIR24-1	grey	VSMC_M10
GO:0043101	0.72	0.52	5	10	purine-containing compound salvage	BP	1	MTAP,PRTFDC1,AMPD3,AMPD1,ADK	grey	VSMC_M10
GO:0010887	0.72	0.55	4	8	negative regulation of cholesterol storage	BP	1	PPARA,TTC39B,NR1H2,NR1H3	grey	VSMC_M10
GO:0031124	0.72	0.38	28	56	mRNA 3'-end processing	BP	1	CPSF6,PABPC1,ZC3H3,HSF1,CPSF1,RNF20,YTHDC1,PNPT1,LSM10,MTPAP,SYMPK,PCF11,CSTF3,CLP1,RPRD1B,TENT2,TENT4B,CPSF2,RPRD2,CSTF1,NCBP2,CPSF4,LEO1,AP002990.1,CSTF2,PAPOLA,RPRD1A,ZNF473	grey	VSMC_M10
GO:0032230	0.72	0.55	4	8	positive regulation of synaptic transmission, GABAergic	BP	1	PRKCE,HAP1,NLGN2,ZDHHC12	grey	VSMC_M10
GO:0035247	0.72	0.55	4	8	peptidyl-arginine omega-N-methylation	BP	1	NDUFAF7,PRMT9,PRMT7,PRMT6	grey	VSMC_M10
GO:0042594	0.72	0.34	81	158	response to starvation	BP	1	MARS,MAP3K5,PPARA,ATF4,PICK1,TFEB,SLC39A4,GPT,NUAK1,BRSK1,ALB,RRAGD,VPS41,ATG5,FOXO3,KPTN,SESN3,FOXA3,DNAJC15,RALB,PRKAG2,SZT2,RPTOR,EIF2AK2,WRN,GAS6,LARS,ULK1,PRKAG1,EIF2AK4,SLC38A2,NUAK2,NUPR2,SRDSA1,SIK1,SLC38A3,HSPA8,GNPAT,CBL,MTMR3,XPR1,TBL2,HMGCL,GLUL,NFE2L2,CPS1,SIK2,COMT,WNT4,PRKAG3,CTSV,MAPK1,BHLHA15,WIPI2,MAX,RRAGB,BNIP1,ZFYVE1,MAPK3,TNRC6A,LARP1,BCAS3,ADSSL1,SREBF1,LAMP2,NIM1K,OXCT1,STK26,JUN,CLEC16A,KIAA1324,WDR59,HSPA5,DHODH,SH3GLB1,RIPOR1,ACADM,IMPACT,DDIT3,UPP1,RNF152	grey	VSMC_M10

GO:1901264	0.72	0.37	31	61	carbohydrate derivative transport	BP	1	SLC35B2,SLC35A1,ABCC4,SLC35A4,SLC33A1,PLTP,SLC37A1,CALHM1,SLC35A5,SLC37A2,ABCC5,SLC37A4,SLC29A2,SLC29A3,SLC25A42,SLC35A2,SLC29A4,RSC1A1,SLC5A2,SLC35B1,SLC50A1,AC138894.1,ABCC3,LRRC8E,SLC25A23,SLC25A41,RALBP1,LRRC8A,SLC25A25,SLC35E3,SLC35C1	grey	VSMC_M10
GO:0020027	0.72	0.48	7	14	hemoglobin metabolic process	BP	1	CAT,HPX,SLC25A37,ALAS1,LDB1,INHA,AHSP	grey	VSMC_M10
GO:0032693	0.72	0.55	4	8	negative regulation of interleukin-10 production	BP	1	AGER,TNFRSF21,VSIR,FOXP3	grey	VSMC_M10
GO:0014068	0.72	0.37	33	66	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	ERBB3,RGL2,PTK2,NTRK2,TEK,KIT,ROR2,SEMA4D,CAT,SOX9,DCN,FLT1,NKX3-1,F2RL1,F2R,TGFB2,NCF1,EGF,HCLS1,GPER1,AGT,FGR,CBL,OSM,CD28,FN1,PTPN6,HAX1,INSR,CCL5,MIR21,HCST,PDGFD	grey	VSMC_M10
GO:0061512	0.72	0.38	27	54	protein localization to cilium	BP	1	TBC1D32,LRRC6,MAPK15,DNAH11,TULP2,TTC26,TTC21A,TUB,CCDC66,ZNF423,ZMYND10,TTC21B,BBS1,LZTFL1,EHD1,FAM149B1,TULP3,TTC25,ROM1,WDR19,ATP6V1D,TMEM107,IFT20,EFCAB7,TCTN2,SNX10,CC2D2B	grey	VSMC_M10
GO:0048280	0.72	0.55	4	8	vesicle fusion with Golgi apparatus	BP	1	YIPF4,SEC22B,VTI1A,STX5	grey	VSMC_M10
GO:0001937	0.72	0.41	17	34	negative regulation of endothelial cell proliferation	BP	1	AIMP1,FLT1,ATP5F1A,MEF2C,IL12A,PDCD10,SYNJ2BP,NGFR,VASH1,TNMD,CCL2,MIR21,MIR222,MIR22,MIR24-1,ACVRL1,RGCC	grey	VSMC_M10
GO:0006662	0.72	0.45	10	20	glycerol ether metabolic process	BP	1	PEX7,PLA2G6,TXN2,TMEM86B,LIPE,GNPAT,PLA2G4A,PLA2G16,NCEH1,TXN	grey	VSMC_M10
GO:0031647	0.72	0.32	129	249	regulation of protein stability	BP	1	NEDD4L,SERF2,TRIM39,RAB21,STK3,ZNF207,HSPA1B,PRKN,RNF5,DERL1,UBE2B,PIM1,SMO,PEX6,FBXO7,BAG1,CDC37L1,GAPDH,PDCL3,ISOC2,RTN4,AAK1,VPS35,QRSL1,PHB,CRTAP,TADA3,USP36,MCM8,PRNP,BAG4,DDRGK1,PRKDC,TRIM44,FAM107A,PIK3R1,CDK7,CASP3,HIP1R,TAF9,CTNND1,CDKN2AIP,PARVA,MTMR9,FBXW7,ADGRV1,PEX2,CCNH,TESC,MARCH7,STK4,MORC3,MYLIP,SIAH1,RPL23,TERT,DAD1,TBRG1,RABL3,GET4,KRAS,USP13,USP19,HSPA8,HPS4,ANK2,CHEK2,USP2,DVL3,BAG3,PEX19,TMEM25,RPL11,SENP2,CREB1,PRKRA,SYVN1,CTSH,MFSD1,SAV1,PDCD10,HTT,TNIP2,DDOST,PINK1,MUL1,OTUD3,ATP1B1,MAPK1,PIM2,EPHA4,DDI2,GNL3L,ATP1B2,TARDBP,TMEM88,AHSP,EFNA1,TAF1,TAF9B,SEL1L,SMAD3,SWSAP1,KDM8,CCDC88C,COG7,MOSMO,RNF128,SREBF1,LAMP2,NLK,NAPG,CREBBP,HCFC1,MAPK8IP3,SEC16A,PER3,PARK7,TSC1,STXBP1,SH3GLB1,TRIM24,SOX4,BAG2,IRGM,SUGT1,CAMLG,USP40,APOPT1	grey	VSMC_M10
GO:0035745	0.72	0.55	4	8	T-helper 2 cell cytokine production	BP	1	RSAD2,DENND1B,TBX21,PRKCZ	grey	VSMC_M10
GO:2000551	0.72	0.55	4	8	regulation of T-helper 2 cell cytokine production	BP	1	RSAD2,DENND1B,TBX21,PRKCZ	grey	VSMC_M10
GO:0098930	0.72	0.37	29	58	axonal transport	BP	1	AP3S1,KIF5A,RAB21,KIF3A,AGTPBP1,MGARP,DLG2,AP3M2,KIF5C,KIF3B,OPA1,AP3B1,DTNBP1,CNIH2,CALY,MAPT,BLOC1S6,AP3M1,KIF1C,HAP1,TRIM46,NDEL1,SNAPIN,MAPK8IP3,TERF2,BLOC1S3,BORCS5,AP3S2,MAP1A	grey	VSMC_M10
GO:0031126	0.72	0.52	5	10	sno(s)RNA 3'-end processing	BP	1	EXOSC4,EXOSC3,TENT4B,PARN,EXOSC5	grey	VSMC_M10
GO:1902624	0.72	0.43	12	24	positive regulation of neutrophil migration	BP	1	RAC2,CXCL8,C5AR1,NCKAP1L,DNM1L,CD99,MOSPD2,ADAM8,MCU,CXCR2,DAPK2,CD74	grey	VSMC_M10
GO:1902176	0.72	0.47	8	16	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	BP	1	PRKN,HTRA2,NFE2L2,NONO,PINK1,MAPK7,PARK7,NOL3	grey	VSMC_M10
GO:0006706	0.72	0.44	10	20	steroid catabolic process	BP	1	CYP27B1,HSD17B14,CYP7A1,SPP1,SRD5A1,HSD11B1,CYP27A1,CYP46A1,CEL,YWHAH	grey	VSMC_M10
GO:2000251	0.72	0.47	8	16	positive regulation of actin cytoskeleton reorganization	BP	1	BAIAP2L2,TEK,CCL27,HCK,HCLS1,HAX1,BCAS3,HRAS	grey	VSMC_M10
GO:0045117	0.72	0.55	4	8	azole transmembrane transport	BP	1	SLC7A1,SLC38A3,SLC38A5,SLC25A29	grey	VSMC_M10
GO:2000480	0.72	0.55	4	8	negative regulation of cAMP-dependent protein kinase activity	BP	1	PRKAR2B,PRKAG2,PKIA,PRKAR1A	grey	VSMC_M10
GO:0032377	0.72	0.55	4	8	regulation of intracellular lipid transport	BP	1	ABCA12,ANXA2,MIR27B,LDLRAP1	grey	VSMC_M10
GO:0043330	0.72	0.41	15	30	response to exogenous dsRNA	BP	1	RALB,TMEM173,MAVS,RIPK2,NOD2,IFIH1,RFTN2,MUL1,MAPK1,SLC3A2,MAPK3,COLEC12,TICAM1,ZCCHC3,KCNJ8	grey	VSMC_M10
GO:1904031	0.72	0.41	15	30	positive regulation of cyclin-dependent protein kinase activity	BP	1	CCND3,TTBK1,EGFR,CCNY,MAPRE3,PKD2,CCND1,CDKN1B,STOX1,PSMD10,CDK5R1,PKD1,PSRC1,SPDYA,RGCC	grey	VSMC_M10
GO:0006940	0.72	0.39	23	46	regulation of smooth muscle contraction	BP	1	ZDHHC21,CHRNA3,SRF,KIT,TNNI3,ADRA2B,PLCE1,GUCY1A1,DOCK5,F2R,CHRM3,ADRA2A,GPER1,ATP1A2,ADRA2C,CALCRL,KCNMA1,NMUR2,SETD3,ABAT,P2RX1,MIR21,RHOA	grey	VSMC_M10
GO:0018126	0.72	0.42	13	26	protein hydroxylation	BP	1	P4HA2,JMJD4,CRTAP,EGLN2,ASPH,HIF1AN,EGLN3,PLOD3,P3H2,P3H4,VIPAS39,P3H3,JMJD7	grey	VSMC_M10
GO:0050930	0.72	0.49	6	12	induction of positive chemotaxis	BP	1	AGER,CXCL8,VEGFC,IL16,PGF,ARTN	grey	VSMC_M10
GO:0071280	0.72	0.49	6	12	cellular response to copper ion	BP	1	HSF1,AQP1,PRNP,BACE1,NFE2L2,MT1X	grey	VSMC_M10
GO:1901659	0.72	0.46	8	16	glycosyl compound biosynthetic process	BP	1	MTAP,NT5E,PRTFDC1,TYW1B,TYW5,LCMT2,DTYMK,ADK	grey	VSMC_M10
GO:0000491	0.72	0.49	6	12	small nucleolar ribonucleoprotein complex assembly	BP	1	C12orf45,TAF9,ZNHIT3,SNU13,ZNHIT6,PIH1D2	grey	VSMC_M10
GO:0015846	0.72	0.54	4	8	polyamine transport	BP	1	TAF7,AZIN2,ATP13A2,OAZ1	grey	VSMC_M10
GO:0060193	0.72	0.38	23	46	positive regulation of lipase activity	BP	1	ESR1,KIT,LPAR1,NR1H2,EGFR,C5AR1,PHB,ABHD5,RASGRP4,FLT1,NR1H3,GNA13,ARHGAP6,AGT,ABL2,FGFR3,NMUR2,CCL5,GNA15,PDPK1,PRKCZ,RHOA,HRAS	grey	VSMC_M10
GO:0009130	0.72	0.49	6	12	pyrimidine nucleoside monophosphate biosynthetic process	BP	1	CMPK1,UPRT,UCK1,DHODH,DCTD,UPP1	grey	VSMC_M10
GO:0034139	0.72	0.54	4	8	regulation of toll-like receptor 3 signaling pathway	BP	1	TNFAIP3,PELI1,F2RL1,WDFY1	grey	VSMC_M10
GO:0010889	0.72	0.49	6	12	regulation of sequestering of triglyceride	BP	1	PPARA,PLIN2,ABHD5,FITM2,FITM1,PLIN3	grey	VSMC_M10
GO:1901799	0.72	0.39	19	38	negative regulation of proteasomal protein catabolic process	BP	1	TRIM39,SDCBP,AQP11,KLHL40,DDRGK1,RYBP,PSMF1,TAF9,USP25,FAM192A,MARCH7,USP19,RPL11,OGT,SGTA,PARK7,CAMLG,STYX,MAP1A	grey	VSMC_M10
GO:0006614	0.72	0.46	8	16	SRP-dependent cotranslational protein targeting to membrane	BP	1	TRAM2,SEC61B,SRP14,SSR3,SRPRA,ZFAND2B,TRAM1L1,SEC61A2	grey	VSMC_M10
GO:0071827	0.72	0.41	16	32	plasma lipoprotein particle organization	BP	1	APOM,NR1H2,APOB,APOC1,NR1H4,SOAT2,PLTP,ABCA5,AGT,SOAT1,ZDHHC8,LPCAT3,LIPC,MPO,ABCA7,PLAGL2	grey	VSMC_M10
GO:0046128	0.72	0.45	9	18	purine ribonucleoside metabolic process	BP	1	MTAP,GNMT,ENPP4,NT5E,PRTFDC1,AHCY,DGUOK,ADK,PEMT	grey	VSMC_M10

GO:0009395	0.72	0.40	18	36	phospholipid catabolic process	BP	1	ABHD16A,PLA2G6,SMPD2,NAPEPLD,APOC1,ABHD6,PLA2G4B,PLBD1,PLA2G4A,ABHD12B,SMPD4,LIPC,GDPD3,LDLR,GDPD1,GDE1,PNPLA6,PLA2G15	grey	VSMC_M10
GO:0060632	0.72	0.41	16	32	regulation of microtubule-based movement	BP	1	CFAP69,DNAH11,ARMC4,DRC1,MKKS,CFAP20,CCDC65,CFAP43,TTC21B,CFAP45,CNIH2,CALY,HAP1,TRIM46,BORCS5,CCSAP	grey	VSMC_M10
GO:0006086	0.72	0.51	5	10	acetyl-CoA biosynthetic process from pyruvate	BP	1	DLD,PDK1,PDHX,PDK3,MPC2	grey	VSMC_M10
GO:0002437	0.72	0.39	20	40	inflammatory response to antigenic stimulus	BP	1	MAPK14,PLK2,HCK,IL37,AHCY,RASGRP1,NOD2,FGR,CD28,SERPINC1,CXCR2,RBPJ,KDM6B,PNMA1,BTK,YES1,C3,PARK7,KARS,IL36G	grey	VSMC_M10
GO:0060563	0.72	0.47	7	14	neuroepithelial cell differentiation	BP	1	WNT11,FAM20C,WNT4,DLX3,TMEM231,SOX4,CEBPB	grey	VSMC_M10
GO:0051084	0.72	0.41	15	30	'de novo' posttranslational protein folding	BP	1	HSPA1B,BAG1,HSPE1,DNAJC18,HSPA8,DNAJB12,SDF2L1,DNAJB1,GAK,CD74,TOR1B,TOR2A,HSPA5,ENTPD5,SDF2	grey	VSMC_M10
GO:0043489	0.72	0.37	26	52	RNA stabilization	BP	1	PABPC1,PHAX,MAPK14,TRAF3IP2,MYD88,TENT2,TENT5C,TENT4B,RBM24,AXIN2,MAPKAPK2,TRAF5,ANGEL2,EIF4ENIF1,YBX3,SLC11A1,RBM10,TARDBP,TENT5D,LARP1,PARN,METTL16,CIRBP,TRAF2,YBX1,TENT5A	grey	VSMC_M10
GO:0060218	0.72	0.41	14	28	hematopoietic stem cell differentiation	BP	1	SRF,ERCC2,EIF2AK2,PRKDC,TCF15,LMBR1L,YTHDF2,OSM,NFE2L2,XRCC5,MEOX1,SETD1A,BATF,SP7	grey	VSMC_M10
GO:0048864	0.72	0.36	36	72	stem cell development	BP	1	SEMA6A,SOX10,SMO,SEMA4D,SEMA4C,SOX9,OVOL2,JAG1,ALX1,SEMA3D,SEMA3A,NRG1,KBTBD8,RET,HAND2,SEMA4F,SEMA3G,SEMA4G,KLHL12,SEMA3F,PEF1,PDCD6,GBX2,LAMA5,SETD2,SEMA6D,FN1,MAPK1,BMPR1A,RADIL,ALDH1A2,SEMA4A,MAPK3,TCOF1,ISL1,SOX8	grey	VSMC_M10
GO:0098760	0.72	0.49	6	12	response to interleukin-7	BP	1	RAD23B,PDIA3,STIP1,BTK,IL7R,YBX1	grey	VSMC_M10
GO:0098761	0.72	0.49	6	12	cellular response to interleukin-7	BP	1	RAD23B,PDIA3,STIP1,BTK,IL7R,YBX1	grey	VSMC_M10
GO:0009886	0.73	0.51	5	10	post-embryonic animal morphogenesis	BP	1	BAK1,MYO7A,FBN1,MFAP2,BCL2L11	grey	VSMC_M10
GO:0042454	0.73	0.51	5	10	ribonucleoside catabolic process	BP	1	APOBEC3H,ENPP4,CDADC1,AHCY,UPP1	grey	VSMC_M10
GO:0070572	0.73	0.51	5	10	positive regulation of neuron projection regeneration	BP	1	LRP1,PTN,NDEL1,MIR222,CNTF	grey	VSMC_M10
GO:2001257	0.73	0.34	59	116	regulation of cation channel activity	BP	1	STAC3,MAPK8IP2,PRRT1,PLA2G6,SHANK1,KCNRG,CACNB2,STAC,CACNB4,SLMAP,MEF2C,PTK2B,KCNJ11,HOMER1,IFNGR2,KCNE2,PKD2,CASQ2,KCNIP2,FAM173B,KCNG1,ANK2,KLHL24,CASQ1,NTSR1,CNIH2,NOS1AP,DLG1,HTT,PINK1,KCNA1,GNB5,MINK1,HAP1,DLG4,NLGN2,CNIH3,STAC2,CACNB1,NLGN3,CALM1,CCL2,FMR1,RNF207,AMIGO1,JPH3,RRAD,MIR24-1,DMD,GPR35,JPH2,FGF11,NETO2,CACNG7,CRBN,CRH,SHISA8,CACNG5,GEM	grey	VSMC_M10
GO:0071712	0.73	0.49	6	12	ER-associated misfolded protein catabolic process	BP	1	RNF5,DERL1,UGGT2,AUP1,RNF185,SDF2L1	grey	VSMC_M10
GO:0048245	0.73	0.54	4	8	eosinophil chemotaxis	BP	1	DAPK2,CCL5,CCL7,CCL2	grey	VSMC_M10
GO:0051583	0.73	0.54	4	8	dopamine uptake involved in synaptic transmission	BP	1	PRKN,SLC6A2,SLC6A3,PARK7	grey	VSMC_M10
GO:0051934	0.73	0.54	4	8	catecholamine uptake involved in synaptic transmission	BP	1	PRKN,SLC6A2,SLC6A3,PARK7	grey	VSMC_M10
GO:0009636	0.73	0.33	90	174	response to toxic substance	BP	1	FECH,LTC4S,APOM,PRKN,BAK1,PRXL2C,KDM3B,FANCC,PIM1,TRPM6,ALDH1A1,SRF,ABCB1,TXNRD1,PRDX1,ADH5,CAT,ALB,PXDN,DDC,MGST2,SLC7A11,TXNRD3,DHFR,DNMT3A,ATP7B,ESD,AKR1A1,GSTK1,PRDX3,CYGB,ERCC6,PXDNL,ABTB2,DNMT3B,GLRX,HTRA2,EPHX2,GPX8,BPHL,TP53INP1,ABCC2,ABCG2,SRD5A1,SLC30A10,FBLN5,CHKA,MARC2,MARC1,OPRD1,MGMT,NFE2L2,DUOX1,SLC30A4,FIS1,CPS1,UBA52,GCH1,PINK1,ABCB6,MAPK1,KDM5C,EPHX1,RDH11,SOD3,KDM6B,FOS,MAPK3,GSTZ1,MPO,CCL5,RALBP1,TXNDC2,PARK7,ADAMTS13,ASS1,LCN2,NQO1,MIR21,MT-CYB,MT1X,SLC22A5,DHRS2,PDZD3,CLDN1,SCN2B,HBA2,TXN,PTGES,ADH4	grey	VSMC_M10
GO:0006108	0.73	0.54	4	8	malate metabolic process	BP	1	ME1,MDH2,D2HGDH,MDH1B	grey	VSMC_M10
GO:0070555	0.73	0.34	50	98	response to interleukin-1	BP	1	YTHDC2,MAPK13,IL1R2,VRK2,CXCL8,MYLK3,BMI1,SOX9,MYD88,IRAK2,HNMT,IKBKB,PLCB1,ST18,TRAF6,OTUD4,TAF9,CCL17,RIPK2,NKX3-1,ABCC2,TOLLIP,CD40,HYAL1,HYAL3,HDAC4,RC3H1,UPF1,TNIP2,CD38,MAPK3,CITED1,RPS6KA5,YY1,CCL14,CCL5,CCL7,CCL2,CCL25,GHR,ADAMTS12,CYBA,LCN2,DAB2IP,MIR21,MIR27A,CCL16,CEBPB,RPS6KA4,CCL22	grey	VSMC_M10
GO:0035107	0.73	0.34	58	115	appendage morphogenesis	BP	1	OSR2,FZD6,TBC1D32,BAK1,PITX1,PTCH1,TFAP2B,ROR2,DLX5,HOXA13,MYCN,OSR1,INTU,HDAC2,SOX9,GLI2,MEGF8,LMBR1,ZNF219,RARB,FREM2,HAND2,FMN1,FRAS1,TBX5,IFT52,RPGRIP1L,TFAP2A,SALL1,FBXW4,BMPR1B,HDAC1,TGFB2,SP9,WNT3,ECE1,TULP3,BMPR1A,WDR19,IQCE,MED1,ALDH1A2,PSEN1,TMEM107,MKS1,RNF165,TBX4,TBX2,GPC3,CREBBP,SKI,ALX3,TMEM231,SOX4,NOG,WNT5A,C2CD3,BCL2L11	grey	VSMC_M10
GO:0035108	0.73	0.34	58	115	limb morphogenesis	BP	1	OSR2,FZD6,TBC1D32,BAK1,PITX1,PTCH1,TFAP2B,ROR2,DLX5,HOXA13,MYCN,OSR1,INTU,HDAC2,SOX9,GLI2,MEGF8,LMBR1,ZNF219,RARB,FREM2,HAND2,FMN1,FRAS1,TBX5,IFT52,RPGRIP1L,TFAP2A,SALL1,FBXW4,BMPR1B,HDAC1,TGFB2,SP9,WNT3,ECE1,TULP3,BMPR1A,WDR19,IQCE,MED1,ALDH1A2,PSEN1,TMEM107,MKS1,RNF165,TBX4,TBX2,GPC3,CREBBP,SKI,ALX3,TMEM231,SOX4,NOG,WNT5A,C2CD3,BCL2L11	grey	VSMC_M10
GO:0002702	0.73	0.35	38	75	positive regulation of production of molecular mediator of immune response	BP	1	CD226,IL5,KIT,EXOSC3,MSH2,RSAD2,TLR4,SPHK2,HMCES,PHB,LACC1,MLH1,PAXIP1,SHLD1,MAVS,HPX,TRAF6,GPI,F2RL1,NOD2,CD40,DENND1B,CD28,FZD5,HK1,SHLD2,SPON2,TBX21,STX4,IL4R,CD74,TICAM1,PRKCZ,TRAF2,SLC7A5,BCL10,WNT5A,INAVA	grey	VSMC_M10
GO:0042308	0.73	0.49	6	12	negative regulation of protein import into nucleus	BP	1	RAB23,FERMT1,PKIA,SUFU,CABP1,APOD	grey	VSMC_M10
GO:1904590	0.73	0.49	6	12	negative regulation of protein import	BP	1	RAB23,FERMT1,PKIA,SUFU,CABP1,APOD	grey	VSMC_M10
GO:2000774	0.73	0.51	5	10	positive regulation of cellular senescence	BP	1	CDKN2A,PAWR,KRAS,YPEL3,MIR22	grey	VSMC_M10

GO:0017148	0.73	0.33	81	158	negative regulation of translation	BP	1	PAN2,SHMT2,CNOT2,CNOT6,RIDA,PABPC1,EIF3E,PNLDC1,MRPL13,AGO2,TNRC6B,ATF4,TUT7,GAPDH,CNOT11,EXOSC3,IGF2BP3,PNPT1,AGO1,TUT4,DHFR,MLH1,TNRC6C,PURA,EIF2AK2,LSM1,PAN3,ENC1,CNOT1,CELF1,CNOT6L,EIF2AK4,EIF4E2,PAIP2B,FTO,TENT4B,RBM24,BANK1,CAPRIN2,DIS3L2,GIGYF2,YTHDF2,DDX6,YTHDF1,EIF4ENIF1,IGF2BP2,EIF4EBP2,DDX3X,RC3H1,UPF1,SAMD4A,STAT3,POLR2G,NT5C3B,DCP1B,FXR2,TARDBP,TOB1,TNRC6A,CNOT8,LARP1,SHMT1,PARN,FMR1,METTL16,PLEKHN1,CIRBP,TSC1,MIR29A,MIR21,MIR222,MIR125B1,MIR27B,MIR27A,AGO4,METTL14,NANOS1,YBX1,ZFP36L2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0046940	0.73	0.54	4	8	nucleoside monophosphate phosphorylation	BP	1	CMPK1,DTYMK,AK8,CMPK2	grey	VSMC_M10
GO:0032008	0.73	0.39	19	38	positive regulation of TOR signaling	BP	1	RRAGD,PIP4P1,RPTOR,NCKAP1L,GAS6,LARS,SLC38A9,GPR137B,SIK3,GPR137,OTUD5,RRAGB,SMCR8,CLEC16A,MLST8,LAMTOR5,WDR59,MIR199A1,LAMTOR2	grey	VSMC_M10
GO:0046825	0.73	0.41	13	26	regulation of protein export from nucleus	BP	1	XPO1,DNAJC27,SIRT7,GAS6,RAPGEF3,SP100,TCF7L2,BAG3,SFN,UHMK1,CTDSPL2,PARK7,TXN	grey	VSMC_M10
GO:0032945	0.73	0.37	24	48	negative regulation of mononuclear cell proliferation	BP	1	TNFRSF21,PELI1,IL4I1,FOXJ1,PAWR,PRNP,CASP3,TMEM131L,MARCH7,BTN2A2,PRKAR1A,DLG1,VSIR,RC3H1,PTPN6,SCGB1A1,FOXP3,ZBTB7B,BTK,TWSG1,GLMN,LST1,CEBPB,HAVCR2	grey	VSMC_M10
GO:0050672	0.73	0.37	24	48	negative regulation of lymphocyte proliferation	BP	1	TNFRSF21,PELI1,IL4I1,FOXJ1,PAWR,PRNP,CASP3,TMEM131L,MARCH7,BTN2A2,PRKAR1A,DLG1,VSIR,RC3H1,PTPN6,SCGB1A1,FOXP3,ZBTB7B,BTK,TWSG1,GLMN,LST1,CEBPB,HAVCR2	grey	VSMC_M10
GO:1903530	0.73	0.31	207	399	regulation of secretion by cell	BP	1	VPS4B,LRP1,RAB21,SNCAIP,SLC12A2,RIMS2,PRKN,GDF9,PLA2G6,PICK1,RAC2,CHRNA3,CHRNA5,CRY1,APBA1,RFX3,TFAP2B,CHMP2A,IL11,PRKCE,RIMS1,HMGN3,RIMS3,BMP8A,RSAD2,NR1H2,EGFR,TLR4,SDCBP,TRPM4,SPHK2,RAB7A,RAB10,GIPR,CACNB2,CLASP2,FRMD4A,GAB2,LLGL2,UNC13D,C1QTNF1,SYT1,RAB5A,APBB3,DPH3,AIMP1,NCKAP1L,SIRT3,SYT9,ADRA2B,NR1H4,NDUFAF2,FAM3D,IL1A,PAX8,FER,OSBP,ARNTL,SCG5,MEF2C,ASIC1,VEGFC,P2RY1,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX3-1,NKX6-1,ACVR1C,F2RL1,F2R,CRY2,VPS18,SPP1,ZBED6,LGI3,ADTRP,DTNBP1,SYT8,GRM2,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,HYAL3,CPT1A,MAP2K6,SLC9B2,TGFB2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GRK2,GPER1,AGT,FGR,PER2,OSM,STX1A,SNX4,NTSR1,PASK,SEPT2,BACE1,GLUL,CSPG5,SIDT2,SLC16A1,ADAM8,KLF7,NSF,CREB1,RAP1B,PLA2G4A,TTN,IL12A,ENY2,ABCA12,CASK,MCU,ADRA2C,PNKD,PPP3CB,RAB3A,PINK1,SYN1,CD38,C12orf4,MPC2,INHA,RAB8A,ATP13A2,HAP1,CPLANE2,SYT7,RAB15,RSC1A1,NLGN2,TNFRSF1B,SEPT1,CPLX1,TARDBP,STX1B,STX4,ITGAM,SYT11,RAB8B,TMED10,CACNA1G,CHRNB2,MYH10,RAB3D,IL4R,CALM1,SYTL4,SNAPIN,GPR68,PRKCB,SCAMP5,CAMK2A,CCL5,STXBP2,SREBF1,ISL1,PRAM1,OXCT1,NOS2,ABAT,FMR1,RPH3AL,NADK,PDPK1,P2RX1,RAB26,ATP6AP1,BAIAP3,CACNA1H,FOXF1,LRRC8A,STXBP1,AP1G1,VPS4A,MIR199A1,FGA,CHRNB4,CHGA,SOX4,DPP4,CRH,RGCC,DOC2B,PTGES,RALA,LIF,UQCC2,VAMP3,PARD6A,KCNMB4	grey	VSMC_M10
GO:0010656	0.73	0.39	18	36	negative regulation of muscle cell apoptotic process	BP	1	PPP1R10,RGL2,HSF1,PAX8,HAND2,PTK2B,SIRT5,SIRT4,BAG3,NFE2L2,PDPK1,MIR199A1,MIR21,MIR24-1,NOL3,C3orf58,NKX2-5,HEY2	grey	VSMC_M10
GO:0140352	0.73	0.30	322	618	export from cell	BP	1	VPS4B,LRP1,CANX,RAB21,SNCAIP,SLC12A2,RIMS2,PRKN,GDF9,GRM4,LY6E,EXOC4,SYNGR1,NTRK2,PLA2G6,COPG2,PICK1,RAC2,MYH9,CHRNA3,CHRNA5,CRY1,ABCB1,STEAP2,APBA1,SCFD2,RFX3,KIT,TFAP2B,CHMP2A,NLRP5,SVBP,STX17,IL11,BRSK1,PRKCE,RIMS1,HMGN3,RIMS3,SLC4A4,CYB5R4,PPT1,SCRN1,BMP8A,PLEK,RSAD2,NR1H2,EGFR,TLR4,VPS41,SDCBP,TRPM4,PPFIA3,LIN7B,SPHK2,NAPA,SLC8A2,RAB7A,RAB10,COPG1,ATP7B,GIPR,CACNB2,SYTL2,CLASP2,FRMD4A,GAB2,LLGL2,RALB,STEAP3,GRIK5,UNC13D,RAF1,ATP1A3,NAPB,ABCC4,C1QTNF1,ANK1,SYT1,RAB5A,LIN7A,APBB3,DPH3,AIMP1,NCKAP1L,SIRT3,STX2,SYT9,ADRA2B,SNPH,NR1H4,HCK,NDUFAF2,FAM3D,IL1A,PAX8,NR4A1,FER,OSBP,TRAPPC11,ARNTL,ERC2,SCG5,MEF2C,ASIC1,VEGFC,P2RY1,RASGRP1,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,EXOC6B,PFKM,SYNJ1,SLC8B1,NKX3-1,NKX6-1,ACVR1C,F2RL1,F2R,SLC40A1,ANO6,CRY2,VPS18,ABCC2,KCNE2,SPP1,ZBED6,LGI3,ABCG2,DMTN,ADTRP,DTNBP1,KCNIP2,SYT8,GRM2,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,HYAL3,CPT1A,MAP2K6,TRPV4,SLC9B2,TGFB2,ADRA2A,MON1A,TCIRG1,TCF7L2,SNAP23,KCNB1,PFKFB2,GRK2,GPER1,RAB11FIP2,LAT2,AGT,FGR,ABCC5,CBL,SYTL1,ATP1A2,SLC9A1,PRSS12,PER2,OSM,STX1A,SNX4,NTSR1,PASK,SEPT2,BACE1,DNAJC5,GLUL,CSPG5,SIDT2,DLG1,SLC16A1,ADAM8,KLF7,NSF,CREB1,MIA3,RAP1B,BLOC1S6,PLA2G4A,CTAGE9,VGF,TTN,IL12A,TANGO2,ENY2,ABCA12,NRXN2,CASK,MCU,ADRA2C,PNKD,PTGDR,PPP3CB,RAB3A,PINK1,SYN1,CAMK2G,SNAP29,EXOC5,PTPRN,ATP1B1,CD38,SLC27A1,C12orf4,MPC2,ILDR2,INHA,RAB8A,ATP13A2,HAP1,CPLANE2,SLC29A4,SYT7,RAB15,RSC1A1,NLGN2,TNFRSF1B,SEPT1,MIA3,SLC16A1,ATP1B2,CPLX1,TARDBP,STX	grey	VSMC_M10
GO:0050832	0.73	0.44	9	18	defense response to fungus	BP	1	USP15,GAPDH,SPON2,MPO,S100A8,BCL10,S100A12,CHGA,COTL1	grey	VSMC_M10
GO:0030808	0.73	0.42	12	24	regulation of nucleotide biosynthetic process	BP	1	PPARA,GUCA1B,SPHK2,PDK1,FAM173B,DNAJC30,PDK3,PINK1,STAT3,PARP1,NOS2,PDZD3	grey	VSMC_M10
GO:1900371	0.73	0.42	12	24	regulation of purine nucleotide biosynthetic process	BP	1	PPARA,GUCA1B,SPHK2,PDK1,FAM173B,DNAJC30,PDK3,PINK1,STAT3,PARP1,NOS2,PDZD3	grey	VSMC_M10
GO:0051126	0.73	0.53	4	8	negative regulation of actin nucleation	BP	1	PICK1,HIP1R,WDR63,GMFG	grey	VSMC_M10
GO:0007157	0.73	0.40	14	29	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	BP	1	FAT4,PVR,TENM3,AMIGO2,ALCAM,NECTIN3,AMIGO3,NECTIN4,CADM1,HMCN1,TENM2,UMOD,AMIGO1,GRID2	grey	VSMC_M10

GO:1902414	0.73	0.35	41	82	protein localization to cell junction	BP	1	KIF5A,KIF3A,ABHD17B,ADAM22,SHANK1,DLG2,KIF5C,ACTG1,LSR,DSP,NECTIN3,DAG1,BSN,MPP4,DLG1,MAPT,NRXN2,VCL,NSG1,GRIPAP1,RAB8A,DLG4,ACTB,IQSEC2,NLGN2,CPLX1,STX1B,ZDHHC15,RAB11A,ARHGAP44,ASIC2,JAK1,PRKCZ,MAPK8IP3,ZDHHC12,MARVELD3,WNT5A,LAMTOR2,CACNG7,HRAS,MAP1A	grey	VSMC_M10
GO:0035384	0.73	0.38	21	42	thioester biosynthetic process	BP	1	PPT2,ACSL6,PPCS,PPT1,DLD,ELOVL1,PDK1,PDHX,ELOVL7,ACSL5,HACD2,PDK3,ACSBG1,MPC2,TECR,GCDH,ACACA,ACSBG2,ACSF3,MLYCD,ELOVL3	grey	VSMC_M10
GO:0071616	0.73	0.38	21	42	acyl-CoA biosynthetic process	BP	1	PPT2,ACSL6,PPCS,PPT1,DLD,ELOVL1,PDK1,PDHX,ELOVL7,ACSL5,HACD2,PDK3,ACSBG1,MPC2,TECR,GCDH,ACACA,ACSBG2,ACSF3,MLYCD,ELOVL3	grey	VSMC_M10
GO:0070231	0.73	0.39	18	36	T cell apoptotic process	BP	1	BAK1,SLC46A2,IDO1,ZC3H8,LMBR1L,RIPK1,GPAM,PDCD1,ADAM8,EFNA1,CCL5,IL7R,DNAJA3,BCL10,FADD,WNT5A,TSC22D3,BCL2L11	grey	VSMC_M10
GO:0051901	0.73	0.53	4	8	positive regulation of mitochondrial depolarization	BP	1	TSPO,DCN,PARP1,MLLT11	grey	VSMC_M10
GO:0009069	0.73	0.41	13	26	serine family amino acid metabolic process	BP	1	SHMT2,RIDA,PSAT1,SLC7A11,DHFR,CSAD,THNSL2,SERINC5,CBSL,AMT,SHMT1,GCSH,PHGDH	grey	VSMC_M10
GO:0042742	0.73	0.33	56	109	defense response to bacterium	BP	1	PLA2G6,FPR2,ANKRD17,NOD1,AQP1,LYPD8,TLR4,C5AR1,OPTN,MYD88,SIRT2,MAVS,FOXP1,OAS3,RIPK2,F2RL1,MAPKBP1,NOD2,TLR5,SLAMF8,FGR,COCH,FCER1G,LYZL6,VGF,IL12A,SLC11A1,CFP,RBPJ,SPON2,SYT11,IL6R,MPO,S100A14,S100A8,SCNN1B,COLEC12,NOS2,IL7R,DROSHA,CYBA,LCN2,FGA,S100A12,OAS1,HIST1H2BK,CHGA,DEFB124,CXCL6,JCHAIN,IRGM,PLAC8,CEBPB,HIST1H2BF,HIST1H2BJ,HAVCR2	grey	VSMC_M10
GO:0006289	0.73	0.37	25	50	nucleotide-excision repair	BP	1	RPA3,FANCC,RAD23B,USP45,ERCC1,XPC,ERCC2,ERCC3,POLR2I,ERCC6,ERCC8,GTF2H2C,DDB2,POLL,FAN1,RAD52,DDB1,RNF111,KAT7,XAB2,ERCC4,SLX4,NTHL1,RPA4,GTF2H5	grey	VSMC_M10
GO:0061003	0.73	0.43	9	19	positive regulation of dendritic spine morphogenesis	BP	1	CUX2,TIAM1,OPA1,ITPKA,DNM1L,CAPRIN2,GPRASP2,BHLHB9,LRP8	grey	VSMC_M10
GO:0072527	0.73	0.36	32	63	pyrimidine-containing compound metabolic process	BP	1	NME1,TBPL1,ENPP3,DPYS,APOBEC3H,CMPK1,CDADC1,MBD4,ENTPD4,NME4,THTPA,CTPS2,DTYMK,TET1,UPB1,CPS1,NME7,MAPK1,ALDH6A1,UPRT,NEIL1,NT5M,NTHL1,TKTL1,NME3,UCK1,DHODH,TPK1,CMPK2,NME6,DCTD,UPP1	grey	VSMC_M10
GO:0072665	0.73	0.36	30	60	protein localization to vacuole	BP	1	TNFAIP3,RTN4,VPS41,KPTN,RAB7A,SZT2,NCOA4,AP3B1,MON1A,GPR137B,HSPA8,SORL1,SH3BP4,RNF215,VPS37D,MFSD1,AP4M1,AP3M1,ATP13A2,VPS13D,VPS13C,RNF128,LAMP2,LAMTOR5,TLDC1,SH3GLB1,VPS4A,CACNG7,SNX16,CACNG5	grey	VSMC_M10
GO:0006290	0.73	0.53	4	8	pyrimidine dimer repair	BP	1	ERCC1,XPC,ERCC6,DDB2	grey	VSMC_M10
GO:0019318	0.73	0.32	95	185	hexose metabolic process	BP	1	FUCA2,PRKN,PPARA,PMM1,AKR1B1,ATF4,MAPK14,GPT,GNMT,CRY1,PGM5,GALT,TFAP2B,SLC25A13,GAPDH,PPP4R3B,ZNF692,FAM3C,RUBCNL,AKR1A1,GLB1,KHK,EPM2AIP1,GCKR,PPP1CB,AKT2,PFKP,PGM2L1,C1QTNF1,SIRT7,PDK1,FUT10,PPP1R3B,POFUT1,GPI,NLN,NCOA2,SORBS1,GPD1,KCNJ11,PFKM,CHST1,GLYCTK,IGF2,GPLD1,IRS1,SIK1,CPT1A,MST1,PPP1R3E,PFKFB2,PC,PPP1R3D,SLC37A4,PER2,PFKFB4,ACTN3,USF1,PASK,DUSP12,APOD,FUOM,PDK3,SORD,HK1,GNB3,SLC35A2,PPP1R3F,IGFBP4,DDB1,DGKQ,OGT,COX11,CRTC2,LCMT1,ADPGK,MPI,INSR,LEPR,ALDOC,PTPN2,PMM2,INPP5K,TKTL1,MLYCD,ACADM,FBP2,OAS1,FABP5,FUT4,FPGT,POFUT2,TIGAR,NNMT,ARPP19	grey	VSMC_M10
GO:0060041	0.73	0.33	54	108	retina development in camera-type eye	BP	1	MDM1,TBC1D32,AGTPBP1,NTRK2,PRPH2,RORB,SLC1A1,TFAP2B,RDH13,PTN,TSPAN12,USP45,SOX9,ZNF513,ACVR2B,TUB,PFDN5,NPHP1,RET,USH1C,TENT2,OPA1,RPGRIP1L,TFAP2A,PAX2,BMPR1B,NECTIN3,LPCAT1,TGFB2,TCIRG1,NRL,CLIC4,DLX1,OBSL1,RHOJ,ROM1,SDK1,MAX,CLN8,MED1,PSEN1,TTLL5,MEGF11,LHX1,LAMA1,GNB1,SKI,SOX8,LAMC3,FJX1,ACVRL1,THY1,DIO3,TGIF2	grey	VSMC_M10
GO:0051058	0.73	0.37	24	49	negative regulation of small GTPase mediated signal transduction	BP	1	SYNGAP1,MET,SPRY1,ARHGAP12,SPRY2,PPP2CB,RASA3,RASA2,ARHGAP24,TGFB2,RASA4,BCL6,ABL2,LZTR1,RASAL3,MFN2,ITGA3,KCTD13,ARHGAP44,TNFAIP1,MAPKAP1,SCAI,DAB2IP,STAMBP	grey	VSMC_M10
GO:0043393	0.73	0.32	83	162	regulation of protein binding	BP	1	LRP1,STK3,PRKN,PPARA,DERL1,LRRC6,CSNK1E,MFNG,HSF1,TTBK1,MITD1,ITGB1BP1,ADD2,MAPRE1,SYMPK,MAPRE3,RALB,PTPRF,TMEM173,EFHB,PLCL2,PPP2CB,TRIB3,PLK2,IDE,HIP1R,TMBIM6,RAPGEF2,FAM192A,TIAM1,RIPK2,AMFR,IFIT2,STK4,DTNBP1,BDNF,SPPL3,CAPRIN2,TERT,TCF7L2,TTBK2,ADNP,EPB41,UBASH3B,DISC1,SORL1,DTX3L,NFATC4,HDAC4,BTBD1,RPL11,ITGA4,MEN1,LRPAP1,MARK2,RAMP2,DNAJB2,GREM2,DDX11,CRMP1,ACTB,NVL,GNL3L,ANXA2,PEX14,PSEN1,TAF1,MAPK3,WFIKKN2,SNAPIN,MARK3,TICAM1,CRK,PKD1,WFIKKN1,PARK7,PRMT7,MIR27B,BAG2,NOG,WNT5A,LDLRAP1,STYX	grey	VSMC_M10
GO:0061178	0.73	0.37	25	50	regulation of insulin secretion involved in cellular response to glucose stimulus	BP	1	LRP1,PLA2G6,PRKCE,HMGN3,TRPM4,NR1H4,NDUFAF2,OSBP,TIAM1,ZBED6,GPLD1,SLC9B2,ADRA2A,SIDT2,KLF7,ENY2,ABCA12,PPP3CB,MPC2,STX4,GPR68,OXCT1,NADK,BAIAP3,CRH	grey	VSMC_M10
GO:0001522	0.74	0.44	9	18	pseudouridine synthesis	BP	1	PUS10,RPUSD2,PUS7L,RPUSD4,GAR1,TRUB1,PUSL1,RPUSD1,RPUSD3	grey	VSMC_M10
GO:0006388	0.74	0.50	5	10	tRNA splicing, via endonucleolytic cleavage and ligation	BP	1	TSEN34,CLP1,ZBTB8OS,RTRAF,TRPT1	grey	VSMC_M10
GO:0042129	0.74	0.33	52	102	regulation of T cell proliferation	BP	1	AGER,HLA-DPB1,TNFRSF13C,RAC2,TNFRSF21,NCK2,PELI1,IL4I1,IL15,BMI1,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,IL1A,CASP3,TMEM131L,RIPK2,MARCH7,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,CD28,DLG1,VSIR,RC3H1,PTPN6,TNFSF18,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,ZBTB7B,CCL5,TWSG1,DNAJA3,GLMN,MIR21,FADD,CD46,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2	grey	VSMC_M10

GO:0019218	0.74	0.35	37	73	regulation of steroid metabolic process	BP	1	CYP27B1,TSPO,TTC39B,KIT,DKKL1,APOB,APOC1,PANK2,NR1H4,CYP7A1,ASAH1,DKK3,EPHX2,ERLIN1,FMO5,SNAI1,ABCB11,AGT,SCAP,POR,ACADL,LPCAT3,GNB3,WNT4,STAT5B,ACADVL,FGFR4,DGKQ,LDLR,SREBF1,GFI1,MIR27B,MIR27A,LDLRAP1,STARD4,INSIG2,FGF1	grey	VSMC_M10
GO:1903587	0.74	0.44	9	18	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	IL12A,PDCD10,NGFR,MIR21,MIR222,MIR23A,MIR27B,MIR24-1,MIR27A	grey	VSMC_M10
GO:0045333	0.74	0.31	101	191	cellular respiration	BP	1	SHMT2,LYRM7,UQCRQ,NDUFA6,ACO2,SLC25A13,CAT,SDHAF4,MSH2,PNPT1,DLD,NDUFB2,NDUFB6,DNAJC15,DHTKD1,NDUFC2,ATP5F1C,MDH2,NDUFS8,PANK2,NDUFA12,SIRT3,COX7A1,SUCLG2,COX4I2,IDE,ATP5F1A,GPD1,NDUFS3,ETFDH,DGUOK,UQCRB,COX15,FAM173B,COX6B1,NDUFV3,TRPV4,COQ10B,OXA1L,NDUFB4,ISCU,COA6,POLG2,NDUFB3,CISD1,NFATC4,ACTN3,NDUFS2,DNAJC30,MLXIPL,SDHC,MDH1B,COX6A1,IDH3A,COX8A,PINK1,NDUFA9,SDHB,COX6A2,NDUFAB1,UQCRC2,COX10,COX5A,TEFM,NDUFA7,NOS2,SLC25A23,NDUFV2,SLC25A14,PRDM16,NDUFB10,UQCR11,PARK7,SLC25A33,ATP5PB,SLC25A25,MT-ND1,MT-ND2,MT-ATP8,MT-ATP6,MT-CO3,MT-ND6,MT-CYB,RHOA,ATP5ME,ATP5MF,NDUFA5,IFNLR1,NDUFC1,COX7A2,FXN,ETFRF1,NDUFA3,NDUFB5,NDUFS6,NDUFA8,SDHAF2,NDUFS5,UQCC2,COX7A2L,PPIF	grey	VSMC_M10
GO:0002698	0.74	0.35	31	62	negative regulation of immune effector process	BP	1	ENPP3,IL4I1,FOXJ1,NCKAP1L,PRKDC,FER,TMBIM6,NOD2,CD96,TGFB2,HLX,SLAMF8,DUSP10,BCL6,RC3H1,PTPN6,TNFSF18,PPP3CB,FOXP3,TBX21,ZBTB7B,IL4R,IL7R,CRK,FOXF1,CD46,A2M,FGL2,SERPINB9,HAVCR2,RC3H2	grey	VSMC_M10
GO:0045601	0.74	0.40	14	29	regulation of endothelial cell differentiation	BP	1	ZDHHC21,S1PR3,IKBKB,JAG1,PLCB1,BTG1,APOLD1,VCL,TMEM100,VEZF1,MIR21,ACVRL1,FOXJ2,MIR99B	grey	VSMC_M10
GO:0032602	0.74	0.35	32	64	chemokine production	BP	1	LRP1,AGER,TRIM32,TLR4,MYD88,EIF2AK2,MAVS,FOXP1,IL7,OAS3,RIPK2,F2RL1,NOD2,HDAC1,TRPV4,APOD,DDX3X,MUL1,IL6R,IL4R,MAP2K5,CD74,CSF1R,SUZ12,TICAM1,OAS1,DEFB124,CXCL6,WNT5A,IL33,TSLP,HAVCR2	grey	VSMC_M10
GO:0032642	0.74	0.35	32	64	regulation of chemokine production	BP	1	LRP1,AGER,TRIM32,TLR4,MYD88,EIF2AK2,MAVS,FOXP1,IL7,OAS3,RIPK2,F2RL1,NOD2,HDAC1,TRPV4,APOD,DDX3X,MUL1,IL6R,IL4R,MAP2K5,CD74,CSF1R,SUZ12,TICAM1,OAS1,DEFB124,CXCL6,WNT5A,IL33,TSLP,HAVCR2	grey	VSMC_M10
GO:0016125	0.74	0.33	58	114	sterol metabolic process	BP	1	APOF,CYP21A2,TTC39B,PLPP6,CAT,APOB,EBP,EBPL,CUBN,LIPE,PRKAG2,TSKU,PIP4P1,NR1H4,SOAT2,CYP7A1,CYP7B1,CEBPA,LIMA1,EPHX2,ERLIN1,CYB5R1,ABCA5,FMO5,MSMO1,SC5D,SCAP,HSD17B7,POR,ACADL,SOAT1,TM7SF2,OSBPL1A,FDX1,LPCAT3,GNB3,CYP27A1,CH25H,LIPA,ACADVL,CLN8,LIPC,DGKQ,ERG28,APOBR,CLN6,LDLR,CYP46A1,NPC1,SREBF1,LEPR,ACAA2,RXRA,CEL,NFE2L1,LDLRAP1,INSIG2,FGF1	grey	VSMC_M10
GO:0006163	0.74	0.30	157	302	purine nucleotide metabolic process	BP	1	NME1,HSD17B4,PDE7B,ATP5MGL,PPT2,PPARA,PDE10A,ACSL6,PRXL2C,GTPBP1,GUCA1B,IMPDH1,GDA,CROT,SLC35B2,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,NT5E,PPT1,BPGM,DLD,SPHK2,ADCY3,NUDT15,DLG2,LACC1,DHTKD1,PRKAG2,ATP5F1C,ELOVL1,PFKP,NUDT16,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,GPI,AMPD3,ATP5F1A,MCCC2,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,GMPR,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,MFN1,PFKFB2,PRPS2,ENO4,HACD2,ARNT,ADCY4,ACTN3,HDAC4,THEM5,DNAJC30,MLXIPL,PDE8A,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,HK1,ACSBG1,ATP5S,CASK,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,ENO3,PARP1,TECR,CARD11,SLC26A1,PSEN1,ACOT2,GUCY2D,PKLR,PANK3,GCDH,OGT,ADPGK,PDE4A,ACSM3,ACACA,NCOR1,INSR,SLC26A2,PRPSAP2,ADSSL1,NOS2,ACSBG2,ALDOC,PIPOX,ACOT11,ATP6V0C,PANK4,NME3,MPP1,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,MLYCD,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,PDZD3,ELOVL3,MTHFD2L,TIGAR,NUDT19,NME6,NUDT2,HINT1	grey	VSMC_M10
GO:1902108	0.74	0.38	17	34	regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	TMEM14A,HIP1R,THEM4,STPG1,FZD9,NMT1,MUL1,TMEM102,CAMK2A,ACAA2,NAIF1,MIR29A,NOL3,BNIP3L,BCL2L11,SLC35F6,AC140504.1	grey	VSMC_M10
GO:0099515	0.74	0.43	9	19	actin filament-based transport	BP	1	MYO1A,SUN2,MYO7B,MYO7A,SYNE2,MYO1D,MYO1F,MYO5B,FNBP1L	grey	VSMC_M10
GO:0048013	0.74	0.37	22	45	ephrin receptor signaling pathway	BP	1	PTK2,ANKS1A,NCK2,EPHA7,EPHA1,ARHGEF7,ANKS1B,EPHB1,ARHGEF28,TIAM1,KALRN,EPHB3,EPHB4,EPHA4,RBPJ,EFNA1,YES1,CDK5R1,CRK,EFNA4,CHN1,EFNB3	grey	VSMC_M10
GO:0051048	0.74	0.33	56	110	negative regulation of secretion	BP	1	VPS4B,ERBB3,PRKN,CRY1,IL11,BMP8A,RSAD2,RAB7A,FRMD4A,DPH3,NRG1,NCKAP1L,ADRA2B,NDUFAF2,FAM3D,ASIC1,P2RY1,KCNJ11,NR1H3,RAB11FIP5,ACVR1C,F2R,CRY2,PLA2R1,ADTRP,SIRT4,IRS1,CD200,HDAC1,PPP3CA,ADRA2A,KCNB1,EGF,OSM,KLF7,RAP1B,IL12A,COMT,ENY2,ADRA2C,PNKD,INHA,RSC1A1,TNFRSF1B,SYT11,SYTL4,CD74,SREBF1,ABAT,FMR1,FOXF1,MIR199A1,CHGA,CRH,LIF,VAMP3	grey	VSMC_M10
GO:1901661	0.74	0.40	14	28	quinone metabolic process	BP	1	AKR1B1,AKR1A1,CBR4,COQ2,NQO2,CRYZL1,CBR3,COQ5,COQ10B,NDUFA9,COQ8A,COQ4,PDSS2,ADH4	grey	VSMC_M10

GO:0002684	0.74	0.29	283	542	positive regulation of immune system process	BP	1	CD226,STX7,ENPP3,AGER,GPSM3,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TNFRSF13C,XRCC6,TRIB1,PTK2,PLA2G6,RAC2,HSF1,TTBK1,TEC,CCL27,KIT,TNFRSF21,NCK2,ROR2,EXOSC3,PRKCE,MSH2,FPR2,ANKRD17,CXCL8,NOD1,AKIRIN2,PELI1,AKIRIN1,RSAD2,PTN,IL4I1,TLR4,IL15,SPHK2,HMCES,BMI1,C5AR2,C5AR1,PRKD2,PHB,LACC1,NECTIN2,PVR,EIF2B3,GAB2,MLH1,GLI2,UNC13D,MYD88,OXSR1,SLC22A13,FOXJ1,PAXIP1,POU4F1,IL15RA,TGFBR2,IKBKB,NMI,TMEM173,PAWR,PLCL2,SHLD1,PRNP,MAVS,NCKAP1L,GAS6,HPX,FOXP1,PRKDC,IRF7,SLC7A1,TRAF6,SOX12,HCK,TOX,IL1A,GPI,CEBPA,FER,PIK3CB,LPXN,PTPRJ,MEF2C,IL7,VEGFC,JAM2,SLA2,PTK2B,RASGRP1,EIF2AK4,NLRC5,RIPK2,AP3B1,F2RL1,TESC,RIPK1,ANO6,POLR3D,SOX13,NOD2,ZNF335,CD40,IGF2,GPLD1,SPPL3,DNM1L,LCK,BANK1,ICOSLG,TRPV4,SLC9B2,TGFB2,BTN2A2,GPAM,CD99,PRSS56,POLR3C,HLX,DENND1B,CMKLR1,ACIN1,HCLS1,MOSPD2,PARP9,THEMIS2,LAT2,BMX,FGR,PLPP4,SNX4,COCH,CD28,FCER1G,RUNX3,ZBTB46,PPP2R3C,ADAM8,CADM1,CREB1,FZD5,MIA3,DUSP10,BLOC1S6,NONO,PLA2G4A,BCL6,HK1,ITGA2B,ITGA4,IL12A,VSIR,XRCC5,RC3H1,PTPN6,MCU,TNFSF18,CXCR2,SLC11A1,LAG3,TNIP2,CFP,CD38,BST1,C12orf4,MAPK1,STAT5B,FOXP3,RASAL3,ZBTB1,SHLD2,GPS2,CARD11,TMEM102,MED1,SPON2,TBX21,STX4,PSEN1,ITGAM,LCP2,PGF,DAPK2,FOS,MAPK3,ZBTB7B,CHRNB2,IL6R,HAX1,CD19,IL4R,S100A14,GPR68,SFPQ,PRKCB,BTK,BDKRB1,SIN3A,CD74,CCL5,RIOK3,CSF1R,PPARGC1B,STXBP2,CCL7,CCL2,FBXO38,YES1,NKAP,CD320,PRAM1,VAV1,C7,EVI2B,C3,NOS2,IL7R,PTPN2,JUN,SOCS1,TICAM1,DNAJA3,CREBBP,PDPK1,PRKCZ,T	grey	VSMC_M10
GO:0014044	0.74	0.40	13	27	Schwann cell development	BP	1	ADGRG6,NTRK2,ADAM22,PRX,AKT2,SIRT2,NRG1,LGI4,DAG1,CNTNAP1,MPP5,SKI,POU3F2	grey	VSMC_M10
GO:0030866	0.74	0.38	17	35	cortical actin cytoskeleton organization	BP	1	EPB41L2,TLN1,PLEK,LCP1,LLGL2,IKBKB,NCKAP1L,PLS1,EPB41L1,RTKN,EPB41,DLG1,NCKAP1,EPB41L3,STRIP1,VPS4A,FHOD1	grey	VSMC_M10
GO:1905330	0.74	0.35	28	56	regulation of morphogenesis of an epithelium	BP	1	ESR1,SMO,SIX2,SOX9,FOXP1,PAX8,PAX2,NKD1,EGF,AGT,STOX1,WNT4,MAGED1,BTBD7,TBX2,LHX1,ADAMTS12,RNF207,SOX8,LCN2,MIR21,NOG,WNT5A,LBX2,SIX1,LIF,FGF1,WNT2	grey	VSMC_M10
GO:1903557	0.74	0.34	36	72	positive regulation of tumor necrosis factor superfamily cytokine production	BP	1	AGER,NOD1,TLR4,SPHK2,HDAC2,MYD88,MAVS,IL1A,PIK3R1,PTPRJ,RASGRP1,OAS3,RIPK2,RIPK1,NOD2,IFIH1,HDAC1,MAPKAPK2,NFATC4,ADAM8,FZD5,STAT3,TNFRSF8,SPON2,PSEN1,ISL1,TICAM1,CYBA,BCL10,MIR27B,OAS1,FADD,WNT5A,IL33,C1QTNF4,HAVCR2	grey	VSMC_M10
GO:0003148	0.74	0.41	11	23	outflow tract septum morphogenesis	BP	1	TGFBR2,PARVA,ROBO1,ROBO2,TGFB2,BMPR1A,TBX2,GATA6,ISL1,ENG,NKX2-5	grey	VSMC_M10
GO:0031076	0.74	0.40	13	27	embryonic camera-type eye development	BP	1	FRS2,IFT172,TFAP2A,PAX2,ALDH1A3,SP3,FZD5,TULP3,WDR19,ALDH1A2,TBX2,STRA6,WNT5A	grey	VSMC_M10
GO:0072521	0.74	0.30	166	319	purine-containing compound metabolic process	BP	1	NME1,HSD17B4,SHMT2,PDE7B,ATP5MGL,PPT2,PPARA,PDE10A,ACSL6,PRXL2C,GTPBP1,OARD1,GUCA1B,IMPDH1,MTAP,GNMT,GDA,CROT,SLC35B2,ENPP4,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,NT5E,PPT1,BPGM,DLD,SPHK2,ADCY3,PRTFDC1,NUDT15,DLG2,LACC1,DHTKD1,PRKAG2,ATP5F1C,ELOVL1,PFKP,NUDT16,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,GPI,AHCY,AMPD3,ATP5F1A,MCCC2,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,GMPR,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,MFN1,PFKFB2,PRPS2,ENO4,HACD2,ARNT,ADCY4,ACTN3,HDAC4,THEM5,DNAJC30,MLXIPL,PDE8A,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,HK1,ACSBG1,ATP5S,CASK,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,ENO3,PARP1,TECR,CARD11,SLC26A1,PSEN1,ACOT2,GUCY2D,PKLR,PANK3,GCDH,OGT,ADPGK,PDE4A,ACSM3,ACACA,NCOR1,INSR,SLC26A2,PRPSAP2,SHMT1,ADSSL1,NOS2,ACSBG2,ALDOC,PIPOX,ACOT11,ATP6V0C,PANK4,NME3,MPP1,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,MLYCD,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,PDZD3,ELOVL3,MTHFD2L,PEMT,TIGAR,NUDT19,NME6,NUDT2,HINT1	grey	VSMC_M10
GO:0086009	0.74	0.38	16	33	membrane repolarization	BP	1	NEDD4L,SCN5A,KCNJ3,KCNE2,CASQ2,KCNIP2,KCNJ2,ANK2,ATP1A2,SCN4B,NOS1AP,ATP1B1,ATP1B2,RNF207,KCNH2,KCNJ8	grey	VSMC_M10
GO:0099173	0.74	0.32	69	137	postsynapse organization	BP	1	SYNGAP1,PICK1,LRRC4,ABHD17B,SHANK1,EPHA7,PTN,VPS35,SLC7A11,MTMR2,LRFN1,FARP1,ACTG1,PRNP,EPHB1,CHMP2B,CUX2,TIAM1,HOMER1,OPA1,ITPKA,DOCK10,INA,DNM1L,CAPRIN2,SEMA3F,GAP43,NLGN4Y,SSH1,CFL1,HSPA8,WASF2,SPTBN2,CDKL5,EPHB3,TANC2,NOS1AP,FZD9,DLG1,SRGN,NRXN2,DNM3,EPHA4,DLG4,ACTB,NLGN2,GPHN,CHRNB1,ITGA3,NLGN3,EFNA1,ZDHHC15,GPRASP2,BHLHB9,ARHGAP44,INSR,CDK5R1,LRP8,DNAJA3,RER1,ABHD17A,CEL,NTNG2,ZDHHC12,GRID2,ABHD17C,WNT5A,MESD,LRRTM2	grey	VSMC_M10

GO:0072657	0.74	0.29	242	466	protein localization to membrane	BP	1	LRP1,STX7,STAC3,MAP7,PEX3,ZDHHC14,EMC2,PRKN,AGER,GOPC,HSPA4,SYNGAP1,PTCH1,SIL1,TOMM22,PICK1,MICALL1,ZDHHC21,TSPAN33,LRRC4,ADAM22,SLC1A1,TRAM2,SEC61B,PRKCE,ASB3,SPTBN1,EMC10,PTN,ITGB1BP1,SEC61G,EGFR,TCAF2,VPS35,SDCBP,SLC7A11,LIN7B,AGK,BRAF,RAB7A,RAB10,ARL5B,CACNB2,CLASP2,DLG2,STAC,OPTN,GOLGA4,AQP11,GRIK5,EMC3,SEC62,MYL12A,AKT2,IKBKB,ANK1,ARL5A,LIN7A,PRNP,BAG4,GAS6,PKP3,ARL6IP5,SRP14,TUB,KCNIP3,LYPLA1,TM9SF4,ZDHHC20,RILPL1,RILPL2,PIK3R1,TMEM150A,VAMP5,SLMAP,PLS1,EMC4,FCHO2,SORBS1,NUP54,P2RY1,RAPGEF2,KCNJ11,TIAM1,SSR3,AP3B1,ZFYVE27,GOLGA7B,TESC,PEX16,DMTN,KIF13A,NHLRC1,NECTIN3,SRPRA,PKP2,PPFIA1,ZDHHC23,ZDHHC6,OXA1L,DAG1,SSH1,GET4,KCNB1,NCF1,ANK2,C2CD5,GPER1,RAB11FIP2,FAM126B,CIB1,AP2M1,ZDHHC18,PPP2R5A,PEX19,ZDHHC24,BBS1,GORASP2,STX1A,LAMA5,VPS37D,PACS1,FZD9,DLG1,LRRC15,NSF,PIKFYVE,FIS1,CEMIP,NMT1,LZTFL1,RTP4,EHD1,ZDHHC8,ITGA4,ABCA12,NRXN2,SAV1,CNPY4,AP4M1,BCS1L,RAB3A,RAMP2,ZFAND2B,EXOC5,ATP1B1,PPIL2,ARL6IP1,NSG1,GRIPAP1,ZDHHC4,RAB8A,CNST,DLG4,ACTB,WDR19,RAB15,IQSEC2,RSC1A1,PEX26,NLGN2,GPHN,MPP5,WNK3,STAC2,ARL5C,SYNJ2BP,TSPAN17,ANXA2,GAK,CPLX1,STX1B,STX4,TMEM88,ITGAM,SSR2,RAB8B,ITGA3,TAOK2,AC138894.1,ZDHHC15,RAB11A,STX8,RAB3D,CALM1,TTC7B,TIMM29,GGA2,CYP46A1,ARHGAP44,NPC1,AP2B1,MIEF2,CDK5R1,PRAM1,EPB41L3,MAIP1,IFT20,EFCAB7,GPC3,INPP5K,DNAJA3,EMC6,PDPK1,PRKCZ,SGTA,RAB26,RER1,ABHD17A,ARHGEF16,UBL4A,SEC16A,PALM,BSG,ATP2C2,ZDHHC12,STXBP1,HSPA5,SH3GLB	grey	VSMC_M10
GO:0003161	0.74	0.39	15	31	cardiac conduction system development	BP	1	MAML1,SMAD5,BVES,SCN5A,NRG1,TBX5,BMPR1A,MSX2,CACNA1G,DSG2,GATA6,ISL1,HCN4,NKX2-5,HEY2	grey	VSMC_M10
GO:0032535	0.74	0.30	167	325	regulation of cellular component size	BP	1	ARPC3,LRP1,SEMA6A,AVIL,RAB21,PRR16,SLC12A2,FSTL4,WASHC5,PLXNA4,BAIAP2L2,PICK1,CDC42EP1,LMOD2,SRF,NCK2,SEMA4D,KIAA1211,SEMA4C,TMOD1,PLEKHH2,PRKCE,SPTBN1,RTN4,RUFY3,AQP1,PLEK,EPHA7,ADD2,KEL,FAM49A,NRCAM,WASF1,SLC26A5,GOLGA4,MEGF8,CLNS1A,AQP11,PLEKHG2,FCHSD2,MKKS,RPTOR,RAB5A,BAG4,SEMA3D,SPART,FCHSD1,SEMA3A,NCKAP1L,LARS,ULK1,ARFIP2,LMOD3,RYK,RET,HCK,TTL,FER,HIP1R,PLS1,FMN1,LIMA1,SEMA4F,P2RX7,PTK2B,DPYSL2,USH1C,NKX6-1,ZFYVE27,F2RL1,IQGAP2,ANO6,SEMA3G,SPP1,CYFIP1,DMTN,SEMA4G,SLC12A5,MAGEL2,BDNF,KIAA0319,CARMIL1,LMOD1,ADD3,SLC12A7,TRPV4,SEMA3F,SSH1,PEX11B,HCLS1,ADNP,AP1AR,DISC1,RAB22A,WASF2,AP2M1,SPTBN2,TMOD4,SLC12A8,EPS8,CDKL5,WHAMM,DLG1,WNT3,CAPZA1,CREB1,CDC42EP2,MAPT,SEMA6D,SLC12A9,TNR,FN1,NCKAP1,GNB3,ARPC1A,KCNMA1,WAS,TMOD2,ATP13A2,SPTB,CLN8,PFN3,WNK3,SEMA4A,TRIM46,NDEL1,AC138894.1,HAX1,RAB11A,NTN1,DNM2,EVL,SIN3A,TRPV2,PEX11G,LRRC8E,CDK5R1,VAV1,IL7R,SSH2,RILP,RAP1GAP2,L1CAM,MLST8,ARHGAP4,PLXNA3,SPIRE2,TSC1,LAMTOR5,VAV3,LRRC8A,BARHL2,WDR63,SLC12A4,CARMIL2,RHOA,CNTN2,VASP,GMFG,WNT5A,PEX11A,GRB2,PPP1R15A,PFN4,PDXP,OLFM1,COTL1	grey	VSMC_M10
GO:1990868	0.74	0.36	24	48	response to chemokine	BP	1	SLC12A2,CXCL8,OXSR1,ACKR2,ROBO1,PTK2B,CCL17,CMKLR1,CIB1,THPO,CXCR2,PADI2,CCL14,CCL5,CCL7,CCL2,CCL25,RHOA,CCL16,GPR35,CCR10,CXCL6,DUSP1,CCL22	grey	VSMC_M10
GO:1990869	0.74	0.36	24	48	cellular response to chemokine	BP	1	SLC12A2,CXCL8,OXSR1,ACKR2,ROBO1,PTK2B,CCL17,CMKLR1,CIB1,THPO,CXCR2,PADI2,CCL14,CCL5,CCL7,CCL2,CCL25,RHOA,CCL16,GPR35,CCR10,CXCL6,DUSP1,CCL22	grey	VSMC_M10
GO:0003177	0.74	0.42	9	19	pulmonary valve development	BP	1	NFATC1,JAG1,ROBO1,ROBO2,TGFB2,RBPJ,TNFRSF1B,STRA6,HEY2	grey	VSMC_M10
GO:0031118	0.74	0.49	5	10	rRNA pseudouridine synthesis	BP	1	RPUSD2,RPUSD4,GAR1,RPUSD1,RPUSD3	grey	VSMC_M10
GO:0034453	0.74	0.40	12	25	microtubule anchoring	BP	1	CCDC68,KIF3A,BICD2,NINL,CLASP2,HOOK3,DAG1,SAXO2,NIN,CCDC120,PEX14,CAMSAP3	grey	VSMC_M10
GO:0043631	0.74	0.36	20	41	RNA polyadenylation	BP	1	CPSF6,PABPC1,ZC3H3,HSF1,CPSF1,RNF20,YTHDC1,PNPT1,MTPAP,SYMPK,PCF11,CSTF3,CLP1,TENT2,TENT4B,CPSF2,LEO1,AP002990.1,CSTF2,PAPOLA	grey	VSMC_M10
GO:0035773	0.74	0.35	29	58	insulin secretion involved in cellular response to glucose stimulus	BP	1	LRP1,PLA2G6,PRKCE,HMGN3,TRPM4,RAF1,NR1H4,NDUFAF2,OSBP,TIAM1,RAB11FIP5,ZBED6,GPLD1,SLC9B2,ADRA2A,RAB11FIP2,SIDT2,KLF7,ENY2,ABCA12,PPP3CB,PTPRN,MPC2,STX4,GPR68,OXCT1,NADK,BAIAP3,CRH	grey	VSMC_M10
GO:1903828	0.75	0.32	50	99	negative regulation of cellular protein localization	BP	1	NEDD4L,GOPC,C6orf106,ABHD17B,RAB23,DNAJA1,ITGB1BP1,UBAC2,FERMT1,BAG4,MFHAS1,NSFL1C,LYPLA1,POLR1A,DCLK2,PKIA,DMTN,SUFU,CABP1,PPFIA1,ANKRD13A,SP100,TTBK2,YOD1,OTUD7B,BAG3,AP2M1,PPP2R5A,FZD9,APOD,LRRC15,MAPT,LZTFL1,DERL3,C11orf65,MAGED1,RSC1A1,SIN3A,INPP5K,TAX1BP3,ABHD17A,SAPCD2,PARK7,ABHD17C,TXN,LEPROT,UBE2G2,MRAP2,MAP1A,DERL2	grey	VSMC_M10
GO:0010565	0.75	0.33	48	95	regulation of cellular ketone metabolic process	BP	1	PPARA,PRKCE,NR1H2,DKKL1,SLC7A11,SOX9,APOC1,PRKAG2,SLC22A13,PIBF1,AKT2,PANK2,PDK1,NR1H4,TRIB3,CYP7A1,DKK3,NR1H3,ERLIN1,PRMT3,SIRT5,LONP2,SIRT4,IRS1,CPT1A,SLC7A7,ABCB11,LPGAT1,MLXIPL,SCAP,PDK3,ACADL,TYSND1,COMT,WNT4,ACADVL,FGFR4,DGKQ,AC138894.1,NCOR1,CD74,SREBF1,PARK7,MLYCD,MIR21,FABP5,STARD4,INSIG2	grey	VSMC_M10

GO:0048593	0.75	0.32	48	96	camera-type eye morphogenesis	BP	1	FRS2,BAK1,ATF4,NTRK2,RORB,SLC1A1,TFAP2B,TDRD7,RDH13,PTN,TSPAN12,FOXE3,SOX9,IFT172,TSKU,JAG1,EPHB1,TENM3,USH1C,RPGRIP1L,TFAP2A,PAX2,NECTIN3,ALDH1A3,SHROOM2,NRL,SP3,FZD5,OBSL1,ROM1,SDK1,MFN2,MEGF11,LCTL,TBX2,LHX1,STRA6,YY1,SKI,SOX8,FJX1,THY1,WNT5A,DIO3,TBC1D20,PITX3,WNT2,COL8A2	grey	VSMC_M10
GO:0050670	0.75	0.31	70	137	regulation of lymphocyte proliferation	BP	1	AGER,IL5,HLA-DPB1,TNFRSF13C,RAC2,TNFRSF21,NCK2,PELI1,IL4I1,TLR4,IL15,BMI1,MYD88,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,IL1A,CASP3,MEF2C,TMEM131L,IL7,RIPK2,MARCH7,ZNF335,CD40,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,CD28,DLG1,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,CD38,BST1,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,ZBTB7B,CHRNB2,BTK,CD74,CCL5,CD320,TWSG1,TICAM1,DNAJA3,VAV3,GLMN,MIR21,LST1,FADD,CD46,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0048799	0.75	0.40	12	25	animal organ maturation	BP	1	SEMA4D,RYR1,RET,PAX2,ACTN3,FGFR3,ALDH1A2,THBS3,RFLNB,RHOA,SNX10,CCDC154	grey	VSMC_M10
GO:0050777	0.75	0.31	65	128	negative regulation of immune response	BP	1	TNFAIP3,USP15,ENPP3,C6orf106,MAPK14,NR1H2,IL4I1,FOXJ1,SEC14L1,SIRT2,NMI,NPLOC4,NCKAP1L,PCBP2,PLK2,HCK,FER,NR1H3,TRAFD1,OAS3,NLRC5,MAPKBP1,NOD2,CD96,HLX,YTHDF2,SLAMF8,PARP14,RNF26,FGR,NLRX1,TRAF3IP1,HTRA1,PDCD1,DUSP10,BCL6,RC3H1,PTPN6,TNFSF18,COL3A1,PPP3CB,MUL1,FOXP3,TKFC,USP18,TBX21,DCST1,ZBTB7B,IL4R,TSPAN6,STAT2,RIOK3,YES1,IL7R,PTPN2,CRK,FOXF1,MIR21,OAS1,CD46,A2M,FGL2,SERPINB9,HAVCR2,RC3H2	grey	VSMC_M10
GO:0099068	0.75	0.39	12	25	postsynapse assembly	BP	1	LRFN1,GAP43,NLGN4Y,NRXN2,NLGN2,NLGN3,CEL,NTNG2,ZDHHC12,GRID2,WNT5A,LRRTM2	grey	VSMC_M10
GO:0099622	0.75	0.39	12	25	cardiac muscle cell membrane repolarization	BP	1	SCN5A,KCNJ3,KCNE2,KCNIP2,KCNJ2,ANK2,SCN4B,NOS1AP,ATP1B1,RNF207,KCNH2,KCNJ8	grey	VSMC_M10
GO:0031057	0.75	0.37	18	37	negative regulation of histone modification	BP	1	PHF1,UBE2B,ATG5,SPHK2,KDM4A,TAF7,SDR16C5,DNMT3B,JARID2,BCOR,KDM5A,FOXP3,OTUB2,SIN3A,SUPT6H,SKI,MTF2,PRMT6	grey	VSMC_M10
GO:0003203	0.75	0.38	15	31	endocardial cushion morphogenesis	BP	1	SOX9,TGFBR2,ROBO1,ROBO2,TGFB2,SNAI1,BMPR1A,RBPJ,TMEM100,TBX2,ISL1,ENG,ACVRL1,NOG,HEY2	grey	VSMC_M10
GO:0007292	0.75	0.32	51	101	female gamete generation	BP	1	YTHDC2,GDF9,MCM9,WASHC5,TOB2,H3F3C,TUT7,DMC1,YTHDC1,PTN,NOBOX,CCDC155,TUT4,FOXO3,PANX1,ERCC1,MLH1,SIRT2,MCM8,SOHLH2,HPGD,M1AP,ADAMTS1,PTK2B,KMT2D,NPM2,BMPR1B,GAS2,HSF2BP,PRKAR1A,CCDC36,YTHDF2,SPO11,ETV6,WNT4,YBX2,SEPT1,IL4R,PAQR5,RAD51C,TAF4B,PARN,MEIOB,WDR77,SPIRE2,MSH4,AURKC,UBB,NANOS1,EREG,ZGLP1	grey	VSMC_M10
GO:0090398	0.75	0.33	34	68	cellular senescence	BP	1	MAP3K5,MAPK14,CDKN2A,SRF,NUAK1,CDK6,PNPT1,ZNF277,PAWR,PRKDC,PLK2,ING2,ARNTL,MAPKAPK5,OPA1,PLA2R1,TERT,MAP2K6,SLC30A10,KRAS,MAP3K3,CDKN1B,BCL6,BMPR1A,YPEL3,VASH1,MAP2K1,TBX2,TERF2,MIR22,PRMT6,YBX1,HRAS,MAP2K7	grey	VSMC_M10
GO:0043255	0.75	0.33	39	78	regulation of carbohydrate biosynthetic process	BP	1	PPARA,GPT,GNMT,CRY1,PPP4R3B,ZNF692,PLEK,FAM3C,EPM2AIP1,PPP1CB,AKT2,SIRT7,PPP1R3B,NLN,SORBS1,P2RY1,PTK2B,IGF2,IRS1,SIK1,MST1,PPP1R3E,EGF,GPER1,PPP1R3D,NTSR1,PASK,PTH1R,PPP1R3F,DDB1,DGKQ,OGT,INSR,LEPR,PTPN2,INPP5K,ACADM,NNMT,ARPP19	grey	VSMC_M10
GO:0051353	0.75	0.35	25	50	positive regulation of oxidoreductase activity	BP	1	CYP27B1,SDHAF4,NOD1,DHFR,SIRT3,PIK3CB,PTK2B,VDR,NOD2,TERT,COX17,KRAS,AGT,NOS1AP,POR,ABL2,GCH1,CALM1,PARK7,GNAI3,CYBA,TERF2,FXN,FCER2,APOPT1	grey	VSMC_M10
GO:0030857	0.75	0.38	15	31	negative regulation of epithelial cell differentiation	BP	1	SMO,S1PR3,HOXA7,OSR1,SPRY1,FOXE3,SOX9,SPRY2,JAG1,SPRED3,SRSF6,CCND1,CITED1,ACVRL1,FOXJ2	grey	VSMC_M10
GO:0021533	0.75	0.42	8	17	cell differentiation in hindbrain	BP	1	AGTPBP1,FAIM2,LDB1,TTC21B,LHX1,GRID2,NOG,CEND1	grey	VSMC_M10
GO:0097242	0.75	0.38	14	29	amyloid-beta clearance	BP	1	LRP1,SRF,C5AR1,RAB5A,IDE,MME,HDAC1,LRPAP1,ITGAM,RAB11A,LDLR,INSR,C3,ABCA7	grey	VSMC_M10
GO:0090151	0.75	0.39	12	24	establishment of protein localization to mitochondrial membrane	BP	1	HSPA4,TOMM22,AGK,AP3B1,OXA1L,NMT1,BCS1L,CALM1,TIMM29,MAIP1,TIMM10B,TIMM8B	grey	VSMC_M10
GO:0001702	0.75	0.42	8	17	gastrulation with mouth forming second	BP	1	FRS2,SRF,MEGF8,ACVR2A,LDB1,LHX1,AMOT,WNT5A	grey	VSMC_M10
GO:0036092	0.75	0.44	7	15	phosphatidylinositol-3-phosphate biosynthetic process	BP	1	SYNJ2,INPP4A,INPP4B,FIG4,PIK3CB,SYNJ1,PIKFYVE	grey	VSMC_M10
GO:0010812	0.75	0.34	26	53	negative regulation of cell-substrate adhesion	BP	1	LRP1,FBLN1,CDKN2A,HOXA7,ITGB1BP1,CLASP2,JAG1,FAM107A,PIK3R1,GCNT2,DMTN,ARHGAP6,AP1AR,FZD7,PTPRO,MELTF,APOD,BCL6,MEN1,CASK,CORO2B,BCAS3,RHOA,ACVRL1,ACER2,DUSP22	grey	VSMC_M10
GO:2001224	0.75	0.43	7	15	positive regulation of neuron migration	BP	1	SEMA6A,SEMA3A,RAPGEF2,SRGAP2C,ZNF609,FBXO31,DAB2IP	grey	VSMC_M10
GO:0043113	0.75	0.35	21	43	receptor clustering	BP	1	SYNGAP1,PICK1,PTN,ITGB1BP1,SLC7A11,DLG2,GRIK5,SSH1,FZD9,DLG1,ITGA4,NRXN2,SAV1,DLG4,WDR19,GPHN,SYNJ2BP,DNAJA3,RER1,THY1,MESD	grey	VSMC_M10
GO:0032607	0.75	0.40	10	21	interferon-alpha production	BP	1	IRF5,TLR4,NMI,MAVS,IRF7,RIPK2,IFIH1,SETD2,DDX3X,HAVCR2	grey	VSMC_M10
GO:0032647	0.75	0.40	10	21	regulation of interferon-alpha production	BP	1	IRF5,TLR4,NMI,MAVS,IRF7,RIPK2,IFIH1,SETD2,DDX3X,HAVCR2	grey	VSMC_M10
GO:0030048	0.75	0.32	48	97	actin filament-based movement	BP	1	NEDD4L,MYO1A,SUN2,MYH9,MYH14,TRPM4,MYO7B,CACNB2,SCN5A,SCN1A,MYO7A,GPD1L,PARVA,STC1,KCNJ3,TNNC1,KCNE2,DSP,RYR2,PKP2,KCNJ2,MYH7,ANK2,WASF2,ATP1A2,ACTC1,SLC9A1,SCN4B,NOS1AP,DLG1,WAS,MYO9B,SYNE2,WIPF2,CACNA1G,ATP2A1,MYH10,CCDC88C,DSG2,MYO1D,MYO1F,MYO5B,RNF207,FNBP1L,KCNH2,SCN2B,KCNJ8,HCN4	grey	VSMC_M10
GO:0003184	0.75	0.43	7	15	pulmonary valve morphogenesis	BP	1	NFATC1,JAG1,ROBO1,ROBO2,TGFB2,STRA6,HEY2	grey	VSMC_M10

GO:1990778	0.75	0.29	143	279	protein localization to cell periphery	BP	1	LRP1,STX7,STAC3,MAP7,GOPC,EPB41L2,PTCH1,TSPAN33,ADAM22,SLC1A1,PRKCE,ASB3,SPTBN1,ITGB1BP1,EGFR,VPS35,LIN7B,RAB7A,RAB10,CACNB2,CLASP2,STAC,OPTN,GOLGA4,MYL12A,AKT2,IKBKB,ANK1,LIN7A,PRNP,BAG4,GAS6,PKP3,ARL6IP5,TUB,KCNIP3,LYPLA1,RILPL1,RILPL2,PIK3R1,TMEM150A,VAMP5,SLMAP,PLS1,FCHO2,SORBS1,P2RY1,RAPGEF2,KCNJ11,ZFYVE27,TESC,KIF13A,NHLRC1,NECTIN3,PKP2,PPFIA1,ZDHHC23,DAG1,KCNB1,EPB41,ANK2,C2CD5,GPER1,RAB11FIP2,FAM126B,CIB1,AP2M1,PPP2R5A,BBS1,GORASP2,LAMA5,PACS1,DLG1,LRRC15,NSF,LZTFL1,EHD1,ZDHHC8,ABCA12,CNPY4,AP4M1,RAB3A,RAMP2,EXOC5,ATP1B1,PPIL2,NSG1,GRIPAP1,RAB8A,CNST,DLG4,ACTB,WDR19,RAB15,IQSEC2,RSC1A1,MPP5,WNK3,STAC2,TSPAN17,ANXA2,GAK,CPLX1,STX1B,STX4,TMEM88,RAB8B,ITGA3,AC138894.1,RAB11A,STX8,RAB3D,TTC7B,GGA2,ARHGAP44,PRAM1,EPB41L3,IFT20,EFCAB7,NUBP1,INPP5K,PDPK1,PRKCZ,RAB26,RER1,ARHGEF16,SAPCD2,SEC16A,PALM,BSG,GPSM2,ATP2C2,STXBP1,VPS4A,C16orf70,FYB1,PDZD3,PDZD11,LDLRAP1,CACNG7,HRAS,VAMP3,MRAP2	grey	VSMC_M10
GO:0021782	0.75	0.32	43	86	glial cell development	BP	1	LRP1,ADGRG6,AGER,NTRK2,PICK1,SOX10,SMO,TTBK1,ADAM22,CDK6,ROR2,FPR2,EGFR,TLR4,C5AR1,HDAC11,ERCC2,EIF2B3,PRX,AKT2,SIRT2,NRG1,LGI4,TSPAN2,DAG1,KRAS,CSPG5,NSUN5,MAPT,CNTNAP1,MPP5,PSEN1,LDLR,S100A8,MXRA8,SKI,LAMC3,CNTN2,SOX4,CNTF,POU3F2,NRROS,PHGDH	grey	VSMC_M10
GO:0032288	0.75	0.41	9	19	myelin assembly	BP	1	FIG4,MTMR2,ERCC2,ANK2,GNPAT,PIKFYVE,CNTNAP1,MPP5,EPB41L3	grey	VSMC_M10
GO:0016064	0.75	0.32	43	85	immunoglobulin mediated immune response	BP	1	CD226,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,EXOSC3,MSH2,TRAF3IP2,HMCES,ERCC1,NECTIN2,MLH1,MYD88,FOXJ1,PAXIP1,SHLD1,HPX,IRF7,GAPT,NBN,NOD2,CD40,TCIRG1,CD28,FCER1G,RNF168,BCL6,PTPN6,FOXP3,SHLD2,TBX21,BATF,CD19,IL4R,BTK,CD74,C7,C3,SUPT6H,BCL10,CD46,FCER2,RNF8	grey	VSMC_M10
GO:0009190	0.75	0.42	8	17	cyclic nucleotide biosynthetic process	BP	1	ADCY3,GUCY1A1,GUCY1B1,ADCY7,ADCY2,ADCY4,ADCY10,GUCY2D	grey	VSMC_M10
GO:0052652	0.75	0.42	8	17	cyclic purine nucleotide metabolic process	BP	1	ADCY3,GUCY1A1,GUCY1B1,ADCY7,ADCY2,ADCY4,ADCY10,GUCY2D	grey	VSMC_M10
GO:1905207	0.75	0.38	13	27	regulation of cardiocyte differentiation	BP	1	FRS2,EGFR,MEF2C,SOX6,TBX5,PRICKLE1,TGFB2,GPER1,FZD7,GATA6,MIR222,NKX2-5,HEY2	grey	VSMC_M10
GO:0001578	0.75	0.32	43	86	microtubule bundle formation	BP	1	ZNF207,UBE2B,LRRC6,CFAP69,WDR92,CDK5RAP2,ARMC2,MAPRE1,ARMC4,TTC26,DRC1,RSPH6A,NCKAP5,FOXJ1,TTLL3,SPEF1,CLIP1,CCDC66,NCKAP5L,CCDC65,DNAH1,DNAH5,NEURL1,CFAP43,ZMYND10,CFAP46,JHY,TTC12,TOGARAM1,DNAAF2,SPAG16,TTC25,DNAAF4,MNS1,TRIM46,CCDC151,CAPN6,SPEF2,C16orf71,TPGS1,PSRC1,HYDIN,WDR63	grey	VSMC_M10
GO:0051480	0.75	0.29	108	212	regulation of cytosolic calcium ion concentration	BP	1	LRP1,ESR1,BAK1,MCHR1,GPR20,PLA2G6,S1PR3,PRKCE,FPR2,IBTK,LPAR1,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,PTGIR,GIPR,CACNB2,ACKR2,C1QTNF1,RYR1,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,RASA3,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,TPCN1,SLC8B1,F2RL1,F2R,PKD2,CASQ2,RYR2,TRPM1,SPPL3,LCK,TRPV4,GNA13,CMKLR1,UBASH3B,ANK2,GPER1,AGT,ATP1A2,CASQ1,NTSR1,FZD9,PTH1R,FIS1,CEMIP,ABL2,CDH23,PTPN6,CXCR2,GNG3,HTT,PTGDR,PTGER2,CD38,HAP1,DLG4,FAM155B,CACNA1A,AC138894.1,CD19,SMAD3,CALM1,BDKRB1,NMUR2,TRPV2,HRH4,PTGER4,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,GPR157,CYBA,JPH3,MCOLN3,PTGFR,MIR199A1,KCNK3,DMD,GPR35,NOL3,CHRNA10,CCR10,JPH2,THY1,WNT5A,DDIT3	grey	VSMC_M10
GO:0006886	0.75	0.27	386	739	intracellular protein transport	BP	1	TIMM21,STX7,AP3S1,KIF5A,PEX7,PEX3,TBC1D30,TBC1D9B,PPP1R10,RAB21,SNX31,ZDHHC14,RIMS2,PRKN,TSPO,HSPA4,DERL1,FAM91A1,FAM53C,TSNARE1,SIL1,SYNGR1,MAPK14,TOMM22,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,SMO,ZDHHC21,PEX6,FBXO7,XPO5,APBA1,PEX1,SCFD2,SLC1A1,TGFBRAP1,TBC1D8,TRAM2,RAB23,SEC61B,STX17,SIX2,RIMS1,TMEM30A,RUFY3,XPO1,ITGB1BP1,YWHAZ,SEC61G,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,AGK,BCAP29,TRAF3IP2,DNAJC27,NAPA,RAB7A,AP2S1,COPG1,KPNA3,ARL5B,LCP1,SYTL2,DLG2,DNAJC15,PLK3,IPO13,AQP11,ZFAND6,TBC1D4,MYO7A,NAPB,GCKR,SEC62,KPNA2,AKT2,PITRM1,TIMM50,SNX5,USP36,TBC1D16,AP3M2,KIF5C,NPLOC4,ARL5A,UBAC2,RAB5A,ASPSCR1,TMCO6,NUP98,SIRT7,FERMT1,HACL1,CEP290,PRNP,ING1,BAG4,MAVS,FUT10,GAS6,ARFIP2,VPS16,COPZ1,STX2,SRP14,NCOA4,KCNIP3,NUP58,MIPEP,TM9SF4,ZDHHC20,IPO11,RILPL1,RILPL2,IMMP1L,PIK3R1,TBC1D12,TNPO1,FBXW7,SCG5,PEX2,PKIA,HTRA2,AUP1,ZFAND1,CSNK2A2,NUP54,KATNB1,SSR3,SPCS1,EXOC6B,SEC31A,RAPGEF3,AP3B1,GOLGA7B,AP4B1,PEX16,CRY2,VPS18,TOMM34,SEC31B,DMTN,PRICKLE1,VPS26C,HERC2,XPO7,LONP2,VPS39,KIF13A,SUFU,SIRT4,EIF2D,CABP1,RHBDD1,SRPRA,RPL23,PPP3CA,IPO9,SP100,ZDHHC23,MON1A,TBCK,ZDHHC6,VTI1A,TCF7L2,ADPRH,PDCD6,OXA1L,UNC93B1,RABL3,KCNB1,NCF1,YOD1,HCLS1,TBC1D10C,HSPA8,VPS45,HPS4,SORL1,C2CD5,ARIH2,AP1B1,AGT,CIB1,RAB22A,SYTL1,BAG3,AP1S2,MLPH,RAB17,AP2M1,SEC23IP,STRADB,SFN,ZDHHC18,PEX19,COPA,ZDHHC24,STX1A,RNF215,SNX27,STX6,RAB1B,TOMM40L,STRADA,VPS37D,UHMK1,EIF4ENIF1,RPL11,SNX6,	grey	VSMC_M10
GO:0060038	0.75	0.35	22	45	cardiac muscle cell proliferation	BP	1	GLI1,MAPK14,PIM1,TGFBR2,MEF2C,TBX5,JARID2,TGFB2,PRKAR1A,KCNK2,SAV1,MAPK1,BMPR1A,RBPJ,TBX2,GATA6,MIR199A1,MIR222,NOG,C3orf58,HEY2,WNT2	grey	VSMC_M10

GO:0032368	0.75	0.32	48	95	regulation of lipid transport	BP	1	LRP1,PRKN,PPARA,TSPO,GDF9,PTCH1,PLA2G6,TTC39B,CRY1,ABCG5,ABCG8,TMEM30A,NR1H2,APOC1,AKT2,C1QTNF1,NR1H3,NKX3-1,CRY2,SPP1,PLA2R1,PLTP,MAP2K6,ABCA5,ACSL5,EGF,AGT,NTSR1,PLA2G4A,FIS1,OSBPL6,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,NAXE,ABCA3,ABCA7,RXRA,MIR27B,MIR27A,ABCA8,MIR33B,LDLRAP1,CRH,LRAT,PTGES	grey	VSMC_M10
GO:0034260	0.75	0.37	15	31	negative regulation of GTPase activity	BP	1	SPRY1,SPRY2,ARRB1,MKKS,FICD,SH3BP4,RASA4,GMIP,BCAS3,AMOT,GPSM1,TSC1,DAB2IP,MIR21,HRAS	grey	VSMC_M10
GO:0001755	0.75	0.35	23	47	neural crest cell migration	BP	1	SEMA6A,SOX10,SMO,SEMA4D,SEMA4C,OVOL2,ALX1,SEMA3D,SEMA3A,RET,HAND2,SEMA4F,SEMA3G,SEMA4G,SEMA3F,GBX2,LAMA5,SEMA6D,FN1,RADIL,SEMA4A,ISL1,SOX8	grey	VSMC_M10
GO:0006476	0.75	0.32	44	88	protein deacetylation	BP	1	BAZ2A,C6orf89,SPHK2,HDAC2,PRKD2,PHB,HDAC11,BEX4,TADA3,SIRT2,SIRT7,SIRT3,MTA3,SDR16C5,ING2,HDAC7,SIRT5,SUDS3,ELK4,SIRT4,HDAC1,RCOR3,PER2,HDAC4,MAPT,BCL6,RCOR2,PINK1,TBL1XR1,KDM5A,FOXP3,AKAP8L,AKAP8,JDP2,ZBTB7B,SFPQ,SIN3A,RCOR1,SREBF1,SKI,MIER2,PRMT6,SAP30BP,NNMT	grey	VSMC_M10
GO:0032677	0.75	0.34	28	56	regulation of interleukin-8 production	BP	1	HSPA1B,NOD1,ANXA4,TLR4,C5AR2,PRKD2,MYD88,ARRB1,MAVS,F2RL1,F2R,RIPK1,MAPKBP1,NOD2,TLR5,OTUD7B,STAT3,MAP2K5,CD74,NOS2,PARK7,LAMTOR5,BCL10,FADD,ZNF580,WNT5A,DDIT3,IL17D	grey	VSMC_M10
GO:0060074	0.75	0.42	8	17	synapse maturation	BP	1	SHANK1,YWHAZ,NEURL1,DISC1,NFATC4,SEZ6,PALM,DAB2IP	grey	VSMC_M10
GO:0051261	0.75	0.31	49	99	protein depolymerization	BP	1	VPS4B,AVIL,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,PLEK,ADD2,CLASP2,TRIM54,NCKAP5,NAV3,SPEF1,LMOD3,ATXN7,LIMA1,NCKAP5L,KATNB1,SYNJ1,F2RL1,DMTN,STMND1,CARMIL1,LMOD1,ADD3,TRPV4,TTBK2,CFL1,HSPA8,CIB1,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,GAK,CAMSAP3,TAOK1,APC2,CAMSAP1,VPS4A,CARMIL2,CCSAP,APC,PDXP,MAP1A,MAP6D1	grey	VSMC_M10
GO:0010165	0.75	0.37	14	29	response to X-ray	BP	1	XRCC6,MSH2,ERCC1,XRCC2,THBD,XRRA1,ERCC6,CASP3,XRCC4,CCND1,XRCC5,DNM2,KARS,BRCC3	grey	VSMC_M10
GO:0033169	0.75	0.45	6	13	histone H3-K9 demethylation	BP	1	KDM3B,KDM4C,KDM7A,KDM4A,PHF8,HSF4	grey	VSMC_M10
GO:0035459	0.75	0.41	9	19	vesicle cargo loading	BP	1	SEC31A,SEC31B,KIF13A,SCAP,MIA3,CTAGE9,SEC24C,TMED10,TBC1D20	grey	VSMC_M10
GO:0045879	0.76	0.37	14	29	negative regulation of smoothened signaling pathway	BP	1	PTCH1,PTCH2,KCTD21,GLI2,MEGF8,IFT172,KCTD6,SUFU,GPR161,TULP3,MOSMO,GPC3,MGRN1,GPR37L1	grey	VSMC_M10
GO:0048384	0.76	0.39	11	23	retinoic acid receptor signaling pathway	BP	1	SNW1,RXRB,NR1H2,RARB,ASXL1,ZNF536,CNOT1,RXRG,DHRS3,ALDH1A2,RXRA	grey	VSMC_M10
GO:0032387	0.76	0.35	23	46	negative regulation of intracellular transport	BP	1	RAB23,ITGB1BP1,UBAC2,FERMT1,BAG4,PKIA,DMTN,SUFU,CABP1,SP100,YOD1,BAG3,CNIH2,APOD,DERL3,C11orf65,SNX12,INPP5K,PARK7,MIR27B,TXN,UBE2G2,DERL2	grey	VSMC_M10
GO:0007041	0.76	0.31	50	100	lysosomal transport	BP	1	VPS4B,LRP1,IGF2R,PRKN,VPS52,TGFBRAP1,VPS41,VPS35,RAB7A,RBSN,HGSNAT,HOOK3,TMEM106B,FAM160A2,VPS16,NCOA4,CHMP2B,AP3B1,VPS18,VPS39,KIF13A,RAB7B,CCDC91,HSPA8,SORL1,DTX3L,SNX27,AP4M1,PINK1,ANKFY1,AP3M1,ATP13A2,GAK,AC138894.1,HOOK2,VIPAS39,STX8,SNAPIN,NPC1,LAMP2,CLEC16A,VPS53,MTM1,MGRN1,RILP,AP1G1,VPS4A,CACNG7,SNX16,CACNG5	grey	VSMC_M10
GO:0008203	0.76	0.31	52	103	cholesterol metabolic process	BP	1	APOF,TTC39B,PLPP6,CAT,APOB,EBP,CUBN,LIPE,TSKU,PIP4P1,NR1H4,SOAT2,CYP7A1,CYP7B1,CEBPA,LIMA1,EPHX2,ERLIN1,ABCA5,FMO5,MSMO1,SC5D,SCAP,HSD17B7,POR,ACADL,SOAT1,TM7SF2,OSBPL1A,FDX1,LPCAT3,GNB3,CYP27A1,CH25H,ACADVL,CLN8,LIPC,DGKQ,APOBR,CLN6,LDLR,CYP46A1,NPC1,SREBF1,LEPR,ACAA2,RXRA,CEL,NFE2L1,LDLRAP1,INSIG2,FGF1	grey	VSMC_M10
GO:0016233	0.76	0.36	18	37	telomere capping	BP	1	MAP3K4,MAPK15,POT1,ERCC1,XRCC1,PRKDC,MAPKAPK5,NBN,STN1,RTEL1,MAPK1,CTC1,MAPK3,ERCC4,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0032486	0.76	0.44	6	13	Rap protein signal transduction	BP	1	PLK2,RAPGEF2,RAPGEF3,CBL,RAP1B,RAP2B	grey	VSMC_M10
GO:0106056	0.76	0.37	15	31	regulation of calcineurin-mediated signaling	BP	1	FHL2,SLC8A2,EFHB,PRNP,NRG1,SPPL3,TBC1D10C,CIB1,SLC9A1,MYOZ2,ACTN3,HOMER2,MYOZ1,MAPK7,CAMTA1	grey	VSMC_M10
GO:0036503	0.76	0.31	50	99	ERAD pathway	BP	1	CANX,PRKN,RNF5,DERL1,FOXRED2,SEC61B,ECPAS,AQP11,UBXN4,UGGT2,FBXO17,DNAJC18,NPLOC4,UBAC2,UBXN8,USP25,AUP1,TMEM67,AMFR,RNFT2,ERLIN1,RHBDD1,GET4,USP13,YOD1,USP19,RNF185,RHBDD2,EDEM3,NFE2L2,SYVN1,DERL3,TMUB2,DNAJC10,DNAJB12,TMEM129,ANKZF1,DNAJB2,SDF2L1,CALR3,FBXO2,SEL1L,BCAP31,SGTA,TMEM259,HSPA5,RNFT1,FAM8A1,UBE2G2,DERL2	grey	VSMC_M10
GO:0034101	0.76	0.31	56	111	erythrocyte homeostasis	BP	1	MPIG6B,HSPA1B,BRD1,SMAD5,L3MBTL3,MAPK14,ZNF16,RBFOX2,SRF,CDK6,KIT,PRDX1,RPS14,SMAP1,EPAS1,PTBP3,BPGM,FOXO3,ERCC2,SLC25A38,ACVR2A,NCKAP1L,PRKDC,MFHAS1,GPI,ACVR1B,CASP3,TMEM14C,DMTN,ALAS1,LDB1,PKNOX1,RPS17,ACIN1,DYRK3,HCLS1,ARNT,SP3,BCL6,STAT3,STAT5B,INHA,THRA,MED1,HOXB6,AHSP,KAT7,DNASE2,SCNN1B,RCOR1,PTPN2,MIR222,ANKRD54,ARID4A,MAFB,FAM210B	grey	VSMC_M10
GO:0051897	0.76	0.31	44	88	positive regulation of protein kinase B signaling	BP	1	STK3,PTK2,TEK,RTN4,ITGB1BP1,MET,EGFR,PHB,SPRY2,C1QTNF1,HBEGF,BAG4,NRG1,GAS6,MFHAS1,RET,PIK3CB,PTPRJ,GCNT2,IGF2,TCF7L2,EGF,HCLS1,CASS4,OSM,THPO,CD28,ADAM8,STOX1,GDF15,PINK1,HAX1,PIK3R5,INSR,PARK7,ENG,MIR29A,MIR199A1,MIR21,MIR222,TXN,MYORG,TSPYL5,RASD2	grey	VSMC_M10
GO:0034433	0.76	0.43	7	14	steroid esterification	BP	1	APOC1,SOAT2,AGT,SOAT1,MIR27B,MIR27A,STARD4	grey	VSMC_M10
GO:0034434	0.76	0.43	7	14	sterol esterification	BP	1	APOC1,SOAT2,AGT,SOAT1,MIR27B,MIR27A,STARD4	grey	VSMC_M10
GO:0034435	0.76	0.43	7	14	cholesterol esterification	BP	1	APOC1,SOAT2,AGT,SOAT1,MIR27B,MIR27A,STARD4	grey	VSMC_M10

GO:0009150	0.76	0.28	148	286	purine ribonucleotide metabolic process	BP	1	NME1,HSD17B4,PDE7B,ATP5MGL,PPT2,PPARA,PDE10A,ACSL6,PRXL2C,GTPBP1,IMPDH1,GDA,CROT,SLC35B2,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,NT5E,PPT1,BPGM,DLD,SPHK2,ADCY3,DLG2,DHTKD1,PRKAG2,ATP5F1C,ELOVL1,PFKP,NUDT16,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,GPI,AMPD3,ATP5F1A,MCC2,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,MFN1,PFKFB2,ENO4,HACD2,ARNT,ADCY4,ACTN3,HDAC4,THEM5,DNAJC30,MLXIPL,PDE8A,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,HK1,ACSBG1,ATP5S,CASK,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,ENO3,PARP1,TECR,CARD11,SLC26A1,PSEN1,ACOT2,GUCY2D,PKLR,PANK3,GCDH,OGT,ADPGK,PDE4A,ACSM3,ACACA,NCOR1,INSR,SLC26A2,ADSSL1,ACSBG2,ALDOC,PIPOX,ACOT11,ATP6V0C,PANK4,NME3,MPP1,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,MLYCD,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,ELOVL3,TIGAR,NUDT19,NME6,NUDT2,HINT1	grey	VSMC_M10
GO:0072538	0.76	0.38	12	25	T-helper 17 type immune response	BP	1	TRAF3IP2,PHB,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,BATF,ZBTB7B,IL6R,MIR21,RC3H2	grey	VSMC_M10
GO:0042267	0.76	0.36	16	33	natural killer cell mediated cytotoxicity	BP	1	CD226,PRDX1,NECTIN2,PVR,UNC13D,RASGRP1,CADM1,IL12A,PTPN6,LAG3,STAT5B,VAV1,CRK,AP1G1,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0048011	0.76	0.39	11	23	neurotrophin TRK receptor signaling pathway	BP	1	WASF1,SPRY1,RAF1,SPRY2,CASP3,ZFYVE27,CYFIP1,DOK5,AGT,PPP2R5B,HAP1	grey	VSMC_M10
GO:0030178	0.76	0.30	72	142	negative regulation of Wnt signaling pathway	BP	1	NFATC1,LRP1,GLI1,STK3,FZD6,PRKN,MAPK14,CBY1,SOX10,MDFI,ROR2,SOSTDC1,GRB10,HECW1,FUZ,SFRP4,DKKL1,FOXO3,SOX9,TSKU,WNT11,RBMS3,CHD8,UBAC2,FERMT1,PFDN5,CTNND1,DKK3,TRABD2A,TMEM131L,LMBR1L,AMFR,SOX13,STK4,PRICKLE1,NKD1,HDAC1,TCF7L2,DKK2,AXIN2,SOX2,ZNRF3,KREMEN1,BICC1,NFATC4,PTPRO,OTUD5,IGFBP4,TMEM88,CITED1,SOX30,AC004687.2,CCDC88C,GSC,G3BP1,ISL1,NLK,GPC3,TLE6,TAX1BP3,APC2,DAB2IP,MIR199A1,TRABD2B,NOG,WNT5A,DDIT3,DACT3,SDHAF2,SHISA2,APC,NKX2-5	grey	VSMC_M10
GO:0006874	0.76	0.28	145	283	cellular calcium ion homeostasis	BP	1	LRP1,ESR1,SMDT1,BAK1,MCHR1,GPR20,PLA2G6,SLC25A27,S1PR3,PRKCE,TNNI3,FPR2,IBTK,LPAR1,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,ATP7B,PTGIR,GIPR,CACNB2,ACKR2,SLC24A3,C1QTNF1,TMTC4,RYR1,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,RASA3,MICU3,IMMT,C19orf12,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,TPCN1,SLC8B1,VDR,STC1,RMDN3,F2RL1,F2R,PKD2,CASQ2,MCUR1,CD40,RYR2,RAP1GDS1,TRPM1,SPPL3,LCK,TRPV4,TCIRG1,GNA13,CMKLR1,MCUB,UBASH3B,DISC1,ANK2,GPER1,TRPM8,PDZD8,AGT,ATP1A2,CASQ1,NTSR1,FZD9,TMCO1,PTH1R,FIS1,CEMIP,ABL2,CDH23,PTPN6,MICU1,MCU,CXCR2,GNG3,HTT,PTGDR,PTGER2,ATP1B1,CD38,ATP13A2,HAP1,DLG4,FAM155B,PSEN1,CACNA1A,AC138894.1,ATP2A1,CD19,SMAD3,CALM1,PRKCB,BDKRB1,NMUR2,TRPV2,HRH4,CCL14,CCL5,CCL7,PTGER4,SLC25A23,MAIP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,GPR157,SYPL2,CYBA,JPH3,ATP2C2,MCOLN3,PTGFR,MIR199A1,KCNK3,DMD,GPR35,NOL3,CHRNA10,CCR10,JPH2,THY1,WNT5A,DDIT3	grey	VSMC_M10
GO:0034695	0.76	0.41	8	17	response to prostaglandin E	BP	1	PRKCE,AANAT,PTGER2,AKAP8,ACACA,PTGER4,GNB1,GNG2	grey	VSMC_M10
GO:0018023	0.76	0.35	19	39	peptidyl-lysine trimethylation	BP	1	IWS1,SUV39H2,KDM4A,NSD3,KMT2D,RTF1,WDR82,ZNF335,FAM173B,SETD2,WDR61,VCPKMT,SETD1A,OGT,SETD3,MECP2,ARID4A,BEND3,ZNF304	grey	VSMC_M10
GO:0010799	0.76	0.36	17	35	regulation of peptidyl-threonine phosphorylation	BP	1	PRKAG2,SPRY2,SIRT2,RPTOR,RIPK2,DMTN,EGF,STOX1,CEMIP,MAPK1,WNK3,DGKQ,CALM1,INPP5K,IRGM,WNT5A,CADM4	grey	VSMC_M10
GO:0048821	0.76	0.37	13	27	erythrocyte development	BP	1	BRD1,L3MBTL3,SRF,PTBP3,BPGM,ERCC2,NCKAP1L,DMTN,ALAS1,BCL6,MED1,ARID4A,FAM210B	grey	VSMC_M10
GO:0010463	0.76	0.36	17	35	mesenchymal cell proliferation	BP	1	MYC,SMO,SIX2,PTN,MYCN,OSR1,SOX9,WNT11,TGFBR2,HAND2,CHRD,BMPR1A,GPC3,FOXF1,WNT5A,SIX1,WNT2	grey	VSMC_M10
GO:0030168	0.76	0.31	48	96	platelet activation	BP	1	FZD6,MAPK14,MYH9,SRF,TEC,TLN1,PLEK,DGKI,TLR4,SLC7A11,THBD,MYL12A,C1QTNF1,ACTG1,CLIC1,ADRA2B,PIK3CB,P2RY1,F2R,DMTN,CD40,LCK,ADRA2A,UBASH3B,DGKD,FCER1G,DGKG,PLA2G4A,ITGA2B,FN1,PTPN6,ADRA2C,FERMT3,COL3A1,VCL,ACTB,PEAR1,DGKQ,DGKE,VAV1,ABAT,P2RX1,ADAMTS13,VAV3,STXBP1,FGA,BLOC1S3,RAP2B	grey	VSMC_M10
GO:0098698	0.76	0.41	8	17	postsynaptic specialization assembly	BP	1	LRFN1,GAP43,NRXN2,NLGN2,NTNG2,ZDHHC12,GRID2,LRRTM2	grey	VSMC_M10
GO:0060119	0.76	0.36	17	35	inner ear receptor cell development	BP	1	ATP8B1,WHRN,USH1G,MYO7A,TSKU,SLC4A7,LRTOMT,AP000812.5,PLS1,ADGRV1,USH1C,TRIP11,STRC,CDH23,MKS1,IFT20,PJVK	grey	VSMC_M10
GO:0045823	0.76	0.38	12	25	positive regulation of heart contraction	BP	1	SLC1A1,TRPM4,ADRA1D,RYR2,TGFB2,ACE2,ATP1A2,GCH1,CHGA,RGS4,NKX2-5,HEY2	grey	VSMC_M10
GO:1903531	0.76	0.31	50	99	negative regulation of secretion by cell	BP	1	VPS4B,PRKN,CRY1,IL11,BMP8A,RSAD2,RAB7A,FRMD4A,DPH3,NCKAP1L,ADRA2B,NDUFAF2,FAM3D,ASIC1,P2RY1,KCNJ11,NR1H3,RAB11FIP5,ACVR1C,F2R,CRY2,ADTRP,SIRT4,IRS1,CD200,HDAC1,PPP3CA,ADRA2A,KCNB1,OSM,KLF7,RAP1B,IL12A,ENY2,ADRA2C,PNKD,INHA,RSC1A1,TNFRSF1B,SYT11,SYTL4,SREBF1,ABAT,FMR1,FOXF1,MIR199A1,CHGA,CRH,LIF,VAMP3	grey	VSMC_M10
GO:0032728	0.76	0.36	16	33	positive regulation of interferon-beta production	BP	1	IRF5,TLR4,TMEM173,MAVS,IRF7,OAS3,RIPK2,POLR3D,IFIH1,POLR3C,DDX3X,POLR3A,RIOK3,RNF135,TICAM1,OAS1	grey	VSMC_M10

GO:0061333	0.76	0.32	31	63	renal tubule morphogenesis	BP	1	MTSS1,MYC,KLHL3,PTCH1,SMO,SIX2,OSR1,SOX9,GZF1,WNT11,PAX8,EYA1,FMN1,MEF2C,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,NOG,SIX1,FGF1	grey	VSMC_M10
GO:0060969	0.76	0.40	9	19	negative regulation of gene silencing	BP	1	ZC3H10,ESR1,BCDIN3D,PPP3CA,TERT,TET1,STAT3,PHF8,NCOR1	grey	VSMC_M10
GO:0014850	0.76	0.39	10	21	response to muscle activity	BP	1	ABCG5,ABCG8,OPA1,RYR2,SRD5A1,AGT,MTFP1,FIS1,PRKAG3,ADSSL1	grey	VSMC_M10
GO:0010821	0.76	0.30	63	124	regulation of mitochondrion organization	BP	1	PRKN,TSPO,BAK1,PLA2G6,FBXO7,TMEM14A,VPS35,MGARP,USP36,SIRT7,DDHD2,DCN,HIP1R,FBXW7,HTRA2,CSNK2A2,OPA1,DNM1L,ZDHHC6,USP30,GPER1,CIDEB,FZD9,PISD,FZD5,MAPT,STOX1,FIS1,NMT1,C11orf65,MCU,HTT,DDHD1,PINK1,MUL1,ATP13A2,TMEM102,VPS13D,VPS13C,HAX1,ADCK1,STAT2,PSMD10,MIEF2,SREBF1,RALBP1,ACAA2,PAM16,PARK7,DHODH,PRMT6,MLLT11,NOL3,BNIP3L,TIGAR,FXN,BCL2L11,SLC35F6,RALA,BCL2L2,MIEF1,PPIF,AC140504.1	grey	VSMC_M10
GO:0001658	0.76	0.34	23	47	branching involved in ureteric bud morphogenesis	BP	1	MYC,PTCH1,SMO,SIX2,SOX9,GZF1,PAX8,EYA1,PKD2,PAX2,SALL1,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,SOX8,NOG,SIX1,FGF1	grey	VSMC_M10
GO:0002931	0.76	0.33	25	51	response to ischemia	BP	1	MAP3K5,BVES,SLC8A2,NDNF,PANX1,SLC26A5,P2RX2,PIK3CB,FAIM2,P2RX7,KCNJ11,MAP2K6,CIB1,HYOU1,PER2,ABRAXAS2,PINK1,CAMK2A,CSF1R,MLYCD,NQO1,NOL3,TIGAR,BCL2L2,PPIF	grey	VSMC_M10
GO:0001556	0.76	0.40	9	19	oocyte maturation	BP	1	WASHC5,TUT7,DMC1,TUT4,FOXO3,SIRT2,PTK2B,YTHDF2,EREG	grey	VSMC_M10
GO:0002695	0.76	0.30	60	118	negative regulation of leukocyte activation	BP	1	TNFAIP3,ENPP3,FBXO7,TNFRSF21,PELI1,IL4I1,CST7,CD300LF,PIBF1,FOXJ1,PAWR,PRNP,NCKAP1L,ZC3H8,FER,CASP3,TMEM131L,PAG1,NR1H3,MARCH7,CD200,BANK1,BTN2A2,PRKAR1A,HLX,TBC1D10C,GPER1,FGR,RUNX3,DLG1,BCL6,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,INHA,SCGB1A1,FOXP3,TBX21,SYT11,ZBTB7B,IL4R,LDLR,BTK,CD74,TWSG1,PTPN2,SOCS1,FOXF1,GLMN,MIR21,MIR27A,LST1,MIR125A,FGL2,LAX1,CEBPB,HAVCR2,RC3H2	grey	VSMC_M10
GO:0032925	0.76	0.41	8	17	regulation of activin receptor signaling pathway	BP	1	ZC3H3,ACVR2B,ACVR2A,ACVR1B,MEN1,SKI,FSTL3,LEMD3	grey	VSMC_M10
GO:0060147	0.76	0.34	20	41	regulation of posttranscriptional gene silencing	BP	1	ZC3H10,ESR1,AGO2,TNRC6B,XPO5,EGFR,MYCN,PUM2,BCDIN3D,EIF4E2,RIPK1,PPP3CA,TERT,AJUBA,DDX6,EIF4ENIF1,STAT3,MAP2K1,NCOR1,FMR1	grey	VSMC_M10
GO:0032958	0.76	0.39	10	21	inositol phosphate biosynthetic process	BP	1	IPPK,PLEK,ITPKC,P2RY1,PTK2B,ITPKA,GPER1,IP6K2,NTSR1,PTH1R	grey	VSMC_M10
GO:0060561	0.76	0.39	10	21	apoptotic process involved in morphogenesis	BP	1	BAK1,PAX8,HAND2,VDR,PAX2,TGFB2,FZD5,TNFRSF1B,JAG2,BCL2L11	grey	VSMC_M10
GO:0043370	0.76	0.36	16	33	regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	HLA-DRA,NCKAP1L,RIPK2,HLX,RUNX3,BCL6,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,SOCS1,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0032881	0.76	0.36	16	33	regulation of polysaccharide metabolic process	BP	1	RUBCNL,KHK,EPM2AIP1,PPP1CB,AKT2,PPP1R3B,SORBS1,IGF2,IRS1,PPP1R3E,EGF,PPP1R3D,PASK,PPP1R3F,INSR,INPP5K	grey	VSMC_M10
GO:0060413	0.76	0.42	7	15	atrial septum morphogenesis	BP	1	SMO,TBX5,TGFB2,ISL1,SOX4,NKX2-5,HEY2	grey	VSMC_M10
GO:2000050	0.76	0.38	12	25	regulation of non-canonical Wnt signaling pathway	BP	1	RSPO3,CSNK1E,DAAM2,SFRP4,SPEF1,TIAM1,NKD1,ZNRF3,MKS1,GPC3,WNT5A,LBX2	grey	VSMC_M10
GO:0014031	0.76	0.31	36	73	mesenchymal cell development	BP	1	SEMA6A,SOX10,SMO,SEMA4D,SEMA4C,SOX9,OVOL2,JAG1,ALX1,SEMA3D,SEMA3A,NRG1,KBTBD8,RET,HAND2,SEMA4F,SEMA3G,SEMA4G,KLHL12,SEMA3F,PEF1,PDCD6,GBX2,LAMA5,SEMA6D,FN1,MAPK1,BMPR1A,RADIL,ALDH1A2,SEMA4A,MAPK3,TCOF1,ISL1,SOX8,HEY2	grey	VSMC_M10
GO:0061081	0.76	0.41	8	17	positive regulation of myeloid leukocyte cytokine production involved in immune response	BP	1	KIT,TLR4,MAVS,SPON2,CD74,TICAM1,BCL10,WNT5A	grey	VSMC_M10
GO:0060964	0.76	0.35	19	39	regulation of gene silencing by miRNA	BP	1	ZC3H10,ESR1,AGO2,TNRC6B,EGFR,MYCN,PUM2,BCDIN3D,EIF4E2,RIPK1,PPP3CA,TERT,AJUBA,DDX6,EIF4ENIF1,STAT3,MAP2K1,NCOR1,FMR1	grey	VSMC_M10
GO:0070169	0.76	0.34	20	41	positive regulation of biomineral tissue development	BP	1	OSR2,PTN,OSR1,SLC4A2,ACVR2B,ACVR2A,KL,ADGRV1,MEF2C,P2RX7,ANO6,TFAP2A,BMPR1B,AMELX,ACTN3,FZD9,WNT4,BMPR1A,SMAD3,CEBPB	grey	VSMC_M10
GO:0010872	0.76	0.46	5	10	regulation of cholesterol esterification	BP	1	APOC1,AGT,MIR27B,MIR27A,STARD4	grey	VSMC_M10
GO:2000637	0.76	0.37	13	27	positive regulation of gene silencing by miRNA	BP	1	AGO2,TNRC6B,EGFR,MYCN,PUM2,EIF4E2,RIPK1,AJUBA,DDX6,EIF4ENIF1,STAT3,MAP2K1,FMR1	grey	VSMC_M10
GO:1904738	0.76	0.37	13	27	vascular associated smooth muscle cell migration	BP	1	LRP1,GRB10,MEF2C,ADAMTS1,DOCK5,TERT,GNA13,SSH1,AGT,NFE2L2,DOCK7,MIR21,RHOA	grey	VSMC_M10
GO:0045599	0.77	0.34	21	43	negative regulation of fat cell differentiation	BP	1	MKX,JAG1,SIRT2,TRIB3,ASXL1,ARNTL,RUNX1T1,TRIO,TRPV4,GPER1,MMP11,GPS2,TGFB1I1,JDP2,SMAD3,MIR27B,MIR27A,WNT5A,DDIT3,ZFP36L2,C1QL4	grey	VSMC_M10
GO:0098869	0.77	0.32	34	67	cellular oxidant detoxification	BP	1	LTC4S,APOM,PRXL2C,KDM3B,FANCC,TXNRD1,PRDX1,CAT,ALB,PXDN,MGST2,TXNRD3,DHFR,GSTK1,PRDX3,CYGB,PXDNL,GLRX,GPX8,TP53INP1,FBLN5,NFE2L2,DUOX1,GCH1,SOD3,GSTZ1,MPO,TXNDC2,PARK7,NQO1,MIR21,HBA2,TXN,PTGES	grey	VSMC_M10
GO:0016266	0.77	0.35	16	33	O-glycan processing	BP	1	C1GALT1,POMGNT1,GALNT11,ST6GALNAC2,GALNT15,GXYLT2,POFUT1,B3GNT4,GALNT5,B3GNT5,GALNT2,XXYLT1,GALNT8,GALNT1,ST6GALNAC4,ST3GAL2	grey	VSMC_M10
GO:0072171	0.77	0.33	26	53	mesonephric tubule morphogenesis	BP	1	MYC,PTCH1,SMO,SIX2,OSR1,SOX9,GZF1,WNT11,PAX8,EYA1,FMN1,PKD2,PAX2,SALL1,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,SOX8,NOG,SIX1,FGF1	grey	VSMC_M10
GO:0043409	0.77	0.29	66	131	negative regulation of MAPK cascade	BP	1	SEMA6A,PRKN,FBLN1,MYC,LEMD2,STK38,WNK2,KLHL31,DNAJA1,FKTN,ITGB1BP1,VRK3,TLR4,SPRY1,PHB,SPRY2,ARRB1,ZMYND11,SPRED3,DUSP6,SH3RF2,SIRT3,PIK3CB,PTPRJ,P2RX7,PAQR3,F2RL1,TAOK3,DUSP8,PRDM15,PDCD4,DAG1,TBC1D10C,SORL1,GPER1,AGT,DUSP16,DLG1,AIDA,DUSP10,MEN1,DUSP19,PTPN6,PINK1,GPS2,RGS14,SYNJ2BP,EFNA1,TNIP1,PSMD10,NCOR1,PTPN2,INPP5K,ABCA7,MARVELD3,DAB2IP,MIR21,DUSP2,CHRNA10,DUSP26,DUSP1,DUSP4,C3orf33,LIF,LAX1,C1QL4	grey	VSMC_M10
GO:0060716	0.77	0.40	8	17	labyrinthine layer blood vessel development	BP	1	OVOL2,VASH2,FZD5,MAPK1,RBPJ,VASH1,HEY2,WNT2	grey	VSMC_M10

GO:0060968	0.77	0.32	29	59	regulation of gene silencing	BP	1	ZC3H10,ESR1,AGO2,TNRC6B,XPO5,EGFR,MYCN,PUM2,SETDB2,FAM208A,BCDIN3D,EIF4E2,RIPK1,PPHLN1,PPP3CA,TERT,AJUBA,DDX6,EIF4ENIF1,TET1,STAT3,PHF8,MAP2K1,NCOR1,FMR1,SETDB1,HIST1H3F,HIST1H3H,ZNF304	grey	VSMC_M10
GO:0006891	0.77	0.36	14	29	intra-Golgi vesicle-mediated transport	BP	1	COPG2,TRAPPC3,NAPA,COPG1,COG1,COPZ1,VTI1A,COG2,COPA,NSF,NAPG,COG8,RAB6B,TRAPPC3L	grey	VSMC_M10
GO:0070861	0.77	0.38	11	23	regulation of protein exit from endoplasmic reticulum	BP	1	TMEM30A,UBAC2,TM9SF4,YOD1,SORL1,DERL3,SEC16B,TMEM30B,BCAP31,UBE2G2,DERL2	grey	VSMC_M10
GO:0043001	0.77	0.35	18	37	Golgi to plasma membrane protein transport	BP	1	GOPC,SPTBN1,RAB10,OPTN,GOLGA4,LYPLA1,VAMP5,KIF13A,BBS1,NSF,CNST,RSC1A1,AC138894.1,GGA2,RAB26,SEC16A,C16orf70,VAMP3	grey	VSMC_M10
GO:0060307	0.77	0.42	7	15	regulation of ventricular cardiac muscle cell membrane repolarization	BP	1	SCN5A,KCNE2,ANK2,SCN4B,NOS1AP,RNF207,KCNH2	grey	VSMC_M10
GO:0043984	0.77	0.40	8	17	histone H4-K16 acetylation	BP	1	KANSL3,ATG5,PHF20,KANSL2,AUTS2,MSL1,OGT,HCFC1	grey	VSMC_M10
GO:1901071	0.77	0.39	9	19	glucosamine-containing compound metabolic process	BP	1	LARGE1,GNPDA2,NANP,CHST1,OVGP1,CHST3,CHST7,CHST5,CTBS	grey	VSMC_M10
GO:0060441	0.77	0.38	11	23	epithelial tube branching involved in lung morphogenesis	BP	1	TNC,SPRY1,SOX9,SPRY2,DAG1,KRAS,CTSH,LAMA1,FOXF1,ESRP2,WNT2	grey	VSMC_M10
GO:0072676	0.77	0.31	36	72	lymphocyte migration	BP	1	SLC12A2,CCL27,OXSR1,GAS6,RET,CYP7B1,JAM2,PTK2B,CCL17,SLC8B1,ADTRP,CD200,CD99,APOD,ADAM8,MIA3,ITGA4,CH25H,PADI2,CXCL16,TMEM102,TBX21,STK10,CCL14,CCL5,CCL7,CCL2,CCL25,CRK,RHOA,CCL16,FADD,WNT5A,ARTN,GCSAM,CCL22	grey	VSMC_M10
GO:2000514	0.77	0.34	20	41	regulation of CD4-positive, alpha-beta T cell activation	BP	1	AGER,HLA-DRA,TGFBR2,NCKAP1L,RIPK2,HLX,RUNX3,BCL6,VSIR,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,TWSG1,SOCS1,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0098969	0.77	0.41	7	15	neurotransmitter receptor transport to postsynaptic membrane	BP	1	NSG1,GRIPAP1,RAB8A,CPLX1,STX1B,RAB11A,ARHGAP44	grey	VSMC_M10
GO:0051307	0.77	0.38	10	21	meiotic chromosome separation	BP	1	MAPK15,MLH1,MOS,M1AP,EME1,ERCC4,SLX4,MEIOB,MSH4,CENPX	grey	VSMC_M10
GO:0008277	0.77	0.30	48	96	regulation of G protein-coupled receptor signaling pathway	BP	1	CRY1,RIC8B,PHF24,CAMKMT,KLK14,CXCL8,PLEK,MET,PHB,GIPR,ARRB1,PDE6G,PLCB1,RASGRP4,TUB,RGS20,ABHD6,PLCE1,RPGRIP1L,RGS1,GIT2,GRK2,GPER1,SAG,PDE6H,HOMER2,NMT1,GRK4,RAMP2,TMOD2,TULP3,GRK6,RGS14,DGKQ,GUCY2D,DNM2,CAMK2A,CCL5,C3,MGRN1,GNG7,USP20,RGS11,CNTN2,CHGA,RGS12,RGS4,MRAP2	grey	VSMC_M10
GO:0060135	0.77	0.33	24	49	maternal process involved in female pregnancy	BP	1	CYP27B1,ESR1,AKR1B1,PLA2G6,PPAT,PTN,PRDX3,VDR,STC1,SPP1,ADCY7,DEDD,MEN1,WNT4,CTSV,MAPK1,MED1,ITGA3,MAPK3,EPOR,BSG,TCF23,LIF,HAVCR2	grey	VSMC_M10
GO:0010042	0.77	0.39	9	19	response to manganese ion	BP	1	PRKN,TSPO,A3GALT2,SLC30A10,BACE1,D2HGDH,ATP13A2,SLFN14,HSPA5	grey	VSMC_M10
GO:0046622	0.77	0.34	20	41	positive regulation of organ growth	BP	1	GLI1,MAPK14,PIM1,SMO,MEF2C,IL7,TBX5,IGF2,HLX,YBX3,MAPK1,BMPR1A,RBPJ,TBX2,GATA6,MIR199A1,MIR222,BASP1,HEY2,WNT2	grey	VSMC_M10
GO:0033363	0.77	0.36	14	29	secretory granule organization	BP	1	TBPL1,NECTIN2,OSBP,AP3B1,F2R,DTNBP1,CREB1,SRGN,PTPRN,SOX30,BAIAP3,MFSD14A,BLOC1S3,TBC1D20	grey	VSMC_M10
GO:1902652	0.77	0.29	56	111	secondary alcohol metabolic process	BP	1	APOF,CYP27B1,ACO2,TTC39B,PLPP6,CAT,APOB,EBP,CUBN,LIPE,TSKU,PIP4P1,NR1H4,SOAT2,CYP7A1,CYP7B1,CEBPA,LIMA1,EPHX2,CYP2R1,ERLIN1,ABCA5,FMO5,MSMO1,SC5D,SCAP,HSD17B7,POR,ACADL,SOAT1,TM7SF2,OSBPL1A,IDH3A,FDX1,LPCAT3,GNB3,CYP27A1,CH25H,ACADVL,CLN8,LIPC,DGKQ,APOBR,CLN6,LDLR,CYP46A1,NPC1,SREBF1,LEPR,ACAA2,RXRA,CEL,NFE2L1,LDLRAP1,INSIG2,FGF1	grey	VSMC_M10
GO:0051782	0.77	0.41	7	15	negative regulation of cell division	BP	1	MYC,PTCH1,INTU,CHMP4C,ZFYVE19,SUSD2,VPS4A	grey	VSMC_M10
GO:0033032	0.77	0.40	8	17	regulation of myeloid cell apoptotic process	BP	1	CDKN2A,SLC7A11,IRF7,PIK3CB,MEF2C,NOD2,CXCR2,THRA	grey	VSMC_M10
GO:0035336	0.77	0.37	12	25	long-chain fatty-acyl-CoA metabolic process	BP	1	ACSL6,ELOVL1,ELOVL7,FAR2,ACSL5,HACD2,THEM5,ACSBG1,TECR,ACSBG2,ACSF3,ELOVL3	grey	VSMC_M10
GO:0001825	0.77	0.35	15	31	blastocyst formation	BP	1	CNOT2,PNLDC1,RRP7A,MFNG,SRF,RTN4,CCNB1IP1,CNOT1,RPL7L1,SP3,TET1,WDR74,MFN2,NLE1,SUPT6H	grey	VSMC_M10
GO:0062098	0.77	0.37	11	23	regulation of programmed necrotic cell death	BP	1	PELI1,ASAH1,RIPK1,SPATA2,FZD9,YBX3,BIRC3,OGT,MIR22,FADD,CASP8	grey	VSMC_M10
GO:0043981	0.77	0.41	7	15	histone H4-K5 acetylation	BP	1	KANSL3,PHF20,KANSL2,ING4,KAT7,OGT,HCFC1	grey	VSMC_M10
GO:0043982	0.77	0.41	7	15	histone H4-K8 acetylation	BP	1	KANSL3,PHF20,KANSL2,ING4,KAT7,OGT,HCFC1	grey	VSMC_M10
GO:0050848	0.77	0.32	27	55	regulation of calcium-mediated signaling	BP	1	FHL2,PLEK,SLC8A2,EFHB,PRNP,P2RX2,NRG1,P2RX3,SLA2,PTK2B,SPPL3,CMKLR1,TBC1D10C,CIB1,SLC9A1,MYOZ2,ACTN3,HOMER2,MAPT,HTT,MYOZ1,BST1,TMEM100,CALM1,RIT2,MAPK7,CAMTA1	grey	VSMC_M10
GO:0021544	0.77	0.40	8	17	subpallium development	BP	1	FOXP2,SLC7A11,MKKS,RARB,ZSWIM6,ALDH1A3,DLX1,BCL11B	grey	VSMC_M10
GO:0051571	0.77	0.41	7	15	positive regulation of histone H3-K4 methylation	BP	1	SNW1,PAXIP1,DNMT3B,RTF1,AUTS2,WDR61,NELFA	grey	VSMC_M10
GO:0045684	0.77	0.37	12	25	positive regulation of epidermis development	BP	1	CYP27B1,PTCH1,SFRP4,PTCH2,OVOL2,VDR,KDF1,SFN,H2AFY2,MED1,MIR125B1,ZBED2	grey	VSMC_M10
GO:0097300	0.77	0.34	17	35	programmed necrotic cell death	BP	1	PELI1,ASAH1,RIPK1,DNM1L,ITPK1,SPATA2,FZD9,YBX3,PYGL,BIRC3,TRPM7,OGT,TRAF2,MIR22,FADD,CASP8,PPIF	grey	VSMC_M10
GO:0046887	0.77	0.30	43	86	positive regulation of hormone secretion	BP	1	LRP1,PLA2G6,PRKCE,EGFR,TRPM4,GIPR,C1QTNF1,AIMP1,SIRT3,OSBP,P2RY1,NNAT,PFKM,NKX3-1,NKX6-1,SPP1,GPLD1,TCF7L2,PFKFB2,GPER1,SNX4,GLUL,CREB1,MCU,PPP3CB,CD38,MPC2,INHA,NLGN2,TARDBP,STX4,RAB8B,GPR68,ISL1,OXCT1,ABAT,NADK,BAIAP3,LRRC8A,FGA,SOX4,CRH,DOC2B	grey	VSMC_M10
GO:0050870	0.77	0.29	66	130	positive regulation of T cell activation	BP	1	AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,NCK2,IL4I1,IL15,BMI1,GLI2,TGFBR2,NCKAP1L,SLC7A1,TRAF6,SOX12,IL1A,IL7,RASGRP1,RIPK2,AP3B1,SOX13,NOD2,IGF2,LCK,ICOSLG,GPAM,HLX,CD28,RUNX3,ADAM8,DUSP10,BCL6,IL12A,VSIR,PTPN6,STAT5B,FOXP3,RASAL3,ZBTB1,CARD11,ZBTB7B,IL4R,CD74,CCL5,CCL2,YES1,NKAP,VAV1,IL7R,SOCS1,DNAJA3,PRKCZ,BCL10,MIR21,RHOA,SOX4,FADD,DPP4,CD46,THY1,CD70,TNFSF9,EFNB3,TNFSF13B,HAVCR2	grey	VSMC_M10

GO:0030502	0.77	0.43	6	13	negative regulation of bone mineralization	BP	1	TRPM4,SOX9,PTK2B,SRGN,BCOR,RFLNB	grey	VSMC_M10
GO:0060260	0.77	0.36	13	27	regulation of transcription initiation from RNA polymerase II promoter	BP	1	ESR1,MED30,SRF,ERCC1,PAXIP1,ERCC6,CREB1,MED14,THRA,MED24,MED1,NKX2-5,HEY2	grey	VSMC_M10
GO:0033631	0.77	0.43	6	13	cell-cell adhesion mediated by integrin	BP	1	PODXL,ITGA4,FERMT3,CCL5,PIEZO1,DPP4	grey	VSMC_M10
GO:1902285	0.77	0.43	6	13	semaphorin-plexin signaling pathway involved in neuron projection guidance	BP	1	PLXNA4,PLXNA1,PLXNC1,SEMA3A,SEMA3F,PLXNA3	grey	VSMC_M10
GO:0051281	0.77	0.36	14	29	positive regulation of release of sequestered calcium ion into cytosol	BP	1	F2R,PKD2,GPER1,CASQ1,NTSR1,CEMIP,HTT,HAP1,CD19,CALM1,BDKRB1,PDPK1,JPH2,THY1	grey	VSMC_M10
GO:0001895	0.77	0.33	21	43	retina homeostasis	BP	1	PRDX1,ALB,WHRN,USP45,USH1G,MKKS,ACTG1,ERCC6,TUB,CCDC66,ADGRV1,USH1C,BBS1,CDH23,ACTB,CLN8,ATP1B2,ESRRB,JCHAIN,DRAM2,BBS10	grey	VSMC_M10
GO:0071514	0.77	0.41	7	15	genetic imprinting	BP	1	DNMT3A,IGF2,PCGF3,MECP2,PRMT7,CTCF,ARID4A	grey	VSMC_M10
GO:0045056	0.77	0.40	8	17	transcytosis	BP	1	LRP1,AGER,FCGRT,VPS35,RAB5A,RAB17,LRPAP1,RAB11A	grey	VSMC_M10
GO:0050951	0.77	0.40	8	17	sensory perception of temperature stimulus	BP	1	BTBD9,GRIK2,ASIC3,EPHB1,TRPM8,NTSR1,KCNK4,TRPV1	grey	VSMC_M10
GO:0030218	0.77	0.29	51	102	erythrocyte differentiation	BP	1	MPIG6B,HSPA1B,BRD1,SMAD5,L3MBTL3,MAPK14,ZNF16,RBFOX2,SRF,CDK6,KIT,RPS14,SMAP1,EPAS1,PTBP3,BPGM,FOXO3,ERCC2,SLC25A38,ACVR2A,NCKAP1L,PRKDC,MFHAS1,ACVR1B,CASP3,TMEM14C,DMTN,ALAS1,LDB1,PKNOX1,ACIN1,DYRK3,HCLS1,ARNT,SP3,BCL6,STAT3,STAT5B,INHA,THRA,MED1,AHSP,KAT7,DNASE2,RCOR1,PTPN2,MIR222,ANKRD54,ARID4A,MAFB,FAM210B	grey	VSMC_M10
GO:1900181	0.77	0.36	13	27	negative regulation of protein localization to nucleus	BP	1	C6orf106,RAB23,FERMT1,MFHAS1,POLR1A,DCLK2,PKIA,SUFU,CABP1,OTUD7B,APOD,MAGED1,SIN3A	grey	VSMC_M10
GO:0048232	0.77	0.26	192	371	male gamete generation	BP	1	TBPL1,GLI1,YTHDC2,B4GALNT1,ATAT1,TSPAN8,IGF2R,MOV10L1,PACRG,QKI,BRD2,ROS1,HSF2,UBE2B,CATSPER3,H3F3C,DMC1,SPATA31D3,CFAP69,FANCG,SMARCA2,TDRD6,KIT,CCIN,TSGA10,TDRD7,DNAJA1,FOXJ3,SCMH1,RAD23B,YTHDC1,CABS1,HERPUD2,GMCL1,CCDC155,CREM,ARMC2,DLD,TXNRD3,APOB,SPATA6,SPATA5,TTC26,DNMT3A,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,MLH1,ACOX1,FOXJ1,WDR48,TTC21A,CCNB1IP1,ACVR2A,MKKS,SPATA24,ADAM18,MCM8,GOLGA3,PANK2,BTG1,SOHLH2,TEX15,KATNAL1,NPHP1,ING2,SPATA9,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,PRKAG1,SFMBT1,AP3B1,CDYL,SYCP1,DNAH1,DPCD,OCA2,ROPN1L,SIAH1,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,TESMIN,SPATA2,RNF114,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,TSSK4,CIB1,CCDC87,DDX6,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,SEPT2,LIMK2,PATZ1,CATSPER2,OVOL1,YBX3,CADM1,SPATA32,GGT2,TTC12,BCL6,RPL10L,SPAG16,ZCWPW1,CTSV,BIRC3,ADCY10,PARP11,CALR3,KDM5A,ZMYND15,MNS1,YBX2,MYCBPAP,VIPAS39,SOX30,CCDC42,CREB3L4,RAD51C,DNM2,YY1,TAF4B,ALKBH5,JAG2,IFT20,ACSBG2,TXNDC2,SPEF2,CATSPERD,ZNF449,HSPB11,BCAP31,RNF151,TMEM203,MEIOB,GAMT,CHD5,SOX8,TPGS1,MFSD14A,LRRC8A,STRBP,TSNAXIP1,MSH4,FSTL3,AURKC,UBB,SYCP3,ARID4A,AGO4,TCFL5,NKAPL,METTL14,FOXJ2,TDRP,ZSCAN21,ZFP41,SPDYA,GGT5,RNF8,BCL2L11,TBC1D20,ZNF35,BCL2L2,ZGLP1,SPA17,ZNF628	grey	VSMC_M10
GO:0072074	0.77	0.40	8	17	kidney mesenchyme development	BP	1	MYC,SIX2,OSR1,PKD2,PAX2,WNT4,BASP1,SIX1	grey	VSMC_M10
GO:0009566	0.77	0.29	57	113	fertilization	BP	1	TRIM36,H3F3C,MYH9,CFAP69,NLRP5,RIMS1,SPACA6,KLK14,DKKL1,APOB,IZUMO1,ADCY3,TRPC3,NECTIN2,WDR48,PLAT,ADAM18,PLCB1,FUT10,UBXN8,STX2,AP3B1,NPM2,NECTIN3,HYAL3,SLC9B1,INTS13,ABHD2,TSSK4,CCDC87,TDRKH,CLIC4,CATSPER2,YBX3,LYZL6,OVGP1,PLCD4,RAB3A,AKAP3,ADAM21,ADAM20,UBE2Q1,UBAP2L,SPESP1,NOX5,ZP2,SNU13,MEIOB,CACNA1H,PARK7,STXBP1,CD46,GLIPR1L2,FAM170A,LHFPL2,SPA17,TMPRSS12	grey	VSMC_M10
GO:0061484	0.77	0.40	8	17	hematopoietic stem cell homeostasis	BP	1	OCIAD1,FOXA3,TCIRG1,UBAP2L,GPRASP2,NLE1,ADGRG1,SOX4	grey	VSMC_M10
GO:1902170	0.77	0.41	7	15	cellular response to reactive nitrogen species	BP	1	AQP1,GUCY1B1,MTR,MMP3,DNM2,CRK,TRAF2	grey	VSMC_M10
GO:0090128	0.77	0.44	5	11	regulation of synapse maturation	BP	1	YWHAZ,NEURL1,DISC1,NFATC4,DAB2IP	grey	VSMC_M10
GO:0019320	0.77	0.36	12	25	hexose catabolic process	BP	1	GALT,GLB1,PFKP,FUT10,PFKM,GLYCTK,PFKFB2,ACTN3,HK1,TKTL1,FUT4,TIGAR	grey	VSMC_M10
GO:0043331	0.77	0.34	17	35	response to dsRNA	BP	1	PELI1,RALB,TMEM173,MAVS,RIPK2,NOD2,IFIH1,RFTN2,MUL1,MAPK1,SLC3A2,MAPK3,RIOK3,COLEC12,TICAM1,ZCCHC3,KCNJ8	grey	VSMC_M10
GO:1900744	0.77	0.34	18	37	regulation of p38MAPK cascade	BP	1	PHLPP1,MAP3K5,MAP3K4,AGER,GADD45G,EMC10,RELL2,MFHAS1,HAND2,NCF1,MAP3K3,DLG1,DUSP10,MINK1,RELL1,DAB2IP,GADD45A,DUSP1	grey	VSMC_M10
GO:0030278	0.77	0.30	45	91	regulation of ossification	BP	1	CYP27B1,OSR2,TOB2,MAPK14,OMD,SIX2,PTN,TRPM4,OSR1,MKX,INTU,SOX9,ACVR2B,ACVR2A,GFRA4,KL,ADGRV1,MEF2C,P2RX7,PTK2B,BMP2K,ANO6,TFAP2A,BMPR1B,TGFB2,SGMS2,KREMEN1,ACTN3,TXLNG,FZD9,SRGN,BCOR,ANKH,ESRRA,WNT4,MAPK1,BMPR1A,DHRS3,RBPJ,MAPK3,SMAD3,PTGER4,RFLNB,BGLAP,WNT5A	grey	VSMC_M10
GO:0032495	0.77	0.40	8	17	response to muramyl dipeptide	BP	1	TNFAIP3,MAPK14,IRF5,NOD1,JAG1,RIPK2,NOD2,INAVA	grey	VSMC_M10
GO:0120254	0.77	0.30	43	86	olefinic compound metabolic process	BP	1	RDH5,RDH16,ALDH8A1,HSD17B3,AKR1B1,ALDH1A1,RDH13,DKKL1,FAAH,LIPE,ELOVL1,SDR16C5,ABHD6,RETSAT,DKK3,EPHX2,PLA2G4B,SRD5A1,ALDH1A3,CYP2U1,DHRS9,PLA2G4A,BCO2,WNT4,STAT5B,DAGLB,EPHX1,DHRS3,RDH11,ALDH1A2,DGKQ,ALOXE3,MAPK3,SCNN1B,CYP46A1,CYP2J2,CACNA1H,PTGES2,PNPLA4,ELOVL3,LRAT,RDH14,ADH4	grey	VSMC_M10
GO:0050856	0.77	0.35	15	31	regulation of T cell receptor signaling pathway	BP	1	CD226,PRKD2,NECTIN2,PAWR,PRNP,PTPRJ,SLA2,LCK,RC3H1,PTPN6,CARD11,PTPN2,IKBKG,BCL10,THY1	grey	VSMC_M10
GO:0031958	0.77	0.42	6	13	corticosteroid receptor signaling pathway	BP	1	CRY1,PHB,ARNTL,CRY2,ARID1A,YWHAH	grey	VSMC_M10

GO:2000756	0.77	0.32	26	53	regulation of peptidyl-lysine acetylation	BP	1	HINT2,ATG5,SPHK2,HDAC2,IWS1,PAXIP1,ARRB1,TAF7,SDR16C5,HDAC1,AUTS2,TADA2B,FOXP3,KAT7,MUC1,MAPK3,NAP1L2,RPS6KA5,SIN3A,ISL1,GLYR1,PARK7,CTCF,SOX4,LIF,RPS6KA4	grey	VSMC_M10
GO:0002548	0.77	0.33	20	40	monocyte chemotaxis	BP	1	FPR2,FLT1,CCL17,ANO6,SLAMF8,MOSPD2,PTPRO,TNFSF18,IL6R,S100A14,CCL14,CCL5,CCL7,CCL2,CCL25,CCL16,S100A12,DEFB124,DUSP1,CCL22	grey	VSMC_M10
GO:0033059	0.77	0.33	21	43	cellular pigmentation	BP	1	BBS7,MYO7A,MKKS,ANKRD27,AP3B1,DTNBP1,KIF13A,SHROOM2,HPS4,MLPH,RAB17,PIKFYVE,BLOC1S6,MREG,ABCB6,RAB11A,SNAPIN,AP1G1,BLOC1S3,RAB32,TRAPPC6A	grey	VSMC_M10
GO:0032944	0.77	0.28	70	138	regulation of mononuclear cell proliferation	BP	1	AGER,IL5,HLA-DPB1,TNFRSF13C,RAC2,TNFRSF21,NCK2,PELI1,IL4I1,TLR4,IL15,BMI1,MYD88,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,IL1A,CASP3,MEF2C,TMEM131L,IL7,RIPK2,MARCH7,ZNF335,CD40,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,CD28,DLG1,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,CD38,BST1,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,ZBTB7B,CHRNB2,BTK,CD74,CCL5,CD320,TWSG1,TICAM1,DNAJA3,VAV3,GLMN,MIR21,LST1,FADD,CD46,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0000041	0.77	0.30	43	86	transition metal ion transport	BP	1	SLC39A5,SLC39A4,STEAP2,SLC1A1,SLC31A2,PGRMC2,TRPC3,HEPHL1,ATP7B,SLC39A12,ASIC3,STEAP3,TMEM163,HPX,SLC39A13,SLC25A37,SLC48A1,SLC40A1,CUTC,ABCC2,SLC30A10,COX17,ISCU,ABCC5,MELTF,SLC30A4,SLC11A1,ABCB6,FTH1,SLC39A9,FLVCR2,NOX5,DNM2,SLC39A6,SLC46A1,C1orf194,ATP2C2,SLC30A7,LCN2,SLC22A17,FTL,SLC39A11,SLC39A3	grey	VSMC_M10
GO:0002718	0.77	0.31	31	63	regulation of cytokine production involved in immune response	BP	1	CD226,KIT,RSAD2,TLR4,ATG5,TRPM4,SPHK2,LACC1,MAVS,TRAF6,F2RL1,NOD2,CD96,TGFB2,DENND1B,FZD5,BCL6,HK1,FOXP3,TNFRSF1B,SPON2,TBX21,BTK,CD74,TICAM1,PRKCZ,TRAF2,SLC7A5,BCL10,WNT5A,INAVA	grey	VSMC_M10
GO:0051851	0.77	0.32	25	51	modulation by host of symbiont process	BP	1	YTHDC2,SNW1,IGF2R,PRKN,NAPEPLD,PHB,FBXL2,SAP30,EIF2AK4,HDAC1,ZNF639,CFL1,HSPA8,POU2F3,PC,PSMC3,TARDBP,CCL5,JUN,FMR1,INPP5K,MIR222,SAP30BP,TBC1D20,ZNF502	grey	VSMC_M10
GO:0035065	0.77	0.32	22	45	regulation of histone acetylation	BP	1	ATG5,SPHK2,IWS1,PAXIP1,ARRB1,TAF7,SDR16C5,AUTS2,TADA2B,FOXP3,KAT7,MUC1,MAPK3,NAP1L2,RPS6KA5,SIN3A,ISL1,GLYR1,PARK7,CTCF,LIF,RPS6KA4	grey	VSMC_M10
GO:0009595	0.77	0.39	8	17	detection of biotic stimulus	BP	1	TSPO,SMO,NOD1,TLR4,DACH1,PTPRJ,NOD2,FAP	grey	VSMC_M10
GO:0002286	0.77	0.31	32	65	T cell activation involved in immune response	BP	1	HLA-DRA,LCP1,EOMES,NCKAP1L,FOXP1,EIF2AK4,RIPK2,F2RL1,HLX,FCER1G,BCL6,RC3H1,TNFSF18,SLC11A1,STAT3,FOXP3,TBX21,PSEN1,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,CD74,PTGER4,PRKCZ,TSC1,MIR21,CD46,FGL2,HAVCR2,RC3H2	grey	VSMC_M10
GO:0051046	0.77	0.26	224	434	regulation of secretion	BP	1	VPS4B,ERBB3,LRP1,RAB21,SNCAIP,SLC12A2,RIMS2,PRKN,GDF9,PLA2G6,PICK1,RAC2,CHRNA3,CHRNA5,CRY1,APBA1,RFX3,TFAP2B,CHMP2A,IL11,PRKCE,RIMS1,HMGN3,RIMS3,BMP8A,AQP1,RSAD2,NR1H2,EGFR,TLR4,ATG5,SDCBP,TRPM4,SPHK2,RAB7A,RAB10,GIPR,CACNB2,CLASP2,FRMD4A,GAB2,LLGL2,UNC13D,SNX5,C1QTNF1,SYT1,RAB5A,APBB3,DPH3,AIMP1,NRG1,NCKAP1L,SIRT3,SYT9,ADRA2B,NR1H4,NDUFAF2,FAM3D,IL1A,PAX8,FER,OSBP,HIP1R,ARNTL,SCG5,MEF2C,ASIC1,VEGFC,P2RY1,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,STC1,NKX3-1,NKX6-1,ACVR1C,F2RL1,F2R,CRY2,VPS18,ABCC2,SPP1,ZBED6,PLA2R1,LGI3,ADTRP,DTNBP1,SYT8,GRM2,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,HYAL3,CPT1A,MAP2K6,SLC9B2,TGFB2,ADRA2A,TCIRG1,TCF7L2,KCNB1,EGF,PFKFB2,GRK2,GPER1,ABCB11,AGT,FGR,PER2,OSM,STX1A,SNX4,NTSR1,PASK,SEPT2,BACE1,GLUL,CSPG5,SIDT2,SLC16A1,ADAM8,KLF7,NSF,CREB1,RAP1B,PLA2G4A,TTN,IL12A,COMT,ENY2,ABCA12,CASK,MCU,ADRA2C,PNKD,PPP3CB,RAB3A,PINK1,SYN1,CD38,C12orf4,MPC2,INHA,RAB8A,ATP13A2,HAP1,CPLANE2,SYT7,RAB15,RSC1A1,NLGN2,TNFRSF1B,SEPT1,CPLX1,TARDBP,STX1B,STX4,ITGAM,SYT11,RAB8B,TMED10,CACNA1G,CHRNB2,MYH10,RAB3D,IL4R,CALM1,SYTL4,SNAPIN,GPR68,S100A8,PRKCB,SCAMP5,CD74,CAMK2A,CCL5,STXBP2,SREBF1,ISL1,PRAM1,OXCT1,NOS2,ABAT,FMR1,RPH3AL,NADK,TRPV1,PDPK1,P2RX1,RAB26,ATP6AP1,BAIAP3,CACNA1H,CYBA,FOXF1,LRRC8A,STXBP1,AP1G1,VPS4A,MIR199A1,FGA,CHRNB4,CHGA,SOX4,DPP4,POFUT2,CRH,RGCC,DOC2B,PTGES,RALA,LIF,UQCC2,VAMP3,PARD6A,KCNMB4	grey	VSMC_M10

GO:0009259	0.77	0.26	156	302	ribonucleotide metabolic process	BP	1	NME1,HSD17B4,PDE7B,ATP5MGL,DPYS,PPT2,PPARA,PDE10A,ACSL6,PRXL2C,GTPBP1,IMPDH1,GDA,CROT,SLC35B2,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,NT5E,PPT1,BPGM,DLD,SPHK2,CMPK1,ADCY3,DLG2,DHTKD1,PRKAG2,ATP5F1C,ELOVL1,PFKP,NUDT16,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,GPI,AMPD3,ATP5F1A,MCCC2,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,MFN1,PFKFB2,ENO4,HACD2,ARNT,ADCY4,CTPS2,ACTN3,HDAC4,THEM5,DNAJC30,MLXIPL,PDE8A,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,UPB1,HK1,ACSBG1,ATP5S,CASK,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,ENO3,PARP1,TECR,CARD11,SLC26A1,PSEN1,ACOT2,GUCY2D,PKLR,PANK3,GCDH,OGT,UPRT,ADPGK,PDE4A,ACSM3,ACACA,NCOR1,INSR,SLC26A2,ADSSL1,ACSBG2,ALDOC,PIPOX,ACOT11,ATP6V0C,PANK4,NME3,MPP1,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,UCK1,MLYCD,DHODH,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,ELOVL3,TIGAR,NUDT19,NME6,NUDT2,HINT1,UPP1	grey	VSMC_M10
GO:0006351	0.77	0.24	1325	2521	transcription, DNA-templated	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ATP8B1,ONECUT2,BAZ2A,TCF4,TBPL1,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,STK3,OSR2,SNW1,TFB1M,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,PRKN,AGER,PPARA,PDE10A,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,SCAF1,LPIN1,SFRP4,UCP1,CREM,TEAD2,SETD7,SDCBP,MYCN,C6orf203,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,FAF1,MAMSTR,GTF3C6,ATAD2B,BEND5,CDCA7,KDM7A,ZNF438,FOXE3,HDAC2,PHF10,M	grey	VSMC_M10
GO:1901201	0.77	0.40	7	15	regulation of extracellular matrix assembly	BP	1	SOX9,CLASP2,DAG1,AGT,PHLDB1,SMAD3,RGCC	grey	VSMC_M10
GO:0034123	0.77	0.37	11	23	positive regulation of toll-like receptor signaling pathway	BP	1	NINJ1,RTN4,PELI1,RSAD2,MFHAS1,NR1H3,F2RL1,TLR5,DDX3X,WDFY1,CYBA	grey	VSMC_M10
GO:0030033	0.77	0.40	7	15	microvillus assembly	BP	1	ATP8B1,MYO1A,PODXL,KLF5,RAPGEF2,RAP1GAP,STK26	grey	VSMC_M10
GO:0010038	0.78	0.26	143	279	response to metal ion	BP	1	NEDD4L,FECH,TPH2,SLC12A2,PRKN,TNFRSF11B,TSPO,CPNE5,HSF1,KIT,SLC1A1,SLC25A13,CAT,ALG2,AQP1,MTF1,EGFR,BRAF,TRPC3,DNMT3A,SLC26A5,ATP7B,ENTPD6,GIPR,ERCC1,DLG2,KHK,SCN5A,AANAT,CPNE9,SYT1,RYR1,PRNP,PPP2CB,SYT9,CYB5A,IL1A,GPI,CEBPA,GSS,CASP3,RYR3,ADGRV1,MEF2C,CYP2R1,HVCN1,XRCC4,PTK2B,SLC39A13,CPNE2,SEC31A,HOMER1,LOXL2,TNNC1,ABCC2,PKD2,TFAP2A,DMTN,CASQ2,ADCY7,KCNIP2,RYR2,SYT8,SLC41A1,GPLD1,A3GALT2,SLC6A3,PPP3CA,CCND1,TERT,TESMIN,SLC30A10,PEF1,TCIRG1,PDCD6,NCF1,FABP4,AMELX,NFATC4,CARF,CLIC4,BACE1,DTYMK,D2HGDH,CDKN1B,NFE2L2,CREB1,RASA4,MAPT,SORD,SLC30A4,CPS1,TTN,RASGRP2,ANXA7,ABCB6,KCNA1,MAPK1,KCNMA1,ATP13A2,DLG4,PARP1,SYT7,GPHN,SOD3,SYT11,PKLR,FOS,MAPK3,CACNA1G,CALM1,S100A8,NPC1,SLFN14,SLC25A23,LONP1,JUN,ABAT,CACNA1H,PARK7,BSG,ADAMTS13,CPNE7,ASS1,LCN2,HSPA5,NQO1,MT-CYB,FGA,FSTL3,KCNK3,MT1X,CASP8,CA2,BGLAP,CLDN1,WNT5A,TIGAR,FXN,DUSP1,PTGES,PPIF,KCNMB4	grey	VSMC_M10
GO:1902882	0.78	0.30	37	74	regulation of response to oxidative stress	BP	1	PRKN,NCOA7,ATF4,GPR37,FBXO7,MET,TLR4,SLC7A11,FOXO3,DHFR,SESN3,PAWR,ACOX2,FBXW7,HTRA2,RIPK1,FBLN5,MCL1,PDE8A,NFE2L2,NONO,STOX1,GCH1,PINK1,MMP3,PARP1,SFPQ,MAPK7,STK26,PARK7,TSC1,TLDC1,MAPKAP1,MIR21,NOL3,GPR37L1,TXN	grey	VSMC_M10
GO:0002687	0.78	0.29	51	101	positive regulation of leukocyte migration	BP	1	AGER,GPSM3,PTK2,RAC2,CCL27,FPR2,CXCL8,AKIRIN1,PTN,C5AR1,OXSR1,NCKAP1L,GAS6,VEGFC,JAM2,PTK2B,F2RL1,ANO6,DNM1L,TRPV4,CD99,PRSS56,CMKLR1,MOSPD2,ADAM8,MIA3,ITGA2B,ITGA4,IL12A,MCU,TNFSF18,CXCR2,MAPK1,TMEM102,PGF,DAPK2,MAPK3,IL6R,S100A14,BDKRB1,CD74,CCL5,CSF1R,CCL7,RHOA,DEFB124,FADD,ZNF580,THY1,WNT5A,PDGFD	grey	VSMC_M10
GO:0010818	0.78	0.40	7	15	T cell chemotaxis	BP	1	SLC12A2,CCL27,OXSR1,CXCL16,TMEM102,CCL5,WNT5A	grey	VSMC_M10
GO:0007029	0.78	0.30	40	80	endoplasmic reticulum organization	BP	1	EMC2,MAPK15,TRAM2,RTN4,EMC10,RAB10,EMC3,ATL2,EMC4,SEC31A,ZFYVE27,COL4A3BP,DOP1B,SEC31B,GET4,CASQ1,MIA3,SEC16B,MOSPD3,LPCAT3,ATL1,SMPD4,ARL6IP1,STX18,GAK,BNIP1,LMAN1L,CXorf56,TLE6,EMC6,SGTA,UBL4A,SEC16A,TOR1B,REEP6,WDR83OS,CAMLG,EMC7,TRAM1L1,POLR2M	grey	VSMC_M10

GO:0032760	0.78	0.30	34	69	positive regulation of tumor necrosis factor production	BP	1	AGER,NOD1,TLR4,SPHK2,HDAC2,MYD88,MAVS,IL1A,PIK3R1,PTPRJ,RASGRP1,OAS3,RIPK2,RIPK1,NOD2,IFIH1,HDAC1,MAPKAPK2,NFATC4,FZD5,STAT3,TNFRSF8,SPON2,PSEN1,ISL1,TICAM1,CYBA,MIR27B,OAS1,FADD,WNT5A,IL33,C1QTNF4,HAVCR2	grey	VSMC_M10
GO:0016577	0.78	0.35	13	28	histone demethylation	BP	1	UBE2B,KDM3B,KDM4C,KDM7A,KDM4A,JARID2,KDM5A,KDM5C,PHF8,KDM6B,RIOX1,KDM8,HSF4	grey	VSMC_M10
GO:2000516	0.78	0.37	11	23	positive regulation of CD4-positive, alpha-beta T cell activation	BP	1	HLA-DRA,TGFBR2,NCKAP1L,RIPK2,HLX,FOXP3,ZBTB7B,IL4R,SOCS1,PRKCZ,MIR21	grey	VSMC_M10
GO:0090161	0.78	0.44	5	11	Golgi ribbon formation	BP	1	OPTN,TRIP11,VTI1A,STX6,TMED5	grey	VSMC_M10
GO:0070986	0.78	0.42	6	13	left/right axis specification	BP	1	SMO,SETDB2,IFT172,PKD1L1,MNS1,HSPB11	grey	VSMC_M10
GO:0006474	0.78	0.40	7	15	N-terminal protein amino acid acetylation	BP	1	AANAT,NAA40,NAA30,CREBBP,NAA60,NAA10,SOX4	grey	VSMC_M10
GO:0006482	0.78	0.35	14	30	protein demethylation	BP	1	UBE2B,KDM3B,KDM4C,KDM7A,KDM4A,PPME1,JARID2,KDM5A,KDM5C,PHF8,KDM6B,RIOX1,KDM8,HSF4	grey	VSMC_M10
GO:0008214	0.78	0.35	14	30	protein dealkylation	BP	1	UBE2B,KDM3B,KDM4C,KDM7A,KDM4A,PPME1,JARID2,KDM5A,KDM5C,PHF8,KDM6B,RIOX1,KDM8,HSF4	grey	VSMC_M10
GO:0071415	0.78	0.44	5	11	cellular response to purine-containing compound	BP	1	RYR1,RYR3,P2RY1,CASQ2,RYR2	grey	VSMC_M10
GO:0006525	0.78	0.39	8	17	arginine metabolic process	BP	1	ASL,SLC7A7,OAT,FAH,AC138894.1,NOS2,ASS1,MIR21	grey	VSMC_M10
GO:0070841	0.78	0.37	10	21	inclusion body assembly	BP	1	SNCAIP,HSPA1B,PRKN,HSF1,SORL1,BAG3,MAPT,DNAJB2,DNAJB1,TRIM37	grey	VSMC_M10
GO:1902001	0.78	0.39	8	17	fatty acid transmembrane transport	BP	1	CPT1B,AKT2,CPT1A,ACSL5,SLC25A20,SLC27A1,ABCD4,ABCD3	grey	VSMC_M10
GO:0007194	0.78	0.44	5	11	negative regulation of adenylate cyclase activity	BP	1	GABBR2,ADGRV1,GRM2,PALM,GNAI3	grey	VSMC_M10
GO:0051349	0.78	0.42	6	13	positive regulation of lyase activity	BP	1	GUCA1B,ORAI1,ISCU,NOS2,PARK7,FXN	grey	VSMC_M10
GO:0032965	0.78	0.35	14	29	regulation of collagen biosynthetic process	BP	1	HDAC2,CYGB,CYP7A1,F2R,AMELX,WNT4,SUCO,LARP6,CIITA,SERPINF2,ENG,MIR29A,RGCC,CBX8	grey	VSMC_M10
GO:0060965	0.78	0.40	7	15	negative regulation of gene silencing by miRNA	BP	1	ZC3H10,ESR1,BCDIN3D,PPP3CA,TERT,STAT3,NCOR1	grey	VSMC_M10
GO:0009651	0.78	0.38	9	19	response to salt stress	BP	1	XRCC6,AKR1B1,AQP1,TRPV4,XRCC5,MICU1,SLC25A23,MT-CYB,CLDN1	grey	VSMC_M10
GO:0007608	0.78	0.39	8	17	sensory perception of smell	BP	1	CFAP69,ADCY3,MKKS,NCAM2,SLC6A3,BBS1,PDE4A,OR5AN1	grey	VSMC_M10
GO:0050730	0.78	0.27	98	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	ERBB3,IL5,HSF1,TEC,KIT,NCK2,SEMA4D,PDCL3,IL11,PRKCE,PPP2R1A,IBTK,EPGN,AREG,EPHA7,TGFA,EGFR,IL15,HDAC2,ABI1,PIBF1,HBEGF,PRNP,NRG1,GAS6,HPX,ERCC6,OSBP,FBXW7,PTPRJ,IL7,PTK2B,ARL2BP,RIPK2,DMTN,NOD2,CNTN1,CD40,IGF2,NEURL1,LRRK1,HDAC1,BANK1,ADRA2A,NCF1,EGF,HCLS1,ADNP,CASS4,PARP9,PARP14,AGT,CBL,OSM,SNX6,PPP2R5B,IL12A,PTPN6,TNFSF18,DOK7,ZFYVE28,FGFR3,SOCS4,BST1,EPHA4,DLG4,DVL2,TMEM102,DGKQ,CTF1,PSEN1,EFNA1,IL6R,HAX1,CD74,CCL5,CSF1R,YES1,ISL1,SUZ12,GHR,UNC119,PTPN2,SOCS1,LRP8,PRKCZ,MLST8,CNTF,MIR125A,THY1,CSPG4,LIF,DUSP22,TSLP,CADM4,EREG,RAP2B,PDGFD	grey	VSMC_M10
GO:0034472	0.78	0.38	9	19	snRNA 3'-end processing	BP	1	EXOSC4,EXOSC3,USB1,INTS8,INTS12,INTS5,AP000990.1,INTS2,EXOSC5	grey	VSMC_M10
GO:0043038	0.78	0.33	20	41	amino acid activation	BP	1	MARS,AASDH,QRSL1,HARS,HARS2,CARS2,LARS,WARS2,GATC,YARS2,TARS2,DALRD3,LARS2,DARS2,FARSB,EARS2,LRRC47,KARS,AARS,MARS2	grey	VSMC_M10
GO:0051412	0.78	0.40	7	15	response to corticosterone	BP	1	FOXO3,AANAT,CCND1,NPAS4,FOS,CALM1,CRH	grey	VSMC_M10
GO:0001574	0.78	0.40	7	15	ganglioside biosynthetic process	BP	1	B4GALNT1,ST8SIA4,ST8SIA2,ST6GALNAC4,ST3GAL2,ST6GALNAC5,ST8SIA6	grey	VSMC_M10
GO:0051145	0.78	0.31	28	57	smooth muscle cell differentiation	BP	1	NFATC1,SRF,KIT,ANKRD17,SOX9,MEF2C,PDCD4,GPER1,NFATC4,EFEMP2,WNT4,RAMP2,FOXO4,RBPMS2,TBX2,GATA6,MRTFB,MECP2,FOXF1,ENG,NFATC3,MIR21,MIR125B1,MIR22,PRDM6,SIX1,EREG,HEY2	grey	VSMC_M10
GO:0071696	0.78	0.43	5	11	ectodermal placode development	BP	1	FRS2,HDAC2,HDAC1,TBX2,SIX1	grey	VSMC_M10
GO:2001056	0.78	0.28	53	105	positive regulation of cysteine-type endopeptidase activity	BP	1	MAP3K5,GRAMD4,BAK1,MYC,HSF1,TTBK1,SLC1A1,NOD1,CASP8AP2,TNFSF15,HSPE1,ARRB1,ARL6IP5,ST18,ASPH,FOXL2,HIP1R,ROBO1,DIABLO,HTRA2,RIPK2,SENP1,NKX3-1,ACVR1C,F2R,PIDD1,LCK,PDCD6,GPER1,CIDEB,EGLN3,MAPT,FIS1,CTSH,DDX3X,MUL1,BCL2L13,NGFR,SMAD3,S100A8,BCAP31,P2RX1,BCL10,MIR27B,RHOA,RPS27L,FADD,CASP8,ACER2,BCL2L11,PERP,PRR7,CRADD	grey	VSMC_M10
GO:0045727	0.78	0.28	55	109	positive regulation of translation	BP	1	RMND1,PRR16,PABPC1,EIF3E,JMJD4,AGO2,HABP4,NCK2,CNBP,CDC123,UPF3A,PRKDC,MRPS27,USP16,PTK2B,EIF2AK4,TENT4B,RPUSD4,RCC1L,RPS6KB2,YTHDF2,RPS4X,YTHDF1,PASK,CD28,UHMK1,NSUN5,YBX3,DDX3X,COA3,SAMD4A,PINK1,MAPK1,POLR2G,ZCCHC4,FXR2,MAPK3,TOB1,EIF3C,LARP6,LARP1,CCL5,UPF3B,FMR1,CIRBP,BARHL2,RHOA,RPS27L,SOX4,METTL14,IMPACT,RPUSD3,PPP1R15A,UQCC2,TRMT10C	grey	VSMC_M10
GO:0030522	0.78	0.26	110	217	intracellular receptor signaling pathway	BP	1	TNFAIP3,CYP27B1,USP15,ESR1,CNOT2,SNW1,HSPA1B,PPARA,RXRB,KDM4C,PIM1,FOXH1,RBFOX2,RORB,CRY1,DNAJA1,ANKRD17,SLC46A2,NR1H2,TLR4,PUM2,PHB,LACC1,EGLN2,SEC14L1,TADA3,CLPB,RARB,NR1D2,NPLOC4,TAF7,RNF14,DDRGK1,FOXP1,IRF7,CALCOCO1,NCOA4,TRAF6,NR1H4,ASXL1,CYP7B1,NR4A1,UFSP2,ZNF536,ZNF366,ARNTL,HNF4G,CNOT1,KMT2D,NR1H3,OAS3,RIPK2,OTULIN,DDX54,VDR,NKX3-1,NR4A2,CRY2,VPS18,NOD2,IFIH1,OASL,HDAC1,MAP2K6,NR5A2,TIFA,ALPK1,GPER1,ARNT,NLRX1,ARID1A,NR1I3,RXRG,PDK3,ESRRA,BIRC3,STAT3,PADI2,DNAAF4,PARP1,GPS2,THRA,TKFC,DHRS3,MED1,ALDH1A2,ALOXE3,PAGR1,ESRRB,TSPAN6,PIAS2,NCOR1,RIOK3,PPARGC1B,SREBF1,ISL1,RHOXF1,RNF135,PARK7,RXRA,NR6A1,RHOA,FABP5,TRIM24,TRIM68,ZCCHC3,AHRR,IRGM,INAVA,YWHAH	grey	VSMC_M10
GO:0035721	0.78	0.43	5	11	intraciliary retrograde transport	BP	1	DYNC2LI1,TTC21A,WDR60,TTC21B,WDR19	grey	VSMC_M10
GO:2001212	0.78	0.41	6	13	regulation of vasculogenesis	BP	1	RIN2,RAPGEF2,HIF1AN,RAMP2,TMEM100,HEY2	grey	VSMC_M10

GO:0048562	0.78	0.26	114	225	embryonic organ morphogenesis	BP	1	GLI1,FRS2,OSR2,FZD6,SMO,MDFI,FOXH1,PTK7,SRF,ROR2,DLX5,SIX2,KCNQ4,HOXA2,HOXA4,HOXA6,HOXA7,WHRN,FUZ,TEAD2,MYCN,SOBP,OSR1,BBS7,BMI1,MYO3A,SETDB2,SOX9,USH1G,GLI2,MEGF8,IFT172,MYO7A,WDR60,SPRY2,WNT11,TGFBR2,OVOL2,MKKS,RARB,ALX1,CEP290,PAX8,HAND2,EYA1,PLS1,FZD3,MEF2C,USH1C,IFT52,PKD2,TFAP2A,PAX2,RYR2,SUFU,HYAL1,ALDH1A3,SATB2,HLX,GBX2,MYO3B,GRHL3,SP3,STRC,DLG1,SETD2,HOXD4,HOXD3,FZD5,STOX1,PRKRA,FBN1,NKX3-2,MAPK1,TULP3,MFAP2,DVL2,WDR19,TCAP,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,EFNA1,RBPMS2,MAPK3,POU3F4,SMAD3,NTN1,GSC,TBX2,LHX1,STRA6,MIB1,RNF207,ALX3,FOXF1,ENG,CHRNA10,FOXG1,MAFB,HOXB3,NOG,LBX1,WNT5A,OTX1,SIX1,C2CD3,INSIG2,SLC39A3,NKX2-5,HOXA3,ZIC1	grey	VSMC_M10
GO:0032968	0.78	0.43	5	11	positive regulation of transcription elongation from RNA polymerase II promoter	BP	1	EAPP,ELL,LEO1,CDK12,SUPT6H	grey	VSMC_M10
GO:2000059	0.78	0.33	19	39	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	TRIM39,PDCL3,SDCBP,KLHL40,DDRGK1,RYBP,TAF9,CSNK2A2,SUFU,RPL23,RPL11,PSEN1,TAF1,OGT,SGTA,PARK7,CAMLG,STYX,MAP1A	grey	VSMC_M10
GO:0030705	0.78	0.27	87	173	cytoskeleton-dependent intracellular transport	BP	1	MYO1A,AP3S1,KIF5A,RAB21,KIF3A,AGTPBP1,SUN2,COPG2,IFT74,APBA1,BICD2,DYNC2LI1,LRPPRC,MGARP,WASF1,TTC26,KIF3C,ARHGAP21,COPG1,MYO7B,KLC3,DLG2,IFT172,MYO7A,TTC21A,WDR60,HOOK3,AP3M2,KIF5C,PURA,TUB,KIF3B,IFT81,RASGRP1,OPA1,AP3B1,IFT52,DTNBP1,TUBA1A,KIF13A,BICDL1,TTC21B,HSPA8,BAG3,TRAF3IP1,CNIH2,TANC2,CALY,TTC30A,SPG11,MAPT,BLOC1S6,MREG,HTT,KIF17,UXT,AP3M1,KIF1C,SYNE2,HAP1,WDR19,PEX14,TRIM46,NDEL1,AC138894.1,HOOK2,SNAPIN,CCDC88C,SFPQ,CAMSAP3,MYO1D,MYO1F,IFT20,MYO5B,HSPB11,BICDL2,PRKCZ,MAPK8IP3,FNBP1L,TERF2,UBB,BLOC1S3,BORCS5,AP3S2,TUBA1C,MAP1A,MAP6D1	grey	VSMC_M10
GO:0015917	0.78	0.46	4	9	aminophospholipid transport	BP	1	ATP8B1,TMEM30A,TMEM30B,ATP11C	grey	VSMC_M10
GO:0003159	0.78	0.38	9	19	morphogenesis of an endothelium	BP	1	PRKD2,FOXP1,RBPJ,ADAMTS12,LCN2,MIR21,RHOA,ACVRL1,FGF1	grey	VSMC_M10
GO:0061154	0.78	0.38	9	19	endothelial tube morphogenesis	BP	1	PRKD2,FOXP1,RBPJ,ADAMTS12,LCN2,MIR21,RHOA,ACVRL1,FGF1	grey	VSMC_M10
GO:0060251	0.78	0.35	12	25	regulation of glial cell proliferation	BP	1	TSPO,SOX10,PTN,EGFR,PLAG1,RNF10,CERS2,CREB1,CHRM1,SKI,MIR222,MIR125B1	grey	VSMC_M10
GO:1903909	0.78	0.43	5	11	regulation of receptor clustering	BP	1	PTN,SLC7A11,SSH1,FZD9,MESD	grey	VSMC_M10
GO:0070922	0.78	0.46	4	9	small RNA loading onto RISC	BP	1	AGO2,AGO1,CLP1,AGO4	grey	VSMC_M10
GO:1901797	0.78	0.35	13	27	negative regulation of signal transduction by p53 class mediator	BP	1	PRKN,ARMC10,TAF9,ING2,MARCH7,DYRK3,SNAI1,MUC1,TAF9B,PSMD10,CD74,MIR21,PTTG1IP	grey	VSMC_M10
GO:0051093	0.78	0.24	350	676	negative regulation of developmental process	BP	1	NFATC1,NME1,SEMA6A,FRS2,STK3,ZNF706,SLC12A2,PRKN,PPARA,FBLN1,TNFRSF11B,TSPO,FSTL4,SYNGAP1,TRIB1,MYC,TOB2,ASAP1,PTCH1,SOX10,PI16,SMO,DAAM2,TEK,FBXO7,RORB,CDK6,SEMA4D,S1PR3,SEMA4C,SOSTDC1,SIX2,RTN4,RUFY3,HOXA2,HOXA7,ANKRD17,AREG,AKIRIN1,EPHA7,NR1H2,PTN,ITGB1BP1,AGO1,EGFR,FUZ,TLR4,CDK5RAP2,MYCN,TRPM4,OSR1,FOXO3,MKX,SPRY1,WISP3,FOXE3,HDAC2,SOX9,GLI2,KDM4A,FOXJ1,TSKU,SPRY2,WNT11,HOOK3,TGFBR2,OVOL2,ISM1,JAG1,SIRT2,RARB,SRA1,FERMT1,SPRED3,LSM1,SEMA3D,DCN,SPART,SEMA3A,GAS6,ULK1,PRKDC,RYK,TCF15,TRIB3,EPHB1,PLK2,ZC3H8,ASXL1,PAX8,PIK3CB,ZNF536,PIK3R1,HAND2,ROBO2,IL17RD,ARNTL,FBXW7,ADGRV1,TMEM131L,SEMA4F,VEGFC,TLX2,ADAMTS1,SOX6,TLL2,PTK2B,RAPGEF2,CCL17,SFMBT1,EIF2AK4,NR1H3,SLIT1,RUNX1T1,NKX3-1,HDAC7,NKX6-1,TRIO,RAPGEF3,LOXL2,TBX5,SRSF6,TP53INP1,SEMA3G,SPP1,ZBED6,STK4,PAX2,DMTN,SEMA4G,PRICKLE1,NKD1,JARID2,LDB1,IGF2,BDNF,SUFU,SRGAP2C,RNF10,KIAA0319,PKP2,DNM1L,NEPRO,PPP3CA,HYAL3,SINHCAF,USF3,CCND1,TERT,TRPV4,SEMA3F,PDCD4,ABCA5,TGFB2,SLC30A10,PTHLH,GPR137B,AXIN2,PIAS3,HLX,KRAS,TCTA,SNAI1,USP19,SOX2,AP1AR,YTHDF2,UBASH3B,SORL1,GPER1,KREMEN1,AGT,CIB1,CERS2,NFATC4,FZD7,DDX6,HDAC4,KCNK2,CHRD,RUNX3,MAP3K3,DLX1,ZBTB46,MELTF,EIF4ENIF1,CDKN1B,E2F2,LRIG2,YBX3,WNT3,KLF7,NFE2L2,DUSP10,MAPT,SRGN,BCL6,SEMA6D,DIXDC1,BCOR,MMP11,MEN1,WDR61,TNR,C11orf65,RC3H1,GPR137,SAV1,FBN1,TNFSF18,WNT4,LAG3,HSPG2,DNM3,COL5A2,MYOZ1,RAP1GAP,GDF	grey	VSMC_M10
GO:0120178	0.78	0.34	14	29	steroid hormone biosynthetic process	BP	1	CYP21A2,TSPO,HSD17B8,HSD17B3,AKR1B1,SRD5A3,DKK3,SRD5A1,HSD17B7,WNT4,MED1,DGKQ,DHRS11,CACNA1H	grey	VSMC_M10
GO:0031453	0.78	0.43	5	11	positive regulation of heterochromatin assembly	BP	1	SETDB2,FAM208A,PPHLN1,SETDB1,ZNF304	grey	VSMC_M10
GO:0120263	0.78	0.43	5	11	positive regulation of heterochromatin organization	BP	1	SETDB2,FAM208A,PPHLN1,SETDB1,ZNF304	grey	VSMC_M10
GO:1905954	0.78	0.29	36	73	positive regulation of lipid localization	BP	1	LRP1,PTCH1,PLA2G6,PLIN2,TMEM30A,NR1H2,APOB,C1QTNF1,NR1H3,NKX3-1,FITM2,SPP1,PLA2R1,PLTP,MAP2K6,ABCA5,ACSL5,FITM1,NTSR1,PLA2G4A,EHD1,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,C3,PLIN3,ABCA3,ABCA7,RXRA,ABCA8,LDLRAP1,CRH,LRAT,PTGES	grey	VSMC_M10
GO:1901017	0.78	0.41	6	13	negative regulation of potassium ion transmembrane transporter activity	BP	1	NEDD4L,KCNRG,OXSR1,KCNE2,CASQ2,CRBN	grey	VSMC_M10
GO:0030011	0.78	0.39	8	17	maintenance of cell polarity	BP	1	LIN7B,WNT11,ANK1,LIN7A,NCKAP1L,SLC9A1,CARMIL2,PDZD11	grey	VSMC_M10
GO:1901679	0.78	0.38	8	17	nucleotide transmembrane transport	BP	1	SLC35B2,ABCC4,SLC25A42,LRRC8E,SLC25A41,SLC25A33,LRRC8A,SLC25A32	grey	VSMC_M10

GO:0055082	0.78	0.25	291	564	cellular chemical homeostasis	BP	1	ZNF236,NME1,ORMDL2,SLC39A5,NEDD4L,LRP1,ESR1,SLC12A2,AGER,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,CKB,TMPRSS6,SLC39A4,SRF,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,PRKCE,TNNI3,RTN4,FPR2,HMGN3,IBTK,SLC4A4,LPAR1,PPT1,AQP1,SLC31A2,KEL,ATG5,TRPM4,FOXO3,FGF21,GRIN2D,TRPC3,SLC8A2,RAB7A,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,FOXA3,GIPR,CACNB2,SLC39A12,ATP6V0E2,LACC1,SLC4A2,AQP11,GRIK5,RAF1,ATP1A3,ACKR2,SLC24A3,C1QTNF1,SLC4A7,TMEM106B,TMTC4,MAFG,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,GAS6,HPX,RASA3,NCOA4,NR1H4,MICU3,ATP6V1H,CYP7A1,TM9SF4,NDUFAF2,IL1A,IMMT,OSBP,C19orf12,PIK3R1,P2RX3,PLCE1,SLC9A9,RYR3,TMBIM6,P2RX7,HVCN1,P2RY1,PTK2B,SLC39A13,KCNJ11,TIAM1,RAB11FIP5,TPCN1,SLC8B1,VDR,STC1,OPA1,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,FITM2,ORMDL1,ABCC2,ZBED6,PKD2,PAX2,TWNK,CASQ2,MCUR1,SLC12A5,CD40,RYR2,SLC41A1,SLC4A10,RAP1GDS1,GPLD1,TRPM1,SPPL3,LCK,PPP3CA,KCNJ2,TESMIN,SLC9B1,TRPV4,SLC9B2,ZBTB20,TMEM9,ADRA2A,SLC30A10,TCIRG1,GNA13,ISCU,KCNB1,CMKLR1,MCUB,HJV,SLC9A8,UBASH3B,DISC1,POLG,ANK2,GPER1,SLAMF8,RHCG,TRPM8,PDZD8,RAB11FIP2,AGT,ATP1A2,SLC9A1,CASQ1,NTSR1,XPR1,CLIC4,MLXIPL,FZD9,SIDT2,TMCO1,PDK3,KLF7,PTH1R,SLC30A4,FIS1,CEMIP,HK1,ABL2,MEN1,CDH23,ENY2,ABCA12,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,SLC9A7,PPP3CB,ATP6V0A1,ABCB6,TRPM7,PTPRN,ATP1B1,CD38,MPC2,MAPK1,DMXL2,KCNMA1,SLC4A3,ATP13A2,FTH1,HAP1,DLG4,CYB561A3,ATP1B2,FAM155B,STX4,PSEN1,CACNA1A,NGFR,MAPK3,AC138894.1,ATP2A	grey	VSMC_M10
GO:0002686	0.78	0.33	16	33	negative regulation of leukocyte migration	BP	1	HOXA7,C5AR2,PLCB1,ADTRP,CD200,SLAMF8,APOD,MIA3,PADI2,CCL2,CCL25,PTGER4,MIR24-1,DPP4,DUSP1,GCSAM	grey	VSMC_M10
GO:1900120	0.78	0.40	7	15	regulation of receptor binding	BP	1	PTPRF,PLCL2,BDNF,GREM2,ANXA2,MIR27B,NOG	grey	VSMC_M10
GO:0006825	0.78	0.40	7	15	copper ion transport	BP	1	STEAP2,SLC31A2,HEPHL1,ATP7B,STEAP3,CUTC,COX17	grey	VSMC_M10
GO:0097659	0.78	0.23	1325	2522	nucleic acid-templated transcription	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ATP8B1,ONECUT2,BAZ2A,TCF4,TBPL1,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,STK3,OSR2,SNW1,TFB1M,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,PRKN,AGER,PPARA,PDE10A,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,SCAF1,LPIN1,SFRP4,UCP1,CREM,TEAD2,SETD7,SDCBP,MYCN,C6orf203,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,FAF1,MAMSTR,GTF3C6,ATAD2B,BEND5,CDCA7,KDM7A,ZNF438,FOXE3,HDAC2,PHF10,M	grey	VSMC_M10
GO:0045618	0.78	0.40	7	15	positive regulation of keratinocyte differentiation	BP	1	CYP27B1,OVOL2,VDR,H2AFY2,MED1,MIR125B1,ZBED2	grey	VSMC_M10
GO:0034767	0.78	0.28	57	114	positive regulation of ion transmembrane transport	BP	1	STAC3,ABCB1,WNK2,CACNB2,STAC,GLRX,P2RX7,KCNJ11,IFNGR2,F2R,TESC,ANO6,KCNE2,PKD2,KCNIP2,RYR2,FAM173B,KCNJ2,COX17,ANK2,GPER1,AGT,ACE2,SLC9A1,CASQ1,NTSR1,NOS1AP,CEMIP,HTT,PINK1,ATP1B1,KCNA1,ARL6IP1,HAP1,WNK3,STAC2,ATP1B2,PSEN1,NLGN3,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,CCL2,PDPK1,P2RX1,RNF207,AMIGO1,LCN2,MIR21,DMD,JPH2,KCNH2,THY1,APOPT1	grey	VSMC_M10
GO:0031214	0.78	0.27	63	126	biomineral tissue development	BP	1	CYP27B1,OSR2,PPARA,ATF4,ROR2,OMD,CNNM4,KLK4,PTN,ITGB1BP1,TRPM4,OSR1,SOX9,ERCC2,SLC4A2,ACVR2B,WNT11,SLC24A3,ACVR2A,KL,GAS6,ADGRV1,MEF2C,P2RX7,PTK2B,BMP2K,ANO6,SPP1,TFAP2A,ITGB6,BMPR1B,FBXL15,SBDS,PTHLH,TCIRG1,FAM20A,FAM20C,SGMS2,AXIN2,AMELX,FGR,ACTN3,TXLNG,FZD9,PTH1R,SRGN,BCOR,ANKH,ZBTB40,WNT4,ALPL,FGFR3,MMP13,BMPR1A,SMAD3,GPC3,RFLNB,BGLAP,MINPP1,SNX10,CCDC154,CEBPB,HEY2	grey	VSMC_M10
GO:0043550	0.78	0.30	28	58	regulation of lipid kinase activity	BP	1	PIP4K2C,AGAP2,PTK2,TEK,KIT,FPR2,WDR91,PIP4K2A,CCKBR,FLT1,PIK3R1,SLA2,PTK2B,NOD2,IRS1,FGR,PPP2R5A,RUBCN,PIK3IP1,FGFR3,SOCS4,SOCS7,CD19,PIK3R5,SOCS1,VAV3,DAB2IP,NRBF2	grey	VSMC_M10
GO:0042446	0.78	0.31	23	47	hormone biosynthetic process	BP	1	CYP27B1,CYP21A2,TSPO,HSD17B8,HSD17B3,AKR1B1,SRD5A3,AANAT,DKK3,SRD5A1,ARNT,HSD17B7,POR,DUOX1,FDX1,WNT4,MED1,DGKQ,DHRS11,CACNA1H,GFI1,DIO3,DIO2	grey	VSMC_M10
GO:0071233	0.78	0.45	4	9	cellular response to leucine	BP	1	RRAGD,SESN3,RPTOR,LARS	grey	VSMC_M10
GO:0000478	0.78	0.40	7	15	endonucleolytic cleavage involved in rRNA processing	BP	1	UTP23,TSR1,BMS1,RPP40,NOP9,KRI1,NOL9	grey	VSMC_M10
GO:0000479	0.78	0.40	7	15	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	1	UTP23,TSR1,BMS1,RPP40,NOP9,KRI1,NOL9	grey	VSMC_M10
GO:0010522	0.78	0.29	35	71	regulation of calcium ion transport into cytosol	BP	1	BAK1,PRKCE,ATG5,TRPC3,PRNP,DIAPH1,P2RX2,P2RX3,TMBIM6,P2RX7,PTK2B,F2R,PKD2,CASQ2,RYR2,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,CD19,CALM1,BDKRB1,PDPK1,P2RX1,CYBA,JPH3,DMD,JPH2,THY1	grey	VSMC_M10

GO:0006810	0.78	0.23	1740	3300	transport	BP	1	ATP9B,TIMM21,NME1,VPS4B,ERBB3,SLC39A5,NEDD4L,APOF,ATP8B1,MIP,STARD6,MYO1A,LRP1,STX7,SLC18B1,STAC3,AP3S1,SLC2A12,KIF5A,SLC26A10,PEX7,AGAP2,HEBP2,REPS1,CYP27B1,PEX3,SLC16A7,CANX,TBC1D30,ATP5MGL,TBC1D9B,PPP1R10,CPSF6,RAB21,NIPAL2,SNCAIP,SNX24,SNX31,MAPK8IP2,CPT1B,PHAX,MARCH3,APOM,ZDHHC14,SLC12A2,HSPA1B,SYNJ2,SERAC1,RIMS2,IGF2R,SLC27A6,CDC42SE2,KCNV1,PRRT1,PRKN,QKI,RNF5,AGER,PPARA,TAP1,SLC22A4,CALHM4,KIF3A,SEPT8,TSPO,GDF9,GOPC,SLC35F1,VPS52,HSPA4,DERL1,SMDT1,BAK1,FAM91A1,CATSPER3,WASHC5,MYC,LRRC6,KLHL3,MCHR1,PKD2L2,KCNK9,GRM4,PTK2,FAM53C,SLC45A4,PTCH1,TSNARE1,LY6E,ZC3H3,EXOC4,SIL1,SYNGR1,MAPK15,AGTPBP1,SUN2,MAPK14,NTRK2,TOMM22,NRBP2,KCNJ4,CSNK1E,TMEM184B,PLA2G6,COPG2,PICK1,MICALL1,PIM1,TBC1D22B,BTBD9,RAC2,SMO,ZDHHC21,TTC39B,HSF1,PLIN2,TOMM6,SLC39A4,ATP6V1F,MYH9,GUCA1B,MFSD3,APOL4,APOL6,IFT74,CHRNA3,CHRNA5,PEX6,TRPM6,FBXO7,CRY1,CROT,ABCB1,SLC25A40,ABCC10,NOL6,STEAP2,GABRA1,XPO5,WASHC4,APBA1,CNGA1,SLC41A2,TMEM63B,PEX1,SLC35B2,OCIAD1,USP46,CLIC5,VPS50,SLC25A27,SCFD2,RFX3,KIT,SLC1A1,CA9,TGFBRAP1,TFAP2B,SLC25A13,TBC1D8,TRAM2,PPAT,TMEM14A,RGP1,WNK2,BICD2,MFSD14C,CHMP2A,CNNM4,TSPAN13,RAB23,DYNC2LI1,NLRP5,ABCG5,SVBP,ABCG8,LRPPRC,SEC61B,SLC3A1,STX17,CLDN19,SIX2,DNAJA1,IL11,BRSK1,PRKCE,SMAP1,ATP6V1E2,RIMS1,ABCB5,TMC4,TMEM30A,DNAH11,SPTBN1,IGF2BP3,FPR2,HMGN3,KCNQ4,YTHDC1,RIMS3,IBTK,PNPT1,RUFY3,SHANK1,SLC4A4,CYB5R4,PPT1,SNX14,ALB,CXCL8,SCRN1,XPO1,	grey	VSMC_M10
GO:1902018	0.78	0.43	5	11	negative regulation of cilium assembly	BP	1	TBC1D30,LIMK2,DNM2,CDK10,ODF2L	grey	VSMC_M10
GO:0055012	0.78	0.41	6	13	ventricular cardiac muscle cell differentiation	BP	1	FHL2,ATG5,RARB,MEF2C,NKX2-5,HEY2	grey	VSMC_M10
GO:0010939	0.78	0.34	15	31	regulation of necrotic cell death	BP	1	HEBP2,TSPO,PELI1,ASAH1,RIPK1,SPATA2,FZD9,YBX3,BIRC3,OGT,MIR22,NOL3,FADD,CASP8,PPIF	grey	VSMC_M10
GO:0060402	0.78	0.28	53	107	calcium ion transport into cytosol	BP	1	BAK1,PRKCE,IBTK,ATG5,GRIN2D,TRPC3,SLC8A2,RYR1,PRNP,DIAPH1,P2RX2,RASA3,P2RX3,RYR3,TMBIM6,P2RX7,PTK2B,TPCN1,SLC8B1,F2R,PKD2,CASQ2,RYR2,TRPM1,LCK,TRPV4,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,FAM155B,CD19,CALM1,BDKRB1,TRPV2,TRPV3,TRPV1,PDPK1,P2RX1,CYBA,JPH3,MCOLN3,DMD,NOL3,JPH2,THY1,DDIT3	grey	VSMC_M10
GO:0021932	0.78	0.45	4	9	hindbrain radial glia guided cell migration	BP	1	RBFOX2,ATP1B2,DAB1,CEND1	grey	VSMC_M10
GO:0150065	0.78	0.43	5	11	regulation of deacetylase activity	BP	1	C6orf89,SPHK2,PRKD2,PINK1,KDM5A	grey	VSMC_M10
GO:2001244	0.78	0.31	23	46	positive regulation of intrinsic apoptotic signaling pathway	BP	1	NCK2,GSDME,FBH1,FBXW7,NKX3-1,SIAH1,DNM1L,LCK,MCL1,RPL11,FIS1,PRKRA,S100A8,SFPQ,PTPN2,PIAS4,BCAP31,PARK7,MIR27B,UBB,DDIT3,BCL2L11,PLAGL2	grey	VSMC_M10
GO:0009306	0.78	0.25	136	266	protein secretion	BP	1	LRP1,CANX,SLC12A2,RIMS2,PRKN,PLA2G6,COPG2,PICK1,RFX3,TFAP2B,SVBP,PRKCE,HMGN3,CYB5R4,BMP8A,PLEK,RSAD2,NR1H2,EGFR,TLR4,TRPM4,RAB10,COPG1,GIPR,FRMD4A,LLGL2,STEAP3,RAF1,APBB3,DPH3,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,IL1A,OSBP,ARNTL,VEGFC,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,ACVR1C,F2RL1,F2R,ZBED6,DMTN,ADTRP,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,CPT1A,SLC9B2,TGFB2,ADRA2A,MON1A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,PER2,STX1A,GLUL,SIDT2,SLC16A1,ADAM8,KLF7,MIA3,BLOC1S6,CTAGE9,VGF,TTN,IL12A,TANGO2,ENY2,ABCA12,MCU,PPP3CB,RAB3A,CAMK2G,PTPRN,CD38,MPC2,ILDR2,RAB8A,ATP13A2,SYT7,RAB15,NLGN2,CPLX1,TARDBP,STX4,RAB8B,TMED10,UBE2Q1,MYH10,SEL1L,RAB3D,SYTL4,GPR68,TVP23C,CCL5,SREBF1,ISL1,OXCT1,NOS2,TVP23A,ABAT,RPH3AL,NADK,BAIAP3,PARK7,LRRC8A,TANGO6,MIR199A1,FGA,BLOC1S3,CHGA,SOX4,DPP4,TMEM167A,CRH,DOC2B,UQCC2,PARD6A	grey	VSMC_M10
GO:0035592	0.78	0.25	136	266	establishment of protein localization to extracellular region	BP	1	LRP1,CANX,SLC12A2,RIMS2,PRKN,PLA2G6,COPG2,PICK1,RFX3,TFAP2B,SVBP,PRKCE,HMGN3,CYB5R4,BMP8A,PLEK,RSAD2,NR1H2,EGFR,TLR4,TRPM4,RAB10,COPG1,GIPR,FRMD4A,LLGL2,STEAP3,RAF1,APBB3,DPH3,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,IL1A,OSBP,ARNTL,VEGFC,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,ACVR1C,F2RL1,F2R,ZBED6,DMTN,ADTRP,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,CPT1A,SLC9B2,TGFB2,ADRA2A,MON1A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,PER2,STX1A,GLUL,SIDT2,SLC16A1,ADAM8,KLF7,MIA3,BLOC1S6,CTAGE9,VGF,TTN,IL12A,TANGO2,ENY2,ABCA12,MCU,PPP3CB,RAB3A,CAMK2G,PTPRN,CD38,MPC2,ILDR2,RAB8A,ATP13A2,SYT7,RAB15,NLGN2,CPLX1,TARDBP,STX4,RAB8B,TMED10,UBE2Q1,MYH10,SEL1L,RAB3D,SYTL4,GPR68,TVP23C,CCL5,SREBF1,ISL1,OXCT1,NOS2,TVP23A,ABAT,RPH3AL,NADK,BAIAP3,PARK7,LRRC8A,TANGO6,MIR199A1,FGA,BLOC1S3,CHGA,SOX4,DPP4,TMEM167A,CRH,DOC2B,UQCC2,PARD6A	grey	VSMC_M10
GO:0050860	0.78	0.39	7	15	negative regulation of T cell receptor signaling pathway	BP	1	PAWR,PRNP,PTPRJ,SLA2,PTPN6,PTPN2,THY1	grey	VSMC_M10
GO:0072182	0.78	0.43	5	11	regulation of nephron tubule epithelial cell differentiation	BP	1	OSR1,PAX8,PAX2,LHX1,LIF	grey	VSMC_M10
GO:0019319	0.78	0.30	30	61	hexose biosynthetic process	BP	1	PPARA,AKR1B1,ATF4,GPT,GNMT,CRY1,SLC25A13,PPP4R3B,ZNF692,FAM3C,SIRT7,GPI,NLN,GPD1,SIK1,MST1,PC,SLC37A4,PER2,SORD,DDB1,DGKQ,OGT,CRTC2,LEPR,PTPN2,ACADM,FBP2,NNMT,ARPP19	grey	VSMC_M10
GO:0006026	0.78	0.37	9	19	aminoglycan catabolic process	BP	1	CEMIP2,GLB1,HYAL1,HYAL3,OVGP1,CEMIP,IDUA,IDS,CTBS	grey	VSMC_M10
GO:0048486	0.78	0.39	7	15	parasympathetic nervous system development	BP	1	PLXNA4,SEMA3A,TFAP2A,SEMA3F,ADARB1,PLXNA3,SIX1	grey	VSMC_M10
GO:0097094	0.78	0.41	6	13	craniofacial suture morphogenesis	BP	1	RAB23,MEGF8,MSX2,TMEM107,FOXN3,INSIG2	grey	VSMC_M10

GO:0098801	0.78	0.36	11	23	regulation of renal system process	BP	1	SNX5,GAS6,STC1,F2RL1,F2R,AGT,PTPRO,COMT,CORO2B,INPP5K,CYBA	grey	VSMC_M10
GO:0006206	0.78	0.39	7	15	pyrimidine nucleobase metabolic process	BP	1	DPYS,CMPK1,CTPS2,CPS1,MAPK1,ALDH6A1,DHODH	grey	VSMC_M10
GO:0000083	0.78	0.38	8	17	regulation of transcription involved in G1/S transition of mitotic cell cycle	BP	1	CDK14,KLF11,BACH1,CDK18,CDK15,ESRRB,GFI1,E2F6	grey	VSMC_M10
GO:1901890	0.78	0.29	40	82	positive regulation of cell junction assembly	BP	1	NTRK2,TEK,LINGO2,SEMA4D,CLDN19,LRRN3,ITGB1BP1,VSTM5,EPHB1,NPHP1,CLSTN2,FMN1,PTPRJ,CUX2,TBX5,AMIGO2,BDNF,COL16A1,AMIGO3,ADNP,AGT,ACE2,EPHB3,WNT4,LRTM2,NLGN2,SEMA4A,NLGN3,SMAD3,GPRASP2,BHLHB9,ASIC2,SLITRK2,AMIGO1,TSC1,ADGRL2,GRID2,THY1,CLDN1,LRRTM2	grey	VSMC_M10
GO:0034368	0.79	0.37	9	19	protein-lipid complex remodeling	BP	1	APOM,APOB,APOC1,NR1H4,PLTP,ABCA5,AGT,LIPC,MPO	grey	VSMC_M10
GO:0034369	0.79	0.37	9	19	plasma lipoprotein particle remodeling	BP	1	APOM,APOB,APOC1,NR1H4,PLTP,ABCA5,AGT,LIPC,MPO	grey	VSMC_M10
GO:0019933	0.79	0.32	19	40	cAMP-mediated signaling	BP	1	PDE7B,ADGRG6,RIMS2,UBE2B,SOX9,GIPR,RAPGEF2,RAPGEF3,CAP2,ADCY2,EIF4EBP2,DGKQ,PDE4A,MAPK7,KSR1,MGRN1,CAP1,CRH,RASD2	grey	VSMC_M10
GO:1903036	0.79	0.30	26	53	positive regulation of response to wounding	BP	1	LRP1,PTK2,ENPP4,PRKCE,PTN,THBD,ACTG1,HBEGF,FERMT1,F2R,ANO6,RREB1,DMTN,ADRA2A,USF1,NFE2L2,DUOX1,F12,NDEL1,SERPINF2,MIR29A,MIR21,MIR222,CNTF,CLDN1,HRAS	grey	VSMC_M10
GO:0032527	0.79	0.31	21	43	protein exit from endoplasmic reticulum	BP	1	DERL1,SEC61B,TMEM30A,NPLOC4,UBAC2,TM9SF4,AUP1,RHBDD1,YOD1,SORL1,SYVN1,DERL3,SEC16B,TMEM129,TMEM30B,SEL1L,TECPR2,BCAP31,SEC16A,UBE2G2,DERL2	grey	VSMC_M10
GO:0043279	0.79	0.28	40	81	response to alkaloid	BP	1	SLC1A1,PRKCE,DDC,HDAC2,DNMT3A,HNMT,RYR1,DNMT3B,GPI,CASP3,RYR3,PTK2B,TIAM1,HOMER1,SPIDR,CASQ2,RYR2,GRM2,SLC6A3,HDAC1,CPT1A,PEA15,HOMER2,BCHE,SDK1,TMED10,CHRNB2,DNM2,GHR,MBD1,ABAT,TRPV1,HSPA5,DHODH,NQO1,MT-ND6,FADD,RGS4,CRH,PITX3	grey	VSMC_M10
GO:0072529	0.79	0.35	12	25	pyrimidine-containing compound catabolic process	BP	1	DPYS,APOBEC3H,CDADC1,MBD4,ENTPD4,TET1,UPB1,ALDH6A1,NEIL1,NT5M,NTHL1,UPP1	grey	VSMC_M10
GO:2001267	0.79	0.39	7	15	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	BP	1	ST18,HTRA2,SMAD3,NLE1,PARK7,CAAP1,PRR7	grey	VSMC_M10
GO:0032753	0.79	0.39	7	15	positive regulation of interleukin-4 production	BP	1	CD28,FCER1G,FOXP3,PRKCZ,SLC7A5,CEBPB,HAVCR2	grey	VSMC_M10
GO:0035461	0.79	0.41	6	13	vitamin transmembrane transport	BP	1	SLC23A2,ABCC5,SLC27A1,STRA6,SLC46A1,SLC25A32	grey	VSMC_M10
GO:0016075	0.79	0.38	8	17	rRNA catabolic process	BP	1	EXOSC4,EXOSC3,DEDD2,DDX49,MRPL44,SLFN14,DROSHA,EXOSC5	grey	VSMC_M10
GO:0000422	0.79	0.29	35	71	autophagy of mitochondrion	BP	1	ATG12,PRKN,TSPO,FBXO7,ATG5,OPTN,USP36,ULK1,FBXW7,HTRA2,CSNK2A2,DNM1L,CISD2,USP30,FZD5,FIS1,ATG2A,FUNDC1,HTT,MARK2,PINK1,MUL1,ATG9A,ATP13A2,WIPI2,VPS13D,MFN2,VPS13C,HAX1,ATG2B,SREBF1,FUNDC2,PARK7,BNIP3L,TIGAR	grey	VSMC_M10
GO:0061726	0.79	0.29	35	71	mitochondrion disassembly	BP	1	ATG12,PRKN,TSPO,FBXO7,ATG5,OPTN,USP36,ULK1,FBXW7,HTRA2,CSNK2A2,DNM1L,CISD2,USP30,FZD5,FIS1,ATG2A,FUNDC1,HTT,MARK2,PINK1,MUL1,ATG9A,ATP13A2,WIPI2,VPS13D,MFN2,VPS13C,HAX1,ATG2B,SREBF1,FUNDC2,PARK7,BNIP3L,TIGAR	grey	VSMC_M10
GO:0030510	0.79	0.29	36	74	regulation of BMP signaling pathway	BP	1	LEMD2,KCP,TFAP2B,SOSTDC1,HOXA13,BMPER,SFRP4,UBE2O,SPART,ZNF423,FBXL15,SORL1,HTRA1,CHRD,DLX1,CTDSPL2,HTRA3,FBN1,FKBP8,GREM2,RBPJ,ITGA3,RBPMS2,TOB1,RNF165,CHRDL1,TWSG1,GPC3,SKI,ENG,FSTL3,LEMD3,ACVRL1,NOG,WNT5A,UBE2D1	grey	VSMC_M10
GO:0007635	0.79	0.42	5	11	chemosensory behavior	BP	1	CFAP69,SHANK1,ADCY3,P2RX3,TRPV1	grey	VSMC_M10
GO:0034497	0.79	0.42	5	11	protein localization to phagophore assembly site	BP	1	STX17,ATG16L1,ATG9A,WIPI2,MFN2	grey	VSMC_M10
GO:0032402	0.79	0.38	8	17	melanosome transport	BP	1	BBS7,MKKS,MLPH,RAB17,BLOC1S6,MREG,RAB11A,BLOC1S3	grey	VSMC_M10
GO:1903671	0.79	0.45	4	9	negative regulation of sprouting angiogenesis	BP	1	SEMA6A,PIK3CB,E2F2,SYNJ2BP	grey	VSMC_M10
GO:0060004	0.79	0.45	4	9	reflex	BP	1	USP46,SLC1A1,SHANK1,ALDH1A3	grey	VSMC_M10
GO:0019693	0.79	0.25	161	312	ribose phosphate metabolic process	BP	1	NME1,HSD17B4,PDE7B,ATP5MGL,DPYS,PPT2,PPARA,PDE10A,ACSL6,PRXL2C,GTPBP1,IMPDH1,GDA,CROT,SLC35B2,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,NT5E,PPT1,BPGM,DLD,SPHK2,CMPK1,ADCY3,DLG2,NUDT5,DHTKD1,PRKAG2,ATP5F1C,ELOVL1,PFKP,NUDT16,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,GPI,AMPD3,ATP5F1A,MCCC2,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,MFN1,PFKFB2,PRPS2,ENO4,HACD2,ARNT,ADCY4,CTPS2,ACTN3,HDAC4,THEM5,DNAJC30,MLXIPL,PDE8A,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,UPB1,HK1,ACSBG1,ATP5S,CASK,PYGL,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,ENO3,PARP1,TECR,CARD11,SLC26A1,PSEN1,ACOT2,GUCY2D,PKLR,PANK3,GCDH,OGT,UPRT,ADPGK,PDE4A,ACSM3,ACACA,NCOR1,INSR,SLC26A2,PRPSAP2,ADSSL1,ACSBG2,ALDOC,PIPOX,ACOT11,ATP6V0C,PANK4,NME3,MPP1,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,UCK1,MLYCD,DHODH,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,ELOVL3,TIGAR,NUDT19,NME6,NUDT2,HINT1,UPP1,RPIA	grey	VSMC_M10
GO:0030889	0.79	0.42	5	11	negative regulation of B cell proliferation	BP	1	TNFRSF21,PAWR,CASP3,RC3H1,BTK	grey	VSMC_M10
GO:0035455	0.79	0.40	6	13	response to interferon-alpha	BP	1	EIF2AK2,GAS6,IFIT2,MX2,KLHL20,IFIT3	grey	VSMC_M10
GO:0001990	0.79	0.35	11	23	regulation of systemic arterial blood pressure by hormone	BP	1	MME,F2RL1,F2R,ENPEP,AGT,ACE2,ECE1,SERPINF2,CYBA,HSD11B2,RHOA	grey	VSMC_M10

GO:0051924	0.79	0.26	87	172	regulation of calcium ion transport	BP	1	STAC3,TSPO,BAK1,MCHR1,PLA2G6,TSPAN13,PRKCE,ATG5,SPHK2,TRPC3,CACNB2,STAC,CACNB4,EFHB,PRNP,DIAPH1,P2RX2,P2RX3,ORAI1,TMBIM6,P2RX7,PTK2B,SLC8B1,HOMER1,STC1,F2R,KCNE2,PKD2,CASQ2,RYR2,ADRA2A,EGF,EPB41,OPRD1,UBASH3B,ANK2,GPER1,AGT,ATP1A2,SLC9A1,PLPP4,C4orf3,CASQ1,NTSR1,NOS1AP,HOMER2,IL16,CEMIP,SESTD1,CASK,PTPN6,HTT,CAMK2G,ATP1B1,GNB5,HAP1,PSEN2,WNK3,STAC2,CACNB1,ATP2A1,CD19,CALM1,VMP1,BDKRB1,TRPV2,CAMK2A,CCL5,CCL2,FMR1,INPP5K,TRPV3,PDPK1,P2RX1,CYBA,JPH3,ATP2C2,RRAD,MIR21,RHOA,DMD,GPR35,JPH2,THY1,RGS4,CRH,GEM	grey	VSMC_M10
GO:0060670	0.79	0.42	5	11	branching involved in labyrinthine layer morphogenesis	BP	1	RSPO3,SPINT2,SPINT1,FZD5,GRB2	grey	VSMC_M10
GO:0019377	0.79	0.40	6	13	glycolipid catabolic process	BP	1	NEU3,GALC,GLA,HEXA,GM2A,NEU2	grey	VSMC_M10
GO:0002029	0.79	0.40	6	13	desensitization of G protein-coupled receptor signaling pathway	BP	1	GIPR,ARRB1,GRK2,SAG,GRK4,DNM2	grey	VSMC_M10
GO:0022401	0.79	0.40	6	13	negative adaptation of signaling pathway	BP	1	GIPR,ARRB1,GRK2,SAG,GRK4,DNM2	grey	VSMC_M10
GO:0023058	0.79	0.40	6	13	adaptation of signaling pathway	BP	1	GIPR,ARRB1,GRK2,SAG,GRK4,DNM2	grey	VSMC_M10
GO:0002732	0.79	0.45	4	9	positive regulation of dendritic cell cytokine production	BP	1	KIT,MAVS,NOD2,TICAM1	grey	VSMC_M10
GO:0043552	0.79	0.34	13	28	positive regulation of phosphatidylinositol 3-kinase activity	BP	1	AGAP2,PTK2,TEK,KIT,FPR2,FLT1,PTK2B,NOD2,IRS1,FGR,FGFR3,CD19,VAV3	grey	VSMC_M10
GO:0002693	0.79	0.40	6	13	positive regulation of cellular extravasation	BP	1	AGER,CD99,ADAM8,FADD,THY1,PDGFD	grey	VSMC_M10
GO:0045662	0.79	0.38	8	17	negative regulation of myoblast differentiation	BP	1	SOSTDC1,SOX9,SRA1,CCL17,PRICKLE1,MBNL3,SOX8,DDIT3	grey	VSMC_M10
GO:0008631	0.79	0.32	19	39	intrinsic apoptotic signaling pathway in response to oxidative stress	BP	1	MAP3K5,PRKN,PDK1,ARL6IP5,DIABLO,FBXW7,HTRA2,MCL1,NFE2L2,NONO,PRODH,PDCD10,PINK1,PARP1,SFPQ,MAPK7,PARK7,ZNF622,NOL3	grey	VSMC_M10
GO:0051100	0.79	0.27	65	129	negative regulation of binding	BP	1	PPARA,HABP4,C6orf106,CSNK1E,SMO,MDFI,TTBK1,MITD1,ZNF462,ITGB1BP1,HDAC2,SYMPK,RALB,RSF1,PTPRF,FBH1,EFHB,BTAF1,HAND2,FBXW7,TMBIM6,P2RY1,FAM192A,IFIT2,DTNBP1,PPP3CA,SP100,TTBK2,ADNP,DISC1,SORL1,NFATC4,PER2,C4orf3,PEX19,GEMIN2,ITGA4,MEPCE,LRPAP1,RAP1GAP,DNAJB2,DDX11,CRMP1,ACTB,GNL3L,MSX2,PEX14,PSEN1,TAF1,MAPK3,WFIKKN2,SIN3A,ERCC4,JUN,WFIKKN1,PARK7,MIR27B,MIR27A,BAG2,NOG,DDIT3,ZNF304,ZNF593,STYX,HEY2	grey	VSMC_M10
GO:0032411	0.79	0.28	42	85	positive regulation of transporter activity	BP	1	STAC3,ABCB1,WNK2,CACNB2,STAC,GLRX,KCNJ11,NR1H3,IFNGR2,TESC,KCNE2,PKD2,KCNIP2,RYR2,FAM173B,COX17,ANK2,SLC9A1,CASQ1,NTSR1,NOS1AP,HTT,PINK1,ATP1B1,KCNA1,HAP1,WNK3,STAC2,ATP1B2,NLGN3,ATP2A1,CALM1,DNM2,VMP1,CCL2,RNF207,PARK7,AMIGO1,RXRA,DMD,JPH2,APOPT1	grey	VSMC_M10
GO:0071871	0.79	0.42	5	11	response to epinephrine	BP	1	SIRT2,RYR2,SRD5A1,SLC9A1,PKLR	grey	VSMC_M10
GO:0006002	0.79	0.42	5	11	fructose 6-phosphate metabolic process	BP	1	GFPT2,PFKP,PFKM,HK1,FBP2	grey	VSMC_M10
GO:0051881	0.79	0.29	33	66	regulation of mitochondrial membrane potential	BP	1	HEBP2,PRKN,TSPO,BAK1,SLC25A27,WISP3,PRDX3,AKT2,DCN,PANK2,SPART,RNF122,CLIC1,ARL6IP5,PPA2,MFN1,OPRD1,IFI6,FZD9,PPP2R3C,MAPT,STOX1,BCO2,PINK1,MUL1,PARP1,TRPV1,PARK7,SLC25A33,PIP5KL1,UBB,MLLT11,BNIP3L	grey	VSMC_M10
GO:0034755	0.79	0.38	8	17	iron ion transmembrane transport	BP	1	STEAP2,SLC25A37,SLC40A1,ISCU,ABCC5,SLC11A1,ABCB6,LCN2	grey	VSMC_M10
GO:0070265	0.79	0.31	22	45	necrotic cell death	BP	1	HEBP2,TSPO,NINJ1,GSDME,PELI1,ASAH1,RIPK1,DNM1L,ITPK1,SPATA2,FZD9,YBX3,PYGL,BIRC3,TRPM7,OGT,TRAF2,MIR22,NOL3,FADD,CASP8,PPIF	grey	VSMC_M10
GO:0033500	0.79	0.26	93	184	carbohydrate homeostasis	BP	1	ZNF236,NME1,LRP1,AGER,PTCH1,PLA2G6,CRY1,SRF,TFAP2B,PRKCE,HMGN3,CYB5R4,TRPM4,FOXO3,FGF21,SESN3,FOXA3,GRIK5,RAF1,GCKR,ASPSCR1,GAS6,NR1H4,CYP7A1,NDUFAF2,GPI,CEBPA,OSBP,PIK3R1,KCNJ11,TIAM1,RAB11FIP5,PFKM,SLC8B1,OPA1,CRY2,ZBED6,PAX2,TWNK,TENT4B,GPLD1,IRS1,PPP3CA,TRPV4,SLC9B2,ZBTB20,ADRA2A,TCF7L2,KCNB1,POLG,GPER1,RAB11FIP2,USF1,MLXIPL,SIDT2,SLC16A1,PDK3,KLF7,FIS1,VGF,HK1,MEN1,ENY2,ABCA12,MCU,PYGL,PPP3CB,STAT3,PTPRN,MPC2,BHLHA15,SLC2A4,FGFR4,STX4,NGFR,CRTC2,GPR68,SIN3A,INSR,OXCT1,LEPR,PTPN2,INPP5K,NADK,BAIAP3,PARK7,CYBA,LRRC8A,OAS1,FABP5,LRRC8D,SOX4,CRH	grey	VSMC_M10
GO:0097531	0.79	0.40	6	13	mast cell migration	BP	1	RAC2,KIT,VEGFC,STAT5B,PGF,CHGA	grey	VSMC_M10
GO:1902894	0.79	0.39	7	15	negative regulation of pri-miRNA transcription by RNA polymerase II	BP	1	PPARA,SRF,SOX9,NFATC4,HDAC4,YY1,NFATC3	grey	VSMC_M10
GO:0035637	0.79	0.27	56	114	multicellular organismal signaling	BP	1	NTRK2,CLDN19,MYH14,CLCN1,TRPM4,SLC8A2,CACNB2,ATP1A3,SCN5A,SCN1A,P2RX3,CHRM5,KCNJ3,TBX5,KCNE2,DSP,CASQ2,RYR2,PKP2,KCNJ2,SCN2A,SCN7A,ANK2,GPER1,AGT,ACE2,ATP1A2,SLC9A1,SCN4B,TNR,CNTNAP1,ATP1B1,KCNA1,SLC4A3,ATP1B2,CACNA1G,ATP2A1,CALM1,OTOA,DSG2,ISL1,FMR1,ATP2B3,P2RX1,RNF207,CACNA1H,GPR35,TMEM65,KCNH2,SCN2B,CACNG7,GPR88,CACNG5,HCN4,NKX2-5,KCNMB4	grey	VSMC_M10
GO:0002639	0.79	0.32	16	33	positive regulation of immunoglobulin production	BP	1	IL5,EXOSC3,MSH2,HMCES,PHB,MLH1,PAXIP1,SHLD1,HPX,GPI,CD40,CD28,SHLD2,TBX21,STX4,IL4R	grey	VSMC_M10
GO:0071679	0.79	0.42	5	11	commissural neuron axon guidance	BP	1	PTCH1,SMO,RYK,FZD3,DAG1	grey	VSMC_M10
GO:0071360	0.79	0.39	7	15	cellular response to exogenous dsRNA	BP	1	RALB,TMEM173,MAVS,IFIH1,MUL1,COLEC12,ZCCHC3	grey	VSMC_M10
GO:0030282	0.79	0.27	48	97	bone mineralization	BP	1	CYP27B1,OSR2,ATF4,ROR2,OMD,PTN,TRPM4,OSR1,SOX9,ERCC2,ACVR2B,WNT11,SLC24A3,ACVR2A,KL,ADGRV1,MEF2C,P2RX7,PTK2B,BMP2K,ANO6,TFAP2A,BMPR1B,FBXL15,SBDS,PTHLH,SGMS2,AXIN2,FGR,ACTN3,TXLNG,FZD9,PTH1R,SRGN,BCOR,ANKH,ZBTB40,WNT4,FGFR3,MMP13,BMPR1A,SMAD3,GPC3,RFLNB,BGLAP,MINPP1,SNX10,CCDC154	grey	VSMC_M10
GO:0090177	0.79	0.42	5	11	establishment of planar polarity involved in neural tube closure	BP	1	PTK7,DVL3,GRHL3,DVL2,WNT5A	grey	VSMC_M10
GO:0006878	0.79	0.42	5	11	cellular copper ion homeostasis	BP	1	SLC31A2,ATP7B,PRNP,ABCB6,SCO1	grey	VSMC_M10
GO:0003157	0.79	0.42	5	11	endocardium development	BP	1	STK3,OVOL2,NRG1,STK4,RBPJ	grey	VSMC_M10

GO:0000212	0.79	0.42	5	11	meiotic spindle organization	BP	1	WASHC5,MYH9,MOS,TUBG1,SEPT1	grey	VSMC_M10
GO:0010528	0.79	0.42	5	11	regulation of transposition	BP	1	TUT7,APOBEC3H,TUT4,SIRT7,TEX15	grey	VSMC_M10
GO:0010529	0.79	0.42	5	11	negative regulation of transposition	BP	1	TUT7,APOBEC3H,TUT4,SIRT7,TEX15	grey	VSMC_M10
GO:0060415	0.79	0.29	27	56	muscle tissue morphogenesis	BP	1	LY6E,FOXH1,TNNI3,POU4F1,NRG1,TNNC1,DSP,RYR2,PKP2,TNNI1,TGFB2,ADARB1,MYH7,ACTC1,EFEMP2,TTN,BMPR1A,TCAP,RBPJ,MED1,ISL1,ENG,NOG,WNT5A,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0061577	0.79	0.42	5	11	calcium ion transmembrane transport via high voltage-gated calcium channel	BP	1	CACNB2,NOS1AP,SESTD1,CACNB1,MIR21	grey	VSMC_M10
GO:1902043	0.79	0.42	5	11	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	1	STK3,FAF1,STK4,BMPR1B,PEA15	grey	VSMC_M10
GO:0055091	0.79	0.42	5	11	phospholipid homeostasis	BP	1	ITGB6,GPAM,ABCB11,ABCA3,TLCD1	grey	VSMC_M10
GO:0045475	0.79	0.42	5	11	locomotor rhythm	BP	1	NCOA2,CIART,USP2,NCOR1,ZFHX3	grey	VSMC_M10
GO:0060560	0.79	0.25	100	200	developmental growth involved in morphogenesis	BP	1	NEDD4L,LRP1,SEMA6A,ESR1,RAB21,RIMS2,PRKN,FSTL4,PLXNA4,CPNE5,PTK7,SRF,SEMA4D,SEMA4C,RIMS1,RTN4,RUFY3,AREG,EPHA7,TNC,NRCAM,WASF1,SPRY1,PLXNA1,SOX9,GOLGA4,MEGF8,SPRY2,WNT11,CPNE9,TGFBR2,SYT1,SLC23A2,SEMA3D,SPART,SEMA3A,ULK1,RYK,TTL,FMN1,SEMA4F,DPYSL2,EIF2AK4,TIAM1,SLIT1,NKX6-1,ZFYVE27,BIN3,SEMA3G,SPP1,CYFIP1,ALCAM,SEMA4G,SALL1,NKD1,BDNF,KIAA0319,SEMA3F,AUTS2,ADNP,DISC1,CDKL5,WNT3,SPG11,MAPT,SEMA6D,ITGA4,TNR,FN1,NIN,FLRT1,PPP3CB,MUL1,VCL,MED1,SEMA4A,NLGN3,TRIM46,NDEL1,RAB11A,NTN1,DNM2,TBX2,LHX1,SIN3A,TRPV2,CDK5R1,SLC9A6,L1CAM,PRKCZ,ARHGAP4,PLXNA3,BARHL2,IMPACT,WNT5A,CACNG7,SIX1,LLPH,FGF1,OLFM1	grey	VSMC_M10
GO:0045579	0.79	0.42	5	11	positive regulation of B cell differentiation	BP	1	NCKAP1L,IL7,PPP2R3C,STAT5B,BTK	grey	VSMC_M10
GO:0043473	0.79	0.28	37	75	pigmentation	BP	1	SOX10,KIT,FIG4,BBS7,MYO7A,SZT2,MKKS,MITF,ANKRD27,MEF2C,HPS3,HPS5,AP3B1,ADAMTS20,VANGL1,DTNBP1,OCA2,KIF13A,SHROOM2,USP13,HPS4,MLPH,RAB17,PIKFYVE,BLOC1S6,MREG,ABCB6,LRMDA,CITED1,RAB11A,SNAPIN,SLC45A2,AP1G1,BLOC1S3,RAB32,BCL2L11,TRAPPC6A	grey	VSMC_M10
GO:2000104	0.79	0.40	6	13	negative regulation of DNA-dependent DNA replication	BP	1	ZRANB3,FBH1,DONSON,BCL6,TIPIN,LIG3	grey	VSMC_M10
GO:1902253	0.79	0.34	12	25	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	PRKN,ARMC10,TAF9,ING2,MARCH7,RPL11,MUC1,TAF9B,CD74,MIR21,UBB,PTTG1IP	grey	VSMC_M10
GO:0016973	0.79	0.37	8	17	poly(A)+ mRNA export from nucleus	BP	1	IWS1,DDX25,ENY2,NXF1,THOC2,DDX19A,SARNP,DDX19B	grey	VSMC_M10
GO:1903894	0.79	0.40	6	13	regulation of IRE1-mediated unfolded protein response	BP	1	BAK1,DDRGK1,FICD,HSPA5,DAB2IP,BCL2L11	grey	VSMC_M10
GO:0044154	0.79	0.41	5	11	histone H3-K14 acetylation	BP	1	BRD1,PHF14,ING5,KAT7,NAP1L2	grey	VSMC_M10
GO:0030262	0.79	0.34	11	23	apoptotic nuclear changes	BP	1	HSF1,DEDD2,FOXL2,ACVR1C,ACIN1,GPER1,DNASE2,PAM16,DFFB,BLCAP,NMNAT1	grey	VSMC_M10
GO:0039692	0.79	0.41	5	11	single stranded viral RNA replication via double stranded DNA intermediate	BP	1	APOBEC3H,CXCL8,FAM208A,INPP5K,SETDB1	grey	VSMC_M10
GO:1901657	0.79	0.29	30	60	glycosyl compound metabolic process	BP	1	FUCA2,AKR1B1,APOBEC3H,OARD1,MTAP,GNMT,GDA,ENPP4,PPAT,NT5E,PRTFDC1,CDADC1,AKR1A1,AHCY,CBR4,DGUOK,NME4,TYW1B,TYW5,PRPS2,LCMT2,DTYMK,UPB1,ADK,UPRT,GLA,PRPSAP2,ABHD10,PEMT,UPP1	grey	VSMC_M10
GO:0007190	0.79	0.39	6	13	activation of adenylate cyclase activity	BP	1	GIPR,RAF1,CAP2,CALM1,ADORA2B,CAP1	grey	VSMC_M10
GO:0002043	0.79	0.34	12	25	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	BMPER,ITGB1BP1,IL12A,PDCD10,NGFR,MIR21,MIR222,MIR23A,MIR27B,MIR24-1,MIR27A,ACVRL1	grey	VSMC_M10
GO:0072659	0.79	0.25	121	239	protein localization to plasma membrane	BP	1	LRP1,STX7,STAC3,MAP7,GOPC,PTCH1,TSPAN33,PRKCE,ASB3,SPTBN1,ITGB1BP1,EGFR,VPS35,RAB7A,RAB10,CACNB2,CLASP2,STAC,OPTN,GOLGA4,MYL12A,AKT2,IKBKB,ANK1,PRNP,BAG4,GAS6,PKP3,ARL6IP5,KCNIP3,LYPLA1,RILPL1,RILPL2,PIK3R1,TMEM150A,VAMP5,SLMAP,PLS1,FCHO2,SORBS1,P2RY1,RAPGEF2,KCNJ11,ZFYVE27,TESC,KIF13A,NHLRC1,NECTIN3,PKP2,PPFIA1,ZDHHC23,KCNB1,ANK2,C2CD5,GPER1,RAB11FIP2,FAM126B,CIB1,AP2M1,PPP2R5A,BBS1,GORASP2,LAMA5,PACS1,DLG1,LRRC15,NSF,EHD1,ZDHHC8,ABCA12,CNPY4,RAB3A,RAMP2,EXOC5,ATP1B1,PPIL2,NSG1,GRIPAP1,RAB8A,CNST,ACTB,RAB15,RSC1A1,MPP5,WNK3,STAC2,TSPAN17,ANXA2,GAK,STX4,TMEM88,RAB8B,ITGA3,AC138894.1,RAB11A,STX8,RAB3D,TTC7B,GGA2,ARHGAP44,PRAM1,EPB41L3,IFT20,INPP5K,PDPK1,PRKCZ,RAB26,RER1,ARHGEF16,SEC16A,PALM,BSG,ATP2C2,STXBP1,VPS4A,C16orf70,FYB1,PDZD3,LDLRAP1,VAMP3,MRAP2	grey	VSMC_M10
GO:0016114	0.79	0.41	5	11	terpenoid biosynthetic process	BP	1	PRMT3,ALDH1A3,GGPS1,DHRS9,ALDH1A2	grey	VSMC_M10
GO:0032637	0.79	0.29	28	57	interleukin-8 production	BP	1	HSPA1B,NOD1,ANXA4,TLR4,C5AR2,PRKD2,MYD88,ARRB1,MAVS,F2RL1,F2R,RIPK1,MAPKBP1,NOD2,TLR5,OTUD7B,STAT3,MAP2K5,CD74,NOS2,PARK7,LAMTOR5,BCL10,FADD,ZNF580,WNT5A,DDIT3,IL17D	grey	VSMC_M10
GO:0032201	0.79	0.44	4	9	telomere maintenance via semi-conservative replication	BP	1	WRN,RTEL1,UPF1,TERF2	grey	VSMC_M10
GO:0070307	0.79	0.41	5	11	lens fiber cell development	BP	1	FRS2,ATF4,TMOD1,BFSP1,TBC1D20	grey	VSMC_M10
GO:0010769	0.79	0.28	39	80	regulation of cell morphogenesis involved in differentiation	BP	1	RAB21,FBLN1,PTK2,ITGB1BP1,UNC13D,SS18L2,RAC3,ARHGEF7,PRKDC,ANKRD27,CUX2,TIAM1,DOCK5,OPA1,RREB1,ITPKA,DMTN,DNM1L,CARMIL1,CAPRIN2,AP1AR,CASS4,CIB1,SS18L1,CDKL5,DOCK1,MELTF,CSPG5,OBSL1,EPHA4,DNM2,PARP6,GPRASP2,BHLHB9,LRP8,CRK,FBXO31,FGA,CNTN2	grey	VSMC_M10
GO:0032905	0.79	0.41	5	11	transforming growth factor beta1 production	BP	1	TSKU,LUM,FOXP3,GATA6,NRROS	grey	VSMC_M10
GO:0002825	0.79	0.39	6	13	regulation of T-helper 1 type immune response	BP	1	RIPK2,HLX,PLA2G4A,SLC11A1,IL4R,HAVCR2	grey	VSMC_M10
GO:0002281	0.79	0.41	5	11	macrophage activation involved in immune response	BP	1	PRKCE,NMI,DYSF,TICAM1,HAVCR2	grey	VSMC_M10

GO:0008610	0.79	0.23	282	544	lipid biosynthetic process	BP	1	KDSR,ORMDL2,PIP4K2C,PEX7,B4GALNT1,CYP27B1,AVIL,LTC4S,SYNJ2,SERAC1,CYP21A2,AGPAT4,AGPAT1,QKI,PPARA,ACSL6,PNPLA3,TSPO,MCAT,HSD17B8,A4GALT,HSD17B3,AKR1B1,PLA2G6,GPAA1,HACD4,LARGE1,CWH43,PLPP6,SRD5A3,SPTLC1,HINT2,INPP4A,TMEM246,PIGF,MBOAT7,NR1H2,MBOAT2,LPIN1,INPP4B,DKKL1,SMPD2,FIG4,APOB,AGK,SPHK2,MTMR2,PIP4K2A,PRKD2,EBP,SELENOI,ABHD5,APOC1,PRKAG2,TAMM41,PIBF1,ITPKC,ACER3,ELOVL1,MTMR14,SPTLC3,PGAP2,CRLS1,CDS2,SIRT3,NR1H4,MTMR7,TRIB3,CYP7A1,ELOVL7,ASAH1,CYP7B1,ABHD6,THNSL2,CBR4,PIGU,PIK3CB,OSBP,PITPNM2,ST8SIA4,PIK3R1,TMEM150A,DKK3,PLCE1,FBXW7,SORBS1,CYP2R1,SLA2,PRKAG1,NR1H3,SERINC5,SYNJ1,COQ2,LPIN3,CDS1,FITM2,ORMDL1,HSD17B13,ITPKA,ERLIN1,PIGT,PRMT3,PRKAB1,SIRT4,GPLD1,SRD5A1,CYB5R1,A3GALT2,LPCAT1,SIK1,ALDH1A3,PGAP1,ZBTB20,GPAM,ACSL5,CHKA,ACP6,ABHD4,ST8SIA2,SGMS2,ALDH3B2,AJUBA,GGPS1,PITPNM1,SNAI1,ABHD2,MSMO1,MECR,B3GALT1,GPER1,SC5D,GNPAT,DGKD,B3GNT5,CERS6,PIGM,FITM1,ABCB11,DHRS9,BMX,HACD2,FAM126B,IP6K2,LPGAT1,CERS2,PIGV,DPAGT1,MTMR3,OSBPL2,PCYT1A,INPP5J,MLXIPL,PIGX,GAL3ST3,PIGZ,SCAP,HSD17B7,PISD,POR,DGKG,CREB1,PIKFYVE,PLA2G4A,OSBPL6,ACADL,MOGAT3,TM7SF2,SACM1L,OSBPL1A,ACSBG1,FDX1,PPM1L,PECR,LPCAT3,GAL3ST4,WNT4,PIGC,CYP27A1,PRKAG3,SMPD4,SOCS4,PLA2G16,PI4KA,SLC27A1,ABHD8,SGMS1,CH25H,DAGLB,SCCPDH,FADS3,LIAS,ACADVL,TECR,HSD17B10,CLN8,PGAP3,DEGS1,PIGH,PRPF19,MED1,PI4K2B,ALDH1A2,FGFR4,LIPC,SOCS7,DGKQ,OSBPL7,ALOXE3,ERG28,AC138894.1,HACD3,DGKE,TTC7B,LDLR,	grey	VSMC_M10
GO:0090527	0.79	0.44	4	9	actin filament reorganization	BP	1	DMTN,CASS4,WHAMM,MCU	grey	VSMC_M10
GO:0048678	0.79	0.28	32	65	response to axon injury	BP	1	LRP1,TSPO,TXN2,SLC1A1,PTN,TNC,DHFR,GIPR,PTPRF,CHL1,DPYSL3,MORN4,SPP1,KIAA0319,MTR,GAP43,DAG1,KREMEN1,CERS2,KCNK2,LRIG2,APOD,TNR,EPHA4,MAX,NDEL1,MAP2K1,ISL1,MAPK8IP3,MIR222,CNTF,RTN4RL1	grey	VSMC_M10
GO:0046854	0.79	0.29	26	54	phosphatidylinositol phosphate biosynthetic process	BP	1	PIP4K2C,SYNJ2,INPP4A,INPP4B,FIG4,PIP4K2A,ITPKC,PIK3CB,PIK3R1,TMEM150A,SLA2,SYNJ1,ITPKA,FAM126B,IP6K2,PIKFYVE,SOCS4,PI4KA,PI4K2B,SOCS7,TTC7B,IMPA2,SOCS1,PIP5K1C,PIP5KL1,INPP1	grey	VSMC_M10
GO:0060174	0.79	0.44	4	9	limb bud formation	BP	1	SOX9,ZNF219,WNT3,SOX4	grey	VSMC_M10
GO:0032253	0.80	0.44	4	9	dense core granule localization	BP	1	KIF5A,TANC2,KIF1C,TRIM46	grey	VSMC_M10
GO:0099519	0.80	0.44	4	9	dense core granule cytoskeletal transport	BP	1	KIF5A,TANC2,KIF1C,TRIM46	grey	VSMC_M10
GO:1901950	0.80	0.44	4	9	dense core granule transport	BP	1	KIF5A,TANC2,KIF1C,TRIM46	grey	VSMC_M10
GO:1900103	0.80	0.41	5	11	positive regulation of endoplasmic reticulum unfolded protein response	BP	1	BAK1,PIK3R1,PTPN2,DAB2IP,BCL2L11	grey	VSMC_M10
GO:1903867	0.80	0.44	4	9	extraembryonic membrane development	BP	1	MAP3K4,PAXIP1,HTRA1,FZD5	grey	VSMC_M10
GO:0002295	0.80	0.41	5	11	T-helper cell lineage commitment	BP	1	TNFSF18,STAT3,TBX21,BATF,IL6R	grey	VSMC_M10
GO:1900227	0.80	0.43	4	9	positive regulation of NLRP3 inflammasome complex assembly	BP	1	ATAT1,TLR4,MYD88,DDX3X	grey	VSMC_M10
GO:0048266	0.80	0.41	5	11	behavioral response to pain	BP	1	TSPO,P2RX2,P2RX3,VWA1,TRPV1	grey	VSMC_M10
GO:0043094	0.80	0.34	11	23	cellular metabolic compound salvage	BP	1	MTAP,PRTFDC1,APIP,AMPD3,ENOPH1,AMPD1,ADK,UCK1,FUK,NAPRT,UPP1	grey	VSMC_M10
GO:0000737	0.80	0.35	10	21	DNA catabolic process, endonucleolytic	BP	1	HSF1,FBH1,FOXL2,DNASE2,PAM16,DNASE1,DFFB,DNASE1L1,DNASE1L2,NMNAT1	grey	VSMC_M10
GO:1904064	0.80	0.26	51	103	positive regulation of cation transmembrane transport	BP	1	STAC3,WNK2,CACNB2,STAC,GLRX,KCNJ11,IFNGR2,FR,TESC,ANO6,KCNE2,PKD2,KCNIP2,RYR2,FAM173B,KCNJ2,ANK2,GPER1,AGT,ACE2,SLC9A1,CASQ1,NTSR1,NOS1AP,CEMIP,HTT,PINK1,ATP1B1,KCNA1,HAP1,WNK3,STAC2,ATP1B2,NLGN3,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,CCL2,PDPK1,P2RX1,RNF207,AMIGO1,LCN2,MIR21,DMD,JPH2,KCNH2,THY1	grey	VSMC_M10
GO:0009158	0.80	0.39	6	13	ribonucleoside monophosphate catabolic process	BP	1	DPYS,GDA,NT5E,AMPD3,UPB1,UPP1	grey	VSMC_M10
GO:0006919	0.80	0.29	28	57	activation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	BAK1,SLC1A1,NOD1,CASP8AP2,TNFSF15,HSPE1,HIP1R,ROBO1,DIABLO,SENP1,NKX3-1,F2R,PIDD1,LCK,PDCD6,EGLN3,MAPT,CTSH,MUL1,BCL2L13,NGFR,SMAD3,S100A8,P2RX1,RPS27L,CASP8,ACER2,CRADD	grey	VSMC_M10
GO:1904925	0.80	0.39	6	13	positive regulation of autophagy of mitochondrion in response to mitochondrial depolarization	BP	1	PRKN,OPTN,PINK1,MUL1,MFN2,VPS13C	grey	VSMC_M10
GO:0009125	0.80	0.38	7	15	nucleoside monophosphate catabolic process	BP	1	DPYS,GDA,NT5E,AMPD3,UPB1,NT5M,UPP1	grey	VSMC_M10
GO:0003197	0.80	0.30	19	40	endocardial cushion development	BP	1	SOX9,TGFBR2,JAG1,ROBO1,ROBO2,TBX5,RBM24,TGFB2,SNAI1,BMPR1A,RBPJ,TMEM100,TBX2,ISL1,FOXF1,ENG,ACVRL1,NOG,HEY2	grey	VSMC_M10
GO:0032310	0.80	0.41	5	11	prostaglandin secretion	BP	1	ABCC4,MAP2K6,PLA2G4A,NOS2,PTGES	grey	VSMC_M10
GO:0044848	0.80	0.43	4	9	biological phase	BP	1	FERMT1,SYCP2L,TGFB2,WNT5A	grey	VSMC_M10
GO:0019216	0.80	0.24	128	251	regulation of lipid metabolic process	BP	1	ORMDL2,PIP4K2C,AGAP2,CYP27B1,AVIL,PPARA,TSPO,PTK2,GOLM1,PLA2G6,TTC39B,TEK,KIT,PRKCE,MBOAT7,FPR2,NR1H2,LPIN1,DKKL1,APOB,FGF21,SPHK2,MTMR2,PIP4K2A,SOX9,OPA3,ABHD5,RUBCNL,APOC1,DNAJC15,PRKAG2,SLC22A13,PIBF1,ALK,AKT2,NR1D2,PANK2,PDK1,SIRT3,FLT1,NR1H4,TRIB3,CYP7A1,ASAH1,ABHD6,DKK3,CHRM5,MTMR9,FBXW7,SORBS1,EPHX2,PTK2B,NR1H3,FITM2,ORMDL1,HSD17B13,ERLIN1,NOD2,PRMT3,LONP2,SIRT4,GPLD1,IRS1,LPCAT1,SIK1,CPT1A,ZBTB20,ADRA2A,FMO5,SNAI1,SORL1,GPER1,ABCB11,AGT,FGR,LPGAT1,CERS2,PPP2R5A,MTMR3,RUBCN,MLXIPL,PIK3IP1,SCAP,APOD,POR,PDK3,CREB1,ACADL,TYSND1,LPCAT3,GNB3,WNT4,FGFR3,SLC27A1,STAT5B,DAGLB,ACADVL,GPS2,THRA,FGFR4,DGKQ,CD19,LDLR,BCL11B,ASXL3,NCOR1,CD74,SREBF1,C3,MTMR1,ABCA3,ABCA7,VAV3,MLYCD,GFI1,DAB2IP,MIR27B,MIR27A,BSCL2,FABP5,LDLRAP1,CNEP1R1,C1QTNF2,STARD4,INSIG2,CCDC3,FGF1,DNAJC19	grey	VSMC_M10
GO:1903541	0.80	0.37	7	15	regulation of exosomal secretion	BP	1	VPS4B,PRKN,CHMP2A,SDCBP,RAB7A,ATP13A2,VPS4A	grey	VSMC_M10
GO:0060442	0.80	0.43	4	9	branching involved in prostate gland morphogenesis	BP	1	ESR1,FRS2,HOXA13,NKX3-1	grey	VSMC_M10

GO:0042278	0.80	0.34	11	23	purine nucleoside metabolic process	BP	1	OARD1,MTAP,GNMT,GDA,ENPP4,NT5E,PRTFDC1,AHCY,DGUOK,ADK,PEMT	grey	VSMC_M10
GO:0010506	0.80	0.24	136	268	regulation of autophagy	BP	1	PIP4K2C,EPM2A,PRKN,RNF5,TSPO,AL096711.2,EXOC4,MAPK15,NRBP2,TFEB,FBXO7,DCAF12,SPTLC1,GAPDH,ATP6V1E2,NOD1,RRAGD,MET,ATP6V1C2,VPS35,SCOC,FOXO3,MFSD8,SESN3,PIP4K2A,ATP6V0E2,FBXL2,PLK3,OPTN,RALB,ATP6V0B,KDM4A,SNX5,USP36,SIRT2,RPTOR,TMEM173,FEZ2,DCN,ULK1,ATP6V1H,TRIB3,PLK2,DEPP1,DRAM1,PIK3CB,CASP3,MTMR9,FBXW7,HTRA2,CSNK2A2,RIPK2,TPCN1,WDR41,TP53INP1,NOD2,LZTS1,ATP6V1B2,DNM1L,SEC22B,CISD2,TMEM39A,DHRSX,GPR137B,USP30,USP13,ATG16L1,SH3BP4,MCL1,BAG3,CISD1,MTMR3,RUBCN,IL10RA,SNX6,SNX32,FZD5,MAPT,TAB3,VPS26A,ABL2,TBC1D14,GPR137,HTT,ATP6V0A1,PINK1,STAT3,TBC1D25,PIM2,RAB8A,ATP13A2,PHF23,ATP6V1D,VPS13D,RRAGB,OSBPL7,VPS13C,DAPK2,MAPK3,AC138894.1,HAX1,LARP1,KEAP1,NPC1,RMC1,SMCR8,CDK5R1,SREBF1,LEPR,ERCC4,CLEC16A,TICAM1,MTM1,ATP6V0C,IKBKG,PARK7,GPSM1,GNAI3,KIAA1324,TSC1,SH3GLB1,MIR199A1,TRIM68,TRIM34,BNIP3L,TRIM65,IRGM,TIGAR,ACER2,DDIT3,DRAM2,CPTP,BCL2L11,HSPB8,CAPNS1,RNF152	grey	VSMC_M10
GO:1990440	0.80	0.41	5	11	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	BP	1	ATF4,CREB3L3,HSPA5,DDIT3,CEBPB	grey	VSMC_M10
GO:0048638	0.80	0.24	130	257	regulation of developmental growth	BP	1	NEDD4L,LRP1,SEMA6A,GLI1,RAB21,STK3,RIMS2,PRKN,PPARA,FSTL4,PTCH1,PLXNA4,MAPK14,CPNE5,PI16,PIM1,SMO,SRF,SEMA4D,SEMA4C,RIMS1,RTN4,RUFY3,EPHA7,NRCAM,GOLGA4,MEGF8,CPNE9,TGFBR2,MKKS,SYT1,PLCB1,SLC23A2,DUSP6,SEMA3D,SPART,SEMA3A,ULK1,PRKDC,RYK,TTL,PLS1,MEF2C,SEMA4F,IL7,HTRA2,CELF1,TLL2,DPYSL2,NKX6-1,TBX5,ZFYVE27,FTO,SEMA3G,SPP1,STK4,CYFIP1,SEMA4G,NKD1,JARID2,IGF2,BDNF,KIAA0319,SLC6A3,SEMA3F,GPAM,HLX,ADNP,DISC1,ACTN3,KCNK2,CDKL5,CDKN1B,YBX3,WNT3,CREB1,DUSP10,MAPT,SEMA6D,TNR,FN1,SAV1,MYOZ1,GDF15,FGFR3,MUL1,STAT3,MAPK1,STAT5B,BMPR1A,RBPJ,SOX15,SEMA4A,TRIM46,NDEL1,WWC1,RAB11A,NTN1,DNM2,TBX2,YY1,SIN3A,TRPV2,INSR,GATA6,CDK5R1,RAI1,GHR,L1CAM,ARHGAP4,GAMT,PLXNA3,BARHL2,MIR199A1,MIR222,MIR25,NOG,WNT5A,BASP1,DIO3,POU3F2,FXN,CACNG7,SIX1,RGS4,PLAC8,BCL2L11,HEY2,OLFM1,WNT2	grey	VSMC_M10
GO:0030204	0.80	0.33	12	26	chondroitin sulfate metabolic process	BP	1	NDNF,CHPF2,CSGALNACT1,DCN,HYAL1,CHST3,SPOCK2,CHST7,CHST12,IDUA,B3GALT6,CHSY3	grey	VSMC_M10
GO:0060487	0.80	0.37	7	15	lung epithelial cell differentiation	BP	1	SOX9,FOXJ1,CREB1,SAV1,THRA,RBPJ,GATA6	grey	VSMC_M10
GO:0002315	0.80	0.43	4	9	marginal zone B cell differentiation	BP	1	MFNG,PTK2B,CDH17,DOCK10	grey	VSMC_M10
GO:0006875	0.80	0.23	195	381	cellular metal ion homeostasis	BP	1	SLC39A5,NEDD4L,LRP1,ESR1,SLC12A2,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,TMPRSS6,SLC39A4,STEAP2,SLC25A27,SLC1A1,S1PR3,PRKCE,TNNI3,FPR2,IBTK,LPAR1,SLC31A2,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,ATP1A3,ACKR2,SLC24A3,C1QTNF1,TMTC4,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,CCKBR,HPX,RASA3,NCOA4,MICU3,IL1A,IMMT,C19orf12,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,PKD2,CASQ2,MCUR1,CD40,RYR2,SLC41A1,RAP1GDS1,TRPM1,SPPL3,LCK,KCNJ2,TESMIN,TRPV4,SLC30A10,TCIRG1,GNA13,ISCU,CMKLR1,MCUB,HJV,UBASH3B,DISC1,ANK2,GPER1,TRPM8,PDZD8,AGT,ATP1A2,SLC9A1,CASQ1,NTSR1,FZD9,TMCO1,PTH1R,SLC30A4,FIS1,CEMIP,ABL2,CDH23,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,ABCB6,TRPM7,ATP1B1,CD38,KCNMA1,ATP13A2,FTH1,HAP1,DLG4,CYB561A3,ATP1B2,FAM155B,PSEN1,CACNA1A,AC138894.1,ATP2A1,CD19,SMAD3,NOX5,CALM1,S100A8,PRKCB,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,C7,PTGER4,SLC25A23,MAIP1,TMEM199,SLC46A1,NUBP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,ATP6AP1,GPR157,SYPL2,CYBA,JPH3,ATP2C2,SLC30A7,FRRS1,LCN2,MCOLN3,PTGFR,MIR199A1,KCNK3,DMD,MT1X,GPR35,NOL3,CHRNA10,CCR10,JPH2,SLC22A17,THY1,WNT5A,FXN,FTL,DDIT3,SCO1	grey	VSMC_M10
GO:0043031	0.80	0.40	5	11	negative regulation of macrophage activation	BP	1	CST7,NR1H3,CD200,SYT11,LDLR	grey	VSMC_M10
GO:0010561	0.80	0.40	5	11	negative regulation of glycoprotein biosynthetic process	BP	1	AGO2,HBEGF,SLC2A10,ABCA7,ACER2	grey	VSMC_M10
GO:0022602	0.80	0.31	15	32	ovulation cycle process	BP	1	ESR1,GDF9,FOXO3,ARRB1,CASP3,ROBO2,ADAMTS1,BMPR1B,GAS2,MAP2K6,TGFB2,PTPRN,STAT5B,HSPA5,EREG	grey	VSMC_M10
GO:0071526	0.80	0.30	18	38	semaphorin-plexin signaling pathway	BP	1	SEMA6A,PLXNA4,SEMA4D,SEMA4C,MET,PLXNA1,SEMA3D,PLXNC1,SEMA3A,HAND2,SEMA4F,SEMA3G,SEMA4G,SEMA3F,FARP2,SEMA6D,SEMA4A,PLXNA3	grey	VSMC_M10
GO:0045471	0.80	0.27	43	87	response to ethanol	BP	1	FECH,PPARA,BAK1,USP46,CAT,PRKCE,TNC,SETD7,HDAC2,DNMT3A,SLC23A2,CYP7A1,HPGD,PTK2B,TP53INP1,ADCY7,SLC6A3,CCND1,CPT1A,CBL,ACTC1,EPS8,MGMT,STAT3,SLC2A4,CHRNB2,S100A8,CCL7,SREBF1,OXCT1,ABAT,SDF4,NQO1,MT-CYB,RHOA,SETDB1,CASP8,BGLAP,PEMT,CLDN1,EEF1B2,RGS4,CRH	grey	VSMC_M10
GO:0030500	0.80	0.28	30	62	regulation of bone mineralization	BP	1	CYP27B1,OSR2,OMD,PTN,TRPM4,OSR1,SOX9,ACVR2B,ACVR2A,KL,ADGRV1,MEF2C,P2RX7,PTK2B,BMP2K,ANO6,TFAP2A,BMPR1B,SGMS2,ACTN3,TXLNG,FZD9,SRGN,BCOR,ANKH,WNT4,BMPR1A,SMAD3,RFLNB,BGLAP	grey	VSMC_M10
GO:0097049	0.80	0.43	4	9	motor neuron apoptotic process	BP	1	SLC1A1,ADARB1,KCNB1,FADD	grey	VSMC_M10

GO:1902513	0.80	0.43	4	9	regulation of organelle transport along microtubule	BP	1	CNIH2,HAP1,TRIM46,BORCS5	grey	VSMC_M10
GO:0043587	0.80	0.43	4	9	tongue morphogenesis	BP	1	INTU,HDAC2,HDAC1,SIX1	grey	VSMC_M10
GO:0021696	0.80	0.32	13	28	cerebellar cortex morphogenesis	BP	1	GLI1,AGTPBP1,SMO,WHRN,GLI2,FAIM2,LDB1,TTC21B,SPTBN2,MAP2K1,LHX1,GRID2,CEND1	grey	VSMC_M10
GO:0051640	0.80	0.23	229	447	organelle localization	BP	1	VPS4B,MYO1A,STX7,AP3S1,KIF5A,PRKN,KIF3A,UBE2B,FAM91A1,TSNARE1,EXOC4,MAPK15,AGTPBP1,SUN2,COPG2,RAC2,TFEB,MYH9,PEX1,SCFD2,KIT,BICD2,CHMP2A,NLRP5,LRPPRC,STX17,BRSK1,ALB,XPO1,TRAPPC12,PLEK,YWHAZ,CDK5RAP2,BVES,STARD3NL,CCDC155,MGARP,PPFIA3,WASF1,SPHK2,SPRY1,BBS7,KIF3C,ARHGAP21,RAB10,COPG1,MYO7B,SYTL2,CLASP2,NECTIN2,GAB2,MLH1,LLGL2,RALB,UNC13D,PIBF1,MYO7A,SPRY2,HOOK3,PIP4P1,AP3M2,KIF5C,MKKS,SYT1,TMEM106B,LIN7A,CEP290,TMEM230,CHAMP1,STX2,NSFL1C,SNPH,MOS,TTL,KIF3B,ARMC1,FER,CHMP2B,CHMP4C,SDAD1,MCPH1,KATNB1,RASGRP1,ARFGAP2,SLIT1,EXOC6B,SYNJ1,OPA1,AP3B1,CHMP7,VPS18,DTNBP1,KIF13A,GBF1,BICDL1,KLHL12,DNM1L,AC112128.1,TRIP11,PEF1,TCIRG1,PDCD6,SNAP23,MARK1,MFN1,CFL1,KCNB1,SHROOM2,AP1AR,PDZD8,LAT2,SPO11,FGR,CBL,NOP9,MLPH,RAB17,STX1A,SNX4,CNIH2,STX6,KLC2,LIMK2,TANC2,DLG1,NSF,TBCCD1,SPG11,MAPT,BLOC1S6,MAJIN,ITGA4,MOSPD3,MAP4K2,MREG,PDCD10,HTT,PTGDR,KXD1,RAB3A,MARK2,PINK1,IFFO1,MUL1,SYN1,UXT,SNAP29,AP3M1,C12orf4,BHLHA15,STX5,KIF1C,RAB8A,SYNE2,HAP1,PSEN2,SLC2A4,RAB15,NLGN2,MFN2,SEPT1,KPNB1,STX1B,STX4,PEX14,PSEN1,SYT11,MSTO1,RAB8B,BORCS6,TMED10,TRIM46,NDEL1,AC138894.1,ATP2A1,RAB11A,LAT,NTN1,STX8,RAB3D,IL4R,CALM1,SYTL4,SNAPIN,S100A13,DNM2,VMP1,BTK,CLMN,AP1M2,STXBP2,MYO1D,C17orf75,PPP6C,MYO1F,DOCK7,DAB1,MYO5B,MTM1,TLE6,CLUH,BICDL2,PDPK1,PRKCZ,SAPCD2,ATP6AP1,IKBKG,TPGS1,DEF8,SPIRE2,CHMP1A,PSRC1,GPSM2,FOXF1,SPOUT1,STXBP1,FNBP1L,VPS4A,RIPOR1,FHOD1,UBB,BLOC1S3,O	grey	VSMC_M10
GO:0060390	0.80	0.32	13	28	regulation of SMAD protein signal transduction	BP	1	LRP1,SPTBN1,OVOL2,RBPMS,VEPH1,KIAA0319,SLC2A10,PBLD,BMPR1A,PARP1,CILP,TOB1,SH2B1	grey	VSMC_M10
GO:0098927	0.80	0.30	19	40	vesicle-mediated transport between endosomal compartments	BP	1	RAB21,WDR91,MTMR2,RAB7A,HOOK3,RAB5A,DNAJC13,FAM160A2,ANKRD27,SORL1,MAPK1,SNX12,MAPK3,HOOK2,MAP2K1,STX8,MYO1D,RILP,SNX16	grey	VSMC_M10
GO:0030730	0.80	0.38	6	13	sequestering of triglyceride	BP	1	PPARA,PLIN2,ABHD5,FITM2,FITM1,PLIN3	grey	VSMC_M10
GO:0030901	0.80	0.27	34	69	midbrain development	BP	1	FZD6,UQCRQ,CSNK1E,CKB,TTBK1,FZD1,KDM7A,SIRT2,RYK,FZD3,NDUFS3,NR4A2,SUDS3,COX6B1,INA,WNT3,CXCR2,PADI2,ACTB,TAF1,CALM1,SEC16A,ATP5PB,SYPL2,MAPKAP1,HSPA5,RHOA,WNT5A,BASP1,OTX1,YWHAH,PITX3,TAL2,WNT2	grey	VSMC_M10
GO:0045778	0.80	0.30	20	42	positive regulation of ossification	BP	1	OSR2,TOB2,PTN,OSR1,ACVR2B,ACVR2A,KL,ADGRV1,MEF2C,P2RX7,ANO6,TFAP2A,BMPR1B,TGFB2,ACTN3,FZD9,WNT4,BMPR1A,SMAD3,WNT5A	grey	VSMC_M10
GO:0042310	0.80	0.28	30	62	vasoconstriction	BP	1	ZDHHC21,EGFR,KEL,TRPM4,MKKS,ADRA1D,ADRA2B,HTR7,DOCK5,F2R,CHRM3,RAP1GDS1,ADRA2A,AGT,ACE2,ATP1A2,PER2,ADRA2C,ECE1,SMTNL2,CD38,HRH2,SCNN1B,ASIC2,P2RX1,MIR21,RHOA,HTR1D,FGA,KCNMB4	grey	VSMC_M10
GO:0072078	0.80	0.28	29	60	nephron tubule morphogenesis	BP	1	MYC,KLHL3,PTCH1,SMO,SIX2,OSR1,SOX9,GZF1,WNT11,PAX8,EYA1,FMN1,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,NOG,SIX1,FGF1	grey	VSMC_M10
GO:0030217	0.80	0.24	90	179	T cell differentiation	BP	1	HLA-DRA,TCF7,SRF,KIT,SLC46A2,RSAD2,IL4I1,IL15,ATG5,TRAF3IP2,BMI1,CLPTM1,GLI2,FOXJ1,TGFBR2,EOMES,NCKAP1L,FOXP1,PRKDC,SOX12,TOX,ZC3H8,IL1A,CAMK4,TMEM131L,IL7,RASGRP1,LMBR1L,RIPK2,AP3B1,SOX13,PKNOX1,LCK,TCIRG1,RABL3,HLX,FZD7,CD28,FCER1G,RUNX3,PATZ1,SP3,ADAM8,FZD5,DUSP10,BCL6,VSIR,RC3H1,TNFSF18,WNT4,LAG3,PPP3CB,STAT3,STAT5B,FOXP3,ZBTB1,CARD11,TBX21,SEMA4A,DOCK2,BATF,ZBTB7B,IL6R,IL4R,BCL11B,CD74,JAG2,NKAP,VAV1,LEPR,PTGER4,IL7R,PTPN2,SOCS1,DROSHA,DNAJA3,PRKCZ,TSC1,MIR21,RHOA,SOX4,MAFB,FADD,CD46,FGL2,TNFSF9,NHEJ1,ZFP36L2,PRR7,RC3H2	grey	VSMC_M10
GO:0009394	0.80	0.30	17	35	2'-deoxyribonucleotide metabolic process	BP	1	TBPL1,DPYS,GDA,NUDT15,MBD4,NUDT16,DGUOK,NUDT18,DTYMK,UPB1,ADK,NEIL1,NT5M,NTHL1,CMPK2,DCTD,UPP1	grey	VSMC_M10
GO:2000736	0.80	0.29	24	50	regulation of stem cell differentiation	BP	1	OCIAD1,PTN,TEAD2,SOX9,JAG1,EIF2AK2,PRKDC,TCF15,SOX6,TBX5,PRICKLE1,RBM24,TGFB2,YTHDF2,OSM,NFE2L2,STAT3,CDK12,SETD1A,ESRRB,GATA6,SP7,ZFP36L2,NKX2-5	grey	VSMC_M10
GO:0001941	0.80	0.31	16	34	postsynaptic membrane organization	BP	1	LRRC4,PTN,SLC7A11,NLGN4Y,SSH1,FZD9,NRXN2,DLG4,NLGN2,GPHN,CHRNB1,NLGN3,DNAJA3,RER1,CEL,MESD	grey	VSMC_M10
GO:0060837	0.80	0.43	4	9	blood vessel endothelial cell differentiation	BP	1	RBPJ,TMEM100,FOXJ2,HEY2	grey	VSMC_M10
GO:0046823	0.80	0.35	9	19	negative regulation of nucleocytoplasmic transport	BP	1	RAB23,FERMT1,PKIA,SUFU,CABP1,SP100,APOD,PARK7,TXN	grey	VSMC_M10
GO:0014066	0.80	0.26	42	86	regulation of phosphatidylinositol 3-kinase signaling	BP	1	ERBB3,RGL2,PTK2,NTRK2,TEK,KIT,ROR2,SEMA4D,CAT,EGFR,SOX9,FBXL2,DCN,FLT1,RASGRP1,NKX3-1,F2RL1,F2R,TGFB2,NCF1,EGF,HCLS1,GPER1,AGT,FGR,CBL,OSM,CD28,PIK3IP1,FN1,PTPN6,HAX1,INSR,CCL5,PIP5K1C,DAB2IP,MIR21,ENTPD5,STAMBP,C3orf58,HCST,PDGFD	grey	VSMC_M10

GO:0050708	0.80	0.24	101	200	regulation of protein secretion	BP	1	LRP1,SLC12A2,PRKN,PLA2G6,PICK1,RFX3,TFAP2B,PRKCE,HMGN3,BMP8A,RSAD2,NR1H2,EGFR,TLR4,TRPM4,GIPR,FRMD4A,LLGL2,APBB3,DPH3,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,IL1A,OSBP,ARNTL,VEGFC,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,ACVR1C,F2RL1,F2R,ZBED6,ADTRP,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,CPT1A,SLC9B2,TGFB2,ADRA2A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,PER2,STX1A,GLUL,SIDT2,SLC16A1,ADAM8,KLF7,TTN,IL12A,ENY2,ABCA12,MCU,PPP3CB,CD38,MPC2,ATP13A2,SYT7,NLGN2,TARDBP,STX4,TMED10,MYH10,SYTL4,GPR68,CCL5,SREBF1,ISL1,OXCT1,NOS2,ABAT,RPH3AL,NADK,BAIAP3,LRRC8A,MIR199A1,FGA,CHGA,SOX4,DPP4,CRH,DOC2B,UQCC2,PARD6A	grey	VSMC_M10
GO:0045064	0.80	0.40	5	11	T-helper 2 cell differentiation	BP	1	HLX,BCL6,BATF,IL4R,PRKCZ	grey	VSMC_M10
GO:0071692	0.80	0.23	138	271	protein localization to extracellular region	BP	1	LRP1,CANX,SLC12A2,RIMS2,PRKN,PLA2G6,COPG2,PICK1,RFX3,TFAP2B,SVBP,PRKCE,HMGN3,CYB5R4,BMP8A,PLEK,RSAD2,NR1H2,EGFR,TLR4,TRPM4,RAB10,COPG1,GIPR,FRMD4A,LLGL2,STEAP3,RAF1,APBB3,DPH3,SIRT3,SYT9,NR1H4,NDUFAF2,FAM3D,IL1A,OSBP,ARNTL,VEGFC,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,ACVR1C,F2RL1,F2R,ZBED6,DMTN,ADTRP,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,CPT1A,SLC9B2,TGFB2,ADRA2A,MON1A,TCIRG1,TCF7L2,KCNB1,PFKFB2,GPER1,RAB11FIP2,PER2,STX1A,GLUL,SIDT2,SLC16A1,ADAM8,KLF7,MIA3,BLOC1S6,CTAGE9,VGF,TTN,IL12A,TANGO2,ENY2,ABCA12,MCU,FBN1,PPP3CB,RAB3A,CAMK2G,PTPRN,CD38,MPC2,ILDR2,RAB8A,ATP13A2,SYT7,RAB15,NLGN2,CPLX1,TARDBP,STX4,RAB8B,TMED10,UBE2Q1,MYH10,SEL1L,RAB3D,SYTL4,GPR68,TVP23C,CCL5,SREBF1,ISL1,OXCT1,NOS2,TVP23A,ABAT,RPH3AL,NADK,BAIAP3,PARK7,LRRC8A,TANGO6,MIR199A1,FGA,BLOC1S3,CHGA,SOX4,DPP4,TMEM167A,CRH,NRROS,DOC2B,UQCC2,PARD6A	grey	VSMC_M10
GO:0072088	0.80	0.27	30	62	nephron epithelium morphogenesis	BP	1	MYC,KLHL3,PTCH1,SMO,SIX2,OSR1,SOX9,GZF1,WNT11,PAX8,EYA1,FMN1,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,NOG,SIX1,LIF,FGF1	grey	VSMC_M10
GO:2000009	0.80	0.42	4	9	negative regulation of protein localization to cell surface	BP	1	NEDD4L,GOPC,TAX1BP3,LEPROT	grey	VSMC_M10
GO:0015749	0.80	0.26	41	84	monosaccharide transmembrane transport	BP	1	SLC2A12,MAPK14,SLC25A27,GRB10,FGF21,BRAF,MFSD4B,SLC26A5,PRKAG2,AKT2,ASPSCR1,SLC23A2,TRIB3,PIK3R1,SORBS1,IRS1,SLC2A10,TERT,C2CD5,PEA15,NFE2L2,CLTCL1,SLC2A2,SLC27A1,SLC2A9,SLC2A4,RSC1A1,SLC5A2,SLC50A1,SLC5A11,PRKCB,INSR,YES1,C3,GPC3,INPP5K,SLC45A1,SLC2A6,TSC1,FABP5,ARPP19	grey	VSMC_M10
GO:0033148	0.80	0.42	4	9	positive regulation of intracellular estrogen receptor signaling pathway	BP	1	KMT2D,PARP1,MED1,PAGR1	grey	VSMC_M10
GO:0072203	0.80	0.42	4	9	cell proliferation involved in metanephros development	BP	1	MYC,PTCH1,OSR1,GPC3	grey	VSMC_M10
GO:0044650	0.80	0.42	4	9	adhesion of symbiont to host cell	BP	1	NECTIN2,GAS6,ACE2,LRRC15	grey	VSMC_M10
GO:2001169	0.80	0.37	7	15	regulation of ATP biosynthetic process	BP	1	PPARA,SPHK2,FAM173B,DNAJC30,PINK1,STAT3,PARP1	grey	VSMC_M10
GO:0046686	0.80	0.29	23	47	response to cadmium ion	BP	1	HSF1,KIT,CAT,MTF1,EGFR,ERCC1,PRNP,CYB5A,GPI,GSS,TERT,NCF1,DTYMK,CDKN1B,SORD,ABCB6,MAPK1,FOS,MAPK3,NPC1,JUN,MT-CYB,MT1X	grey	VSMC_M10
GO:0097084	0.80	0.42	4	9	vascular associated smooth muscle cell development	BP	1	EFEMP2,RAMP2,ENG,HEY2	grey	VSMC_M10
GO:0002292	0.80	0.28	24	50	T cell differentiation involved in immune response	BP	1	HLA-DRA,EOMES,FOXP1,RIPK2,HLX,FCER1G,BCL6,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,PTGER4,PRKCZ,TSC1,MIR21,CD46,FGL2,RC3H2	grey	VSMC_M10
GO:1904753	0.80	0.40	5	11	negative regulation of vascular associated smooth muscle cell migration	BP	1	MEF2C,GNA13,NFE2L2,MIR21,RHOA	grey	VSMC_M10
GO:0046470	0.80	0.28	27	55	phosphatidylcholine metabolic process	BP	1	PLA2G6,TMEM86B,MBOAT7,NR1H2,MBOAT2,APOC1,NR1H3,CDS1,GPLD1,LPCAT1,CHKA,ABHD4,PCYT1A,PLA2G4A,LPCAT3,PLA2G16,SLC27A1,LIPC,GDPD3,LDLR,ABHD3,PNPLA6,ABCA3,MECP2,PLA2G15,FABP5,PEMT	grey	VSMC_M10
GO:0060674	0.80	0.32	12	26	placenta blood vessel development	BP	1	OVOL2,SPINT1,PKD2,VASH2,FZD5,MAPK1,RBPJ,VASH1,MAP2K1,PKD1,HEY2,WNT2	grey	VSMC_M10
GO:0035019	0.80	0.31	15	32	somatic stem cell population maintenance	BP	1	MYC,KIT,SIX2,SOX9,RAF1,PAX8,PAX2,LDB1,SOX2,VPS72,RBPJ,SKI,SOX4,NOG,ZFP36L2	grey	VSMC_M10
GO:0032616	0.80	0.40	5	11	interleukin-13 production	BP	1	TNFRSF21,SPHK2,SCGB1A1,PRKCZ,TSLP	grey	VSMC_M10
GO:0032656	0.80	0.40	5	11	regulation of interleukin-13 production	BP	1	TNFRSF21,SPHK2,SCGB1A1,PRKCZ,TSLP	grey	VSMC_M10
GO:0034219	0.80	0.26	42	86	carbohydrate transmembrane transport	BP	1	SLC2A12,MAPK14,SLC25A27,GRB10,FGF21,BRAF,MFSD4B,SLC26A5,PRKAG2,AKT2,ASPSCR1,SLC23A2,TRIB3,PIK3R1,SORBS1,TMEM144,IRS1,SLC2A10,TERT,C2CD5,PEA15,NFE2L2,CLTCL1,SLC2A2,SLC27A1,SLC2A9,SLC2A4,RSC1A1,SLC5A2,SLC50A1,SLC5A11,PRKCB,INSR,YES1,C3,GPC3,INPP5K,SLC45A1,SLC2A6,TSC1,FABP5,ARPP19	grey	VSMC_M10

GO:0050767	0.80	0.23	144	285	regulation of neurogenesis	BP	1	LRP1,SEMA6A,RAB21,SNW1,TIAM2,TSPO,FSTL4,SYNGAP1,PLXNA4,NTRK2,SOX10,SMO,DAAM2,SRF,TTBK1,KIT,SEMA4D,SEMA4C,RTN4,RUFY3,EPHA7,PTN,EGFR,TRIM32,MYCN,PLXNA1,HDAC2,GOLGA4,MEGF8,KDM4A,XRCC2,NUMBL,POU4F1,SS18L2,HOOK3,BHLHE40,SIRT2,SEMA3D,SPART,PLXNC1,SEMA3A,ULK1,RYK,PLAG1,ANKRD27,FAIM,ROBO1,ROBO2,ARNTL,FZD3,SEMA4F,VEGFC,TLX2,CUX2,MME,RAPGEF2,TIAM1,SYNJ1,OPA1,NKX6-1,ZFYVE27,SPINT1,SEMA3G,ITPKA,SPP1,CYFIP1,SEMA4G,ZNF335,BDNF,RNF10,KIAA0319,NEURL1,DNM1L,HDAC1,PPP3CA,CAPRIN2,SEMA3F,DAG1,ADNP,YTHDF2,DISC1,SORL1,GPER1,CERS2,NFATC4,HES6,PER2,SS18L1,CDKL5,DLX1,WNT3,DUSP10,MAPT,SEMA6D,TNR,FN1,XRCC5,NIN,OBSL1,HAP1,EPHA4,BMPR1A,SPEN,TNFRSF1B,RGS14,PRPF19,PSEN1,SEMA4A,TRIM46,NDEL1,RAB11A,MAP2K1,NTN1,LDLR,PARP6,GPRASP2,BHLHB9,TRPV2,CDK5R1,DOCK7,MBD1,DAB1,LRP8,L1CAM,SKI,ARHGAP4,PLXNA3,SOX8,AMIGO1,FBXO31,MIR222,MIR125B1,FOXG1,GPR37L1,HOXB3,NOG,THY1,WNT5A,LIF,YWHAH,EFNB3,PITX3,HEY2,WNT2	grey	VSMC_M10
GO:0010637	0.80	0.42	4	9	negative regulation of mitochondrial fusion	BP	1	PRKN,DNM1L,MUL1,ADCK1	grey	VSMC_M10
GO:0002521	0.80	0.23	196	383	leukocyte differentiation	BP	1	NME1,AGER,HLA-DRA,IL5,TCF7,BAK1,XRCC6,TRIB1,MYC,TOB2,L3MBTL3,MAPK14,MFNG,HSF1,MYH9,FBXO7,SRF,CDK6,KIT,ROR2,NFIL3,IL11,MSH2,CD109,HOXA7,SLC46A2,RSAD2,IL4I1,TLR4,IL15,ATG5,OSTM1,TRAF3IP2,BMI1,CLPTM1,GAB2,GLI2,FOXJ1,POU4F1,IL15RA,KLF6,CMTM7,TGFBR2,EOMES,PLCL2,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,TRAF6,SOX12,TOX,ZC3H8,IL1A,CAMK4,CEBPA,PIK3R1,FBXW7,PTPRJ,TMEM131L,IL7,TPD52,PTK2B,RASGRP1,LMBR1L,RIPK2,CDH17,AP3B1,F2RL1,TESC,RIPK1,SOX13,TSPAN2,ITGB6,DCAF1,DOCK10,SH3PXD2A,PKNOX1,LRRK1,LCK,SLC9B2,TCIRG1,GPR137B,RABL3,PIAS3,HLX,ACIN1,TCTA,HCLS1,UBASH3B,SLAMF8,FZD7,HDAC4,CD28,FCER1G,RUNX3,FARP2,ZBTB46,PATZ1,FZD9,SP3,PPP2R3C,ADAM8,CREB1,FZD5,DUSP10,BCL6,SYVN1,BATF2,ITGA4,VSIR,RC3H1,ESRRA,PTPN6,GPR137,FBN1,TNFSF18,WNT4,LAG3,PPP3CB,LTBR,STAT3,STAT5B,INHA,TFE3,FOXP3,ZBTB1,PARP1,GPS2,CARD11,RBPJ,MED1,ANXA2,TBX21,PSEN1,SEMA4A,KAT7,DOCK2,FOS,BATF,ZBTB7B,IL6R,HAX1,CD19,IL4R,GPR68,BTK,BCL11B,YY1,CD74,CSF1R,PPARGC1B,JAG2,NKAP,VAV1,LEPR,PTGER4,EVI2B,IL7R,PTPN2,GPC3,JUN,SOCS1,DROSHA,DNAJA3,PRKCZ,ATP6AP1,TSC1,LRRC8A,MIR21,MIR125B1,RHOA,FSTL3,SOX4,MAFB,FADD,CD46,CASP8,CA2,DHRS2,BGLAP,SNX10,GLO1,FGL2,NRROS,TNFSF9,NHEJ1,LIF,ZFP36L2,CEBPB,PRR7,TNFSF13B,BATF3,RC3H2	grey	VSMC_M10
GO:0060675	0.80	0.28	25	52	ureteric bud morphogenesis	BP	1	MYC,PTCH1,SMO,SIX2,SOX9,GZF1,WNT11,PAX8,EYA1,FMN1,PKD2,PAX2,SALL1,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,SOX8,NOG,SIX1,FGF1	grey	VSMC_M10
GO:0032940	0.80	0.22	296	574	secretion by cell	BP	1	VPS4B,LRP1,CANX,RAB21,SNCAIP,SLC12A2,RIMS2,PRKN,GDF9,GRM4,LY6E,EXOC4,SYNGR1,NTRK2,PLA2G6,COPG2,PICK1,RAC2,MYH9,CHRNA3,CHRNA5,CRY1,STEAP2,APBA1,SCFD2,RFX3,KIT,TFAP2B,CHMP2A,NLRP5,SVBP,STX17,IL11,BRSK1,PRKCE,RIMS1,HMGN3,RIMS3,CYB5R4,PPT1,SCRN1,BMP8A,PLEK,RSAD2,NR1H2,EGFR,TLR4,VPS41,SDCBP,TRPM4,PPFIA3,LIN7B,SPHK2,NAPA,RAB7A,RAB10,COPG1,GIPR,CACNB2,SYTL2,CLASP2,FRMD4A,GAB2,LLGL2,RALB,STEAP3,GRIK5,UNC13D,RAF1,NAPB,ABCC4,C1QTNF1,ANK1,SYT1,RAB5A,LIN7A,APBB3,DPH3,AIMP1,NCKAP1L,SIRT3,STX2,SYT9,ADRA2B,SNPH,NR1H4,HCK,NDUFAF2,FAM3D,IL1A,PAX8,NR4A1,FER,OSBP,TRAPPC11,ARNTL,ERC2,SCG5,MEF2C,ASIC1,VEGFC,P2RY1,RASGRP1,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,EXOC6B,PFKM,SYNJ1,SLC8B1,NKX3-1,NKX6-1,ACVR1C,F2RL1,F2R,CRY2,VPS18,SPP1,ZBED6,LGI3,DMTN,ADTRP,DTNBP1,SYT8,GRM2,SIRT4,GPLD1,IRS1,CD200,DNM1L,HDAC1,PPP3CA,HYAL3,CPT1A,MAP2K6,TRPV4,SLC9B2,TGFB2,ADRA2A,MON1A,TCIRG1,TCF7L2,SNAP23,KCNB1,PFKFB2,GRK2,GPER1,RAB11FIP2,LAT2,AGT,FGR,CBL,SYTL1,PRSS12,PER2,OSM,STX1A,SNX4,NTSR1,PASK,SEPT2,BACE1,DNAJC5,GLUL,CSPG5,SIDT2,SLC16A1,ADAM8,KLF7,NSF,CREB1,MIA3,RAP1B,BLOC1S6,PLA2G4A,CTAGE9,VGF,TTN,IL12A,TANGO2,ENY2,ABCA12,NRXN2,CASK,MCU,ADRA2C,PNKD,PTGDR,PPP3CB,RAB3A,PINK1,SYN1,CAMK2G,SNAP29,EXOC5,PTPRN,CD38,C12orf4,MPC2,ILDR2,INHA,RAB8A,ATP13A2,HAP1,CPLANE2,SYT7,RAB15,RSC1A1,NLGN2,TNFRSF1B,SEPT1,WASHC3,CPLX1,TARDBP,STX1B,STX4,PSEN1,RAB25,ITGAM,SYT11,RAB8B,TMED10,CA	grey	VSMC_M10
GO:0009263	0.80	0.38	6	13	deoxyribonucleotide biosynthetic process	BP	1	TBPL1,DGUOK,DTYMK,ADK,CMPK2,DCTD	grey	VSMC_M10
GO:0070242	0.80	0.38	6	13	thymocyte apoptotic process	BP	1	BAK1,ZC3H8,ADAM8,EFNA1,WNT5A,BCL2L11	grey	VSMC_M10
GO:1901993	0.81	0.42	4	9	regulation of meiotic cell cycle phase transition	BP	1	MAPK15,TOPAZ1,MOS,OVOL1	grey	VSMC_M10
GO:0060907	0.81	0.42	4	9	positive regulation of macrophage cytokine production	BP	1	TLR4,SPON2,CD74,WNT5A	grey	VSMC_M10
GO:2000303	0.81	0.40	5	11	regulation of ceramide biosynthetic process	BP	1	ORMDL2,PLA2G6,SPHK2,SIRT3,ORMDL1	grey	VSMC_M10
GO:0007567	0.81	0.42	4	9	parturition	BP	1	HPGD,PLA2G4B,PTGFR,CRH	grey	VSMC_M10

GO:0008544	0.81	0.24	101	201	epidermis development	BP	1	GLI1,CYP27B1,FZD6,PPARA,PTCH1,SMO,ZDHHC21,IFT74,SOSTDC1,CD109,KLK14,HOXA7,MYCL,WHRN,GRHL1,EGFR,FUZ,GJB5,SFRP4,MYCN,NTF4,INTU,HDAC2,SOX9,ERCC2,ERCC3,PTCH2,GLI2,EVPL,IFT172,MYO7A,SCEL,OVOL2,SLC4A7,JAG1,LRTOMT,AP000812.5,MAFG,FERMT1,TFDP1,ASAH1,ACVR1B,FLNB,CASP3,PLS1,TRPC4AP,FZD3,USH1C,VDR,AP3B1,SRSF6,DSP,STK4,PPHLN1,LDB1,COL17A1,HDAC1,TGFB2,PTHLH,SNAI1,LAMB3,POU2F3,TGM1,KDF1,SFN,COL7A1,LAMA5,CLIC4,GRHL3,CST6,STRC,OVOL1,KLF7,PLOD3,H2AFY2,ABCA12,SAV1,GORAB,WAS,RBPJ,MED1,NGFR,MAP2K1,KEAP1,BCL11B,LAMA3,GATA6,TMEM132E,JAG2,AGPAT2,MCOLN3,MIR125B1,FABP5,WNT5A,POU3F2,DNASE1L2,ZBED2,YBX1,EREG,SGPP1,HEY2	grey	VSMC_M10
GO:0031272	0.81	0.40	5	11	regulation of pseudopodium assembly	BP	1	CDC42EP1,KIT,F2RL1,CDC42EP2,APC	grey	VSMC_M10
GO:0031274	0.81	0.40	5	11	positive regulation of pseudopodium assembly	BP	1	CDC42EP1,KIT,F2RL1,CDC42EP2,APC	grey	VSMC_M10
GO:0090649	0.81	0.40	5	11	response to oxygen-glucose deprivation	BP	1	DNM1L,CBL,BNIP1,TSC1,LCN2	grey	VSMC_M10
GO:0034063	0.81	0.32	11	24	stress granule assembly	BP	1	PUM2,YTHDF2,DDX6,YTHDF1,MAPT,DDX3X,PRRC2C,ATXN2L,UBAP2L,G3BP1,CIRBP	grey	VSMC_M10
GO:0010642	0.81	0.40	5	11	negative regulation of platelet-derived growth factor receptor signaling pathway	BP	1	LRP1,PTGIR,PTPRJ,APOD,PTPN2	grey	VSMC_M10
GO:0120163	0.81	0.29	21	44	negative regulation of cold-induced thermogenesis	BP	1	ATF4,ALDH1A1,NR1H2,TLR4,IL15,LAMA4,ACVR2B,PLCL2,ABHD6,ARNTL,NR1H3,ZNF423,MAP2K6,ACTN3,TFE3,RBPJ,PCTP,DOCK7,ACOT11,NOVA1,DDIT3	grey	VSMC_M10
GO:0097050	0.81	0.42	4	9	type B pancreatic cell apoptotic process	BP	1	SRSF6,RYR2,HDAC1,TCF7L2	grey	VSMC_M10
GO:0010612	0.81	0.40	5	11	regulation of cardiac muscle adaptation	BP	1	TRPC3,PPP3CA,SMAD3,MIR199A1,MIR25	grey	VSMC_M10
GO:1903242	0.81	0.40	5	11	regulation of cardiac muscle hypertrophy in response to stress	BP	1	TRPC3,PPP3CA,SMAD3,MIR199A1,MIR25	grey	VSMC_M10
GO:0009200	0.81	0.36	7	15	deoxyribonucleoside triphosphate metabolic process	BP	1	TBPL1,NUDT15,NUDT16,DGUOK,DTYMK,ADK,CMPK2	grey	VSMC_M10
GO:0002532	0.81	0.27	29	59	production of molecular mediator involved in inflammatory response	BP	1	PPARA,GPSM3,MAPK14,IL1R2,TLR4,MYD88,CHID1,NOD2,ADCY7,PDCD4,SNAP23,NCF1,SLAMF8,SNX4,APOD,DUSP10,STAT3,IL4R,BTK,PLD4,NOS2,TICAM1,P2RX1,MIR21,MIR222,C5orf30,MIR125A,IL17D,IL17B	grey	VSMC_M10
GO:0042073	0.81	0.30	16	34	intraciliary transport	BP	1	IFT74,DYNC2LI1,TTC26,IFT172,TTC21A,WDR60,TUB,KIF3B,IFT81,IFT52,TTC21B,TRAF3IP1,TTC30A,WDR19,IFT20,HSPB11	grey	VSMC_M10
GO:1901387	0.81	0.40	5	11	positive regulation of voltage-gated calcium channel activity	BP	1	STAC3,CACNB2,STAC,KCNE2,STAC2	grey	VSMC_M10
GO:0010248	0.81	0.42	4	9	establishment or maintenance of transmembrane electrochemical gradient	BP	1	BAK1,ATP1A3,ATP1A2,ATP1B1	grey	VSMC_M10
GO:0006833	0.81	0.40	5	11	water transport	BP	1	MIP,AQP1,AQP11,INPP5K,PDZD3	grey	VSMC_M10
GO:0009164	0.81	0.36	7	15	nucleoside catabolic process	BP	1	APOBEC3H,GDA,ENPP4,CDADC1,AHCY,UPB1,UPP1	grey	VSMC_M10
GO:0051974	0.81	0.42	4	9	negative regulation of telomerase activity	BP	1	POT1,MEN1,PIF1,TEN1	grey	VSMC_M10
GO:0071470	0.81	0.29	19	40	cellular response to osmotic stress	BP	1	TSPO,XRCC6,AKR1B1,AQP1,OXSR1,CASP3,PKD2,TRPV4,SCN2A,YBX3,DDX3X,XRCC5,MICU1,SLC2A4,WNK3,AC138894.1,LRRC8E,SLC25A23,LRRC8D	grey	VSMC_M10
GO:0001890	0.81	0.25	58	117	placenta development	BP	1	CYP27B1,STK3,MAP3K4,CCDC134,RSPO3,PTK2,MAPK14,MDFI,TFEB,EPAS1,PTN,GJB5,PRDX3,OVOL2,EOMES,SPINT2,DCN,CEBPA,MME,VDR,STC1,SPINT1,SPP1,PKD2,STK4,IGF2,SNAI1,ARNT,VASH2,HTRA1,DEDD,SP3,CDKN1B,SETD2,FZD5,MEN1,CTSV,MAPK1,RBPJ,MED1,SOX15,DLX3,MAPK3,VASH1,CITED1,ALKBH1,MAP2K1,EPOR,PKD1,BSG,KRT19,CASP8,TCF23,GRB2,LIF,CEBPB,HEY2,WNT2	grey	VSMC_M10
GO:0150115	0.81	0.25	46	95	cell-substrate junction organization	BP	1	LRP1,PTK2,TEK,TLN1,ITGB1BP1,IQSEC1,CLASP2,ACTG1,ARHGEF7,PTPRA,FAM107A,PIK3R1,FMN1,SORBS1,PTPRJ,PTK2B,DMTN,LDB1,SLK,COL17A1,COL16A1,AJUBA,ARHGAP6,SLC9A1,ACTN3,WHAMM,LAMC1,APOD,TRIP6,FN1,WNT4,VCL,RAB8B,TAOK2,SMAD3,CORO2B,BCAS3,CAMSAP3,PDPK1,TSC1,RHOA,ACVRL1,PEAK1,THY1,LAMTOR2,DUSP22	grey	VSMC_M10
GO:0007095	0.81	0.30	15	32	mitotic G2 DNA damage checkpoint signaling	BP	1	MRNIP,TRIM39,BRSK1,NBN,ABRAXAS1,DONSON,TAOK3,SYF2,UIMC1,FOXO4,TAOK2,FOXN3,TAOK1,FZR1,BRCC3	grey	VSMC_M10
GO:0070141	0.81	0.39	5	11	response to UV-A	BP	1	OPN1SW,EGFR,MME,CCND1,MMP3	grey	VSMC_M10
GO:0014820	0.81	0.42	4	9	tonic smooth muscle contraction	BP	1	MKKS,AGT,CD38,SCNN1B	grey	VSMC_M10
GO:1903543	0.81	0.38	6	13	positive regulation of exosomal secretion	BP	1	VPS4B,CHMP2A,SDCBP,RAB7A,ATP13A2,VPS4A	grey	VSMC_M10
GO:0051642	0.81	0.31	14	30	centrosome localization	BP	1	SUN2,BICD2,INTS13,DLG1,TBCCD1,NIN,SYNE2,NDEL1,IFT20,NUBP1,GPSM2,SPOUT1,FHOD1,DYNC1LI2	grey	VSMC_M10
GO:0090343	0.81	0.38	6	13	positive regulation of cell aging	BP	1	CDKN2A,PAWR,KRAS,YPEL3,MIR21,MIR22	grey	VSMC_M10
GO:0110148	0.81	0.24	63	127	biomineralization	BP	1	CYP27B1,OSR2,PPARA,ATF4,ROR2,OMD,CNNM4,KLK4,PTN,ITGB1BP1,TRPM4,OSR1,SOX9,ERCC2,SLC4A2,ACVR2B,WNT11,SLC24A3,ACVR2A,KL,GAS6,ADGRV1,MEF2C,P2RX7,PTK2B,BMP2K,ANO6,SPP1,TFAP2A,ITGB6,BMPR1B,FBXL15,SBDS,PTHLH,TCIRG1,FAM20A,FAM20C,SGMS2,AXIN2,AMELX,FGR,ACTN3,TXLNG,FZD9,PTH1R,SRGN,BCOR,ANKH,ZBTB40,WNT4,ALPL,FGFR3,MMP13,BMPR1A,SMAD3,GPC3,RFLNB,BGLAP,MINPP1,SNX10,CCDC154,CEBPB,HEY2	grey	VSMC_M10
GO:0010745	0.81	0.42	4	9	negative regulation of macrophage derived foam cell differentiation	BP	1	PPARA,NR1H2,NR1H3,ABCA5	grey	VSMC_M10
GO:0010968	0.81	0.42	4	9	regulation of microtubule nucleation	BP	1	HSPA1B,EML2,ARHGEF7,MECP2	grey	VSMC_M10
GO:0090481	0.81	0.39	5	11	pyrimidine nucleotide-sugar transmembrane transport	BP	1	SLC35A1,SLC35A4,SLC35A5,SLC35A2,SLC35B1	grey	VSMC_M10
GO:0055015	0.81	0.42	4	9	ventricular cardiac muscle cell development	BP	1	FHL2,ATG5,NKX2-5,HEY2	grey	VSMC_M10
GO:0031279	0.81	0.30	15	32	regulation of cyclase activity	BP	1	MAPK14,GUCA1B,GABBR2,RAF1,ADGRV1,ORAI1,CAP2,GRM2,MAPK3,CALM1,NOS2,PALM,GNAI3,CAP1,PDZD3	grey	VSMC_M10
GO:0060966	0.81	0.29	20	42	regulation of gene silencing by RNA	BP	1	ZC3H10,ESR1,AGO2,TNRC6B,XPO5,EGFR,MYCN,PUM2,BCDIN3D,EIF4E2,RIPK1,PPP3CA,TERT,AJUBA,DDX6,EIF4ENIF1,STAT3,MAP2K1,NCOR1,FMR1	grey	VSMC_M10
GO:0002679	0.81	0.39	5	11	respiratory burst involved in defense response	BP	1	HCK,NCF1,SLAMF8,DUSP10,MPO	grey	VSMC_M10
GO:1900247	0.81	0.42	4	9	regulation of cytoplasmic translational elongation	BP	1	DPH2,DPH3,DPH1,AARS	grey	VSMC_M10

GO:1903975	0.81	0.39	5	11	regulation of glial cell migration	BP	1	LRP1,TIAM1,CERS2,ATP1B2,MIR222	grey	VSMC_M10
GO:0006360	0.81	0.28	24	50	transcription by RNA polymerase I	BP	1	BAZ2A,MARS,ATF4,IPPK,ERCC2,ERCC3,POU4F1,SIRT7,ERCC6,RASL11A,POLR1A,HEATR1,DEDD,TAF1A,H2AFY2,DDX11,PHF8,TAF1,TCOF1,RRN3,TTF1,TAF1C,POLR2K,GTF2H5	grey	VSMC_M10
GO:0050673	0.81	0.22	161	316	epithelial cell proliferation	BP	1	NME1,GLI1,TNFAIP3,ESR1,FRS2,RIDA,OSR2,MTSS1,MYC,PTCH1,C6orf89,SMO,IFT74,TEK,CDK6,KIT,DLX5,PDCL3,CD109,RTN4,EMC10,EPGN,AREG,BMPER,TGFA,PTN,ITGB1BP1,EGFR,OSR1,INTU,FOXE3,C5AR2,C5AR1,PRKD2,SOX9,AQP11,IFT172,SCN5A,WDR48,THAP1,OVOL2,ACVR2A,RPTOR,PURA,FERMT1,AIMP1,PRKDC,FLT1,SDR16C5,CYP7B1,NR4A1,ATP5F1A,EYA1,ROBO1,FBXW7,MEF2C,PEX2,VEGFC,VDR,NKX3-1,NKX6-1,LOXL2,AGGF1,SERPINB1,SRSF6,IFT52,RREB1,PAX2,NOD2,IGF2,FAP,HYAL1,CCND1,TGFB2,SULF2,TCF7L2,PDCD6,PRKX,EGF,SOX2,ARNT,TGM1,KDF1,SFN,VASH2,FZD7,RPS6KA1,HTRA1,RUNX3,GLUL,SIDT2,LAMC1,CDKN1B,DLG1,DUSP10,STOX1,ITGA4,MEN1,IL12A,CASK,SAV1,PDCD10,GPBAR1,RAP1GAP,STAT3,PTPRN,MAPK1,WDR13,MAGED1,IGFBP4,BMPR1A,MED1,ALDH1A2,SYNJ2BP,PSEN1,NGFR,PGF,VASH1,MAP2K1,SMAD3,MAP2K5,NOX5,TNMD,BCL11B,CCL2,ISL1,SUZ12,GPC3,PDPK1,WDR77,CYBA,MARVELD3,DAB2IP,ESRP2,MIR29A,MIR21,MIR222,MIR23A,MIR125B1,MIR22,MIR27B,MIR24-1,MIR27A,SERPINB5,LAMB1,ACVRL1,TINF2,ZNF580,NOG,CLDN1,WNT5A,SIX1,ZNF304,RGCC,HRAS,BCL2L2,CEBPB,EREG,FGF1,WNT2,COL8A2	grey	VSMC_M10
GO:0002449	0.81	0.24	80	159	lymphocyte mediated immunity	BP	1	CD226,STX7,AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,PRDX1,EXOSC3,MSH2,RSAD2,IL4I1,TRPM4,TRAF3IP2,HMCES,ERCC1,NECTIN2,PVR,MLH1,UNC13D,MYD88,SLC22A13,FOXJ1,PAXIP1,JAG1,SHLD1,NCKAP1L,HPX,IRF7,TRAF6,GAPT,SLA2,RASGRP1,NBN,NOD2,CD40,CD96,TCIRG1,DENND1B,CD28,FCER1G,RNF168,CADM1,FZD5,BCL6,CTSH,IL12A,PTPN6,LAG3,PPP3CB,STAT5B,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,TBX21,BATF,CD19,IL4R,BTK,CD74,FBXO38,VAV1,C7,C3,IL7R,SUPT6H,CRK,PRKCZ,TRAF2,AP1G1,BCL10,FADD,CD46,FCER2,RNF8,CD70,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0007492	0.81	0.27	28	59	endoderm development	BP	1	ITGA7,EOMES,MMP15,RTF1,LDB1,HDAC1,SOX2,LAMB3,COL7A1,ITGB5,LAMC1,SETD2,ITGA4,FN1,COL5A2,LEO1,BMPR1A,SMAD3,LHX1,LAMA3,GATA6,COL5A1,DUSP2,LAMB1,HOXC11,NOG,DUSP1,DUSP4	grey	VSMC_M10
GO:0000209	0.81	0.23	102	203	protein polyubiquitination	BP	1	NEDD4L,TNFAIP3,PRKN,RNF5,SKP1,UBE2B,RNF217,RNF146,KLHL3,RNF20,UBE3D,PELI1,HECW1,TRIM32,TRAF1,HACE1,TRAF3IP2,KBTBD6,UBE2E2,UBE2O,UBE3C,UBE2E1,NMI,TPP2,NHLRC3,RNF14,UBOX5,TRIM3,TRAF6,TRIM44,MARCH8,ERCC8,SPSB4,ZFP91,UBE2L6,TRIM2,ANAPC5,ANAPC7,DDB2,AMFR,MARCH7,TTC3,NOD2,MAGEL2,NHLRC1,RNF144B,DZIP3,HECW2,KLHL42,RNF115,RNF114,DTX3L,ARIH2,RNF26,CBL,TRAF5,PELI3,RNF168,SYVN1,DDX3X,RC3H1,KLHL20,RNF4,TMEM129,MUL1,PPIL2,RNF167,RNF216,GPS2,PRPF19,ANAPC4,RNF111,NPEPPS,AREL1,TAF1,UBE2Q1,OTUB2,RNF165,TRAF3,FBXO22,UBE2Q2,FBXO38,RNF135,MGRN1,FZR1,TRAF2,RNF126,WWP2,TRIM68,TRIM34,UBE2G1,RNF8,UBE2QL1,UBE2N,UBE2U,CDC26,DDA1,UBE2G2,UBE2R2,RNF152,UBE2D1,RC3H2	grey	VSMC_M10
GO:0045682	0.81	0.28	24	50	regulation of epidermis development	BP	1	CYP27B1,PTCH1,CD109,HOXA7,MYCL,GRHL1,SFRP4,MYCN,PTCH2,OVOL2,MAFG,VDR,SRSF6,KDF1,SFN,KLF7,H2AFY2,ABCA12,MED1,KEAP1,MIR125B1,ZBED2,SGPP1,HEY2	grey	VSMC_M10
GO:2000291	0.81	0.42	4	9	regulation of myoblast proliferation	BP	1	SOX15,ZNF609,GATA6,MIR199A1	grey	VSMC_M10
GO:1904375	0.81	0.25	53	107	regulation of protein localization to cell periphery	BP	1	LRP1,STX7,STAC3,GOPC,EPB41L2,PRKCE,SPTBN1,EGFR,STAC,PRNP,LYPLA1,PIK3R1,PLS1,SORBS1,KCNJ11,NHLRC1,PPFIA1,DAG1,EPB41,GPER1,RAB11FIP2,CIB1,AP2M1,PPP2R5A,DLG1,LRRC15,LZTFL1,ZDHHC8,CNPY4,GRIPAP1,CNST,ACTB,IQSEC2,RSC1A1,WNK3,STAC2,STX4,ITGA3,AC138894.1,RAB11A,STX8,ARHGAP44,EFCAB7,PDPK1,PRKCZ,RER1,ARHGEF16,SAPCD2,GPSM2,VPS4A,LDLRAP1,HRAS,MRAP2	grey	VSMC_M10
GO:0110151	0.81	0.29	20	42	positive regulation of biomineralization	BP	1	OSR2,PTN,OSR1,SLC4A2,ACVR2B,ACVR2A,KL,ADGRV1,MEF2C,P2RX7,ANO6,TFAP2A,BMPR1B,AMELX,ACTN3,FZD9,WNT4,BMPR1A,SMAD3,CEBPB	grey	VSMC_M10
GO:0032966	0.81	0.41	4	9	negative regulation of collagen biosynthetic process	BP	1	CYGB,CYP7A1,CIITA,MIR29A	grey	VSMC_M10
GO:0051865	0.81	0.27	30	62	protein autoubiquitination	BP	1	PRKN,UBE2B,RNF146,UHRF2,NFX1,UBE3D,CNOT4,RNF122,SH3RF2,TRAF6,ERCC8,RNF181,DDB2,AMFR,MARCH7,RNF10,RNF115,KLHL24,DTX3L,TRIM52,RNF185,RNF4,TAF1,TRIM37,RNF208,TRAF2,WWP2,TRIM68,RNFT1,RNF8	grey	VSMC_M10
GO:0045616	0.81	0.31	13	28	regulation of keratinocyte differentiation	BP	1	CYP27B1,CD109,HOXA7,GRHL1,OVOL2,VDR,SRSF6,H2AFY2,ABCA12,MED1,MIR125B1,ZBED2,SGPP1	grey	VSMC_M10
GO:0060840	0.81	0.26	39	81	artery development	BP	1	LRP1,TAB1,FOXH1,SRF,TFAP2B,HOXA13,CNTRL,APOB,ACVR2B,WNT11,JAG1,HAND2,HPGD,EYA1,ROBO1,ROBO2,NKX3-1,PKD2,PRICKLE1,SUFU,SLC2A10,TGFB2,EFEMP2,LUZP1,BMPR1A,RBPJ,NGFR,LDLR,DCTN5,TBX2,STRA6,AP2B1,FOXF1,ENG,SOX4,ACVRL1,NOG,SIX1,HEY2	grey	VSMC_M10

GO:0042593	0.81	0.23	92	183	glucose homeostasis	BP	1	ZNF236,NME1,LRP1,AGER,PTCH1,PLA2G6,CRY1,SRF,TFAP2B,PRKCE,HMGN3,CYB5R4,TRPM4,FOXO3,FGF21,SESN3,FOXA3,GRIK5,RAF1,GCKR,ASPSCR1,GAS6,NR1H4,CYP7A1,NDUFAF2,GPI,CEBPA,OSBP,PIK3R1,KCNJ11,TIAM1,RAB11FIP5,PFKM,SLC8B1,OPA1,CRY2,ZBED6,PAX2,TWNK,GPLD1,IRS1,PPP3CA,TRPV4,SLC9B2,ZBTB20,ADRA2A,TCF7L2,KCNB1,POLG,GPER1,RAB11FIP2,USF1,MLXIPL,SIDT2,SLC16A1,PDK3,KLF7,FIS1,VGF,HK1,MEN1,ENY2,ABCA12,MCU,PYGL,PPP3CB,STAT3,PTPRN,MPC2,BHLHA15,SLC2A4,FGFR4,STX4,NGFR,CRTC2,GPR68,SIN3A,INSR,OXCT1,LEPR,PTPN2,INPP5K,NADK,BAIAP3,PARK7,CYBA,LRRC8A,OAS1,FABP5,LRRC8D,SOX4,CRH	grey	VSMC_M10
GO:0043244	0.81	0.25	52	107	regulation of protein-containing complex disassembly	BP	1	AVIL,JMJD4,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,PLEK,ADD2,CLASP2,MTRF1,TRIM54,NAV3,SPEF1,LMOD3,ATXN7,LIMA1,KATNB1,SCAF4,F2RL1,DMTN,CARMIL1,LMOD1,ADD3,TRPV4,TMEM39A,TTBK2,CIB1,SPTBN2,TMOD4,EPS8,RUBCN,CAPZA1,UPF1,TBC1D25,TMOD2,PHF23,SPTB,AC138894.1,INSR,SMCR8,CAMSAP3,TAOK1,CLEC16A,APC2,CAMSAP1,CARMIL2,IRGM,APC,PDXP,MAP1A,MAP6D1	grey	VSMC_M10
GO:0031641	0.81	0.29	17	36	regulation of myelination	BP	1	SOX10,TNFRSF21,PTN,LPIN1,FIG4,MTMR2,CST7,SIRT2,RARB,LGI4,JAM2,CYFIP1,RNF10,DAG1,NSUN5,DLG1,TNFRSF1B	grey	VSMC_M10
GO:0002031	0.81	0.41	4	9	G protein-coupled receptor internalization	BP	1	ARRB1,SAG,GRK4,DNM2	grey	VSMC_M10
GO:0090090	0.81	0.24	56	113	negative regulation of canonical Wnt signaling pathway	BP	1	GLI1,STK3,FZD6,PRKN,MAPK14,SOX10,ROR2,SOSTDC1,HECW1,FUZ,SFRP4,DKKL1,FOXO3,SOX9,WNT11,RBMS3,CHD8,UBAC2,FERMT1,PFDN5,CTNND1,DKK3,TMEM131L,LMBR1L,AMFR,SOX13,STK4,PRICKLE1,NKD1,HDAC1,TCF7L2,DKK2,AXIN2,SOX2,ZNRF3,KREMEN1,BICC1,PTPRO,OTUD5,IGFBP4,TMEM88,CCDC88C,G3BP1,ISL1,GPC3,TLE6,APC2,DAB2IP,MIR199A1,NOG,WNT5A,DDIT3,DACT3,SDHAF2,APC,NKX2-5	grey	VSMC_M10
GO:0032774	0.81	0.20	1329	2534	RNA biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ATP8B1,ONECUT2,BAZ2A,TCF4,TBPL1,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,HELB,ZBTB2,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,STK3,OSR2,SNW1,TFB1M,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,PRKN,AGER,PPARA,PDE10A,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,SCAF1,LPIN1,SFRP4,UCP1,CREM,TEAD2,SETD7,SDCBP,MYCN,C6orf203,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,FAF1,MAMSTR,GTF3C6,ATAD2B,BEND5,CDCA7,KDM7A,ZNF438,FOXE3,HDAC2,	grey	VSMC_M10
GO:0098901	0.81	0.32	10	22	regulation of cardiac muscle cell action potential	BP	1	TRPM4,DSP,RYR2,PKP2,ANK2,NOS1AP,DLG1,CALM1,DSG2,HCN4	grey	VSMC_M10
GO:0006622	0.81	0.32	10	22	protein targeting to lysosome	BP	1	RAB7A,NCOA4,AP3B1,HSPA8,SORL1,AP4M1,AP3M1,LAMP2,VPS4A,SNX16	grey	VSMC_M10
GO:0033692	0.81	0.27	25	52	cellular polysaccharide biosynthetic process	BP	1	HAS1,EPM2AIP1,PPP1CB,CSGALNACT1,AKT2,PPP1R3B,GBE1,B3GNT4,SORBS1,IGF2,NHLRC1,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PRKAG3,AC022400.6,PPP1R3F,INSR,INPP5K,AGL,HAS3,ACADM,HS2ST1	grey	VSMC_M10
GO:0006959	0.81	0.25	42	84	humoral immune response	BP	1	CXCL14,PLA2G6,TFEB,TNFRSF21,GAPDH,CXCL8,TRAF3IP2,BMI1,PHB,FOXJ1,HPX,GPI,MEF2C,IL7,NOD2,YTHDF2,CD28,PDCD1,PPP2R3C,PTPN6,SLC11A1,CFP,BST1,TFE3,RBPJ,SPON2,GATA6,CCL2,C7,C3,FGA,S100A12,HIST1H2BK,CXCL6,CD46,A2M,JCHAIN,CFD,FCER2,RGCC,HIST1H2BF,HIST1H2BJ	grey	VSMC_M10
GO:2000036	0.81	0.31	12	26	regulation of stem cell population maintenance	BP	1	CNOT2,ZNF706,MYC,SMO,PTN,PAX8,CNOT1,LOXL2,PAX2,SAV1,ESRRB,ZNF322	grey	VSMC_M10
GO:0003002	0.81	0.22	127	251	regionalization	BP	1	GLI1,FRS2,TBC1D32,PTCH1,SMO,MDFI,FOXH1,SRF,ROR2,MEOX2,SOSTDC1,SIX2,SCMH1,HOXA2,HOXA4,HOXA6,HOXA7,FUZ,OSR1,NTF4,INTU,SPRY1,BMI1,SETDB2,ABI1,GLI2,MEGF8,PCDH8,XRCC2,ACVR2B,IFT172,FOXJ1,WNT11,OVOL2,ACVR2A,BHLHE40,SEMA3A,PRKDC,HOXC6,TCF15,POFUT1,PAX8,ROBO1,ROBO2,FAM208A,MEF2C,NKX3-1,IFT52,RPGRIP1L,PAX2,NKD1,DPCD,LDB1,BMPR1B,FBXL15,SUFU,IRX2,PGAP1,SEMA3F,POGLUT1,AXIN2,SNAI1,TTC21B,GBX2,HES6,CHRD,DLX1,WNT3,HOXD8,HOXD4,HOXD3,AIDA,FZD5,MEOX1,PKD1L1,FKBP8,GORAB,GPR161,TULP3,MNS1,DVL2,BMPR1A,WDR19,TCAP,RBPJ,ALDH1A2,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,ITGAM,TMEM107,SMAD3,MKS1,GSC,LHX1,YY1,CDX1,MIB1,NLE1,ISL1,C3,GPC3,HSPB11,HES4,SKI,WDR77,CELSR2,FOXF1,MTF2,ADGRG1,FOXG1,MAFB,ACVRL1,HOXB3,NOG,WNT5A,BASP1,OTX1,SIX1,DDIT3,FGF1,PIFO,HEY2,WNT2,HOXA3	grey	VSMC_M10

GO:0002367	0.81	0.26	31	64	cytokine production involved in immune response	BP	1	CD226,KIT,RSAD2,TLR4,ATG5,TRPM4,SPHK2,LACC1,MAVS,TRAF6,F2RL1,NOD2,CD96,TGFB2,DENND1B,FZD5,BCL6,HK1,FOXP3,TNFRSF1B,SPON2,TBX21,BTK,CD74,TICAM1,PRKCZ,TRAF2,SLC7A5,BCL10,WNT5A,INAVA	grey	VSMC_M10
GO:1900026	0.81	0.30	14	30	positive regulation of substrate adhesion-dependent cell spreading	BP	1	UNC13D,RAC3,ARHGEF7,DOCK5,RREB1,DMTN,CARMIL1,CASS4,CIB1,DOCK1,CSPG5,DNM2,CRK,FGA	grey	VSMC_M10
GO:0032885	0.81	0.30	14	30	regulation of polysaccharide biosynthetic process	BP	1	EPM2AIP1,PPP1CB,AKT2,PPP1R3B,SORBS1,IGF2,IRS1,PPP1R3E,EGF,PPP1R3D,PASK,PPP1R3F,INSR,INPP5K	grey	VSMC_M10
GO:0070884	0.81	0.30	14	30	regulation of calcineurin-NFAT signaling cascade	BP	1	FHL2,EFHB,PRNP,NRG1,SPPL3,TBC1D10C,CIB1,SLC9A1,MYOZ2,ACTN3,HOMER2,MYOZ1,MAPK7,CAMTA1	grey	VSMC_M10
GO:0002263	0.81	0.23	93	185	cell activation involved in immune response	BP	1	LRP1,ENPP3,HLA-DRA,MFNG,RAC2,KIT,EXOSC3,PRKCE,MSH2,TLR4,SPHK2,HMCES,ERCC1,LCP1,GAB2,MLH1,UNC13D,MYD88,PAXIP1,EOMES,NMI,TCIM,PLCL2,SHLD1,NCKAP1L,FOXP1,GAPT,FER,PTK2B,RASGRP1,EIF2AK4,RIPK2,NBN,DYSF,CDH17,F2RL1,CD40,GBF1,DOCK10,SNAP23,HLX,LAT2,FGR,CBL,SNX4,CD28,FCER1G,RNF168,BCL6,RC3H1,TNFSF18,SLC11A1,PTGDR,STAT3,C12orf4,FOXP3,SHLD2,TBX21,STX4,PSEN1,SEMA4A,ITGAM,DOCK2,BATF,ZBTB7B,IL6R,CD19,LAT,IL4R,S100A13,BTK,SCNN1B,CD74,STXBP2,PRAM1,PTGER4,SUPT6H,TICAM1,DNASE1,PDPK1,PRKCZ,TSC1,FOXF1,KARS,STXBP1,AP1G1,MIR21,CHGA,CD46,FGL2,RNF8,HAVCR2,RC3H2	grey	VSMC_M10
GO:0070663	0.81	0.23	77	153	regulation of leukocyte proliferation	BP	1	TNFAIP3,ENPP3,AGER,IL5,HLA-DPB1,TNFRSF13C,PTK2,RAC2,TNFRSF21,NCK2,PELI1,IL4I1,TLR4,IL15,BMI1,MYD88,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,IL1A,CASP3,MEF2C,TMEM131L,IL7,RIPK2,MARCH7,ZNF335,CD40,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,CD28,DLG1,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,CD38,BST1,MAPK1,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,MAPK3,ZBTB7B,CHRNB2,BTK,CD74,CCL5,CSF1R,CD320,TWSG1,TICAM1,DNAJA3,VAV3,GLMN,MIR21,LST1,FADD,CD46,IL33,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0006111	0.81	0.28	19	40	regulation of gluconeogenesis	BP	1	PPARA,GPT,GNMT,CRY1,PPP4R3B,ZNF692,FAM3C,SIRT7,NLN,SIK1,MST1,DDB1,DGKQ,OGT,LEPR,PTPN2,ACADM,NNMT,ARPP19	grey	VSMC_M10
GO:0007220	0.81	0.41	4	9	Notch receptor processing	BP	1	GALNT11,PSEN2,PSEN1,APH1B	grey	VSMC_M10
GO:0051569	0.81	0.31	12	26	regulation of histone H3-K4 methylation	BP	1	SNW1,PAXIP1,DNMT3B,RTF1,ZNF335,AUTS2,BCOR,WDR61,NELFA,GFI1,PRMT6,NNMT	grey	VSMC_M10
GO:0034121	0.81	0.27	26	54	regulation of toll-like receptor signaling pathway	BP	1	TNFAIP3,ESR1,GRAMD4,LRRC14,NINJ1,RTN4,PELI1,RSAD2,CD300LF,IRF7,MFHAS1,OTUD4,NR1H3,F2RL1,NOD2,RAB7B,TLR5,DDX3X,BIRC3,GPS2,WDFY1,GPR108,PDPK1,CYBA,GFI1,DAB2IP	grey	VSMC_M10
GO:0034375	0.81	0.38	5	11	high-density lipoprotein particle remodeling	BP	1	APOM,APOC1,PLTP,ABCA5,LIPC	grey	VSMC_M10
GO:1902415	0.81	0.41	4	9	regulation of mRNA binding	BP	1	EIF3E,EIF3C,LARP6,FMR1	grey	VSMC_M10
GO:0032414	0.81	0.25	39	80	positive regulation of ion transmembrane transporter activity	BP	1	STAC3,ABCB1,WNK2,CACNB2,STAC,GLRX,KCNJ11,IFNGR2,TESC,KCNE2,PKD2,KCNIP2,RYR2,FAM173B,COX17,ANK2,SLC9A1,CASQ1,NTSR1,NOS1AP,HTT,PINK1,ATP1B1,KCNA1,HAP1,WNK3,STAC2,ATP1B2,NLGN3,ATP2A1,CALM1,DNM2,VMP1,CCL2,RNF207,AMIGO1,DMD,JPH2,APOPT1	grey	VSMC_M10
GO:0071702	0.81	0.20	991	1891	organic substance transport	BP	1	ATP9B,TIMM21,VPS4B,APOF,ATP8B1,STARD6,LRP1,STX7,AP3S1,SLC2A12,KIF5A,SLC26A10,PEX7,AGAP2,PEX3,SLC16A7,CANX,TBC1D30,TBC1D9B,PPP1R10,CPSF6,RAB21,SNX24,SNX31,CPT1B,PHAX,APOM,ZDHHC14,SLC12A2,SERAC1,RIMS2,SLC27A6,PRKN,QKI,PPARA,TAP1,SLC22A4,KIF3A,TSPO,GDF9,GOPC,VPS52,HSPA4,DERL1,FAM91A1,WASHC5,FAM53C,SLC45A4,PTCH1,TSNARE1,LY6E,ZC3H3,EXOC4,SIL1,SYNGR1,MAPK15,MAPK14,NTRK2,TOMM22,PLA2G6,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,SMO,ZDHHC21,TTC39B,HSF1,PLIN2,TOMM6,MYH9,APOL4,APOL6,CHRNA3,PEX6,FBXO7,CRY1,CROT,ABCB1,ABCC10,NOL6,XPO5,WASHC4,APBA1,PEX1,SLC35B2,VPS50,SLC25A27,SCFD2,RFX3,SLC1A1,TGFBRAP1,TFAP2B,SLC25A13,TBC1D8,TRAM2,BICD2,CHMP2A,RAB23,ABCG5,SVBP,ABCG8,LRPPRC,SEC61B,SLC3A1,STX17,SIX2,DNAJA1,PRKCE,RIMS1,TMEM30A,SPTBN1,IGF2BP3,HMGN3,YTHDC1,PNPT1,RUFY3,SLC4A4,CYB5R4,PPT1,SNX14,XPO1,SNX30,SLC35A1,BMP8A,AQP1,EHBP1,AFTPH,SLC1A4,PLEK,RSAD2,NR1H2,ITGB1BP1,DDC,GRB10,YWHAZ,SEC61G,EGFR,FUZ,ARHGEF5,TLR4,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,TRPM4,SLC7A11,PGRMC2,LIN7B,EPS15,APOB,AGK,FGF21,BRAF,BCAP29,MFSD4B,MFSD2B,TRAF3IP2,ANKRD50,TTC26,DNAJC27,NAPA,BBS7,RAB7A,SLC26A5,PIP4K2A,AP2S1,RAB10,COPG1,KPNA3,GIPR,ARL5B,IWS1,LCP1,SYTL2,COG1,SLC25A30,DLG2,CUBN,RBSN,APOC1,SLC4A2,DNAJC15,ASIC3,PLK3,FRMD4A,OPTN,GOLGA4,LLGL2,IPO13,STEAP3,AQP11,PRKAG2,CCDC93,RAF1,ZFAND6,SLC22A13,TBC1D4,MYO7A,SLC25A38,NAPB,GCKR,SEC14L1,TSKU,SEC62,SEC22C,KPNA2,AKT2,PITRM1,LRP1B,HOOK3,ARRB1,ABCC4,	grey	VSMC_M10
GO:0048668	0.81	0.32	10	22	collateral sprouting	BP	1	LRP1,FSTL4,SEMA4D,EPHA7,SPART,ULK1,SPP1,BDNF,WNT3,NIN	grey	VSMC_M10
GO:0002562	0.81	0.27	26	54	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	TCF7,EXOSC3,MSH2,CYREN,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,PRKDC,XRCC4,NBN,CD40,DCAF1,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,BCL11B,YY1,SUPT6H,RNF8,NHEJ1	grey	VSMC_M10
GO:0016444	0.81	0.27	26	54	somatic cell DNA recombination	BP	1	TCF7,EXOSC3,MSH2,CYREN,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,PRKDC,XRCC4,NBN,CD40,DCAF1,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,BCL11B,YY1,SUPT6H,RNF8,NHEJ1	grey	VSMC_M10
GO:0009159	0.81	0.38	5	11	deoxyribonucleoside monophosphate catabolic process	BP	1	DPYS,GDA,UPB1,NT5M,UPP1	grey	VSMC_M10
GO:2000107	0.81	0.29	16	34	negative regulation of leukocyte apoptotic process	BP	1	SLC46A2,GAS6,FOXP1,IRF7,NOD2,GPAM,HCLS1,BCL6,CXCR2,EFNA1,CD74,CCL5,IL7R,BCL10,FADD,TSC22D3	grey	VSMC_M10

GO:0072089	0.81	0.27	26	54	stem cell proliferation	BP	1	FBLN1,PIM1,ABCB1,SIX2,EPCAM,OVOL2,FERMT1,EIF2AK2,VEGFC,TERT,SART3,YTHDF2,ZNRF3,ARIH2,KDF1,THPO,OVOL1,ETV6,WNT3,KAT7,CTC1,CITED1,AC004687.2,MIR222,ATXN1L,WNT5A	grey	VSMC_M10
GO:2000142	0.81	0.29	15	32	regulation of DNA-templated transcription, initiation	BP	1	ESR1,MED30,SRF,ERCC1,PAXIP1,MITF,ERCC6,CREB1,MED14,THRA,MED24,MED1,JUN,NKX2-5,HEY2	grey	VSMC_M10
GO:0034969	0.81	0.41	4	9	histone arginine methylation	BP	1	PRDM4,NR1H4,PRMT7,PRMT6	grey	VSMC_M10
GO:0002438	0.81	0.38	5	11	acute inflammatory response to antigenic stimulus	BP	1	SERPINC1,CXCR2,BTK,C3,PARK7	grey	VSMC_M10
GO:0006984	0.81	0.28	21	44	ER-nucleus signaling pathway	BP	1	ATF4,NCK2,C12orf49,FBXW7,ATG10,AMFR,ERLIN1,QRICH1,SCAP,TMCO1,NFE2L2,LPCAT3,ZBTB7B,SREBF1,PTPN2,ABCA7,HSPA5,DDIT3,BCL2L11,PPP1R15A,INSIG2	grey	VSMC_M10
GO:0042255	0.81	0.28	22	45	ribosome assembly	BP	1	RRP7A,RPS14,MDN1,RPSA,PRKDC,DHX37,RPL6,SBDS,MRPS11,RPS27,DHX30,RPL11,EFL1,RPL10L,DDX3X,XRCC5,MRPL22,NLE1,RPL23A,ERAL1,MRPS2,RPS27L	grey	VSMC_M10
GO:1901021	0.81	0.29	17	36	positive regulation of calcium ion transmembrane transporter activity	BP	1	STAC3,CACNB2,STAC,KCNE2,PKD2,RYR2,ANK2,SLC9A1,CASQ1,HTT,ATP1B1,HAP1,STAC2,ATP2A1,CALM1,VMP1,JPH2	grey	VSMC_M10
GO:0051791	0.81	0.41	4	9	medium-chain fatty acid metabolic process	BP	1	CROT,ABHD2,ABHD3,ACADM	grey	VSMC_M10
GO:0021612	0.82	0.41	4	9	facial nerve structural organization	BP	1	PLXNA4,SEMA3A,SEMA3F,PLXNA3	grey	VSMC_M10
GO:1903332	0.82	0.38	5	11	regulation of protein folding	BP	1	PDCL3,DNAJB2,SGTA,HSPA5,POFUT2	grey	VSMC_M10
GO:0021697	0.82	0.33	9	20	cerebellar cortex formation	BP	1	AGTPBP1,WHRN,FAIM2,LDB1,TTC21B,MAP2K1,LHX1,GRID2,CEND1	grey	VSMC_M10
GO:0016447	0.82	0.27	23	48	somatic recombination of immunoglobulin gene segments	BP	1	EXOSC3,MSH2,CYREN,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,PRKDC,XRCC4,NBN,CD40,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,YY1,SUPT6H,RNF8,NHEJ1	grey	VSMC_M10
GO:0048880	0.82	0.22	144	286	sensory system development	BP	1	SLC39A5,MDM1,FRS2,OSR2,TBC1D32,BAK1,ATF4,AGTPBP1,NTRK2,PRPH2,RORB,SRF,SLC1A1,TFAP2B,TDRD7,TMOD1,RDH13,ABCB5,PTN,TSPAN12,USP45,SLC7A11,SPRY1,FOXE3,HDAC2,BBS7,SOX9,CRYGN,ZNF513,ACVR2B,IFT172,MYO7A,POU4F1,TSKU,SPRY2,DZANK1,TGFBR2,BFSP1,JAG1,RARB,FSCN2,SPRED3,FREM2,CEP290,KERA,SEMA3A,MAB21L1,MITF,FLT1,TUB,EPHB1,PFDN5,NPHP1,RET,FOXL2,MAB21L2,TENM3,USH1C,TENT2,OPA1,RPGRIP1L,TFAP2A,PAX2,NKD1,BMPR1B,MYH15,NECTIN3,LPCAT1,PKNOX1,SLC6A3,HDAC1,ALDH1A3,TGFB2,TCIRG1,PRSS56,SHROOM2,SOX2,CRYBA4,NRL,CLIC4,DLX1,GRHL3,LIMK2,SP3,CDKN1B,DLG1,FZD5,FBN1,FKBP8,COL5A2,PLA2G16,STAT3,TULP3,OBSL1,RHOJ,ROM1,MFAP2,WDR19,SDK1,MAX,CLN8,MED1,ALDH1A2,MFN2,PSEN1,ITGAM,TTLL5,MEGF11,LCTL,SMAD3,TBX2,BCL11B,LHX1,STRA6,YY1,CHRDL1,UNC45B,TMEM132E,ISL1,LAMA1,C3,TWSG1,GNB1,FZR1,SKI,SOX8,COL5A1,LAMC3,OLFM3,TMEM231,SLC25A25,HSF4,BLOC1S3,FJX1,CNTF,ACVRL1,THY1,WNT5A,DIO3,TGIF2,TBC1D20,PITX3,WNT2,COL8A2	grey	VSMC_M10
GO:0034341	0.82	0.24	47	95	response to interferon-gamma	BP	1	CYP27B1,GAPDH,NR1H2,TLR4,NMI,ACTG1,HPX,HCK,FLNB,CCL17,NR1H3,NLRC5,IFNGR2,CD40,RAB7B,SP100,PARP9,PARP14,CDC42EP2,SLC11A1,GCH1,WAS,CXCL16,MED1,STX4,CITED1,STX8,CD74,CCL14,CCL5,CCL7,CCL2,CCL25,JAK1,NOS2,PTPN2,SOCS1,CIITA,ADAMTS13,ASS1,STXBP1,CCL16,IRGM,CLDN1,WNT5A,VAMP3,CCL22	grey	VSMC_M10
GO:0007281	0.82	0.23	89	177	germ cell development	BP	1	TBPL1,YTHDC2,MOV10L1,PACRG,QKI,GDF9,UBE2B,CATSPER3,WASHC5,SMAD5,H3F3C,FANCC,TUT7,DMC1,CFAP69,FANCG,SMARCA2,KIT,MSH2,YTHDC1,GMCL1,PTN,NOBOX,CCDC155,TUT4,FOXO3,ARMC2,DLD,TTC26,PANX1,RSPH6A,TOPAZ1,ERCC1,NECTIN2,MLH1,TTC21A,CCNB1IP1,SIRT2,MKKS,PANK2,SOHLH2,ING2,CELF1,JAM2,PTK2B,KMT2D,CDYL,SYCP1,DNAH1,NPM2,OCA2,ROPN1L,BMPR1B,NECTIN3,NEURL1,DDX25,CFAP43,ABHD2,CCDC36,YTHDF2,SPO11,TSSK4,CIB1,OSBP2,CATSPER2,TTC12,SPAG16,WNT4,ZMYND15,MNS1,YBX2,SOX30,CCDC42,PAQR5,TAF4B,SPEF2,CATSPERD,CHD5,TPGS1,WDR77,MFSD14A,STRBP,AURKC,SYCP3,NANOS1,RNF8,TBC1D20,EREG,ZGLP1	grey	VSMC_M10
GO:0006040	0.82	0.29	15	32	amino sugar metabolic process	BP	1	GFPT2,LARGE1,ALDH1A1,GNPDA2,NANP,CSGALNACT1,CHST1,CMAS,DPAGT1,MGAT1,OVGP1,CHST3,CHST7,CHST5,CTBS	grey	VSMC_M10
GO:0051602	0.82	0.31	12	26	response to electrical stimulus	BP	1	BRD1,NR4A1,FZD3,OPA1,KCNJ3,CYFIP1,DISC1,SLC9A1,RAB3A,ADSSL1,PALM,NQO1	grey	VSMC_M10
GO:0090503	0.82	0.28	20	42	RNA phosphodiester bond hydrolysis, exonucleolytic	BP	1	PAN2,CNOT2,CNOT6,PNLDC1,EXOSC4,EXOSC3,PNPT1,PAN3,CNOT1,USB1,CNOT6L,DIS3L2,ANGEL2,EXD2,ISG20L2,ANGEL1,CNOT8,ERI2,PARN,EXOSC5	grey	VSMC_M10
GO:0086003	0.82	0.26	27	57	cardiac muscle cell contraction	BP	1	NEDD4L,TRPM4,CACNB2,SCN5A,SCN1A,GPD1L,STC1,KCNJ3,KCNE2,DSP,RYR2,PKP2,KCNJ2,ANK2,ATP1A2,SLC9A1,SCN4B,NOS1AP,DLG1,CACNA1G,ATP2A1,DSG2,RNF207,KCNH2,SCN2B,KCNJ8,HCN4	grey	VSMC_M10
GO:0150116	0.82	0.26	31	65	regulation of cell-substrate junction organization	BP	1	LRP1,PTK2,TEK,ITGB1BP1,IQSEC1,CLASP2,ACTG1,PTPRA,FAM107A,PIK3R1,FMN1,PTPRJ,DMTN,LDB1,SLK,COL16A1,ARHGAP6,SLC9A1,APOD,WNT4,VCL,SMAD3,BCAS3,CAMSAP3,TSC1,RHOA,ACVRL1,PEAK1,THY1,LAMTOR2,DUSP22	grey	VSMC_M10
GO:0060976	0.82	0.28	18	39	coronary vasculature development	BP	1	TAB1,PTK7,SRF,CNTRL,MEGF8,HAND2,TBX5,PRICKLE1,SUFU,GPER1,MMP21,SETD2,DCTN5,GATA6,AP2B1,ZBTB14,GPC3,HEY2	grey	VSMC_M10
GO:0043030	0.82	0.28	18	38	regulation of macrophage activation	BP	1	TTBK1,TLR4,CST7,MFHAS1,CEBPA,NR1H3,CD200,GPR137B,PLA2G4A,TNIP2,SYT11,IL4R,LDLR,CD74,KARS,WNT5A,IL33,HAVCR2	grey	VSMC_M10

GO:0045926	0.82	0.22	98	195	negative regulation of growth	BP	1	SEMA6A,CYP27B1,STK3,HSPA1B,PPARA,GDF9,FSTL4,PTCH1,PI16,CDKN2A,SMARCA2,SEMA4D,SEMA4C,RTN4,PPP2R1A,PNPT1,PPT1,EPHA7,SPHK2,PHB,WNT11,SERTAD3,TGFBR2,ING1,SEMA3D,BTG1,SPART,SEMA3A,ULK1,RYK,ACVR1B,CDKN2AIP,PTPRJ,SEMA4F,NDUFS3,TLL2,TBX5,PRDM11,SEMA3G,SPP1,STK4,SEMA4G,NKD1,JARID2,KIAA0319,HYAL1,CAPRIN2,SEMA3F,TGFB2,EI24,SH3BP4,AGT,IP6K2,KCNK2,ING5,CDKN1B,WNT3,DUSP10,BCL6,SEMA6D,DDX3X,TNR,SAV1,ING4,MYOZ1,GDF15,FGFR3,MUL1,DNAJB2,TSPYL2,SEMA4A,TRIM46,WWC1,SMAD3,NTN1,BDKRB1,DCUN1D3,YY1,CDK5R1,RAI1,GPC3,ARHGAP4,PLXNA3,PSRC1,NAIF1,MIR199A1,MIR25,SERTAD2,MT1X,ACVRL1,NOG,WNT5A,FXN,RGS4,PLAC8,DACT3,NME6,CGRRF1	grey	VSMC_M10
GO:0090303	0.82	0.27	20	42	positive regulation of wound healing	BP	1	PTK2,ENPP4,PRKCE,THBD,ACTG1,HBEGF,FERMT1,F2R,ANO6,RREB1,DMTN,ADRA2A,USF1,NFE2L2,DUOX1,F12,SERPINF2,MIR29A,CLDN1,HRAS	grey	VSMC_M10
GO:0019748	0.82	0.29	14	30	secondary metabolic process	BP	1	AKR1B1,DDC,SLC7A11,AKR1A1,CBR4,RAPGEF2,ABCC2,OCA2,BDH2,NFE2L2,CITED1,SLC45A2,WNT5A,N6AMT1	grey	VSMC_M10
GO:0071711	0.82	0.29	14	30	basement membrane organization	BP	1	PXDN,CLASP2,FERMT1,SPINT2,GAS2,DAG1,LAMB3,PHLDB1,PLOD3,MMP11,NID2,RAMP2,NTNG2,LAMB1	grey	VSMC_M10
GO:0072595	0.82	0.28	18	38	maintenance of protein localization in organelle	BP	1	TSPO,SKP1,SUN2,GPAA1,TAF8,GRIK5,TAF3,ARL2BP,MORC3,SP100,HK1,PINK1,RER1,PARK7,HSPA5,SUPT7L,TXN,INSIG2	grey	VSMC_M10
GO:0000394	0.82	0.38	5	11	RNA splicing, via endonucleolytic cleavage and ligation	BP	1	TSEN34,CLP1,ZBTB8OS,RTRAF,TRPT1	grey	VSMC_M10
GO:0006094	0.82	0.26	28	58	gluconeogenesis	BP	1	PPARA,ATF4,GPT,GNMT,CRY1,SLC25A13,PPP4R3B,ZNF692,FAM3C,SIRT7,GPI,NLN,GPD1,SIK1,MST1,PC,SLC37A4,PER2,DDB1,DGKQ,OGT,CRTC2,LEPR,PTPN2,ACADM,FBP2,NNMT,ARPP19	grey	VSMC_M10
GO:0000956	0.82	0.24	50	102	nuclear-transcribed mRNA catabolic process	BP	1	PAN2,CNOT2,CNOT6,PABPC1,SKIV2L,DXO,EIF3E,PNLDC1,AGO2,TNRC6B,TUT7,EXOSC4,EXOSC3,AGO1,TUT4,MTPAP,DHX34,MLH1,TNRC6C,LSM1,UPF3A,PAN3,TTC37,CNOT1,CNOT6L,TENT2,TENT4B,DIS3L2,NCBP2,EIF4ENIF1,RC3H1,UPF1,SAMD4A,POLR2G,NT5C3B,DCP1B,CASC3,SMG5,TOB1,TNRC6A,CNOT8,UPF3B,PARN,LSM7,EDC4,NANOS1,ZFP36L2,MAGOHB,RC3H2,EXOSC5	grey	VSMC_M10
GO:0140353	0.82	0.30	13	28	lipid export from cell	BP	1	GDF9,CRY1,ABCC4,C1QTNF1,NKX3-1,CRY2,SPP1,MAP2K6,AGT,PLA2G4A,NOS2,CRH,PTGES	grey	VSMC_M10
GO:1905332	0.82	0.28	16	34	positive regulation of morphogenesis of an epithelium	BP	1	SMO,SOX9,PAX8,PAX2,EGF,AGT,STOX1,WNT4,MAGED1,LHX1,SOX8,LCN2,NOG,LBX2,SIX1,LIF	grey	VSMC_M10
GO:0033280	0.82	0.29	14	30	response to vitamin D	BP	1	CYP27B1,SNW1,PIM1,PTN,TNC,IL15,VDR,STC1,SPP1,ALPL,MED1,MIR125B1,TRIM24,BGLAP	grey	VSMC_M10
GO:0030042	0.82	0.26	24	51	actin filament depolymerization	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,PLEK,ADD2,LMOD3,LIMA1,F2RL1,DMTN,CARMIL1,LMOD1,ADD3,CFL1,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,CARMIL2,PDXP	grey	VSMC_M10
GO:0038094	0.82	0.31	11	24	Fc-gamma receptor signaling pathway	BP	1	PTK2,PLA2G6,PRKCE,HCK,PTPRJ,FGR,PLPP4,FCER1G,YES1,VAV1,VAV3	grey	VSMC_M10
GO:0043408	0.82	0.20	258	502	regulation of MAPK cascade	BP	1	PHLPP1,LRP1,SEMA6A,MAP3K5,FRS2,STK3,MAPK8IP2,MAP3K4,PRKN,AGER,FBLN1,ROS1,SYNGAP1,MYC,LEMD2,PRXL2C,GRM4,TAB1,NTRK2,STK38,TEK,GPR37,KIT,ROR2,GADD45G,WNK2,KLHL31,PRDX1,SEMA4C,DNAJA1,IL11,PRKCE,FKTN,FPR2,GSDME,VRK2,EMC10,LPAR1,MTURN,EPGN,NOD1,BMPER,EPHA7,TGFA,ITGB1BP1,VRK3,YWHAZ,EGFR,ARHGEF5,TLR4,TRAF1,SDCBP,FGF21,BRAF,SPRY1,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,RAF1,MYD88,SPRY2,ALK,ARRB1,C1QTNF1,NEK10,ZMYND11,PDE6G,PLCB1,SPRED3,EIF2AK2,ADRA1D,DUSP6,RELL2,SEMA3A,KL,NRG1,SH3RF2,GAS6,SIRT3,ARL6IP5,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,APIP,ST5,EPHB1,MOS,RET,PIK3CB,HAND2,ROBO1,PLCE1,FBXW7,PTPRJ,P2RX7,WDR54,P2RY1,MADD,PTK2B,RASGRP1,RAPGEF2,CCL17,TIAM1,PAQR3,RIPK2,F2RL1,F2R,NQO2,RIPK1,PRDM11,STK4,GCNT2,NOD2,TAOK3,CD40,DSTYK,DUSP8,IGF2,PRDM15,BANK1,MAP2K6,TRPV4,PDCD4,TGFB2,ADRA2A,SLC30A10,DAG1,AJUBA,NCF1,KRAS,EGF,TBC1D10C,SOX2,SORL1,GPER1,DOK5,AGT,CIB1,TRAF5,DVL3,FZD7,OSM,THPO,PDE6H,MAP3K3,PDE8A,MAGI3,DUSP16,DLG1,MAP3K11,ADAM8,AIDA,FZD5,DUSP10,MBIP,RAP1B,MEN1,MAP4K2,FN1,DUSP19,PTPN6,PDCD10,ADRA2C,GPBAR1,GDF15,FGFR3,PINK1,LTBR,MAPK1,MINK1,EPHA4,MAGED1,DVL2,IGFBP4,GPS2,RELL1,RGS14,FGFR4,SYNJ2BP,PSEN1,FGF18,TAOK2,EFNA1,WWC1,MAPK3,MAP2K1,PIK3R5,MAP2K5,RIT2,TNIP1,PSMD10,GAREM1,NCOR1,TRAF3,CD74,HRH4,CCL14,INSR,CCL5,CSF1R,CCL7,CCL2,CCL25,GHR,KSR1,PTPN2,TAOK1,INPP5K,SERPINF2,PRKCZ,MAPK8IP3,TRAF2,ATP6AP1,ABCA7,CDK10,MARVELD3,DAB2IP,MIR21,MIR222,MIR23A,MIR27B,MIR24-1,MIR23A,EGA,SCN1A,DUSP2,S100A12,TNFSF13,SUSN	grey	VSMC_M10
GO:0034766	0.82	0.25	33	68	negative regulation of ion transmembrane transport	BP	1	NEDD4L,GOPC,PRKCE,HECW1,TCAF2,KEL,OSR1,SLC26A5,KCNRG,OXSR1,ARL6IP5,SLC43A1,KCNE2,PKD2,CASQ2,HECW2,ADRA2A,ISCU,ATP1A2,C4orf3,NTSR1,SESTD1,GNB5,CALM1,FMR1,RRAD,MIR24-1,GPR35,KCNH2,CRBN,RGS4,GEM,PPIF	grey	VSMC_M10
GO:0045933	0.82	0.29	14	30	positive regulation of muscle contraction	BP	1	SRF,KIT,ADRA2B,F2R,CHRM3,TRPV4,GPER1,ACE2,ACTN3,ATP2A1,ABAT,MIR21,RHOA,CHGA	grey	VSMC_M10
GO:0110110	0.82	0.29	14	30	positive regulation of animal organ morphogenesis	BP	1	FRS2,SPRY1,SOX9,WNT11,ROBO1,ROBO2,STOX1,WNT4,NGFR,SOX8,WNT5A,SIX1,FGF1,WNT2	grey	VSMC_M10
GO:0034380	0.82	0.40	4	9	high-density lipoprotein particle assembly	BP	1	APOM,NR1H2,ZDHHC8,ABCA7	grey	VSMC_M10
GO:0048102	0.82	0.40	4	9	autophagic cell death	BP	1	TP53INP1,CDKN1B,CTSV,SH3GLB1	grey	VSMC_M10
GO:0051250	0.82	0.24	49	99	negative regulation of lymphocyte activation	BP	1	TNFAIP3,FBXO7,TNFRSF21,PELI1,IL4I1,PIBF1,FOXJ1,PAWR,PRNP,NCKAP1L,ZC3H8,CASP3,TMEM131L,PAG1,MARCH7,BANK1,BTN2A2,PRKAR1A,HLX,TBC1D10C,FGR,RUNX3,DLG1,BCL6,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,INHA,SCGB1A1,FOXP3,TBX21,ZBTB7B,IL4R,BTK,CD74,TWSG1,PTPN2,SOCS1,GLMN,MIR21,MIR27A,LST1,FGL2,LAX1,CEBPB,HAVCR2,RC3H2	grey	VSMC_M10

GO:1901857	0.82	0.40	4	9	positive regulation of cellular respiration	BP	1	ISCU,PINK1,PARK7,IFNLR1	grey	VSMC_M10
GO:0014009	0.82	0.28	18	38	glial cell proliferation	BP	1	SNW1,TSPO,SOX10,AREG,PTN,EGFR,PLAG1,LGI4,PTK2B,RNF10,CERS2,CREB1,CHRM1,LEPR,SKI,MIR222,MIR125B1,SOX4	grey	VSMC_M10
GO:1904861	0.82	0.31	10	22	excitatory synapse assembly	BP	1	LRRC4,VSTM5,LRFN1,NRXN2,NLGN2,SEMA4A,ZDHHC12,GRID2,WNT5A,LRRTM2	grey	VSMC_M10
GO:0001776	0.82	0.25	34	70	leukocyte homeostasis	BP	1	TNFAIP3,BAK1,SLC46A2,SLC7A11,TRAF3IP2,NCKAP1L,GAPT,ZC3H8,PIK3CB,CASP3,MEF2C,DOCK10,GPAM,TCIRG1,PPP2R3C,RC3H1,CXCR2,PPP3CB,STAT5B,FOXP3,LAT,CD74,DNAJA3,BCL10,FADD,CXCL6,CAMLG,TSC22D3,BCL2L11,SH2B2,SLC39A3,TNFSF13B,XKR8,RC3H2	grey	VSMC_M10
GO:0071674	0.82	0.23	63	126	mononuclear cell migration	BP	1	SLC12A2,AGER,PTK2,CCL27,FPR2,AKIRIN1,TRPM4,C5AR1,OXSR1,PLCB1,GAS6,FLT1,RET,CYP7B1,JAM2,PTK2B,CCL17,SLC8B1,ANO6,ADTRP,CD200,TRPV4,CD99,CMKLR1,SLAMF8,MOSPD2,EPS8,PTPRO,APOD,ADAM8,MIA3,ITGA4,IL12A,TNFSF18,CXCR2,MAPK1,CH25H,PADI2,CXCL16,TMEM102,TBX21,STK10,MAPK3,IL6R,S100A14,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,CRK,RHOA,CCL16,S100A12,DEFB124,FADD,WNT5A,DUSP1,ARTN,GCSAM,CCL22,PDGFD	grey	VSMC_M10
GO:0045191	0.82	0.29	13	28	regulation of isotype switching	BP	1	EXOSC3,MSH2,HMCES,MLH1,PAXIP1,SHLD1,CD40,CD28,BCL6,FOXP3,SHLD2,TBX21,SUPT6H	grey	VSMC_M10
GO:1905049	0.82	0.40	4	9	negative regulation of metallopeptidase activity	BP	1	LRP1,SORL1,MIR199A1,MIR24-1	grey	VSMC_M10
GO:0009612	0.82	0.22	88	176	response to mechanical stimulus	BP	1	BAK1,PKD2L2,HABP4,PTK2,PTCH1,MAPK14,PHF24,KIT,ETV1,AQP1,CASP8AP2,WHRN,PTN,TNC,EGFR,TLR4,SMPD2,MKX,SLC26A5,SOX9,XPC,ASIC3,RAF1,MYD88,SCN1A,SCEL,WNT11,TGFBR2,MKKS,CNN2,DCN,GPI,P2RX3,ADGRV1,P2RY1,PTK2B,TMEM150C,SLC38A2,PKD2,CD40,RYR2,KIAA0319,KCNJ2,TRPV4,DAG1,TLR5,AGT,ATP1A2,BAG3,SLC9A1,HDAC4,KCNK2,BACE1,STRC,TTN,NRXN2,KCNK4,HTT,PKD1L1,COL3A1,LTBR,KCNA1,TCAP,TNFRSF8,FOS,MAPK3,MPO,BDKRB1,STRA6,ASIC2,PTGER4,JUN,PKD1,PIEZO1,CYBA,ENG,PKD1L3,STRBP,BCL10,RHOA,DMD,PJVK,CHRNA10,FADD,CASP8,BGLAP,GADD45A,CRADD	grey	VSMC_M10
GO:0032727	0.82	0.33	8	18	positive regulation of interferon-alpha production	BP	1	IRF5,TLR4,MAVS,IRF7,RIPK2,IFIH1,SETD2,DDX3X	grey	VSMC_M10
GO:0006862	0.82	0.29	13	28	nucleotide transport	BP	1	SLC35B2,ABCC4,SLC33A1,CALHM1,ABCC5,SLC25A42,LRRC8E,SLC25A23,SLC25A41,SLC25A33,LRRC8A,SLC25A25,SLC25A32	grey	VSMC_M10
GO:1903421	0.82	0.30	11	24	regulation of synaptic vesicle recycling	BP	1	BTBD9,CYFIP1,DNM1L,AP2M1,DNM3,PPP3CB,GRIPAP1,DGKQ,STX1B,SYT11,CALM1	grey	VSMC_M10
GO:0031669	0.82	0.22	91	182	cellular response to nutrient levels	BP	1	MARS,MAP3K5,CYP27B1,SNW1,PPARA,ATF4,PICK1,PIM1,TXN2,TFEB,SLC39A4,SRF,NUAK1,BRSK1,ALB,RRAGD,PTN,TNC,VPS41,IL15,ATG5,FOXO3,KPTN,SESN3,FOXA3,DNAJC15,RALB,PRKAG2,SZT2,RPTOR,EIF2AK2,WRN,GAS6,LARS,ULK1,NR1H4,USF2,FAM107A,PRKAG1,EIF2AK4,VDR,SLC38A2,NUAK2,NUPR2,SRD5A1,DNM1L,SIK1,SLC38A3,KCNB1,HSPA8,CBL,MTMR3,UCN2,USF1,XPR1,TBL2,GLUL,NFE2L2,SIK2,COMT,WNT4,PRKAG3,CTSV,MAPK1,BHLHA15,WIPI2,MAX,MED1,RRAGB,ZFYVE1,MAPK3,TNRC6A,SREBF1,LAMP2,NIM1K,STK26,JUN,CLEC16A,KIAA1324,TSC1,LCN2,WDR59,HSPA5,SH3GLB1,RIPOR1,MIR125B1,TRIM24,BGLAP,IMPACT,UPP1,RNF152	grey	VSMC_M10
GO:0003208	0.82	0.25	27	57	cardiac ventricle morphogenesis	BP	1	LY6E,FOXH1,TNNI3,POU4F1,TGFBR2,JAG1,NRG1,HAND2,MEF2C,TBX5,TNNC1,DSP,RYR2,PKP2,TNNI1,TGFB2,MYH7,BMPR1A,RBPJ,MED1,ISL1,FOXF1,ENG,SOX4,NOG,NKX2-5,HEY2	grey	VSMC_M10
GO:0097320	0.82	0.32	8	18	plasma membrane tubulation	BP	1	ASAP1,MICALL1,BIN3,WHAMM,DNM2,FNBP1L,SH3GLB1,CAVIN2	grey	VSMC_M10
GO:0043039	0.82	0.27	19	40	tRNA aminoacylation	BP	1	MARS,QRSL1,HARS,HARS2,CARS2,LARS,WARS2,GATC,YARS2,TARS2,DALRD3,LARS2,DARS2,FARSB,EARS2,LRRC47,KARS,AARS,MARS2	grey	VSMC_M10
GO:0001764	0.82	0.23	55	113	neuron migration	BP	1	SEMA6A,CEP85L,GFRA3,NTRK2,SRF,ADGRL3,NRCAM,NDNF,SEMA3A,UNC5D,NRG1,GAS6,FZD3,MEF2C,ELP3,IGSF10,RAPGEF2,NKX6-1,NR4A2,TUBB2A,SRGAP2C,KIAA0319,SATB2,AUTS2,MARK1,DISC1,CDKL5,LRIG2,COL3A1,MARK2,STAT3,SDCCAG8,DNAAF4,PSEN1,ITGA3,TRIM46,NDEL1,ZNF609,ALKBH1,NTN1,LHX1,CAMK2A,CDK5R1,DAB1,CRK,CELSR2,NTNG2,FBXO31,BARHL2,DAB2IP,ADGRG1,CNTN2,FOXG1,POMK,POMGNT2	grey	VSMC_M10
GO:0006826	0.82	0.26	23	48	iron ion transport	BP	1	STEAP2,PGRMC2,HEPHL1,ASIC3,STEAP3,HPX,SLC25A37,SLC48A1,SLC40A1,ISCU,ABCC5,MELTF,SLC11A1,ABCB6,FTH1,FLVCR2,NOX5,DNM2,SLC46A1,C1orf194,LCN2,SLC22A17,FTL	grey	VSMC_M10
GO:1904752	0.82	0.30	12	26	regulation of vascular associated smooth muscle cell migration	BP	1	LRP1,MEF2C,ADAMTS1,DOCK5,TERT,GNA13,SSH1,AGT,NFE2L2,DOCK7,MIR21,RHOA	grey	VSMC_M10
GO:0120162	0.82	0.24	38	78	positive regulation of cold-induced thermogenesis	BP	1	HSF1,GADD45G,EPAS1,GRB10,LPIN1,UCP1,FGF21,ALMS1,EBF2,KSR2,PRKAB1,CMKLR1,FABP4,TRPM8,GPR3,PER2,ACADL,MFAP2,YBX2,THRA,MFN2,KDM6B,ZBTB7B,OGT,IL4R,TRPV2,PPARGC1B,LEPR,PRDM16,LCN2,BSCL2,FABP5,ELOVL3,PEMT,PLAC8,APC,CEBPB,DIO2	grey	VSMC_M10
GO:0033138	0.82	0.24	36	74	positive regulation of peptidyl-serine phosphorylation	BP	1	NTRK2,IL11,EGFR,NTF4,BRAF,PRKD2,RAF1,SPRY2,RPTOR,BAG4,GAS6,RET,FNIP2,RIPK2,RAPGEF3,STK4,BDNF,CAPRIN2,HCLS1,OPRD1,OSM,STOX1,PDCD10,PINK1,ARAF,HAX1,SH2D3A,DOCK7,MTCP1,PARK7,MAPKAP1,IRGM,SMYD3,WNT5A,TXN,LIF	grey	VSMC_M10
GO:0015718	0.82	0.25	32	66	monocarboxylic acid transport	BP	1	ATP8B1,SLC16A7,PLA2G6,SLC22A13,ABCC4,SLC5A8,CYP7A1,SLC10A6,ABCC2,PLA2R1,ABCG2,MAP2K6,SLC16A6,SLCO3A1,ABCB11,SLCO1A2,SLCO1C1,NTSR1,SLC16A1,PLA2G4A,SLC27A1,MPC2,SLC16A13,ABCC3,NMUR2,EMB,NOS2,PROCA1,SLC16A4,ABCD3,PLA2G2C,PTGES	grey	VSMC_M10
GO:1903035	0.82	0.25	31	64	negative regulation of response to wounding	BP	1	SERPINB2,TSPAN8,SLC12A2,CLDN19,CD109,CLASP2,THBD,PLAT,C1QTNF1,SPP1,ADTRP,FAP,KIAA0319,UBASH3B,KREMEN1,CERS2,USF1,LRIG2,TNR,CASK,WNT4,MYOZ1,EPHA4,F12,ANXA2,SMAD3,ABAT,CRK,SERPINF2,FGA,RTN4RL1	grey	VSMC_M10

GO:1905476	0.82	0.29	13	28	negative regulation of protein localization to membrane	BP	1	GOPC,ITGB1BP1,LYPLA1,DMTN,PPFIA1,AP2M1,PPP2R5A,FZD9,LRRC15,LZTFL1,RSC1A1,INPP5K,MRAP2	grey	VSMC_M10
GO:0055065	0.82	0.20	224	438	metal ion homeostasis	BP	1	SLC39A5,NEDD4L,LRP1,CYP27B1,ESR1,SLC12A2,PRKN,SMDT1,BAK1,MYC,MCHR1,GPR20,PLA2G6,BTBD9,TMPRSS6,SLC39A4,STEAP2,SLC25A27,SLC1A1,TFAP2B,S1PR3,CNNM4,PRKCE,TNNI3,EPAS1,FPR2,IBTK,LPAR1,SLC31A2,EGFR,KEL,ATG5,TRPM4,GRIN2D,TRPC3,SLC8A2,C5AR2,C5AR1,HEPHL1,ATP7B,PTGIR,GIPR,CACNB2,SLC39A12,STEAP3,ATP1A3,ACKR2,SLC24A3,SNX5,C1QTNF1,TMTC4,RYR1,LETM2,PRNP,ADRA1D,DIAPH1,P2RX2,KL,CCKBR,HPX,RASA3,NCOA4,MICU3,IL1A,IMMT,C19orf12,P2RX3,PLCE1,RYR3,TMBIM6,P2RX7,P2RY1,PTK2B,SLC39A13,TPCN1,SLC8B1,VDR,STC1,SLC25A37,AP3B1,RMDN3,F2RL1,F2R,SLC40A1,CUTC,PKD2,CASQ2,MCUR1,SLC12A5,CD40,RYR2,SLC41A1,RAP1GDS1,TRPM1,SPPL3,LCK,KCNJ2,TESMIN,SLC12A7,TRPV4,BDH2,SLC30A10,TCIRG1,FAM20A,GNA13,ISCU,CMKLR1,MCUB,HJV,SCN7A,UBASH3B,DISC1,ANK2,GPER1,TRPM8,PDZD8,AGT,ATP1A2,SLC9A1,CASQ1,SLC12A8,NTSR1,MELTF,FZD9,TMCO1,PTH1R,SLC30A4,FIS1,CEMIP,ABL2,SLC12A9,CDH23,COMT,PTPN6,MICU1,MCU,CXCR2,GNG3,SLC11A1,HTT,PTGDR,PTGER2,ABCB6,TRPM7,ATP1B1,KCNA1,CD38,KCNMA1,ATP13A2,FTH1,HAP1,DLG4,CYB561A3,ATP1B2,FAM155B,PSEN1,CACNA1A,AC138894.1,ATP2A1,CD19,COX11,SMAD3,NOX5,CALM1,S100A14,S100A8,PRKCB,SCNN1B,BDKRB1,NMUR2,SLC39A6,TRPV2,HRH4,CCL14,CCL5,CCL7,C7,PTGER4,SLC25A23,MAIP1,TMEM199,SLC46A1,NUBP1,GNB1,ATP2B3,BCAP31,GNA15,TRPV3,TRPV1,PDPK1,P2RX1,PKD1,TMEM203,ATP6AP1,GPR157,SYPL2,CYBA,JPH3,ATP2C2,SLC30A7,FRRS1,LCN2,MCOLN3,SLC12A4,PTGFR,MIR199A1,KCNK3,DMD,MT1X,GPR35,NOL3,CHRNA10,TRIM24,CCR10,JPH2,SLC22A17,KCN	grey	VSMC_M10
GO:0030239	0.82	0.26	24	51	myofibril assembly	BP	1	OBSCN,LMOD2,SRF,PGM5,TMOD1,MYLK3,ACTG1,LMOD3,LMOD1,PRKAR1A,ACTC1,MYOZ2,CASQ1,TMOD4,MYPN,TTN,MYOZ1,TMOD2,OBSL1,LDB3,TCAP,MYH11,CSRP2,KRT19	grey	VSMC_M10
GO:0048639	0.82	0.23	66	134	positive regulation of developmental growth	BP	1	NEDD4L,LRP1,GLI1,RIMS2,PRKN,MAPK14,CPNE5,PIM1,SMO,SRF,SEMA4D,RIMS1,RUFY3,GOLGA4,MEGF8,CPNE9,TGFBR2,MKKS,SYT1,PLCB1,SLC23A2,PRKDC,PLS1,MEF2C,IL7,CELF1,TBX5,ZFYVE27,CYFIP1,IGF2,BDNF,SLC6A3,GPAM,HLX,ADNP,DISC1,ACTN3,CDKL5,YBX3,WNT3,CREB1,MAPT,FN1,MUL1,MAPK1,STAT5B,BMPR1A,RBPJ,SOX15,NDEL1,RAB11A,NTN1,TBX2,TRPV2,INSR,GATA6,GHR,L1CAM,MIR199A1,MIR222,BASP1,DIO3,POU3F2,CACNG7,HEY2,WNT2	grey	VSMC_M10
GO:0003229	0.82	0.26	22	47	ventricular cardiac muscle tissue development	BP	1	LY6E,FOXH1,TNNI3,POU4F1,NRG1,TBX5,TNNC1,DSP,RYR2,PKP2,TNNI1,TGFB2,MYH7,BMPR1A,RBPJ,MED1,DSG2,ISL1,ENG,NOG,NKX2-5,HEY2	grey	VSMC_M10
GO:0006493	0.82	0.24	36	74	protein O-linked glycosylation	BP	1	RXYLT1,LARGE1,C1GALT1,FKTN,IL15,POMGNT1,GALNT11,ST6GALNAC2,MGAT5B,TMTC4,GALNT15,GXYLT2,EOGT,POFUT1,B3GNT4,GALNT5,POGLUT1,B3GNT5,GALNT2,XXYLT1,TET1,PLOD3,KDELC2,GALNT8,GALNT16,OGT,POMT2,GALNT1,ST6GALNAC4,ST3GAL2,POFUT2,POMK,POMGNT2,ISPD,SLC35C1,ST8SIA6	grey	VSMC_M10
GO:0001659	0.82	0.22	70	141	temperature homeostasis	BP	1	ATF4,HSF1,ALDH1A1,GADD45G,EPAS1,NR1H2,GRB10,TLR4,LPIN1,IL15,UCP1,FGF21,LAMA4,NAPEPLD,ACVR2B,PLCL2,IL1A,ABHD6,ARNTL,NR1H3,ALMS1,EBF2,FTO,KSR2,ZNF423,PRKAB1,MAP2K6,CMKLR1,FABP4,TRPM8,GPR3,PER2,ACTN3,NTSR1,ACADL,STAT3,SLC27A1,TFE3,MFAP2,ACADVL,YBX2,THRA,RBPJ,MFN2,KDM6B,SLC25A44,ZBTB7B,OGT,PCTP,IL4R,TRPV2,PPARGC1B,LEPR,DOCK7,ACOT11,ABAT,TRPV1,PRDM16,LCN2,BSCL2,FABP5,ELOVL3,PEMT,NOVA1,PLAC8,DDIT3,PTGES,APC,CEBPB,DIO2	grey	VSMC_M10
GO:0051235	0.82	0.21	125	248	maintenance of location	BP	1	B4GALNT1,PPARA,TSPO,GOPC,SKP1,SUN2,MEST,GPAA1,TTC39B,MDFI,PLIN2,TAF8,CRY1,NFKBIE,PRKCE,IBTK,ALB,NR1H2,ATG5,LDAH,APOB,FAF1,ARHGAP21,ATP7B,ABHD5,GRIK5,TAF3,NFKBIB,RYR1,CDS2,DIAPH1,RASA3,ASXL1,RYR3,FBXW7,AUP1,PTK2B,ARL2BP,NR1H3,TPCN1,SLC8B1,CDS1,ACVR1C,F2R,FITM2,CRY2,FTO,PKD2,MORC3,CASQ2,RYR2,SUFU,LCK,SP100,CPT1A,IGSF11,GET4,UBASH3B,SORL1,ANK2,GPER1,FITM1,ATP1A2,CASQ1,NTSR1,TBCCD1,SLC30A4,SRGN,CEMIP,SOAT1,HK1,EHD1,PTPN6,FBN1,HTT,PINK1,STAT5B,FTH1,HAP1,VPS13D,VPS13C,ZFYVE1,PSEN1,ATP2A1,CD19,CALM1,S100A8,RIT2,BDKRB1,KEAP1,TMEM159,GM2A,PSMD10,SREBF1,C3,SLC25A23,PTPN2,PLIN3,TRPV1,PDPK1,RER1,PKD1,PARK7,GPSM2,CYBA,JPH3,SLC30A7,SPOUT1,LCN2,HSPA5,MCOLN3,DMD,BSCL2,NOL3,JPH2,THY1,SUPT7L,FTL,DDIT3,TXN,NRROS,STARD4,INSIG2,PFN4,POLR2M	grey	VSMC_M10
GO:0055003	0.82	0.35	6	14	cardiac myofibril assembly	BP	1	SRF,MYLK3,ACTC1,TTN,OBSL1,TCAP	grey	VSMC_M10
GO:2000241	0.82	0.23	52	105	regulation of reproductive process	BP	1	YTHDC2,ESR1,STK3,FBXO43,GDF9,UBE2B,AGO2,MAPK15,MYH9,CFAP69,NLRP5,HDAC2,SOX9,TOPAZ1,PLAT,SIRT2,PLCB1,SEMA3A,DHX37,MOS,ACVR1B,P2RY1,NKX3-1,ACVR1C,STK4,NPM2,HYAL3,PRKAR1A,INTS13,SNAI1,CCDC36,YTHDF2,CIB1,GPR3,CCDC87,HDAC4,CDKN1B,OVOL1,OVGP1,WNT4,SYDE1,NOX5,ZP2,FZR1,CACNA1H,WDR77,STXBP1,OOEP,WNT5A,DUSP1,LIF,LHFPL2	grey	VSMC_M10
GO:0032611	0.82	0.26	25	52	interleukin-1 beta production	BP	1	TNFAIP3,AGER,S1PR3,NOD1,TLR4,PANX1,MYD88,FOXP1,P2RX7,RIPK2,SERPINB1,F2RL1,F2R,NOD2,FZD5,HK1,STAT3,PYDC1,SMAD3,ISL1,MIR27B,CASP8,WNT5A,INAVA,CPTP	grey	VSMC_M10
GO:0032651	0.82	0.26	25	52	regulation of interleukin-1 beta production	BP	1	TNFAIP3,AGER,S1PR3,NOD1,TLR4,PANX1,MYD88,FOXP1,P2RX7,RIPK2,SERPINB1,F2RL1,F2R,NOD2,FZD5,HK1,STAT3,PYDC1,SMAD3,ISL1,MIR27B,CASP8,WNT5A,INAVA,CPTP	grey	VSMC_M10

GO:0002691	0.83	0.29	12	26	regulation of cellular extravasation	BP	1	AGER,PLCB1,CD99,ADAM8,ITGA4,BST1,CCL25,PTGER4,FADD,FUT4,THY1,PDGFD	grey	VSMC_M10
GO:0002861	0.83	0.30	11	24	regulation of inflammatory response to antigenic stimulus	BP	1	MAPK14,PLK2,HCK,NOD2,FGR,CD28,BTK,YES1,C3,PARK7,KARS	grey	VSMC_M10
GO:0034249	0.83	0.22	92	183	negative regulation of cellular amide metabolic process	BP	1	ORMDL2,PAN2,SHMT2,CNOT2,CNOT6,RIDA,PABPC1,EIF3E,PNLDC1,MRPL13,AGO2,TNRC6B,ATF4,TUT7,NTRK2,GAPDH,CNOT11,EXOSC3,IGF2BP3,RTN4,PNPT1,AGO1,TUT4,DHFR,MLH1,TNRC6C,PURA,EIF2AK2,PRNP,LSM1,PAN3,ENC1,CNOT1,CELF1,CNOT6L,EIF2AK4,EIF4E2,PAIP2B,ORMDL1,FTO,TENT4B,RBM24,BANK1,CAPRIN2,DIS3L2,GIGYF2,YTHDF2,SORL1,DDX6,YTHDF1,EIF4ENIF1,IGF2BP2,EIF4EBP2,DDX3X,RC3H1,UPF1,SAMD4A,STAT3,POLR2G,RTN1,NT5C3B,HAP1,DCP1B,FXR2,TARDBP,TOB1,TNRC6A,CNOT8,LARP1,SHMT1,PARN,FMR1,METTL16,PLEKHN1,CIRBP,ABCA7,TSC1,MIR29A,MIR21,MIR222,MIR125B1,MIR27B,MIR24-1,MIR27A,AGO4,METTL14,NANOS1,MIR339,YBX1,ZFP36L2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0019048	0.83	0.39	4	9	modulation by virus of host process	BP	1	ANO6,DAG1,INSR,RXRA	grey	VSMC_M10
GO:0010876	0.83	0.21	158	311	lipid localization	BP	1	ATP9B,VPS4B,APOF,ATP8B1,STARD6,LRP1,B4GALNT1,CPT1B,APOM,SERAC1,SLC27A6,PRKN,PPARA,TSPO,GDF9,PTCH1,PLA2G6,MEST,TTC39B,PLIN2,APOL4,APOL6,CRY1,CROT,ABCB1,ABCG5,ABCG8,TMEM30A,NR1H2,LDAH,APOB,MFSD2B,PIP4K2A,ABHD5,APOC1,TSKU,AKT2,ABCC4,C1QTNF1,CDS2,ANO4,SLC5A8,SOAT2,CYP7A1,ASXL1,OSBP,PITPNM2,XKR6,FBXW7,PLSCR4,LIMA1,P2RX7,AUP1,NR1H3,NKX3-1,CDS1,ACVR1C,ANO6,FITM2,CRY2,SLC10A6,FTO,COL4A3BP,ABCC2,SPP1,PLA2R1,PLTP,NME4,CPT1A,MAP2K6,ABCA5,ABCA9,ACSL5,CHKA,SLCO3A1,PITPNM1,FABP4,PITPNC1,EGF,GRAMD1B,TEX2,FITM1,PDZD8,ABCB11,AGT,SLC25A20,ABCG4,SLCO1A2,SLCO1C1,OSBPL2,NTSR1,OSBP2,APOLD1,APOD,PLA2G4A,STARD5,FIS1,OSBPL6,SOAT1,OSBPL1A,EHD1,ZDHHC8,ABCA12,LPCAT3,SPNS3,SLC27A1,STAT5B,TMEM30B,SYT7,GPS2,CLN8,LIPC,ANXA2,OSBPL7,NAXE,ZFYVE1,ABCD4,APOBR,AC138894.1,ABCC3,PCTP,LDLR,ATG2B,NMUR2,TMEM159,STRA6,GM2A,NPC1,SREBF1,C3,NOS2,PROCA1,PRELID3A,PTPN2,PLIN3,ATP11C,PITPNA,ABCA3,ABCA7,RXRA,CEL,ABCD3,VPS4A,MIR27B,MIR27A,BSCL2,FABP5,ABCA8,MIR33B,PLA2G2C,LDLRAP1,CRH,CPTP,LRAT,STARD4,PTGES,SGPP1,XKR8	grey	VSMC_M10
GO:0000045	0.83	0.23	43	88	autophagosome assembly	BP	1	ATG12,PIP4K2C,RNF5,RAB23,STX17,ATG5,RAB7A,PIP4K2A,RALB,ATG16L2,TMEM173,RAB5A,FEZ2,ULK1,NSFL1C,TBC1D12,TP53INP1,SEC22B,TMEM39A,TCIRG1,ADPRH,ATG16L1,BAG3,MTMR3,RAB1B,PIKFYVE,ATG2A,TBC1D14,PINK1,ATG9A,WIPI2,PHF23,MFN2,PSEN1,VMP1,ATG2B,SMCR8,IFT20,MTM1,EMC6,KIAA1324,SH3GLB1,IRGM	grey	VSMC_M10
GO:0030206	0.83	0.33	7	16	chondroitin sulfate biosynthetic process	BP	1	CHPF2,CSGALNACT1,CHST3,CHST7,CHST12,B3GALT6,CHSY3	grey	VSMC_M10
GO:0036003	0.83	0.30	10	22	positive regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	ATF4,HSF1,NFE2L2,RBPJ,MUC1,MAPK7,CREB3L3,HSPA5,DDIT3,CEBPB	grey	VSMC_M10
GO:0006355	0.83	0.19	1262	2411	regulation of transcription, DNA-templated	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ATP8B1,ONECUT2,BAZ2A,TCF4,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,STK3,OSR2,SNW1,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,PRKN,AGER,PPARA,MED30,IL5,BRD2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,LPIN1,SFRP4,UCP1,CREM,TEAD2,SETD7,SDCBP,MYCN,C6orf203,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,FAF1,MAMSTR,ATAD2B,BEND5,CDCA7,KDM7A,ZNF438,FOXE3,HDAC2,PHF10,MAML2,BBS7,MLLT10,DNMT3A,BMI1,ZC3H4,PRKD2,CNBP,SET	grey	VSMC_M10
GO:0051351	0.83	0.39	4	9	positive regulation of ligase activity	BP	1	XRCC1,XRCC4,FAM173B,NHEJ1	grey	VSMC_M10
GO:0007218	0.83	0.27	17	36	neuropeptide signaling pathway	BP	1	TAC3,MCHR1,GPR37,CYSLTR2,SCG5,RAPGEF2,NPY1R,SORCS3,CRCP,OPRD1,SORL1,NTSR1,PYY,NMUR2,NPB,NXPH4,GPR83	grey	VSMC_M10
GO:1905037	0.83	0.23	45	92	autophagosome organization	BP	1	ATG12,PIP4K2C,RNF5,RAB23,STX17,ATG5,RAB7A,PIP4K2A,RALB,ATG16L2,TMEM173,RAB5A,FEZ2,ULK1,NSFL1C,TBC1D12,TP53INP1,SEC22B,TMEM39A,TCIRG1,ADPRH,ATG16L1,BAG3,MTMR3,RAB1B,PIKFYVE,ATG2A,TBC1D14,PINK1,ATG9A,ATP13A2,WIPI2,PHF23,MFN2,PSEN1,AC138894.1,VMP1,ATG2B,SMCR8,IFT20,MTM1,EMC6,KIAA1324,SH3GLB1,IRGM	grey	VSMC_M10
GO:0048268	0.83	0.32	8	18	clathrin coat assembly	BP	1	EPS15,AP2S1,HIP1R,FCHO2,CALY,NSG1,AP2B1,SGIP1	grey	VSMC_M10
GO:0072599	0.83	0.27	16	34	establishment of protein localization to endoplasmic reticulum	BP	1	TRAM2,SEC61B,SEC61G,RAB10,SEC62,SRP14,SSR3,SPCS1,RYR2,SRPRA,ZFAND2B,SGTA,HSPA5,TRAM1L1,SPCS2,SEC61A2	grey	VSMC_M10

GO:0010591	0.83	0.27	16	34	regulation of lamellipodium assembly	BP	1	AVIL,RAC2,AKIRIN1,FER,PIK3R1,PLCE1,BIN3,CYFIP1,DMTN,AUTS2,WASF2,HDAC4,NCKAP1,WAS,DNM2,CARMIL2	grey	VSMC_M10
GO:0051154	0.83	0.28	15	32	negative regulation of striated muscle cell differentiation	BP	1	FRS2,PPARA,PI16,SOX6,BDNF,FZD7,HDAC4,BHLHA15,YY1,PLPP7,MIR199A1,MIR222,RGS4,YBX1,NKX2-5	grey	VSMC_M10
GO:0010712	0.83	0.27	16	34	regulation of collagen metabolic process	BP	1	HDAC2,CYGB,CYP7A1,F2R,FAP,AMELX,VSIR,WNT4,SUCO,LARP6,CIITA,SERPINF2,ENG,MIR29A,RGCC,CBX8	grey	VSMC_M10
GO:0061179	0.83	0.39	4	9	negative regulation of insulin secretion involved in cellular response to glucose stimulus	BP	1	NDUFAF2,ADRA2A,KLF7,ENY2	grey	VSMC_M10
GO:0016180	0.83	0.29	11	24	snRNA processing	BP	1	EXOSC4,EXOSC3,INTS10,USB1,INTS8,INTS12,INTS5,AP002990.1,INTS2,INTS11,EXOSC5	grey	VSMC_M10
GO:0014033	0.83	0.24	37	77	neural crest cell differentiation	BP	1	SEMA6A,SOX10,SMO,SEMA4D,SEMA4C,SOX9,OVOL2,JAG1,ALX1,SEMA3D,SEMA3A,NRG1,KBTBD8,RET,HAND2,MEF2C,SEMA4F,SEMA3G,SEMA4G,KLHL12,SEMA3F,PEF1,PDCD6,GBX2,LAMA5,SEMA6D,FN1,MAPK1,BMPR1A,RADIL,ALDH1A2,SEMA4A,MAPK3,GSC,TCOF1,ISL1,SOX8	grey	VSMC_M10
GO:0060428	0.83	0.29	12	26	lung epithelium development	BP	1	SOX9,FOXJ1,SRSF6,CREB1,SAV1,THRA,RBPJ,MAP2K1,STRA6,GATA6,PKD1,WNT2	grey	VSMC_M10
GO:0048857	0.83	0.26	22	46	neural nucleus development	BP	1	CKB,TTBK1,FOXP2,SIRT2,NDUFS3,SUDS3,COX6B1,INA,ALDH1A3,PADI2,ACTB,CHRNB2,CALM1,CDK5R1,SEC16A,ATP5PB,SYPL2,MAPKAP1,HSPA5,RHOA,BASP1,YWHAH	grey	VSMC_M10
GO:0030433	0.83	0.24	38	78	ubiquitin-dependent ERAD pathway	BP	1	CANX,RNF5,DERL1,FOXRED2,SEC61B,ECPAS,UBXN4,FBXO17,DNAJC18,NPLOC4,UBXN8,AUP1,TMEM67,AMFR,ERLIN1,YOD1,USP19,RNF185,RHBDD2,EDEM3,NFE2L2,SYVN1,DERL3,TMUB2,DNAJC10,DNAJB12,TMEM129,ANKZF1,DNAJB2,CALR3,FBXO2,SEL1L,BCAP31,SGTA,HSPA5,FAM8A1,UBE2G2,DERL2	grey	VSMC_M10
GO:0032482	0.83	0.32	8	18	Rab protein signal transduction	BP	1	RAB21,MADD,RAB4A,RAB15,DENND4A,RAB33A,DEND1A,RAB39A	grey	VSMC_M10
GO:0033574	0.83	0.27	16	34	response to testosterone	BP	1	NME1,TSPO,HSF1,MTAP,CA9,FOXP2,NCOA4,GPI,KCNJ11,NKX3-1,SPP1,SRD5A1,CBL,NQO1,BGLAP,DUSP1	grey	VSMC_M10
GO:0006775	0.83	0.30	10	22	fat-soluble vitamin metabolic process	BP	1	CYP27B1,CYP2R1,CBR3,PLTP,SNAI1,CYP27A1,ALDH1A2,PIAS4,GFI1,LRAT	grey	VSMC_M10
GO:0060021	0.83	0.24	34	71	roof of mouth development	BP	1	OSR2,COL11A2,TBC1D32,BNC2,DLX5,MEOX2,OSR1,INTU,BBS7,IFT172,CSRNP1,WNT11,TGFBR2,HAND2,FRAS1,TFAP2A,ITGB6,TGFB2,SATB2,SNAI1,EPHB3,DLG1,BCOR,BMPR1A,DHRS3,TMEM107,WFIKKN2,TBX2,JAG2,MMP25,SKI,WFIKKN1,WNT5A,INSIG2	grey	VSMC_M10
GO:0072080	0.83	0.23	36	75	nephron tubule development	BP	1	MTSS1,MYC,KLHL3,PTCH1,SMO,TFAP2B,SIX2,POU3F3,OSR1,SOX9,AQP11,GZF1,WNT11,JAG1,PAX8,EYA1,FMN1,MEF2C,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,NOG,SIX1,LIF,FGF1	grey	VSMC_M10
GO:0009117	0.83	0.20	196	381	nucleotide metabolic process	BP	1	NME1,HSD17B4,TBPL1,PDE7B,ENPP3,ATP5MGL,DPYS,PPT2,PPARA,PDE10A,ACSL6,PRXL2C,GTPBP1,GUCA1B,IMPDH1,NMRK1,GDA,CROT,SLC35B2,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,ME1,NT5E,PPT1,BPGM,DLD,SPHK2,CMPK1,ADCY3,NUDT15,DLG2,LACC1,NUDT5,DHTKD1,MBD4,PRKAG2,SLC22A13,ATP5F1C,ELOVL1,PFKP,IDO2,IDO1,NUDT16,PANK2,PDK1,SUCLG2,PDHX,SLC5A8,ELOVL7,PANK1,GPI,NUDT12,AMPD3,ATP5F1A,MCCC2,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,GMPR,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,PUDP,NUDT17,MFN1,PFKFB2,PRPS2,ENO4,PARP9,HACD2,ARNT,ADCY4,CTPS2,ACTN3,HDAC4,THEM5,DNAJC30,MLXIPL,PDE8A,DTYMK,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,UPB1,HK1,ACSBG1,ATP5S,CASK,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,MAPK1,ENO3,NT5C3B,PARP1,TECR,CARD11,SLC26A1,NAXE,PSEN1,ACOT2,GUCY2D,PKLR,PANK3,GCDH,OGT,UPRT,ADPGK,PDE4A,ACSM3,ACACA,NEIL1,NCOR1,INSR,SLC26A2,PRPSAP2,ADSSL1,NT5M,NOS2,ACSBG2,ALDOC,PIPOX,ACOT11,NADK,ATP6V0C,PANK4,NTHL1,NME3,MPP1,PARK7,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,AK8,UCK1,MLYCD,KARS,FUK,DHODH,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,PDZD3,ELOVL3,MTHFD2L,CMPK2,TIGAR,NUDT19,NNMT,NME6,DCTD,NUDT2,NAPRT,HINT1,UPP1,NMNAT1	grey	VSMC_M10
GO:0002637	0.83	0.25	23	48	regulation of immunoglobulin production	BP	1	IL5,EXOSC3,MSH2,HMCES,PHB,MLH1,PAXIP1,SHLD1,HPX,PRKDC,TRAF6,GPI,TMBIM6,CD40,CD28,BCL6,FOXP3,SHLD2,TBX21,STX4,IL4R,SUPT6H,TRAF2	grey	VSMC_M10
GO:0032309	0.83	0.29	11	24	icosanoid secretion	BP	1	PLA2G6,ABCC4,PLA2R1,MAP2K6,NTSR1,PLA2G4A,NMUR2,NOS2,PROCA1,PLA2G2C,PTGES	grey	VSMC_M10
GO:0032922	0.83	0.25	26	55	circadian regulation of gene expression	BP	1	PPARA,ATF4,CSNK1E,CRY1,HDAC2,MYCBP2,PPP1CB,BHLHE40,NUDT12,NCOA2,ARNTL,TOP1,CRY2,HDAC1,CIART,USP2,PER2,KDM5A,MAGED1,NGFR,OGT,KDM8,RAI1,PER3,ZFHX3,PASD1	grey	VSMC_M10
GO:0097553	0.83	0.23	46	95	calcium ion transmembrane import into cytosol	BP	1	PRKCE,IBTK,ATG5,GRIN2D,SLC8A2,RYR1,PRNP,DIAPH1,RASA3,RYR3,PTK2B,TPCN1,SLC8B1,F2R,PKD2,CASQ2,RYR2,LCK,TRPV4,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,FAM155B,CD19,CALM1,BDKRB1,TRPV2,TRPV3,TRPV1,PDPK1,P2RX1,CYBA,JPH3,MCOLN3,DMD,NOL3,JPH2,THY1,DDIT3	grey	VSMC_M10

GO:0007186	0.83	0.19	234	458	G protein-coupled receptor signaling pathway	BP	1	TAC3,LRP1,ADGRG6,ESR1,FRS2,ADM2,FZD6,IGF2R,MCHR1,GRM4,GPR20,PICK1,RAC2,SMO,ZDHHC21,OPN1SW,GRM8,GPR37,RORB,CRY1,RIC8B,FZD1,PHF24,ADGRF1,S1PR3,ADGRL3,OXER1,GABBR2,CAMKMT,FPR2,KLK14,LPAR1,CXCL8,AREG,CRHR2,PLEK,GPR85,DGKI,MET,SPHK2,TPRA1,ADCY3,C5AR2,C5AR1,PTGIR,PHB,GIPR,CYSLTR2,TMEM145,GPR180,ACKR2,ARRB1,ZNF219,PDE6G,PLCB1,RASGRP4,ADRA1D,CCKBR,ADRA2B,TUB,PDGFRL,RGS20,HTR7,RGS7BP,PAX8,ABHD6,NLN,PIK3CB,PREX2,HPGD,PLCE1,CHRM5,ADGRV1,SCG5,FZD3,P2RY1,PTK2B,ADGRG5,RAPGEF2,CCL17,NPY1R,HOMER1,CHRM4,F2RL1,F2R,IQGAP2,RPGRIP1L,ADCY7,CHRM3,GRM2,APLP2,ADCY2,TRPM1,LGR6,RGS1,SORCS3,GIT2,CRCP,ADRA2A,GAP43,PTHLH,GNA13,GPR156,CMKLR1,RRH,OPRD1,GRK2,SORL1,GPER1,SAG,DGKD,AGT,WASF2,GPR3,ADCY4,FZD7,UCN2,ECE2,KCNK2,NTSR1,XPR1,PDE6H,FZD9,HOMER2,GPRC5D,GPR19,DGKG,FZD5,PTH1R,NMT1,PYY,PTPN6,GNB1L,ADRA2C,CXCR2,GPBAR1,GNG3,GNB3,PTGDR,GRK4,PTGER2,CALCRL,ECE1,RAMP2,GPR161,BHLHA15,CHRM1,TMOD2,TULP3,GNB5,DAGLB,GPR173,ADGRE5,GRK6,RGS14,ARHGEF11,ADGRA3,AGTRAP,DGKQ,HRH2,GUCY2D,DGKE,PIK3R5,CALM1,GPR68,DNM2,RIT2,BDKRB1,PDE4A,NMUR2,ADORA2B,HRH4,CAMK2A,CCL14,INSR,CCL5,CCL7,CCL2,CCL25,CDK5R1,RASD1,VAV1,PTGER4,C3,GNAL,ADGRG4,INPP5K,MGRN1,GNB1,GNA15,GNG10,GNG7,GPR153,BAIAP3,GNG13,PALM,GPR157,GNAT2,GNAI3,CELSR2,GPSM2,USP20,ADGRL2,PTGFR,HTR1D,CCL16,GPR35,RGS11,ADGRE3,ADGRG1,GPR182,CNTN2,TAS2R3,CHGA,CCR10,GPR37L1,CA2,GNG12,NPB,NXPH4,RGS12,CELSR3,RGS4,OR5AN1,GPR88,MLNR,G	grey	VSMC_M10
GO:0045987	0.83	0.30	9	20	positive regulation of smooth muscle contraction	BP	1	SRF,KIT,ADRA2B,F2R,CHRM3,GPER1,ABAT,MIR21,RHOA	grey	VSMC_M10
GO:0032743	0.83	0.30	10	22	positive regulation of interleukin-2 production	BP	1	SPTBN1,PRKD2,TRAF6,IL1A,RIPK2,CD28,STAT5B,CARD11,TRAF2,GLMN	grey	VSMC_M10
GO:0006734	0.83	0.29	11	24	NADH metabolic process	BP	1	PFKP,MDH2,NUDT12,GPD1,PFKM,NUDT17,ACTN3,MDH1B,HK1,NQO1,TIGAR	grey	VSMC_M10
GO:0071346	0.83	0.23	39	80	cellular response to interferon-gamma	BP	1	GAPDH,NR1H2,TLR4,NMI,ACTG1,HPX,HCK,FLNB,CCL17,NR1H3,NLRC5,IFNGR2,RAB7B,SP100,PARP9,PARP14,CDC42EP2,WAS,MED1,STX4,STX8,CCL14,CCL5,CCL7,CCL2,CCL25,JAK1,NOS2,PTPN2,SOCS1,ADAMTS13,ASS1,STXBP1,CCL16,IRGM,CLDN1,WNT5A,VAMP3,CCL22	grey	VSMC_M10
GO:0060353	0.83	0.38	4	9	regulation of cell adhesion molecule production	BP	1	CXCL8,COLEC12,MIR222,MIR27B	grey	VSMC_M10
GO:0016925	0.83	0.26	20	42	protein sumoylation	BP	1	UHRF2,TRPM4,SUMO2,CBX4,EYA1,HDAC7,TOLLIP,IFIH1,PIAS3,ARNT,HDAC4,STX1A,MUL1,GNL3L,PIAS2,PIAS4,PARK7,RNF212B,RWDD3,RASD2	grey	VSMC_M10
GO:0060019	0.83	0.38	4	9	radial glial cell differentiation	BP	1	STAT3,GPR157,RHOA,METTL14	grey	VSMC_M10
GO:1903506	0.83	0.18	1262	2412	regulation of nucleic acid-templated transcription	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ATP8B1,ONECUT2,BAZ2A,TCF4,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,STK3,OSR2,SNW1,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,PRKN,AGER,PPARA,MED30,IL5,BRD2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,LPIN1,SFRP4,UCP1,CREM,TEAD2,SETD7,SDCBP,MYCN,C6orf203,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,FAF1,MAMSTR,ATAD2B,BEND5,CDCA7,KDM7A,ZNF438,FOXE3,HDAC2,PHF10,MAML2,BBS7,MLLT10,DNMT3A,BMI1,ZC3H4,PRKD2,CNBP,SET	grey	VSMC_M10
GO:0043491	0.83	0.21	73	147	protein kinase B signaling	BP	1	PHLPP1,STK3,PPARA,LEMD2,PTK2,NTRK2,TEK,RTN4,ITGB1BP1,MET,EGFR,SESN3,PHB,SOX9,PLK3,SPRY2,C1QTNF1,SIRT2,HBEGF,BAG4,NRG1,GAS6,MFHAS1,RET,PIK3CB,PTPRJ,NKX3-1,GCNT2,PAX2,ADTRP,CD40,IGF2,GRM2,BANK1,TCF7L2,PDCD6,DAG1,EGF,HCLS1,RPS6KB2,GPER1,CASS4,CIB1,OSM,THPO,CD28,THEM4,DLG1,ADAM8,STOX1,GDF15,PINK1,MUL1,OTUD3,PEAR1,HAX1,TMEM100,PIK3R5,INSR,CCL5,CCL2,INPP5K,PARK7,ENG,MIR29A,MIR199A1,MIR21,MIR222,DDIT3,TXN,MYORG,TSPYL5,RASD2	grey	VSMC_M10
GO:0071333	0.83	0.22	54	110	cellular response to glucose stimulus	BP	1	ZNF236,NME1,LRP1,AGER,PLA2G6,SRF,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,GRIK5,RAF1,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,KCNJ11,TIAM1,RAB11FIP5,OPA1,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,SLC9B2,ZBTB20,ADRA2A,KCNB1,POLG,GPER1,RAB11FIP2,MLXIPL,SIDT2,PDK3,KLF7,FIS1,MEN1,ENY2,ABCA12,PPP3CB,PTPRN,MPC2,STX4,GPR68,SIN3A,OXCT1,NADK,BAIAP3,CYBA,SOX4,CRH	grey	VSMC_M10
GO:0008645	0.83	0.23	40	83	hexose transmembrane transport	BP	1	SLC2A12,MAPK14,SLC25A27,GRB10,FGF21,BRAF,MFSD4B,SLC26A5,PRKAG2,AKT2,ASPSCR1,TRIB3,PIK3R1,SORBS1,IRS1,SLC2A10,TERT,C2CD5,PEA15,NFE2L2,CLTCL1,SLC2A2,SLC27A1,SLC2A9,SLC2A4,RSC1A1,SLC5A2,SLC50A1,SLC5A11,PRKCB,INSR,YES1,C3,GPC3,INPP5K,SLC45A1,SLC2A6,TSC1,FABP5,ARPP19	grey	VSMC_M10
GO:0072202	0.83	0.29	10	22	cell differentiation involved in metanephros development	BP	1	SMO,SIX2,POU3F3,OSR1,PAX8,PAX2,SALL1,WNT4,CITED1,LIF	grey	VSMC_M10

GO:1904707	0.83	0.27	16	34	positive regulation of vascular associated smooth muscle cell proliferation	BP	1	MAP3K5,HPGD,ADAMTS1,NQO2,TERT,AGT,BMPR1A,MFN2,JUN,GNAI3,MIR21,MIR222,MIR27B,MIR27A,FOXJ2,LDLRAP1	grey	VSMC_M10
GO:0030212	0.83	0.29	10	22	hyaluronan metabolic process	BP	1	PIM1,CEMIP2,HAS1,IL15,HYAL1,HYAL3,EGF,ABCC5,CEMIP,HAS3	grey	VSMC_M10
GO:0007160	0.83	0.20	95	192	cell-matrix adhesion	BP	1	ITGA7,ONECUT2,LRP1,TNXB,PARVG,PTK2,CDKN2A,TEK,SRF,CDK6,SGCE,HOXA7,ITGB1BP1,EPHA1,CLASP2,BCAM,RIN2,JAG1,ACTG1,FERMT1,ARHGEF7,PTPRA,FAM107A,PIK3CB,PIK3R1,FMN1,SORBS1,PTPRJ,PTK2B,TIAM1,DMTN,ITGB6,LDB1,PXN,CD96,SLK,PPFIA1,COL17A1,FBLN5,COL16A1,DAG1,AJUBA,ITGA10,ARHGAP6,DISC1,CIB1,SLC9A1,ITGB5,ACTN3,WHAMM,STRC,EFEMP2,APOD,HOXD3,BCL6,COL13A1,TRIP6,ITGA2B,ITGA4,FN1,CASK,FERMT3,WNT4,NID2,COL3A1,TRPM7,VCL,BST1,MINK1,ITGA3,THBS3,TAOK2,SMAD3,ITGA11,CORO2B,OTOA,BCAS3,CAMSAP3,CCL25,ADAMTS12,PDPK1,L1CAM,PRKCZ,PKD1,ADAMTS13,TSC1,RHOA,FGA,ACVRL1,PEAK1,THY1,TIMM10B,ACER2,BCL2L11,DUSP22	grey	VSMC_M10
GO:0010640	0.83	0.30	9	20	regulation of platelet-derived growth factor receptor signaling pathway	BP	1	LRP1,PTGIR,HIP1R,PTPRJ,CBL,LRIG2,APOD,IFT20,PTPN2	grey	VSMC_M10
GO:0006623	0.83	0.26	16	35	protein targeting to vacuole	BP	1	VPS41,RAB7A,NCOA4,AP3B1,MON1A,HSPA8,SORL1,RNF215,VPS37D,AP4M1,AP3M1,VPS13D,VPS13C,LAMP2,VPS4A,SNX16	grey	VSMC_M10
GO:0001759	0.83	0.30	9	20	organ induction	BP	1	FRS2,SPRY1,WNT11,ROBO1,ROBO2,WNT5A,SIX1,FGF1,WNT2	grey	VSMC_M10
GO:0002369	0.83	0.29	10	22	T cell cytokine production	BP	1	RSAD2,TRPM4,TRAF6,DENND1B,FZD5,FOXP3,TNFRSF1B,TBX21,PRKCZ,TRAF2	grey	VSMC_M10
GO:0002724	0.83	0.29	10	22	regulation of T cell cytokine production	BP	1	RSAD2,TRPM4,TRAF6,DENND1B,FZD5,FOXP3,TNFRSF1B,TBX21,PRKCZ,TRAF2	grey	VSMC_M10
GO:0045595	0.84	0.18	597	1153	regulation of cell differentiation	BP	1	NFATC1,NME1,TCF4,LRP1,SEMA6A,GLI1,CYP27B1,MAML1,ATAT1,FRS2,RAB21,STK3,SNW1,TIAM2,HSPA1B,BRD1,AGER,PPARA,HLA-DRA,FBLN1,IL5,TSPO,FSTL4,TCF7,SYNGAP1,XRCC6,TRIB1,MYC,TOB2,SMAD5,PTK2,PTCH1,ATF4,PLXNA4,MAPK14,NTRK2,CSNK1E,KDM4C,SOX10,PI16,PIM1,SMO,ZDHHC21,HSF1,DAAM2,TAF8,ZNF16,RBFOX2,FBXO7,RORB,SRF,TTBK1,DLK2,OCIAD1,CDK6,RFX3,KIT,TNFRSF21,TFAP2B,ROR2,SEMA4D,S1PR3,SEMA4C,SOSTDC1,BEND6,ZNF268,SIX2,SMAP1,CD109,RTN4,PPP2R1A,RUFY3,HOXA2,HOXA7,ANKRD17,PTBP3,MYCL,SLC46A2,MTURN,AREG,AKIRIN1,CNOT4,EPHA7,NR1H2,MBOAT2,PTN,ITGB1BP1,GRHL1,ST7,IL4I1,EGFR,FUZ,TRIM32,TLR4,CDK5RAP2,IL15,SFRP4,MYLK3,DKKL1,TEAD2,SDCBP,MYCN,NRCAM,TRPM4,OSR1,FOXO3,NTF4,MKX,APOB,MAMSTR,SPRY1,PLXNA1,FOXE3,HDAC2,NAPEPLD,SOX9,CLASP2,CLPTM1,PTCH2,GOLGA4,GLI2,MEGF8,AAMDC,KDM4A,UNC13D,RAF1,XRCC2,ACVR2B,KLF5,FOXJ1,NUMBL,POU4F1,TSKU,IL15RA,SPRY2,SS18L2,ALK,RIN2,HOOK3,TGFBR2,OVOL2,ZNF219,ACVR2A,IKBKB,PLEKHB1,BHLHE40,JAG1,SIRT2,RARB,NR1D2,PTPRQ,SRA1,PLCB1,MAFG,SPRED3,RAC3,ALX1,EIF2AK2,LSM1,ARHGEF7,SEMA3D,BTG1,SPART,PLXNC1,SEMA3A,CLIC1,NRG1,NCKAP1L,GAS6,ULK1,FOXP1,MITF,LMOD3,PRKDC,IRF7,RYK,ADRA2B,TRAF6,TCF15,TRIB3,EPHB1,SOX12,PLAG1,RET,TOX,ZC3H8,ASXL1,DNMT3B,PAX8,ACVR1B,CAMK4,CEBPA,SMYD1,NLN,ANKRD27,FAIM,ZNF536,PIK3R1,HAND2,EYA1,ROBO1,ROBO2,IL17RD,ARNTL,FBXW7,ADGRV1,FZD3,MEF2C,TMEM131L,SEMA4F,IL7,VEGFC,TLX2,CUX2,SOX6,PTK2B,RASGRP1,MME,RAPGEF2,DPYSL2,CCL17,EIF2AK4,NR	grey	VSMC_M10
GO:0031113	0.84	0.25	23	49	regulation of microtubule polymerization	BP	1	HSPA1B,SLAIN2,MET,CDK5RAP2,MAPRE1,EML2,SLC39A12,MAPRE3,SLAIN1,NAV3,ARHGEF7,CLIP1,INPP5J,CDKN1B,MAPT,TOGARAM1,NIN,CAMSAP3,CDK5R1,MECP2,CAMSAP1,PSRC1,DRG1	grey	VSMC_M10
GO:1903540	0.84	0.32	7	16	establishment of protein localization to postsynaptic membrane	BP	1	NSG1,GRIPAP1,RAB8A,CPLX1,STX1B,RAB11A,ARHGAP44	grey	VSMC_M10
GO:0002052	0.84	0.32	7	16	positive regulation of neuroblast proliferation	BP	1	SOX10,SMO,FZD3,VEGFC,ZNF335,DISC1,FOXG1	grey	VSMC_M10
GO:0045773	0.84	0.26	17	37	positive regulation of axon extension	BP	1	LRP1,SRF,RUFY3,GOLGA4,MEGF8,ZFYVE27,CYFIP1,ADNP,DISC1,CDKL5,MAPT,FN1,NDEL1,RAB11A,NTN1,TRPV2,L1CAM	grey	VSMC_M10
GO:0006892	0.84	0.22	48	99	post-Golgi vesicle-mediated transport	BP	1	AP3S1,GOPC,VPS52,EXOC4,STEAP2,SPTBN1,EPS15,RAB10,RBSN,OPTN,GOLGA4,CCDC93,LYPLA1,VAMP5,EXOC6B,DOP1B,KIF13A,GBF1,CCDC91,VTI1A,SNAP23,AP1AR,SORL1,BBS1,RNF215,NSF,SCAMP3,KLHL20,AP4M1,ANKFY1,EXOC5,CNST,RSC1A1,GAK,VPS13C,AC138894.1,DNM2,GGA2,SCAMP2,VPS35L,CORO7,RAB26,SEC16A,AP1G1,C16orf70,AP3S2,RABIF,VAMP3	grey	VSMC_M10
GO:0006007	0.84	0.32	7	16	glucose catabolic process	BP	1	PFKP,PFKM,PFKFB2,ACTN3,HK1,TKTL1,TIGAR	grey	VSMC_M10
GO:0007338	0.84	0.22	42	86	single fertilization	BP	1	TRIM36,H3F3C,MYH9,NLRP5,RIMS1,SPACA6,DKKL1,IZUMO1,ADCY3,TRPC3,WDR48,PLAT,ADAM18,PLCB1,UBXN8,STX2,AP3B1,NPM2,HYAL3,SLC9B1,ABHD2,CCDC87,LYZL6,OVGP1,PLCD4,RAB3A,AKAP3,ADAM21,ADAM20,UBAP2L,SPESP1,NOX5,ZP2,SNU13,CACNA1H,PARK7,STXBP1,CD46,GLIPR1L2,LHFPL2,SPA17,TMPRSS12	grey	VSMC_M10
GO:0048199	0.84	0.30	9	20	vesicle targeting, to, from or within Golgi	BP	1	MAPK15,ARFGAP2,GBF1,KLHL12,PEF1,PDCD6,AP1AR,TMED10,PPP6C	grey	VSMC_M10
GO:0010457	0.84	0.33	6	14	centriole-centriole cohesion	BP	1	KIF3A,CNTLN,CEP68,CEP44,CEP250,NIN	grey	VSMC_M10
GO:0035335	0.84	0.23	37	77	peptidyl-tyrosine dephosphorylation	BP	1	EYA4,PTP4A3,PTPDC1,ACP4,RNGTT,MTMR2,PTPRF,TIMM50,MTMR14,PTPRQ,DUSP6,PTPRA,MTMR7,EYA1,PTPRJ,PTPN5,SSH1,UBASH3B,EYA3,MTMR3,PTPRO,DUSP18,DUSP12,DUSP10,DUSP19,PTPN6,PTPN21,DUSP14,PTPN2,SSH2,MTM1,MTMR1,CDC14A,DUSP26,DUSP1,DUSP22,PTPMT1	grey	VSMC_M10

GO:0043405	0.84	0.21	72	146	regulation of MAP kinase activity	BP	1	MAP3K5,TNXB,MAP3K4,AGER,TRIB1,TAB1,STK38,KIT,ROR2,DNAJA1,EPGN,TGFA,EGFR,ARHGEF5,TLR4,SPRY1,SPRY2,NEK10,FLT1,TRAF6,TRIB3,PIK3CB,ROBO1,PTPRJ,PTK2B,RASGRP1,TIAM1,PAQR3,NOD2,DTNBP1,TAOK3,CD40,PDCD4,ADRA2A,AJUBA,KRAS,EGF,SORL1,AGT,DVL3,MAP3K11,ADAM8,AIDA,FZD5,DUSP10,MAP4K2,DUSP19,PTPN6,PDCD10,EPHA4,MAGED1,DVL2,CDK12,RGS14,PSEN1,FGF18,PIK3R5,MAP2K5,INSR,GHR,KSR1,INPP5K,TRAF2,DAB2IP,S100A12,WNT5A,DUSP1,HRAS,LAX1,MAP2K7,FGF1,PDGFD	grey	VSMC_M10
GO:0030865	0.84	0.24	26	55	cortical cytoskeleton organization	BP	1	EPB41L2,RAC2,TLN1,PLEK,LCP1,LLGL2,IKBKB,RAC3,NCKAP1L,PLS1,EPB41L1,RTKN,RND1,RHOBTB2,TRPV4,EPB41,RHOBTB1,DLG1,PPP2R3C,NCKAP1,EPB41L3,STRIP1,VPS4A,FHOD1,RHOA,RND3	grey	VSMC_M10
GO:0006006	0.84	0.21	77	155	glucose metabolic process	BP	1	PRKN,PPARA,ATF4,MAPK14,GPT,GNMT,CRY1,PGM5,TFAP2B,SLC25A13,GAPDH,PPP4R3B,ZNF692,FAM3C,RUBCNL,AKR1A1,KHK,EPM2AIP1,GCKR,PPP1CB,AKT2,PFKP,PGM2L1,C1QTNF1,SIRT7,PDK1,PPP1R3B,GPI,NLN,NCOA2,SORBS1,GPD1,KCNJ11,PFKM,IGF2,GPLD1,IRS1,SIK1,CPT1A,MST1,PPP1R3E,PFKFB2,PC,PPP1R3D,SLC37A4,PER2,ACTN3,USF1,PASK,DUSP12,APOD,PDK3,SORD,HK1,GNB3,PPP1R3F,IGFBP4,DDB1,DGKQ,OGT,COX11,CRTC2,LCMT1,ADPGK,INSR,LEPR,PTPN2,INPP5K,TKTL1,MLYCD,ACADM,FBP2,OAS1,FABP5,TIGAR,NNMT,ARPP19	grey	VSMC_M10
GO:0072163	0.84	0.22	38	79	mesonephric epithelium development	BP	1	MYC,SMAD5,PTCH1,SMO,CAT,SIX2,EPCAM,BMPER,OSR1,SPRY1,SOX9,FOXJ1,GZF1,WNT11,RARB,RET,PAX8,EYA1,ROBO2,FMN1,PKD2,PAX2,SALL1,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,SMAD3,LHX1,GPC3,PKD1,SOX8,NOG,BASP1,SIX1,FGF1	grey	VSMC_M10
GO:0072164	0.84	0.22	38	79	mesonephric tubule development	BP	1	MYC,SMAD5,PTCH1,SMO,CAT,SIX2,EPCAM,BMPER,OSR1,SPRY1,SOX9,FOXJ1,GZF1,WNT11,RARB,RET,PAX8,EYA1,ROBO2,FMN1,PKD2,PAX2,SALL1,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,SMAD3,LHX1,GPC3,PKD1,SOX8,NOG,BASP1,SIX1,FGF1	grey	VSMC_M10
GO:1905153	0.84	0.33	6	14	regulation of membrane invagination	BP	1	NCKAP1L,F2RL1,ANO6,SYT11,C3,ABCA7	grey	VSMC_M10
GO:0045047	0.84	0.27	14	30	protein targeting to ER	BP	1	TRAM2,SEC61B,SEC61G,SEC62,SRP14,SSR3,SPCS1,SRPRA,ZFAND2B,SGTA,HSPA5,TRAM1L1,SPCS2,SEC61A2	grey	VSMC_M10
GO:0034105	0.84	0.37	4	9	positive regulation of tissue remodeling	BP	1	IL15,PPP3CA,MIR199A1,MIR27B	grey	VSMC_M10
GO:0021987	0.84	0.22	42	87	cerebral cortex development	BP	1	LRP1,SUN2,NTRK2,SMO,EFHC1,MBOAT7,RTN4,FOXP2,POU3F3,FAT4,MKKS,PLCB1,ROBO1,CELF1,CSNK2A2,MCPH1,SLC38A2,SRGAP2C,SRD5A1,DISC1,NSUN5,BCL2A1,DIXDC1,COL3A1,MPP5,PSEN1,NDEL1,XAB2,CDK5R1,DAB1,LRP8,CRK,TSC1,DAB2IP,RHOA,ADGRG1,FOXG1,LAMB1,GNG12,CCDC85C,POU3F2,BTBD3	grey	VSMC_M10
GO:0150011	0.84	0.33	6	14	regulation of neuron projection arborization	BP	1	DVL3,DLG4,DVL2,MYO9A,NTNG2,WNT5A	grey	VSMC_M10
GO:0097107	0.84	0.33	6	14	postsynaptic density assembly	BP	1	LRFN1,NRXN2,NLGN2,ZDHHC12,GRID2,LRRTM2	grey	VSMC_M10
GO:0098742	0.84	0.20	74	152	cell-cell adhesion via plasma-membrane adhesion molecules	BP	1	MAPK14,LRRC4,CLDN12,ADGRL3,CLDN19,EPCAM,PCDH10,FAT4,NECTIN2,PVR,PCDH8,PTPRF,TGFBR2,PCDHGC5,PCDH1,UNC5D,LRFN3,RET,CLSTN2,ROBO1,ROBO2,TENM3,CDH17,AMIGO2,SPARCL1,ALCAM,NECTIN3,TGFB2,IGSF11,AMIGO3,AJUBA,CDH24,NECTIN4,CADM1,MYPN,HMCN1,CDH23,ARVCF,OBSL1,CLDN7,SDK1,PCDH7,ITGAM,TENM2,MAP2K5,PCDH11X,PCDH19,UMOD,DSG2,DSC3,MAPK7,EMB,DAB1,CDH6,CDH10,SLITRK2,L1CAM,PKD1,BSG,AMIGO1,CELSR2,CDH15,NTNG2,CDH16,PCDHAC2,PCDHA6,CLDN15,CNTN2,GRID2,CLDN1,CDHR4,CELSR3,PCDHGA2,PCDHB15	grey	VSMC_M10
GO:0006044	0.84	0.31	7	16	N-acetylglucosamine metabolic process	BP	1	LARGE1,GNPDA2,NANP,CHST1,CHST3,CHST7,CHST5	grey	VSMC_M10
GO:1990845	0.84	0.21	65	132	adaptive thermogenesis	BP	1	ATF4,HSF1,ALDH1A1,GADD45G,EPAS1,BMP8A,NR1H2,GRB10,TLR4,LPIN1,IL15,UCP1,FGF21,LAMA4,ACVR2B,PLCL2,ABHD6,ARNTL,NR1H3,ALMS1,EBF2,KSR2,ZNF423,PRKAB1,PM20D1,MAP2K6,TRPV4,CMKLR1,FABP4,SORL1,TRPM8,GPR3,PER2,ACTN3,ACADL,TFE3,MFAP2,YBX2,THRA,RBPJ,MFN2,KDM6B,SLC25A44,ZBTB7B,OGT,PCTP,IL4R,TRPV2,PPARGC1B,LEPR,DOCK7,ACOT11,TRPV1,PRDM16,LCN2,BSCL2,FABP5,ELOVL3,PEMT,NOVA1,PLAC8,DDIT3,APC,CEBPB,DIO2	grey	VSMC_M10
GO:0009156	0.84	0.27	14	30	ribonucleoside monophosphate biosynthetic process	BP	1	IMPDH1,PPAT,CMPK1,AMPD3,GMPS,AMPD1,PRPS2,ADK,UPRT,ADSSL1,UCK1,DHODH,NUDT2,UPP1	grey	VSMC_M10
GO:1902992	0.84	0.28	11	24	negative regulation of amyloid precursor protein catabolic process	BP	1	NTRK2,RTN4,PRNP,SORL1,RTN1,HAP1,TMED10,ABCA7,MIR29A,MIR24-1,MIR339	grey	VSMC_M10
GO:0086004	0.84	0.27	13	29	regulation of cardiac muscle cell contraction	BP	1	TRPM4,SCN5A,STC1,DSP,RYR2,PKP2,KCNJ2,ANK2,ATP1A2,DLG1,ATP2A1,DSG2,HCN4	grey	VSMC_M10
GO:0060249	0.84	0.20	109	218	anatomical structure homeostasis	BP	1	TNFAIP3,SLC12A2,PRKN,TNFRSF11B,AKR1B1,RAC2,SMO,LARGE1,ALDH1A1,SRF,CLDN12,SLC1A1,KIAA1211,PRDX1,EPAS1,HOXA13,ALB,MTF1,WHRN,EGFR,USP45,TRIM32,TLR4,NCDN,SLC8A2,SOX9,CACNB2,CUBN,USH1G,MKKS,ACTG1,RAC3,ERCC6,TRAF6,TUB,LSR,CHMP2B,CCDC66,ADGRV1,IL7,P2RX7,JAM2,P2RY1,PTK2B,USH1C,PFKM,HOMER1,F2R,SLC6A2,SPP1,NELL2,GCNT2,NOD2,ITGB6,LDB1,LPCAT1,LRRK1,TCIRG1,GPR137B,KRAS,GIGYF2,UBASH3B,BAG3,BBS1,HOMER2,LAMC1,ADAM8,PTH1R,PBLD,CTSH,CDH23,ABCA12,GPR137,DNAJB2,VCL,CD38,ILDR2,LIPA,ACTB,CLN8,WNK3,ATP1B2,ESRRB,RAB3D,MKS1,ACACA,CSF1R,PPARGC1B,FGGY,TAOK1,MTM1,ATP2B3,P2RX1,ABCA3,ATP6AP1,DEF8,OAS1,DMD,SLC22A5,CA2,NANOS1,JCHAIN,BGLAP,SNX10,CLDN1,INAVA,DRAM2,BBS10,MAP1A	grey	VSMC_M10
GO:0016486	0.84	0.30	8	18	peptide hormone processing	BP	1	PCSK1,SCG5,MME,ENPEP,ACE2,ECE2,PCSK7,ECE1	grey	VSMC_M10
GO:0140448	0.84	0.30	8	18	signaling receptor ligand precursor processing	BP	1	PCSK1,SCG5,MME,ENPEP,ACE2,ECE2,PCSK7,ECE1	grey	VSMC_M10
GO:0060149	0.84	0.31	7	16	negative regulation of posttranscriptional gene silencing	BP	1	ZC3H10,ESR1,BCDIN3D,PPP3CA,TERT,STAT3,NCOR1	grey	VSMC_M10

GO:0060967	0.84	0.31	7	16	negative regulation of gene silencing by RNA	BP	1	ZC3H10,ESR1,BCDIN3D,PPP3CA,TERT,STAT3,NCOR1	grey	VSMC_M10
GO:0045176	0.84	0.32	6	14	apical protein localization	BP	1	ATP8B1,GOPC,NAPA,MAL,SHROOM2,ACTB	grey	VSMC_M10
GO:0007263	0.84	0.30	8	18	nitric oxide mediated signal transduction	BP	1	EGFR,NDNF,GUCY1A1,GUCY1B1,AGT,NOS1AP,RASD1,NOS2	grey	VSMC_M10
GO:0071359	0.84	0.30	8	18	cellular response to dsRNA	BP	1	RALB,TMEM173,MAVS,IFIH1,MUL1,RIOK3,COLEC12,ZCCHC3	grey	VSMC_M10
GO:2000316	0.84	0.31	7	16	regulation of T-helper 17 type immune response	BP	1	RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,MIR21,RC3H2	grey	VSMC_M10
GO:0045165	0.84	0.20	85	172	cell fate commitment	BP	1	ONECUT2,PITX1,SMAD5,PTCH1,SMO,ROR2,SOSTDC1,SIX2,EPAS1,HOXA2,HOXA13,NTF4,RAB10,SOX9,PTCH2,GLI2,MNX1,POU4F1,SPRY2,WNT11,EOMES,JAG1,NRG1,MITF,PRKDC,SOX12,TOX,CASP3,EYA1,MEF2C,IL7,SOX6,EBF2,TBX5,RTF1,SOX13,MGA,PAX2,SUFU,GAP43,SATB2,TCF7L2,SOX2,SLAMF8,MCL1,FZD7,DLX1,WNT3,TNFSF18,WNT4,FKBP8,STAT3,TBX19,LEO1,FOXP3,BMPR1A,RBPJ,EPOP,TBX21,PSEN1,KDM6B,TGFB1I1,BATF,IL6R,GSC,TBX4,TBX2,BCL11B,GATA6,JAG2,ISL1,DOCK7,APC2,SOX8,BARHL2,RHOA,FOXG1,ISL2,LBX1,WNT5A,POU3F2,SIX1,APC,HEY2,WNT2	grey	VSMC_M10
GO:0001823	0.84	0.22	39	81	mesonephros development	BP	1	OSR2,MYC,SMAD5,PTCH1,SMO,CAT,SIX2,EPCAM,BMPER,OSR1,SPRY1,SOX9,FOXJ1,GZF1,WNT11,RARB,RET,PAX8,EYA1,ROBO2,FMN1,PKD2,PAX2,SALL1,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,SMAD3,LHX1,GPC3,PKD1,SOX8,NOG,BASP1,SIX1,FGF1	grey	VSMC_M10
GO:0065005	0.84	0.28	10	22	protein-lipid complex assembly	BP	1	APOM,NR1H2,APOB,APOC1,SOAT2,SOAT1,ZDHHC8,LPCAT3,ABCA7,PLAGL2	grey	VSMC_M10
GO:0033233	0.84	0.28	10	22	regulation of protein sumoylation	BP	1	TOLLIP,PIAS3,ARNT,HDAC4,MUL1,GNL3L,PIAS4,PARK7,RWDD3,RASD2	grey	VSMC_M10
GO:0031529	0.84	0.24	23	49	ruffle organization	BP	1	EPS8L1,PLEK,BAG4,ARFIP2,LIMA1,ARHGEF26,ARHGAP24,CYFIP1,CARMIL1,TCIRG1,EPS8,NDEL1,EVL,CSF1R,INPP5K,EPS8L3,DEF8,MTSS1L,CARMIL2,EPS8L2,SNX10,CSPG4,HRAS	grey	VSMC_M10
GO:0002027	0.84	0.22	35	73	regulation of heart rate	BP	1	SLC1A1,EPAS1,BVES,TRPM4,CACNB2,SCN5A,GPD1L,ADRA1D,SEMA3A,KCNJ3,KCNE2,DSP,CASQ2,RYR2,PKP2,KCNJ2,MYH7,ANK2,AGT,SCN4B,NOS1AP,GCH1,CACNA1G,CALM1,DSG2,SREBF1,ISL1,TRPV1,DMD,KCNH2,SCN2B,RGS4,POPDC2,HCN4,HEY2	grey	VSMC_M10
GO:0090110	0.84	0.32	6	14	COPII-coated vesicle cargo loading	BP	1	SEC31A,SEC31B,SCAP,MIA3,SEC24C,TBC1D20	grey	VSMC_M10
GO:0035794	0.84	0.26	16	34	positive regulation of mitochondrial membrane permeability	BP	1	HEBP2,TMEM14A,HIP1R,SLC9A1,STPG1,FZD9,NMT1,MUL1,TMEM102,ACAA2,MIR29A,BNIP3L,BCL2L11,SLC35F6,PPIF,AC140504.1	grey	VSMC_M10
GO:0032682	0.84	0.31	7	16	negative regulation of chemokine production	BP	1	OAS3,F2RL1,APOD,MUL1,MAP2K5,SUZ12,OAS1	grey	VSMC_M10
GO:0003323	0.84	0.30	8	18	type B pancreatic cell development	BP	1	SMO,CDK6,RFX3,ARNTL,NKX6-1,SIDT2,PDPK1,WNT5A	grey	VSMC_M10
GO:0071604	0.84	0.25	16	35	transforming growth factor beta production	BP	1	TSKU,WNT11,FERMT1,LUM,ITGB6,CD200,TGFB2,CREB1,FN1,FOXP3,BMPR1A,SMAD3,GATA6,SERPINF2,CD46,NRROS	grey	VSMC_M10
GO:0045814	0.84	0.24	20	43	negative regulation of gene expression, epigenetic	BP	1	BAZ2A,H3F3C,DNMT3A,BMI1,SETDB2,SIRT2,FAM208A,BAHD1,PPHLN1,HDAC1,ZNFX1,TET1,H2AFY2,PHF8,NRDE2,SMCHD1,SETDB1,CREBZF,BEND3,ZNF304	grey	VSMC_M10
GO:0010518	0.84	0.25	19	41	positive regulation of phospholipase activity	BP	1	ESR1,KIT,LPAR1,EGFR,C5AR1,PHB,RASGRP4,FLT1,GNA13,ARHGAP6,AGT,ABL2,FGFR3,NMUR2,CCL5,GNA15,PDPK1,PRKCZ,HRAS	grey	VSMC_M10
GO:0006122	0.84	0.37	4	9	mitochondrial electron transport, ubiquinol to cytochrome c	BP	1	UQCRQ,UQCRB,UQCR11,MT-CYB	grey	VSMC_M10
GO:0045600	0.84	0.23	25	53	positive regulation of fat cell differentiation	BP	1	STK3,MAPK14,PIM1,DKKL1,TRPM4,NAPEPLD,AAMDC,KLF5,CEBPA,CDS1,RREB1,SOX13,STK4,CMKLR1,SYAP1,CREB1,SAV1,TFE3,ZBTB7B,ZBTB7C,MIR21,SIX1,CCDC3,CEBPB,CCDC71L	grey	VSMC_M10
GO:0009214	0.84	0.33	5	12	cyclic nucleotide catabolic process	BP	1	PDE7B,PDE10A,PDE9A,PDE8A,PDE4A	grey	VSMC_M10
GO:0046426	0.84	0.29	9	20	negative regulation of receptor signaling pathway via JAK-STAT	BP	1	PPP2R1A,PIBF1,PARP14,SUZ12,PTPN2,SOCS1,DAB1,MIR125A,LEPROT	grey	VSMC_M10
GO:0070849	0.84	0.24	19	41	response to epidermal growth factor	BP	1	MARS,EGFR,SOX9,BAG4,PAX2,CBL,SYAP1,PDE8A,SNX6,MAPK1,STAT5B,MED1,MAPK3,GAREM1,INPP5K,PDPK1,DAB2IP,DUSP22,ZFP36L2	grey	VSMC_M10
GO:0098780	0.84	0.30	8	18	response to mitochondrial depolarisation	BP	1	PRKN,OPTN,HTRA2,PINK1,MUL1,GPS2,MFN2,VPS13C	grey	VSMC_M10
GO:0045666	0.84	0.23	29	61	positive regulation of neuron differentiation	BP	1	TCF4,CSNK1E,KDM4C,BEND6,TRIM32,NRCAM,GLI2,KDM4A,ADRA2B,DNMT3B,MEF2C,NKX6-1,DLX1,SH3GL3,HOXD3,BCL6,BRINP2,ADRA2C,CYB5D2,PRPF19,NAP1L2,SIN3A,DAB1,RHOA,FOXG1,IMPACT,MMD,TGIF2,NKX2-5	grey	VSMC_M10
GO:1901983	0.84	0.23	30	63	regulation of protein acetylation	BP	1	HINT2,ATG5,SPHK2,HDAC2,IWS1,PAXIP1,ARRB1,TAF7,SDR16C5,ARNTL,RAPGEF3,HDAC1,AUTS2,DDX3X,TADA2B,FOXP3,KAT7,MUC1,MAPK3,NAP1L2,RPS6KA5,SIN3A,ISL1,TAOK1,GLYR1,PARK7,CTCF,SOX4,LIF,RPS6KA4	grey	VSMC_M10
GO:0021955	0.84	0.26	13	29	central nervous system neuron axonogenesis	BP	1	PLXNA4,GLI2,MYCBP2,TSKU,SZT2,EPHB1,NR4A2,ADARB1,EPHB3,NIN,EPHA4,NDEL1,CHRNB2	grey	VSMC_M10
GO:0110154	0.84	0.31	7	16	RNA decapping	BP	1	DXO,LSM1,NUDT16,NUDT12,EIF4ENIF1,DCP1B,EDC4	grey	VSMC_M10
GO:0045747	0.84	0.25	15	33	positive regulation of Notch signaling pathway	BP	1	MFNG,KIT,AAK1,ITGB1BP1,JAG1,ROBO1,ROBO2,BMP2K,NOD2,NEPRO,TGFB2,POGLUT1,PDCD10,STAT3,JAG2	grey	VSMC_M10
GO:0002088	0.84	0.22	30	63	lens development in camera-type eye	BP	1	FRS2,TBC1D32,ATF4,TDRD7,TMOD1,SLC7A11,SPRY1,FOXE3,CRYGN,SPRY2,TGFBR2,BFSP1,SPRED3,NECTIN3,SHROOM2,CRYBA4,CDKN1B,DLG1,PLA2G16,MED1,LCTL,SMAD3,UNC45B,FZR1,SKI,HSF4,WNT5A,TBC1D20,PITX3,WNT2	grey	VSMC_M10
GO:1903020	0.84	0.29	9	20	positive regulation of glycoprotein metabolic process	BP	1	IL15,PAWR,PLCB1,SLC2A10,TCF7L2,RAB1B,SOAT1,POMT2,IL33	grey	VSMC_M10
GO:0031638	0.84	0.25	18	38	zymogen activation	BP	1	BAK1,PLGRKT,PLAT,ASPH,RIPK2,CIDEB,PRSS12,MELTF,CTSH,VSIR,HGFAC,F12,SERPINF2,HPR,FGA,FADD,CASP8,PERP	grey	VSMC_M10
GO:1903319	0.84	0.28	10	22	positive regulation of protein maturation	BP	1	MYH9,PLGRKT,RHBDD1,MELTF,ADAM8,LPCAT3,F12,CNTN2,SOX4,BAG2	grey	VSMC_M10
GO:1902430	0.84	0.28	10	22	negative regulation of amyloid-beta formation	BP	1	NTRK2,RTN4,PRNP,SORL1,RTN1,HAP1,ABCA7,MIR29A,MIR24-1,MIR339	grey	VSMC_M10

GO:0071634	0.84	0.25	15	33	regulation of transforming growth factor beta production	BP	1	TSKU,WNT11,FERMT1,LUM,ITGB6,CD200,TGFB2,CREB1,FN1,FOXP3,BMPR1A,SMAD3,GATA6,SERPINF2,CD46	grey	VSMC_M10
GO:0014823	0.84	0.23	27	57	response to activity	BP	1	TPH2,HSF1,CRY1,ABCG5,CAT,ABCG8,PTN,FGF21,PRKDC,DNMT3B,OPA1,CRY2,RYR2,SRD5A1,AGT,CBL,MTFP1,CREB1,FIS1,PRKAG3,BNIP1,KDM6B,ADSSL1,OXCT1,CYBA,SLC25A25,BGLAP	grey	VSMC_M10
GO:0046903	0.84	0.17	346	673	secretion	BP	1	NME1,VPS4B,ERBB3,LRP1,CANX,RAB21,SNCAIP,SLC12A2,RIMS2,PRKN,SLC22A4,GDF9,GRM4,LY6E,EXOC4,SYNGR1,NTRK2,PLA2G6,COPG2,PICK1,RAC2,MYH9,GUCA1B,CHRNA3,CHRNA5,CRY1,STEAP2,APBA1,SCFD2,RFX3,KIT,CA9,TFAP2B,PPAT,CHMP2A,NLRP5,SVBP,STX17,IL11,BRSK1,PRKCE,RIMS1,HMGN3,RIMS3,CYB5R4,PPT1,SCRN1,BMP8A,AQP1,PLEK,RSAD2,NR1H2,EGFR,TLR4,VPS41,ATG5,SDCBP,TRPM4,PPFIA3,LIN7B,TRAF3IP2,SPHK2,NAPA,RAB7A,RAB10,COPG1,GIPR,CACNB2,SYTL2,CLASP2,FRMD4A,GAB2,LLGL2,RALB,STEAP3,GRIK5,UNC13D,RAF1,NAPB,ABCC4,SNX5,C1QTNF1,ANK1,SYT1,RAB5A,LIN7A,APBB3,DPH3,AIMP1,NRG1,CCKBR,NCKAP1L,SIRT3,STX2,SYT9,ADRA2B,SNPH,NR1H4,USF2,HCK,NDUFAF2,FAM3D,IL1A,PAX8,NR4A1,FER,OSBP,HIP1R,TRAPPC11,CHRM5,ARNTL,ERC2,SCG5,MEF2C,ASIC1,TPD52,VEGFC,P2RY1,RASGRP1,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,EXOC6B,PFKM,SYNJ1,SLC8B1,VDR,STC1,NKX3-1,NKX6-1,ACVR1C,F2RL1,F2R,CRY2,VPS18,ABCC2,SPP1,ZBED6,PLA2R1,LGI3,DMTN,ADTRP,DTNBP1,CHRM3,SYT8,GRM2,SIRT4,GPLD1,IRS1,NEURL1,CD200,DNM1L,SLC6A3,HDAC1,PPP3CA,HYAL3,CCND1,CPT1A,MAP2K6,TRPV4,SLC9B2,TGFB2,ADRA2A,FBLN5,MON1A,TCIRG1,TCF7L2,SNAP23,KCNB1,EGF,PFKFB2,GRK2,GPER1,ABCB11,RAB11FIP2,LAT2,AGT,FGR,CBL,SYTL1,PRSS12,PER2,OSM,COPA,STX1A,SNX4,NTSR1,PASK,SEPT2,BACE1,DNAJC5,GLUL,CSPG5,SIDT2,SLC16A1,ADAM8,KLF7,NSF,CREB1,MIA3,RAP1B,BLOC1S6,PLA2G4A,CTAGE9,VGF,TTN,IL12A,TANGO2,COMT,ENY2,ABCA12,NRXN2,CASK,SERPINC1,MCU,ADRA2C,PNKD,PTGDR,PPP3CB,RAB3A,PINK1,SYN1,CAMK2G,SNAP29,EXOC5,PTPRN,	grey	VSMC_M10
GO:0046485	0.85	0.29	8	18	ether lipid metabolic process	BP	1	PEX7,PLA2G6,TMEM86B,LIPE,GNPAT,PLA2G4A,PLA2G16,NCEH1	grey	VSMC_M10
GO:2001141	0.85	0.17	1263	2416	regulation of RNA biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,ATP8B1,ONECUT2,BAZ2A,TCF4,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,STK3,OSR2,SNW1,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,PRKN,AGER,PPARA,MED30,IL5,BRD2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,LPIN1,SFRP4,UCP1,CREM,TEAD2,SETD7,SDCBP,MYCN,C6orf203,ELF2,OSR1,FOXO3,ZXDC,ZBTB24,MKX,FAF1,MAMSTR,ATAD2B,BEND5,CDCA7,KDM7A,ZNF438,FOXE3,HDAC2,PHF10,MAML2,BBS7,MLLT10,DNMT3A,BMI1,ZC3H4,PRKD2,CNBP,SET	grey	VSMC_M10
GO:1901550	0.85	0.33	5	12	regulation of endothelial cell development	BP	1	ZDHHC21,S1PR3,IKBKB,PLCB1,VCL	grey	VSMC_M10
GO:1903140	0.85	0.33	5	12	regulation of establishment of endothelial barrier	BP	1	ZDHHC21,S1PR3,IKBKB,PLCB1,VCL	grey	VSMC_M10
GO:0006921	0.85	0.27	11	24	cellular component disassembly involved in execution phase of apoptosis	BP	1	HSF1,DEDD2,FOXL2,ACVR1C,ACIN1,GPER1,DNASE2,PAM16,DFFB,BLCAP,NMNAT1	grey	VSMC_M10
GO:0045022	0.85	0.24	17	37	early endosome to late endosome transport	BP	1	RAB21,WDR91,MTMR2,RAB7A,HOOK3,RAB5A,DNAJC13,FAM160A2,ANKRD27,MAPK1,SNX12,MAPK3,HOOK2,MAP2K1,STX8,RILP,SNX16	grey	VSMC_M10
GO:0010560	0.85	0.29	8	18	positive regulation of glycoprotein biosynthetic process	BP	1	IL15,PAWR,PLCB1,SLC2A10,TCF7L2,SOAT1,POMT2,IL33	grey	VSMC_M10
GO:0002443	0.85	0.19	111	221	leukocyte mediated immunity	BP	1	CD226,STX7,AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,RAC2,KIT,PRDX1,EXOSC3,MSH2,RSAD2,IL4I1,TLR4,TRPM4,TRAF3IP2,SPHK2,HMCES,ERCC1,NECTIN2,PVR,GAB2,MLH1,UNC13D,MYD88,SLC22A13,FOXJ1,PAXIP1,JAG1,SHLD1,MAVS,NCKAP1L,HPX,IRF7,TRAF6,GAPT,FER,SLA2,RASGRP1,NBN,F2RL1,NOD2,CD40,CD96,TCIRG1,SNAP23,DENND1B,LAT2,FGR,CBL,SNX4,CD28,FCER1G,RNF168,CADM1,FZD5,BCL6,CTSH,IL12A,PTPN6,LAG3,PTGDR,PPP3CB,C12orf4,STAT5B,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,SPON2,TBX21,STX4,ITGAM,BATF,CD19,LAT,IL4R,S100A13,BTK,SCNN1B,CD74,STXBP2,FBXO38,PRAM1,VAV1,C7,C3,NOS2,IL7R,SUPT6H,TICAM1,CRK,DNASE1,PDPK1,PRKCZ,TRAF2,FOXF1,STXBP1,AP1G1,BCL10,CHGA,FADD,CXCL6,CD46,FCER2,RNF8,CD70,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0043271	0.85	0.21	45	93	negative regulation of ion transport	BP	1	NEDD4L,GOPC,WNK2,PRKCE,HECW1,TCAF2,SFRP4,KEL,OSR1,SLC26A5,KCNRG,OXSR1,ARL6IP5,PXK,SLC43A1,TMBIM6,PTK2B,STC1,KCNE2,PKD2,PLA2R1,CASQ2,HECW2,ADRA2A,ISCU,ATP1A2,C4orf3,NTSR1,SESTD1,GNB5,WNK3,SYT11,CALM1,ABAT,FMR1,GABRE,INPP5K,RRAD,MIR24-1,GPR35,KCNH2,CRBN,RGS4,GEM,PPIF	grey	VSMC_M10
GO:0043652	0.85	0.31	6	14	engulfment of apoptotic cell	BP	1	RAC2,XKR6,RHOBTB2,RHOBTB1,ABCA7,XKR8	grey	VSMC_M10

GO:0045214	0.85	0.25	15	33	sarcomere organization	BP	1	OBSCN,LMOD2,SRF,MYLK3,ACTG1,PRKAR1A,MYOZ2,CASQ1,MYPN,TTN,MYOZ1,LDB3,TCAP,CSRP2,KRT19	grey	VSMC_M10
GO:0006749	0.85	0.24	20	42	glutathione metabolic process	BP	1	CLIC5,SLC1A1,CHAC2,MGST2,SLC7A11,MMACHC,GSTK1,CLIC1,ARL6IP5,GSS,GLRX2,NFE2L2,GGT2,GGT6,GSTZ1,PARK7,PTGES2,GSTT4,GLO1,GGT5	grey	VSMC_M10
GO:0007000	0.85	0.31	6	14	nucleolus organization	BP	1	BAZ2A,USP36,SIRT2,DDX11,PHF8,BEND3	grey	VSMC_M10
GO:0051770	0.85	0.31	6	14	positive regulation of nitric-oxide synthase biosynthetic process	BP	1	TLR4,NOD2,MAP2K6,CCL2,FCER2,IL33	grey	VSMC_M10
GO:0009127	0.85	0.28	9	20	purine nucleoside monophosphate biosynthetic process	BP	1	IMPDH1,PPAT,AMPD3,DGUOK,GMPS,AMPD1,ADK,ADSSL1,NUDT2	grey	VSMC_M10
GO:0050772	0.85	0.22	32	68	positive regulation of axonogenesis	BP	1	LRP1,TIAM2,PLXNA4,NTRK2,SRF,SEMA4D,RUFY3,PLXNA1,GOLGA4,MEGF8,PLXNC1,ROBO1,ROBO2,TIAM1,ZFYVE27,CYFIP1,BDNF,ADNP,DISC1,CDKL5,WNT3,MAPT,FN1,NIN,NDEL1,RAB11A,MAP2K1,NTN1,TRPV2,L1CAM,PLXNA3,AMIGO1	grey	VSMC_M10
GO:0010738	0.85	0.33	5	12	regulation of protein kinase A signaling	BP	1	AKAP7,TCIM,ADGRV1,SPATC1L,PDE4A	grey	VSMC_M10
GO:1901019	0.85	0.22	32	67	regulation of calcium ion transmembrane transporter activity	BP	1	STAC3,PLA2G6,CACNB2,STAC,CACNB4,KCNE2,PKD2,CASQ2,RYR2,ADRA2A,ANK2,ATP1A2,SLC9A1,C4orf3,CASQ1,NOS1AP,HTT,ATP1B1,GNB5,HAP1,STAC2,CACNB1,ATP2A1,CALM1,VMP1,FMR1,JPH3,RRAD,DMD,GPR35,JPH2,GEM	grey	VSMC_M10
GO:0034620	0.85	0.21	42	86	cellular response to unfolded protein	BP	1	HSPA1B,PRKN,PACRG,DERL1,BAK1,ATF4,HSF1,NCK2,ERMP1,HERPUD2,FGF21,OPTN,TMTC4,EIF2AK2,DDRGK1,PIK3R1,TMBIM6,AMFR,RHBDD1,CCND1,FICD,YOD1,HSPA8,QRICH1,BAG3,TBL2,RHBDD2,NFE2L2,DERL3,BHLHA15,CREB3L4,PTPN2,CREB3L3,ABCA7,HSPA5,DAB2IP,MIR199A1,DDIT3,BCL2L11,HSPB8,PPP1R15A,DERL2	grey	VSMC_M10
GO:1904355	0.85	0.30	7	16	positive regulation of telomere capping	BP	1	MAP3K4,MAPK15,MAPKAPK5,RTEL1,MAPK1,MAPK3,MAP2K7	grey	VSMC_M10
GO:0006949	0.85	0.25	16	35	syncytium formation	BP	1	MAPK14,MYH9,CD109,ERCC1,DYRK1B,MYOF,JAM2,RAPGEF3,ADAMTS15,SH3PXD2A,TCTA,VASH2,EHD1,GDF15,IL4R,CACNA1H	grey	VSMC_M10
GO:0046112	0.85	0.29	8	18	nucleobase biosynthetic process	BP	1	SHMT2,PPAT,CMPK1,GMPS,CTPS2,CPS1,SHMT1,DHODH	grey	VSMC_M10
GO:0032252	0.85	0.33	5	12	secretory granule localization	BP	1	KIF5A,RASGRP1,TANC2,KIF1C,TRIM46	grey	VSMC_M10
GO:0030728	0.85	0.31	6	14	ovulation	BP	1	FOXO3,HPGD,ADAMTS1,GAS2,IL4R,EREG	grey	VSMC_M10
GO:0002366	0.85	0.19	90	181	leukocyte activation involved in immune response	BP	1	ENPP3,HLA-DRA,MFNG,RAC2,KIT,EXOSC3,PRKCE,MSH2,TLR4,SPHK2,HMCES,ERCC1,LCP1,GAB2,MLH1,UNC13D,MYD88,PAXIP1,EOMES,NMI,PLCL2,SHLD1,NCKAP1L,FOXP1,GAPT,FER,PTK2B,RASGRP1,EIF2AK4,RIPK2,NBN,DYSF,CDH17,F2RL1,CD40,DOCK10,SNAP23,HLX,LAT2,FGR,CBL,SNX4,CD28,FCER1G,RNF168,BCL6,RC3H1,TNFSF18,SLC11A1,PTGDR,STAT3,C12orf4,FOXP3,SHLD2,TBX21,STX4,PSEN1,SEMA4A,ITGAM,DOCK2,BATF,ZBTB7B,IL6R,CD19,LAT,IL4R,S100A13,BTK,SCNN1B,CD74,STXBP2,PRAM1,PTGER4,SUPT6H,TICAM1,DNASE1,PDPK1,PRKCZ,TSC1,FOXF1,KARS,STXBP1,AP1G1,MIR21,CHGA,CD46,FGL2,RNF8,HAVCR2,RC3H2	grey	VSMC_M10
GO:0010894	0.85	0.28	9	20	negative regulation of steroid biosynthetic process	BP	1	CYP27B1,DKKL1,DKK3,ERLIN1,SNAI1,SCAP,WNT4,GFI1,INSIG2	grey	VSMC_M10
GO:0051893	0.85	0.22	28	60	regulation of focal adhesion assembly	BP	1	LRP1,PTK2,TEK,ITGB1BP1,CLASP2,ACTG1,PTPRA,FAM107A,FMN1,PTPRJ,DMTN,LDB1,SLK,COL16A1,ARHGAP6,SLC9A1,APOD,WNT4,VCL,SMAD3,BCAS3,CAMSAP3,TSC1,RHOA,ACVRL1,PEAK1,THY1,DUSP22	grey	VSMC_M10
GO:0090109	0.85	0.22	28	60	regulation of cell-substrate junction assembly	BP	1	LRP1,PTK2,TEK,ITGB1BP1,CLASP2,ACTG1,PTPRA,FAM107A,FMN1,PTPRJ,DMTN,LDB1,SLK,COL16A1,ARHGAP6,SLC9A1,APOD,WNT4,VCL,SMAD3,BCAS3,CAMSAP3,TSC1,RHOA,ACVRL1,PEAK1,THY1,DUSP22	grey	VSMC_M10
GO:0032413	0.85	0.23	23	49	negative regulation of ion transmembrane transporter activity	BP	1	NEDD4L,GOPC,PRKCE,HECW1,TCAF2,OSR1,KCNRG,OXSR1,KCNE2,PKD2,CASQ2,HECW2,ADRA2A,ATP1A2,C4orf3,GNB5,CALM1,FMR1,RRAD,MIR24-1,GPR35,CRBN,GEM	grey	VSMC_M10
GO:1904427	0.85	0.22	26	55	positive regulation of calcium ion transmembrane transport	BP	1	STAC3,CACNB2,STAC,F2R,KCNE2,PKD2,RYR2,ANK2,GPER1,SLC9A1,CASQ1,NTSR1,CEMIP,HTT,ATP1B1,HAP1,STAC2,ATP2A1,CD19,CALM1,VMP1,BDKRB1,PDPK1,P2RX1,JPH2,THY1	grey	VSMC_M10
GO:0030501	0.85	0.24	17	37	positive regulation of bone mineralization	BP	1	OSR2,PTN,OSR1,ACVR2B,ACVR2A,KL,ADGRV1,MEF2C,P2RX7,ANO6,TFAP2A,BMPR1B,ACTN3,FZD9,WNT4,BMPR1A,SMAD3	grey	VSMC_M10
GO:0006925	0.85	0.30	7	16	inflammatory cell apoptotic process	BP	1	CDKN2A,SLC7A11,IRF7,PIK3CB,MEF2C,NOD2,CXCR2	grey	VSMC_M10
GO:0051788	0.85	0.27	10	22	response to misfolded protein	BP	1	RNF5,DERL1,UGGT2,DNAJC18,AUP1,RNF185,DNAJB12,SDF2L1,F12,RNF126	grey	VSMC_M10
GO:1904380	0.85	0.31	6	14	endoplasmic reticulum mannose trimming	BP	1	RNF5,UGGT2,AMFR,RNF185,EDEM3,SYVN1	grey	VSMC_M10
GO:0050778	0.85	0.18	155	306	positive regulation of immune response	BP	1	CD226,STX7,HLA-DRA,HLA-DPB1,XRCC6,PTK2,PLA2G6,TEC,TNFRSF21,EXOSC3,PRKCE,MSH2,FPR2,AKIRIN2,RSAD2,TLR4,IL15,SPHK2,HMCES,C5AR2,C5AR1,PRKD2,PHB,NECTIN2,PVR,EIF2B3,GAB2,MLH1,SLC22A13,PAXIP1,IKBKB,NMI,TMEM173,PAWR,PLCL2,SHLD1,PRNP,MAVS,NCKAP1L,HPX,FOXP1,PRKDC,IRF7,TRAF6,HCK,LPXN,PTPRJ,MEF2C,SLA2,RASGRP1,EIF2AK4,NLRC5,RIPK2,F2RL1,POLR3D,NOD2,CD40,GPLD1,SPPL3,LCK,BANK1,ICOSLG,TGFB2,BTN2A2,POLR3C,HLX,DENND1B,CMKLR1,PARP9,THEMIS2,LAT2,BMX,FGR,PLPP4,SNX4,COCH,CD28,FCER1G,ADAM8,CADM1,FZD5,NONO,PLA2G4A,IL12A,XRCC5,RC3H1,PTPN6,SLC11A1,LAG3,CFP,CD38,MAPK1,STAT5B,FOXP3,ZBTB1,SHLD2,GPS2,CARD11,MED1,TBX21,STX4,PSEN1,ITGAM,LCP2,CD19,IL4R,SFPQ,PRKCB,BTK,SIN3A,CD74,CCL5,RIOK3,FBXO38,YES1,PRAM1,VAV1,C7,C3,PTPN2,CREBBP,PRKCZ,TRAF2,IKBKG,PARK7,CYBA,VAV3,KARS,STXBP1,AP1G1,BCL10,CMTM3,MIR21,FYB1,FADD,BTN1A1,CD46,ZCCHC3,A2M,CFD,IRGM,CD247,THY1,WNT5A,FCER2,RGCC,UBE2N,GCSAM,HRAS,LAX1,SH2B2,EREG,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10

GO:0009416	0.85	0.18	120	239	response to light stimulus	BP	1	FECH,CPT1B,MAP3K4,SYNGAP1,UBE2B,BAK1,MYC,ATF4,MAPK13,FBXL6,OPN1SW,PRPH2,CRY1,KIT,REV1,CAT,CAMKMT,BRSK1,RDH13,MSH2,AQP1,GJA10,PTN,EGFR,TRIM32,SLC7A11,TRPC3,ERCC1,XPC,ERCC2,ERCC3,B4GALT2,ZRANB3,AANAT,PPP1CB,AKT2,PLEKHB1,BHLHE40,DDHD2,WRN,ERCC6,NPHP1,ERCC8,PIK3R1,PRIMPOL,CASP3,ATR,CEP250,CCDC66,SCARA3,MME,EIF2AK4,DDB2,TENT2,CDS1,CRY2,TP53INP1,SLC4A10,TRPM1,RHBDD1,SIK1,HYAL1,HYAL3,CCND1,KRAS,PITPNM1,RRH,POLG,SPRTN,SAG,USP2,ATP1A2,NFATC4,PER2,USF1,CREB1,NMT1,MEN1,IL12A,CRTC1,GRK4,MMP3,RHNO1,GNB5,ROM1,ZBTB1,PARP1,DDB1,RGS14,GUCY2D,FBXL22,FOS,TAF1,CHRNB2,TIPIN,DNM2,DCUN1D3,YY1,ASIC2,CUL4B,IFT20,UNC119,ERCC4,TP53I13,FMR1,CREBBP,SDF4,MECP2,CIRBP,ABCA7,PER3,GNAT2,LCN2,FBXL8,FBXL12,REEP6,IMPACT,DUSP1,GPR88,MAP2K7	grey	VSMC_M10
GO:0033865	0.85	0.20	50	102	nucleoside bisphosphate metabolic process	BP	1	HSD17B4,PPT2,ACSL6,CROT,SLC35B2,PPCS,PPT1,DLD,ELOVL1,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,MCCC2,ACOT12,FITM2,MCEE,TPST1,GPAM,FAR2,ACSL5,HACD2,THEM5,HMGCL,ACOT9,PDK3,SLC25A16,ACSBG1,COASY,MPC2,TECR,SLC26A1,ACOT2,PANK3,GCDH,ACSM3,ACACA,SLC26A2,ACSBG2,PIPOX,ACOT11,PANK4,ACSF3,MLYCD,SULT1C3,ACOT4,ELOVL3,NUDT19	grey	VSMC_M10
GO:0033875	0.85	0.20	50	102	ribonucleoside bisphosphate metabolic process	BP	1	HSD17B4,PPT2,ACSL6,CROT,SLC35B2,PPCS,PPT1,DLD,ELOVL1,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,MCCC2,ACOT12,FITM2,MCEE,TPST1,GPAM,FAR2,ACSL5,HACD2,THEM5,HMGCL,ACOT9,PDK3,SLC25A16,ACSBG1,COASY,MPC2,TECR,SLC26A1,ACOT2,PANK3,GCDH,ACSM3,ACACA,SLC26A2,ACSBG2,PIPOX,ACOT11,PANK4,ACSF3,MLYCD,SULT1C3,ACOT4,ELOVL3,NUDT19	grey	VSMC_M10
GO:0034032	0.85	0.20	50	102	purine nucleoside bisphosphate metabolic process	BP	1	HSD17B4,PPT2,ACSL6,CROT,SLC35B2,PPCS,PPT1,DLD,ELOVL1,PANK2,PDK1,SUCLG2,PDHX,ELOVL7,PANK1,MCCC2,ACOT12,FITM2,MCEE,TPST1,GPAM,FAR2,ACSL5,HACD2,THEM5,HMGCL,ACOT9,PDK3,SLC25A16,ACSBG1,COASY,MPC2,TECR,SLC26A1,ACOT2,PANK3,GCDH,ACSM3,ACACA,SLC26A2,ACSBG2,PIPOX,ACOT11,PANK4,ACSF3,MLYCD,SULT1C3,ACOT4,ELOVL3,NUDT19	grey	VSMC_M10
GO:1902116	0.85	0.25	15	33	negative regulation of organelle assembly	BP	1	TBC1D30,MDM1,CDK5RAP2,FEZ2,SEC22B,TMEM39A,LIMK2,PINK1,PHF23,TRIM37,DNM2,SMCR8,MTM1,CDK10,ODF2L	grey	VSMC_M10
GO:0010950	0.85	0.20	63	127	positive regulation of endopeptidase activity	BP	1	MAP3K5,GRAMD4,AGER,BAK1,MYC,HSF1,TTBK1,SLC1A1,NOD1,AKIRIN2,CASP8AP2,TNFSF15,HSPE1,ARRB1,ARL6IP5,ST18,ASPH,FOXL2,HIP1R,ROBO1,DIABLO,HTRA2,RIPK2,SENP1,NKX3-1,ACVR1C,F2R,PIDD1,LCK,PDCD6,GPER1,PSME1,CIDEB,EGLN3,MAPT,FIS1,CTSH,DDX3X,VSIR,PSME3,MUL1,STAT3,EPHA4,BCL2L13,NGFR,EFNA1,SMAD3,S100A8,BCAP31,P2RX1,BCL10,MIR21,MIR27B,RHOA,RPS27L,FADD,CASP8,ACER2,BCL2L11,PERP,APH1B,PRR7,CRADD	grey	VSMC_M10
GO:1905269	0.85	0.32	5	12	positive regulation of chromatin organization	BP	1	SETDB2,FAM208A,PPHLN1,SETDB1,ZNF304	grey	VSMC_M10
GO:0009168	0.85	0.29	8	18	purine ribonucleoside monophosphate biosynthetic process	BP	1	IMPDH1,PPAT,AMPD3,GMPS,AMPD1,ADK,ADSSL1,NUDT2	grey	VSMC_M10
GO:0060100	0.85	0.32	5	12	positive regulation of phagocytosis, engulfment	BP	1	NCKAP1L,F2RL1,ANO6,C3,ABCA7	grey	VSMC_M10
GO:1905155	0.85	0.32	5	12	positive regulation of membrane invagination	BP	1	NCKAP1L,F2RL1,ANO6,C3,ABCA7	grey	VSMC_M10
GO:0010801	0.85	0.29	7	16	negative regulation of peptidyl-threonine phosphorylation	BP	1	SPRY2,SIRT2,DMTN,DGKQ,CALM1,INPP5K,CADM4	grey	VSMC_M10
GO:0072310	0.85	0.34	4	10	glomerular epithelial cell development	BP	1	PODXL,FOXJ1,JAG1,ASXL1	grey	VSMC_M10
GO:0010954	0.85	0.28	9	20	positive regulation of protein processing	BP	1	MYH9,PLGRKT,RHBDD1,MELTF,ADAM8,LPCAT3,F12,CNTN2,BAG2	grey	VSMC_M10
GO:0051482	0.85	0.29	7	16	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	BP	1	GPR20,LPAR1,F2RL1,F2R,GNA15,GPR157,GPR35	grey	VSMC_M10
GO:0050920	0.85	0.19	83	167	regulation of chemotaxis	BP	1	SEMA6A,AGER,GPSM3,PTK2,PLXNA4,RAC2,CCL27,SEMA4D,SEMA4C,FPR2,CXCL8,AKIRIN1,PTN,MET,C5AR2,C5AR1,PRKD2,MEGF8,OXSR1,MYCBP2,SEMA3D,SEMA3A,NCKAP1L,GAS6,RYK,MTUS1,ROBO1,ROBO2,SEMA4F,VEGFC,PTK2B,TIAM1,SLC8B1,F2RL1,ANO6,SEMA3G,SEMA4G,NOD2,DNM1L,TRPV4,SEMA3F,PRSS56,CMKLR1,SLAMF8,MOSPD2,YTHDF1,PTPRO,WNT3,IL16,SEMA6D,IL12A,MCU,TNFSF18,CXCR2,BST1,MAPK1,PADI2,TMEM102,STX4,SEMA4A,FGF18,PGF,DAPK2,MAPK3,IL6R,SMAD3,S100A14,CD74,CCL5,CSF1R,CCL7,CCL2,PTPN2,PLXNA3,MPP1,DEFB124,DPP4,ZNF580,WNT5A,DUSP1,ARTN,FGF1,PDGFD	grey	VSMC_M10
GO:1903670	0.85	0.25	13	29	regulation of sprouting angiogenesis	BP	1	SEMA6A,CEMIP2,BMPER,SLC39A12,PIK3CB,GLUL,E2F2,RHOJ,SYNJ2BP,JAK1,PDPK1,MIR125A,FGF1	grey	VSMC_M10
GO:0034198	0.85	0.23	18	39	cellular response to amino acid starvation	BP	1	MAP3K5,ATF4,TFEB,RRAGD,KPTN,SESN3,SZT2,EIF2AK2,LARS,EIF2AK4,SLC38A2,MAPK1,RRAGB,MAPK3,WDR59,SH3GLB1,IMPACT,RNF152	grey	VSMC_M10
GO:1905952	0.85	0.19	58	118	regulation of lipid localization	BP	1	LRP1,PRKN,PPARA,TSPO,GDF9,PTCH1,PLA2G6,TTC39B,PLIN2,CRY1,ABCG5,ABCG8,TMEM30A,NR1H2,APOB,ABHD5,APOC1,AKT2,C1QTNF1,ASXL1,NR1H3,NKX3-1,FITM2,CRY2,SPP1,PLA2R1,PLTP,MAP2K6,ABCA5,ACSL5,EGF,FITM1,AGT,NTSR1,PLA2G4A,FIS1,OSBPL6,EHD1,ZDHHC8,ABCA12,LPCAT3,GPS2,ANXA2,NAXE,C3,PTPN2,PLIN3,ABCA3,ABCA7,RXRA,MIR27B,MIR27A,ABCA8,MIR33B,LDLRAP1,CRH,LRAT,PTGES	grey	VSMC_M10
GO:0002730	0.85	0.32	5	12	regulation of dendritic cell cytokine production	BP	1	KIT,TLR4,MAVS,NOD2,TICAM1	grey	VSMC_M10
GO:0045844	0.85	0.30	6	14	positive regulation of striated muscle tissue development	BP	1	LMOD3,MEF2C,IGF2,ACTN3,CREB1,MRTFB	grey	VSMC_M10
GO:0048636	0.85	0.30	6	14	positive regulation of muscle organ development	BP	1	LMOD3,MEF2C,IGF2,ACTN3,CREB1,MRTFB	grey	VSMC_M10

GO:0043280	0.85	0.20	47	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MAP3K5,GRAMD4,BAK1,MYC,HSF1,SLC1A1,NOD1,CASP8AP2,TNFSF15,HSPE1,ARRB1,ARL6IP5,ST18,FOXL2,HIP1R,ROBO1,DIABLO,HTRA2,SENP1,NKX3-1,ACVR1C,F2R,PIDD1,LCK,PDCD6,GPER1,EGLN3,MAPT,FIS1,CTSH,DDX3X,MUL1,BCL2L13,NGFR,SMAD3,S100A8,BCAP31,P2RX1,BCL10,MIR27B,RHOA,RPS27L,CASP8,ACER2,BCL2L11,PRR7,CRADD	grey	VSMC_M10
GO:0010332	0.85	0.22	25	53	response to gamma radiation	BP	1	BAK1,XRCC6,MYC,HSF1,XRCC2,WRN,PRKDC,ERCC6,ATR,POLG,CHEK2,CBL,MEN1,XRCC5,PARP1,DCUN1D3,CCL7,CYBA,HSPA5,MIR21,TIGAR,HRAS,TMEM109,TSPYL5,GTF2H5	grey	VSMC_M10
GO:1990182	0.85	0.28	8	18	exosomal secretion	BP	1	VPS4B,PRKN,CHMP2A,SDCBP,RAB7A,ATP13A2,RAB11A,VPS4A	grey	VSMC_M10
GO:0061842	0.85	0.25	14	31	microtubule organizing center localization	BP	1	SUN2,BICD2,INTS13,DLG1,TBCCD1,NIN,SYNE2,NDEL1,IFT20,NUBP1,GPSM2,SPOUT1,FHOD1,DYNC1LI2	grey	VSMC_M10
GO:0046364	0.85	0.21	31	65	monosaccharide biosynthetic process	BP	1	PPARA,AKR1B1,ATF4,GPT,GNMT,CRY1,SLC25A13,PPP4R3B,ZNF692,FAM3C,AKR1A1,SIRT7,GPI,NLN,GPD1,SIK1,MST1,PC,SLC37A4,PER2,SORD,DDB1,DGKQ,OGT,CRTC2,LEPR,PTPN2,ACADM,FBP2,NNMT,ARPP19	grey	VSMC_M10
GO:0045598	0.85	0.20	53	109	regulation of fat cell differentiation	BP	1	ATAT1,STK3,MAPK14,PIM1,TAF8,DLK2,DKKL1,TRPM4,MKX,NAPEPLD,AAMDC,KLF5,JAG1,SIRT2,PTPRQ,TRIB3,ASXL1,CEBPA,ARNTL,RUNX1T1,TRIO,CDS1,FTO,RREB1,SOX13,STK4,TRPV4,CMKLR1,GPER1,SYAP1,CREB1,DUSP10,MMP11,SAV1,GNB3,TFE3,GPS2,TGFB1I1,JDP2,ZBTB7B,SMAD3,ZBTB7C,MIR21,MIR27B,MIR27A,WNT5A,SIX1,DDIT3,CCDC3,ZFP36L2,CEBPB,CCDC71L,C1QL4	grey	VSMC_M10
GO:0048705	0.85	0.18	92	186	skeletal system morphogenesis	BP	1	OSR2,MAPK14,MDFI,TEK,ZFAND5,ROR2,DLX5,RAB23,SIX2,HOXA2,HOXA4,HOXA6,HOXA7,COL27A1,FUZ,SFRP4,MYCN,OSR1,BMI1,SOX9,MEGF8,WDR48,CSRNP1,TSKU,WDR60,TGFBR2,RARB,ALX1,RYK,TCF15,EYA1,FMN1,MEF2C,SOX6,STC1,TFAP2A,BMPR1B,HYAL1,TRPV4,TRIP11,SATB2,AXIN2,FGR,ACTN3,DLG1,SETD2,HOXD8,HOXD4,HOXD3,POR,PRKRA,COL13A1,ALPL,FGFR3,MMP13,NKX3-2,TULP3,WDR19,THRA,DHRS3,MSX2,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,FGF18,TMEM107,THBS3,CHAD,SMAD3,FOXN3,GSC,TBX4,LHX1,CDX1,PPARGC1B,NLE1,GHR,SPEF2,RFLNB,SKI,PKD1,ALX3,ANKRD11,HOXB3,NOG,SIX1,OTOR,INSIG2,SLC39A3,HOXA3	grey	VSMC_M10
GO:0036297	0.85	0.23	17	37	interstrand cross-link repair	BP	1	MCM9,ERCC6L2,FANCC,FANCG,FANCL,ERCC1,MCM8,ATR,FAN1,RNF168,POLN,RAD51D,ERCC4,SLX4,FAAP24,FANCF,RNF8	grey	VSMC_M10
GO:0060337	0.85	0.23	19	41	type I interferon signaling pathway	BP	1	MYD88,MAVS,IRF7,OAS3,NLRC5,SP100,YTHDF2,PTPN6,MUL1,USP18,DCST1,STAT2,TYK2,JAK1,PTPN2,MIR21,OAS1,FADD,WNT5A	grey	VSMC_M10
GO:0071218	0.85	0.27	9	20	cellular response to misfolded protein	BP	1	RNF5,DERL1,UGGT2,DNAJC18,AUP1,RNF185,DNAJB12,SDF2L1,RNF126	grey	VSMC_M10
GO:0062009	0.85	0.27	9	21	secondary palate development	BP	1	COL11A2,WNT11,TGFBR2,ITGB6,TGFB2,DLG1,JAG2,MMP25,WNT5A	grey	VSMC_M10
GO:0007175	0.85	0.32	5	12	negative regulation of epidermal growth factor-activated receptor activity	BP	1	CBL,SNX6,ZFYVE28,SOCS4,PSEN1	grey	VSMC_M10
GO:0050966	0.85	0.32	5	12	detection of mechanical stimulus involved in sensory perception of pain	BP	1	PHF24,ASIC3,SCN1A,BACE1,KCNA1	grey	VSMC_M10
GO:0051491	0.85	0.25	12	27	positive regulation of filopodium assembly	BP	1	SRF,DPYSL3,PIK3R1,NEURL1,DNM3,MIEN1,TENM2,BCAS3,FMR1,PALM,FNBP1L,RALA	grey	VSMC_M10
GO:0010715	0.85	0.29	7	16	regulation of extracellular matrix disassembly	BP	1	LRP1,CLASP2,FAP,MELTF,FGFR4,CARMIL2,DPP4	grey	VSMC_M10
GO:0030324	0.85	0.19	69	141	lung development	BP	1	GLI1,RIDA,TAB1,PTK7,SRF,EPAS1,PTN,TNC,YWHAZ,EGFR,MYCN,SLC7A11,SPRY1,SOX9,GLI2,FOXJ1,SPRY2,WNT11,TGFBR2,ASXL1,CEBPA,FBXW7,MME,TBX5,AP3B1,SRSF6,ITGB6,DAG1,KRAS,HSD11B1,LAMA5,SP3,CREB1,PLOD3,CTSH,ABCA12,SAV1,RAB3A,MAPK1,LIPA,TTC25,BMPR1A,THRA,RBPJ,ALDH1A2,FGF18,ITGA3,MAPK3,MAP2K1,TBX4,STRA6,GATA6,SREBF1,LAMA1,GPC3,HSPB11,ABCA3,PKD1,FOXF1,ESRP2,FSTL3,ATXN1L,NOG,WNT5A,HIKESHI,LIF,FGF1,WNT2,RC3H2	grey	VSMC_M10
GO:0051797	0.85	0.32	5	12	regulation of hair follicle development	BP	1	SMO,FERMT1,TGFB2,NGFR,WNT5A	grey	VSMC_M10
GO:0006244	0.85	0.28	8	18	pyrimidine nucleotide catabolic process	BP	1	DPYS,MBD4,ENTPD4,UPB1,NEIL1,NT5M,NTHL1,UPP1	grey	VSMC_M10
GO:0050482	0.85	0.29	7	16	arachidonic acid secretion	BP	1	PLA2G6,PLA2R1,NTSR1,PLA2G4A,NMUR2,PROCA1,PLA2G2C	grey	VSMC_M10
GO:1903963	0.85	0.29	7	16	arachidonate transport	BP	1	PLA2G6,PLA2R1,NTSR1,PLA2G4A,NMUR2,PROCA1,PLA2G2C	grey	VSMC_M10
GO:0000387	0.85	0.23	18	38	spliceosomal snRNP assembly	BP	1	PRPF31,SRSF10,CLNS1A,TGS1,AAR2,SART3,GEMIN2,SNRPD3,PRPF19,COIL,PRMT7,RNU5E-1,RNU5B-1,RNU4ATAC,SNRPC,RNU4-2,SRSF12,RNU4-1	grey	VSMC_M10
GO:0039702	0.85	0.28	8	18	viral budding via host ESCRT complex	BP	1	VPS4B,CHMP2A,CHMP2B,CHMP4C,CHMP7,VPS37D,CHMP1A,VPS4A	grey	VSMC_M10
GO:0051451	0.85	0.32	5	12	myoblast migration	BP	1	SMO,AKIRIN1,ITGB1BP1,BIN3,SIX1	grey	VSMC_M10
GO:0001836	0.85	0.22	23	48	release of cytochrome c from mitochondria	BP	1	PRKN,BAK1,PLA2G6,GGCT,TIMM50,OPA1,DNM1L,GPER1,IFI6,CIDEB,SFN,FZD9,FIS1,PINK1,PSMD10,JUN,PAM16,MLLT11,NOL3,FXN,BCL2L11,BCL2L2,PPIF	grey	VSMC_M10
GO:0098586	0.85	0.21	30	63	cellular response to virus	BP	1	USP15,MAPK14,GSDME,ANKRD17,PUM2,PHB,SEC14L1,CLPB,NPLOC4,IRF7,OAS3,GBF1,IFIH1,OASL,IFI6,NLRX1,IL12A,DDX3X,BIRC3,TKFC,SMAD3,TSPAN6,CCL5,RIOK3,RNF135,FMR1,MIR21,OAS1,ZCCHC3,IRGM	grey	VSMC_M10
GO:0006700	0.86	0.30	6	14	C21-steroid hormone biosynthetic process	BP	1	TSPO,AKR1B1,DKK3,WNT4,DGKQ,CACNA1H	grey	VSMC_M10
GO:0060306	0.86	0.26	10	23	regulation of membrane repolarization	BP	1	NEDD4L,SCN5A,KCNE2,CASQ2,KCNJ2,ANK2,SCN4B,NOS1AP,RNF207,KCNH2	grey	VSMC_M10
GO:0045744	0.86	0.23	17	37	negative regulation of G protein-coupled receptor signaling pathway	BP	1	CRY1,KLK14,CXCL8,PLEK,MET,GIPR,ARRB1,RPGRIP1L,GRK2,SAG,GRK4,RGS14,DNM2,CCL5,MGRN1,RGS4,MRAP2	grey	VSMC_M10
GO:0035269	0.86	0.29	7	16	protein O-linked mannosylation	BP	1	RXYLT1,LARGE1,FKTN,TMTC4,POMT2,POMGNT2,ISPD	grey	VSMC_M10
GO:0090025	0.86	0.27	9	20	regulation of monocyte chemotaxis	BP	1	FPR2,ANO6,SLAMF8,MOSPD2,TNFSF18,S100A14,CCL5,DEFB124,DUSP1	grey	VSMC_M10

GO:0031167	0.86	0.27	9	20	rRNA methylation	BP	1	TFB1M,DIMT1,NSUN3,NSUN5,MRM2,ZCCHC4,MRM3,METTL16,TRMT61B	grey	VSMC_M10
GO:0019827	0.86	0.19	51	106	stem cell population maintenance	BP	1	CNOT2,ZNF706,MED30,MYC,FANCC,SMO,KIT,SIX2,PTN,TUT4,FOXO3,SOX9,RAF1,HOOK3,JAG1,LSM1,TCF15,PAX8,CNOT1,SETD6,MCPH1,LOXL2,RTF1,PAX2,LDB1,DIS3L2,SOX2,FZD7,DDX6,VPS72,EIF4ENIF1,TET1,MED14,SAV1,STAT3,LEO1,BMPR1A,RBPJ,MED6,ESRRB,MED7,SKI,MED27,MTF2,SOX4,METTL14,NOG,ZNF322,LIF,ZFP36L2,MED21	grey	VSMC_M10
GO:0030216	0.86	0.20	35	74	keratinocyte differentiation	BP	1	CYP27B1,IFT74,CD109,HOXA7,GRHL1,INTU,EVPL,SCEL,OVOL2,JAG1,ASAH1,FLNB,CASP3,VDR,SRSF6,DSP,STK4,PPHLN1,TGM1,KDF1,SFN,CLIC4,H2AFY2,ABCA12,SAV1,RBPJ,MED1,MAP2K1,BCL11B,MIR125B1,WNT5A,DNASE1L2,ZBED2,EREG,SGPP1	grey	VSMC_M10
GO:0000578	0.86	0.25	11	25	embryonic axis specification	BP	1	FRS2,PTCH1,FAM208A,HOXD8,FZD5,CITED1,LHX1,WDR77,WNT5A,BASP1,C2CD3	grey	VSMC_M10
GO:0030323	0.86	0.18	71	145	respiratory tube development	BP	1	GLI1,HECA,RIDA,TAB1,PTK7,SRF,EPAS1,PTN,TNC,YWHAZ,EGFR,MYCN,SLC7A11,SPRY1,SOX9,GLI2,FOXJ1,SPRY2,WNT11,TGFBR2,ASXL1,CEBPA,FBXW7,MME,TBX5,AP3B1,SRSF6,ITGB6,DAG1,KRAS,HSD11B1,LAMA5,SP3,CREB1,PLOD3,CTSH,ABCA12,SAV1,RAB3A,MAPK1,TULP3,LIPA,TTC25,BMPR1A,THRA,RBPJ,ALDH1A2,FGF18,ITGA3,MAPK3,MAP2K1,TBX4,STRA6,GATA6,SREBF1,LAMA1,GPC3,HSPB11,ABCA3,PKD1,FOXF1,ESRP2,FSTL3,ATXN1L,NOG,WNT5A,HIKESHI,LIF,FGF1,WNT2,RC3H2	grey	VSMC_M10
GO:0051447	0.86	0.30	6	14	negative regulation of meiotic cell cycle	BP	1	FBXO43,MOS,PRKAR1A,OVOL1,DUSP1,LIF	grey	VSMC_M10
GO:0000077	0.86	0.19	51	105	DNA damage checkpoint signaling	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,MAPK14,CRY1,BRSK1,MSH2,ETAA1,XPC,PLK3,NEK11,PRKDC,ERCC6,CEP63,STK33,PLK2,RAD17,ATR,RAD9B,EIF2AK4,NBN,ABRAXAS1,DONSON,PIDD1,TAOK3,CCND1,GIGYF2,CHEK2,ATRIP,SYF2,CDKN1B,TIPRL,RHNO1,PRPF19,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,FOXN3,TAOK1,FZR1,DOT1L,FBXO31,RPA4,RPS27L,SOX4,BRCC3,CRADD	grey	VSMC_M10
GO:0032410	0.86	0.21	27	57	negative regulation of transporter activity	BP	1	NEDD4L,GOPC,PRKCE,HECW1,TCAF2,OSR1,KCNRG,OXSR1,KCNE2,PKD2,CASQ2,HECW2,ADRA2A,ATP1A2,C4orf3,CTTNBP2NL,GNB5,CALM1,FMR1,WWP2,RRAD,MIR24-1,GPR35,MIR33B,CRBN,GEM,PPIF	grey	VSMC_M10
GO:0022037	0.86	0.20	40	84	metencephalon development	BP	1	GLI1,UQCRQ,AGTPBP1,CKB,SMO,SEMA4C,WHRN,PTN,XRCC1,GLI2,B4GALT2,SCN5A,CLP1,FAIM2,RPGRIP1L,CNTN1,LDB1,TTBK2,TTC21B,GNPAT,GBX2,SPTBN2,HAP1,PSEN1,MAP2K1,LHX1,CDK5R1,SEZ6,DAB1,ABAT,CRK,SDF4,MECP2,AARS,HSPA5,GRID2,NANOS1,CEND1,OTX1,PDSS2	grey	VSMC_M10
GO:0072497	0.86	0.33	4	10	mesenchymal stem cell differentiation	BP	1	FZD1,SOX9,SOX6,WNT3	grey	VSMC_M10
GO:0001675	0.86	0.31	5	12	acrosome assembly	BP	1	TBPL1,NECTIN2,SOX30,MFSD14A,TBC1D20	grey	VSMC_M10
GO:0007097	0.86	0.27	8	19	nuclear migration	BP	1	SUN2,HOOK3,SLIT1,SYNE2,NTN1,CLMN,DOCK7,FHOD1	grey	VSMC_M10
GO:0006085	0.86	0.28	7	16	acetyl-CoA biosynthetic process	BP	1	PPCS,DLD,PDK1,PDHX,PDK3,MPC2,MLYCD	grey	VSMC_M10
GO:0060644	0.86	0.30	6	14	mammary gland epithelial cell differentiation	BP	1	PTCH1,SMO,AKT2,MGMT,FOXF1,CEBPB	grey	VSMC_M10
GO:0055002	0.86	0.21	24	52	striated muscle cell development	BP	1	OBSCN,LMOD2,SRF,PGM5,TMOD1,MYLK3,ACTG1,LMOD3,LMOD1,PRKAR1A,ACTC1,MYOZ2,CASQ1,TMOD4,MYPN,TTN,MYOZ1,TMOD2,OBSL1,LDB3,TCAP,MYH11,CSRP2,KRT19	grey	VSMC_M10
GO:0007044	0.86	0.20	42	89	cell-substrate junction assembly	BP	1	LRP1,PTK2,TEK,TLN1,ITGB1BP1,CLASP2,ACTG1,ARHGEF7,PTPRA,FAM107A,FMN1,SORBS1,PTPRJ,PTK2B,DMTN,LDB1,SLK,COL17A1,COL16A1,AJUBA,ARHGAP6,SLC9A1,ACTN3,WHAMM,LAMC1,APOD,TRIP6,FN1,WNT4,VCL,TAOK2,SMAD3,CORO2B,BCAS3,CAMSAP3,PDPK1,TSC1,RHOA,ACVRL1,PEAK1,THY1,DUSP22	grey	VSMC_M10
GO:0060541	0.86	0.18	80	163	respiratory system development	BP	1	GLI1,RIDA,TAB1,PTK7,SRF,DLX5,EPAS1,PTN,TNC,YWHAZ,EGFR,MYCN,SLC7A11,SPRY1,SOX9,GLI2,FOXJ1,SPRY2,WNT11,TGFBR2,ASXL1,CEBPA,FBXW7,MME,TBX5,AP3B1,SRSF6,RPGRIP1L,ITGB6,ALDH1A3,DAG1,KRAS,HSD11B1,LAMA5,SP3,CREB1,PLOD3,CTSH,ABCA12,SAV1,RAB3A,MAPK1,TULP3,LIPA,TTC25,BMPR1A,THRA,RBPJ,ALDH1A2,FGF18,ITGA3,MAPK3,MAP2K1,TBX4,STRA6,GATA6,SMCHD1,SREBF1,LAMA1,SPEF2,GPC3,HSPB11,ABCA3,SKI,PKD1,FOXF1,ASS1,HYDIN,ESRP2,FSTL3,ATXN1L,NOG,WNT5A,BASP1,SIX1,HIKESHI,LIF,FGF1,WNT2,RC3H2	grey	VSMC_M10
GO:0010885	0.86	0.30	6	14	regulation of cholesterol storage	BP	1	PPARA,TTC39B,NR1H2,APOB,NR1H3,EHD1	grey	VSMC_M10
GO:0030953	0.86	0.33	4	10	astral microtubule organization	BP	1	LIMK2,DLG1,KPNB1,RAB11A	grey	VSMC_M10
GO:0071248	0.86	0.18	69	141	cellular response to metal ion	BP	1	TPH2,SLC12A2,PRKN,TSPO,CPNE5,HSF1,SLC1A1,AQP1,MTF1,EGFR,BRAF,DLG2,SCN5A,CPNE9,SYT1,RYR1,PRNP,SYT9,CEBPA,RYR3,ADGRV1,MEF2C,HVCN1,XRCC4,CPNE2,PKD2,TFAP2A,DMTN,ADCY7,SYT8,SLC41A1,GPLD1,A3GALT2,SLC30A10,NCF1,FABP4,NFATC4,CARF,CLIC4,BACE1,CDKN1B,NFE2L2,CREB1,RASA4,RASGRP2,ABCB6,KCNA1,MAPK1,ATP13A2,DLG4,PARP1,SYT7,SYT11,FOS,MAPK3,SLFN14,SLC25A23,JUN,CACNA1H,CPNE7,HSPA5,NQO1,FSTL3,KCNK3,MT1X,CLDN1,WNT5A,TIGAR,PPIF	grey	VSMC_M10
GO:0055070	0.86	0.30	6	14	copper ion homeostasis	BP	1	SLC31A2,ATP7B,PRNP,CUTC,ABCB6,SCO1	grey	VSMC_M10
GO:0033262	0.86	0.31	5	12	regulation of nuclear cell cycle DNA replication	BP	1	DACH1,NUGGC,BCL6,DBF4B,TIPIN	grey	VSMC_M10
GO:1904659	0.86	0.20	38	80	glucose transmembrane transport	BP	1	SLC2A12,MAPK14,SLC25A27,GRB10,FGF21,BRAF,MFSD4B,PRKAG2,AKT2,ASPSCR1,TRIB3,PIK3R1,SORBS1,IRS1,SLC2A10,TERT,C2CD5,PEA15,NFE2L2,CLTCL1,SLC2A2,SLC27A1,SLC2A9,SLC2A4,RSC1A1,SLC5A2,SLC5A11,PRKCB,INSR,YES1,C3,GPC3,INPP5K,SLC45A1,SLC2A6,TSC1,FABP5,ARPP19	grey	VSMC_M10
GO:0010883	0.86	0.22	19	41	regulation of lipid storage	BP	1	PPARA,MEST,TTC39B,PLIN2,NR1H2,APOB,ABHD5,ASXL1,FBXW7,NR1H3,FITM2,FTO,CPT1A,FITM1,EHD1,SREBF1,C3,PTPN2,PLIN3	grey	VSMC_M10
GO:0033013	0.86	0.22	23	49	tetrapyrrole metabolic process	BP	1	FECH,TSPO,MMACHC,SLC25A38,HPX,MMAA,CPOX,COX15,ABCC2,TMEM14C,ALAS1,MTR,BDH2,MMAB,ABCB6,ABCD4,COX10,CD320,SLC46A1,NFE2L1,FXN,MMADHC,CLYBL	grey	VSMC_M10

GO:0010863	0.86	0.24	13	29	positive regulation of phospholipase C activity	BP	1	ESR1,KIT,LPAR1,EGFR,C5AR1,PHB,RASGRP4,FLT1,ARHGAP6,AGT,ABL2,GNA15,HRAS	grey	VSMC_M10
GO:0043567	0.86	0.29	6	14	regulation of insulin-like growth factor receptor signaling pathway	BP	1	PHIP,NKX3-1,ZFAND2B,IGFBP4,CILP,MYORG	grey	VSMC_M10
GO:0046434	0.86	0.19	62	126	organophosphate catabolic process	BP	1	PDE7B,ENPP3,ABHD16A,SYNJ2,DPYS,PDE10A,SMPDL3A,PLA2G6,GDA,NT5E,INPP4B,SMPD2,MTMR2,NAPEPLD,ENTPD6,NUDT15,APOC1,NUDT5,MBD4,GPD1L,NUDT16,MTMR7,ABHD6,NUDT12,AMPD3,GPD1,SYNJ1,ENTPD4,FITM2,NUDT18,PLA2G4B,PDE9A,INPP5A,NUDT17,NTSR1,INPP5J,PDE8A,PLBD1,PLA2G4A,UPB1,ABHD12B,SMPD4,LIPC,GDPD3,LDLR,GDPD1,PDE4A,NEIL1,GDE1,PNPLA6,NT5M,IMPA2,INPP5K,NTHL1,MLYCD,PLA2G15,ENTPD5,NUDT19,INPP1,PDXP,HINT1,UPP1	grey	VSMC_M10
GO:2000679	0.86	0.28	7	16	positive regulation of transcription regulatory region DNA binding	BP	1	POU4F1,DDRGK1,TRAF6,HAND2,PARP1,PARK7,LAMTOR5	grey	VSMC_M10
GO:0071322	0.86	0.19	59	121	cellular response to carbohydrate stimulus	BP	1	ZNF236,NME1,LRP1,AGER,MAPK13,PLA2G6,SRF,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,GRIK5,RAF1,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,KCNJ11,TIAM1,RAB11FIP5,OPA1,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,MAP2K6,SLC9B2,ZBTB20,ADRA2A,KCNB1,POLG,GPER1,RAB11FIP2,MLXIPL,SIDT2,PDK3,KLF7,FIS1,MEN1,ENY2,ABCA12,CALCRL,PPP3CB,PTPRN,MPC2,STX4,GPR68,PRKCB,SIN3A,COLEC12,OXCT1,NADK,BAIAP3,CYBA,SOX4,CRH	grey	VSMC_M10
GO:0002689	0.86	0.29	6	14	negative regulation of leukocyte chemotaxis	BP	1	C5AR2,SLAMF8,PADI2,CCL2,DPP4,DUSP1	grey	VSMC_M10
GO:0045746	0.86	0.23	15	33	negative regulation of Notch signaling pathway	BP	1	DLK2,BEND6,ARRB1,TCIM,CBFA2T2,FBXW7,HIF1AN,NEURL1,YTHDF2,DLX1,BCL6,ARRDC1,WWP2,SLC35C1,HEY2	grey	VSMC_M10
GO:0006753	0.86	0.16	198	387	nucleoside phosphate metabolic process	BP	1	NME1,HSD17B4,TBPL1,PDE7B,ENPP3,ATP5MGL,DPYS,PPT2,PPARA,PDE10A,ACSL6,SMPDL3A,PRXL2C,GTPBP1,GUCA1B,IMPDH1,NMRK1,GDA,CROT,SLC35B2,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,ME1,NT5E,PPT1,BPGM,DLD,SPHK2,CMPK1,ADCY3,ENTPD6,NUDT15,DLG2,LACC1,NUDT5,DHTKD1,MBD4,PRKAG2,SLC22A13,ATP5F1C,ELOVL1,PFKP,IDO2,IDO1,NUDT16,PANK2,PDK1,SUCLG2,PDHX,SLC5A8,ELOVL7,PANK1,GPI,NUDT12,AMPD3,ATP5F1A,MCCC2,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,GMPR,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,PUDP,NUDT17,MFN1,PFKFB2,PRPS2,ENO4,PARP9,HACD2,ARNT,ADCY4,CTPS2,ACTN3,HDAC4,THEM5,DNAJC30,MLXIPL,PDE8A,DTYMK,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,UPB1,HK1,ACSBG1,ATP5S,CASK,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,MAPK1,ENO3,NT5C3B,PARP1,TECR,CARD11,SLC26A1,NAXE,PSEN1,ACOT2,GUCY2D,PKLR,PANK3,GCDH,OGT,UPRT,ADPGK,PDE4A,ACSM3,ACACA,NEIL1,NCOR1,INSR,SLC26A2,PRPSAP2,ADSSL1,NT5M,NOS2,ACSBG2,ALDOC,PIPOX,ACOT11,NADK,ATP6V0C,PANK4,NTHL1,NME3,MPP1,PARK7,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,AK8,UCK1,MLYCD,KARS,FUK,DHODH,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,PDZD3,ELOVL3,MTHFD2L,CMPK2,TIGAR,NUDT19,NNMT,NME6,DCTD,NUDT2,NAPRT,HINT1,UPP1,NMNAT1	grey	VSMC_M10
GO:0014855	0.86	0.21	26	56	striated muscle cell proliferation	BP	1	GLI1,MAPK14,PIM1,AKIRIN1,TGFBR2,EPHB1,MEF2C,TBX5,JARID2,TGFB2,PRKAR1A,KCNK2,SAV1,STAT3,MAPK1,BMPR1A,RBPJ,TBX2,GATA6,MIR199A1,MIR222,NOG,SIX1,C3orf58,HEY2,WNT2	grey	VSMC_M10
GO:0106106	0.86	0.18	60	123	cold-induced thermogenesis	BP	1	ATF4,HSF1,ALDH1A1,GADD45G,EPAS1,NR1H2,GRB10,TLR4,LPIN1,IL15,UCP1,FGF21,LAMA4,ACVR2B,PLCL2,ABHD6,ARNTL,NR1H3,ALMS1,EBF2,KSR2,ZNF423,PRKAB1,MAP2K6,CMKLR1,FABP4,TRPM8,GPR3,PER2,ACTN3,ACADL,TFE3,MFAP2,YBX2,THRA,RBPJ,MFN2,KDM6B,SLC25A44,ZBTB7B,OGT,PCTP,IL4R,TRPV2,PPARGC1B,LEPR,DOCK7,ACOT11,PRDM16,LCN2,BSCL2,FABP5,ELOVL3,PEMT,NOVA1,PLAC8,DDIT3,APC,CEBPB,DIO2	grey	VSMC_M10
GO:0120161	0.86	0.18	60	123	regulation of cold-induced thermogenesis	BP	1	ATF4,HSF1,ALDH1A1,GADD45G,EPAS1,NR1H2,GRB10,TLR4,LPIN1,IL15,UCP1,FGF21,LAMA4,ACVR2B,PLCL2,ABHD6,ARNTL,NR1H3,ALMS1,EBF2,KSR2,ZNF423,PRKAB1,MAP2K6,CMKLR1,FABP4,TRPM8,GPR3,PER2,ACTN3,ACADL,TFE3,MFAP2,YBX2,THRA,RBPJ,MFN2,KDM6B,SLC25A44,ZBTB7B,OGT,PCTP,IL4R,TRPV2,PPARGC1B,LEPR,DOCK7,ACOT11,PRDM16,LCN2,BSCL2,FABP5,ELOVL3,PEMT,NOVA1,PLAC8,DDIT3,APC,CEBPB,DIO2	grey	VSMC_M10
GO:0060479	0.86	0.28	7	16	lung cell differentiation	BP	1	SOX9,FOXJ1,CREB1,SAV1,THRA,RBPJ,GATA6	grey	VSMC_M10
GO:1990416	0.86	0.33	4	10	cellular response to brain-derived neurotrophic factor stimulus	BP	1	NTRK2,WASF1,MAPT,PDPK1	grey	VSMC_M10
GO:0055023	0.86	0.24	14	31	positive regulation of cardiac muscle tissue growth	BP	1	GLI1,MAPK14,PIM1,MEF2C,TBX5,MAPK1,BMPR1A,RBPJ,TBX2,GATA6,MIR199A1,MIR222,HEY2,WNT2	grey	VSMC_M10
GO:0060340	0.86	0.31	5	12	positive regulation of type I interferon-mediated signaling pathway	BP	1	MAVS,IRF7,NLRC5,FADD,WNT5A	grey	VSMC_M10
GO:0048634	0.86	0.24	13	29	regulation of muscle organ development	BP	1	SIRT2,LMOD3,MEF2C,SFMBT1,IGF2,USP19,ACTN3,YBX3,CREB1,SOX15,SMAD3,MRTFB,JPH2	grey	VSMC_M10
GO:0033627	0.86	0.20	28	60	cell adhesion mediated by integrin	BP	1	PTK2,PODXL,IFT74,ITGB1BP1,FERMT1,RAC3,NCKAP1L,RET,LPXN,TESC,ITGB6,TGFB2,COL16A1,CIB1,ITGB5,ITGA4,PTPN6,FBN1,FERMT3,MUC1,EFNA1,ITGA11,CCL5,CRK,PIEZO1,DPP4,ACER2,LIF	grey	VSMC_M10
GO:0090201	0.86	0.27	8	18	negative regulation of release of cytochrome c from mitochondria	BP	1	PRKN,OPA1,PSMD10,PAM16,NOL3,FXN,BCL2L2,PPIF	grey	VSMC_M10
GO:0043247	0.86	0.31	5	12	telomere maintenance in response to DNA damage	BP	1	ERCC1,XRCC1,RTEL1,ERCC4,TERF2	grey	VSMC_M10
GO:0043558	0.86	0.31	5	12	regulation of translational initiation in response to stress	BP	1	NCK2,EIF2AK2,EIF2AK4,IMPACT,PPP1R15A	grey	VSMC_M10

GO:0072091	0.86	0.23	15	33	regulation of stem cell proliferation	BP	1	FBLN1,PIM1,EPCAM,OVOL2,FERMT1,EIF2AK2,VEGFC,TERT,KDF1,THPO,OVOL1,KAT7,CITED1,MIR222,ATXN1L	grey	VSMC_M10
GO:0070167	0.86	0.20	35	74	regulation of biomineral tissue development	BP	1	CYP27B1,OSR2,OMD,PTN,TRPM4,OSR1,SOX9,SLC4A2,ACVR2B,ACVR2A,KL,GAS6,ADGRV1,MEF2C,P2RX7,PTK2B,BMP2K,ANO6,TFAP2A,BMPR1B,SGMS2,AMELX,ACTN3,TXLNG,FZD9,SRGN,BCOR,ANKH,WNT4,BMPR1A,SMAD3,RFLNB,BGLAP,CEBPB,HEY2	grey	VSMC_M10
GO:0051764	0.86	0.31	5	12	actin crosslink formation	BP	1	BAIAP2L2,LCP1,DPYSL3,GAS2,EPS8	grey	VSMC_M10
GO:0060350	0.86	0.21	21	46	endochondral bone morphogenesis	BP	1	TEK,DLX5,COL27A1,SOX9,TSKU,TGFBR2,RARB,MEF2C,STC1,BMPR1B,TRPV4,TRIP11,AXIN2,POR,COL13A1,ALPL,FGFR3,MMP13,FGF18,THBS3,GHR	grey	VSMC_M10
GO:0048863	0.86	0.18	84	171	stem cell differentiation	BP	1	SEMA6A,ESR1,SOX10,SMO,SRF,FZD1,OCIAD1,KIT,SEMA4D,SEMA4C,EPCAM,HOXA7,PTN,TEAD2,OSR1,SOX9,ERCC2,OVOL2,JAG1,ALX1,EIF2AK2,SEMA3D,SEMA3A,NRG1,PRKDC,KBTBD8,TCF15,RET,HAND2,MEF2C,SEMA4F,SETD6,SOX6,LMBR1L,TBX5,SEMA3G,PAX2,SEMA4G,PRICKLE1,JARID2,RBM24,KLHL12,SEMA3F,TGFB2,PEF1,PDCD6,YTHDF2,GBX2,OSM,LAMA5,SETD2,WNT3,NFE2L2,SEMA6D,FN1,XRCC5,MEOX1,SHC4,STAT3,MAPK1,BMPR1A,RADIL,RBPJ,CDK12,ALDH1A2,EPOP,SETD1A,SEMA4A,FOXO4,BATF,MAPK3,ESRRB,GSC,TBX2,TCOF1,GATA6,JSL1,SOX8,MTF2,SP7,A2M,LIF,ZFP36L2,NKX2-5	grey	VSMC_M10
GO:0019722	0.86	0.18	72	147	calcium-mediated signaling	BP	1	NFATC1,RCAN2,FHL2,TNNI3,FPR2,CXCL8,PLEK,EGFR,TRPM4,GRIN2D,SLC8A2,ACKR2,EFHB,PRNP,P2RX2,NRG1,P2RX3,PLCE1,PTPRJ,P2RX7,SLA2,PTK2B,PLA2G4B,DMTN,CASQ2,KSR2,CHRM3,RYR2,SPPL3,PPP3CA,NR5A2,CMKLR1,TBC1D10C,ANK2,TRPM8,LAT2,CIB1,ATP1A2,SLC9A1,NFATC4,MYOZ2,CASQ1,ACTN3,HDAC4,RCAN3,HOMER2,MAPT,FIS1,MCU,CXCR2,HTT,PPP3CB,MYOZ1,ATP1B1,BST1,BHLHA15,LAT,TMEM100,CALM1,BTK,RIT2,NMUR2,MAPK7,BCAP31,PDPK1,CAMTA1,NFATC3,PTGFR,DMD,CCR10,IRGM,SAMD14	grey	VSMC_M10
GO:0031349	0.86	0.17	88	177	positive regulation of defense response	BP	1	CD226,GPSM3,XRCC6,MAPK13,TTBK1,NINJ1,FPR2,NOD1,AKIRIN2,EGFR,TLR4,IL15,MGST2,CDK19,NAPEPLD,NECTIN2,PVR,OPTN,IKBKB,NMI,TMEM173,MAVS,HPX,PRKDC,IRF7,TRAF6,HCK,CEBPA,MEF2C,RASGRP1,NLRC5,RIPK2,F2RL1,RIPK1,POLR3D,NOD2,TRPV4,PDCD4,POLR3C,FABP4,PARP9,AGT,OSM,SNX4,COCH,CD28,ADAM8,CADM1,NONO,IL16,IL12A,XRCC5,TNFSF18,LAG3,STAT5B,MED1,MAPK3,LDLR,S100A8,SFPQ,BTK,TNIP1,SIN3A,CCL5,RIOK3,VAV1,PTGER4,C3,OSMR,CREB3L3,CREBBP,PARK7,CYBA,KARS,AP1G1,MIR21,MIR22,S100A12,FADD,ZCCHC3,IRGM,WNT5A,IL33,CRH,TSLP,CEBPB,EREG,HAVCR2	grey	VSMC_M10
GO:0043010	0.86	0.17	120	242	camera-type eye development	BP	1	MDM1,FRS2,OSR2,TBC1D32,BAK1,ATF4,AGTPBP1,NTRK2,PRPH2,RORB,SRF,SLC1A1,TFAP2B,TDRD7,TMOD1,RDH13,PTN,TSPAN12,USP45,SLC7A11,SPRY1,FOXE3,HDAC2,SOX9,CRYGN,ZNF513,ACVR2B,IFT172,TSKU,SPRY2,TGFBR2,BFSP1,JAG1,SPRED3,CEP290,KERA,MAB21L1,MITF,FLT1,TUB,EPHB1,PFDN5,NPHP1,RET,FOXL2,MAB21L2,TENM3,USH1C,TENT2,OPA1,RPGRIP1L,TFAP2A,PAX2,BMPR1B,MYH15,NECTIN3,LPCAT1,PKNOX1,SLC6A3,HDAC1,ALDH1A3,TGFB2,TCIRG1,PRSS56,SHROOM2,CRYBA4,NRL,CLIC4,DLX1,GRHL3,LIMK2,SP3,CDKN1B,DLG1,FZD5,FBN1,FKBP8,PLA2G16,TULP3,OBSL1,RHOJ,ROM1,WDR19,SDK1,MAX,CLN8,MED1,ALDH1A2,MFN2,PSEN1,TTLL5,MEGF11,LCTL,SMAD3,TBX2,BCL11B,LHX1,STRA6,YY1,UNC45B,LAMA1,TWSG1,GNB1,FZR1,SKI,SOX8,LAMC3,TMEM231,SLC25A25,HSF4,FJX1,ACVRL1,THY1,WNT5A,DIO3,TGIF2,TBC1D20,PITX3,WNT2,COL8A2	grey	VSMC_M10
GO:0031053	0.86	0.30	5	12	primary miRNA processing	BP	1	PUS10,DDX3X,STAT3,SMAD3,DROSHA	grey	VSMC_M10
GO:0032623	0.86	0.22	20	43	interleukin-2 production	BP	1	TNFAIP3,SPTBN1,PRKD2,NAV3,PRNP,TRAF6,IL1A,RIPK2,HDAC7,NOD2,CD28,HOMER2,LAG3,STAT5B,FOXP3,CARD11,TBX21,TRAF2,GLMN,HAVCR2	grey	VSMC_M10
GO:0032663	0.86	0.22	20	43	regulation of interleukin-2 production	BP	1	TNFAIP3,SPTBN1,PRKD2,NAV3,PRNP,TRAF6,IL1A,RIPK2,HDAC7,NOD2,CD28,HOMER2,LAG3,STAT5B,FOXP3,CARD11,TBX21,TRAF2,GLMN,HAVCR2	grey	VSMC_M10
GO:0019079	0.86	0.19	48	99	viral genome replication	BP	1	YTHDC2,PABPC1,PRKN,PPARA,APOBEC3H,CXCL8,RSAD2,PCBP1,ATG5,ZC3HAV1,PHB,FBXL2,ATG16L2,RAB5A,EIF2AK2,MAVS,GAS6,PCBP2,FAM208A,EIF2AK4,OAS3,IFIH1,OASL,TMEM39A,ADARB1,NR5A2,STAU1,HSPA8,GRK2,ATG16L1,CD28,DDX3X,PI4KA,DDB1,HACD3,LARP1,TNIP1,CCL5,CCL2,FMR1,INPP5K,LAMTOR5,MIR222,HTATSF1,SETDB1,OAS1,TBC1D20,FAM111A	grey	VSMC_M10
GO:0050851	0.86	0.18	57	117	antigen receptor-mediated signaling pathway	BP	1	CD226,HLA-DPB1,TEC,TNFRSF21,PRKD2,NECTIN2,EIF2B3,IKBKB,PAWR,PLCL2,PRNP,NCKAP1L,FOXP1,TRAF6,LPXN,PTPRJ,MEF2C,SLA2,RIPK2,SPPL3,LCK,BANK1,ICOSLG,BTN2A2,DENND1B,THEMIS2,LAT2,BMX,CD28,RC3H1,PTPN6,CD38,MAPK1,FOXP3,GPS2,CARD11,PSEN1,LCP2,CD19,PRKCB,BTK,PRAM1,PTPN2,IKBKG,VAV3,BCL10,CMTM3,FYB1,BTN1A1,CD247,THY1,UBE2N,GCSAM,HRAS,LAX1,SH2B2,RC3H2	grey	VSMC_M10
GO:0045721	0.86	0.30	5	12	negative regulation of gluconeogenesis	BP	1	CRY1,FAM3C,SIK1,MST1,LEPR	grey	VSMC_M10
GO:0071168	0.86	0.24	12	27	protein localization to chromatin	BP	1	MRNIP,ESR1,MCM9,LEMD2,MSH2,MCM8,FAM208A,CHMP7,PPHLN1,SETD2,H2AFY2,MAU2	grey	VSMC_M10
GO:0014842	0.86	0.32	4	10	regulation of skeletal muscle satellite cell proliferation	BP	1	AKIRIN1,EPHB1,STAT3,SIX1	grey	VSMC_M10
GO:0014857	0.86	0.32	4	10	regulation of skeletal muscle cell proliferation	BP	1	AKIRIN1,EPHB1,STAT3,SIX1	grey	VSMC_M10

GO:0048736	0.86	0.18	68	140	appendage development	BP	1	OSR2,FZD6,TBC1D32,BAK1,PITX1,PTCH1,TFAP2B,ROR2,DLX5,MEOX2,HOXA13,MYCN,SLC7A11,OSR1,INTU,HDAC2,BBS7,SOX9,GLI2,MEGF8,IFT172,LMBR1,ZNF219,RARB,FREM2,HAND2,FMN1,FRAS1,TBX5,IFT52,RPGRIP1L,TFAP2A,SALL1,FBXW4,PRKAB1,BMPR1B,HDAC1,TGFB2,ZNRF3,KREMEN1,KDF1,SP9,WNT3,ECE1,TULP3,BMPR1A,WDR19,IQCE,MED1,ALDH1A2,PSEN1,TMEM107,MKS1,RNF165,TBX4,TBX2,GPC3,CREBBP,SKI,ALX3,TMEM231,SOX4,NOG,WNT5A,C2CD3,BCL2L11,SLC39A3,RC3H2	grey	VSMC_M10
GO:0060173	0.86	0.18	68	140	limb development	BP	1	OSR2,FZD6,TBC1D32,BAK1,PITX1,PTCH1,TFAP2B,ROR2,DLX5,MEOX2,HOXA13,MYCN,SLC7A11,OSR1,INTU,HDAC2,BBS7,SOX9,GLI2,MEGF8,IFT172,LMBR1,ZNF219,RARB,FREM2,HAND2,FMN1,FRAS1,TBX5,IFT52,RPGRIP1L,TFAP2A,SALL1,FBXW4,PRKAB1,BMPR1B,HDAC1,TGFB2,ZNRF3,KREMEN1,KDF1,SP9,WNT3,ECE1,TULP3,BMPR1A,WDR19,IQCE,MED1,ALDH1A2,PSEN1,TMEM107,MKS1,RNF165,TBX4,TBX2,GPC3,CREBBP,SKI,ALX3,TMEM231,SOX4,NOG,WNT5A,C2CD3,BCL2L11,SLC39A3,RC3H2	grey	VSMC_M10
GO:0038034	0.86	0.21	23	49	signal transduction in absence of ligand	BP	1	ERBB3,EYA4,HSPA1B,BAK1,ZC3HC1,FOXO3,RET,IL1A,EYA1,IL7,HTRA2,TERT,EYA3,IFI6,MCL1,BAG3,STRADB,BCL2A1,MAP2K5,MAPK7,FADD,BCL2L11,BCL2L2	grey	VSMC_M10
GO:0097192	0.86	0.21	23	49	extrinsic apoptotic signaling pathway in absence of ligand	BP	1	ERBB3,EYA4,HSPA1B,BAK1,ZC3HC1,FOXO3,RET,IL1A,EYA1,IL7,HTRA2,TERT,EYA3,IFI6,MCL1,BAG3,STRADB,BCL2A1,MAP2K5,MAPK7,FADD,BCL2L11,BCL2L2	grey	VSMC_M10
GO:0042178	0.86	0.29	6	14	xenobiotic catabolic process	BP	1	NUDT15,CYP2R1,ABCC2,CYP2U1,CYP2J2,CRYZ	grey	VSMC_M10
GO:0030397	0.86	0.30	5	12	membrane disassembly	BP	1	LPIN1,PLA2G16,AKAP8L,NDEL1,PRKCB	grey	VSMC_M10
GO:0008654	0.86	0.17	111	222	phospholipid biosynthetic process	BP	1	PIP4K2C,SYNJ2,SERAC1,AGPAT4,AGPAT1,PNPLA3,PLA2G6,GPAA1,CWH43,SRD5A3,INPP4A,TMEM246,PIGF,MBOAT7,MBOAT2,LPIN1,INPP4B,FIG4,SPHK2,MTMR2,PIP4K2A,SELENOI,ABHD5,TAMM41,ITPKC,MTMR14,PGAP2,CRLS1,CDS2,NR1H4,MTMR7,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,SLA2,SERINC5,SYNJ1,CDS1,FITM2,ITPKA,PIGT,LPCAT1,PGAP1,GPAM,CHKA,ACP6,ABHD4,SGMS2,AJUBA,GGPS1,PITPNM1,GNPAT,DGKD,PIGM,FITM1,BMX,FAM126B,IP6K2,LPGAT1,PIGV,DPAGT1,MTMR3,PCYT1A,INPP5J,PIGX,PIGZ,PISD,DGKG,PIKFYVE,PLA2G4A,SACM1L,LPCAT3,PIGC,SOCS4,PLA2G16,PI4KA,SLC27A1,ABHD8,SGMS1,PGAP3,PIGH,PI4K2B,SOCS7,DGKQ,AC138894.1,DGKE,TTC7B,PIGL,ABHD3,MPPE1,IMPA2,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,AGPAT2,PIP5KL1,FABP5,ABCA8,DHDDS,PEMT,PYURF,LCLAT1,PIGB,PIGA,INPP1,PTPMT1,CDIPT	grey	VSMC_M10
GO:0030947	0.86	0.25	10	23	regulation of vascular endothelial growth factor receptor signaling pathway	BP	1	GRB10,PRKD2,VEGFC,PDCD6,ARNT,FGF18,TNMD,PRKCB,DAB2IP,CADM4	grey	VSMC_M10
GO:0045986	0.86	0.30	5	12	negative regulation of smooth muscle contraction	BP	1	GUCY1A1,DOCK5,ADRA2C,CALCRL,KCNMA1	grey	VSMC_M10
GO:0007030	0.86	0.18	59	122	Golgi organization	BP	1	ATP8B1,TJAP1,STX17,TRAPPC12,YWHAZ,HACE1,ARHGAP21,COG1,CLASP2,RBSN,PLK3,OPTN,YIPF4,NPLOC4,ARHGEF7,ATL2,NSFL1C,TRAPPC11,KIFC3,ARMH3,GBF1,SEC22B,TRIP11,VTI1A,COG2,SEC23IP,GORASP2,STX6,SEC16B,TANGO2,PDCD10,HTT,MAPK1,BHLHA15,STX5,OBSL1,STX18,PI4K2B,GAK,TMED10,MAPK3,MAP2K1,DNM2,VMP1,COG7,BCAS3,LMAN1L,CAMSAP3,SEC16A,SURF4,GOLGA8M,TMED5,COG4,PLK5,HIKESHI,TBC1D20,FAM174B,TMED3,ZFP69B	grey	VSMC_M10
GO:0021681	0.86	0.32	4	10	cerebellar granular layer development	BP	1	FAIM2,TTBK2,GRID2,CEND1	grey	VSMC_M10
GO:0014902	0.86	0.19	41	86	myotube differentiation	BP	1	STAC3,MAML1,MAPK14,SMO,MYH9,KEL,MAMSTR,KLF5,KLHL40,DYRK1B,RYR1,P2RX2,LMOD3,SMYD1,NLN,MYOF,MEF2C,JAM2,HOMER1,BIN3,RBM24,ADAMTS15,BDNF,SIK1,PPP3CA,ACTN3,HDAC4,EHD1,GDF15,BHLHA15,IL4R,FBXO22,SKI,CACNA1H,PIEZO1,PLPP7,SMYD3,SIX1,MYORG,NKX2-5,RBM38	grey	VSMC_M10
GO:0006418	0.86	0.22	17	37	tRNA aminoacylation for protein translation	BP	1	MARS,HARS,HARS2,CARS2,LARS,WARS2,YARS2,TARS2,DALRD3,LARS2,DARS2,FARSB,EARS2,LRRC47,KARS,AARS,MARS2	grey	VSMC_M10
GO:0007617	0.86	0.30	5	12	mating behavior	BP	1	MAPK8IP2,HDAC2,HDAC4,THRA,UBE2Q1	grey	VSMC_M10
GO:0032011	0.86	0.27	7	17	ARF protein signal transduction	BP	1	IQSEC1,PSD3,FBXO8,GBF1,PSD,CYTH3,IQSEC2	grey	VSMC_M10
GO:0032012	0.86	0.27	7	17	regulation of ARF protein signal transduction	BP	1	IQSEC1,PSD3,FBXO8,GBF1,PSD,CYTH3,IQSEC2	grey	VSMC_M10
GO:0002431	0.86	0.24	12	27	Fc receptor mediated stimulatory signaling pathway	BP	1	CD226,PTK2,PLA2G6,PRKCE,HCK,PTPRJ,FGR,PLPP4,FCER1G,YES1,VAV1,VAV3	grey	VSMC_M10
GO:0008593	0.86	0.19	36	76	regulation of Notch signaling pathway	BP	1	MFNG,DLK2,KIT,BEND6,AAK1,ITGB1BP1,LLGL2,GALNT11,ARRB1,JAG1,TCIM,POFUT1,CBFA2T2,ROBO1,ROBO2,FBXW7,BMP2K,HIF1AN,NOD2,GAS2,NEURL1,NEPRO,TGFB2,POGLUT1,YTHDF2,DLX1,BCL6,PDCD10,STAT3,SYNJ2BP,JAG2,ARRDC1,WWP2,CD46,SLC35C1,HEY2	grey	VSMC_M10
GO:1903573	0.86	0.22	18	39	negative regulation of response to endoplasmic reticulum stress	BP	1	PRKN,NCK2,NR1H2,AQP11,DDRGK1,USP25,TMBIM6,NR1H3,OPA1,HYOU1,SYVN1,LPCAT3,SGTA,ABCA7,PARK7,HSPA5,MIR199A1,PPP1R15A	grey	VSMC_M10
GO:1901888	0.86	0.17	80	165	regulation of cell junction assembly	BP	1	LRP1,PTK2,NTRK2,TEK,LINGO2,SEMA4D,CLDN19,LRRN3,EPHA7,ITGB1BP1,VPS35,VSTM5,CLASP2,SLITRK5,IKBKB,LRFN1,FARP1,ACTG1,PTPRA,LRFN3,EPHB1,NPHP1,FAM107A,CLSTN2,ROBO2,FMN1,PTPRJ,MEF2C,CUX2,RAPGEF2,SLIT1,TBX5,AMIGO2,DMTN,LDB1,BDNF,SLK,COL16A1,AMIGO3,SNAI1,ADNP,ARHGAP6,AGT,ACE2,SLC9A1,RAB17,EPHB3,APOD,FZD5,RAP1B,GPBAR1,WNT4,VCL,LRTM2,NLGN2,SEMA4A,NLGN3,CHRNB2,SMAD3,NTN1,BCAS3,GPRASP2,BHLHB9,CAMSAP3,ASIC2,SLITRK2,AMIGO1,TSC1,NTNG2,ADGRL2,RHOA,GRID2,ACVRL1,PEAK1,THY1,CLDN1,WNT5A,SIX1,DUSP22,LRRTM2	grey	VSMC_M10
GO:0035067	0.86	0.30	5	12	negative regulation of histone acetylation	BP	1	ATG5,TAF7,SDR16C5,FOXP3,SIN3A	grey	VSMC_M10
GO:0007530	0.86	0.30	5	12	sex determination	BP	1	MAP3K4,SOX9,SRD5A1,WNT4,INSRR	grey	VSMC_M10

GO:0070886	0.86	0.30	5	12	positive regulation of calcineurin-NFAT signaling cascade	BP	1	NRG1,SPPL3,CIB1,SLC9A1,CAMTA1	grey	VSMC_M10
GO:0106058	0.86	0.30	5	12	positive regulation of calcineurin-mediated signaling	BP	1	NRG1,SPPL3,CIB1,SLC9A1,CAMTA1	grey	VSMC_M10
GO:0048016	0.86	0.21	22	48	inositol phosphate-mediated signaling	BP	1	NFATC1,FHL2,EFHB,PRNP,NRG1,PLCE1,SPPL3,PPP3CA,INPP5A,TBC1D10C,CIB1,SLC9A1,NFATC4,MYOZ2,ACTN3,HOMER2,PPP3CB,MYOZ1,NMUR2,MAPK7,CAMTA1,NFATC3	grey	VSMC_M10
GO:1904779	0.87	0.32	4	10	regulation of protein localization to centrosome	BP	1	NSFL1C,CEP250,APC,PARD6A	grey	VSMC_M10
GO:0009223	0.87	0.27	7	16	pyrimidine deoxyribonucleotide catabolic process	BP	1	DPYS,MBD4,UPB1,NEIL1,NT5M,NTHL1,UPP1	grey	VSMC_M10
GO:0001657	0.87	0.19	37	78	ureteric bud development	BP	1	MYC,SMAD5,PTCH1,SMO,CAT,SIX2,EPCAM,BMPER,OSR1,SPRY1,SOX9,FOXJ1,GZF1,WNT11,RARB,RET,PAX8,EYA1,ROBO2,FMN1,PKD2,PAX2,SALL1,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,SMAD3,LHX1,GPC3,SOX8,NOG,BASP1,SIX1,FGF1	grey	VSMC_M10
GO:0071825	0.87	0.22	16	35	protein-lipid complex subunit organization	BP	1	APOM,NR1H2,APOB,APOC1,NR1H4,SOAT2,PLTP,ABCA5,AGT,SOAT1,ZDHHC8,LPCAT3,LIPC,MPO,ABCA7,PLAGL2	grey	VSMC_M10
GO:0019637	0.87	0.15	384	743	organophosphate metabolic process	BP	1	NME1,HSD17B4,TBPL1,PDE7B,PIP4K2C,ENPP3,ATP5MGL,GFPT2,ABHD16A,SYNJ2,SERAC1,DPYS,AGPAT4,PPT2,AGPAT1,PPARA,PDE10A,ACSL6,PNPLA3,SMPDL3A,PRXL2C,GTPBP1,PLA2G6,CKB,GPAA1,MOCS1,GUCA1B,IMPDH1,NMRK1,GDA,CROT,SLC35B2,CWH43,SRD5A3,SLC25A13,GAPDH,PPAT,IPPK,INPP4A,RAB23,PPCS,PLPPR1,TMEM246,TMEM86B,PIGF,MBOAT7,SLC4A4,ME1,NT5E,PPT1,BPGM,PLEK,NR1H2,MBOAT2,LPIN1,INPP4B,SMPD2,DLD,FIG4,SPHK2,CMPK1,ADCY3,MTMR2,PIP4K2A,NAPEPLD,HADHA,SELENOI,ENTPD6,NUDT15,ABHD5,DLG2,AKR1A1,LACC1,APOC1,NUDT5,DHTKD1,MBD4,PRKAG2,TAMM41,SLC22A13,ATP5F1C,XYLB,ITPKC,RBKS,ELOVL1,GPD1L,PIP4P1,MTMR14,PFKP,IDO2,IDO1,PLCB1,PGAP2,CRLS1,CDS2,PLPP5,NUDT16,PANK2,PDK1,SUCLG2,NR1H4,PDHX,MTMR7,SLC5A8,ELOVL7,PANK1,GPI,ABHD6,NUDT12,AMPD3,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,GK5,ATP5F1A,MCCC2,CHRM5,MTMR9,GPD1,P2RX7,GUCY1A1,GUCY1B1,SLA2,P2RY1,PTK2B,ACOT12,CKMT2,DGUOK,PRKAG1,GMPS,NR1H3,SERINC5,PFKM,SYNJ1,OPA1,ENTPD4,CDS1,FITM2,AMPD1,ITPKA,NUDT18,PIGT,PLA2G4B,GLYCTK,ADCY7,GMPR,FAM173B,ADCY2,GPLD1,MCEE,NME4,PDE9A,LPCAT1,PGAP1,TPST1,ZBTB20,GPAM,FAR2,ACSL5,CHKA,PTHLH,PLA1A,ITPK1,ACP6,INPP5A,ABHD4,SGMS2,AJUBA,PUDP,NUDT17,GGPS1,MFN1,PITPNM1,PFKFB2,THTPA,MTMR11,PRPS2,GPER1,GNPAT,DGKD,PIGM,ENO4,FITM1,PARP9,BMX,HACD2,FAM126B,IP6K2,ARNT,LPGAT1,ADCY4,PIGV,DPAGT1,PLPP4,CTPS2,MTMR3,PFKFB4,ACTN3,HDAC4,NTSR1,THEM5,DNAJC30,PCYT1A,INPP5J,MLXIPL,PDE8A,PIGX,DTYMK,HMGCL,PLBD1,PIGZ,MAGI3,CKMT1B,PISD,DL	grey	VSMC_M10
GO:0002433	0.87	0.25	10	23	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	BP	1	PTK2,PLA2G6,PRKCE,HCK,PTPRJ,FGR,PLPP4,YES1,VAV1,VAV3	grey	VSMC_M10
GO:0038096	0.87	0.25	10	23	Fc-gamma receptor signaling pathway involved in phagocytosis	BP	1	PTK2,PLA2G6,PRKCE,HCK,PTPRJ,FGR,PLPP4,YES1,VAV1,VAV3	grey	VSMC_M10
GO:0010717	0.87	0.19	38	80	regulation of epithelial to mesenchymal transition	BP	1	FUZ,SDCBP,SPRY1,HDAC2,CLASP2,SPRY2,TGFBR2,OVOL2,JAG1,SPRED3,ALX1,IL17RD,TIAM1,LOXL2,TBX5,GCNT2,USF3,TGFB2,TCF7L2,DAG1,AXIN2,SNAI1,PHLDB1,TGFB1I1,EFNA1,SMAD3,ISL1,ENG,DAB2IP,MIR21,MIR222,POFUT2,NOG,DACT3,SDHAF2,RGCC,LDLRAD4,OLFM1	grey	VSMC_M10
GO:0002551	0.87	0.30	5	12	mast cell chemotaxis	BP	1	RAC2,KIT,VEGFC,PGF,CHGA	grey	VSMC_M10
GO:0035458	0.87	0.28	6	14	cellular response to interferon-beta	BP	1	PNPT1,TMEM173,HTRA2,OAS1,IRGM,UBE2G2	grey	VSMC_M10
GO:0043624	0.87	0.18	57	119	cellular protein complex disassembly	BP	1	VPS4B,AVIL,JMJD4,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,PLEK,ADD2,NAPA,CLASP2,MTRF1,TRIM54,NCKAP5,NAPB,NAV3,SPEF1,LMOD3,ATXN7,C12orf65,LIMA1,NCKAP5L,KATNB1,SYNJ1,F2RL1,DMTN,STMND1,CARMIL1,LMOD1,ADD3,TRPV4,TTBK2,CFL1,HSPA8,CIB1,SPTBN2,TMOD4,EPS8,CAPZA1,NSF,UPF1,TMOD2,SPTB,GAK,PEX14,CAMSAP3,TAOK1,APC2,CAMSAP1,VPS4A,CARMIL2,CCSAP,APC,PDXP,MAP1A,MAP6D1	grey	VSMC_M10
GO:0034086	0.87	0.32	4	10	maintenance of sister chromatid cohesion	BP	1	SLF1,SLF2,MAU2,NAA10	grey	VSMC_M10
GO:0034088	0.87	0.32	4	10	maintenance of mitotic sister chromatid cohesion	BP	1	SLF1,SLF2,MAU2,NAA10	grey	VSMC_M10
GO:0071241	0.87	0.17	81	165	cellular response to inorganic substance	BP	1	TPH2,SLC12A2,PRKN,TSPO,CPNE5,HSF1,SLC1A1,AQP1,MTF1,EGFR,BRAF,DLG2,SCN5A,CPNE9,SYT1,RYR1,PRNP,SYT9,CEBPA,RYR3,ADGRV1,MEF2C,HVCN1,GUCY1B1,XRCC4,CPNE2,SPIDR,PKD2,TFAP2A,DMTN,ADCY7,SYT8,SLC41A1,GPLD1,A3GALT2,MTR,SLC30A10,NCF1,FABP4,RTF2,NFATC4,CARF,CLIC4,BACE1,CDKN1B,NFE2L2,CREB1,RASA4,RASGRP2,MMP3,ABCB6,KCNA1,ADCY10,MAPK1,DDX11,ATP13A2,DLG4,PARP1,SYT7,DDI2,SYT11,FOS,MAPK3,DNM2,SLFN14,SLC25A23,JUN,FMR1,CRK,TRAF2,CACNA1H,CPNE7,HSPA5,NQO1,FSTL3,KCNK3,MT1X,CLDN1,WNT5A,TIGAR,PPIF	grey	VSMC_M10
GO:0016073	0.87	0.22	16	35	snRNA metabolic process	BP	1	EXOSC4,EXOSC3,INTS10,ZCCHC8,USB1,INTS8,INTS12,RBM7,MEPCE,INTS5,AP002990.1,INTS2,METTL4,INTS11,METTL16,EXOSC5	grey	VSMC_M10
GO:0034250	0.87	0.18	64	130	positive regulation of cellular amide metabolic process	BP	1	RMND1,PRR16,PABPC1,EIF3E,JMJD4,AGO2,HABP4,PLA2G6,NCK2,SPHK2,CNBP,CDC123,SIRT3,UPF3A,PRKDC,CASP3,MRPS27,USP16,PTK2B,EIF2AK4,NOD2,TENT4B,SLC2A13,RPUSD4,RCC1L,RPS6KB2,YTHDF2,RPS4X,YTHDF1,PASK,CD28,UHMK1,NSUN5,YBX3,NFE2L2,DDX3X,COA3,SAMD4A,PINK1,MAPK1,POLR2G,EPHA4,ZCCHC4,FXR2,EFNA1,MAPK3,TOB1,EIF3C,LARP6,LARP1,CCL5,UPF3B,FMR1,CIRBP,BARHL2,RHOA,RPS27L,SOX4,METTL14,IMPACT,RPUSD3,PPP1R15A,UQCC2,TRMT10C	grey	VSMC_M10
GO:0048041	0.87	0.19	38	81	focal adhesion assembly	BP	1	LRP1,PTK2,TEK,ITGB1BP1,CLASP2,ACTG1,ARHGEF7,PTPRA,FAM107A,FMN1,SORBS1,PTPRJ,PTK2B,DMTN,LDB1,SLK,COL16A1,AJUBA,ARHGAP6,SLC9A1,ACTN3,WHAMM,APOD,TRIP6,WNT4,VCL,TAOK2,SMAD3,CORO2B,BCAS3,CAMSAP3,PDPK1,TSC1,RHOA,ACVRL1,PEAK1,THY1,DUSP22	grey	VSMC_M10
GO:0046033	0.87	0.28	6	14	AMP metabolic process	BP	1	NT5E,AMPD3,AMPD1,ADK,ADSSL1,NUDT2	grey	VSMC_M10

GO:0001767	0.87	0.32	4	10	establishment of lymphocyte polarity	BP	1	MYH9,TRAF3IP2,SNX27,DOCK2	grey	VSMC_M10
GO:0001704	0.87	0.18	44	93	formation of primary germ layer	BP	1	ITGA7,EXOC4,SRF,TXNRD1,SIX2,WNT11,EOMES,GPI,EYA1,TLX2,MMP15,RTF1,PAX2,PRKAR1A,SNAI1,SOX2,LAMB3,COL7A1,FZD7,ITGB5,SETD2,WNT3,ITGA4,FN1,COL5A2,TBX19,LEO1,BMPR1A,KDM6B,ITGA3,SMAD3,LHX1,LAMA3,GATA6,TWSG1,COL5A1,FOXF1,DUSP2,LAMB1,POFUT2,NOG,WNT5A,DUSP1,DUSP4	grey	VSMC_M10
GO:0045429	0.87	0.23	12	27	positive regulation of nitric oxide biosynthetic process	BP	1	TLR4,PTK2B,PKD2,AGT,NOS1AP,SMAD3,DNM2,INSR,TICAM1,TRPV1,ASS1,MIR99B	grey	VSMC_M10
GO:0030851	0.87	0.24	11	25	granulocyte differentiation	BP	1	IL5,TRIB1,L3MBTL3,CEBPA,AP3B1,TESC,HCLS1,ZBTB46,SP3,HAX1,EVI2B	grey	VSMC_M10
GO:0070278	0.87	0.30	5	12	extracellular matrix constituent secretion	BP	1	ADTRP,AGT,TNFRSF1B,ENG,RGCC	grey	VSMC_M10
GO:1905475	0.87	0.17	72	147	regulation of protein localization to membrane	BP	1	LRP1,STX7,STAC3,PRKN,GOPC,SLC1A1,PRKCE,SPTBN1,PTN,ITGB1BP1,EGFR,TCAF2,SLC7A11,STAC,AKT2,PRNP,LYPLA1,PIK3R1,PLS1,SORBS1,KCNJ11,DMTN,NHLRC1,PPFIA1,DAG1,SSH1,KCNB1,C2CD5,GPER1,RAB11FIP2,CIB1,AP2M1,PPP2R5A,FZD9,DLG1,LRRC15,FIS1,CEMIP,NMT1,LZTFL1,ZDHHC8,CNPY4,GRIPAP1,CNST,ACTB,IQSEC2,RSC1A1,WNK3,STAC2,STX4,ITGAM,ITGA3,AC138894.1,RAB11A,STX8,ARHGAP44,AP2B1,MIEF2,CDK5R1,EFCAB7,GPC3,INPP5K,PDPK1,PRKCZ,RER1,ARHGEF16,VPS4A,LDLRAP1,HRAS,MIEF1,MRAP2,MESD	grey	VSMC_M10
GO:0001656	0.87	0.19	35	74	metanephros development	BP	1	OSR2,MYC,PTCH1,AKR1B1,SMO,TFAP2B,SIX2,POU3F3,OSR1,SPRY1,SOX9,FOXJ1,RET,PAX8,EYA1,ROBO2,FMN1,FRAS1,NKX3-1,PKD2,PAX2,SALL1,IRX2,CTSH,FBN1,CXCR2,WNT4,CITED1,LHX1,GPC3,PKD1,SOX8,BASP1,SIX1,LIF	grey	VSMC_M10
GO:0010832	0.87	0.29	5	12	negative regulation of myotube differentiation	BP	1	BDNF,HDAC4,BHLHA15,PLPP7,NKX2-5	grey	VSMC_M10
GO:2001239	0.87	0.22	15	33	regulation of extrinsic apoptotic signaling pathway in absence of ligand	BP	1	EYA4,HSPA1B,ZC3HC1,RET,IL1A,EYA1,IL7,HTRA2,TERT,EYA3,IFI6,MCL1,STRADB,MAP2K5,MAPK7	grey	VSMC_M10
GO:0048251	0.87	0.31	4	10	elastic fiber assembly	BP	1	TNXB,FBLN5,EFEMP2,MYH11	grey	VSMC_M10
GO:0018158	0.87	0.29	5	12	protein oxidation	BP	1	PRDX3,TRABD2A,LOXL2,LOXL4,TRABD2B	grey	VSMC_M10
GO:0032435	0.87	0.23	13	29	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	TRIM39,SDCBP,KLHL40,DDRGK1,RYBP,TAF9,RPL11,OGT,SGTA,PARK7,CAMLG,STYX,MAP1A	grey	VSMC_M10
GO:0048557	0.87	0.29	5	12	embryonic digestive tract morphogenesis	BP	1	SIX2,OVOL2,HLX,RBPMS2,FOXF1	grey	VSMC_M10
GO:0061311	0.87	0.24	11	25	cell surface receptor signaling pathway involved in heart development	BP	1	GALNT11,WNT11,JAG1,HAND2,SNAI1,BMPR1A,RBPJ,MKS1,NOG,WNT5A,HEY2	grey	VSMC_M10
GO:0051592	0.87	0.18	55	114	response to calcium ion	BP	1	TPH2,CPNE5,SLC25A13,ALG2,EGFR,BRAF,TRPC3,ENTPD6,GIPR,SCN5A,AANAT,CPNE9,SYT1,RYR1,SYT9,RYR3,ADGRV1,MEF2C,PTK2B,CPNE2,SEC31A,HOMER1,PKD2,DMTN,CASQ2,KCNIP2,RYR2,SYT8,GPLD1,PPP3CA,CCND1,PEF1,PDCD6,AMELX,CARF,CLIC4,RASA4,TTN,RASGRP2,ANXA7,KCNMA1,SYT7,SYT11,FOS,CALM1,SLC25A23,CPNE7,HSPA5,MT-CYB,FGA,WNT5A,DUSP1,PTGES,PPIF,KCNMB4	grey	VSMC_M10
GO:0015867	0.87	0.29	5	12	ATP transport	BP	1	CALHM1,SLC25A42,SLC25A23,SLC25A41,SLC25A25	grey	VSMC_M10
GO:0032634	0.87	0.29	5	12	interleukin-5 production	BP	1	TNFRSF21,SCGB1A1,FOXP3,PRKCZ,TSLP	grey	VSMC_M10
GO:0032674	0.87	0.29	5	12	regulation of interleukin-5 production	BP	1	TNFRSF21,SCGB1A1,FOXP3,PRKCZ,TSLP	grey	VSMC_M10
GO:0003205	0.87	0.17	65	135	cardiac chamber development	BP	1	ADGRG6,MAML1,FRS2,LY6E,TAB1,SMO,FOXH1,TEK,PTK7,SRF,FHL2,TNNI3,DNAH11,HOXA13,CNTRL,SCN5A,POU4F1,WNT11,TGFBR2,OVOL2,JAG1,NRG1,PAX8,HAND2,PARVA,ROBO1,ROBO2,MEF2C,ADAMTS1,TBX5,TNNC1,DSP,SALL1,RYR2,SUFU,PKP2,TNNI1,TGFB2,TRIP11,MYH7,ANK2,KCNK2,LUZP1,SAV1,BMPR1A,DHRS3,RBPJ,MED1,MKS1,DCTN5,TBX2,STRA6,GATA6,AP2B1,ISL1,ZBTB14,FOXF1,ENG,SOX4,TMEM65,NOG,WNT5A,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0051960	0.87	0.16	172	344	regulation of nervous system development	BP	1	LRP1,SEMA6A,RAB21,SNW1,TIAM2,TSPO,FSTL4,SYNGAP1,PLXNA4,NTRK2,SOX10,SMO,DAAM2,LINGO2,SRF,TTBK1,KIT,TNFRSF21,SEMA4D,SEMA4C,RTN4,RUFY3,LRRN3,EPHA7,PTN,EGFR,TRIM32,LPIN1,MYCN,FIG4,PLXNA1,HDAC2,MTMR2,VSTM5,CST7,GOLGA4,MEGF8,KDM4A,XRCC2,NUMBL,POU4F1,SS18L2,HOOK3,BHLHE40,SIRT2,RARB,SEMA3D,SPART,PLXNC1,SEMA3A,ULK1,RYK,EPHB1,PLAG1,LGI4,ANKRD27,FAIM,CLSTN2,ROBO1,ROBO2,ARNTL,FZD3,SEMA4F,VEGFC,TLX2,JAM2,CUX2,MME,RAPGEF2,TIAM1,SLIT1,SYNJ1,OPA1,NKX6-1,AMIGO2,ZFYVE27,SPINT1,SEMA3G,ITPKA,SPP1,CYFIP1,SEMA4G,ZNF335,BDNF,RNF10,KIAA0319,NEURL1,DNM1L,HDAC1,PPP3CA,CAPRIN2,SEMA3F,DAG1,AMIGO3,ADNP,YTHDF2,DISC1,SORL1,GPER1,GBX2,CERS2,NFATC4,HES6,PER2,SS18L1,CDKL5,DLX1,EPHB3,NSUN5,DLG1,WNT3,DUSP10,MAPT,SEMA6D,TNR,FN1,XRCC5,NIN,OBSL1,HAP1,EPHA4,LRTM2,BMPR1A,SPEN,NLGN2,TNFRSF1B,RGS14,PRPF19,PSEN1,SEMA4A,NLGN3,TRIM46,NDEL1,RAB11A,MAP2K1,NTN1,LDLR,PARP6,GPRASP2,BHLHB9,TRPV2,ASIC2,CDK5R1,DOCK7,MBD1,DAB1,SLITRK2,LRP8,L1CAM,SKI,ARHGAP4,PLXNA3,SOX8,AMIGO1,FBXO31,ADGRL2,MIR222,MIR125B1,FOXG1,GRID2,GPR37L1,HOXB3,NOG,THY1,WNT5A,LIF,YWHAH,EFNB3,PITX3,HEY2,WNT2,LRRTM2	grey	VSMC_M10
GO:0008360	0.87	0.17	65	134	regulation of cell shape	BP	1	ITGA7,CDC42SE2,PTK2,PLXNA4,CDC42EP1,RAC2,STRIP2,MYH9,KIT,SEMA4D,FGD3,PHIP,LPAR1,MYH14,PTN,BVES,PLXNA1,SLC26A5,MYL12A,RAC3,DIAPH1,PLXNC1,FGD6,HCK,PARVA,P2RY1,PTK2B,RND1,RHOBTB2,CYFIP1,DMTN,BRWD1,GAS2,FGD4,DAG1,EPB41,FGR,EPS8,COCH,RHOBTB1,DLG1,TBCCD1,CDC42EP2,FN1,MARK2,RHOJ,FBLIM1,FGD1,SEMA4A,TAOK2,MYH10,BRWD3,CSF1R,CCL7,CCL2,EPB41L3,CRK,PLXNA3,PALM,CFDP1,MIR21,RHOA,LST1,RND3,RHOU	grey	VSMC_M10
GO:0060009	0.87	0.31	4	10	Sertoli cell development	BP	1	HSD17B4,SOX9,SOX8,ARID4A	grey	VSMC_M10
GO:0002028	0.87	0.19	31	66	regulation of sodium ion transport	BP	1	NEDD4L,WNK2,PRKCE,HECW1,OSR1,SCN5A,GPD1L,SLMAP,GLRX,P2RX7,TESC,CNTN1,PKP2,SIK1,HECW2,KLHL24,ATP1A2,SLC9A1,SCN4B,DLG1,ATP1B1,WNK3,ATP1B2,DNM2,MIR24-1,DMD,FGF11,SCN2B,NETO2,YWHAH,NKX2-5	grey	VSMC_M10

GO:0019068	0.87	0.22	14	31	virion assembly	BP	1	VPS4B,CHMP2A,CHMP2B,CHMP4C,SPCS1,CHMP7,PC ,DDX6,RAB1B,VPS37D,CHMP1A,MVB12B,VPS4A,TBC 1D20	grey	VSMC_M10
GO:1903441	0.87	0.31	4	10	protein localization to ciliary membrane	BP	1	TUB,LZTFL1,WDR19,EFCAB7	grey	VSMC_M10
GO:0060795	0.87	0.24	10	23	cell fate commitment involved in formation of primary germ layer	BP	1	SIX2,EOMES,EYA1,RTF1,PAX2,SOX2,FZD7,LEO1,BMPR 1A,GATA6	grey	VSMC_M10
GO:1903725	0.87	0.22	14	31	regulation of phospholipid metabolic process	BP	1	LPIN1,MTMR2,APOC1,NR1H4,CHRM5,MTMR9,LPCAT 1,MTMR3,GNB3,SLC27A1,LDLR,MTMR1,ABCA3,DNAJ C19	grey	VSMC_M10
GO:0060295	0.87	0.29	5	12	regulation of cilium movement involved in cell motility	BP	1	CFAP69,MKKS,CFAP20,CFAP45,CCSAP	grey	VSMC_M10
GO:1902019	0.87	0.29	5	12	regulation of cilium-dependent cell motility	BP	1	CFAP69,MKKS,CFAP20,CFAP45,CCSAP	grey	VSMC_M10
GO:0046636	0.87	0.22	13	29	negative regulation of alpha-beta T cell activation	BP	1	HLX,RUNX3,BCL6,VSIR,RC3H1,TNFSF18,FOXP3,TBX21 ,ZBTB7B,IL4R,TWSG1,SOCS1,RC3H2	grey	VSMC_M10
GO:0006942	0.87	0.19	32	68	regulation of striated muscle contraction	BP	1	TNNI3,ASB3,TRPM4,SCN5A,NR4A1,STC1,DSP,CASQ2, RYR2,PKP2,KCNJ2,TNNI1,TRPV4,MYH7,GRK2,ANK2,A CE2,ATP1A2,SLC9A1,CASQ1,ACTN3,HDAC4,DLG1,ATP 1B1,ATP2A1,CALM1,DSG2,RNF207,DMD,CHGA,HCN4 ,NKX2-5	grey	VSMC_M10
GO:2000644	0.87	0.31	4	10	regulation of receptor catabolic process	BP	1	MTMR2,MYLIP,DTX3L,ANXA2	grey	VSMC_M10
GO:0046626	0.87	0.20	23	50	regulation of insulin receptor signaling pathway	BP	1	PIP4K2C,GKAP1,CCND3,GRB10,SESN3,PIP4K2A,SNX5, PIK3R1,SORBS1,OPA1,IGF2,IRS1,GRB14,SORL1,AGT,SI K2,ZBTB7B,OGT,PRKCB,PTPN2,SOCS1,INPP5K,PRKCZ	grey	VSMC_M10
GO:0150063	0.87	0.16	140	282	visual system development	BP	1	SLC39A5,MDM1,FRS2,OSR2,TBC1D32,BAK1,ATF4,AG TPBP1,NTRK2,PRPH2,RORB,SRF,SLC1A1,TFAP2B,TDR D7,TMOD1,RDH13,ABCB5,PTN,TSPAN12,USP45,SLC7 A11,SPRY1,FOXE3,HDAC2,BBS7,SOX9,CRYGN,ZNF513 ,ACVR2B,IFT172,MYO7A,TSKU,SPRY2,DZANK1,TGFBR 2,BFSP1,JAG1,RARB,FSCN2,SPRED3,FREM2,CEP290,K ERA,MAB21L1,MITF,FLT1,TUB,EPHB1,PFDN5,NPHP1, RET,FOXL2,MAB21L2,TENM3,USH1C,TENT2,OPA1,RP GRIP1L,TFAP2A,PAX2,NKD1,BMPR1B,MYH15,NECTIN 3,LPCAT1,PKNOX1,SLC6A3,HDAC1,ALDH1A3,TGFB2,T CIRG1,PRSS56,SHROOM2,SOX2,CRYBA4,NRL,CLIC4,D LX1,GRHL3,LIMK2,SP3,CDKN1B,DLG1,FZD5,FBN1,FKB P8,COL5A2,PLA2G16,STAT3,TULP3,OBSL1,RHOJ,ROM 1,MFAP2,WDR19,SDK1,MAX,CLN8,MED1,ALDH1A2, MFN2,PSEN1,ITGAM,TTLL5,MEGF11,LCTL,SMAD3,TB X2,BCL11B,LHX1,STRA6,YY1,CHRDL1,UNC45B,LAMA1 ,C3,TWSG1,GNB1,FZR1,SKI,SOX8,COL5A1,LAMC3,OLF M3,TMEM231,SLC25A25,HSF4,BLOC1S3,FJX1,CNTF,A CVRL1,THY1,WNT5A,DIO3,TGIF2,TBC1D20,PITX3,WN T2,COL8A2	grey	VSMC_M10
GO:0070977	0.87	0.24	9	21	bone maturation	BP	1	SEMA4D,RYR1,ACTN3,FGFR3,THBS3,RFLNB,RHOA,SN X10,CCDC154	grey	VSMC_M10
GO:0010927	0.87	0.18	41	87	cellular component assembly involved in morphogenesis	BP	1	TBPL1,OBSCN,LMOD2,SRF,PGM5,TMOD1,MYLK3,FIG 4,MTMR2,ERCC2,CLASP2,NECTIN2,ACTG1,LMOD3,L MOD1,PRKAR1A,DAG1,ANK2,GNPAT,ACTC1,MYOZ2, CASQ1,TMOD4,PHLDB1,MYPN,PIKFYVE,TTN,MYOZ1, CNTNAP1,TMOD2,OBSL1,LDB3,MPP5,TCAP,SOX30,M YH11,EPB41L3,MFSD14A,CSRP2,KRT19,TBC1D20	grey	VSMC_M10
GO:0010623	0.87	0.31	4	10	programmed cell death involved in cell development	BP	1	KIT,PRKDC,IL1A,CNTF	grey	VSMC_M10
GO:0000122	0.87	0.15	355	694	negative regulation of transcription by RNA polymerase II	BP	1	PLAGL1,ZBTB2,ESR1,CNOT2,OSR2,SNW1,ZBTB12,PRK N,PPARA,MYC,SMAD5,PTCH1,ATF4,CBX7,SOX10,TMP RSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CRY1,SR F,NFX1,SMARCA2,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D ,RPS14,ZNF550,ZNF268,NFE2L3,HOXA2,HOXA7,JAZF1 ,XPO1,AKIRIN2,BACH2,ZNF692,NR1H2,ZNF350,FOXP 2,MED25,KLF11,CREM,SDCBP,OSR1,FOXO3,HDAC2,D NMT3A,BMI1,CNBP,PHB,SOX9,ZNF746,EED,SUV39H2 ,ZNF404,PLK3,GLI2,DACH1,TAF3,ACVR2B,KLF5,KLF12, FOXJ1,GZF1,POU4F1,THAP1,EID2,OVOL2,ZNF219,EO MES,CBX4,BHLHE40,CHD8,SIRT2,RARB,PURA,NR1D2, PAWR,SIRT7,ALX1,TAF7,RYBP,FOXP1,MITF,MTA3,ARI D5A,IRF7,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,SDR16C 5,ZC3H8,DNMT3B,CEBPA,CBFA2T2,ZNF536,IRF2,NCO A2,SAP30,ZNF366,HMBOX1,MEF2C,PEX2,PKIA,TMBI M6,CNOT1,SLA2,CUX2,MCPH1,FNIP2,BACH1,NR1H3, SCAF4,LCOR,VDR,HDAC7,NKX6-1,LOXL2,NR4A2,PHF21A,CRY2,RREB1,RTF1,ZBED6,SO X13,ZNF248,TFAP2A,RIPPLY3,HIF1AN,SALL1,HIVEP1,J ARID2,ATXN1,SUDS3,LDB1,IGF2,MAGEL2,ELK4,NUPR 2,DCAF1,SUFU,TAGLN3,PCGF6,IRX2,RPL23,HDAC1,CC ND1,SP100,TRPV4,ZBTB20,SATB2,TCF7L2,AJUBA,PIAS 3,HJV,SNAI1,ZNF202,HCLS1,SOX2,OTUD7B,GTF2IRD1 ,ZNF217,PARP9,PARP15,TFAP2C,USP2,ORC2,BAG3,N FATC4,HES6,MYOZ2,PER2,AEBP2,VPS72,HDAC4,RUN X3,NR1I3,DLX1,MLXIPL,PATZ1,SP3,DLG1,OVOL1,ETV6 ,YBX3,HOXD8,KLF7,HEXIM2,BCL6,H2AFY2,BCOR,MEN 1,MEPCE,ZBTB37,MYOZ1,RBM10,UXT,STAT3,NKX3-2,TBL1XR1,PPM1A,SCGB1A1,FOXP3,ZBTB25,ZBTB1,M AGED1,MAGED4B,PARP1,SPEN,GPS2,THRA,MAX,DNA JB1,PRDM2,RBPJ,MED1,NSD1,MAGEH1,MAFK,KLF8,C	grey	VSMC_M10
GO:0060324	0.87	0.21	18	40	face development	BP	1	ZFAND5,SRF,DLX5,RAF1,CSRNP1,MKKS,CRISPLD1,ALD H1A3,MAPK1,ALDH1A2,MAPK3,MAP2K1,STRA6,SKI,A NKRD11,HOXB3,NOG,WNT5A	grey	VSMC_M10
GO:0006527	0.87	0.31	4	10	arginine catabolic process	BP	1	OAT,FAH,NOS2,MIR21	grey	VSMC_M10
GO:0071480	0.87	0.22	13	29	cellular response to gamma radiation	BP	1	XRCC6,HSF1,WRN,ATR,CHEK2,XRCC5,CYBA,HSPA5,MI R21,HRAS,TMEM109,TSPYL5,GTF2H5	grey	VSMC_M10
GO:0090153	0.87	0.29	5	12	regulation of sphingolipid biosynthetic process	BP	1	ORMDL2,PLA2G6,SPHK2,SIRT3,ORMDL1	grey	VSMC_M10
GO:1905038	0.87	0.29	5	12	regulation of membrane lipid metabolic process	BP	1	ORMDL2,PLA2G6,SPHK2,SIRT3,ORMDL1	grey	VSMC_M10
GO:1904019	0.87	0.18	41	86	epithelial cell apoptotic process	BP	1	MAP3K5,TNFAIP3,STK3,PPARA,TEK,SFRP4,FOXO3,FG F21,DNMT3A,NDNF,TGFBR2,TMTC4,GAS6,SRSF6,AN O6,PLA2R1,STK4,CD40,RYR2,HDAC1,TERT,PDCD4,TCF 7L2,GPER1,E2F2,NFE2L2,ITGA4,TNIP2,RAMP2,EXOC5 ,MAPK7,CCL2,JAG2,PIAS4,PDPK1,DAB2IP,MIR24-1,FGA,MIR125A,CD248,RGCC	grey	VSMC_M10
GO:0051489	0.87	0.20	20	44	regulation of filopodium assembly	BP	1	SRF,RAB5A,DPYSL3,PIK3R1,DMTN,SRGAP2C,NEURL1, GAP43,RAB17,DNM3,MIEN1,FXR2,TENM2,AC138894 .1,BCAS3,ARHGAP44,FMR1,PALM,FNBP1L,RALA	grey	VSMC_M10

GO:0009161	0.87	0.20	24	51	ribonucleoside monophosphate metabolic process	BP	1	DPYS,IMPDH1,GDA,PPAT,NT5E,CMPK1,DLG2,AMPD3,GMPS,AMPD1,PRPS2,MAGI3,DLG1,UPB1,CASK,ADK,CARD11,UPRT,ADSSL1,MPP1,UCK1,DHODH,NUDT2,UPP1	grey	VSMC_M10
GO:0045185	0.87	0.18	38	80	maintenance of protein location	BP	1	TSPO,GOPC,SKP1,SUN2,GPAA1,MDFI,TAF8,NFKBIE,FAF1,GRIK5,TAF3,NFKBIB,ARL2BP,PKD2,MORC3,SUFU,SP100,IGSF11,GET4,SORL1,SRGN,HK1,FBN1,PINK1,VPS13D,VPS13C,RIT2,KEAP1,PSMD10,RER1,PKD1,PARK7,HSPA5,SUPT7L,TXN,NRROS,INSIG2,PFN4	grey	VSMC_M10
GO:0031061	0.87	0.25	8	19	negative regulation of histone methylation	BP	1	PHF1,KDM4A,DNMT3B,JARID2,BCOR,SUPT6H,MTF2,PRMT6	grey	VSMC_M10
GO:0072337	0.87	0.23	11	25	modified amino acid transport	BP	1	SLC22A4,SLC3A1,SLC1A4,SLC7A11,ABCC4,SLC38A2,SLC25A20,ABCC5,SLC46A1,SLC22A5,SLC25A32	grey	VSMC_M10
GO:0021846	0.87	0.25	8	19	cell proliferation in forebrain	BP	1	AKNA,POU3F3,NUMBL,HOOK3,DISC1,DIXDC1,DOCK7,POU3F2	grey	VSMC_M10
GO:1903034	0.87	0.17	60	123	regulation of response to wounding	BP	1	SERPINB2,LRP1,TNFAIP3,TSPAN8,SLC12A2,PTK2,ENPP4,CLDN19,PRKCE,CD109,PTN,CLASP2,PTPRF,THBD,PLAT,C1QTNF1,ACTG1,HBEGF,FERMT1,F2RL1,F2R,SRSF6,ANO6,RREB1,SPP1,DMTN,ADTRP,FAP,KIAA0319,ADRA2A,UBASH3B,KREMEN1,CERS2,USF1,LRIG2,NFE2L2,DUOX1,TNR,CASK,SERPINC1,WNT4,MYOZ1,EPHA4,F12,ANXA2,NDEL1,MAP2K1,SMAD3,ABAT,CRK,SERPINF2,MIR29A,MIR21,MIR222,FGA,CNTF,RTN4RL1,CLDN1,HRAS,CADM4	grey	VSMC_M10
GO:1905214	0.87	0.29	5	12	regulation of RNA binding	BP	1	EIF3E,GEMIN2,EIF3C,LARP6,FMR1	grey	VSMC_M10
GO:0009743	0.87	0.16	92	186	response to carbohydrate	BP	1	ZNF236,NME1,LRP1,APOM,AGER,PNPLA3,MAPK13,PLA2G6,TXN2,SRF,CAT,PRKCE,HMGN3,ME1,TRPM4,FOXO3,APOB,FGF21,GIPR,ERCC1,KHK,EIF2B3,GRIK5,RAF1,GCKR,TGFBR2,P2RX2,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,CASP3,P2RX3,PTK2B,KCNJ11,TIAM1,RAB11FIP5,OPA1,NKX6-1,ACVR1C,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,MAP2K6,SLC9B2,ZBTB20,ADRA2A,GPAM,TCF7L2,KCNB1,PFKFB2,ADNP,POLG,GPER1,RAB11FIP2,MLXIPL,GLUL,SIDT2,CDKN1B,PDK3,KLF7,RAP1B,FIS1,MEN1,ENY2,ABCA12,CALCRL,PPP3CB,CTSV,PTPRN,NDUFA9,MPC2,ILDR2,STX4,KAT7,PKLR,GPR68,PRKCB,SIN3A,COLEC12,SREBF1,OXCT1,NADK,BAIAP3,CYBA,NQO1,RHOA,SOX4,CRH	grey	VSMC_M10
GO:0045923	0.87	0.24	10	23	positive regulation of fatty acid metabolic process	BP	1	PPARA,NR1H2,AKT2,NR1H3,IRS1,CPT1A,LPGAT1,MLXIPL,CD74,MLYCD	grey	VSMC_M10
GO:0051252	0.87	0.14	1386	2654	regulation of RNA metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,GLI1,MARS,CLK4,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PABPC1,SNW1,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DXO,ZBED4,PNLDC1,PRKN,QKI,AGER,PPARA,MED30,IL5,BRD2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,HABP4,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,ATF4,TUT7,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,PUF60,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,IGF2BP3,PPP2R1A,ZNF462,TRA2A,PHIP,HMGN3,YTHDC1,NFYC,NFE2L3,PNPT1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,PTBP3,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,LPIN1,SFRP4,UCP1,CREM,TEAD2,SETD7,SDCBP,MYCN,C6orf203,E	grey	VSMC_M10
GO:1903076	0.87	0.18	43	90	regulation of protein localization to plasma membrane	BP	1	LRP1,STX7,STAC3,GOPC,PRKCE,SPTBN1,EGFR,STAC,PRNP,LYPLA1,PIK3R1,PLS1,SORBS1,KCNJ11,NHLRC1,PPFIA1,GPER1,RAB11FIP2,CIB1,AP2M1,PPP2R5A,DLG1,LRRC15,ZDHHC8,CNPY4,GRIPAP1,CNST,ACTB,RSC1A1,WNK3,STAC2,STX4,ITGA3,AC138894.1,RAB11A,STX8,ARHGAP44,PDPK1,RER1,ARHGEF16,VPS4A,LDLRAP1,MRAP2	grey	VSMC_M10
GO:2001269	0.87	0.31	4	10	positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	BP	1	ST18,HTRA2,SMAD3,PRR7	grey	VSMC_M10
GO:0010517	0.87	0.20	23	50	regulation of phospholipase activity	BP	1	LRP1,ESR1,KIT,LPAR1,PPT1,EGFR,C5AR1,PHB,RASGRP4,FLT1,PLA2R1,GNA13,ARHGAP6,AGT,ABL2,FGFR3,ANXA8,NMUR2,CCL5,GNA15,PDPK1,PRKCZ,HRAS	grey	VSMC_M10
GO:0021537	0.87	0.16	90	184	telencephalon development	BP	1	NME1,LRP1,ATAT1,UQCRQ,AGTPBP1,PLXNA4,SUN2,NTRK2,SMO,SRF,CDK6,DLX5,EFHC1,MBOAT7,RTN4,AQP1,FOXP2,POU3F3,SLC7A11,FAT4,EIF2B3,XRCC1,SCN5A,NUMBL,TSKU,SZT2,ALK,MKKS,RARB,PLCB1,SEMA3A,NRG1,RYK,ZSWIM6,CASP3,DCLK2,ROBO1,ROBO2,CELF1,CSNK2A2,MCPH1,TENT2,SLC38A2,RPGRIP1L,SALL1,DNAH5,DPCD,SRGAP2C,SRD5A1,HDAC1,ALDH1A3,DISC1,ATP1A2,DLX1,EPHB3,NSUN5,BCL2A1,DIXDC1,TNR,NIN,COL3A1,KCNA1,MPP5,ATP1B2,PSEN1,KDM6B,NDEL1,BCL11B,LHX1,XAB2,CDK5R1,DAB1,LRP8,CRK,SKI,PLXNA3,TSC1,PHLPP2,DAB2IP,RHOA,ADGRG1,CNTN2,FOXG1,LAMB1,RTN4RL1,GNG12,CCDC85C,WNT5A,POU3F2,BTBD3	grey	VSMC_M10

GO:0007569	0.87	0.17	47	98	cell aging	BP	1	MAP3K5,MAPK14,CDKN2A,SRF,NUAK1,CDK6,PNPT1,ZNF277,ERCC1,PAWR,WRN,PRKDC,PLK2,ATR,ING2,ARNTL,MME,MAPKAPK5,OPA1,PRELP,PLA2R1,MORC3,TERT,MAP2K6,PDCD4,SLC30A10,KRAS,CHEK2,MAP3K3,CDKN1B,BCL6,BMPR1A,CTC1,YPEL3,VASH1,MAP2K1,TBX2,DNAJA3,FZR1,TERF2,MIR21,MIR22,PRMT6,BGLAP,YBX1,HRAS,MAP2K7	grey	VSMC_M10
GO:0030050	0.87	0.26	7	17	vesicle transport along actin filament	BP	1	MYO1A,MYO7B,MYO7A,MYO1D,MYO1F,MYO5B,FNBP1L	grey	VSMC_M10
GO:0006458	0.87	0.21	15	33	'de novo' protein folding	BP	1	HSPA1B,BAG1,HSPE1,DNAJC18,HSPA8,DNAJB12,SDF2L1,DNAJB1,GAK,CD74,TOR1B,TOR2A,HSPA5,ENTPD5,SDF2	grey	VSMC_M10
GO:1900101	0.87	0.22	12	27	regulation of endoplasmic reticulum unfolded protein response	BP	1	BAK1,NCK2,DDRGK1,PIK3R1,FICD,PTPN2,ABCA7,HSPA5,DAB2IP,MIR199A1,BCL2L11,PPP1R15A	grey	VSMC_M10
GO:0051279	0.87	0.19	27	58	regulation of release of sequestered calcium ion into cytosol	BP	1	PRKCE,ATG5,DIAPH1,PTK2B,F2R,PKD2,CASQ2,RYR2,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,CD19,CALM1,BDKRB1,PDPK1,CYBA,JPH3,DMD,JPH2,THY1	grey	VSMC_M10
GO:0014889	0.87	0.30	4	10	muscle atrophy	BP	1	IL15,FOXO3,ACTN3,NOL3	grey	VSMC_M10
GO:0006298	0.87	0.22	12	27	mismatch repair	BP	1	RPA3,MCM9,MSH2,ERCC1,XPC,MLH1,PMS1,AXIN2,SETD2,PMS2,RNASEH2A,MSH4	grey	VSMC_M10
GO:2001259	0.87	0.19	24	52	positive regulation of cation channel activity	BP	1	STAC3,CACNB2,STAC,KCNJ11,IFNGR2,KCNE2,PKD2,KCNIP2,FAM173B,ANK2,CASQ1,NTSR1,NOS1AP,HTT,PINK1,KCNA1,HAP1,STAC2,NLGN3,CALM1,CCL2,RNF207,AMIGO1,JPH2	grey	VSMC_M10
GO:1903170	0.87	0.22	13	29	negative regulation of calcium ion transmembrane transport	BP	1	PKD2,CASQ2,ADRA2A,ATP1A2,C4orf3,NTSR1,SESTD1,GNB5,CALM1,FMR1,RRAD,GPR35,GEM	grey	VSMC_M10
GO:0006304	0.87	0.18	40	84	DNA modification	BP	1	BAZ2A,MOV10L1,MYC,APOBEC3H,PICK1,EXOSC4,EXOSC3,STPG4,ASCC3,DNMT3A,BMI1,CDADC1,MBD4,TEX15,ALKBH3,TOX,DNMT3B,OTUD4,FTO,MTRR,HEMK1,ALKBH2,TDRKH,MGMT,TET1,PARP1,FOS,ALKBH1,NEIL1,METTL4,MBD1,NTHL1,MECP2,MPG,PRMT7,CTCF,MIR29A,BEND3,N6AMT1,EXOSC5	grey	VSMC_M10
GO:0061615	0.87	0.30	4	10	glycolytic process through fructose-6-phosphate	BP	1	PFKP,PFKM,HK1,ADPGK	grey	VSMC_M10
GO:0061620	0.87	0.30	4	10	glycolytic process through glucose-6-phosphate	BP	1	PFKP,PFKM,HK1,ADPGK	grey	VSMC_M10
GO:0048730	0.87	0.23	10	23	epidermis morphogenesis	BP	1	SMO,SOSTDC1,KLK14,INTU,GLI2,TGFB2,SNAI1,PLOD3,GORAB,NGFR	grey	VSMC_M10
GO:0097529	0.87	0.16	70	142	myeloid leukocyte migration	BP	1	AGER,PTK2,RAC2,KIT,ROR2,FPR2,CXCL8,AKIRIN1,C5AR2,C5AR1,MYD88,PLCB1,NCKAP1L,FAM19A4,FLT1,MTUS1,VEGFC,PTK2B,CCL17,ANO6,NOD2,GBF1,CD200,DNM1L,TRPV4,TGFB2,CD99,CMKLR1,SLAMF8,MOSPD2,PTPRO,FCER1G,ADAM8,PIKFYVE,MCU,TNFSF18,CXCR2,BST1,MAPK1,STAT5B,PGF,DAPK2,MAPK3,IL6R,S100A14,S100A8,UMOD,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,VAV1,PTGER4,PIP5K1C,MPP1,BSG,VAV3,MIR24-1,CCL16,S100A12,CHGA,DEFB124,DPP4,CXCL6,DUSP1,CCL22,PDGFD	grey	VSMC_M10
GO:0002903	0.87	0.30	4	10	negative regulation of B cell apoptotic process	BP	1	FOXP1,BCL6,CD74,BCL10	grey	VSMC_M10
GO:0090085	0.87	0.28	5	12	regulation of protein deubiquitination	BP	1	WDR48,OTUD4,SART3,TNIP1,PARK7	grey	VSMC_M10
GO:0002685	0.88	0.16	75	152	regulation of leukocyte migration	BP	1	AGER,GPSM3,PTK2,RAC2,CCL27,FPR2,HOXA7,CXCL8,AKIRIN1,PTN,C5AR2,C5AR1,MYD88,OXSR1,PLCB1,NCKAP1L,GAS6,MTUS1,VEGFC,JAM2,PTK2B,SLC8B1,F2RL1,ANO6,ADTRP,NOD2,CD200,DNM1L,TRPV4,CD99,PRSS56,CMKLR1,SLAMF8,MOSPD2,APOD,ADAM8,MIA3,ITGA2B,ITGA4,IL12A,MCU,TNFSF18,CXCR2,BST1,MAPK1,PADI2,TMEM102,STK10,PGF,DAPK2,MAPK3,IL6R,S100A14,BDKRB1,CD74,CCL5,CSF1R,CCL7,CCL2,CCL25,PTGER4,CRK,MPP1,MIR24-1,RHOA,DEFB124,FADD,DPP4,FUT4,ZNF580,THY1,WNT5A,DUSP1,GCSAM,PDGFD	grey	VSMC_M10
GO:0034975	0.88	0.30	4	10	protein folding in endoplasmic reticulum	BP	1	CANX,PDIA3,DNAJC10,HSPA5	grey	VSMC_M10
GO:0008333	0.88	0.19	23	50	endosome to lysosome transport	BP	1	VPS4B,TGFBRAP1,VPS41,RAB7A,HOOK3,FAM160A2,VPS16,CHMP2B,VPS18,VPS39,KIF13A,RAB7B,DTX3L,SNX27,HOOK2,VIPAS39,STX8,SNAPIN,CLEC16A,MTM1,MGRN1,RILP,SNX16	grey	VSMC_M10
GO:0042118	0.88	0.30	4	10	endothelial cell activation	BP	1	BMPER,TCIM,FOXP1,APOLD1	grey	VSMC_M10
GO:0051284	0.88	0.28	5	12	positive regulation of sequestering of calcium ion	BP	1	PKD2,CASQ2,RYR2,NTSR1,CALM1	grey	VSMC_M10
GO:0070816	0.88	0.30	4	10	phosphorylation of RNA polymerase II C-terminal domain	BP	1	CDK7,CCNH,CDK12,GTF2H5	grey	VSMC_M10
GO:0006465	0.88	0.28	5	12	signal peptide processing	BP	1	SEC11C,IMMP1L,SPCS1,SPPL3,SPCS2	grey	VSMC_M10
GO:0023035	0.88	0.28	5	12	CD40 signaling pathway	BP	1	TNFAIP3,TRAF3IP2,PHB,CD40,TNIP2	grey	VSMC_M10
GO:0001678	0.88	0.16	60	124	cellular glucose homeostasis	BP	1	ZNF236,NME1,LRP1,AGER,PLA2G6,SRF,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,FOXA3,GRIK5,RAF1,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,PIK3R1,KCNJ11,TIAM1,RAB11FIP5,OPA1,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,SLC9B2,ZBTB20,ADRA2A,KCNB1,POLG,GPER1,RAB11FIP2,MLXIPL,SIDT2,PDK3,KLF7,FIS1,HK1,MEN1,ENY2,ABCA12,PPP3CB,PTPRN,MPC2,STX4,NGFR,GPR68,SIN3A,OXCT1,NADK,BAIAP3,CYBA,LRRC8A,LRRC8D,SOX4,CRH	grey	VSMC_M10
GO:0032908	0.88	0.30	4	10	regulation of transforming growth factor beta1 production	BP	1	TSKU,LUM,FOXP3,GATA6	grey	VSMC_M10
GO:0090101	0.88	0.17	48	101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ONECUT2,LRP1,PPARA,LEMD2,SOSTDC1,CD109,BMPER,SPRY1,SPRY2,EID2,SPRED3,SPART,SNX25,IL17RD,VEPH1,SLC2A10,SORL1,HTRA1,CHRD,DLX1,SNX6,CTDSPL2,PBLD,HTRA3,FBN1,PPM1A,GREM2,TGFB1I1,RBPMS2,CILP,TOB1,WFIKKN2,DNM2,CHRDL1,TWSG1,PDPK1,SKI,PRDM16,WFIKKN1,HSPA5,FSTL3,LEMD3,NOG,WNT5A,NRROS,LDLRAD4,UBE2D1,PEG10	grey	VSMC_M10
GO:0046322	0.88	0.30	4	10	negative regulation of fatty acid oxidation	BP	1	SOX9,SIRT4,ACADL,ACADVL	grey	VSMC_M10
GO:0035404	0.88	0.30	4	10	histone-serine phosphorylation	BP	1	MST1,RPS6KA5,AURKC,RPS6KA4	grey	VSMC_M10
GO:0106049	0.88	0.30	4	10	regulation of cellular response to osmotic stress	BP	1	YBX3,MICU1,AC138894.1,SLC25A23	grey	VSMC_M10
GO:0072666	0.88	0.20	19	42	establishment of protein localization to vacuole	BP	1	TNFAIP3,VPS41,RAB7A,NCOA4,AP3B1,MON1A,HSPA8,SORL1,RNF215,VPS37D,AP4M1,AP3M1,VPS13D,VPS13C,LAMP2,VPS4A,CACNG7,SNX16,CACNG5	grey	VSMC_M10
GO:0090030	0.88	0.30	4	10	regulation of steroid hormone biosynthetic process	BP	1	DKK3,POR,WNT4,DGKQ	grey	VSMC_M10

GO:0097306	0.88	0.18	33	71	cellular response to alcohol	BP	1	PTCH1,SMO,PRKCE,TNC,LANCL2,FOXO3,SPHK2,ADCY3,DNMT3A,MAP4K1,SLC23A2,CYP7A1,SPIDR,TP53INP1,ADCY7,ADCY2,GPLD1,DAG1,GRAMD1B,NPAS4,FDX1,PTGER2,AKAP8,OSBPL7,LARP1,SCNN1B,ACACA,CCL7,PTGER4,LRP8,GNB1,PTGFR,GNG2	grey	VSMC_M10
GO:1901617	0.88	0.16	88	178	organic hydroxy compound biosynthetic process	BP	1	CYP27B1,TPH2,HSD17B3,AKR1B1,PSAT1,GPR37,PLPP6,SRD5A3,SPTLC1,IPPK,PLEK,DDC,DKKL1,SLC7A11,APOB,SPHK2,DHFR,EBP,PRKAG2,ITPKC,ACER3,SPTLC3,NR1H4,CYP7A1,ASAH1,CYP7B1,OSBP,DKK3,HAND2,CYP2R1,P2RY1,PTK2B,RAPGEF2,SPR,NR4A2,ITPKA,ERLIN1,PLTP,OCA2,CYB5R1,SLC6A3,TGFB2,SNAI1,MSMO1,GPER1,SC5D,ABCB11,IP6K2,PER2,OSBPL2,NTSR1,SCAP,HSD17B7,POR,PTH1R,OSBPL6,TM7SF2,OSBPL1A,LPCAT3,WNT4,CYP27A1,GCH1,HDC,CH25H,HSD17B10,FGFR4,DGKQ,OSBPL7,PNPO,ERG28,CITED1,CYP46A1,SREBF1,IMPA2,SLC45A2,ACAA2,CACNA1H,PARK7,ABCD3,GFI1,DHDDS,WNT5A,AMACR,ACER2,STARD4,INSIG2,FGF1,PCBD2	grey	VSMC_M10
GO:0006935	0.88	0.14	215	426	chemotaxis	BP	1	LRP1,SEMA6A,KIF5A,SLC12A2,AGER,GPSM3,CXCL14,GFRA3,PTK2,PTCH1,PLXNA4,MAPK14,PLA2G6,RAC2,SMO,CCL27,KIT,PLGRKT,SEMA4D,DLX5,NINJ1,ETV1,SEMA4C,FPR2,HOXA2,LPAR1,CXCL8,AKIRIN1,EPHA7,PTN,MET,EPHA1,GAB1,NRCAM,TRPM4,PLXNA1,C5AR2,C5AR1,PRKD2,GLI2,MEGF8,OXSR1,MYCBP2,ACKR2,CMTM7,CMTM8,KIF5C,HBEGF,FEZ2,SEMA3D,PLXNC1,SEMA3A,CHL1,UNC5D,NRG1,NCKAP1L,GAS6,FAM19A4,FLT1,RYK,EPHB1,MTUS1,RET,CYP7B1,NR4A1,FER,PIK3CB,PARVA,ROBO1,ROBO2,PTPRJ,FZD3,SEMA4F,VEGFC,PTK2B,DPYSL2,CCL17,TIAM1,SLIT1,SLC8B1,TRIO,F2RL1,ANO6,SEMA3G,CYFIP1,ALCAM,SEMA4G,NOD2,SIAH1,BMPR1B,GBF1,BDNF,ELMO2,LGR6,DNM1L,TRPV4,SBDS,SEMA3F,TGFB2,GAP43,DAG1,PRSS56,LHX9,CMKLR1,SLAMF8,MOSPD2,GBX2,KALRN,LAMA5,YTHDF1,PTPRO,MACO1,FCER1G,EPHB3,ADAM8,WNT3,KLF7,CREB1,MYPN,PIKFYVE,IL16,SEMA6D,EPHB4,IL12A,TNR,MCU,TNFSF18,CXCR2,BST1,MAPK1,CH25H,CRMP1,PADI2,CXCL16,EPHA4,LRTM2,TMEM102,UNC5A,STX4,SEMA4A,HOXB9,FGF18,NGFR,DOCK2,PGF,DAPK2,EFNA1,MAPK3,IL6R,ALKBH1,MAP2K1,SMAD3,NTN1,RPS6KA5,S100A14,S100A8,RNF165,BCL11B,LHX1,CD74,CCL14,CCL5,LAMA3,AMOT,CSF1R,CCL7,CCL2,CCL25,CDK5R1,ISL1,EMB,VAV1,LAMA1,RALBP1,PTPN2,CRK,PIP5K1C,L1CAM,NTN3,ARHGEF16,PLXNA3,MPP1,BSG,TUBB3,VAV3,CMTM3,RHOA,CCL16,DPYSL5,S100A12,EFNA4,CNTN2,VASP,FOXG1,CHGA,DEFB124,CCR10,DPP4,CXCL6,ZNF580,ISL2,NOG,WNT5A,CHN1,DUSP1,ARTN,NRXN3,LYPLA2,RALA,HRAS,EFNB3,ISPD,FGF1,CCL22,PDGFD	grey	VSMC_M10
GO:0044771	0.88	0.30	4	10	meiotic cell cycle phase transition	BP	1	MAPK15,TOPAZ1,MOS,OVOL1	grey	VSMC_M10
GO:0071025	0.88	0.28	5	12	RNA surveillance	BP	1	DXO,EXOSC4,EXOSC3,SUPV3L1,EXOSC5	grey	VSMC_M10
GO:0009749	0.88	0.16	75	153	response to glucose	BP	1	ZNF236,NME1,LRP1,APOM,AGER,PLA2G6,TXN2,SRF,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,GIPR,KHK,EIF2B3,GRIK5,RAF1,TGFBR2,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,CASP3,PTK2B,KCNJ11,TIAM1,RAB11FIP5,OPA1,NKX6-1,ACVR1C,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,SLC9B2,ZBTB20,ADRA2A,GPAM,TCF7L2,KCNB1,PFKFB2,POLG,GPER1,RAB11FIP2,MLXIPL,GLUL,SIDT2,CDKN1B,PDK3,KLF7,FIS1,MEN1,ENY2,ABCA12,PPP3CB,CTSV,PTPRN,NDUFA9,MPC2,ILDR2,STX4,PKLR,GPR68,SIN3A,SREBF1,OXCT1,NADK,BAIAP3,CYBA,RHOA,SOX4,CRH	grey	VSMC_M10
GO:0031848	0.88	0.30	4	10	protection from non-homologous end joining at telomere	BP	1	ERCC1,XRCC1,ERCC4,TERF2	grey	VSMC_M10
GO:0045927	0.88	0.15	98	199	positive regulation of growth	BP	1	ADNP2,NEDD4L,LRP1,GLI1,RIMS2,PRKN,H3F3C,MAPK14,CPNE5,PIM1,EXOSC4,SMO,SRF,SEMA4D,RIMS1,RUFY3,EGFR,TRIM32,SDCBP,GOLGA4,MEGF8,CPNE9,TGFBR2,MKKS,RPTOR,HBEGF,SYT1,PLCB1,SLC23A2,PRKDC,CDKN2AIP,PLS1,MEF2C,IL7,CELF1,PTK2B,TBX5,ZFYVE27,CYFIP1,IGF2,BDNF,SLC6A3,HYAL1,TGFB2,GPAM,ZNF639,HLX,ADNP,DISC1,CIB1,SLC9A1,SFN,RPS6KA1,ACTN3,CDKL5,YBX3,WNT3,CREB1,MAPT,SUPV3L1,DDX3X,FN1,DDX49,MUL1,CD38,MAPK1,STAT5B,CXCL16,BMPR1A,RBPJ,SOX15,NDEL1,RAB11A,TAF9B,NTN1,MAP2K5,S100A8,TBX2,PSMD10,TRPV2,INSR,GATA6,GHR,L1CAM,SLC25A33,CYBA,MIR199A1,MIR222,RHOA,BASP1,DIO3,POU3F2,FXN,CACNG7,N6AMT1,HEY2,DERL2,WNT2	grey	VSMC_M10
GO:0071331	0.88	0.17	54	112	cellular response to hexose stimulus	BP	1	ZNF236,NME1,LRP1,AGER,PLA2G6,SRF,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,GRIK5,RAF1,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,KCNJ11,TIAM1,RAB11FIP5,OPA1,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,SLC9B2,ZBTB20,ADRA2A,KCNB1,POLG,GPER1,RAB11FIP2,MLXIPL,SIDT2,PDK3,KLF7,FIS1,MEN1,ENY2,ABCA12,PPP3CB,PTPRN,MPC2,STX4,GPR68,SIN3A,OXCT1,NADK,BAIAP3,CYBA,SOX4,CRH	grey	VSMC_M10

GO:0016050	0.88	0.15	127	255	vesicle organization	BP	1	VPS4B,STX7,TBPL1,PRKN,SEPT8,WASHC5,TSNARE1,MAPK15,WASHC4,TGFBRAP1,CHMP2A,STX17,VPS41,SDCBP,EPS15,RAB7A,PIP4K2A,RUBCNL,NECTIN2,AQP11,GRIK5,TBC1D4,MYO7A,AKT2,HOOK3,YIPF4,SYT1,DNAJC13,FAM160A2,STX2,SYT9,TMEM127,ANKRD27,OSBP,CHMP2B,CHMP4C,ARFGAP2,SEC31A,DYSF,SYNJ1,AP3B1,CHMP7,F2R,VPS18,SEC31B,DTNBP1,VPS39,KIF13A,GBF1,RAB7B,KLHL12,SEC22B,TMEM9,PEF1,VTI1A,PDCD6,SNAP23,SHROOM2,HPS4,C2CD5,RNF26,RAB22A,AP2M1,STX1A,STX6,VPS37D,VPS8,SCAP,CREB1,MIA3,SPG11,PIKFYVE,ALS2CL,BLOC1S6,SRGN,SEC24C,RAB3A,ABCB6,VAMP1,SNAP29,ANKFY1,PTPRN,STX5,RAB8A,ATP13A2,CPLANE2,DLG4,SYT7,SLC2A4,ANXA8,PI4K2B,ANXA2,CPLX1,STX1B,STX4,SYT11,RAB8B,TMED10,AC138894.1,HOOK2,ZDHHC15,RAB11A,SOX30,STX8,SNAPIN,PPP6C,RILP,BAIAP3,CHMP1A,GNAI3,VAV3,MFSD14A,STXBP1,FNBP1L,AP1G1,VPS4A,PHETA1,BLOC1S3,SNAP47,SNX10,RAB32,DOC2B,TBC1D20,VAMP3,PLEKHJ1,TRAPPC6A,RAB39A	grey	VSMC_M10
GO:0042551	0.88	0.20	17	38	neuron maturation	BP	1	ANKS1A,PICK1,NRCAM,RAC3,RET,LGI4,RND1,OPA1,NR4A2,KCNIP2,FARP2,C1QL1,GLDN,C3,MECP2,SRRM4,CNTN2	grey	VSMC_M10
GO:0060068	0.88	0.30	4	10	vagina development	BP	1	ESR1,BAK1,LHX1,WNT5A	grey	VSMC_M10
GO:0031123	0.88	0.17	45	94	RNA 3'-end processing	BP	1	CPSF6,PABPC1,ZC3H3,TUT7,EXOSC4,HSF1,CPSF1,EXOSC3,RNF20,YTHDC1,PNPT1,LSM10,TUT4,MTPAP,SYMPK,PCF11,TRNT1,CSTF3,CLP1,USB1,RPRD1B,TENT2,INTS8,TENT4B,INTS12,CPSF2,RPRD2,CSTF1,NCBP2,SUPV3L1,CPSF4,LEO1,INTS5,AP002990.1,HSD17B10,CSTF2,INTS2,PAPOLA,RPRD1A,ERI2,PARN,POLR3K,TRMT10C,ZNF473,EXOSC5	grey	VSMC_M10
GO:0031348	0.88	0.16	73	149	negative regulation of defense response	BP	1	TNFAIP3,USP15,ENPP3,PPARA,C6orf106,MAPK14,TEK,FPR2,NT5E,NR1H2,VPS35,CST7,FNDC4,SEC14L1,SIRT2,NMI,NR1D2,NPLOC4,MFHAS1,PCBP2,NR1H4,PLK2,HCK,NR1H3,TRAFD1,OAS3,NLRC5,OTULIN,MAPKBP1,NOD2,CD96,CD200,YTHDF2,GPER1,SLAMF8,PARP14,RNF26,FGR,NLRX1,TRAF3IP1,HTRA1,DUSP10,LPCAT3,CALCRL,MUL1,FOXP3,GPS2,TKFC,USP18,TNFRSF1B,SYT11,DCST1,SMAD3,TSPAN6,LDLR,STAT2,RIOK3,MAPK7,YES1,ISL1,PTGER4,PTPN2,CRK,FOXF1,MIR199A1,MIR21,MIR222,C5orf30,OAS1,A2M,FGL2,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0043087	0.88	0.15	141	285	regulation of GTPase activity	BP	1	ARHGAP9,TBC1D30,TBC1D9B,TIAM2,SYNGAP1,ASAP1,PTK2,PLXNA4,NTRK2,TBC1D22B,SEMA4D,TBC1D8,RGP1,FGD3,ASAP2,ITGB1BP1,MET,ARHGEF5,EPHA1,BVES,TBC1D9,SPRY1,PLXNA1,ARHGAP12,IQSEC1,RSU1,TBC1D4,FOXJ1,SPRY2,WNT11,AKT2,ARRB1,TBC1D16,MKKS,ARHGEF7,PLXNC1,FGD6,LARS,RASA3,SBF2,RASA2,TBC1D12,ARHGEF26,PTK2B,RASGRP1,RAPGEF2,CCL17,TIAM1,RAPGEF3,F2RL1,F2R,IQGAP2,ARHGAP24,CD40,RAP1GDS1,DOCK10,FGD4,RGS1,TBCK,ADPRH,GPR137B,AJUBA,ADAP1,DENND1B,FICD,ARHGAP6,TBC1D10C,RAB11FIP2,SH3BP4,DVL3,CDKL5,GRHL3,EPHB3,RASA4,TRAPPC6B,BCL6,RASAL2,TBC1D2B,GMIP,RASGRP2,TBC1D14,RABGAP1L,RUNDC1,WNT4,ELMOD1,RAP1GAP,TBC1D25,GNB5,EPHA4,ARHGEF19,RASAL3,DVL2,SYDE1,TBC1D1,ARAP2,RGS14,FGD1,TBC1D10B,NDEL1,MYO9A,BCAS3,ARHGAP44,TBC1D8B,CCL14,CCL5,AMOT,CCL7,CCL2,CCL25,ADAP2,VAV1,RALBP1,DOCK7,ABR,CRK,RAP1GAP2,TAX1BP3,MLST8,ARHGEF16,APC2,ARHGAP45,PLXNA3,GPSM1,TSC1,VAV3,MTSS1L,GAPVD1,DENND1A,RABGAP1,DAB2IP,MIR21,CCL16,ASAP3,THY1,WNT5A,CHN1,RGS4,TBC1D20,HRAS,TRAPPC6A,CCL22	grey	VSMC_M10
GO:0001952	0.88	0.17	50	105	regulation of cell-matrix adhesion	BP	1	ONECUT2,LRP1,PTK2,CDKN2A,TEK,CDK6,HOXA7,ITGB1BP1,EPHA1,CLASP2,RIN2,JAG1,ACTG1,FERMT1,PTPRA,FAM107A,PIK3CB,PIK3R1,FMN1,PTPRJ,PTK2B,DMTN,LDB1,SLK,COL16A1,DAG1,ARHGAP6,DISC1,CIB1,SLC9A1,EFEMP2,APOD,BCL6,CASK,WNT4,VCL,BST1,MINK1,SMAD3,BCAS3,CAMSAP3,CCL25,PRKCZ,TSC1,RHOA,ACVRL1,PEAK1,THY1,ACER2,DUSP22	grey	VSMC_M10
GO:0002694	0.88	0.14	178	352	regulation of leukocyte activation	BP	1	CD226,TNFAIP3,ENPP3,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,XRCC6,RAC2,FBXO7,TTBK1,TNFRSF21,NCK2,EXOSC3,MSH2,SLC46A2,PELI1,IL4I1,TLR4,IL15,SPHK2,HMCES,BMI1,CST7,CD300LF,CLPTM1,NECTIN2,GAB2,MLH1,GLI2,UNC13D,MYD88,PIBF1,FOXJ1,PAXIP1,IL15RA,TGFBR2,PAWR,SHLD1,PRNP,NCKAP1L,GAS6,PRKDC,SLC7A1,MFHAS1,TRAF6,SOX12,TOX,ZC3H8,IL1A,CAMK4,CEBPA,FER,CASP3,MEF2C,TMEM131L,IL7,PAG1,RASGRP1,NR1H3,RIPK2,AP3B1,F2RL1,MARCH7,SOX13,NOD2,ZNF335,CD40,IGF2,CD200,LCK,BANK1,ICOSLG,BTN2A2,GPAM,PRKAR1A,GPR137B,HLX,TBC1D10C,GPER1,SLAMF8,THEMIS2,FGR,SNX4,CD28,RUNX3,DLG1,PPP2R3C,ADAM8,DUSP10,BLOC1S6,PLA2G4A,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,TNIP2,CD38,BST1,C12orf4,STAT5B,INHA,SCGB1A1,FOXP3,RASAL3,ZBTB1,SHLD2,CARD11,TNFRSF1B,TBX21,STX4,ITGAM,SYT11,ZBTB7B,CHRNB2,CD19,LAT,IL4R,LDLR,BTK,CD74,CCL5,STXBP2,CCL2,YES1,NKAP,CD320,PRAM1,VAV1,TWSG1,IL7R,SUPT6H,PTPN2,SOCS1,DROSHA,TICAM1,DNAJA3,PDPK1,PRKCZ,FOXF1,VAV3,KARS,STXBP1,GLMN,AP1G1,BCL10,MIR21,MIR27A,RHOA,HAVCR1,LST1,BLOC1S3,SOX4,FADD,DPP4,CD46,MIR125A,THY1,WNT5A,FGL2,IL33,CD70,TNFSF9,TSLP,ZFP36L2,LAX1,EFNB3,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10

GO:0044091	0.88	0.19	20	44	membrane biogenesis	BP	1	PEX3,CHMP2A,SPTBN1,SIRT2,STX2,NSFL1C,CHMP7,PEX16,NLGN4Y,NRXN2,NLGN2,ANXA2,GAK,STX4,SYT11,NLGN3,CEL,VPS4A,TLCD1,PEX11A	grey	VSMC_M10
GO:1902065	0.88	0.30	4	10	response to L-glutamate	BP	1	TMBIM6,OPA1,CREB1,AMIGO1	grey	VSMC_M10
GO:0060272	0.88	0.30	4	10	embryonic skeletal joint morphogenesis	BP	1	OSR2,OSR1,HYAL1,NOG	grey	VSMC_M10
GO:0034374	0.88	0.30	4	10	low-density lipoprotein particle remodeling	BP	1	APOB,AGT,LIPC,MPO	grey	VSMC_M10
GO:0048844	0.88	0.18	26	57	artery morphogenesis	BP	1	LRP1,FOXH1,SRF,TFAP2B,HOXA13,APOB,WNT11,JAG1,HAND2,HPGD,EYA1,PKD2,TGFB2,EFEMP2,BMPR1A,RBPJ,LDLR,TBX2,STRA6,FOXF1,ENG,SOX4,ACVRL1,NOG,SIX1,HEY2	grey	VSMC_M10
GO:0002089	0.88	0.24	8	19	lens morphogenesis in camera-type eye	BP	1	ATF4,TDRD7,NECTIN3,SHROOM2,LCTL,SKI,TBC1D20,PITX3	grey	VSMC_M10
GO:1904063	0.88	0.18	29	62	negative regulation of cation transmembrane transport	BP	1	NEDD4L,PRKCE,HECW1,KEL,OSR1,KCNRG,OXSR1,SLC43A1,KCNE2,PKD2,CASQ2,HECW2,ADRA2A,ISCU,ATP1A2,C4orf3,NTSR1,SESTD1,GNB5,CALM1,FMR1,RRAD,MIR24-1,GPR35,KCNH2,CRBN,RGS4,GEM,PPIF	grey	VSMC_M10
GO:0099623	0.88	0.25	7	17	regulation of cardiac muscle cell membrane repolarization	BP	1	SCN5A,KCNE2,ANK2,SCN4B,NOS1AP,RNF207,KCNH2	grey	VSMC_M10
GO:1903169	0.88	0.16	53	110	regulation of calcium ion transmembrane transport	BP	1	STAC3,PLA2G6,TSPAN13,PRKCE,ATG5,CACNB2,STAC,CACNB4,PRNP,DIAPH1,PTK2B,F2R,KCNE2,PKD2,CASQ2,RYR2,ADRA2A,UBASH3B,ANK2,GPER1,ATP1A2,SLC9A1,C4orf3,CASQ1,NTSR1,NOS1AP,CEMIP,SESTD1,PTPN6,HTT,ATP1B1,GNB5,HAP1,PSEN2,STAC2,CACNB1,ATP2A1,CD19,CALM1,VMP1,BDKRB1,FMR1,PDPK1,P2RX1,CYBA,JPH3,RRAD,MIR21,DMD,GPR35,JPH2,THY1,GEM	grey	VSMC_M10
GO:0032025	0.88	0.29	4	10	response to cobalt ion	BP	1	CASP3,D2HGDH,CASP8,TIGAR	grey	VSMC_M10
GO:0010596	0.88	0.19	22	48	negative regulation of endothelial cell migration	BP	1	MEOX2,SVBP,ITGB1BP1,DCN,MEF2C,STC1,SP100,PATZ1,PDCD10,SYNJ2BP,VASH1,MAP2K5,MECP2,DAB2IP,MIR199A1,MIR21,MIR22,MIR24-1,RHOA,ACVRL1,GADD45A,RGCC	grey	VSMC_M10
GO:0043931	0.88	0.24	8	19	ossification involved in bone maturation	BP	1	SEMA4D,RYR1,ACTN3,THBS3,RFLNB,RHOA,SNX10,CCDC154	grey	VSMC_M10
GO:0051208	0.88	0.17	41	87	sequestering of calcium ion	BP	1	PRKCE,IBTK,ATG5,ATP7B,RYR1,DIAPH1,RASA3,RYR3,PTK2B,TPCN1,SLC8B1,F2R,PKD2,CASQ2,RYR2,LCK,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,PSEN1,CD19,CALM1,BDKRB1,SLC25A23,TRPV1,PDPK1,CYBA,JPH3,MCOLN3,DMD,NOL3,JPH2,THY1,DDIT3	grey	VSMC_M10
GO:0016445	0.88	0.18	25	54	somatic diversification of immunoglobulins	BP	1	EXOSC3,MSH2,CYREN,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,PRKDC,XRCC4,NBN,POLL,CD40,CD28,RNF168,BCL6,PMS2,FOXP3,SHLD2,TBX21,BATF,YY1,SUPT6H,RNF8,NHEJ1	grey	VSMC_M10
GO:0045944	0.88	0.13	463	904	positive regulation of transcription by RNA polymerase II	BP	1	NFATC1,ZNF407,ONECUT2,TCF4,GLI1,PLAGL1,MAML1,ESR1,OSR2,SNW1,ZBED4,PRKN,PPARA,MED30,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,ATF4,MAPK14,SOX10,NRF1,TMPRSS6,SMO,HSF1,TFEB,IRF5,FOXH1,IFT74,RORB,ZNF300,PRDM4,DMTF1,SRF,SMARCA2,RFX3,NCK2,TFAP2B,DLX5,ETV1,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,IL11,EPAS1,EPCAM,ZNF462,PHIP,HMGN3,NFYC,HOXA2,HOXA7,HOXA13,REL,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TLR4,CCNC,BCL2L12,LPIN1,TEAD2,MYCN,OSR1,FOXO3,MAMSTR,ATAD2B,ZNF438,HDAC2,PHF10,MAML2,MLLT10,PRKD2,CNBP,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,UTF1,SUMO2,GLI2,RSF1,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,SS18L2,KLF6,ARRB1,OVOL2,ZNF219,ACVR2A,EOMES,IKBKB,CHD8,JAG1,SIRT2,TMEM173,RARB,NR1D2,SIRT7,MAFG,DPF1,ALX1,TAF7,LUM,DCN,MAVS,TFDP1,DDRGK1,MITF,PRKDC,IRF7,ERCC6,CALCOCO1,ST18,TRAF6,NR1H4,TCF15,SOX12,PLAG1,USF2,LMO2,ASXL1,IL1A,PAX8,NR4A1,ACVR1B,ZNF143,CEBPA,NCOA6,PIK3R1,TFDP2,CDK7,IRF2,TAF9,NCOA2,MED19,CCDC62,TFCP2,HAND2,CSRNP2,EYA1,MLXIP,ARNTL,HLTF,HNF4G,ZNF395,MEF2C,TLX2,ZNF319,P2RY1,USP16,SSBP2,KMT2D,BACH1,NR1H3,RPRD1B,EAPP,EBF2,NLRC5,RIPK2,PFKM,SENP1,VDR,NKX3-1,LPIN3,NKX6-1,TBX5,AP3B1,NR4A2,F2RL1,RIPK1,RREB1,PKD2,TFAP2A,PAX2,SALL1,HIVEP1,NOD2,ZNF335,CD40,LDB1,IGF2,BMPR1B,ELK4,NFKB2,PRDM15,MED10,RNF10,PKNOX1,HDAC1,ELF3,PPP3CA,CAPRIN2,TERT,SLC38A3,TGFB2,SATB2,TCF7L2,ARNTL2,NR5A2,AUTS2,ZNF639,	grey	VSMC_M10
GO:0019692	0.88	0.20	17	37	deoxyribose phosphate metabolic process	BP	1	TBPL1,DPYS,GDA,NUDT15,MBD4,NUDT16,DGUOK,NUDT18,DTYMK,UPB1,ADK,NEIL1,NT5M,NTHL1,CMPK2,DCTD,UPP1	grey	VSMC_M10
GO:1903115	0.88	0.21	14	32	regulation of actin filament-based movement	BP	1	TRPM4,SCN5A,STC1,TNNC1,DSP,RYR2,PKP2,KCNJ2,ANK2,ATP1A2,DLG1,ATP2A1,DSG2,HCN4	grey	VSMC_M10
GO:0006336	0.88	0.22	11	25	DNA replication-independent nucleosome assembly	BP	1	ASF1A,UBN2,RBBP4,HIRA,HIST1H4B,HIST2H4A,HIST1H4H,ITGB3BP,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0071364	0.88	0.20	17	38	cellular response to epidermal growth factor stimulus	BP	1	MARS,EGFR,SOX9,BAG4,PAX2,CBL,SYAP1,PDE8A,SNX6,STAT5B,MED1,GAREM1,INPP5K,PDPK1,DAB2IP,DUSP22,ZFP36L2	grey	VSMC_M10
GO:0090594	0.88	0.29	4	10	inflammatory response to wounding	BP	1	TLR4,IL1A,F2R,MIR21	grey	VSMC_M10
GO:1902686	0.88	0.21	14	31	mitochondrial outer membrane permeabilization involved in programmed cell death	BP	1	TMEM14A,HIP1R,STPG1,FZD9,NMT1,MUL1,TMEM102,ACAA2,MIR29A,BNIP3L,BCL2L11,SLC35F6,PPIF,AC140504.1	grey	VSMC_M10
GO:2000279	0.88	0.20	14	32	negative regulation of DNA biosynthetic process	BP	1	POT1,DACH1,TENT4B,STN1,KCNK2,MEN1,GNL3L,CTC1,PIF1,TERF2,ACVRL1,TINF2,TEN1,DUSP1	grey	VSMC_M10
GO:1901163	0.88	0.29	4	10	regulation of trophoblast cell migration	BP	1	AGO2,ACVR1B,ACVR1C,SYDE1	grey	VSMC_M10
GO:0035967	0.88	0.16	50	103	cellular response to topologically incorrect protein	BP	1	HSPA1B,PRKN,PACRG,RNF5,DERL1,BAK1,ATF4,HSF1,NCK2,ERMP1,HERPUD2,FGF21,OPTN,UGGT2,DNAJC18,TMTC4,EIF2AK2,DDRGK1,PIK3R1,TMBIM6,AUP1,AMFR,RHBDD1,CCND1,FICD,YOD1,HSPA8,QRICH1,BAG3,RNF185,TBL2,RHBDD2,NFE2L2,DERL3,DNAJB12,SDF2L1,BHLHA15,CREB3L4,PTPN2,CREB3L3,ABCA7,RNF126,HSPA5,DAB2IP,MIR199A1,DDIT3,BCL2L11,HSPB8,PPP1R15A,DERL2	grey	VSMC_M10
GO:0046637	0.88	0.19	20	44	regulation of alpha-beta T cell differentiation	BP	1	HLA-DRA,TGFBR2,NCKAP1L,RIPK2,AP3B1,HLX,RUNX3,BCL6,RC3H1,TNFSF18,FOXP3,TBX21,ZBTB7B,IL4R,NKAP,SOCS1,PRKCZ,MIR21,RHOA,RC3H2	grey	VSMC_M10

GO:1901020	0.88	0.22	11	25	negative regulation of calcium ion transmembrane transporter activity	BP	1	PKD2,CASQ2,ADRA2A,ATP1A2,C4orf3,GNB5,CALM1,FMR1,RRAD,GPR35,GEM	grey	VSMC_M10
GO:0031110	0.88	0.17	37	79	regulation of microtubule polymerization or depolymerization	BP	1	HSPA1B,SLAIN2,MET,CDK5RAP2,MAPRE1,EML2,SLC39A12,CLASP2,MAPRE3,TRIM54,SLAIN1,NAV3,ARHGEF7,SPEF1,ATXN7,CLIP1,KATNB1,STMND1,TRPV4,TTBK2,CIB1,INPP5J,CDKN1B,MAPT,TOGARAM1,NIN,CAMSAP3,CDK5R1,TAOK1,MECP2,APC2,CAMSAP1,PSRC1,APC,MAP1A,DRG1,MAP6D1	grey	VSMC_M10
GO:0019985	0.88	0.24	7	17	translesion synthesis	BP	1	POLI,REV1,REV3L,PRIMPOL,SPRTN,POLN,ZBTB1	grey	VSMC_M10
GO:0097009	0.88	0.20	14	32	energy homeostasis	BP	1	BMP8A,TSKU,ALK,NR1D2,PM20D1,TRPV4,PASK,MLXIPL,CRTC1,STAT3,SGIP1,LEPR,UBB,MRAP2	grey	VSMC_M10
GO:0061326	0.88	0.17	36	77	renal tubule development	BP	1	MTSS1,MYC,KLHL3,PTCH1,SMO,TFAP2B,SIX2,POU3F3,OSR1,SOX9,AQP11,GZF1,WNT11,JAG1,PAX8,EYA1,FMN1,MEF2C,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,NOG,SIX1,LIF,FGF1	grey	VSMC_M10
GO:0060767	0.88	0.29	4	10	epithelial cell proliferation involved in prostate gland development	BP	1	SOX9,NKX3-1,CDKN1B,WDR77	grey	VSMC_M10
GO:0008299	0.88	0.22	10	23	isoprenoid biosynthetic process	BP	1	SRD5A3,COQ2,PRMT3,ALDH1A3,GGPS1,DHRS9,ALDH1A2,DHDDS,PDSS2,ISPD	grey	VSMC_M10
GO:1901741	0.88	0.29	4	10	positive regulation of myoblast fusion	BP	1	MAPK14,EHD1,GDF15,IL4R	grey	VSMC_M10
GO:0046931	0.88	0.23	8	19	pore complex assembly	BP	1	TSPAN33,RTN4,NUP98,P2RX7,PLEKHA7,ANO6,AHCTF1,PDZD11	grey	VSMC_M10
GO:1903902	0.88	0.23	9	21	positive regulation of viral life cycle	BP	1	CHMP2A,KPNA2,CHMP2B,PC,DDB1,CD74,FMR1,VPS4A,ZNF502	grey	VSMC_M10
GO:0045740	0.88	0.20	16	36	positive regulation of DNA replication	BP	1	GLI1,EGFR,SSBP1,FAF1,GLI2,NPM2,STN1,EGF,DBF4B,KAT7,KCTD13,CTC1,TNFAIP1,JUN,HRAS,EREG	grey	VSMC_M10
GO:0046916	0.88	0.17	41	86	cellular transition metal ion homeostasis	BP	1	SLC39A5,MYC,TMPRSS6,SLC39A4,STEAP2,SLC1A1,SLC31A2,HEPHL1,ATP7B,SLC39A12,PRNP,HPX,NCOA4,SLC39A13,AP3B1,SLC40A1,LCK,SLC30A10,ISCU,HJV,SLC30A4,SLC11A1,ABCB6,ATP13A2,FTH1,CYB561A3,NOX5,S100A8,SLC39A6,TMEM199,SLC46A1,NUBP1,ATP6AP1,SLC30A7,FRRS1,LCN2,MT1X,SLC22A17,FXN,FTL,SCO1	grey	VSMC_M10
GO:2000191	0.88	0.22	10	23	regulation of fatty acid transport	BP	1	PPARA,PLA2G6,AKT2,PLA2R1,MAP2K6,ACSL5,NTSR1,PLA2G4A,FIS1,PTGES	grey	VSMC_M10
GO:1902110	0.88	0.21	13	29	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	TMEM14A,HIP1R,STPG1,FZD9,NMT1,MUL1,TMEM102,ACAA2,MIR29A,BNIP3L,BCL2L11,SLC35F6,AC140504.1	grey	VSMC_M10
GO:1903055	0.88	0.22	10	23	positive regulation of extracellular matrix organization	BP	1	SOX9,CLASP2,DAG1,AGT,PHLDB1,MELTF,EFEMP2,SMAD3,CARMIL2,RGCC	grey	VSMC_M10
GO:0010882	0.88	0.22	10	23	regulation of cardiac muscle contraction by calcium ion signaling	BP	1	TNNI3,CASQ2,RYR2,ANK2,ATP1A2,SLC9A1,HDAC4,ATP1B1,CALM1,DMD	grey	VSMC_M10
GO:1902117	0.88	0.18	28	61	positive regulation of organelle assembly	BP	1	VPS4B,PAN2,PIP4K2C,CNOT2,CNOT6,IL5,ASAP1,MAPK15,FUZ,SDCBP,PIP4K2A,LCP1,RALB,ULK1,PAN3,CNOT1,CNOT6L,ZMYND10,HTT,STX18,HAP1,MNS1,G3BP1,WRAP73,KIAA1324,GPSM2,SH3GLB1,RHOA	grey	VSMC_M10
GO:0007020	0.88	0.20	14	32	microtubule nucleation	BP	1	HSPA1B,TUBGCP6,SLAIN2,EML2,CLASP2,SLAIN1,ARHGEF7,TUBGCP5,TUBGCP4,NIN,TUBG1,NDEL1,CEP192,MECP2	grey	VSMC_M10
GO:1902914	0.88	0.22	10	23	regulation of protein polyubiquitination	BP	1	PRKN,NMI,TRIM44,SPSB4,MARCH7,NOD2,DDX3X,GPS2,OTUB2,UBE2D1	grey	VSMC_M10
GO:0010713	0.88	0.29	4	10	negative regulation of collagen metabolic process	BP	1	CYGB,CYP7A1,CIITA,MIR29A	grey	VSMC_M10
GO:0007131	0.88	0.19	20	44	reciprocal meiotic recombination	BP	1	UBE2B,DMC1,KLHDC3,MLH1,CCNB1IP1,RAD54B,SYCP1,HSF2BP,SPO11,C11orf80,RAD51B,EME1,RAD51C,RAD51D,ERCC4,SLX4,MEIOB,MSH4,RNF212B,CENPX	grey	VSMC_M10
GO:0140527	0.88	0.19	20	44	reciprocal homologous recombination	BP	1	UBE2B,DMC1,KLHDC3,MLH1,CCNB1IP1,RAD54B,SYCP1,HSF2BP,SPO11,C11orf80,RAD51B,EME1,RAD51C,RAD51D,ERCC4,SLX4,MEIOB,MSH4,RNF212B,CENPX	grey	VSMC_M10
GO:0060993	0.88	0.17	36	77	kidney morphogenesis	BP	1	MYC,KLHL3,PTCH1,SMO,SIX2,OSR1,SOX9,FOXJ1,GZF1,WNT11,ASXL1,PAX8,EYA1,FMN1,FRAS1,PKD2,PAX2,SALL1,IRX2,PRKX,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,SOX4,NOG,BASP1,SIX1,LIF,FGF1	grey	VSMC_M10
GO:0043588	0.88	0.15	83	171	skin development	BP	1	CYP27B1,FZD6,SMO,ZDHHC21,IFT74,SRF,TFAP2B,SOSTDC1,CD109,HOXA7,GRHL1,MET,EGFR,FUZ,INTU,TRAF3IP2,HDAC2,SOX9,ERCC2,PTCH2,GLI2,EVPL,WDR48,SCEL,ELOVL1,OVOL2,JAG1,RYR1,FERMT1,TCF15,LSR,ASAH1,ACVR1B,FLNB,CASP3,TRPC4AP,FZD3,FRAS1,VDR,AP3B1,SRSF6,DSP,STK4,PPHLN1,ITGB6,LDB1,SUFU,HDAC1,SLC2A10,TGFB2,SNAI1,TGM1,KDF1,SFN,LAMA5,CLIC4,GRHL3,OVOL1,H2AFY2,ABCA12,SAV1,COL3A1,COL5A2,GORAB,ABCB6,RBPJ,MED1,PSEN1,NGFR,ALOXE3,ITGA3,MAP2K1,BCL11B,GATA6,PKD1,COL5A1,MIR125B1,CLDN1,WNT5A,DNASE1L2,ZBED2,EREG,SGPP1	grey	VSMC_M10
GO:0140059	0.88	0.29	4	10	dendrite arborization	BP	1	SULT4A1,PTN,SEMA3A,TAOK2	grey	VSMC_M10
GO:0002673	0.88	0.22	10	23	regulation of acute inflammatory response	BP	1	OSM,ADAM8,F12,BTK,C3,OSMR,CREB3L3,DNASE1,PARK7,PTGES	grey	VSMC_M10
GO:0097178	0.88	0.19	17	38	ruffle assembly	BP	1	EPS8L1,BAG4,ARHGEF26,ARHGAP24,CYFIP1,EPS8,NDEL1,EVL,INPP5K,EPS8L3,DEF8,MTSS1L,CARMIL2,EPS8L2,SNX10,CSPG4,HRAS	grey	VSMC_M10
GO:0038179	0.88	0.20	15	34	neurotrophin signaling pathway	BP	1	NTRK2,NTF4,WASF1,SPRY1,RAF1,SPRY2,CASP3,RAPGEF2,ZFYVE27,CYFIP1,BDNF,DOK5,AGT,PPP2R5B,HAP1	grey	VSMC_M10
GO:1990928	0.88	0.19	19	42	response to amino acid starvation	BP	1	MAP3K5,ATF4,TFEB,RRAGD,KPTN,SESN3,SZT2,EIF2AK2,LARS,EIF2AK4,SLC38A2,MAPK1,RRAGB,MAPK3,LARP1,WDR59,SH3GLB1,IMPACT,RNF152	grey	VSMC_M10
GO:0043462	0.88	0.19	17	37	regulation of ATPase activity	BP	1	TNNI3,NAPA,CHTOP,PXK,TNNC1,OXA1L,TOR1AIP1,VCPKMT,DNAJC10,DNAJB2,ATP1B1,DNAJB1,ATP1B2,PAM16,TSC1,VMA21,PPIF	grey	VSMC_M10

GO:0010959	0.88	0.14	131	263	regulation of metal ion transport	BP	1	NEDD4L,STAC3,TSPO,BAK1,MCHR1,PLA2G6,WNK2,TSPAN13,PRKCE,SLC31A2,HECW1,KEL,ATG5,OSR1,SPHK2,TRPC3,KCNRG,CACNB2,STAC,OXSR1,SCN5A,GPD1L,CACNB4,EFHB,PRNP,DIAPH1,P2RX2,KCNIP3,SLMAP,GLRX,P2RX3,ORAI1,TMBIM6,P2RX7,PTK2B,SLC8B1,HOMER1,STC1,F2R,TESC,ANO6,KCNE2,PKD2,CASQ2,CNTN1,KCNIP2,RYR2,PKP2,SIK1,HECW2,KCNJ2,ADRA2A,SLC30A10,ISCU,EGF,KCNG1,EPB41,OPRD1,UBASH3B,ANK2,GPER1,KLHL24,AGT,ATP1A2,SLC9A1,PLPP4,C4orf3,CASQ1,NTSR1,SCN4B,NOS1AP,HOMER2,DLG1,IL16,CEMIP,SESTD1,CASK,PTPN6,HTT,CAMK2G,ATP1B1,KCNA1,GNB5,HAP1,PSEN2,WNK3,STAC2,CACNB1,ATP1B2,KCNAB3,KCNIP1,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,TRPV2,CAMK2A,CCL5,CCL2,FMR1,INPP5K,TRPV3,PDPK1,P2RX1,RNF207,AMIGO1,CYBA,JPH3,ATP2C2,LCN2,WWP2,RRAD,MIR21,MIR24-1,RHOA,DMD,GPR35,JPH2,KCNH2,FGF11,THY1,SCN2B,NETO2,CRBN,RGS4,CRH,YWHAH,GEM,NKX2-5	grey	VSMC_M10
GO:0051099	0.88	0.15	69	141	positive regulation of binding	BP	1	NME1,LRP1,STK3,EIF3E,PRKN,DERL1,MFNG,HSF1,ZNF618,MED25,MET,ADD2,MAPRE1,ERCC2,MAPRE3,RALB,POU4F1,SIRT2,TMEM173,PLCL2,DPH3,DDRGK1,PPP2CB,TRAF6,TRIB3,PLK2,IDE,HIP1R,HAND2,HMBOX1,RAPGEF2,TIAM1,EBF2,RIPK2,AMFR,STK4,BDNF,SPPL3,CAPRIN2,TERT,TCF7L2,EGF,EPB41,PARP9,DTX3L,RPL11,MEN1,RAMP2,DDX11,EPHA4,PARP1,NVL,ANXA2,PSEN1,TAF1,EIF3C,CALM1,LARP6,MARK3,ISL1,TICAM1,FMR1,SKI,PKD1,PARK7,GPSM1,LAMTOR5,WNT5A,TXN	grey	VSMC_M10
GO:0019835	0.88	0.29	4	10	cytolysis	BP	1	NINJ1,LYZL6,C7,MMD	grey	VSMC_M10
GO:0051668	0.88	0.13	273	537	localization within membrane	BP	1	LRP1,STX7,STAC3,MAP7,PEX3,ZDHHC14,EMC2,PRKN,AGER,GOPC,VPS52,HSPA4,SYNGAP1,PTCH1,EXOC4,SIL1,TOMM22,PICK1,MICALL1,ZDHHC21,TSPAN33,LRRC4,ADAM22,STEAP2,VPS50,SLC1A1,TRAM2,SEC61B,PRKCE,ASB3,SPTBN1,EMC10,PTN,ITGB1BP1,SEC61G,EGFR,TCAF2,BVES,VPS35,SDCBP,SLC7A11,LIN7B,EPS15,AGK,BRAF,ANKRD50,RAB7A,RAB10,ARL5B,CACNB2,CLASP2,DLG2,STAC,OPTN,GOLGA4,AQP11,CCDC93,GRIK5,EMC3,SEC62,MYL12A,AKT2,IKBKB,ANK1,ARL5A,LIN7A,PRNP,BAG4,GAS6,PKP3,ARL6IP5,SRP14,TUB,KCNIP3,LYPLA1,MAL,TM9SF4,ZDHHC20,RILPL1,RILPL2,ANKRD27,PIK3R1,TMEM150A,VAMP5,SLMAP,PLS1,EMC4,FCHO2,SORBS1,NUP54,P2RY1,RAPGEF2,KCNJ11,TIAM1,SSR3,EXOC6B,AP3B1,ZFYVE27,GOLGA7B,TESC,PEX16,DMTN,VPS26C,VPS39,KIF13A,NHLRC1,NECTIN3,SRPRA,PKP2,PPFIA1,ZDHHC23,ZDHHC6,OXA1L,DAG1,SSH1,GET4,DENND1B,KCNB1,NCF1,SORL1,ANK2,C2CD5,GPER1,RAB11FIP2,FAM126B,CIB1,RAB17,AP2M1,ZDHHC18,PPP2R5A,PEX19,ZDHHC24,BBS1,GORASP2,STX1A,SNX4,LAMA5,SNX27,CNIH2,STX6,VPS37D,PACS1,FZD9,DLG1,LRRC15,NSF,PIKFYVE,FIS1,VPS26A,CEMIP,NMT1,LZTFL1,RTP4,EHD1,ZDHHC8,ITGA4,ABCA12,NRXN2,SAV1,CNPY4,AP4M1,BCS1L,RAB3A,RAMP2,ZFAND2B,EXOC5,ATP1B1,PPIL2,ARL6IP1,NSG1,GRIPAP1,ZDHHC4,RAB8A,CNST,DLG4,ACTB,WDR19,RAB15,IQSEC2,RSC1A1,PEX26,NLGN2,GPHN,MPP5,WNK3,STAC2,ARL5C,SYNJ2BP,TSPAN17,ANXA2,GAK,CPLX1,STX1B,STX4,NAXE,TMEM88,ITGAM,SSR2,SNX12,DOCK2,RAB8B,ITGA3,TAOK2,AC138894.1,ZDHHC15,RAB11A,STX8,RAB3D,CALM1,TTC7B,TIMM29,DNM2,GGA2,CYP46A1,ARHGAP44,VPS35L,NPC1,AP2B1,MIEF2,CDK5	grey	VSMC_M10
GO:0000768	0.88	0.20	15	34	syncytium formation by plasma membrane fusion	BP	1	MAPK14,MYH9,CD109,DYRK1B,MYOF,JAM2,RAPGEF3,ADAMTS15,SH3PXD2A,TCTA,VASH2,EHD1,GDF15,IL4R,CACNA1H	grey	VSMC_M10
GO:0140253	0.88	0.20	15	34	cell-cell fusion	BP	1	MAPK14,MYH9,CD109,DYRK1B,MYOF,JAM2,RAPGEF3,ADAMTS15,SH3PXD2A,TCTA,VASH2,EHD1,GDF15,IL4R,CACNA1H	grey	VSMC_M10
GO:0036037	0.88	0.24	7	17	CD8-positive, alpha-beta T cell activation	BP	1	EOMES,NCKAP1L,TOX,RUNX3,VSIR,ZBTB7B,SOCS1	grey	VSMC_M10
GO:0050732	0.88	0.18	21	46	negative regulation of peptidyl-tyrosine phosphorylation	BP	1	SEMA4D,PPP2R1A,IBTK,PIBF1,DMTN,LRRK1,PARP14,CBL,SNX6,PTPN6,ZFYVE28,SOCS4,PSEN1,SUZ12,PTPN2,SOCS1,PRKCZ,MIR125A,THY1,DUSP22,CADM4	grey	VSMC_M10
GO:0038066	0.89	0.18	20	44	p38MAPK cascade	BP	1	PHLPP1,MAP3K5,MAP3K4,AGER,MAPK14,GADD45G,EMC10,RELL2,MFHAS1,HAND2,NCF1,MAPKAPK2,MAP3K3,DLG1,DUSP10,MINK1,RELL1,DAB2IP,GADD45A,DUSP1	grey	VSMC_M10
GO:0035743	0.89	0.28	4	10	CD4-positive, alpha-beta T cell cytokine production	BP	1	RSAD2,DENND1B,TBX21,PRKCZ	grey	VSMC_M10
GO:0051608	0.89	0.28	4	10	histamine transport	BP	1	SNAP23,SNX4,SLC29A4,BTK	grey	VSMC_M10
GO:0002182	0.89	0.28	4	10	cytoplasmic translational elongation	BP	1	DPH2,DPH3,DPH1,AARS	grey	VSMC_M10
GO:0034763	0.89	0.16	42	88	negative regulation of transmembrane transport	BP	1	NEDD4L,GOPC,PRKCE,GRB10,HECW1,TCAF2,KEL,OSR1,SLC26A5,KCNRG,OXSR1,AKT2,ARL6IP5,SLC43A1,KCNE2,PKD2,CASQ2,HECW2,ADRA2A,ISCU,ATP1A2,C4orf3,PEA15,NTSR1,CTTNBP2NL,SESTD1,GNB5,RSC1A1,CALM1,PRKCB,FMR1,INPP5K,OAZ1,RRAD,MIR24-1,GPR35,FABP5,KCNH2,CRBN,RGS4,GEM,PPIF	grey	VSMC_M10
GO:0110149	0.89	0.17	35	75	regulation of biomineralization	BP	1	CYP27B1,OSR2,OMD,PTN,TRPM4,OSR1,SOX9,SLC4A2,ACVR2B,ACVR2A,KL,GAS6,ADGRV1,MEF2C,P2RX7,PTK2B,BMP2K,ANO6,TFAP2A,BMPR1B,SGMS2,AMELX,ACTN3,TXLNG,FZD9,SRGN,BCOR,ANKH,WNT4,BMPR1A,SMAD3,RFLNB,BGLAP,CEBPB,HEY2	grey	VSMC_M10
GO:0072683	0.89	0.28	4	10	T cell extravasation	BP	1	CD99,CCL2,CRK,FADD	grey	VSMC_M10
GO:0009155	0.89	0.28	4	10	purine deoxyribonucleotide catabolic process	BP	1	GDA,NUDT15,NUDT16,NUDT18	grey	VSMC_M10
GO:0016048	0.89	0.24	7	17	detection of temperature stimulus	BP	1	GRIK2,ASIC3,EPHB1,TRPM8,NTSR1,NGFR,TRPV1	grey	VSMC_M10
GO:0060049	0.89	0.28	4	10	regulation of protein glycosylation	BP	1	FKTN,IL15,POMT2,ACER2	grey	VSMC_M10
GO:0031648	0.89	0.19	19	42	protein destabilization	BP	1	SERF2,PRKN,RNF5,DERL1,ISOC2,PRNP,PRKDC,FBXW7,PEX2,MYLIP,SIAH1,SENP2,CTSH,HTT,MUL1,KDM8,CCDC88C,CREBBP,IRGM	grey	VSMC_M10
GO:0001783	0.89	0.23	8	19	B cell apoptotic process	BP	1	BAK1,TNFRSF21,TRAF3IP2,FOXP1,BCL6,BTK,CD74,BCL10	grey	VSMC_M10

GO:0070227	0.89	0.18	24	52	lymphocyte apoptotic process	BP	1	BAK1,TNFRSF21,SLC46A2,TRAF3IP2,IDO1,FOXP1,ZC3H8,LMBR1L,RIPK1,GPAM,PDCD1,ADAM8,BCL6,EFNA1,BTK,CD74,CCL5,IL7R,DNAJA3,BCL10,FADD,WNT5A,TSC22D3,BCL2L11	grey	VSMC_M10
GO:0071357	0.89	0.18	19	42	cellular response to type I interferon	BP	1	MYD88,MAVS,IRF7,OAS3,NLRC5,SP100,YTHDF2,PTPN6,MUL1,USP18,DCST1,STAT2,TYK2,JAK1,PTPN2,MIR21,OAS1,FADD,WNT5A	grey	VSMC_M10
GO:0060612	0.89	0.20	14	32	adipose tissue development	BP	1	TRPM4,PGRMC2,PAXIP1,DYRK1B,SPART,EBF2,FTO,SORL1,KLF7,PLA2G16,OXCT1,SOX8,SLC25A25,UBB	grey	VSMC_M10
GO:0042330	0.89	0.13	215	427	taxis	BP	1	LRP1,SEMA6A,KIF5A,SLC12A2,AGER,GPSM3,CXCL14,GFRA3,PTK2,PTCH1,PLXNA4,MAPK14,PLA2G6,RAC2,SMO,CCL27,KIT,PLGRKT,SEMA4D,DLX5,NINJ1,ETV1,SEMA4C,FPR2,HOXA2,LPAR1,CXCL8,AKIRIN1,EPHA7,PTN,MET,EPHA1,GAB1,NRCAM,TRPM4,PLXNA1,C5AR2,C5AR1,PRKD2,GLI2,MEGF8,OXSR1,MYCBP2,ACKR2,CMTM7,CMTM8,KIF5C,HBEGF,FEZ2,SEMA3D,PLXNC1,SEMA3A,CHL1,UNC5D,NRG1,NCKAP1L,GAS6,FAM19A4,FLT1,RYK,EPHB1,MTUS1,RET,CYP7B1,NR4A1,FER,PIK3CB,PARVA,ROBO1,ROBO2,PTPRJ,FZD3,SEMA4F,VEGFC,PTK2B,DPYSL2,CCL17,TIAM1,SLIT1,SLC8B1,TRIO,F2RL1,ANO6,SEMA3G,CYFIP1,ALCAM,SEMA4G,NOD2,SIAH1,BMPR1B,GBF1,BDNF,ELMO2,LGR6,DNM1L,TRPV4,SBDS,SEMA3F,TGFB2,GAP43,DAG1,PRSS56,LHX9,CMKLR1,SLAMF8,MOSPD2,GBX2,KALRN,LAMA5,YTHDF1,PTPRO,MACO1,FCER1G,EPHB3,ADAM8,WNT3,KLF7,CREB1,MYPN,PIKFYVE,IL16,SEMA6D,EPHB4,IL12A,TNR,MCU,TNFSF18,CXCR2,BST1,MAPK1,CH25H,CRMP1,PADI2,CXCL16,EPHA4,LRTM2,TMEM102,UNC5A,STX4,SEMA4A,HOXB9,FGF18,NGFR,DOCK2,PGF,DAPK2,EFNA1,MAPK3,IL6R,ALKBH1,MAP2K1,SMAD3,NTN1,RPS6KA5,S100A14,S100A8,RNF165,BCL11B,LHX1,CD74,CCL14,CCL5,LAMA3,AMOT,CSF1R,CCL7,CCL2,CCL25,CDK5R1,ISL1,EMB,VAV1,LAMA1,RALBP1,PTPN2,CRK,PIP5K1C,L1CAM,NTN3,ARHGEF16,PLXNA3,MPP1,BSG,TUBB3,VAV3,CMTM3,RHOA,CCL16,DPYSL5,S100A12,EFNA4,CNTN2,VASP,FOXG1,CHGA,DEFB124,CCR10,DPP4,CXCL6,ZNF580,ISL2,NOG,WNT5A,CHN1,DUSP1,ARTN,NRXN3,LYPLA2,RALA,HRAS,EFNB3,ISPD,FGF1,CCL22,PDGFD	grey	VSMC_M10
GO:0051095	0.89	0.28	4	10	regulation of helicase activity	BP	1	POT1,MSH2,SSBP1,CHTOP	grey	VSMC_M10
GO:0055090	0.89	0.22	9	21	acylglycerol homeostasis	BP	1	SLC25A27,ABCG5,ABCG8,GCKR,NR1H4,NR1H3,FITM2,MLXIPL,LIPC	grey	VSMC_M10
GO:0070328	0.89	0.22	9	21	triglyceride homeostasis	BP	1	SLC25A27,ABCG5,ABCG8,GCKR,NR1H4,NR1H3,FITM2,MLXIPL,LIPC	grey	VSMC_M10
GO:0060575	0.89	0.23	7	17	intestinal epithelial cell differentiation	BP	1	KLF5,CBFA2T2,PYY,SAV1,NKX3-2,GATA6,TIGAR	grey	VSMC_M10
GO:0006869	0.89	0.14	136	273	lipid transport	BP	1	ATP9B,VPS4B,APOF,ATP8B1,STARD6,LRP1,CPT1B,APOM,SERAC1,SLC27A6,PRKN,PPARA,TSPO,GDF9,PTCH1,PLA2G6,TTC39B,PLIN2,APOL4,APOL6,CRY1,CROT,ABCB1,ABCG5,ABCG8,TMEM30A,NR1H2,APOB,MFSD2B,PIP4K2A,APOC1,TSKU,AKT2,ABCC4,C1QTNF1,ANO4,SLC5A8,SOAT2,CYP7A1,OSBP,PITPNM2,XKR6,PLSCR4,LIMA1,P2RX7,NR1H3,NKX3-1,ANO6,CRY2,SLC10A6,COL4A3BP,ABCC2,SPP1,PLA2R1,PLTP,NME4,CPT1A,MAP2K6,ABCA5,ABCA9,ACSL5,CHKA,SLCO3A1,PITPNM1,FABP4,PITPNC1,EGF,GRAMD1B,TEX2,PDZD8,ABCB11,AGT,SLC25A20,ABCG4,SLCO1A2,SLCO1C1,OSBPL2,NTSR1,OSBP2,APOLD1,APOD,PLA2G4A,STARD5,FIS1,OSBPL6,SOAT1,OSBPL1A,ZDHHC8,ABCA12,LPCAT3,SPNS3,SLC27A1,TMEM30B,SYT7,GPS2,CLN8,LIPC,ANXA2,OSBPL7,NAXE,ABCD4,APOBR,AC138894.1,ABCC3,PCTP,LDLR,ATG2B,NMUR2,STRA6,GM2A,NPC1,NOS2,PROCA1,PRELID3A,ATP11C,PITPNA,ABCA3,ABCA7,RXRA,CEL,ABCD3,VPS4A,MIR27B,MIR27A,FABP5,ABCA8,MIR33B,PLA2G2C,LDLRAP1,CRH,CPTP,LRAT,STARD4,PTGES,SGPP1,XKR8	grey	VSMC_M10
GO:0150172	0.89	0.28	4	10	regulation of phosphatidylcholine metabolic process	BP	1	APOC1,LPCAT1,LDLR,ABCA3	grey	VSMC_M10
GO:0030031	0.89	0.13	223	443	cell projection assembly	BP	1	ATP8B1,ONECUT2,MYO1A,AVIL,TBC1D30,ATAT1,PARVG,KIF3A,TBC1D32,UBE2B,MTSS1,ASAP1,LRRC6,MAPK15,PODXL,CDC42EP1,RAC2,IFT74,SRF,CFAP69,RFX3,KIT,NCK2,PTPDC1,FGD3,RAB23,DYNC2LI1,EPS8L1,CEP162,TMEM17,AKIRIN1,WDR92,FUZ,IQUB,ATG5,SDCBP,ARMC2,MAPRE1,ARMC4,INTU,SPATA6,TTC26,BBS7,VSTM5,ARHGEF4,DRC1,RSPH6A,GALNT11,FBF1,PIBF1,KLF5,IFT172,FOXJ1,WDR60,TTLL3,CCDC13,ABCC4,MKKS,RAB5A,RAC3,CEP290,BAG4,ARHGEF7,SPEF1,FGD6,NCKAP1L,ARFIP2,TMEM80,DPYSL3,AL359736.1,KIF3B,FER,RILPL1,RILPL2,CEP70,PIK3R1,PARVA,PLCE1,CEP250,CCDC66,P2RX7,TCTN3,IFT81,CCDC113,CFAP20,ARHGEF26,RAPGEF2,CCDC65,TMEM67,BIN3,F2RL1,IFT52,ARHGAP24,ANO6,RPGRIP1L,DNAH1,CYFIP1,DMTN,DNAH5,ZNF423,GBF1,SRGAP2C,NEURL1,CARMIL1,CFAP43,FGD4,ZMYND10,GAP43,ARMC9,CFAP46,TBK2,AUTS2,AJUBA,CLCN4,ALPK1,JHY,DISC1,OFD1,WASF2,RAB17,TMEM237,TRAF3IP1,HDAC4,BBS1,LAMA5,EPS8,PTPRO,CDKL5,SEPT2,LIMK2,WHAMM,CDC42EP2,CFAP161,TTC12,TOGARAM1,EHD1,DNAAF2,SPAG16,NCKAP1,ABLIM2,FAM149B1,HTT,CFAP70,DNM3,RAP1GAP,STK36,GORAB,CEP126,SNAP29,EXOC5,VCL,WAS,RHOJ,TTC25,RAB8A,SDCCAG8,HAP1,DNAAF4,CPLANE2,MNS1,WDR19,TMEM138,MIEN1,ATP6V1D,PLEK2,FGD1,FXR2,BBOF1,CNTROB,TMEM107,NDEL1,TENM2,AC138894.1,CCDC151,NTN1,DYNLL2,MKS1,DNM2,BCAS3,ARHGAP44,EVL,TEKT3,IFT20,SPEF2,STK26,CFAP53,ARHGEF6,FMR1,INPP5K,C16orf71,RILP,CLUAP1,WRAP73,PALM,TPGS1,EPS8L3,DEF8,CDK10,CELSR2,VAV3,CDC14A,TMEM231,FNBP1L,MTSS1L,HYDIN,ODF2L,WDR63,CARMIL2,C5orf30,TCTN2,EPS8L2,HYLS1	grey	VSMC_M10
GO:0009113	0.89	0.28	4	10	purine nucleobase biosynthetic process	BP	1	SHMT2,PPAT,GMPS,SHMT1	grey	VSMC_M10
GO:0003230	0.89	0.20	13	30	cardiac atrium development	BP	1	SMO,WNT11,TBX5,TGFB2,ANK2,ISL1,ENG,SOX4,NOG,WNT5A,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0006646	0.89	0.28	4	10	phosphatidylethanolamine biosynthetic process	BP	1	SELENOI,CHKA,PISD,SLC27A1	grey	VSMC_M10

GO:0045104	0.89	0.20	13	30	intermediate filament cytoskeleton organization	BP	1	RAF1,EVPL,BFSP1,NEFM,DSP,INA,PKP2,SYNM,KLHL24,DES,CLN8,NDEL1,MTM1	grey	VSMC_M10
GO:0010884	0.89	0.23	8	19	positive regulation of lipid storage	BP	1	PLIN2,NR1H2,APOB,FITM2,FITM1,EHD1,C3,PLIN3	grey	VSMC_M10
GO:1905897	0.89	0.17	33	70	regulation of response to endoplasmic reticulum stress	BP	1	PRKN,BAK1,NCK2,NR1H2,AQP11,DDRGK1,PIK3R1,USP25,TMBIM6,NR1H3,OPA1,RNFT2,FICD,USP13,USP19,HYOU1,RNF185,NFE2L2,SYVN1,LPCAT3,PTPN2,BCAP31,SGTA,ABCA7,TMEM259,PARK7,HSPA5,DAB2IP,MIR199A1,RNFT1,DDIT3,BCL2L11,PPP1R15A	grey	VSMC_M10
GO:0098773	0.89	0.17	30	65	skin epidermis development	BP	1	FZD6,SMO,ZDHHC21,SOSTDC1,CD109,EGFR,FUZ,INTU,HDAC2,SOX9,ERCC2,GLI2,FERMT1,ACVR1B,TRPC4AP,FZD3,AP3B1,LDB1,HDAC1,TGFB2,SNAI1,KDF1,LAMA5,SAV1,GORAB,RBPJ,NGFR,GATA6,WNT5A,DNASE1L2	grey	VSMC_M10
GO:0019935	0.89	0.17	26	57	cyclic-nucleotide-mediated signaling	BP	1	PDE7B,ADGRG6,RIMS2,PDE10A,UBE2B,AQP1,SOX9,GIPR,GUCY1B1,PTK2B,RAPGEF2,RAPGEF3,CAP2,ADCY2,PDE9A,ADNP,EIF4EBP2,DGKQ,PDE4A,MAPK7,KSR1,MGRN1,CAP1,PDZD3,CRH,RASD2	grey	VSMC_M10
GO:0002204	0.89	0.18	18	40	somatic recombination of immunoglobulin genes involved in immune response	BP	1	EXOSC3,MSH2,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,NBN,CD40,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,SUPT6H,RNF8	grey	VSMC_M10
GO:0002208	0.89	0.18	18	40	somatic diversification of immunoglobulins involved in immune response	BP	1	EXOSC3,MSH2,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,NBN,CD40,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,SUPT6H,RNF8	grey	VSMC_M10
GO:0045190	0.89	0.18	18	40	isotype switching	BP	1	EXOSC3,MSH2,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,NBN,CD40,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,SUPT6H,RNF8	grey	VSMC_M10
GO:0006707	0.89	0.28	4	10	cholesterol catabolic process	BP	1	CYP7A1,CYP27A1,CYP46A1,CEL	grey	VSMC_M10
GO:0016127	0.89	0.28	4	10	sterol catabolic process	BP	1	CYP7A1,CYP27A1,CYP46A1,CEL	grey	VSMC_M10
GO:0055086	0.89	0.13	224	439	nucleobase-containing small molecule metabolic process	BP	1	NME1,HSD17B4,SHMT2,TBPL1,PDE7B,ENPP3,ATP5MGL,GFPT2,DPYS,PPT2,PPARA,PDE10A,ACSL6,SMPDL3A,PMM1,PRXL2C,APOBEC3H,GTPBP1,OARD1,GUCA1B,IMPDH1,MTAP,NMRK1,GNMT,GDA,CROT,GNPDA2,GALT,SLC35B2,ENPP4,UXS1,SLC25A13,GAPDH,PPAT,RAB23,PPCS,SLC4A4,ME1,NT5E,PPT1,BPGM,DLD,SPHK2,CMPK1,ADCY3,PRTFDC1,ENTPD6,CDADC1,NUDT15,DLG2,LACC1,NUDT5,DHTKD1,MBD4,PRKAG2,SLC22A13,ATP5F1C,ELOVL1,TGDS,CSGALNACT1,PFKP,UGGT2,IDO2,IDO1,NUDT16,PANK2,PDK1,SUCLG2,PDHX,SLC5A8,ELOVL7,PANK1,GPI,NUDT12,AHCY,AMPD3,ATP5F1A,MCCC2,GLRX,GPD1,P2RX7,GUCY1A1,GUCY1B1,ACOT12,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,FITM2,AMPD1,NUDT18,ADCY7,GMPR,FAM173B,ADCY2,MCEE,NME4,PDE9A,TPST1,ZBTB20,GPAM,FAR2,ACSL5,PTHLH,PUDP,NUDT17,MFN1,PFKFB2,PRPS2,ENO4,PARP9,HACD2,ARNT,ADCY4,DPAGT1,CTPS2,ACTN3,HDAC4,THEM5,MGAT1,DNAJC30,MLXIPL,PDE8A,DTYMK,HMGCL,MAGI3,DLG1,ACOT9,PDK3,EFL1,SLC25A16,UPB1,HK1,CPS1,ACSBG1,ATP5S,CASK,COASY,PRKAG3,PINK1,STAT3,NME7,ADK,MPC2,ADCY10,MAPK1,ENO3,NT5C3B,PARP1,TECR,CARD11,SLC26A1,NAXE,PSEN1,ACOT2,ALDH6A1,GUCY2D,PKLR,PANK3,GCDH,OGT,UPRT,ADPGK,PDE4A,ACSM3,MPI,ACACA,NEIL1,NCOR1,INSR,SLC26A2,PRPSAP2,SHMT1,ADSSL1,NT5M,NOS2,ACSBG2,ALDOC,PIPOX,PMM2,ACOT11,NADK,ATP6V0C,PANK4,NTHL1,NME3,MPP1,PARK7,ATP5PB,SLC2A6,VPS9D1,GNAI3,ACSF3,AK8,UCK1,MLYCD,KARS,FUK,DHODH,MT-ATP8,MT-ATP6,RHOA,SULT1C3,ATP5ME,ACOT4,ATP5MF,ENTPD5,PDZD3,ELOVL3,MTHFD2L,PEMT,CMPK2,TIGAR,NNDNF,CHPF2,CSGALNACT1,DCN,HYAL1,CHST3,SPOCK2,CHST7,CHST12,IDUA,B3GALT6,CHSY3	grey	VSMC_M10
GO:0050654	0.89	0.20	12	28	chondroitin sulfate proteoglycan metabolic process	BP	1		grey	VSMC_M10
GO:0002262	0.89	0.15	65	134	myeloid cell homeostasis	BP	1	MPIG6B,HSPA1B,BRD1,BAK1,SMAD5,L3MBTL3,FANCC,MAPK14,ZNF16,RBFOX2,SRF,CDK6,KIT,PRDX1,RPS14,SMAP1,EPAS1,PTBP3,BPGM,SLC7A11,FOXO3,TRAF3IP2,ERCC2,SLC25A38,ACVR2A,NCKAP1L,PRKDC,MFHAS1,GPI,ACVR1B,PIK3CB,CASP3,TMEM14C,DMTN,ALAS1,LDB1,PKNOX1,RPS17,ACIN1,DYRK3,HCLS1,ARNT,SP3,BCL6,CXCR2,STAT3,STAT5B,INHA,FOXP3,THRA,MED1,HOXB6,AHSP,KAT7,DNASE2,SCNN1B,RCOR1,PTPN2,MIR222,ANKRD54,ARID4A,MAFB,BCL2L11,FAM210B,XKR8	grey	VSMC_M10
GO:2000648	0.89	0.23	7	17	positive regulation of stem cell proliferation	BP	1	EPCAM,VEGFC,TERT,THPO,KAT7,CITED1,ATXN1L	grey	VSMC_M10
GO:0006213	0.89	0.26	5	12	pyrimidine nucleoside metabolic process	BP	1	APOBEC3H,CDADC1,DTYMK,UPB1,UPP1	grey	VSMC_M10
GO:0000470	0.89	0.21	10	23	maturation of LSU-rRNA	BP	1	URB1,WDR12,RPL7L1,LAS1L,ZNHIT3,SNU13,NOL9,RPL35,ZNHIT6,NSA2	grey	VSMC_M10
GO:0009116	0.89	0.18	21	45	nucleoside metabolic process	BP	1	APOBEC3H,OARD1,MTAP,GNMT,GDA,ENPP4,PPAT,NT5E,PRTFDC1,CDADC1,AHCY,DGUOK,NME4,PRPS2,DTYMK,UPB1,ADK,UPRT,PRPSAP2,PEMT,UPP1	grey	VSMC_M10
GO:0060117	0.89	0.23	7	17	auditory receptor cell development	BP	1	WHRN,MYO7A,SLC4A7,LRTOMT,AP000812.5,PLS1,STRC	grey	VSMC_M10
GO:0002429	0.89	0.15	72	148	immune response-activating cell surface receptor signaling pathway	BP	1	CD226,HLA-DPB1,PTK2,PLA2G6,TEC,TNFRSF21,PRKCE,FPR2,C5AR2,C5AR1,PRKD2,NECTIN2,EIF2B3,IKBKB,PAWR,PLCL2,PRNP,NCKAP1L,FOXP1,TRAF6,HCK,LPXN,PTPRJ,MEF2C,SLA2,RIPK2,GPLD1,SPPL3,LCK,BANK1,ICOSLG,BTN2A2,DENND1B,CMKLR1,THEMIS2,LAT2,BMX,FGR,PLPP4,CD28,FCER1G,RC3H1,PTPN6,CD38,MAPK1,FOXP3,GPS2,CARD11,PSEN1,LCP2,CD19,PRKCB,BTK,YES1,PRAM1,VAV1,PTPN2,CREBBP,IKBKG,VAV3,BCL10,CMTM3,FYB1,BTN1A1,CD247,THY1,UBE2N,GCSAM,HRAS,LAX1,SH2B2,RC3H2	grey	VSMC_M10
GO:0002757	0.89	0.15	72	148	immune response-activating signal transduction	BP	1	CD226,HLA-DPB1,PTK2,PLA2G6,TEC,TNFRSF21,PRKCE,FPR2,C5AR2,C5AR1,PRKD2,NECTIN2,EIF2B3,IKBKB,PAWR,PLCL2,PRNP,NCKAP1L,FOXP1,TRAF6,HCK,LPXN,PTPRJ,MEF2C,SLA2,RIPK2,GPLD1,SPPL3,LCK,BANK1,ICOSLG,BTN2A2,DENND1B,CMKLR1,THEMIS2,LAT2,BMX,FGR,PLPP4,CD28,FCER1G,RC3H1,PTPN6,CD38,MAPK1,FOXP3,GPS2,CARD11,PSEN1,LCP2,CD19,PRKCB,BTK,YES1,PRAM1,VAV1,PTPN2,CREBBP,IKBKG,VAV3,BCL10,CMTM3,FYB1,BTN1A1,CD247,THY1,UBE2N,GCSAM,HRAS,LAX1,SH2B2,RC3H2	grey	VSMC_M10

GO:0031334	0.89	0.14	98	199	positive regulation of protein-containing complex assembly	BP	1	ARPC3,ATAT1,ESR1,HSPA1B,IL5,BAK1,WASHC5,ASAP1,BAIAP2L2,PICK1,CDC42EP1,LMOD2,TTBK1,SLAIN2,NCK2,KIAA1211,PRKCE,PLEK,NR1H2,MED25,MET,TLR4,CDK5RAP2,MAPRE1,WASF1,FAF1,LCP1,MYD88,SLAIN1,FCHSD2,NAV3,FERMT1,BAG4,FCHSD1,NRG1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,ATR,TRABD2A,CLIP1,SLF1,FMN1,PTK2B,FNIP2,SPIDR,CDH17,IQGAP2,CYFIP1,SLF2,MAGEL2,CARMIL1,LMOD1,AJUBA,AP1AR,WASF2,WHAMM,CDKN1B,DLG1,CALY,CREB1,CDC42EP2,MAPT,RAP1B,TOGARAM1,PPP2R5B,DDX3X,NCKAP1,NIN,PINK1,MMP3,ARPC1A,WAS,GNL3L,EVL,CDK5R1,ABCA3,MLST8,MECP2,PARK7,SPIRE2,PSRC1,PIEZO1,SH3GLB1,DAB2IP,WDR63,CARMIL2,RHOA,TRABD2B,VASP,GMFG,CRBN,GRB2,BCL2L11,DRG1	grey	VSMC_M10
GO:0006637	0.89	0.16	37	78	acyl-CoA metabolic process	BP	1	HSD17B4,PPT2,ACSL6,PPCS,PPT1,DLD,ELOVL1,PDK1,SUCLG2,PDHX,ELOVL7,ACOT12,FITM2,MCEE,GPAM,FAR2,ACSL5,HACD2,THEM5,HMGCL,ACOT9,PDK3,ACSBG1,MPC2,TECR,ACOT2,GCDH,ACSM3,ACACA,ACSBG2,PIPOX,ACOT11,ACSF3,MLYCD,ACOT4,ELOVL3,NUDT19	grey	VSMC_M10
GO:0035383	0.89	0.16	37	78	thioester metabolic process	BP	1	HSD17B4,PPT2,ACSL6,PPCS,PPT1,DLD,ELOVL1,PDK1,SUCLG2,PDHX,ELOVL7,ACOT12,FITM2,MCEE,GPAM,FAR2,ACSL5,HACD2,THEM5,HMGCL,ACOT9,PDK3,ACSBG1,MPC2,TECR,ACOT2,GCDH,ACSM3,ACACA,ACSBG2,PIPOX,ACOT11,ACSF3,MLYCD,ACOT4,ELOVL3,NUDT19	grey	VSMC_M10
GO:0051004	0.89	0.28	4	10	regulation of lipoprotein lipase activity	BP	1	NR1H2,ABHD5,APOC1,NR1H3	grey	VSMC_M10
GO:0006012	0.89	0.28	4	10	galactose metabolic process	BP	1	GALT,GLB1,CHST1,SLC35A2	grey	VSMC_M10
GO:0010460	0.89	0.23	7	17	positive regulation of heart rate	BP	1	SLC1A1,TRPM4,ADRA1D,RYR2,GCH1,RGS4,HEY2	grey	VSMC_M10
GO:0036507	0.89	0.23	7	17	protein demannosylation	BP	1	RNF5,UGGT2,AMFR,MAN1C1,RNF185,EDEM3,SYVN1	grey	VSMC_M10
GO:0036508	0.89	0.23	7	17	protein alpha-1,2-demannosylation	BP	1	RNF5,UGGT2,AMFR,MAN1C1,RNF185,EDEM3,SYVN1	grey	VSMC_M10
GO:0055078	0.89	0.19	15	34	sodium ion homeostasis	BP	1	NEDD4L,SLC12A2,TFAP2B,ATP1A3,SNX5,IL1A,SCN7A,AGT,ATP1A2,SLC9A1,COMT,ATP1B1,ATP1B2,SCNN1B,C7	grey	VSMC_M10
GO:0030279	0.89	0.20	11	26	negative regulation of ossification	BP	1	TRPM4,MKX,SOX9,GFRA4,MEF2C,PTK2B,KREMEN1,SRGN,BCOR,RBPJ,RFLNB	grey	VSMC_M10
GO:0072028	0.89	0.16	30	65	nephron morphogenesis	BP	1	MYC,KLHL3,PTCH1,SMO,SIX2,OSR1,SOX9,GZF1,WNT11,PAX8,EYA1,FMN1,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,NOG,SIX1,LIF,FGF1	grey	VSMC_M10
GO:0032479	0.89	0.16	35	75	regulation of type I interferon production	BP	1	C6orf106,IRF5,GAPDH,REL,TLR4,MYD88,NMI,TMEM173,NPLOC4,MAVS,IRF7,DTX4,OAS3,RIPK2,POLR3D,IFIH1,POLR3C,RNF26,NLRX1,TRAF3IP1,SETD2,DDX3X,POLR3A,OTUD5,RNF216,G3BP1,YY1,TRAF3,RIOK3,RNF135,TICAM1,MIR21,OAS1,ZCCHC3,HAVCR2	grey	VSMC_M10
GO:0032606	0.89	0.16	35	75	type I interferon production	BP	1	C6orf106,IRF5,GAPDH,REL,TLR4,MYD88,NMI,TMEM173,NPLOC4,MAVS,IRF7,DTX4,OAS3,RIPK2,POLR3D,IFIH1,POLR3C,RNF26,NLRX1,TRAF3IP1,SETD2,DDX3X,POLR3A,OTUD5,RNF216,G3BP1,YY1,TRAF3,RIOK3,RNF135,TICAM1,MIR21,OAS1,ZCCHC3,HAVCR2	grey	VSMC_M10
GO:0044728	0.89	0.16	31	67	DNA methylation or demethylation	BP	1	BAZ2A,MOV10L1,MYC,APOBEC3H,PICK1,STPG4,DNMT3A,BMI1,TEX15,ALKBH3,TOX,DNMT3B,OTUD4,FTO,MTRR,HEMK1,ALKBH2,TDRKH,MGMT,TET1,PARP1,FOS,ALKBH1,METTL4,MBD1,MECP2,PRMT7,CTCF,MIR29A,BEND3,N6AMT1	grey	VSMC_M10
GO:0006515	0.89	0.21	11	25	protein quality control for misfolded or incompletely synthesized proteins	BP	1	RNF5,DERL1,ZYG11B,UGGT2,AUP1,LONP2,RNF185,SDF2L1,LONP1,RNF126,ZER1	grey	VSMC_M10
GO:0042113	0.89	0.14	95	193	B cell activation	BP	1	TNFAIP3,IL5,TNFRSF13C,BAK1,MFNG,KIT,TNFRSF21,EXOSC3,IL11,MSH2,SKAP2,PELI1,IL4I1,TLR4,TRAF3IP2,HMCES,BMI1,PHB,ERCC1,MLH1,FOXJ1,PAXIP1,KLF6,CMTM7,PAWR,PLCL2,SHLD1,NCKAP1L,PRKDC,GAPT,PIK3R1,CASP3,PTPRJ,MEF2C,IL7,TPD52,PTK2B,RASGRP1,NBN,CDH17,NOD2,CD40,DCAF1,DOCK10,BANK1,ICOSLG,TCIRG1,RABL3,TBC1D10C,SLAMF8,THEMIS2,LAT2,HDAC4,CD28,RNF168,FZD9,SP3,PPP2R3C,BCL6,SYVN1,ITGA4,RC3H1,PTPN6,TNIP2,CD38,BST1,STAT5B,INHA,FOXP3,SHLD2,GPS2,CARD11,RBPJ,TBX21,BATF,CHRNB2,CD19,PRKCB,BTK,YY1,CD74,CD320,IL7R,SUPT6H,PTPN2,TICAM1,VAV3,LRRC8A,CASP8,RNF8,CD70,NHEJ1,ZFP36L2,LAX1,TNFSF13B	grey	VSMC_M10
GO:0006308	0.89	0.20	11	25	DNA catabolic process	BP	1	HSF1,FBH1,FOXL2,DNASE2,TREX2,PAM16,DNASE1,DFFB,DNASE1L1,DNASE1L2,NMNAT1	grey	VSMC_M10
GO:2000234	0.89	0.28	4	10	positive regulation of rRNA processing	BP	1	SIRT7,DIMT1,RIOK1,HEATR1	grey	VSMC_M10

GO:0061564	0.89	0.13	189	380	axon development	BP	1	LRP1,SEMA6A,KIF5A,RAB21,TIAM2,TSPO,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,RAC2,SMO,SRF,TNFRSF21,SEMA4D,DLX5,ETV1,SEMA4C,SVBP,BRSK1,RTN4,RUFY3,HOXA2,EPHA7,PTN,TNC,TRIM32,EPHA1,KEL,NRCAM,DHFR,PLXNA1,RAB10,GOLGA4,GLI2,MEGF8,PTPRF,MYCBP2,NUMBL,POU4F1,TSKU,SZT2,SLITRK5,KIF5C,FEZ2,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,ULK1,RYK,EPHB1,RET,TTL,CASP3,ROBO1,ROBO2,FZD3,SEMA4F,NCAM2,DPYSL2,TIAM1,SLIT1,NKX6-1,TRIO,NR4A2,ZFYVE27,CRTAC1,SEMA3G,SPP1,PAX2,CYFIP1,ALCAM,TSPAN2,SEMA4G,SIAH1,BMPR1B,BDNF,KIAA0319,MTR,LGR6,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,ADNP,DISC1,KREMEN1,GBX2,KALRN,CERS2,VASH2,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,LRIG2,APOD,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,SEMA6D,EPHB4,ITGA4,TNR,FN1,ATL1,NIN,PPP3CB,RAB3A,MARK2,VCL,RAB8A,CRMP1,EPHA4,LRTM2,ACTB,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,TRIM46,EFNA1,NDEL1,CHRNB2,RAB11A,MAP2K1,NTN1,RPS6KA5,RNF165,DNM2,BCL11B,LHX1,SIN3A,TRPV2,LAMA3,CDK5R1,ISL1,EMB,LAMA1,DOCK7,SLC9A6,DAB1,SLITRK2,L1CAM,NTN3,ARHGAP4,MAPK8IP3,PLXNA3,BSG,TUBB3,AMIGO1,NTNG2,STXBP1,BARHL2,MIR222,DPYSL5,EFNA4,CNTN2,VASP,FOXG1,CNTF,RTN4RL1,ISL2,NOG,THY1,WNT5A,POU3F2,CHN1,ARTN,NRXN3,LYPLA2,EFNB3,ISPD,MAP1A,OLFM1	grey	VSMC_M10
GO:0007369	0.89	0.15	66	138	gastrulation	BP	1	ITGA7,FRS2,EXOC4,SRF,TXNRD1,SIX2,OSR1,DLD,CLASP2,MEGF8,WNT11,TGFBR2,ACVR2A,EOMES,MKKS,GPI,EYA1,FAM208A,TLX2,MMP15,RTF1,PAX2,LDB1,POGLUT1,PRKAR1A,DAG1,SNAI1,SOX2,LAMB3,COL7A1,FZD7,ITGB5,PHLDB1,SYF2,SETD2,WNT3,ITGA4,FN1,COL5A2,TBX19,LEO1,DVL2,BMPR1A,KDM6B,ITGA3,SMAD3,MAP2K5,GSC,LHX1,LAMA3,MAPK7,AMOT,GATA6,TWSG1,GPC3,COL5A1,FOXF1,DUSP2,LAMB1,POFUT2,NOG,WNT5A,LBX2,DUSP1,DUSP4,TGIF2	grey	VSMC_M10
GO:0032633	0.89	0.21	9	21	interleukin-4 production	BP	1	CD28,FCER1G,SCGB1A1,FOXP3,PRKCZ,SLC7A5,DDIT3,CEBPB,HAVCR2	grey	VSMC_M10
GO:0032673	0.89	0.21	9	21	regulation of interleukin-4 production	BP	1	CD28,FCER1G,SCGB1A1,FOXP3,PRKCZ,SLC7A5,DDIT3,CEBPB,HAVCR2	grey	VSMC_M10
GO:0006690	0.89	0.17	29	62	icosanoid metabolic process	BP	1	LTC4S,AKR1B1,ABCC10,MGST2,FAAH,ACOX1,PIBF1,ABHD6,HPGD,PLA2G4B,CYP2U1,MAPKAPK2,PLA2G4A,GGT2,GGT6,DAGLB,EPHX1,AC005520.1,ALOXE3,MAPK3,CD74,CYP2J2,PTGES2,CES2,CYP4F22,FABP5,DPEP2,GGT5,PTGES	grey	VSMC_M10
GO:0031330	0.89	0.14	102	207	negative regulation of cellular catabolic process	BP	1	TRIM39,PABPC1,PHAX,RNF5,TSPO,MAPK14,NRBP2,RGP1,PDCL3,LRPPRC,MET,SDCBP,TRAF3IP2,MTMR2,DHX34,APOC1,KDM4A,AQP11,MYD88,TIMP4,KLHL40,USP36,SIRT2,FEZ2,DDRGK1,RYBP,PKP3,PSMF1,TAF9,MTMR9,USP25,CSNK2A2,FAM192A,TENT2,MARCH7,TENT5C,TENT4B,RBM24,LZTS1,SUFU,GPLD1,RPL23,SEC22B,TMEM39A,USP30,AXIN2,MAPKAPK2,USP19,SORL1,MCL1,TRAF5,ANGEL2,RUBCN,IL10RA,EIF4ENIF1,RPL11,LRIG2,YBX3,TAB3,TBC1D14,SLC11A1,RBM10,PINK1,STAT3,ATP13A2,EPHA4,PHF23,ANXA2,TARDBP,PSEN1,EFNA1,TAF1,OGT,TOB1,TENT5D,NRDE2,LARP1,NPC1,SMCR8,LEPR,PARN,CLEC16A,FMR1,MTM1,PAM16,METTL16,SGTA,CIRBP,TRAF2,PARK7,TSC1,DAB2IP,MIR199A1,MIR21,TIGAR,CAMLG,CPTP,YBX1,STYX,TENT5A,MAP1A,NMNAT1	grey	VSMC_M10
GO:0048588	0.89	0.14	95	195	developmental cell growth	BP	1	NEDD4L,LRP1,SEMA6A,RAB21,RIMS2,PRKN,PPARA,GDF9,FSTL4,PLXNA4,CPNE5,PI16,SRF,SEMA4D,SEMA4C,RIMS1,RTN4,RUFY3,EPHA7,NRCAM,WASF1,PLXNA1,SOX9,GOLGA4,MEGF8,CPNE9,TGFBR2,SYT1,SLC23A2,SEMA3D,SPART,SEMA3A,ULK1,RYK,TTL,SEMA4F,KMT2D,DPYSL2,EIF2AK4,TIAM1,SLIT1,NKX6-1,ZFYVE27,SEMA3G,SPP1,CYFIP1,ALCAM,SEMA4G,BDNF,KIAA0319,SEMA3F,AUTS2,ADNP,DISC1,ARIH2,AGT,CDKL5,WNT3,SPG11,MAPT,SEMA6D,ITGA4,TNR,FN1,NIN,FLRT1,PPP3CB,MUL1,VCL,SEMA4A,NLGN3,TRIM46,NDEL1,RAB11A,NTN1,DNM2,YY1,SIN3A,TRPV2,CDK5R1,SLC9A6,L1CAM,PRKCZ,ARHGAP4,PLXNA3,BARHL2,MIR199A1,MIR23A,MIR24-1,IMPACT,WNT5A,CACNG7,RGS4,LLPH,OLFM1	grey	VSMC_M10
GO:0000154	0.89	0.19	14	31	rRNA modification	BP	1	TFB1M,DIMT1,NSUN3,RPUSD2,RPUSD4,GAR1,NSUN5,MRM2,ZCCHC4,MRM3,METTL16,RPUSD1,RPUSD3,TRMT61B	grey	VSMC_M10
GO:0070228	0.89	0.18	17	38	regulation of lymphocyte apoptotic process	BP	1	SLC46A2,IDO1,FOXP1,ZC3H8,GPAM,PDCD1,ADAM8,BCL6,EFNA1,BTK,CD74,CCL5,IL7R,BCL10,FADD,WNT5A,TSC22D3	grey	VSMC_M10
GO:0022408	0.89	0.15	63	130	negative regulation of cell-cell adhesion	BP	1	PPARA,PTK2,PODXL,TNFRSF21,EPCAM,PELI1,AKNA,IL4I1,FOXJ1,C1QTNF1,JAG1,PAWR,SPINT2,PRNP,NCKAP1L,ZC3H8,CASP3,TMEM131L,PAG1,MARCH7,ADTRP,TRPV4,BTN2A2,PRKAR1A,HLX,YTHDF2,UBASH3B,RUNX3,DLG1,MIA3,BCL6,ABCA12,TNR,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,SCGB1A1,FOXP3,TBX21,ZBTB7B,IL4R,MAP2K5,CD74,MAPK7,CCL25,TWSG1,PTPN2,SOCS1,ABAT,ASS1,GLMN,MIR21,MIR222,MIR27A,MIR125A,FGL2,RGCC,LAX1,CEBPB,HAVCR2,RC3H2	grey	VSMC_M10
GO:0140112	0.89	0.21	9	21	extracellular vesicle biogenesis	BP	1	VPS4B,PRKN,CHMP2A,SDCBP,RAB7A,ATP13A2,RAB11A,ARRDC1,VPS4A	grey	VSMC_M10

GO:0030900	0.89	0.13	139	282	forebrain development	BP	1	NME1,LRP1,GLI1,ATAT1,FRS2,UQCRQ,PITX1,AGTPBP1,PLXNA4,SUN2,NTRK2,SMO,SRF,CDK6,DLX5,EFHC1,MBOAT7,RTN4,AQP1,AKNA,PTN,FOXP2,POU3F3,SLC7A11,FAT4,NDNF,EIF2B3,XRCC1,GLI2,SCN5A,NUMBL,POU4F1,TSKU,SZT2,ALK,HOOK3,MKKS,RARB,PLCB1,RAC3,SEMA3A,NRG1,RYK,TOX,ZSWIM6,CASP3,DCLK2,ROBO1,ROBO2,HTRA2,CELF1,CSNK2A2,MCPH1,RAPGEF2,SLIT1,TENT2,NR4A2,SLC38A2,RPGRIP1L,SALL1,DNAH5,ZNF335,DPCD,SRGAP2C,SLC4A10,SRD5A1,SLC6A3,HDAC1,ALDH1A3,PGAP1,SATB2,KRAS,TTC21B,SOX2,DISC1,GBX2,ATP1A2,DLX1,EPHB3,NSUN5,SETD2,CREB1,BCL2A1,DIXDC1,TNR,NIN,WNT4,COL3A1,TBX19,KCNA1,HAP1,BMPR1A,DNAJB1,MPP5,RBPJ,ALDH1A2,ATP1B2,PSEN1,KDM6B,ITGAM,NDEL1,CHRNB2,GSC,BCL11B,LHX1,SIN3A,XAB2,MYO1D,CDK5R1,ISL1,TWSG1,DOCK7,DAB1,LRP8,CRK,SKI,CHD5,PLXNA3,TSC1,PHLPP2,DAB2IP,LHX8,RHOA,UBB,ADGRG1,CNTN2,FOXG1,LAMB1,METTL14,RTN4RL1,GNG12,CCDC85C,NOG,WNT5A,POU3F2,OTX1,CRH,BTBD3,TAL2	grey	VSMC_M10
GO:0000338	0.89	0.27	4	10	protein deneddylation	BP	1	GPS1,COPS7B,COPS7A,COPS8	grey	VSMC_M10
GO:0033119	0.89	0.22	8	19	negative regulation of RNA splicing	BP	1	PTBP3,SRSF10,TMBIM6,SRSF6,SRSF4,RBM10,SRSF12,SAP18	grey	VSMC_M10
GO:1900242	0.89	0.23	7	17	regulation of synaptic vesicle endocytosis	BP	1	BTBD9,DNM1L,AP2M1,PPP3CB,DGKQ,SYT11,CALM1	grey	VSMC_M10
GO:0009261	0.89	0.18	18	40	ribonucleotide catabolic process	BP	1	PDE7B,DPYS,PDE10A,GDA,NT5E,NUDT16,AMPD3,ENTPD4,FITM2,NUDT18,PDE9A,PDE8A,UPB1,PDE4A,MLYCD,NUDT19,HINT1,UPP1	grey	VSMC_M10
GO:0003209	0.89	0.20	11	26	cardiac atrium morphogenesis	BP	1	SMO,TBX5,TGFB2,ISL1,ENG,SOX4,NOG,WNT5A,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0042451	0.89	0.27	4	10	purine nucleoside biosynthetic process	BP	1	MTAP,NT5E,PRTFDC1,ADK	grey	VSMC_M10
GO:0042455	0.89	0.27	4	10	ribonucleoside biosynthetic process	BP	1	MTAP,NT5E,PRTFDC1,ADK	grey	VSMC_M10
GO:0046129	0.89	0.27	4	10	purine ribonucleoside biosynthetic process	BP	1	MTAP,NT5E,PRTFDC1,ADK	grey	VSMC_M10
GO:0006396	0.89	0.12	500	950	RNA processing	BP	1	ZC3H10,PAN2,RNMT,CLK4,ADAT2,HELB,RPP21,CPSF6,ESR1,ZFC3H1,PABPC1,SNW1,TFB1M,SF3A3,QKI,TRMU,UTP23,RRP7A,CSDC2,TRMT11,AGO2,HABP4,ZC3H3,TUT7,PUF60,C9orf64,CMTR1,EXOSC4,HSF1,CPSF1,USP49,RBM28,RBFOX2,SMU1,NOL6,TSR1,EXOSC3,RPS14,RNF20,MTO1,TSEN34,PRPF31,PPP2R1A,TRA2A,ELP1,YTHDC1,PNPT1,UTP3,PUS10,PTBP3,TRIT1,RNGTT,SRSF10,MDN1,PRPF4,SNIP1,SNRNP27,LSM10,AGO1,EGFR,FCF1,SCAF1,MYCN,TUT4,PRPF38A,PUM2,DUS4L,MTPAP,SYMPK,NSUN6,IWS1,ERCC2,CLASRP,PCF11,FASTK,RPS8,WBP4,DEDD2,CLNS1A,CELF2,KIN,RPL14,RBM26,CRNKL1,PRX,INTS10,THUMPD3,USP36,ESF1,KRR1,IK,NUP98,DPH3,SIRT7,ZMAT2,CWC15,TRMT6,TRNT1,LSM1,NUDT16,WTAP,PPP4R2,THUMPD2,RBPMS,PHRF1,PRKDC,PAN3,TRMT9B,THOC7,DHX37,TGS1,BMS1,DIMT1,CSTF3,SREK1IP1,GPATCH1,ELP4,SREK1,PIK3R1,POP4,USP39,PRMT9,CLP1,ZCCHC8,GCFC2,ELP3,RBM39,M1AP,BCDIN3D,TMBIM6,AAR2,CELF1,USB1,CNOT6L,TPRKB,RPRD1B,SCAF4,URB1,DDX54,NSUN3,RRP12,DHX35,TENT2,HELQ,RBM12B,RPUSD2,SLC38A2,SRSF6,SCAF11,RIPK1,OSGEPL1,PRPF4B,INTS8,RPP40,BCAS2,RIOK1,ATXN1,TENT4B,RBM24,CDKAL1,POP5,PDCD11,RPUSD4,TRMT10A,ZBTB8OS,PPP3CA,RPS17,SMNDC1,TERT,QTRT2,SBDS,RBM5,TYW1B,INTS12,CPSF2,HEATR1,TYW5,FAM207A,ADARB1,SART3,ACIN1,MRPS11,GAR1,HSPA8,SRSF4,TRUB1,YTHDF2,RTRAF,RPRD2,CSTF1,DALRD3,YBEY,LCMT2,ZRSR2,NOP9,RPS27,ZMAT5,FASTKD1,PPIG,WDR12,METTL8,CELF3,RPL7L1,SYF2,WBP11,NCBP2,ELP6,NSUN5,DDX47,RPL11,METTL2B,KIAA0391,BUD13,MFAP1,RBM7,TRMT1L,IVNS1ABP,NONO,SUPV3L1,PRKRA,GEMIN2,SNRPD3,PRP	grey	VSMC_M10
GO:0002440	0.89	0.14	67	138	production of molecular mediator of immune response	BP	1	CD226,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,KIT,EXOSC3,MSH2,CYREN,RSAD2,TLR4,ATG5,TRPM4,TRAF3IP2,SPHK2,HMCES,PHB,ERCC1,LACC1,MLH1,PAXIP1,SHLD1,MAVS,HPX,PRKDC,TRAF6,GAPT,GPI,TMBIM6,XRCC4,NBN,F2RL1,NOD2,POLL,CD40,CD96,TGFB2,DENND1B,CD28,RNF168,FZD5,BCL6,HK1,PMS2,FOXP3,SHLD2,TNFRSF1B,SPON2,TBX21,STX4,BATF,IL4R,BTK,YY1,CD74,SUPT6H,TICAM1,PRKCZ,TRAF2,SLC7A5,BCL10,WNT5A,TRDV3,INAVA,RNF8,NHEJ1	grey	VSMC_M10
GO:0071276	0.89	0.21	9	21	cellular response to cadmium ion	BP	1	HSF1,EGFR,NCF1,ABCB6,MAPK1,FOS,MAPK3,JUN,MT1X	grey	VSMC_M10
GO:0044766	0.89	0.23	7	17	multi-organism transport	BP	1	EPS15,RAB7A,KPNA3,KPNA2,TPCN1,PIKFYVE,FMR1	grey	VSMC_M10
GO:1902579	0.89	0.23	7	17	multi-organism localization	BP	1	EPS15,RAB7A,KPNA3,KPNA2,TPCN1,PIKFYVE,FMR1	grey	VSMC_M10
GO:0051767	0.89	0.23	7	17	nitric-oxide synthase biosynthetic process	BP	1	PGGT1B,TLR4,NOD2,MAP2K6,CCL2,FCER2,IL33	grey	VSMC_M10
GO:0051769	0.89	0.23	7	17	regulation of nitric-oxide synthase biosynthetic process	BP	1	PGGT1B,TLR4,NOD2,MAP2K6,CCL2,FCER2,IL33	grey	VSMC_M10
GO:0010508	0.89	0.15	50	105	positive regulation of autophagy	BP	1	PIP4K2C,EPM2A,PRKN,TFEB,FBXO7,SPTLC1,NOD1,SCOC,FOXO3,SESN3,PIP4K2A,PLK3,OPTN,RALB,TMEM173,DCN,ULK1,PLK2,PIK3CB,RIPK2,TPCN1,TP53INP1,NOD2,DHRSX,ATG16L1,SH3BP4,BAG3,HTT,PINK1,PIM2,VPS13D,MAPK3,LARP1,SMCR8,TICAM1,IKBKG,PARK7,GPSM1,GNAI3,KIAA1324,TSC1,SH3GLB1,TRIM68,TRIM34,BNIP3L,TRIM65,IRGM,BCL2L11,HSPB8,RNF152	grey	VSMC_M10
GO:0010453	0.89	0.23	7	17	regulation of cell fate commitment	BP	1	SOSTDC1,WNT11,FZD7,TNFSF18,BMPR1A,TBX21,WNT5A	grey	VSMC_M10
GO:0045939	0.89	0.21	9	21	negative regulation of steroid metabolic process	BP	1	CYP27B1,DKKL1,DKK3,ERLIN1,SNAI1,SCAP,WNT4,GFI1,INSIG2	grey	VSMC_M10
GO:0032069	0.89	0.23	7	17	regulation of nuclease activity	BP	1	TMBIM6,OAS3,OASL,DDX11,NEIL1,TERF2,OAS1	grey	VSMC_M10
GO:1901658	0.89	0.20	10	23	glycosyl compound catabolic process	BP	1	FUCA2,APOBEC3H,GDA,ENPP4,CDADC1,AHCY,UPB1,GLA,ABHD10,UPP1	grey	VSMC_M10
GO:0061158	0.89	0.23	6	15	3'-UTR-mediated mRNA destabilization	BP	1	RBM24,RC3H1,UPF1,TARDBP,PLEKHN1,ZFP36L2	grey	VSMC_M10
GO:0000731	0.89	0.20	11	26	DNA synthesis involved in DNA repair	BP	1	POLI,REV1,REV3L,WRN,PRIMPOL,WRNIP1,SYCP1,SPRTN,TEX12,POLN,ZBTB1	grey	VSMC_M10
GO:0044550	0.89	0.22	7	17	secondary metabolite biosynthetic process	BP	1	SLC7A11,RAPGEF2,OCA2,BDH2,CITED1,SLC45A2,WNT5A	grey	VSMC_M10

GO:0035590	0.89	0.22	8	19	purinergic nucleotide receptor signaling pathway	BP	1	P2RX2,P2RX3,P2RX7,P2RY1,ANO6,ADORA2B,P2RX1,CNTN2	grey	VSMC_M10
GO:1903037	0.89	0.13	102	206	regulation of leukocyte cell-cell adhesion	BP	1	AGER,PPARA,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,ZDHHC21,TNFRSF21,NCK2,PELI1,IL4I1,IL15,BMI1,GLI2,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,SOX12,ZC3H8,IL1A,CASP3,TMEM131L,IL7,PAG1,RASGRP1,RIPK2,AP3B1,MARCH7,SOX13,ADTRP,NOD2,IGF2,LCK,ICOSLG,BTN2A2,GPAM,PRKAR1A,HLX,CD28,RUNX3,DLG1,ADAM8,MIA3,DUSP10,BCL6,ITGA4,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,STAT5B,SCGB1A1,FOXP3,RASAL3,ZBTB1,CARD11,TBX21,ZBTB7B,IL4R,CD74,CCL5,CCL2,CCL25,YES1,NKAP,VAV1,TWSG1,IL7R,PTPN2,SOCS1,DNAJA3,PRKCZ,ASS1,GLMN,BCL10,MIR21,MIR222,MIR27A,RHOA,SOX4,FADD,DPP4,CD46,FUT4,MIR125A,THY1,FGL2,CD70,TNFSF9,LAX1,EFNB3,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:1905209	0.89	0.23	6	15	positive regulation of cardiocyte differentiation	BP	1	MEF2C,TBX5,TGFB2,GPER1,GATA6,NKX2-5	grey	VSMC_M10
GO:1904994	0.89	0.21	9	21	regulation of leukocyte adhesion to vascular endothelial cell	BP	1	ZDHHC21,TRAF6,ITGA4,CCL25,MIR21,MIR222,RHOA,FUT4,MIR125A	grey	VSMC_M10
GO:0048259	0.89	0.15	40	85	regulation of receptor-mediated endocytosis	BP	1	RAB21,PICK1,USP46,SMAP1,PPT1,RSPO1,AAK1,SFRP4,SDCBP,MTMR2,APOC1,ARRB1,NEU3,PIK3CB,HIP1R,WDR54,BMP2K,SYNJ1,ANKRD13A,EGF,ANKRD13D,DGKD,CBL,AP2M1,SH3GL3,LRPAP1,DLG4,ANXA2,SYT11,DNM2,INSR,SGIP1,C3,UNC119,FMR1,MIR199A1,MIR27B,MIR27A,LDLRAP1,LRRTM2	grey	VSMC_M10
GO:0001654	0.89	0.13	138	280	eye development	BP	1	SLC39A5,MDM1,FRS2,OSR2,TBC1D32,BAK1,ATF4,AGTPBP1,NTRK2,PRPH2,RORB,SRF,SLC1A1,TFAP2B,TDRD7,TMOD1,RDH13,ABCB5,PTN,TSPAN12,USP45,SLC7A11,SPRY1,FOXE3,HDAC2,BBS7,SOX9,CRYGN,ZNF513,ACVR2B,IFT172,MYO7A,TSKU,SPRY2,DZANK1,TGFBR2,BFSP1,JAG1,RARB,FSCN2,SPRED3,FREM2,CEP290,KERA,MAB21L1,MITF,FLT1,TUB,EPHB1,PFDN5,NPHP1,RET,FOXL2,MAB21L2,TENM3,USH1C,TENT2,OPA1,RPGRIP1L,TFAP2A,PAX2,NKD1,BMPR1B,MYH15,NECTIN3,LPCAT1,PKNOX1,SLC6A3,HDAC1,ALDH1A3,TGFB2,TCIRG1,PRSS56,SHROOM2,SOX2,CRYBA4,NRL,CLIC4,DLX1,GRHL3,LIMK2,SP3,CDKN1B,DLG1,FZD5,FBN1,FKBP8,COL5A2,PLA2G16,STAT3,TULP3,OBSL1,RHOJ,ROM1,MFAP2,WDR19,SDK1,MAX,CLN8,MED1,ALDH1A2,MFN2,PSEN1,TTLL5,MEGF11,LCTL,SMAD3,TBX2,BCL11B,LHX1,STRA6,YY1,CHRDL1,UNC45B,LAMA1,TWSG1,GNB1,FZR1,SKI,SOX8,COL5A1,LAMC3,OLFM3,TMEM231,SLC25A25,HSF4,BLOC1S3,FJX1,CNTF,ACVRL1,THY1,WNT5A,DIO3,TGIF2,TBC1D20,PITX3,WNT2,COL8A2	grey	VSMC_M10
GO:0046638	0.89	0.18	15	34	positive regulation of alpha-beta T cell differentiation	BP	1	HLA-DRA,TGFBR2,NCKAP1L,RIPK2,AP3B1,HLX,RUNX3,FOXP3,ZBTB7B,IL4R,NKAP,SOCS1,PRKCZ,MIR21,RHOA	grey	VSMC_M10
GO:0034764	0.89	0.14	75	155	positive regulation of transmembrane transport	BP	1	STAC3,MAPK14,ABCB1,WNK2,FGF21,BRAF,CACNB2,STAC,AKT2,PIK3R1,GLRX,SORBS1,P2RX7,KCNJ11,IFNGR2,F2R,TESC,ANO6,KCNE2,PKD2,KCNIP2,RYR2,FAM173B,AZIN2,IRS1,KCNJ2,TERT,ACSL5,COX17,ANK2,C2CD5,GPER1,AGT,ACE2,SLC9A1,CASQ1,NTSR1,NOS1AP,NFE2L2,CEMIP,HTT,CLTCL1,PINK1,ATP1B1,KCNA1,ARL6IP1,HAP1,WNK3,STAC2,ATP1B2,PSEN1,NLGN3,ATP2A1,CD19,CALM1,DNM2,VMP1,BDKRB1,INSR,CCL2,C3,GPC3,PDPK1,P2RX1,RNF207,AMIGO1,LCN2,MIR21,DMD,JPH2,CA2,KCNH2,THY1,APOPT1,ARPP19	grey	VSMC_M10
GO:0060603	0.89	0.19	11	26	mammary gland duct morphogenesis	BP	1	ESR1,PTCH1,SOSTDC1,AREG,GLI2,VDR,WNT4,MED1,NTN1,CSF1R,WNT5A	grey	VSMC_M10
GO:1904893	0.90	0.20	10	23	negative regulation of receptor signaling pathway via STAT	BP	1	PPP2R1A,PIBF1,PARP14,SUZ12,PTPN2,SOCS1,DAB1,MIR125B1,MIR125A,LEPROT	grey	VSMC_M10
GO:0071326	0.90	0.14	54	113	cellular response to monosaccharide stimulus	BP	1	ZNF236,NME1,LRP1,AGER,PLA2G6,SRF,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,GRIK5,RAF1,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,KCNJ11,TIAM1,RAB11FIP5,OPA1,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,SLC9B2,ZBTB20,ADRA2A,KCNB1,POLG,GPER1,RAB11FIP2,MLXIPL,SIDT2,PDK3,KLF7,FIS1,MEN1,ENY2,ABCA12,PPP3CB,PTPRN,MPC2,STX4,GPR68,SIN3A,OXCT1,NADK,BAIAP3,CYBA,SOX4,CRH	grey	VSMC_M10
GO:0090051	0.90	0.22	7	17	negative regulation of cell migration involved in sprouting angiogenesis	BP	1	MEOX2,ITGB1BP1,PDCD10,MAP2K5,MIR199A1,MIR22,RHOA	grey	VSMC_M10
GO:0070262	0.90	0.23	6	15	peptidyl-serine dephosphorylation	BP	1	PPP2CB,PPP3CA,PPP2R2D,DUSP26,DUSP1,PPP1R15A	grey	VSMC_M10
GO:0046849	0.90	0.15	32	69	bone remodeling	BP	1	TNFAIP3,TNFRSF11B,RAC2,PTN,EGFR,NCDN,MITF,TRAF6,IL7,P2RX7,PTK2B,SPP1,LRRK1,TCIRG1,GPR137B,UBASH3B,ADAM8,PTH1R,GPR137,SUCO,CD38,P3H4,SYT7,RAB3D,CSF1R,PPARGC1B,LEPR,ATP6AP1,DEF8,CA2,BGLAP,SNX10	grey	VSMC_M10
GO:0034394	0.90	0.16	27	59	protein localization to cell surface	BP	1	NEDD4L,PRRT1,GOPC,WNT11,GPD1L,TM9SF4,PIGU,RAB11FIP5,AP3B1,GBF1,BDNF,FBLN5,EGF,ANK2,LRIG2,ABCA12,VCL,STX4,RAB11A,GGA2,TAX1BP3,ABCA7,CD247,TMEM35A,LEPROT,MESD,MAP1A	grey	VSMC_M10
GO:0071320	0.90	0.18	16	37	cellular response to cAMP	BP	1	AQP1,AANAT,GPD1,RAPGEF2,STC1,RAPGEF3,PKD2,DMTN,SRD5A1,RAP1B,CPS1,FDX1,INPP5K,ASS1,HSPA5,HCN4	grey	VSMC_M10
GO:0048565	0.90	0.15	43	92	digestive tract development	BP	1	GLI1,VPS52,SOX10,SMO,KIT,SIX2,CXCL8,EGFR,BBS7,SLC4A2,GLI2,MEGF8,KLF5,IFT172,WNT11,TGFBR2,OVOL2,CHD8,RARB,CCKBR,RET,CBFA2T2,SALL1,TGFB2,HLX,EPHB3,CPS1,PYY,SAV1,NKX3-2,ALDH1A2,RBPMS2,SMAD3,TBX2,STRA6,GATA6,DAB1,PKD1,FOXL1,FOXF1,ASS1,WNT5A,TIGAR	grey	VSMC_M10
GO:0045840	0.90	0.18	14	32	positive regulation of mitotic nuclear division	BP	1	PHIP,HOXA13,EPGN,TGFA,IL1A,ANAPC5,ANAPC7,IGF2,EGF,CD28,ANAPC4,INSR,RGCC,EREG	grey	VSMC_M10
GO:0033146	0.90	0.18	14	32	regulation of intracellular estrogen receptor signaling pathway	BP	1	CNOT2,FOXH1,DDRGK1,CYP7B1,UFSP2,ZNF366,CNOT1,KMT2D,VPS18,DNAAF4,PARP1,MED1,PAGR1,ISL1	grey	VSMC_M10
GO:0046337	0.90	0.20	9	21	phosphatidylethanolamine metabolic process	BP	1	PLA2G6,NAPEPLD,SELENOI,CHKA,ABHD4,PISD,PLA2G16,SLC27A1,PLA2G15	grey	VSMC_M10

GO:0045070	0.90	0.19	12	28	positive regulation of viral genome replication	BP	1	PABPC1,PPARA,TMEM39A,ADARB1,NR5A2,STAU1,CD28,DDX3X,DDB1,HACD3,LARP1,CCL5	grey	VSMC_M10
GO:0060338	0.90	0.18	15	34	regulation of type I interferon-mediated signaling pathway	BP	1	MAVS,IRF7,OAS3,NLRC5,YTHDF2,PTPN6,MUL1,USP18,DCST1,STAT2,PTPN2,MIR21,OAS1,FADD,WNT5A	grey	VSMC_M10
GO:0046902	0.90	0.16	23	50	regulation of mitochondrial membrane permeability	BP	1	HEBP2,BAK1,TMEM14A,HIP1R,SLC9A1,THEM4,STPG1,FZD9,NMT1,MUL1,STAT3,TMEM102,CAMK2A,ACAA2,NAIF1,MIR29A,NOL3,BNIP3L,BCL2L11,SLC35F6,BCL2L2,PPIF,AC140504.1	grey	VSMC_M10
GO:0050995	0.90	0.23	6	15	negative regulation of lipid catabolic process	BP	1	APOC1,ALK,GPLD1,ADRA2A,SORL1,BSCL2	grey	VSMC_M10
GO:0006900	0.90	0.16	25	55	vesicle budding from membrane	BP	1	PRKN,MAPK15,RAB7A,CHMP4C,ARFGAP2,SEC31A,AP3B1,CHMP7,SEC31B,GBF1,KLHL12,PEF1,PDCD6,AP2M1,SCAP,MIA3,SEC24C,SLC2A4,ANXA2,TMED10,PPP6C,RILP,FNBP1L,VPS4A,TBC1D20	grey	VSMC_M10
GO:2000242	0.90	0.17	19	42	negative regulation of reproductive process	BP	1	FBXO43,MYH9,NLRP5,PLAT,MOS,NKX3-1,ACVR1C,HYAL3,PRKAR1A,SNAI1,CDKN1B,OVOL1,OVGP1,WNT4,ZP2,WDR77,WNT5A,DUSP1,LIF	grey	VSMC_M10
GO:0071763	0.90	0.18	14	32	nuclear membrane organization	BP	1	NEMP1,CHMP2A,LPIN1,SIRT2,NSFL1C,CHMP7,GPER1,TOR1AIP1,AKAP8L,TARDBP,NDEL1,PRKCB,TOR1B,VPS4A	grey	VSMC_M10
GO:0032104	0.90	0.23	6	15	regulation of response to extracellular stimulus	BP	1	CYP27B1,SNW1,PPARA,MKKS,MED1,TRIM24	grey	VSMC_M10
GO:0032107	0.90	0.23	6	15	regulation of response to nutrient levels	BP	1	CYP27B1,SNW1,PPARA,MKKS,MED1,TRIM24	grey	VSMC_M10
GO:0098727	0.90	0.14	51	108	maintenance of cell number	BP	1	CNOT2,ZNF706,MED30,MYC,FANCC,SMO,KIT,SIX2,PTN,TUT4,FOXO3,SOX9,RAF1,HOOK3,JAG1,LSM1,TCF15,PAX8,CNOT1,SETD6,MCPH1,LOXL2,RTF1,PAX2,LDB1,DIS3L2,SOX2,FZD7,DDX6,VPS72,EIF4ENIF1,TET1,MED14,SAV1,STAT3,LEO1,BMPR1A,RBPJ,MED6,ESRRB,MED7,SKI,MED27,MTF2,SOX4,METTL14,NOG,ZNF322,LIF,ZFP36L2,MED21	grey	VSMC_M10
GO:0097734	0.90	0.21	8	19	extracellular exosome biogenesis	BP	1	VPS4B,PRKN,CHMP2A,SDCBP,RAB7A,ATP13A2,RAB11A,VPS4A	grey	VSMC_M10
GO:0030490	0.90	0.17	21	46	maturation of SSU-rRNA	BP	1	HELB,UTP23,TSR1,RPS14,UTP3,ERCC2,RPS8,DHX37,BMS1,RPP40,RIOK1,HEATR1,FAM207A,MRPS11,NOP9,TSR2,KRI1,RIOK3,UTP6,SNU13,GTF2H5	grey	VSMC_M10
GO:0002115	0.90	0.23	6	15	store-operated calcium entry	BP	1	EFHB,ORAI1,SLC8B1,HOMER1,CASQ1,HOMER2	grey	VSMC_M10
GO:0010888	0.90	0.22	7	17	negative regulation of lipid storage	BP	1	PPARA,TTC39B,NR1H2,ABHD5,ASXL1,NR1H3,PTPN2	grey	VSMC_M10
GO:0045039	0.90	0.26	4	10	protein insertion into mitochondrial inner membrane	BP	1	AGK,TIMM29,TIMM10B,TIMM8B	grey	VSMC_M10
GO:1903522	0.90	0.13	87	179	regulation of blood circulation	BP	1	AGER,ZDHHC21,SLC1A1,TNNI3,EPAS1,ASB3,EGFR,BVES,TRPM4,SLC8A2,CACNB2,ATP1A3,CELF2,SCN5A,GPD1L,HBEGF,ADRA1D,SEMA3A,ADRA2B,DOCK5,STC1,KCNJ3,TBX5,F2R,KCNE2,DSP,CASQ2,KCNIP2,CHRM3,RYR2,PKP2,KCNJ2,TGFB2,ADRA2A,MYH7,GRK2,ANK2,AGT,ACE2,ATP1A2,SLC9A1,PER2,HDAC4,SCN4B,NOS1AP,DLG1,ADRA2C,PTGER2,ECE1,GCH1,ATP1B1,SMTNL2,CD38,DES,SLC4A3,THRA,ATP1B2,HRH2,CACNA1G,ATP2A1,CALM1,TBX2,DSG2,ASIC2,SREBF1,ISL1,CYP2J2,ATP2B3,TRPV1,P2RX1,RNF207,CACNA1H,MIR21,RHOA,FGA,DMD,CHGA,TMEM65,KCNH2,SCN2B,RGS4,POPDC2,HCN4,NKX2-5,KCNMB4,HEY2,KCNG2	grey	VSMC_M10
GO:0051123	0.90	0.21	8	19	RNA polymerase II preinitiation complex assembly	BP	1	ESR1,TAF7,TAF9,CREB1,TAF6,THRA,TAF1,TAF12	grey	VSMC_M10
GO:0070252	0.90	0.15	32	70	actin-mediated cell contraction	BP	1	NEDD4L,TRPM4,CACNB2,SCN5A,SCN1A,GPD1L,PARVA,STC1,KCNJ3,TNNC1,KCNE2,DSP,RYR2,PKP2,KCNJ2,MYH7,ANK2,ATP1A2,ACTC1,SLC9A1,SCN4B,NOS1AP,DLG1,CACNA1G,ATP2A1,CCDC88C,DSG2,RNF207,KCNH2,SCN2B,KCNJ8,HCN4	grey	VSMC_M10
GO:0044272	0.90	0.14	61	127	sulfur compound biosynthetic process	BP	1	PPT2,ACSL6,MTAP,SLC35B2,SLC1A1,PPCS,CHAC2,PPT1,MGST2,SLC7A11,DLD,AKR1A1,CHPF2,ELOVL1,CSGALNACT1,PDK1,PDHX,APIP,CSAD,ELOVL7,GSS,B3GNT4,ENOPH1,ST3GAL6,CHST1,MTRR,MTR,CBSL,ACSL5,HACD2,PDK3,NFE2L2,GGT2,ACSBG1,CHST3,CHST7,AC022400.6,GGT6,MPC2,MAT1A,LIAS,TECR,CHST12,SLC26A1,GCDH,GLCE,ACACA,SLC26A2,ACSBG2,METTL16,B3GALT6,ACSF3,MLYCD,CHST5,ST3GAL2,MIR21,TPK1,ELOVL3,MTHFD2L,GGT5,CHSY3	grey	VSMC_M10
GO:1903589	0.90	0.26	4	10	positive regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	MIR21,MIR23A,MIR27B,MIR27A	grey	VSMC_M10
GO:1901863	0.90	0.23	6	15	positive regulation of muscle tissue development	BP	1	LMOD3,MEF2C,IGF2,ACTN3,CREB1,MRTFB	grey	VSMC_M10
GO:0051896	0.90	0.14	60	125	regulation of protein kinase B signaling	BP	1	PHLPP1,STK3,PPARA,LEMD2,PTK2,NTRK2,TEK,RTN4,ITGB1BP1,MET,EGFR,SESN3,PHB,SPRY2,C1QTNF1,HBEGF,BAG4,NRG1,GAS6,MFHAS1,RET,PIK3CB,PTPRJ,GCNT2,IGF2,GRM2,BANK1,TCF7L2,PDCD6,DAG1,EGF,HCLS1,GPER1,CASS4,CIB1,OSM,THPO,CD28,DLG1,ADAM8,STOX1,GDF15,PINK1,MUL1,OTUD3,HAX1,PIK3R5,INSR,INPP5K,PARK7,ENG,MIR29A,MIR199A1,MIR21,MIR222,DDIT3,TXN,MYORG,TSPYL5,RASD2	grey	VSMC_M10
GO:0090114	0.90	0.19	12	28	COPII-coated vesicle budding	BP	1	MAPK15,SEC31A,SEC31B,KLHL12,PEF1,PDCD6,SCAP,MIA3,SEC24C,TMED10,PPP6C,TBC1D20	grey	VSMC_M10
GO:0050764	0.90	0.16	27	59	regulation of phagocytosis	BP	1	LRP1,FPR2,IL15,ATG5,CD300LF,IL15RA,CNN2,NCKAP1L,GAS6,TUB,HCK,PTPRJ,DYSF,F2RL1,ANO6,NOD2,FGR,FCER1G,SLC11A1,SYT7,SYT11,DOCK2,DNM2,CCL2,C3,ABCA7,CYBA	grey	VSMC_M10
GO:0009880	0.90	0.16	21	47	embryonic pattern specification	BP	1	FRS2,SMAD5,PTCH1,MEOX2,SEMA3A,FAM208A,RIPPLY3,PGAP1,SEMA3F,SATB2,HOXD8,FZD5,MEOX1,CITED1,SMAD3,LHX1,WDR77,OOEP,WNT5A,BASP1,C2CD3	grey	VSMC_M10

GO:0044089	0.90	0.12	221	441	positive regulation of cellular component biogenesis	BP	1	VPS4B,PAN2,ARPC3,PIP4K2C,AVIL,ATAT1,ESR1,CNOT2,CNOT6,HSPA1B,IL5,BAK1,MTSS1,WASHC5,ASAP1,MAPK15,NTRK2,BAIAP2L2,PICK1,CDC42EP1,RAC2,HSF1,TEK,LINGO2,LMOD2,SRF,TTBK1,SLAIN2,KIT,NCK2,SEMA4D,KIAA1211,CHMP2A,CLDN19,PRKCE,EPS8L1,LPAR1,AKIRIN1,PLEK,LRRN3,NR1H2,ITGB1BP1,MED25,MET,FUZ,ARHGEF5,TLR4,CDK5RAP2,EPHA1,SDCBP,MAPRE1,WASF1,FAF1,RAB7A,PIP4K2A,VSTM5,SETDB2,SOX9,ERCC1,LCP1,CLASP2,RALB,MYD88,SLAIN1,WNT11,FCHSD2,NAV3,FERMT1,BAG4,FCHSD1,NRG1,NCKAP1L,ULK1,ARFIP2,LMOD3,DPYSL3,PAN3,EPHB1,NPHP1,HCK,FER,PIK3R1,CLSTN2,HIP1R,ATR,TRABD2A,CLIP1,PLCE1,SLF1,FAM20BA,FMN1,PTPRJ,P2RX7,CNOT1,CUX2,PTK2B,CNOT6L,FNIP2,SPIDR,CDH17,RAPGEF3,TBX5,AMIGO2,F2RL1,IQGAP2,CYFIP1,SLF2,PPHLN1,MAGEL2,BDNF,PXN,NEURL1,CARMIL1,HYAL1,ZMYND10,LMOD1,COL16A1,DAG1,AUTS2,AMIGO3,AJUBA,ADNP,AP1AR,AGT,WASF2,ACE2,PHLDB1,HDAC4,EPS8,EPHB3,WHAMM,CDKN1B,DLG1,CALY,CREB1,CDC42EP2,MAPT,RAP1B,TOGARAM1,PPP2R5B,DDX3X,NCKAP1,NIN,WNT4,HTT,DNM3,PINK1,MMP3,ARPC1A,WAS,STX18,ATP13A2,HAP1,LRTM2,MNS1,NLGN2,MIEN1,PLEK2,PFN3,GNL3L,SEMA4A,NLGN3,NDEL1,TENM2,SMAD3,DNM2,BCAS3,GPRASP2,BHLHB9,G3BP1,EVL,ASIC2,CDK5R1,SLITRK2,FMR1,SERPINF2,SLX4,ABCA3,MLST8,MECP2,WRAP73,PARK7,PALM,EPS8L3,DEF8,SPIRE2,AMIGO1,PSRC1,KIAA1324,PIEZO1,GPSM2,TSC1,FNBP1L,SH3GLB1,VPS4A,DAB2IP,WDR63,HAS3,ADGRL2,CARMIL2,FHOD1,RHOA,SETDB1,TRABD2B,VASP,CHGA,GRID2,EPS8L2,GMFG,THY1,CLDN1,CRBN,ZNF304,GRB2,BCL2L11,RGCC,APC,RALA,HRAS,DRG1,LRRT	grey	VSMC_M10
GO:0035728	0.90	0.22	6	15	response to hepatocyte growth factor	BP	1	GAB1,SIRT2,CREB1,MED1,ADAMTS12,CRK	grey	VSMC_M10
GO:0002200	0.90	0.15	28	61	somatic diversification of immune receptors	BP	1	TCF7,EXOSC3,MSH2,CYREN,HMCES,ERCC1,MLH1,PAXIP1,SHLD1,PRKDC,XRCC4,NBN,POLL,CD40,DCAF1,CD28,RNF168,BCL6,PMS2,FOXP3,SHLD2,TBX21,BATF,BCL11B,YY1,SUPT6H,RNF8,NHEJ1	grey	VSMC_M10
GO:1990089	0.90	0.16	21	47	response to nerve growth factor	BP	1	ARPC3,NTRK2,MICALL1,PTN,FOXO3,NTF4,WASF1,RAPGEF2,BDNF,CIB1,CBL,CREB1,MAPT,EHD1,CSTF2,CRK,TRPV1,PDPK1,LCN2,HSPA5,DYNC1LI2	grey	VSMC_M10
GO:0072111	0.90	0.21	7	17	cell proliferation involved in kidney development	BP	1	MYC,PTCH1,OSR1,IL6R,GPC3,MIR125A,PDGFD	grey	VSMC_M10
GO:0046794	0.90	0.22	6	15	transport of virus	BP	1	EPS15,KPNA3,KPNA2,TPCN1,PIKFYVE,FMR1	grey	VSMC_M10
GO:1904036	0.90	0.17	15	34	negative regulation of epithelial cell apoptotic process	BP	1	TNFAIP3,PPARA,TEK,FGF21,NDNF,GAS6,SRSF6,TERT,TCF7L2,NFE2L2,TNIP2,RAMP2,MAPK7,PDPK1,FGA	grey	VSMC_M10
GO:0099172	0.90	0.17	16	37	presynapse organization	BP	1	FZD1,VPS35,SDCBP,C5AR1,SLITRK5,FARP1,LRFN3,NLGN4Y,BSN,NLGN2,NLGN3,SNAPIN,SLITRK2,CEL,NTNG2,WNT5A	grey	VSMC_M10
GO:0006027	0.90	0.21	7	17	glycosaminoglycan catabolic process	BP	1	CEMIP2,GLB1,HYAL1,HYAL3,CEMIP,IDUA,IDS	grey	VSMC_M10
GO:0019400	0.90	0.21	7	17	alditol metabolic process	BP	1	AKR1B1,GK5,COQ2,SORD,PLA2G4A,MOGAT3,TKFC	grey	VSMC_M10
GO:0071705	0.90	0.11	835	1609	nitrogen compound transport	BP	1	TIMM21,VPS4B,ATP8B1,LRP1,STX7,AP3S1,KIF5A,PEX7,AGAP2,PEX3,CANX,TBC1D30,TBC1D9B,PPP1R10,CPSF6,RAB21,SNX24,SNX31,PHAX,ZDHHC14,SLC12A2,RIMS2,PRKN,QKI,TAP1,SLC22A4,KIF3A,TSPO,GOPC,VPS52,HSPA4,DERL1,FAM91A1,WASHC5,FAM53C,TSNARE1,LY6E,ZC3H3,EXOC4,SIL1,SYNGR1,MAPK15,MAPK14,NTRK2,TOMM22,PLA2G6,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,SMO,ZDHHC21,HSF1,TOMM6,MYH9,CHRNA3,PEX6,FBXO7,ABCB1,NOL6,XPO5,WASHC4,APBA1,PEX1,SLC35B2,VPS50,SCFD2,RFX3,SLC1A1,TGFBRAP1,TFAP2B,SLC25A13,TBC1D8,TRAM2,BICD2,CHMP2A,RAB23,SVBP,LRPPRC,SEC61B,SLC3A1,STX17,SIX2,DNAJA1,PRKCE,RIMS1,TMEM30A,SPTBN1,IGF2BP3,HMGN3,YTHDC1,PNPT1,RUFY3,CYB5R4,PPT1,SNX14,XPO1,SNX30,SLC35A1,BMP8A,AQP1,EHBP1,AFTPH,SLC1A4,PLEK,RSAD2,NR1H2,ITGB1BP1,DDC,YWHAZ,SEC61G,EGFR,FUZ,ARHGEF5,TLR4,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,TRPM4,SLC7A11,PGRMC2,LIN7B,EPS15,APOB,AGK,BCAP29,TRAF3IP2,ANKRD50,TTC26,DNAJC27,NAPA,BBS7,RAB7A,AP2S1,RAB10,COPG1,KPNA3,GIPR,ARL5B,IWS1,LCP1,SYTL2,COG1,DLG2,CUBN,RBSN,DNAJC15,PLK3,FRMD4A,OPTN,GOLGA4,LLGL2,IPO13,STEAP3,AQP11,CCDC93,RAF1,ZFAND6,SLC22A13,TBC1D4,MYO7A,SLC25A38,NAPB,GCKR,SEC14L1,SEC62,SEC22C,KPNA2,AKT2,PITRM1,LRP1B,HOOK3,ARRB1,ABCC4,TIMM50,TGFBR2,SNX5,USP36,TBC1D16,AP3M2,KIF5C,FCHSD2,RINL,ATG16L2,SLC38A10,NPLOC4,ARL5A,SYT1,UBAC2,RAB5A,LIN7A,APBB3,ASPSCR1,TMCO6,NUP98,DPH3,SIRT7,FERMT1,CHTOP,SLC6A15,HACL1,SLC25A15,HEATR5B,CEP290,PRNP,ING1,BAG4,TAF7,MAVS,AP5S1,DNAJC13,AIMP1,FUT1	grey	VSMC_M10
GO:0042339	0.90	0.22	6	15	keratan sulfate metabolic process	BP	1	GLB1,B3GNT4,ST3GAL6,CHST1,CHST5,ST3GAL2	grey	VSMC_M10
GO:0016202	0.90	0.18	12	28	regulation of striated muscle tissue development	BP	1	SIRT2,LMOD3,MEF2C,IGF2,USP19,ACTN3,YBX3,CREB1,SOX15,SMAD3,MRTFB,JPH2	grey	VSMC_M10
GO:0021915	0.90	0.13	62	130	neural tube development	BP	1	STK3,FZD6,BRD2,TBC1D32,PTCH1,SMO,PTK7,SEMA4C,FUZ,TEAD2,INTU,BMI1,GLI2,IFT172,OVOL2,SPINT2,TRAF6,CASP3,FZD3,OPA1,IFT52,SPINT1,RPGRIP1L,PKD2,STK4,PAX2,PRICKLE1,SUFU,TGFB2,ITPK1,GBX2,DVL3,CHRD,GRHL3,LUZP1,SETD2,PLOD3,FKBP8,GORAB,GPR161,TULP3,LIAS,DVL2,WDR19,ALDH1A2,PSEN1,TMEM107,MKS1,GSC,MIB1,SKI,PKD1,TSC1,GLMN,BCL10,VASP,SOX4,NOG,WNT5A,C2CD3,PHGDH,RALA	grey	VSMC_M10
GO:1903321	0.90	0.14	39	82	negative regulation of protein modification by small protein conjugation or removal	BP	1	TNFAIP3,HSPA1B,TSPO,CRY1,SVBP,DNAJA1,PRKCE,ATG5,SPOPL,SPRY2,KLHL40,ARRB1,SIRT7,USP44,SH3RF2,TRIM44,MARCH7,PRMT3,RPL23,PIAS3,DTX3L,PER2,RPL11,SENP2,IVNS1ABP,GPS2,GNL3L,PSEN1,TAF1,OGT,OTUB2,DCUN1D3,PARK7,GLMN,SOX4,BAG2,CAMLG,PRR7,RASD2	grey	VSMC_M10
GO:0032613	0.90	0.18	14	32	interleukin-10 production	BP	1	AGER,TNFRSF21,TLR4,PIBF1,F2RL1,NOD2,CD28,VSIR,STAT3,FOXP3,PRKCZ,CD46,INAVA,TSLP	grey	VSMC_M10
GO:0032653	0.90	0.18	14	32	regulation of interleukin-10 production	BP	1	AGER,TNFRSF21,TLR4,PIBF1,F2RL1,NOD2,CD28,VSIR,STAT3,FOXP3,PRKCZ,CD46,INAVA,TSLP	grey	VSMC_M10
GO:2000106	0.90	0.15	27	59	regulation of leukocyte apoptotic process	BP	1	CDKN2A,SLC46A2,SLC7A11,IDO1,GAS6,FOXP1,IRF7,ZC3H8,PIK3CB,MEF2C,RAPGEF2,NOD2,GPAM,HCLS1,PDCD1,ADAM8,BCL6,CXCR2,EFNA1,BTK,CD74,CCL5,IL7R,BCL10,FADD,WNT5A,TSC22D3	grey	VSMC_M10

GO:0120031	0.90	0.12	218	435	plasma membrane bounded cell projection assembly	BP	1	ATP8B1,ONECUT2,MYO1A,AVIL,TBC1D30,ATAT1,KIF3A,TBC1D32,UBE2B,MTSS1,ASAP1,LRRC6,MAPK15,PODXL,CDC42EP1,RAC2,IFT74,SRF,CFAP69,RFX3,KIT,NCK2,PTPDC1,FGD3,RAB23,DYNC2LI1,EPS8L1,CEP162,TMEM17,AKIRIN1,WDR92,FUZ,IQUB,ATG5,SDCBP,ARMC2,MAPRE1,ARMC4,INTU,SPATA6,TTC26,BBS7,VSTM5,ARHGEF4,DRC1,RSPH6A,GALNT11,FBF1,PIBF1,KLF5,IFT172,FOXJ1,WDR60,TTLL3,CCDC13,ABCC4,MKKS,RAB5A,CEP290,BAG4,ARHGEF7,SPEF1,FGD6,ARFIP2,TMEM80,DPYSL3,AL359736.1,KIF3B,FER,RILPL1,RILPL2,CEP70,PIK3R1,PARVA,PLCE1,CEP250,CCDC66,P2RX7,TCTN3,IFT81,CCDC113,CFAP20,ARHGEF26,RAPGEF2,CCDC65,TMEM67,BIN3,F2RL1,IFT52,ARHGAP24,ANO6,RPGRIP1L,DNAH1,CYFIP1,DMTN,DNAH5,ZNF423,GBF1,SRGAP2C,NEURL1,CARMIL1,CFAP43,FGD4,ZMYND10,GAP43,ARMC9,CFAP46,TTBK2,AUTS2,AJUBA,CLCN4,ALPK1,JHY,DISC1,OFD1,WASF2,RAB17,TMEM237,TRAF3IP1,HDAC4,BBS1,LAMA5,EPS8,PTPRO,CDKL5,SEPT2,LIMK2,WHAMM,CDC42EP2,CFAP161,TTC12,TOGARAM1,EHD1,DNAAF2,SPAG16,NCKAP1,ABLIM2,FAM149B1,HTT,CFAP70,DNM3,RAP1GAP,STK36,GORAB,CEP126,SNAP29,EXOC5,VCL,WAS,TTC25,RAB8A,SDCCAG8,HAP1,DNAAF4,CPLANE2,MNS1,WDR19,TMEM138,MIEN1,ATP6V1D,PLEK2,FGD1,FXR2,BBOF1,CNTROB,TMEM107,NDEL1,TENM2,AC138894.1,CCDC151,NTN1,DYNLL2,MKS1,DNM2,BCAS3,ARHGAP44,EVL,TEKT3,IFT20,SPEF2,STK26,CFAP53,ARHGEF6,FMR1,INPP5K,C16orf71,RILP,CLUAP1,WRAP73,PALM,TPGS1,EPS8L3,DEF8,CDK10,CELSR2,VAV3,CDC14A,TMEM231,FNBP1L,MTSS1L,HYDIN,ODF2L,WDR63,CARMIL2,C5orf30,TCTN2,EPS8L2,HYLS1,SNX10,C2CD3,CSPG4,CC2	grey	VSMC_M10
GO:0035850	0.90	0.16	18	41	epithelial cell differentiation involved in kidney development	BP	1	MTSS1,PODXL,SMO,SIX2,OSR1,FOXJ1,JAG1,ASXL1,PAX8,MEF2C,PAX2,SALL1,PRKX,PTPRO,CITED1,LHX1,BASP1,LIF	grey	VSMC_M10
GO:0033189	0.90	0.23	5	13	response to vitamin A	BP	1	CAT,DNMT3A,DNMT3B,ALDH1A2,LRAT	grey	VSMC_M10
GO:0006644	0.90	0.12	157	314	phospholipid metabolic process	BP	1	PIP4K2C,ABHD16A,SYNJ2,SERAC1,AGPAT4,AGPAT1,PNPLA3,PLA2G6,GPAA1,CWH43,SRD5A3,INPP4A,PLPPR1,TMEM246,TMEM86B,PIGF,MBOAT7,PLEK,NR1H2,MBOAT2,LPIN1,INPP4B,SMPD2,FIG4,SPHK2,MTMR2,PIP4K2A,NAPEPLD,HADHA,SELENOI,ABHD5,APOC1,TAMM41,ITPKC,PIP4P1,MTMR14,PLCB1,PGAP2,CRLS1,CDS2,PLPP5,NR1H4,MTMR7,ABHD6,PIGU,PIK3CB,PITPNM2,PIK3R1,TMEM150A,CHRM5,MTMR9,SLA2,NR1H3,SERINC5,SYNJ1,CDS1,FITM2,ITPKA,PIGT,PLA2G4B,GPLD1,LPCAT1,PGAP1,GPAM,CHKA,PLA1A,ACP6,INPP5A,ABHD4,SGMS2,AJUBA,GGPS1,PITPNM1,MTMR11,GNPAT,DGKD,PIGM,FITM1,BMX,FAM126B,IP6K2,LPGAT1,PIGV,DPAGT1,PLPP4,MTMR3,THEM5,PCYT1A,INPP5J,PIGX,PLBD1,PIGZ,PISD,DGKG,PIKFYVE,PLA2G4A,SACM1L,LPCAT3,ABHD12B,GNB3,PIGC,PLCD4,SMPD4,SOCS4,PLA2G16,PI4KA,SLC27A1,ABHD8,SGMS1,CLN8,PGAP3,PIGH,PI4K2B,LIPC,SOCS7,DGKQ,GDPD3,AC138894.1,DGKE,PLPPR2,TTC7B,LDLR,GDPD1,PIGL,GDE1,CSF1R,GATA6,ABHD3,PNPLA6,PROCA1,MPPE1,IMPA2,MTMR12,SOCS1,MTM1,MTMR1,INPP5K,PIP5K1C,ABCA3,MECP2,AGPAT2,PIP5KL1,PLA2G15,FABP5,ABCA8,DHDDS,PEMT,PLA2G2C,PYURF,LCLAT1,PIGB,PIGA,INPP1,SGPP1,PTPMT1,DNAJC19,CDIPT	grey	VSMC_M10
GO:0009410	0.90	0.12	157	314	response to xenobiotic stimulus	BP	1	NME1,FECH,TNFRSF11B,TSPO,UBE2B,BAK1,MYC,PTCH1,SOX10,TXN2,PLIN2,ABCB1,FZD1,CA9,TFAP2B,PPAT,ABCG5,CAT,ABCG8,XPO1,TGFA,PTN,DDC,EGFR,ATG5,FOXO3,FGF21,TRAF3IP2,HDAC2,DNMT3A,SLC26A5,HADHA,GAD2,NUDT15,XPC,XRCC1,TIMP4,ARRB1,ABCC4,TGFBR2,RPTOR,PRNP,DUSP6,NCKAP1L,GAS6,RET,DNMT3B,PARP4,GSS,CASP3,ATR,FZD3,MEF2C,VEGFC,CYP2R1,PTK2B,KCNJ11,RPN2,NKX6-1,RAD54B,BPHL,PMS1,SLC6A2,ABCC2,KCNE2,CBR3,SLC12A5,CMBL,GRM2,TPMT,GPLD1,SRD5A1,SLC6A3,HDAC1,LCK,CPT1A,MAP2K6,TGFB2,FMO5,DAD1,CYP2U1,AMELX,SLAMF8,GNPAT,CHEK2,ABCB11,DVL3,ACTC1,HDAC4,CDKN1B,MGMT,APOD,POR,NFE2L2,CREB1,SORD,RAP1B,CPS1,COMT,XRCC5,BCHE,STAT3,CD38,PMS2,ENO3,SCGB1A1,EPHX1,ITGA3,PGF,FOS,SCNN1B,UQCRC2,PDE4A,CYP46A1,NPC1,GATA6,ADSSL1,SREBF1,OXCT1,NOS2,CYP2J2,JUN,MBD1,DAB1,ABAT,RPH3AL,LRP8,ABCA3,AGPAT2,CYBA,ASS1,VAV3,LCN2,ENG,ABCD3,HSPA5,DHODH,NQO1,HSD11B2,CRYZ,MT-ND1,MT-CYB,RHOA,S100A12,KCNK3,SULT1C3,BLOC1S3,AHRR,KCNH2,BGLAP,PEMT,NCEH1,TIGAR,CRH,NNMT,AOC2,N6AMT1	grey	VSMC_M10
GO:0051282	0.90	0.14	39	84	regulation of sequestering of calcium ion	BP	1	PRKCE,IBTK,ATG5,RYR1,DIAPH1,RASA3,RYR3,PTK2B,TPCN1,SLC8B1,F2R,PKD2,CASQ2,RYR2,LCK,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,CD19,CALM1,BDKRB1,SLC25A23,TRPV1,PDPK1,CYBA,JPH3,MCOLN3,DMD,NOL3,JPH2,THY1,DDIT3	grey	VSMC_M10
GO:0033598	0.90	0.19	10	24	mammary gland epithelial cell proliferation	BP	1	ESR1,RTN4,AREG,ROBO1,RREB1,CCND1,MAPK1,MED1,WNT5A,CEBPB	grey	VSMC_M10
GO:0051209	0.90	0.14	38	82	release of sequestered calcium ion into cytosol	BP	1	PRKCE,IBTK,ATG5,RYR1,DIAPH1,RASA3,RYR3,PTK2B,TPCN1,SLC8B1,F2R,PKD2,CASQ2,RYR2,LCK,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,CD19,CALM1,BDKRB1,TRPV1,PDPK1,CYBA,JPH3,MCOLN3,DMD,NOL3,JPH2,THY1,DDIT3	grey	VSMC_M10
GO:0030540	0.90	0.22	6	15	female genitalia development	BP	1	ESR1,BAK1,SRD5A1,LHX1,STRA6,WNT5A	grey	VSMC_M10

GO:2000027	0.90	0.14	51	108	regulation of animal organ morphogenesis	BP	1	FRS2,FZD6,TNFRSF11B,RSPO3,SMO,PTK7,ROR2,SIX2,SPRY1,SOX9,WNT11,SPEF1,RYK,PAX8,ROBO1,ROBO2,FZD3,TIAM1,PAX2,VANGL1,PRICKLE1,NKD1,JHY,ZNRF3,AGT,DVL3,FZD7,GRHL3,STOX1,WNT4,DAAM1,ARHGEF19,MAGED1,DVL2,BMPR1A,SP6,NGFR,MKS1,BTBD7,LHX1,GPC3,SAPCD2,SOX8,CELSR2,RHOA,NOG,WNT5A,SIX1,CELSR3,FGF1,WNT2	grey	VSMC_M10
GO:0006450	0.90	0.21	7	17	regulation of translational fidelity	BP	1	LARS,GATC,TARS2,LARS2,AARS,DTD1,DTD2	grey	VSMC_M10
GO:0006266	0.90	0.22	6	15	DNA ligation	BP	1	XRCC6,XRCC1,XRCC4,MGMT,LIG3,NHEJ1	grey	VSMC_M10
GO:0043486	0.90	0.21	7	17	histone exchange	BP	1	ACTR6,SPTY2D1,VPS72,CHD5,SYCP3,ITGB3BP,RNF8	grey	VSMC_M10
GO:1904407	0.90	0.18	12	28	positive regulation of nitric oxide metabolic process	BP	1	TLR4,PTK2B,PKD2,AGT,NOS1AP,SMAD3,DNM2,INSR,TICAM1,TRPV1,ASS1,MIR99B	grey	VSMC_M10
GO:1905907	0.90	0.25	4	10	negative regulation of amyloid fibril formation	BP	1	PFDN5,PFDN4,LDLR,VBP1	grey	VSMC_M10
GO:0060099	0.90	0.23	5	13	regulation of phagocytosis, engulfment	BP	1	NCKAP1L,F2RL1,ANO6,C3,ABCA7	grey	VSMC_M10
GO:0090200	0.90	0.20	9	21	positive regulation of release of cytochrome c from mitochondria	BP	1	BAK1,PLA2G6,DNM1L,GPER1,CIDEB,PINK1,MLLT11,BCL2L11,PPIF	grey	VSMC_M10
GO:0031281	0.90	0.23	5	13	positive regulation of cyclase activity	BP	1	MAPK14,GUCA1B,ORAI1,MAPK3,NOS2	grey	VSMC_M10
GO:0060749	0.90	0.22	6	15	mammary gland alveolus development	BP	1	ESR1,AREG,TGFA,CCND1,EGF,FOXF1	grey	VSMC_M10
GO:0061377	0.90	0.22	6	15	mammary gland lobule development	BP	1	ESR1,AREG,TGFA,CCND1,EGF,FOXF1	grey	VSMC_M10
GO:0043547	0.90	0.12	98	202	positive regulation of GTPase activity	BP	1	TBC1D30,TBC1D9B,TIAM2,ASAP1,TBC1D22B,SEMA4D,TBC1D8,RGP1,ASAP2,ARHGEF5,EPHA1,TBC1D9,IQSEC1,RSU1,TBC1D4,FOXJ1,WNT11,AKT2,TBC1D16,ARHGEF7,LARS,TBC1D12,ARHGEF26,PTK2B,RASGRP1,RAPGEF2,CCL17,TIAM1,RAPGEF3,F2RL1,F2R,ARHGAP24,CD40,RAP1GDS1,DOCK10,RGS1,TBCK,ADPRH,ADAP1,DENND1B,ARHGAP6,TBC1D10C,RAB11FIP2,DVL3,CDKL5,GRHL3,TBC1D2B,GMIP,RASGRP2,TBC1D14,RABGAP1L,RUNDC1,WNT4,ELMOD1,RAP1GAP,TBC1D25,GNB5,EPHA4,ARHGEF19,DVL2,SYDE1,TBC1D1,ARAP2,RGS14,TBC1D10B,NDEL1,MYO9A,BCAS3,TBC1D8B,CCL14,CCL5,CCL7,CCL2,CCL25,ADAP2,VAV1,RALBP1,DOCK7,ABR,CRK,RAP1GAP2,TAX1BP3,ARHGEF16,APC2,ARHGAP45,TSC1,MTSS1L,DENND1A,RABGAP1,CCL16,ASAP3,THY1,WNT5A,CHN1,RGS4,TBC1D20,HRAS,CCL22	grey	VSMC_M10
GO:0060191	0.90	0.15	29	63	regulation of lipase activity	BP	1	LRP1,ESR1,KIT,LPAR1,PPT1,NR1H2,EGFR,C5AR1,PHB,ABHD5,APOC1,RASGRP4,FLT1,NR1H3,PLA2R1,GNA13,ARHGAP6,AGT,POR,ABL2,FGFR3,ANXA8,NMUR2,CCL5,GNA15,PDPK1,PRKCZ,RHOA,HRAS	grey	VSMC_M10
GO:0010718	0.90	0.16	20	45	positive regulation of epithelial to mesenchymal transition	BP	1	SDCBP,HDAC2,TGFBR2,JAG1,ALX1,TIAM1,LOXL2,GCNT2,TGFB2,TCF7L2,AXIN2,SNAI1,TGFB1I1,SMAD3,ISL1,ENG,MIR21,MIR222,RGCC,OLFM1	grey	VSMC_M10
GO:1903428	0.90	0.21	7	17	positive regulation of reactive oxygen species biosynthetic process	BP	1	TLR4,FOXO3,HDAC4,PARK7,CYBA,LCN2,MIR24-1	grey	VSMC_M10
GO:0090083	0.90	0.22	6	15	regulation of inclusion body assembly	BP	1	SNCAIP,HSPA1B,HSF1,SORL1,DNAJB2,DNAJB1	grey	VSMC_M10
GO:2000095	0.90	0.22	6	15	regulation of Wnt signaling pathway, planar cell polarity pathway	BP	1	RSPO3,SPEF1,NKD1,ZNRF3,MKS1,GPC3	grey	VSMC_M10
GO:0061082	0.90	0.19	10	24	myeloid leukocyte cytokine production	BP	1	KIT,TLR4,MAVS,TGFB2,BCL6,SPON2,CD74,TICAM1,BCL10,WNT5A	grey	VSMC_M10
GO:0046068	0.90	0.23	5	13	cGMP metabolic process	BP	1	PDE10A,GUCY1A1,GUCY1B1,PDE9A,GUCY2D	grey	VSMC_M10
GO:0051147	0.90	0.13	55	115	regulation of muscle cell differentiation	BP	1	NFATC1,MAML1,FRS2,PPARA,MAPK14,PI16,SRF,KIT,ANKRD17,TRIM32,MYLK3,MAMSTR,NRG1,LMOD3,SMYD1,NLN,MEF2C,SOX6,ZBED6,RBM24,IGF2,BDNF,SIK1,PDCD4,GPER1,FZD7,ACTN3,HDAC4,EFEMP2,BHLHA15,BMPR1A,FOXO4,RBPMS2,SETD3,YY1,FBXO22,SUPT6H,MECP2,PIEZO1,PLPP7,ENG,NFATC3,MIR199A1,MIR21,MIR222,MIR125B1,MIR22,PRDM6,RGS4,TCF23,YBX1,EREG,NKX2-5,RBM38,HEY2	grey	VSMC_M10
GO:1903651	0.90	0.23	5	13	positive regulation of cytoplasmic transport	BP	1	RAB21,PRKN,MTMR2,SORL1,TRIM46	grey	VSMC_M10
GO:0043628	0.90	0.17	16	36	ncRNA 3'-end processing	BP	1	EXOSC4,EXOSC3,TRNT1,USB1,INTS8,TENT4B,INTS12,INTS5,AP002990.1,HSD17B10,INTS2,ERI2,PARN,POLR3K,TRMT10C,EXOSC5	grey	VSMC_M10
GO:0031424	0.90	0.23	5	13	keratinization	BP	1	EVPL,PPHLN1,TGM1,SFN,ABCA12	grey	VSMC_M10
GO:0048026	0.90	0.21	7	17	positive regulation of mRNA splicing, via spliceosome	BP	1	SNW1,TRA2A,NUP98,HSPA8,CELF3,PRPF19,CIRBP	grey	VSMC_M10
GO:2000179	0.90	0.16	17	39	positive regulation of neural precursor cell proliferation	BP	1	GLI1,SOX10,SMO,GLI2,TOX,FZD3,VEGFC,ZNF335,ZNF423,EGF,DISC1,FZD9,LHX1,ADGRG1,FOXG1,GPR37L1,PITX3	grey	VSMC_M10
GO:0007183	0.90	0.23	5	13	SMAD protein complex assembly	BP	1	EID2,PPM1A,PARP1,SMAD3,LDLRAD4	grey	VSMC_M10
GO:0003231	0.90	0.13	47	101	cardiac ventricle development	BP	1	FRS2,LY6E,FOXH1,PTK7,TNNI3,HOXA13,CNTRL,SCN5A,POU4F1,WNT11,TGFBR2,JAG1,NRG1,PAX8,HAND2,ROBO1,ROBO2,MEF2C,TBX5,TNNC1,DSP,SALL1,RYR2,SUFU,PKP2,TNNI1,TGFB2,TRIP11,MYH7,KCNK2,LUZP1,SAV1,BMPR1A,RBPJ,MED1,DCTN5,STRA6,AP2B1,ISL1,FOXF1,ENG,SOX4,TMEM65,NOG,WNT5A,NKX2-5,HEY2	grey	VSMC_M10
GO:0051044	0.90	0.23	5	13	positive regulation of membrane protein ectodomain proteolysis	BP	1	SH3D19,GPLD1,ADRA2A,ADAM8,TNFRSF1B	grey	VSMC_M10
GO:0009167	0.90	0.16	16	36	purine ribonucleoside monophosphate metabolic process	BP	1	IMPDH1,GDA,PPAT,NT5E,DLG2,AMPD3,GMPS,AMPD1,MAGI3,DLG1,CASK,ADK,CARD11,ADSSL1,MPP1,NUDT2	grey	VSMC_M10
GO:0040014	0.91	0.15	21	47	regulation of multicellular organism growth	BP	1	PTCH1,SMO,MKKS,PLS1,HTRA2,CELF1,FTO,IGF2,SLC6A3,GPAM,CREB1,GDF15,STAT3,STAT5B,RAI1,GHR,GAMT,DIO3,POU3F2,FXN,PLAC8	grey	VSMC_M10
GO:0030512	0.91	0.14	29	64	negative regulation of transforming growth factor beta receptor signaling pathway	BP	1	ONECUT2,PPARA,CD109,SPRY1,SPRY2,EID2,SPRED3,SNX25,IL17RD,VEPH1,SLC2A10,HTRA1,SNX6,PBLD,HTRA3,FBN1,PPM1A,TGFB1I1,WFIKKN2,DNM2,PDPK1,SKI,PRDM16,WFIKKN1,HSPA5,LEMD3,NRROS,LDLRAD4,PEG10	grey	VSMC_M10
GO:0038093	0.91	0.16	17	39	Fc receptor signaling pathway	BP	1	PTK2,PLA2G6,KIT,PRKCE,IKBKB,TRAF6,HCK,FER,PTPRJ,FGR,PLPP4,FCER1G,BTK,YES1,VAV1,VAV3,MAP2K7	grey	VSMC_M10
GO:2000052	0.91	0.21	6	15	positive regulation of non-canonical Wnt signaling pathway	BP	1	RSPO3,CSNK1E,NKD1,GPC3,WNT5A,LBX2	grey	VSMC_M10

GO:0051051	0.91	0.12	157	314	negative regulation of transport	BP	1	VPS4B,ERBB3,NEDD4L,PRKN,GOPC,CRY1,WNK2,RAB23,ABCG5,ABCG8,IL11,PRKCE,BMP8A,RSAD2,NR1H2,ITGB1BP1,GRB10,HECW1,TCAF2,SFRP4,KEL,VPS35,ATG5,SDCBP,OSR1,MTMR2,RAB7A,SLC26A5,KCNRG,CD300LF,APOC1,FRMD4A,OXSR1,TBC1D4,AKT2,NEU3,UBAC2,DPH3,FERMT1,CNN2,BAG4,NRG1,NCKAP1L,ARL6IP5,ADRA2B,LYPLA1,NDUFAF2,FAM3D,PXK,ANKRD27,SLC43A1,ASIC1,PKIA,TMBIM6,WDR54,P2RY1,PTK2B,KCNJ11,NR1H3,RAB11FIP5,DYSF,STC1,ACVR1C,F2R,CRY2,KCNE2,PKD2,PLA2R1,CYFIP1,DMTN,CASQ2,ADTRP,SUFU,SIRT4,IRS1,CABP1,CD200,HDAC1,ANKRD13A,PPP3CA,HECW2,SP100,ADRA2A,ISCU,KCNB1,YOD1,EGF,ANKRD13D,ATP1A2,BAG3,C4orf3,OSM,PEA15,NTSR1,RUBCN,CNIH2,SH3GL3,APOD,KLF7,CTTNBP2NL,RAP1B,FIS1,DERL3,SESTD1,IL12A,COMT,ENY2,C11orf65,ADRA2C,LRPAP1,PNKD,INHA,GNB5,DLG4,RSC1A1,TNFRSF1B,WNK3,STX1B,SYT11,SNX12,CALM1,SYTL4,PRKCB,SCAMP5,CD74,SREBF1,UNC119,ABAT,FMR1,GABRE,INPP5K,OAZ1,ABCA7,PARK7,FOXF1,WWP2,RRAD,MIR199A1,MIR27B,MIR24-1,MIR27A,GPR35,FABP5,CHGA,KCNH2,MIR33B,CRBN,RGS4,CRH,TXN,LIF,VAMP3,UBE2G2,GEM,PPIF,DERL2,LRRTM2	grey	VSMC_M10
GO:0001894	0.91	0.12	92	189	tissue homeostasis	BP	1	TNFAIP3,SLC12A2,TNFRSF11B,AKR1B1,RAC2,SMO,ALDH1A1,SRF,CLDN12,SLC1A1,KIAA1211,PRDX1,EPAS1,HOXA13,ALB,MTF1,WHRN,EGFR,USP45,TRIM32,TLR4,NCDN,SOX9,CUBN,USH1G,MKKS,ACTG1,RAC3,ERCC6,TRAF6,TUB,LSR,CCDC66,ADGRV1,IL7,P2RX7,JAM2,PTK2B,USH1C,HOMER1,F2R,SPP1,GCNT2,NOD2,ITGB6,LDB1,LPCAT1,LRRK1,TCIRG1,GPR137B,KRAS,GIGYF2,UBASH3B,BBS1,HOMER2,LAMC1,ADAM8,PTH1R,PBLD,CTSH,CDH23,ABCA12,GPR137,VCL,CD38,ILDR2,LIPA,ACTB,CLN8,WNK3,ATP1B2,ESRRB,RAB3D,MKS1,ACACA,CSF1R,PPARGC1B,ABCA3,ATP6AP1,DEF8,OAS1,DMD,SLC22A5,CA2,NANOS1,JCHAIN,BGLAP,SNX10,CLDN1,INAVA,DRAM2,BBS10	grey	VSMC_M10
GO:0009187	0.91	0.17	14	33	cyclic nucleotide metabolic process	BP	1	PDE7B,PDE10A,ADCY3,GUCY1A1,GUCY1B1,ADCY7,ADCY2,PDE9A,PTHLH,ADCY4,PDE8A,ADCY10,GUCY2D,PDE4A	grey	VSMC_M10
GO:0046827	0.91	0.21	6	15	positive regulation of protein export from nucleus	BP	1	GAS6,RAPGEF3,TCF7L2,BAG3,SFN,CTDSPL2	grey	VSMC_M10
GO:0010771	0.91	0.22	5	13	negative regulation of cell morphogenesis involved in differentiation	BP	1	FBLN1,ITGB1BP1,DMTN,AP1AR,MELTF	grey	VSMC_M10
GO:1900025	0.91	0.22	5	13	negative regulation of substrate adhesion-dependent cell spreading	BP	1	FBLN1,ITGB1BP1,DMTN,AP1AR,MELTF	grey	VSMC_M10
GO:0060765	0.91	0.18	10	24	regulation of androgen receptor signaling pathway	BP	1	KDM4C,FOXH1,PHB,RNF14,FOXP1,HDAC1,PIAS2,NCOR1,PARK7,TRIM68	grey	VSMC_M10
GO:1900102	0.91	0.21	6	15	negative regulation of endoplasmic reticulum unfolded protein response	BP	1	NCK2,DDRGK1,ABCA7,HSPA5,MIR199A1,PPP1R15A	grey	VSMC_M10
GO:0099560	0.91	0.19	8	20	synaptic membrane adhesion	BP	1	MAPK14,LRRC4,PCDH8,PTPRF,LRFN3,SPARCL1,SLITRK2,NTNG2	grey	VSMC_M10
GO:0060628	0.91	0.22	5	13	regulation of ER to Golgi vesicle-mediated transport	BP	1	MAPK15,PGAP1,SORL1,STX18,TBC1D20	grey	VSMC_M10
GO:0051101	0.91	0.13	43	91	regulation of DNA binding	BP	1	NME1,PRKN,AGER,HABP4,C6orf106,SMO,MDFI,ZNF462,HDAC2,ERCC2,RSF1,POU4F1,SIRT2,DDRGK1,TAF10,TRAF6,HAND2,FBXW7,SP100,EGF,PER2,PARP1,NSD1,MSX2,PSEN1,TAF1,WFIKKN2,CALM1,SIN3A,ISL1,ERCC4,JUN,ZBTB7C,SKI,DOT1L,WFIKKN1,PARK7,LAMTOR5,DDIT3,TXN,ZNF593,LIF,HEY2	grey	VSMC_M10
GO:0038084	0.91	0.16	18	41	vascular endothelial growth factor signaling pathway	BP	1	SEMA6A,PTP4A3,ADAMTS3,TSPAN12,GAB1,PRKD2,SPRY2,DCN,FLT1,PIK3CB,ROBO1,VEGFC,IL12A,PGF,DAB2IP,MIR199A1,MIR21,CADM4	grey	VSMC_M10
GO:0002371	0.91	0.22	5	13	dendritic cell cytokine production	BP	1	KIT,TLR4,MAVS,NOD2,TICAM1	grey	VSMC_M10
GO:0035025	0.91	0.19	9	22	positive regulation of Rho protein signal transduction	BP	1	GPR20,LPAR1,ARRB1,ROBO1,F2RL1,F2R,COL3A1,GPR35,ADGRG1	grey	VSMC_M10
GO:0090231	0.91	0.21	6	15	regulation of spindle checkpoint	BP	1	CDK5RAP2,DYNC1LI1,ANAPC15,USP44,LCMT1,DUSP1	grey	VSMC_M10
GO:0090266	0.91	0.21	6	15	regulation of mitotic cell cycle spindle assembly checkpoint	BP	1	CDK5RAP2,DYNC1LI1,ANAPC15,USP44,LCMT1,DUSP1	grey	VSMC_M10
GO:1903504	0.91	0.21	6	15	regulation of mitotic spindle checkpoint	BP	1	CDK5RAP2,DYNC1LI1,ANAPC15,USP44,LCMT1,DUSP1	grey	VSMC_M10
GO:0006402	0.91	0.12	98	201	mRNA catabolic process	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,HSPA1B,SKIV2L,DXO,EIF3E,PNLDC1,CSDC2,AGO2,TNRC6B,TUT7,GTPBP1,MAPK14,EXOSC4,CNOT11,EXOSC3,PNPT1,AGO1,TUT4,PUM2,TRAF3IP2,MTPAP,ZC3HAV1,DHX34,FASTK,MLH1,MYD88,TNRC6C,LSM1,NUDT16,PKP3,UPF3A,PAN3,NUDT12,TTC37,CNOT1,CELF1,CNOT6L,TENT2,FTO,TENT5C,TENT4B,RBM24,DIS3L2,AXIN2,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,NCBP2,EIF4ENIF1,YBX3,SUPV3L1,RC3H1,UPF1,SLC11A1,RBM10,SAMD4A,POLR2G,SCGB1A1,NT5C3B,DCP1B,CASC3,FXR2,TARDBP,SMG5,TOB1,TENT5D,TNRC6A,CNOT8,LARP1,SLFN14,ALKBH5,UPF3B,PARN,FMR1,METTL16,PLEKHN1,LSM7,CIRBP,TRAF2,EDC4,AGO4,METTL14,NANOS1,CACNG7,YBX1,ZFP36L2,TENT5A,MAGOHB,RC3H2,EXOSC5	grey	VSMC_M10
GO:1904035	0.91	0.14	30	65	regulation of epithelial cell apoptotic process	BP	1	TNFAIP3,PPARA,TEK,SFRP4,FOXO3,FGF21,NDNF,GAS6,SRSF6,ANO6,PLA2R1,CD40,HDAC1,TERT,PDCD4,TCF7L2,GPER1,NFE2L2,ITGA4,TNIP2,RAMP2,MAPK7,CCL2,PIAS4,PDPK1,MIR24-1,FGA,MIR125A,CD248,RGCC	grey	VSMC_M10
GO:0032735	0.91	0.18	11	26	positive regulation of interleukin-12 production	BP	1	AGER,MAPK14,IRF5,TLR4,PLCB1,TRAF6,RIPK2,NOD2,CD40,IL16,ISL1	grey	VSMC_M10
GO:0006939	0.91	0.14	39	84	smooth muscle contraction	BP	1	PLA2G6,ZDHHC21,CHRNA3,SRF,KIT,TNNI3,MKKS,P2RX2,ADRA2B,HTR7,P2RX3,PLCE1,GUCY1A1,DOCK5,F2R,CHRM3,RAP1GDS1,ADRA2A,SULF2,GPER1,AGT,ATP1A2,DLG1,ADRA2C,CALCRL,CD38,KCNMA1,CHRNB2,SCNN1B,TBX2,NMUR2,SETD3,MYH11,ABAT,TRPV1,P2RX1,MIR21,RHOA,HTR1D	grey	VSMC_M10

GO:0070723	0.91	0.19	9	22	response to cholesterol	BP	1	PTCH1,SMO,TGFBR2,CYP7A1,GPLD1,DAG1,GRAMD1B,OSBPL7,LRP8	grey	VSMC_M10
GO:1900027	0.91	0.18	11	26	regulation of ruffle assembly	BP	1	EPS8L1,ARHGAP24,CYFIP1,EPS8,NDEL1,EVL,EPS8L3,DEF8,CARMIL2,EPS8L2,HRAS	grey	VSMC_M10
GO:0051249	0.91	0.11	143	287	regulation of lymphocyte activation	BP	1	TNFAIP3,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,XRCC6,RAC2,FBXO7,TNFRSF21,NCK2,EXOSC3,MSH2,SLC46A2,PELI1,IL4I1,TLR4,IL15,HMCES,BMI1,CLPTM1,MLH1,GLI2,MYD88,PIBF1,FOXJ1,PAXIP1,IL15RA,TGFBR2,PAWR,SHLD1,PRNP,NCKAP1L,GAS6,PRKDC,SLC7A1,TRAF6,SOX12,TOX,ZC3H8,IL1A,CAMK4,CASP3,MEF2C,TMEM131L,IL7,PAG1,RASGRP1,RIPK2,AP3B1,MARCH7,SOX13,NOD2,ZNF335,CD40,IGF2,LCK,BANK1,ICOSLG,BTN2A2,GPAM,PRKAR1A,HLX,TBC1D10C,SLAMF8,THEMIS2,FGR,CD28,RUNX3,DLG1,PPP2R3C,ADAM8,DUSP10,BLOC1S6,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,TNIP2,CD38,BST1,STAT5B,INHA,SCGB1A1,FOXP3,RASAL3,ZBTB1,SHLD2,CARD11,TNFRSF1B,TBX21,ZBTB7B,CHRNB2,CD19,LAT,IL4R,BTK,CD74,CCL5,CCL2,YES1,NKAP,CD320,VAV1,TWSG1,IL7R,SUPT6H,PTPN2,SOCS1,DROSHA,TICAM1,DNAJA3,PRKCZ,VAV3,GLMN,AP1G1,BCL10,MIR21,MIR27A,RHOA,LST1,BLOC1S3,SOX4,FADD,DPP4,CD46,THY1,FGL2,CD70,TNFSF9,ZFP36L2,LAX1,EFNB3,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0051973	0.91	0.17	13	30	positive regulation of telomerase activity	BP	1	MAP3K4,MYC,MAPK15,POT1,HMBOX1,MAPKAPK5,XRCC5,MAPK1,NVL,WRAP53,MAPK3,PARN,MAP2K7	grey	VSMC_M10
GO:0051656	0.91	0.11	166	334	establishment of organelle localization	BP	1	VPS4B,MYO1A,AP3S1,KIF5A,PRKN,KIF3A,UBE2B,FAM91A1,EXOC4,MAPK15,AGTPBP1,SUN2,COPG2,RAC2,MYH9,KIT,BICD2,CHMP2A,NLRP5,LRPPRC,XPO1,TRAPPC12,YWHAZ,CDK5RAP2,STARD3NL,CCDC155,MGARP,WASF1,SPHK2,SPRY1,BBS7,KIF3C,ARHGAP21,COPG1,MYO7B,CLASP2,NECTIN2,GAB2,MLH1,LLGL2,UNC13D,PIBF1,MYO7A,SPRY2,HOOK3,AP3M2,KIF5C,MKKS,LIN7A,TMEM230,CHAMP1,NSFL1C,MOS,TTL,KIF3B,FER,CHMP2B,CHMP4C,SDAD1,MCPH1,KATNB1,RASGRP1,ARFGAP2,SLIT1,EXOC6B,SYNJ1,OPA1,AP3B1,CHMP7,DTNBP1,KIF13A,GBF1,BICDL1,KLHL12,AC112128.1,TRIP11,PEF1,TCIRG1,PDCD6,SNAP23,MARK1,CFL1,SHROOM2,AP1AR,LAT2,SPO11,FGR,CBL,NOP9,MLPH,RAB17,SNX4,CNIH2,LIMK2,TANC2,DLG1,SPG11,MAPT,BLOC1S6,MAJIN,ITGA4,MAP4K2,MREG,PDCD10,HTT,PTGDR,RAB3A,PINK1,UXT,SNAP29,AP3M1,C12orf4,KIF1C,SYNE2,HAP1,SLC2A4,SEPT1,KPNB1,PEX14,PSEN1,SYT11,TMED10,TRIM46,NDEL1,AC138894.1,RAB11A,LAT,NTN1,IL4R,SNAPIN,S100A13,DNM2,BTK,CLMN,AP1M2,STXBP2,MYO1D,C17orf75,PPP6C,MYO1F,DOCK7,MYO5B,TLE6,BICDL2,PDPK1,PRKCZ,SAPCD2,ATP6AP1,IKBKG,SPIRE2,CHMP1A,PSRC1,GPSM2,FOXF1,STXBP1,FNBP1L,VPS4A,RIPOR1,FHOD1,UBB,BLOC1S3,OOEP,CHGA,BORCS5,AP3S2,GEM	grey	VSMC_M10
GO:1904889	0.91	0.22	5	13	regulation of excitatory synapse assembly	BP	1	VSTM5,LRFN1,SEMA4A,GRID2,LRRTM2	grey	VSMC_M10
GO:0071542	0.91	0.18	10	24	dopaminergic neuron differentiation	BP	1	CSNK1E,FZD1,CDNF,RYK,TIAM1,NR4A2,WNT3,WNT5A,PITX3,WNT2	grey	VSMC_M10
GO:0062014	0.91	0.14	34	73	negative regulation of small molecule metabolic process	BP	1	CYP27B1,PPARA,CRY1,PLEK,FAM3C,DKKL1,SOX9,APOC1,SLC22A13,PIBF1,TRIB3,CYP7A1,DKK3,ERLIN1,PRMT3,SIRT4,SIK1,MST1,SNAI1,ACTN3,HDAC4,SCAP,ACADL,WNT4,STAT3,ACADVL,PARP1,NCOR1,LEPR,GFI1,MIR21,PDZD3,TIGAR,INSIG2	grey	VSMC_M10
GO:0097581	0.91	0.14	36	78	lamellipodium organization	BP	1	AVIL,RAC2,KIT,NCK2,AKIRIN1,WASF1,ARHGEF4,ABI1,ARHGEF7,SPEF1,ARFIP2,AL359736.1,FER,PIK3R1,PLCE1,BIN3,RREB1,CYFIP1,DMTN,CARMIL1,AUTS2,AJUBA,WASF2,HDAC4,PTPRO,WHAMM,NCKAP1,ABLIM2,VCL,WAS,SNX1,DNM2,ARHGEF6,VAV3,MTSS1L,CARMIL2	grey	VSMC_M10
GO:2001235	0.91	0.13	47	98	positive regulation of apoptotic signaling pathway	BP	1	TRIM39,STK3,NCK2,GSDME,FAF1,PDIA3,DEDD2,FBH1,RET,FBXW7,HTRA2,NKX3-1,RIPK1,STK4,SIAH1,BMPR1B,DNM1L,LCK,GPER1,MCL1,AGT,NFATC4,PEA15,ING5,RPL11,FIS1,PRKRA,CTSH,LTBR,MAGED1,NGFR,S100A8,SFPQ,PTPN2,PIAS4,BCAP31,TRAF2,PARK7,BCL10,DAB2IP,MIR27B,UBB,FADD,DDIT3,BCL2L11,PLAGL2,CRADD	grey	VSMC_M10
GO:1905710	0.91	0.16	16	36	positive regulation of membrane permeability	BP	1	HEBP2,TMEM14A,HIP1R,SLC9A1,STPG1,FZD9,NMT1,MUL1,TMEM102,ACAA2,MIR29A,BNIP3L,BCL2L11,SLC35F6,PPIF,AC140504.1	grey	VSMC_M10
GO:0050678	0.91	0.11	136	275	regulation of epithelial cell proliferation	BP	1	NME1,GLI1,TNFAIP3,FRS2,RIDA,OSR2,MTSS1,MYC,PTCH1,SMO,IFT74,TEK,CDK6,DLX5,PDCL3,CD109,RTN4,EMC10,EPGN,AREG,TGFA,PTN,EGFR,OSR1,INTU,FOXE3,C5AR2,C5AR1,PRKD2,SOX9,AQP11,IFT172,SCN5A,WDR48,OVOL2,RPTOR,AIMP1,PRKDC,FLT1,CYP7B1,NR4A1,ATP5F1A,EYA1,ROBO1,FBXW7,MEF2C,PEX2,VEGFC,VDR,NKX3-1,AGGF1,SRSF6,IFT52,RREB1,PAX2,NOD2,IGF2,HYAL1,CCND1,TGFB2,SULF2,TCF7L2,PDCD6,EGF,SOX2,ARNT,TGM1,KDF1,SFN,VASH2,FZD7,HTRA1,RUNX3,GLUL,LAMC1,CDKN1B,DLG1,DUSP10,STOX1,ITGA4,MEN1,IL12A,CASK,SAV1,PDCD10,GPBAR1,RAP1GAP,STAT3,PTPRN,WDR13,MAGED1,BMPR1A,MED1,ALDH1A2,SYNJ2BP,NGFR,PGF,VASH1,SMAD3,MAP2K5,TNMD,BCL11B,CCL2,ISL1,SUZ12,GPC3,PDPK1,WDR77,CYBA,MARVELD3,DAB2IP,ESRP2,MIR29A,MIR21,MIR222,MIR23A,MIR125B1,MIR22,MIR27B,MIR24-1,MIR27A,SERPINB5,LAMB1,ACVRL1,TINF2,ZNF580,NOG,CLDN1,WNT5A,SIX1,ZNF304,RGCC,HRAS,EREG,FGF1,WNT2	grey	VSMC_M10

GO:0006941	0.91	0.13	61	128	striated muscle contraction	BP	1	NEDD4L,STAC3,SMAD5,TNNI3,ASB3,MYH14,TRPM4,CACNB2,STAC,SCN5A,SCN1A,GPD1L,LMOD3,NR4A1,HOMER1,STC1,KCNJ3,TNNC1,KCNE2,DSP,CASQ2,RYR2,PKP2,KCNJ2,MAP2K6,TNNI1,TRPV4,SYNM,MYH7,GRK2,ANK2,ACE2,ATP1A2,ACTC1,SLC9A1,CASQ1,ACTN3,HDAC4,SCN4B,NOS1AP,DLG1,TTN,ATP1B1,CHRNB1,TCAP,STAC2,ARHGEF11,CACNA1G,ATP2A1,CALM1,DTNA,DSG2,RNF207,DMD,CHGA,KCNH2,TNNC2,SCN2B,KCNJ8,HCN4,NKX2-5	grey	VSMC_M10
GO:0002726	0.91	0.21	6	15	positive regulation of T cell cytokine production	BP	1	RSAD2,TRAF6,DENND1B,FZD5,PRKCZ,TRAF2	grey	VSMC_M10
GO:0009896	0.91	0.11	211	420	positive regulation of catabolic process	BP	1	NEDD4L,PAN2,LRP1,PIP4K2C,TNFAIP3,EPM2A,CNOT2,CNOT6,RIDA,PABPC1,HSPA1B,DXO,PNLDC1,PRKN,PPARA,RNF217,TRIB1,AGO2,PRXL2C,PTK2,TNRC6B,TUT7,AGTPBP1,GTPBP1,CSNK1E,HSF1,TFEB,FBXO7,SPTLC1,EXOSC3,PRKCE,PNPT1,SLC4A4,NOD1,HECW1,TRIM32,HACE1,VPS35,SCOC,ZYG11B,TUT4,FOXO3,FAF1,FGF21,ZC3HAV1,SESN3,BBS7,RAB7A,PIP4K2A,SOX9,ABHD5,PLK3,SUMO2,OPTN,MLH1,RALB,EGLN2,TNRC6C,KLHL40,AKT2,SIRT2,TMEM173,LSM1,DCN,RNF14,DDRGK1,SH3RF2,ULK1,PAN3,TRIB3,PLK2,CEBPA,IDE,PIK3CB,SH3D19,FBXW7,GPD1,P2RX7,CNOT1,CELF1,PTK2B,CNOT6L,RIPK2,TPCN1,RNFT2,TP53INP1,FTO,KCNE2,PRICKLE1,NOD2,NKD1,MYLIP,TENT4B,RBM24,RNF144B,GPLD1,IRS1,LPCAT1,HECW2,SEC22B,CPT1A,ZBTB20,ADRA2A,DHRSX,DIS3L2,USP13,GIGYF2,AC013489.1,EGF,YTHDF2,DISC1,SORL1,ATG16L1,ASB11,DTX3L,SH3BP4,ARIH2,ARNT,BAG3,ACTN3,YTHDF1,MLXIPL,RNF185,EIF4ENIF1,CDKN1B,ADAM8,NSF,NFE2L2,SUPV3L1,COP1,VSIR,RC3H1,UPF1,HTT,SAMD4A,ZSWIM8,SOCS4,PINK1,DNAJB2,POLR2G,STX5,PIM2,DAGLB,NT5C3B,DCP1B,DDB1,VPS13D,TNFRSF1B,PSMC3,TARDBP,OSBPL7,PSEN1,AREL1,SNX1,TAF1,MAPK3,TOB1,TNRC6A,LDLR,CNOT8,LARP1,KEAP1,RNF128,PSMD10,FBXO22,INSR,SMCR8,PARN,GPC3,TICAM1,FMR1,RILP,FZR1,BCAP31,METTL16,PLEKHN1,SGTA,OAZ1,APC2,IKBKG,TMEM259,PARK7,GPSM1,GNAI3,KIAA1324,TSC1,ZER1,SH3GLB1,WWP2,DAB2IP,TRIM68,TRIM34,BNIP3L,ENTPD5,METTL14,PSMC1,TRIM65,NANOS1,BAG2,RNFT1,IRGM,WNT5A,BCL2L11,HSPB8,APC,PTTG1IP,ZFP36L2,DDA1,RNF152,RC3H2,EXOSC5	grey	VSMC_M10
GO:0055021	0.91	0.15	24	53	regulation of cardiac muscle tissue growth	BP	1	GLI1,PPARA,MAPK14,PI16,PIM1,TGFBR2,MEF2C,TBX5,JARID2,KCNK2,SAV1,MAPK1,BMPR1A,RBPJ,TBX2,YY1,GATA6,MIR199A1,MIR222,MIR25,NOG,RGS4,HEY2,WNT2	grey	VSMC_M10
GO:0055057	0.91	0.24	4	11	neuroblast division	BP	1	AKNA,RAB10,NUMBL,DOCK7	grey	VSMC_M10
GO:0018146	0.91	0.22	5	13	keratan sulfate biosynthetic process	BP	1	B3GNT4,ST3GAL6,CHST1,CHST5,ST3GAL2	grey	VSMC_M10
GO:0009262	0.91	0.16	17	38	deoxyribonucleotide metabolic process	BP	1	TBPL1,DPYS,GDA,NUDT15,MBD4,NUDT16,DGUOK,NUDT18,DTYMK,UPB1,ADK,NEIL1,NT5M,NTHL1,CMPK2,DCTD,UPP1	grey	VSMC_M10
GO:0006744	0.91	0.20	7	17	ubiquinone biosynthetic process	BP	1	COQ2,COQ5,COQ10B,NDUFA9,COQ8A,COQ4,PDSS2	grey	VSMC_M10
GO:1901663	0.91	0.20	7	17	quinone biosynthetic process	BP	1	COQ2,COQ5,COQ10B,NDUFA9,COQ8A,COQ4,PDSS2	grey	VSMC_M10
GO:0046599	0.91	0.19	8	20	regulation of centriole replication	BP	1	VPS4B,MDM1,CDK5RAP2,CEP295NL,PLK2,ALMS1,AC112128.1,TRIM37	grey	VSMC_M10
GO:0046889	0.91	0.14	28	61	positive regulation of lipid biosynthetic process	BP	1	PPARA,PLA2G6,NR1H2,SPHK2,SIRT3,NR1H4,CYP7A1,ABHD6,SORBS1,NR1H3,HSD17B13,SIRT4,GPLD1,ZBTB20,LPGAT1,MLXIPL,SCAP,POR,CREB1,WNT4,SLC27A1,LDLR,CD74,SREBF1,CNEP1R1,STARD4,CCDC3,FGF1	grey	VSMC_M10
GO:0003091	0.91	0.22	5	13	renal water homeostasis	BP	1	AKR1B1,TFAP2B,AQP1,MYO5B,INPP5K	grey	VSMC_M10
GO:2001185	0.91	0.22	5	13	regulation of CD8-positive, alpha-beta T cell activation	BP	1	NCKAP1L,RUNX3,VSIR,ZBTB7B,SOCS1	grey	VSMC_M10
GO:0050961	0.91	0.22	5	13	detection of temperature stimulus involved in sensory perception	BP	1	GRIK2,ASIC3,EPHB1,NTSR1,TRPV1	grey	VSMC_M10
GO:0043201	0.91	0.23	4	11	response to leucine	BP	1	RRAGD,SESN3,RPTOR,LARS	grey	VSMC_M10
GO:0045761	0.91	0.19	8	20	regulation of adenylate cyclase activity	BP	1	GABBR2,ADGRV1,ORAI1,CAP2,GRM2,PALM,GNAI3,CAP1	grey	VSMC_M10
GO:0120034	0.91	0.13	43	92	positive regulation of plasma membrane bounded cell projection assembly	BP	1	AVIL,CDC42EP1,RAC2,SRF,KIT,EPS8L1,AKIRIN1,FUZ,DPYSL3,PIK3R1,PLCE1,P2RX7,F2RL1,CYFIP1,NEURL1,ZMYND10,AUTS2,WASF2,HDAC4,EPS8,CDC42EP2,NCKAP1,HTT,DNM3,HAP1,MNS1,MIEN1,PLEK2,NDEL1,TENM2,DNM2,BCAS3,FMR1,WRAP73,PALM,EPS8L3,DEF8,FNBP1L,CARMIL2,EPS8L2,APC,RALA,HRAS	grey	VSMC_M10
GO:0090218	0.91	0.16	13	31	positive regulation of lipid kinase activity	BP	1	AGAP2,PTK2,TEK,KIT,FPR2,FLT1,PTK2B,NOD2,IRS1,FGR,FGFR3,CD19,VAV3	grey	VSMC_M10
GO:1901836	0.91	0.21	6	15	regulation of transcription of nucleolar large rRNA by RNA polymerase I	BP	1	MARS,IPPK,SIRT7,DEDD,H2AFY2,DDX11	grey	VSMC_M10
GO:0008210	0.91	0.21	6	15	estrogen metabolic process	BP	1	HSD17B4,HSD17B8,HSD17B7,COMT,HSD17B10,DHRS11	grey	VSMC_M10
GO:0060395	0.91	0.14	28	62	SMAD protein signal transduction	BP	1	LRP1,GDF9,SMAD5,ROR2,SPTBN1,BMP8A,OVOL2,RBPMS,SLC33A1,VEPH1,ITGB6,KIAA0319,SLC2A10,TGFB2,PBLD,GDF15,INHA,BMPR1A,PARP1,FOS,CILP,TOB1,CITED1,SH2B1,SMAD3,JUN,SKI,NCEH1	grey	VSMC_M10
GO:0071549	0.91	0.18	10	24	cellular response to dexamethasone stimulus	BP	1	FECH,AQP1,EGFR,BMI1,DNMT3B,ABCC2,SRD5A1,ASS1,SMYD3,CRH	grey	VSMC_M10
GO:0019369	0.91	0.17	11	26	arachidonic acid metabolic process	BP	1	FAAH,ABHD6,PLA2G4B,CYP2U1,PLA2G4A,DAGLB,EPHX1,ALOXE3,MAPK3,CYP2J2,PTGES2	grey	VSMC_M10
GO:0006103	0.91	0.21	6	15	2-oxoglutarate metabolic process	BP	1	DLD,D2HGDH,L2HGDH,MRPS36,KYAT3,PHYH	grey	VSMC_M10
GO:0010828	0.91	0.16	15	35	positive regulation of glucose transmembrane transport	BP	1	MAPK14,FGF21,BRAF,AKT2,PIK3R1,SORBS1,IRS1,TERT,C2CD5,NFE2L2,CLTCL1,INSR,C3,GPC3,ARPP19	grey	VSMC_M10
GO:0019511	0.91	0.21	6	15	peptidyl-proline hydroxylation	BP	1	P4HA2,CRTAP,EGLN2,EGLN3,P3H2,P3H3	grey	VSMC_M10
GO:0035970	0.91	0.22	5	13	peptidyl-threonine dephosphorylation	BP	1	PPP2CB,DUSP18,DUSP10,PPM1A,DUSP1	grey	VSMC_M10
GO:0070542	0.91	0.15	22	49	response to fatty acid	BP	1	NME1,CAT,UCP1,FOXO3,SOX9,GIPR,NR1H4,SMARCD1,IRS1,CPT1A,GNPAT,HMGCL,PDK3,CREB1,CPS1,XRCC5,KCNK4,LDLR,SREBF1,ASS1,CLDN1,INSIG2	grey	VSMC_M10
GO:0034340	0.91	0.15	21	47	response to type I interferon	BP	1	SHMT2,MYD88,MAVS,IRF7,OAS3,NLRC5,SP100,YTHDF2,SETD2,PTPN6,MUL1,USP18,DCST1,STAT2,TYK2,JAK1,PTPN2,MIR21,OAS1,FADD,WNT5A	grey	VSMC_M10

GO:0110156	0.91	0.22	5	13	methylguanosine-cap decapping	BP	1	LSM1,NUDT12,EIF4ENIF1,DCP1B,EDC4	grey	VSMC_M10
GO:0018212	0.91	0.11	143	290	peptidyl-tyrosine modification	BP	1	ERBB3,CLK4,IL5,ROS1,PTK2,NTRK2,HSF1,TEK,TTBK1,TEC,KIT,NCK2,ROR2,SEMA4D,PDCL3,IL11,PRKCE,PPP2R1A,IBTK,EPGN,AREG,EPHA7,TGFA,MET,EGFR,EPHA1,IL15,HDAC2,ABI1,PIBF1,ALK,DYRK1B,AATK,HBEGF,EIF2AK2,PRNP,NRG1,GAS6,HPX,ERCC6,FLT1,EPHB1,RET,HCK,TTL,FER,OSBP,FBXW7,PTPRJ,IL7,PTK2B,ARL2BP,RIPK2,DMTN,NOD2,CNTN1,CD40,DSTYK,IGF2,NEURL1,LRRK1,HDAC1,LCK,BANK1,MAP2K6,TPST1,ADRA2A,NCF1,DYRK3,EGF,HCLS1,ADNP,CASS4,PARP9,PARP14,BMX,AGT,FGR,CBL,OSM,EPHB3,BAZ1B,SNX6,ABL2,TTN,PPP2R5B,EPHB4,IL12A,PTPN6,TNFSF18,DOK7,ZFYVE28,FGFR3,SOCS4,STK16,BST1,EPHA4,DLG4,DVL2,TNK1,TMEM102,FGFR4,DGKQ,CTF1,PSEN1,EFNA1,MAPK3,IL6R,HAX1,MAP2K1,MAP2K5,BTK,TYK2,CLK3,CD74,INSR,CCL5,CSF1R,YES1,ISL1,SUZ12,GHR,JAK1,UNC119,PTPN2,SOCS1,LRP8,PRKCZ,MLST8,INSRR,CNTF,PEAK1,MIR125A,THY1,CSPG4,LIF,DUSP22,TSLP,CADM4,EREG,MAP2K7,RAP2B,PDGFD	grey	VSMC_M10
GO:0032352	0.91	0.22	5	13	positive regulation of hormone metabolic process	BP	1	PAX8,ARNT,SLCO1C1,POR,WNT4	grey	VSMC_M10
GO:0008156	0.91	0.18	10	24	negative regulation of DNA replication	BP	1	ZRANB3,FBH1,RAD17,ATR,DONSON,BCL6,TSPYL2,TIPIN,LIG3,TTF1	grey	VSMC_M10
GO:2000404	0.91	0.17	12	28	regulation of T cell migration	BP	1	CCL27,OXSR1,CD200,APOD,ADAM8,ITGA4,TMEM102,CCL5,CRK,RHOA,FADD,WNT5A	grey	VSMC_M10
GO:1903131	0.91	0.11	147	297	mononuclear cell differentiation	BP	1	AGER,HLA-DRA,TCF7,BAK1,XRCC6,MYC,MFNG,MYH9,FBXO7,SRF,CDK6,KIT,NFIL3,IL11,MSH2,HOXA7,SLC46A2,RSAD2,IL4I1,IL15,ATG5,TRAF3IP2,BMI1,CLPTM1,GLI2,FOXJ1,IL15RA,KLF6,CMTM7,TGFBR2,EOMES,PLCL2,NCKAP1L,GAS6,FOXP1,PRKDC,IRF7,TRAF6,SOX12,TOX,ZC3H8,IL1A,CAMK4,PIK3R1,PTPRJ,TMEM131L,IL7,TPD52,PTK2B,RASGRP1,LMBR1L,RIPK2,CDH17,AP3B1,F2RL1,SOX13,ITGB6,DCAF1,DOCK10,PKNOX1,LCK,TCIRG1,RABL3,HLX,ACIN1,SLAMF8,FZD7,HDAC4,CD28,FCER1G,RUNX3,ZBTB46,PATZ1,FZD9,SP3,PPP2R3C,ADAM8,FZD5,DUSP10,BCL6,SYVN1,BATF2,ITGA4,VSIR,RC3H1,PTPN6,TNFSF18,WNT4,LAG3,PPP3CB,LTBR,STAT3,STAT5B,INHA,FOXP3,ZBTB1,GPS2,CARD11,RBPJ,MED1,TBX21,PSEN1,SEMA4A,KAT7,DOCK2,BATF,ZBTB7B,IL6R,CD19,IL4R,GPR68,BTK,BCL11B,YY1,CD74,CSF1R,JAG2,NKAP,VAV1,LEPR,PTGER4,IL7R,PTPN2,JUN,SOCS1,DROSHA,DNAJA3,PRKCZ,TSC1,LRRC8A,MIR21,MIR125B1,RHOA,SOX4,MAFB,FADD,CD46,DHRS2,FGL2,TNFSF9,NHEJ1,ZFP36L2,CEBPB,PRR7,TNFSF13B,BATF3,RC3H2	grey	VSMC_M10
GO:0042274	0.91	0.14	30	64	ribosomal small subunit biogenesis	BP	1	HELB,UTP23,RRP7A,TSR1,RPS14,UTP3,ERCC2,RPS8,RPSA,METTL17,PRKDC,DHX37,BMS1,RPP40,RIOK1,RPS17,HEATR1,FAM207A,MRPS11,NOP9,RPS27,XRCC5,TSR2,KRI1,RIOK3,UTP6,SNU13,ERAL1,RPS27L,GTF2H5	grey	VSMC_M10
GO:0071709	0.91	0.15	17	39	membrane assembly	BP	1	CHMP2A,SPTBN1,SIRT2,STX2,NSFL1C,CHMP7,NLGN4Y,NRXN2,NLGN2,ANXA2,GAK,STX4,SYT11,NLGN3,CEL,VPS4A,TLCD1	grey	VSMC_M10
GO:0051204	0.91	0.19	8	19	protein insertion into mitochondrial membrane	BP	1	HSPA4,TOMM22,AGK,NMT1,TIMM29,MAIP1,TIMM10B,TIMM8B	grey	VSMC_M10
GO:0009952	0.91	0.12	72	150	anterior/posterior pattern specification	BP	1	FRS2,SMO,FOXH1,SRF,ROR2,MEOX2,SIX2,SCMH1,HOXA2,HOXA4,HOXA6,HOXA7,FUZ,OSR1,BMI1,ABI1,GLI2,PCDH8,XRCC2,ACVR2B,ACVR2A,BHLHE40,PRKDC,HOXC6,TCF15,POFUT1,FAM208A,NKX3-1,NKD1,LDB1,PGAP1,POGLUT1,AXIN2,GBX2,HES6,WNT3,HOXD8,HOXD4,HOXD3,FZD5,MEOX1,TULP3,BMPR1A,TCAP,RBPJ,ALDH1A2,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,SMAD3,LHX1,YY1,CDX1,MIB1,NLE1,GPC3,HES4,SKI,WDR77,CELSR2,FOXF1,HOXB3,NOG,WNT5A,BASP1,OTX1,DDIT3,HEY2,WNT2,HOXA3	grey	VSMC_M10
GO:0031468	0.91	0.21	5	13	nuclear membrane reassembly	BP	1	CHMP2A,SIRT2,NSFL1C,CHMP7,VPS4A	grey	VSMC_M10
GO:0000165	0.91	0.10	293	579	MAPK cascade	BP	1	PHLPP1,LRP1,SEMA6A,MAP3K5,FRS2,STK3,MAPK8IP2,MAP3K4,PRKN,AGER,FBLN1,ROS1,SYNGAP1,TRIB1,MYC,LEMD2,PRXL2C,GRM4,TAB1,MAPK15,MAPK14,NTRK2,MAPK13,STK38,HSF1,TEK,GPR37,KIT,ROR2,GADD45G,WNK2,KLHL31,PRDX1,SEMA4C,DNAJA1,IL11,PRKCE,FKTN,FPR2,GSDME,VRK2,EMC10,LPAR1,MTURN,EPGN,NOD1,BMPER,EPHA7,TGFA,ITGB1BP1,VRK3,GRB10,YWHAZ,EGFR,ARHGEF5,TLR4,TRAF1,SDCBP,FGF21,BRAF,SPRY1,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,SOX9,RAF1,MYD88,PPP1CB,SPRY2,ALK,ARRB1,IKBKB,C1QTNF1,NEK10,ZMYND11,PDE6G,PLCB1,MAP4K1,SPRED3,GPS1,EIF2AK2,ADRA1D,DUSP6,RELL2,SEMA3A,KL,NRG1,SH3RF2,GAS6,SIRT3,ARL6IP5,ERCC6,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,APIP,ST5,EPHB1,MOS,RET,PIK3CB,HAND2,ROBO1,PLCE1,FBXW7,PTPRJ,MEF2C,P2RX7,WDR54,P2RY1,MADD,PTK2B,RASGRP1,RAPGEF2,MAPKAPK5,CCL17,TIAM1,PAQR3,RIPK2,F2RL1,F2R,NQO2,RIPK1,PRDM11,STK4,GCNT2,NOD2,TAOK3,CD40,DSTYK,DUSP8,IGF2,PRDM15,MAPKAPK3,BANK1,MAP2K6,TRPV4,PDCD4,TGFB2,ADRA2A,SLC30A10,DAG1,AJUBA,NCF1,KRAS,MAPKAPK2,EGF,MAP3K21,TBC1D10C,SOX2,SORL1,GPER1,DOK5,AGT,CIB1,TRAF5,MAP3K6,DVL3,STRADB,FZD7,OSM,PEA15,THPO,PDE6H,MAP3K3,PDE8A,MAP3K15,MAGI3,DUSP16,DLG1,MAP3K11,ADAM8,AIDA,FZD5,DUSP10,MBIP,RAP1B,CTSH,MEN1,MAP4K2,PPM1L,FN1,DUSP19,PTPN6,PDCD10,ADRA2C,GPBAR1,GDF15,FGFR3,PINK1,ARAF,LTBR,MAPK1,MINK1,EPHA4,MAGED1,DVL2,IGFBP4,GPS2,RELL1,RGS14,FGFR4,SYNJ2BP,MAP3K9,PSEN1,FGF18,TAOK2,EFNA1,WWC1,MAPK3,HACD3,MAP2K1,PIK3R5,SMAD3,MAP2K5,RIT2,TNIP1,PSMD10,GAREM1,N	grey	VSMC_M10

GO:0016485	0.91	0.12	83	170	protein processing	BP	1	SEC11C,ATP23,CPM,MYRFL,BAK1,XPNPEP3,PTCH1,MYH9,PLGRKT,IL1R2,ACP4,ADAMTS3,BCL2L12,KEL,CST7,IFT172,PLAT,PITRM1,PRNP,CPXM1,MIPEP,ASPH,IMMP1L,CASP3,PCSK1,SCG5,HTRA2,MME,SPCS1,RIPK2,IFT52,PIDD1,CPN1,LONP2,SIRT4,RHBDD1,SPPL3,HJV,ENPEP,SPRTN,ACE2,CIDEB,PRSS12,ECE2,CPXM2,BACE1,MELTF,PCSK7,PISD,ADAM8,SRGN,TYSND1,CTSH,VSIR,LPCAT3,CPZ,HGFAC,ECE1,PSEN2,PARP1,DDI2,F12,PSEN1,SNX12,OGT,AC138894.1,SERPINF2,ADAMTS13,HPR,TMEM208,FGA,NOL3,CNTN2,FADD,CASP8,BAG2,FXN,C2CD3,PERP,APH1B,FAM111A,TMPRSS12,SPCS2	grey	VSMC_M10
GO:0009151	0.91	0.20	6	15	purine deoxyribonucleotide metabolic process	BP	1	GDA,NUDT15,NUDT16,DGUOK,NUDT18,ADK	grey	VSMC_M10
GO:0060996	0.91	0.13	40	87	dendritic spine development	BP	1	FSTL4,ASAP1,NCK2,SHANK1,HDAC2,IQSEC1,EPHB1,PLK2,MEF2C,CUX2,TIAM1,OPA1,ITPKA,SLC12A5,SRGAP2C,DOCK10,NEURL1,DNM1L,CAPRIN2,CFL1,DISC1,CDKL5,EPHB3,TANC2,DNM3,EPHA4,DLG4,SDK1,PSEN1,EFNA1,ZDHHC15,GPRASP2,BHLHB9,ARHGAP44,CAMK2A,CDK5R1,FMR1,LRP8,LLPH,FOXO6	grey	VSMC_M10
GO:0045892	0.91	0.10	482	943	negative regulation of transcription, DNA-templated	BP	1	SMARCC2,ATP8B1,PLAGL1,ZBTB2,ESR1,CNOT2,OSR2,SNW1,ZNF706,ZBTB12,PRKN,PPARA,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,PTCH1,ATF4,CBX7,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,RPS14,ZNF550,BEND6,ZNF268,SCMH1,NFE2L3,HOXA2,HOXA7,JAZF1,XPO1,AKIRIN2,CASP8AP2,BACH2,ZNF692,NR1H2,ZNF350,FOXP2,MED25,KLF11,POU3F3,LANCL2,CREM,SDCBP,OSR1,FOXO3,BEND5,HDAC2,PHF10,DNMT3A,BMI1,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,SUV39H2,ZNF404,PLK3,GLI2,DEDD2,RSF1,KDM4A,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,SFMBT2,GZF1,POU4F1,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,TAF7,NRG1,GAS6,RYBP,FOXP1,MITF,MTA3,ARID5A,IRF7,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,NCOA2,DKK3,SAP30,ZNF366,ARNTL,GCFC2,HMBOX1,MEF2C,PEX2,PKIA,TMBIM6,CNOT1,SLA2,CUX2,MCPH1,SOX6,FNIP2,BACH1,SFMBT1,NR1H3,EAPP,SCAF4,LCOR,DDX54,RUNX1T1,VDR,NKX3-1,BAHD1,HDAC7,NKX6-1,LOXL2,NR4A2,PHF21A,CRY2,PRDM11,CDYL,RREB1,RTF1,ZBED6,SOX13,ZNF248,TFAP2A,RIPPLY3,HIF1AN,PAX2,SALL1,PPHLN1,PRICKLE1,HIVEP1,JARID2,ATXN1,SUDS3,ZNF423,LDB1,IGF2,MAGEL2,ELK4,NUPR2,DCAF1,SUFU,TAGLN3,PCGF6,IRX2,RPL23,HDAC1,ELF3,CCND1,SP100,TRPV4,PDCD4,ZBTB20,SATB2,TCF7L2,AJUBA,ZNF639,PIAS3,LHX9,HJV,FABP4,SNAI1,ZNF202,HCLS1,FOXJ2,HSPA8,OTUD7B,CTF1IRP1,CIART,ZNF217	grey	VSMC_M10
GO:0050829	0.91	0.16	14	32	defense response to Gram-negative bacterium	BP	1	AQP1,LYPD8,TLR4,OPTN,F2RL1,SLC11A1,IL6R,NOS2,DROSHA,HIST1H2BK,CHGA,CXCL6,IRGM,HIST1H2BJ	grey	VSMC_M10
GO:0034724	0.91	0.17	11	26	DNA replication-independent nucleosome organization	BP	1	ASF1A,UBN2,RBBP4,HIRA,HIST1H4B,HIST2H4A,HIST1H4H,ITGB3BP,HIST1H4D,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0042092	0.91	0.17	11	26	type 2 immune response	BP	1	RSAD2,TRAF3IP2,NOD2,HLX,DENND1B,BCL6,TBX21,BATF,IL4R,CD74,PRKCZ	grey	VSMC_M10
GO:1900221	0.91	0.21	5	13	regulation of amyloid-beta clearance	BP	1	LRP1,SRF,HDAC1,LRPAP1,ABCA7	grey	VSMC_M10
GO:0010259	0.91	0.17	10	24	multicellular organism aging	BP	1	MSH2,DDC,ERCC1,WRN,IDE,RAD54B,CISD2,CTSV,PRDM2,RNF165	grey	VSMC_M10
GO:0030968	0.91	0.13	32	69	endoplasmic reticulum unfolded protein response	BP	1	DERL1,BAK1,ATF4,NCK2,ERMP1,HERPUD2,FGF21,TMTC4,EIF2AK2,DDRGK1,PIK3R1,AMFR,CCND1,FICD,YOD1,QRICH1,TBL2,RHBDD2,NFE2L2,DERL3,BHLHA15,CREB3L4,PTPN2,CREB3L3,ABCA7,HSPA5,DAB2IP,MIR199A1,DDIT3,BCL2L11,PPP1R15A,DERL2	grey	VSMC_M10
GO:0062149	0.91	0.18	8	20	detection of stimulus involved in sensory perception of pain	BP	1	PHF24,ASIC3,SCN1A,EPHB1,NTSR1,BACE1,KCNA1,TRPV1	grey	VSMC_M10
GO:0007420	0.91	0.10	295	587	brain development	BP	1	NME1,LRP1,GLI1,ATAT1,FRS2,RIDA,SYNJ2,FZD6,UQCRQ,CCDC134,BAK1,XRCC6,PITX1,PTCH1,FANCC,AGTPBP1,PLXNA4,SUN2,NTRK2,CSNK1E,CKB,SMO,RBFOX2,SRF,TTBK1,FZD1,CDK6,SLC1A1,DLX5,EFHC1,CCIN,ADGRL3,SEMA4C,MBOAT7,RTN4,UTP3,HOXA2,PPT1,AQP1,EPHA7,AKNA,WHRN,PTN,FOXP2,CTTNBP2,POU3F3,CDK5RAP2,SLC7A11,FOXO3,ARMC4,SPHK2,FAT4,SPATA5,KDM7A,GRIN2D,NAPA,BBS7,BMI1,NDNF,C5AR1,EIF2B3,XRCC1,GLI2,B4GALT2,IFT172,FOXJ1,SCN5A,NUMBL,HNMT,POU4F1,TSKU,SZT2,ALK,HOOK3,TGFBR2,EOMES,CHD8,SIRT2,MKKS,AATK,RARB,SYT1,PLCB1,RAC3,CEP290,SEMA3A,NRG1,WRN,PRKDC,RYK,SNPH,DHX37,TOX,ZSWIM6,NCOA6,CASP3,CTNND1,CLP1,DCLK2,ROBO1,ROBO2,FZD3,FAIM2,HTRA2,NDUFS3,CELF1,CSNK2A2,MCPH1,SOX6,RAPGEF2,DPYSL2,NNAT,SLIT1,SYNJ1,TENT2,NR4A2,AMIGO2,SLC38A2,RPGRIP1L,PAX2,TSPAN2,SALL1,DNAH5,CNTN1,ZNF335,DPCD,ATXN1,SUDS3,ZNF423,LDB1,COX6B1,SRGAP2C,SLC4A10,SRD5A1,INA,NEURL1,CFAP43,SLC6A3,HDAC1,ALDH1A3,PPP3CA,PGAP1,SLC38A3,SATB2,COX17,TTBK2,AMIGO3,SHROOM2,KRAS,PITPNM1,EGF,TTC21B,SOX2,ZFHX2,JHY,DISC1,GNPAT,B3GNT5,GBX2,ATP1A2,BAG3,SPTBN2,UFC1,MACO1,DLX1,DNAJC30,EPHB3,NSUN5,APOD,SETD2,WNT3,CREB1,SEMA6D,BCL2A1,H2AFY2,DIXDC1,MEN1,TNR,XRCC5,NIN,CXCR2,WNT4,HSPG2,COL3A1,STK36,ABCB6,TBX19,KCNA1,TULP3,TTC25,PADI2,HAP1,ACTB,SHROOM4,BMPR1A,DNAJB1,MPP5,RBPJ,PHF8,MED1,ALDH1A2,ATP1B2,SETD1A,PSEN1,KDM6B,ITGAM,NDEL1,TAF1,CITED1,CHRNB2,MAP2K1,POU3F4,EPOR,PCDH19,CALM1,GSC,BCL11B,LHX1,SIN3A,XAB2,MYO1D,CDK5R1,ISL1,OXCT1,TWSG1,POGK,SPEG,SETX,DAB1,ARAP1,AFG3L1,PPP2R5C,POGZ	grey	VSMC_M10

GO:1905114	0.91	0.10	224	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	NFATC1,LRP1,RPS12,GLI1,TNFAIP3,STK3,MAPK8IP2,FZD6,RIMS2,PRKN,TCF7,UBE2B,RSPO3,RNF146,MAPK14,CBY1,CSNK1E,SOX10,SMO,DAAM2,MDFI,CHRNA3,CHRNA5,PTK7,CDK14,FZD1,ROR2,DLX5,WNK2,SOSTDC1,RIMS1,PPP2R1A,SHANK1,RSPO1,GRB10,ATP6V1C2,EGFR,HECW1,FUZ,GRIK2,SFRP4,CCNY,DKKL1,VPS35,TRPM4,FOXO3,GRIN2D,MTMR2,SLC8A2,SOX9,PPM1N,LRRFIP2,GLI2,GRIK5,SCEL,TSKU,WNT11,CHRNA6,RBMS3,CHD8,UBAC2,RAB5A,FERMT1,RAC3,SPEF1,P2RX2,MITF,CALCOCO1,RYK,PFDN5,CTNND1,DKK3,TRABD2A,P2RX3,ARNTL,FZD3,MEF2C,TMEM131L,P2RX7,CSNK2A2,CUX2,PTK2B,LMBR1L,TIAM1,OTULIN,AMFR,NR4A2,RTF1,PKD2,SOX13,STK4,SALL1,VANGL1,PRICKLE1,NKD1,FBXW4,ZNF423,LDB1,PRDM15,KLHL12,LGR6,LRRK1,HDAC1,PPP3CA,CCND1,CAPRIN2,TERT,TMEM9,SULF2,IGSF11,TCF7L2,DKK2,AXIN2,SSH1,MARK1,EGF,TTC21B,SOX2,DISC1,ZNRF3,KREMEN1,DVL3,TMEM237,BICC1,NFATC4,FZD7,STX1A,TMEM25,NPAS4,NTSR1,GID8,PTPRO,GRHL3,FZD9,SENP2,WNT3,CCNYL1,FZD5,DIXDC1,WDR61,DDX3X,MPP2,CPZ,WNT4,MARK2,DAAM1,TBL1XR1,PPM1A,LEO1,OTUD5,ARHGEF19,DLG4,DVL2,IGFBP4,DDB1,NLGN2,CHRNB1,RBPJ,GRK6,STX1B,PSEN1,TMEM88,ITGAM,TGFB1I1,ITGA3,NLGN3,CSNK1G1,CITED1,CHRNB2,SOX30,SMAD3,MKS1,AC004687.2,CCDC88C,GSC,G3BP1,NLE1,ISL1,C3,NLK,IFT20,SEZ6,GPC3,ABAT,PIAS4,TLE6,TRPV1,TAX1BP3,P2RX1,ATP6V0C,PRKCZ,SKI,PKD1,MECP2,APC2,CELSR2,FOXL1,DAB2IP,MIR199A1,MIR222,MIR32,RHOA,ZBTB33,BCL7B,CHRNB4,TRABD2B,CHRNA10,CHRNG,SOX4,GRID2,NOG,WNT5A,LBX2,CELSR3,RGS4,DDIT3,DACT3,SDHAF2,SHISA2,APC,INSYN1,NKX2-5,MESD,WNT2	grey	VSMC_M10
GO:0038095	0.91	0.18	8	20	Fc-epsilon receptor signaling pathway	BP	1	IKBKB,TRAF6,FER,FCER1G,BTK,VAV1,VAV3,MAP2K7	grey	VSMC_M10
GO:1903312	0.91	0.13	34	74	negative regulation of mRNA metabolic process	BP	1	PABPC1,MAPK14,RNF20,SRSF10,TRAF3IP2,DHX34,MYD88,BAG4,PKP3,SRSF6,TENT5C,TENT4B,RBM24,AXIN2,MAPKAPK2,SRSF4,TRAF5,ANGEL2,EIF4ENIF1,YBX3,SLC11A1,RBM10,TARDBP,TOB1,TENT5D,LARP1,FMR1,METTL16,CIRBP,TRAF2,SRSF12,YBX1,TENT5A,SAP18	grey	VSMC_M10
GO:0051016	0.91	0.18	8	20	barbed-end actin filament capping	BP	1	AVIL,KIAA1211,ADD2,CARMIL1,ADD3,EPS8,CAPZA1,CARMIL2	grey	VSMC_M10
GO:0001541	0.91	0.15	17	39	ovarian follicle development	BP	1	ESR1,DMC1,FANCG,KIT,FOXO3,ARRB1,FOXL2,BMPR1B,GAS2,HYAL3,SPO11,TAF4,VGF,INHA,MSH4,CEBPB,EREG	grey	VSMC_M10
GO:0006998	0.91	0.15	19	43	nuclear envelope organization	BP	1	NEMP1,LEMD2,SUN2,CHMP2A,LPIN1,SIRT2,NSFL1C,SPAG4,CHMP7,GPER1,TOR1AIP1,PARP11,AKAP8L,TARDBP,NDEL1,PRKCB,TOR1B,VPS4A,LEMD3	grey	VSMC_M10
GO:0010827	0.91	0.14	26	58	regulation of glucose transmembrane transport	BP	1	MAPK14,SLC25A27,GRB10,FGF21,BRAF,PRKAG2,AKT2,ASPSCR1,TRIB3,PIK3R1,SORBS1,IRS1,TERT,C2CD5,PEA15,NFE2L2,CLTCL1,RSC1A1,PRKCB,INSR,YES1,C3,GPC3,INPP5K,FABP5,ARPP19	grey	VSMC_M10
GO:0072498	0.91	0.21	5	13	embryonic skeletal joint development	BP	1	OSR2,OSR1,HYAL1,SLC2A10,NOG	grey	VSMC_M10
GO:0060538	0.91	0.12	63	132	skeletal muscle organ development	BP	1	STAC3,VGLL2,PITX1,LEMD2,MAPK14,SMO,LARGE1,CNTFR,MEOX2,HIVEP3,MYH14,AKIRIN1,BVES,KEL,KLF5,KLHL40,NR1D2,RYR1,DCN,P2RX2,LMOD3,EPHB1,NR4A1,SMYD1,NLN,FOXL2,FLNB,VAMP5,SAP30,ARNTL,MEF2C,TLL2,HOMER1,BIN3,RBM24,IGF2,MYH15,NEURL1,PPP3CA,DAG1,HLX,USP19,MYOZ2,CASQ1,ACTN3,HDAC4,YBX3,MYOZ1,MYLPF,ZNF689,FOS,STRA6,FBXO22,SKI,SOX8,ASS1,RHOA,DMD,BASP1,SIX1,POPDC2,MYORG,UQCC2	grey	VSMC_M10
GO:0072593	0.91	0.11	86	176	reactive oxygen species metabolic process	BP	1	GLS2,PRKN,PPARA,TSPO,FANCC,MAPK14,RAC2,SLC1A1,PRDX1,CAT,FPR2,CYB5R4,PXDN,EGFR,TLR4,UCP1,ATG5,MYCN,FOXO3,SPHK2,DHFR,WISP3,ACOX1,PRDX3,TGFBR2,SIRT2,SIRT3,FAM19A4,PXDNL,NDUFS3,HVCN1,PTK2B,F2RL1,NQO2,RIPK1,PLA2R1,TFAP2A,PAX2,SIRT5,GBF1,SH3PXD2A,SLC30A10,FBLN5,NCF1,IFI6,AGT,ACE2,HDAC4,NCF2,PDK3,NFE2L2,MAPT,PIKFYVE,DUOX1,BCO2,GCH1,PINK1,MMP3,STAT3,BST1,SOD3,ITGAM,MPO,NOX5,VAV1,NOS2,NOXA1,PARK7,SLC25A33,GNAI3,CYBA,LCN2,NQO1,MIR21,MIR27B,MIR24-1,MT-ND2,RHOA,TIGAR,GADD45A,INAVA,HBA2,NRROS,GRB2,APOPT1,AC140504.1	grey	VSMC_M10
GO:0051923	0.91	0.21	5	13	sulfation	BP	1	SULT4A1,HS3ST5,TPST1,CHST5,SULT1C3	grey	VSMC_M10
GO:0042759	0.91	0.21	5	13	long-chain fatty acid biosynthetic process	BP	1	LTC4S,QKI,ACSBG1,ALOXE3,ACSBG2	grey	VSMC_M10
GO:0036490	0.91	0.22	4	11	regulation of translation in response to endoplasmic reticulum stress	BP	1	NCK2,EIF2AK4,DDX3X,PPP1R15A	grey	VSMC_M10
GO:0060711	0.91	0.15	16	37	labyrinthine layer development	BP	1	RSPO3,GJB5,OVOL2,SPINT2,SPINT1,VASH2,FZD5,MAPK1,RBPJ,VASH1,CITED1,MAP2K1,CASP8,GRB2,HEY2,WNT2	grey	VSMC_M10
GO:0035437	0.91	0.21	5	13	maintenance of protein localization in endoplasmic reticulum	BP	1	GPAA1,GRIK5,RER1,HSPA5,INSIG2	grey	VSMC_M10
GO:0045143	0.91	0.14	21	47	homologous chromosome segregation	BP	1	UBE2B,DMC1,CCDC155,MLH1,CCNB1IP1,SIRT7,TEX15,SYCP1,CCDC36,SPO11,TEX12,MAJIN,ZCWPW1,STAG3,P3H4,SYCE2,MEIOB,MSH4,RNF212B,AGO4,SYCE1L	grey	VSMC_M10
GO:0007171	0.91	0.22	4	11	activation of transmembrane receptor protein tyrosine kinase activity	BP	1	CHRNA3,NRG1,EGF,DGKQ	grey	VSMC_M10
GO:0008542	0.91	0.16	13	31	visual learning	BP	1	SYNGAP1,KIT,SLC7A11,B4GALT2,DDHD2,KRAS,ATP1A2,CREB1,RGS14,CHRNB2,IFT20,MECP2,ABCA7	grey	VSMC_M10
GO:0099150	0.91	0.22	4	11	regulation of postsynaptic specialization assembly	BP	1	LRFN1,GAP43,GRID2,LRRTM2	grey	VSMC_M10
GO:0055123	0.91	0.12	46	99	digestive system development	BP	1	GLI1,VPS52,SOX10,SMO,KIT,SIX2,CXCL8,EGFR,BBS7,SLC4A2,GLI2,MEGF8,KLF5,IFT172,WNT11,TGFBR2,OVOL2,CHD8,RARB,CCKBR,RET,CBFA2T2,HIP1R,SALL1,IGF2,TGFB2,HLX,EPHB3,CPS1,PYY,SAV1,NKX3-2,WDR19,ALDH1A2,RBPMS2,SMAD3,TBX2,STRA6,GATA6,DAB1,PKD1,FOXL1,FOXF1,ASS1,WNT5A,TIGAR	grey	VSMC_M10
GO:0045624	0.91	0.21	5	13	positive regulation of T-helper cell differentiation	BP	1	RIPK2,HLX,IL4R,PRKCZ,MIR21	grey	VSMC_M10
GO:0006361	0.91	0.22	4	11	transcription initiation from RNA polymerase I promoter	BP	1	BAZ2A,TAF1,RRN3,TAF1C	grey	VSMC_M10

GO:0045912	0.91	0.15	17	39	negative regulation of carbohydrate metabolic process	BP	1	PRKN,PPARA,CRY1,PLEK,FAM3C,GCKR,SIK1,MST1,ACTN3,HDAC4,PASK,STAT3,COX11,NCOR1,LEPR,INPP5K,TIGAR	grey	VSMC_M10
GO:0030202	0.91	0.22	4	11	heparin metabolic process	BP	1	CSGALNACT1,AC022400.6,IDUA,GLCE	grey	VSMC_M10
GO:0061298	0.92	0.19	6	16	retina vasculature development in camera-type eye	BP	1	ACVR2B,CLIC4,RHOJ,ROM1,LAMA1,ACVRL1	grey	VSMC_M10
GO:0010458	0.92	0.16	11	26	exit from mitosis	BP	1	CHMP2A,CLASP2,SIRT2,SIRT7,CHMP7,NPM2,PPP2R2D,EPS8,CDKN1B,CDC14A,RGCC	grey	VSMC_M10
GO:0050863	0.92	0.11	101	206	regulation of T cell activation	BP	1	AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TCF7,TNFRSF13C,RAC2,TNFRSF21,NCK2,SLC46A2,PELI1,IL4I1,IL15,BMI1,CLPTM1,GLI2,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,SOX12,TOX,ZC3H8,IL1A,CAMK4,CASP3,TMEM131L,IL7,PAG1,RASGRP1,RIPK2,AP3B1,MARCH7,SOX13,NOD2,IGF2,LCK,ICOSLG,BTN2A2,GPAM,PRKAR1A,HLX,CD28,RUNX3,DLG1,ADAM8,DUSP10,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,STAT5B,SCGB1A1,FOXP3,RASAL3,ZBTB1,CARD11,TNFRSF1B,TBX21,ZBTB7B,LAT,IL4R,CD74,CCL5,CCL2,YES1,NKAP,VAV1,TWSG1,IL7R,PTPN2,SOCS1,DROSHA,DNAJA3,PRKCZ,GLMN,BCL10,MIR21,MIR27A,RHOA,SOX4,FADD,DPP4,CD46,THY1,FGL2,CD70,TNFSF9,LAX1,EFNB3,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0072009	0.92	0.12	41	89	nephron epithelium development	BP	1	MTSS1,MYC,KLHL3,PTCH1,PODXL,SMO,TFAP2B,SIX2,POU3F3,OSR1,SOX9,AQP11,FOXJ1,GZF1,WNT11,JAG1,ASXL1,PAX8,EYA1,FMN1,MEF2C,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,PTPRO,DLG1,WNT4,MAGED1,CITED1,LHX1,GPC3,PKD1,SOX8,NOG,BASP1,SIX1,LIF,FGF1	grey	VSMC_M10
GO:0046635	0.92	0.14	18	41	positive regulation of alpha-beta T cell activation	BP	1	HLA-DRA,TGFBR2,NCKAP1L,RIPK2,AP3B1,HLX,CD28,RUNX3,IL12A,FOXP3,RASAL3,ZBTB7B,IL4R,NKAP,SOCS1,PRKCZ,MIR21,RHOA	grey	VSMC_M10
GO:0021543	0.92	0.12	60	127	pallium development	BP	1	NME1,LRP1,ATAT1,UQCRQ,SUN2,NTRK2,SMO,SRF,CDK6,EFHC1,MBOAT7,RTN4,FOXP2,POU3F3,FAT4,EIF2B3,XRCC1,TSKU,ALK,MKKS,PLCB1,CASP3,DCLK2,ROBO1,CELF1,CSNK2A2,MCPH1,TENT2,SLC38A2,SRGAP2C,SRD5A1,HDAC1,DISC1,DLX1,NSUN5,BCL2A1,DIXDC1,COL3A1,KCNA1,MPP5,PSEN1,KDM6B,NDEL1,XAB2,CDK5R1,DAB1,LRP8,CRK,PLXNA3,TSC1,PHLPP2,DAB2IP,RHOA,ADGRG1,FOXG1,LAMB1,GNG12,CCDC85C,POU3F2,BTBD3	grey	VSMC_M10
GO:0006309	0.92	0.19	6	15	apoptotic DNA fragmentation	BP	1	HSF1,FOXL2,DNASE2,PAM16,DFFB,NMNAT1	grey	VSMC_M10
GO:0043243	0.92	0.16	12	29	positive regulation of protein-containing complex disassembly	BP	1	JMJD4,KIAA1211,PLEK,KATNB1,F2RL1,CARMIL1,TRPV4,INSR,SMCR8,CARMIL2,IRGM,PDXP	grey	VSMC_M10
GO:0002768	0.92	0.11	76	158	immune response-regulating cell surface receptor signaling pathway	BP	1	CD226,HLA-DPB1,PTK2,PLA2G6,TEC,KIT,TNFRSF21,PRKCE,FPR2,C5AR2,C5AR1,PRKD2,NECTIN2,EIF2B3,IKBKB,PAWR,PLCL2,PRNP,NCKAP1L,FOXP1,TRAF6,HCK,FER,LPXN,PTPRJ,MEF2C,SLA2,RIPK2,CD40,GPLD1,SPPL3,LCK,BANK1,ICOSLG,BTN2A2,DENND1B,CMKLR1,THEMIS2,LAT2,BMX,FGR,PLPP4,CD28,FCER1G,RC3H1,PTPN6,CD38,MAPK1,FOXP3,GPS2,CARD11,PSEN1,LCP2,CD19,PRKCB,BTK,YES1,PRAM1,VAV1,PTPN2,CREBBP,IKBKG,VAV3,BCL10,CMTM3,FYB1,BTN1A1,CD247,THY1,UBE2N,GCSAM,HRAS,LAX1,SH2B2,MAP2K7,RC3H2	grey	VSMC_M10
GO:0043928	0.92	0.21	5	13	exonucleolytic catabolism of deadenylated mRNA	BP	1	CNOT6,EXOSC3,NT5C3B,CNOT8,EXOSC5	grey	VSMC_M10
GO:0014911	0.92	0.15	15	35	positive regulation of smooth muscle cell migration	BP	1	LRP1,TLR4,ADAMTS1,DOCK5,TERT,SSH1,AGT,HDAC4,SEMA6D,FOXO4,CCL5,DOCK7,CRK,MIR21,PDGFD	grey	VSMC_M10
GO:0045103	0.92	0.15	13	31	intermediate filament-based process	BP	1	RAF1,EVPL,BFSP1,NEFM,DSP,INA,PKP2,SYNM,KLHL24,DES,CLN8,NDEL1,MTM1	grey	VSMC_M10
GO:0051567	0.92	0.16	12	29	histone H3-K9 methylation	BP	1	SETD7,SETDB2,SUV39H2,KDM4A,DNMT3B,JARID2,MECP2,PRDM16,SETDB1,ARID4A,BEND3,ZNF304	grey	VSMC_M10
GO:0030850	0.92	0.15	16	37	prostate gland development	BP	1	GLI1,ESR1,FRS2,PTCH1,HOXA13,TNC,SOX9,GLI2,PLAG1,CYP7B1,NKX3-1,CDKN1B,WDR77,SERPINB5,NOG,WNT5A	grey	VSMC_M10
GO:0031069	0.92	0.18	8	20	hair follicle morphogenesis	BP	1	SMO,SOSTDC1,INTU,GLI2,TGFB2,SNAI1,GORAB,NGFR	grey	VSMC_M10
GO:0032729	0.92	0.15	15	35	positive regulation of interferon-gamma production	BP	1	CD226,HLA-DPB1,TLR4,RASGRP1,RIPK2,F2RL1,FZD5,IL12A,SLC11A1,ISL1,SLC7A5,FADD,WNT5A,HRAS,HAVCR2	grey	VSMC_M10
GO:0045116	0.92	0.19	6	15	protein neddylation	BP	1	EPAS1,RNF7,NEDD8,RPL11,DCUN1D3,NAE1	grey	VSMC_M10
GO:0006983	0.92	0.20	5	13	ER overload response	BP	1	ATG10,TMCO1,HSPA5,DDIT3,BCL2L11	grey	VSMC_M10
GO:0007250	0.92	0.20	5	13	activation of NF-kappaB-inducing kinase activity	BP	1	TNFSF15,TRAF6,ZFP91,TRAF2,COPS8	grey	VSMC_M10
GO:0006893	0.92	0.13	25	56	Golgi to plasma membrane transport	BP	1	GOPC,EXOC4,STEAP2,SPTBN1,RAB10,OPTN,GOLGA4,CCDC93,LYPLA1,VAMP5,EXOC6B,KIF13A,BBS1,NSF,EXOC5,CNST,RSC1A1,AC138894.1,DNM2,GGA2,VPS35L,RAB26,SEC16A,C16orf70,VAMP3	grey	VSMC_M10
GO:0006898	0.92	0.11	93	192	receptor-mediated endocytosis	BP	1	LRP1,REPS1,CANX,RAB21,IGF2R,PICK1,MICALL1,USP46,SMAP1,FPR2,PPT1,CXCL8,RSPO1,AAK1,SFRP4,SDCBP,WASF1,EPS15,MTMR2,AP2S1,CUBN,APOC1,LRP1B,ARRB1,TGFBR2,NEU3,FCHSD2,RAB5A,DNAJC13,PIK3CB,HIP1R,FCHO2,WDR54,LMBR1L,BMP2K,SYNJ1,PLA2R1,ANKRD13A,SLC9B2,EGF,ANKRD13D,GRK2,SORL1,SAG,DGKD,CBL,AP2M1,FCER1G,SH3GL3,CALY,PIKFYVE,ITGA4,LRPAP1,CXCR2,GRK4,CLTCL1,CALCRL,HSPG2,DNM3,RAMP2,CXCL16,DLG4,PDLIM7,ANXA2,GAK,ITGAM,SYT11,NLGN3,SNX1,AC138894.1,LDLR,DNM2,INSR,AP2B1,SGIP1,C3,UNC119,FMR1,PIP5K1C,GPR107,FNBP1L,BTBD8,AP1G1,CAP1,MIR199A1,MIR27B,MIR27A,CNTN2,LDLRAP1,CACNG7,GRB2,CACNG5,LRRTM2	grey	VSMC_M10
GO:0030513	0.92	0.16	11	27	positive regulation of BMP signaling pathway	BP	1	KCP,UBE2O,ZNF423,FBXL15,FKBP8,RBPJ,RNF165,TWSG1,GPC3,ENG,ACVRL1	grey	VSMC_M10
GO:0046456	0.92	0.16	12	28	icosanoid biosynthetic process	BP	1	LTC4S,MGST2,PIBF1,PLA2G4A,GGT2,GGT6,DAGLB,CD74,PTGES2,FABP5,GGT5,PTGES	grey	VSMC_M10
GO:1903019	0.92	0.20	5	13	negative regulation of glycoprotein metabolic process	BP	1	AGO2,HBEGF,SLC2A10,ABCA7,ACER2	grey	VSMC_M10

GO:0018108	0.92	0.10	141	287	peptidyl-tyrosine phosphorylation	BP	1	ERBB3,CLK4,IL5,ROS1,PTK2,NTRK2,HSF1,TEK,TTBK1,TEC,KIT,NCK2,ROR2,SEMA4D,PDCL3,IL11,PRKCE,PPP2R1A,IBTK,EPGN,AREG,EPHA7,TGFA,MET,EGFR,EPHA1,IL15,HDAC2,ABI1,PIBF1,ALK,DYRK1B,AATK,HBEGF,EIF2AK2,PRNP,NRG1,GAS6,HPX,ERCC6,FLT1,EPHB1,RET,HCK,FER,OSBP,FBXW7,PTPRJ,IL7,PTK2B,ARL2BP,RIPK2,DMTN,NOD2,CNTN1,CD40,DSTYK,IGF2,NEURL1,LRRK1,HDAC1,LCK,BANK1,MAP2K6,ADRA2A,NCF1,DYRK3,EGF,HCLS1,ADNP,CASS4,PARP9,PARP14,BMX,AGT,FGR,CBL,OSM,EPHB3,BAZ1B,SNX6,ABL2,TTN,PPP2R5B,EPHB4,IL12A,PTPN6,TNFSF18,DOK7,ZFYVE28,FGFR3,SOCS4,STK16,BST1,EPHA4,DLG4,DVL2,TNK1,TMEM102,FGFR4,DGKQ,CTF1,PSEN1,EFNA1,MAPK3,IL6R,HAX1,MAP2K1,MAP2K5,BTK,TYK2,CLK3,CD74,INSR,CCL5,CSF1R,YES1,ISL1,SUZ12,GHR,JAK1,UNC119,PTPN2,SOCS1,LRP8,PRKCZ,MLST8,INSRR,CNTF,PEAK1,MIR125A,THY1,CSPG4,LIF,DUSP22,TSLP,CADM4,EREG,MAP2K7,RAP2B,PDGFD	grey	VSMC_M10
GO:0034035	0.92	0.20	5	13	purine ribonucleoside bisphosphate metabolic process	BP	1	SLC35B2,TPST1,SLC26A1,SLC26A2,SULT1C3	grey	VSMC_M10
GO:0050427	0.92	0.20	5	13	3'-phosphoadenosine 5'-phosphosulfate metabolic process	BP	1	SLC35B2,TPST1,SLC26A1,SLC26A2,SULT1C3	grey	VSMC_M10
GO:1902115	0.92	0.11	77	161	regulation of organelle assembly	BP	1	VPS4B,PAN2,PIP4K2C,TBC1D30,MDM1,CNOT2,CNOT6,HSPA1B,RNF5,IL5,ASAP1,MAPK15,CHMP2A,DYNC2LI1,TRAPPC12,FUZ,CDK5RAP2,ATG5,SDCBP,PIP4K2A,LCP1,RALB,CEP295NL,LRFN1,RAB5A,FEZ2,ULK1,PAN3,PLK2,HCK,CHMP2B,TBC1D12,CNOT1,CHMP4C,CNOT6L,ALMS1,ZMYND10,AC112128.1,SEC22B,GAP43,TMEM39A,ADPRH,MTMR3,CDKL5,RAB1B,LIMK2,KIF9,PIKFYVE,TBC1D14,HTT,RNF4,PINK1,STX18,SDCCAG8,HAP1,MNS1,PHF23,CNTROB,CCDC151,TRIM37,DNM2,G3BP1,SMCR8,IFT20,MTM1,WRAP73,CDK10,CHMP1A,KIAA1324,GPSM2,SH3GLB1,ODF2L,RHOA,GRID2,CCSAP,DRG1,LRRTM2	grey	VSMC_M10
GO:0008637	0.92	0.12	41	87	apoptotic mitochondrial changes	BP	1	PRKN,BAK1,PLA2G6,TMEM14A,GGCT,VPS35,TIMM50,PPP2CB,HIP1R,OPA1,IFIT2,DNM1L,GPER1,IFI6,CIDEB,SFN,THEM4,STPG1,FZD9,FIS1,NMT1,PINK1,MUL1,TMEM102,ATP2A1,PSMD10,CAMK2A,JUN,ACAA2,PAM16,NAIF1,MIR29A,MLLT11,NOL3,BNIP3L,FXN,BCL2L11,SLC35F6,BCL2L2,PPIF,AC140504.1	grey	VSMC_M10
GO:0060421	0.92	0.15	15	35	positive regulation of heart growth	BP	1	GLI1,MAPK14,PIM1,MEF2C,TBX5,MAPK1,BMPR1A,RBPJ,TBX2,GATA6,MIR199A1,MIR222,BASP1,HEY2,WNT2	grey	VSMC_M10
GO:0086065	0.92	0.14	20	46	cell communication involved in cardiac conduction	BP	1	TRPM4,CACNB2,ATP1A3,SCN5A,KCNJ3,TBX5,DSP,CASQ2,RYR2,PKP2,ANK2,ATP1A2,SCN4B,ATP1B1,ATP1B2,CACNA1G,CALM1,DSG2,RNF207,HCN4	grey	VSMC_M10
GO:0050650	0.92	0.18	7	18	chondroitin sulfate proteoglycan biosynthetic process	BP	1	CHPF2,CSGALNACT1,CHST3,CHST7,CHST12,B3GALT6,CHSY3	grey	VSMC_M10
GO:0032232	0.92	0.15	12	29	negative regulation of actin filament bundle assembly	BP	1	PRKN,SHANK1,MET,CLASP2,PIK3R1,PPFIA1,ARHGAP6,WASF2,WAS,CORO2B,INPP5K,MIR21	grey	VSMC_M10
GO:0032102	0.92	0.10	131	266	negative regulation of response to external stimulus	BP	1	SERPINB2,SEMA6A,TNFAIP3,USP15,ENPP3,TSPAN8,SLC12A2,PPARA,TRIB1,C6orf106,MAPK14,TEK,SEMA4D,SEMA4C,CLDN19,CD109,FPR2,NT5E,NR1H2,VPS35,C5AR2,CST7,CLASP2,FNDC4,THBD,SEC14L1,PLAT,C1QTNF1,CHD8,SIRT2,MKKS,NMI,NR1D2,NPLOC4,SEMA3D,SEMA3A,MFHAS1,RYK,PCBP2,NR1H4,PLK2,HCK,ROBO1,ROBO2,SEMA4F,NR1H3,TRAFD1,OAS3,NLRC5,OTULIN,SEMA3G,SPP1,MAPKBP1,SEMA4G,ADTRP,NOD2,CD96,FAP,KIAA0319,CD200,SLC6A3,SEMA3F,YTHDF2,UBASH3B,GPER1,SLAMF8,PARP14,KREMEN1,RNF26,FGR,NLRX1,CERS2,TRAF3IP1,HTRA1,USF1,PTPRO,BACE1,LRIG2,WNT3,DUSP10,SEMA6D,TNR,CASK,LPCAT3,WNT4,CALCRL,MYOZ1,MUL1,PADI2,FOXP3,EPHA4,GPS2,TKFC,USP18,F12,TNFRSF1B,ANXA2,SEMA4A,SYT11,DCST1,SMAD3,TSPAN6,LDLR,STAT2,RIOK3,MAPK7,CCL2,YES1,ISL1,PTGER4,PTPN2,ABAT,CRK,SERPINF2,PLXNA3,FOXF1,MIR199A1,MIR21,MIR222,FGA,C5orf30,OAS1,GRID2,DPP4,A2M,RTN4RL1,WNT5A,DUSP1,FGL2,SERPINB9,HAVCR2	grey	VSMC_M10
GO:0071466	0.92	0.12	43	92	cellular response to xenobiotic stimulus	BP	1	NME1,MYC,SOX10,PPAT,DDC,EGFR,FGF21,NUDT15,PRNP,GAS6,MEF2C,CYP2R1,BPHL,ABCC2,KCNE2,CBR3,CMBL,TPMT,GPLD1,FMO5,CYP2U1,SLAMF8,CHEK2,ABCB11,POR,NFE2L2,RAP1B,EPHX1,PDE4A,CYP46A1,ADSSL1,NOS2,CYP2J2,HSPA5,NQO1,CRYZ,S100A12,SULT1C3,AHRR,KCNH2,NCEH1,AOC2,N6AMT1	grey	VSMC_M10
GO:0036005	0.92	0.22	4	11	response to macrophage colony-stimulating factor	BP	1	TLR4,FER,CSF1R,PTPN2	grey	VSMC_M10
GO:0036006	0.92	0.22	4	11	cellular response to macrophage colony-stimulating factor stimulus	BP	1	TLR4,FER,CSF1R,PTPN2	grey	VSMC_M10
GO:0003188	0.92	0.21	4	11	heart valve formation	BP	1	SOX9,EFNA1,HEY2,OLFM1	grey	VSMC_M10
GO:0042659	0.92	0.21	4	11	regulation of cell fate specification	BP	1	WNT11,FZD7,BMPR1A,WNT5A	grey	VSMC_M10
GO:0051283	0.92	0.12	38	83	negative regulation of sequestering of calcium ion	BP	1	PRKCE,IBTK,ATG5,RYR1,DIAPH1,RASA3,RYR3,PTK2B,TPCN1,SLC8B1,F2R,PKD2,CASQ2,RYR2,LCK,UBASH3B,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,CEMIP,PTPN6,HTT,HAP1,CD19,CALM1,BDKRB1,TRPV1,PDPK1,CYBA,JPH3,MCOLN3,DMD,NOL3,JPH2,THY1,DDIT3	grey	VSMC_M10
GO:0009123	0.92	0.12	30	65	nucleoside monophosphate metabolic process	BP	1	DPYS,IMPDH1,GDA,PPAT,NT5E,CMPK1,DLG2,AMPD3,DGUOK,GMPS,AMPD1,PRPS2,DTYMK,MAGI3,DLG1,UPB1,CASK,ADK,CARD11,UPRT,ADSSL1,NT5M,MPP1,AK8,UCK1,DHODH,CMPK2,DCTD,NUDT2,UPP1	grey	VSMC_M10
GO:0006971	0.92	0.21	4	11	hypotonic response	BP	1	TSPO,OXSR1,SLC12A5,TRPV4	grey	VSMC_M10
GO:0046620	0.92	0.12	36	78	regulation of organ growth	BP	1	GLI1,STK3,PPARA,MAPK14,PI16,PIM1,SMO,TGFBR2,DUSP6,MEF2C,IL7,TBX5,STK4,JARID2,IGF2,HLX,KCNK2,YBX3,SAV1,MAPK1,BMPR1A,RBPJ,WWC1,TBX2,YY1,GATA6,MIR199A1,MIR222,MIR25,NOG,BASP1,FXN,RGS4,BCL2L11,HEY2,WNT2	grey	VSMC_M10

GO:0002218	0.92	0.15	14	33	activation of innate immune response	BP	1	XRCC6,TLR4,IKBKB,TMEM173,MAVS,PRKDC,TRAF6,HCK,NONO,XRCC5,SFPQ,SIN3A,CREBBP,ZCCHC3	grey	VSMC_M10
GO:0060394	0.92	0.21	4	11	negative regulation of pathway-restricted SMAD protein phosphorylation	BP	1	LRP1,SNX25,NOG,LDLRAD4	grey	VSMC_M10
GO:0000271	0.92	0.13	26	58	polysaccharide biosynthetic process	BP	1	HAS1,EPM2AIP1,PPP1CB,CSGALNACT1,AKT2,PPP1R3B,GBE1,B3GNT4,SORBS1,IGF2,NHLRC1,IRS1,PPP1R3E,EGF,PPP1R3D,PER2,PASK,PRKAG3,AC022400.6,PPP1R3F,INSR,INPP5K,AGL,HAS3,ACADM,HS2ST1	grey	VSMC_M10
GO:0003279	0.92	0.12	40	88	cardiac septum development	BP	1	MAML1,FRS2,TAB1,SMO,PTK7,DNAH11,HOXA13,CNTRL,WNT11,TGFBR2,JAG1,PAX8,PARVA,ROBO1,ROBO2,TBX5,SALL1,SUFU,TGFB2,TRIP11,ANK2,LUZP1,SAV1,BMPR1A,DHRS3,RBPJ,MKS1,DCTN5,TBX2,STRA6,GATA6,AP2B1,ISL1,ZBTB14,ENG,SOX4,NOG,WNT5A,NKX2-5,HEY2	grey	VSMC_M10
GO:0071482	0.92	0.12	44	94	cellular response to light stimulus	BP	1	BAK1,MYC,ATF4,MAPK13,OPN1SW,CRY1,CAMKMT,AQP1,PTN,ERCC1,XPC,AKT2,PIK3R1,ATR,MME,EIF2AK4,DDB2,TENT2,CRY2,TP53INP1,TRPM1,RHBDD1,HYAL1,HYAL3,RRH,SAG,NFATC4,NMT1,GRK4,MMP3,RHNO1,GNB5,ZBTB1,PARP1,DDB1,GUCY2D,TAF1,YY1,CUL4B,ERCC4,FMR1,CREBBP,IMPACT,GPR88	grey	VSMC_M10
GO:0045444	0.92	0.10	91	188	fat cell differentiation	BP	1	ATAT1,STK3,PSMB8,PNPLA3,MAPK14,CBY1,PIM1,TAF8,DLK2,TFAP2B,IL11,TRIM32,DKKL1,UCP1,TRPM4,MKX,BBS7,NAPEPLD,AAMDC,KLF5,AKT2,JAG1,SIRT2,MKS,PTPRQ,PLCB1,TRIB3,ASXL1,NR4A1,CEBPA,ERAP1,NOC3L,ARNTL,TMEM120B,EBF2,RUNX1T1,TRIO,CDS1,NR4A2,FTO,RREB1,SOX13,STK4,CCND1,TRPV4,TCF7L2,CMKLR1,FABP4,GPER1,LAMB3,PER2,SYAP1,SENP2,CREB1,DUSP10,MMP11,SAV1,GNB3,TFE3,SLC2A4,GPS2,MED1,TGFB1I1,ALDH6A1,ALOXE3,JDP2,ZBTB7B,SMAD3,SREBF1,SOCS1,ZBTB7C,SDF4,PRDM16,SOX8,MIR21,MIR27B,MIR27A,BSCL2,MAFB,WNT5A,SIX1,PLAC8,DDIT3,PEX11A,CCDC3,ZFP36L2,SH2B2,CEBPB,CCDC71L,C1QL4,DIO2	grey	VSMC_M10
GO:0050665	0.92	0.20	5	13	hydrogen peroxide biosynthetic process	BP	1	ACOX1,DUOX1,STAT3,CYBA,AC140504.1	grey	VSMC_M10
GO:0002828	0.92	0.16	9	22	regulation of type 2 immune response	BP	1	RSAD2,NOD2,HLX,DENND1B,BCL6,TBX21,IL4R,CD74,PRKCZ	grey	VSMC_M10
GO:0048873	0.92	0.16	9	22	homeostasis of number of cells within a tissue	BP	1	SMO,SOX9,RAC3,IL7,F2R,KRAS,GIGYF2,ILDR2,LIPA	grey	VSMC_M10
GO:0009264	0.92	0.15	11	26	deoxyribonucleotide catabolic process	BP	1	DPYS,GDA,NUDT15,MBD4,NUDT16,NUDT18,UPB1,NEIL1,NT5M,NTHL1,UPP1	grey	VSMC_M10
GO:0045472	0.92	0.21	4	11	response to ether	BP	1	OPA1,FOXP3,LARP1,CRH	grey	VSMC_M10
GO:0010523	0.92	0.20	5	13	negative regulation of calcium ion transport into cytosol	BP	1	TMBIM6,PKD2,CASQ2,NTSR1,CALM1	grey	VSMC_M10
GO:0034333	0.92	0.21	4	11	adherens junction assembly	BP	1	RAMP2,VCL,ACTB,PIP5K1C	grey	VSMC_M10
GO:0048012	0.92	0.20	5	13	hepatocyte growth factor receptor signaling pathway	BP	1	MET,SIRT2,ESM1,ADAMTS12,PTPN2	grey	VSMC_M10
GO:0150077	0.92	0.16	9	22	regulation of neuroinflammatory response	BP	1	TTBK1,CST7,CD200,CD200R1L,MMP3,TNFRSF1B,SYT11,LDLR,IL33	grey	VSMC_M10
GO:0051081	0.92	0.21	4	11	nuclear membrane disassembly	BP	1	LPIN1,AKAP8L,NDEL1,PRKCB	grey	VSMC_M10
GO:1904705	0.92	0.13	24	53	regulation of vascular associated smooth muscle cell proliferation	BP	1	MAP3K5,HPGD,MEF2C,ADAMTS1,NQO2,TERT,PDCD4,GNA13,GPER1,AGT,EFEMP2,CDKN1B,BMPR1A,MFN2,JUN,GNAI3,MIR21,MIR222,MIR27B,MIR27A,RHOA,FOXJ2,MIR339,LDLRAP1	grey	VSMC_M10
GO:0060088	0.92	0.21	4	11	auditory receptor cell stereocilium organization	BP	1	WHRN,MYO7A,PLS1,STRC	grey	VSMC_M10
GO:0090066	0.92	0.09	208	418	regulation of anatomical structure size	BP	1	ARPC3,LRP1,SEMA6A,AVIL,RAB21,PRR16,SLC12A2,FSTL4,WASHC5,PLXNA4,PLA2G6,BAIAP2L2,PICK1,CDC42EP1,ZDHHC21,LMOD2,SRF,NCK2,SEMA4D,KIAA1211,SEMA4C,TMOD1,PLEKHH2,PRKCE,SPTBN1,RTN4,RUFY3,AQP1,PLEK,EPHA7,ITGB1BP1,ADD2,EGFR,KEL,ATG5,FAM49A,NRCAM,TRPM4,WASF1,SLC26A5,GOLGA4,MEGF8,CLNS1A,AQP11,PLEKHG2,FCHSD2,MKKS,RPTOR,RAB5A,ADRA1D,BAG4,SEMA3D,SPART,FCHSD1,SEMA3A,NCKAP1L,LARS,ULK1,ARFIP2,LMOD3,RYK,ADRA2B,RET,HCK,TTL,ASXL1,HTR7,FER,HIP1R,PLS1,FMN1,LIMA1,SEMA4F,P2RX7,GUCY1A1,P2RY1,PTK2B,DPYSL2,USH1C,DOCK5,NKX6-1,ZFYVE27,F2RL1,F2R,IQGAP2,ANO6,SEMA3G,SPP1,PAX2,CYFIP1,DMTN,SEMA4G,SLC12A5,CHRM3,MAGEL2,BDNF,RAP1GDS1,KIAA0319,CARMIL1,LMOD1,ADD3,SLC12A7,TRPV4,SEMA3F,ADRA2A,SSH1,PEX11B,HCLS1,ADNP,AP1AR,DISC1,GPER1,AGT,RAB22A,WASF2,ACE2,ATP1A2,AP2M1,SPTBN2,PER2,TMOD4,SLC12A8,EPS8,CDKL5,WHAMM,DLG1,WNT3,CAPZA1,CREB1,CDC42EP2,MAPT,PLOD3,SEMA6D,CPS1,SLC12A9,TNR,FN1,NCKAP1,ADRA2C,GNB3,ECE1,GCH1,ARPC1A,SMTNL2,CD38,KCNMA1,WAS,TMOD2,ATP13A2,SPTB,CLN8,PFN3,WNK3,SOD3,HRH2,SEMA4A,TRIM46,NDEL1,AC138894.1,HAX1,RAB11A,NTN1,SCPEP1,DNM2,SCNN1B,EVL,SIN3A,TRPV2,PEX11G,LRRC8E,ASIC2,CDK5R1,VAV1,IL7R,SSH2,RILP,SERPINF2,RAP1GAP2,P2RX1,L1CAM,MLST8,ARHGAP4,PLXNA3,SPIRE2,TSC1,LAMTOR5,VAV3,LRRC8A,BARHL2,WDR63,SLC12A4,CARMIL2,MIR21,RHOA,HTR1D,FGA,CNTN2,VASP,GMFG,WNT5A,PEX11A,GRB2,PPP1R15A,PFN4,PDXP,KCNMB4,OLFM1,COTL1	grey	VSMC_M10

GO:0007409	0.92	0.10	167	341	axonogenesis	BP	1	LRP1,SEMA6A,KIF5A,RAB21,TIAM2,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,RAC2,SMO,SRF,SEMA4D,DLX5,ETV1,SEMA4C,BRSK1,RTN4,RUFY3,HOXA2,EPHA7,EPHA1,KEL,NRCAM,PLXNA1,RAB10,GOLGA4,GLI2,MEGF8,MYCBP2,NUMBL,POU4F1,TSKU,SZT2,SLITRK5,KIF5C,FEZ2,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,ULK1,RYK,EPHB1,RET,TTL,ROBO1,ROBO2,FZD3,SEMA4F,DPYSL2,TIAM1,SLIT1,NKX6-1,TRIO,NR4A2,ZFYVE27,SEMA3G,SPP1,PAX2,CYFIP1,ALCAM,SEMA4G,SIAH1,BMPR1B,BDNF,KIAA0319,LGR6,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,ADNP,DISC1,GBX2,KALRN,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,SEMA6D,EPHB4,ITGA4,TNR,FN1,ATL1,NIN,PPP3CB,RAB3A,MARK2,VCL,RAB8A,CRMP1,EPHA4,LRTM2,ACTB,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,TRIM46,EFNA1,NDEL1,CHRNB2,RAB11A,MAP2K1,NTN1,RPS6KA5,RNF165,DNM2,BCL11B,LHX1,SIN3A,TRPV2,LAMA3,CDK5R1,ISL1,EMB,LAMA1,DOCK7,SLC9A6,DAB1,SLITRK2,L1CAM,NTN3,ARHGAP4,PLXNA3,BSG,TUBB3,AMIGO1,NTNG2,STXBP1,BARHL2,DPYSL5,EFNA4,CNTN2,VASP,FOXG1,ISL2,NOG,THY1,WNT5A,POU3F2,CHN1,ARTN,NRXN3,LYPLA2,EFNB3,ISPD,MAP1A,OLFM1	grey	VSMC_M10
GO:0007034	0.92	0.11	65	137	vacuolar transport	BP	1	VPS4B,LRP1,AP3S1,IGF2R,PRKN,VPS52,TGFBRAP1,CHMP2A,VPS41,VPS35,RAB7A,RBSN,HGSNAT,HOOK3,TMEM106B,FAM160A2,LEPROTL1,VPS16,SLC46A3,NCOA4,CHMP2B,CHMP4C,AP3B1,CHMP7,VPS18,VPS39,KIF13A,RAB7B,MON1A,CCDC91,VTI1A,HSPA8,SORL1,DTX3L,RNF215,SNX27,VPS37D,AP4M1,PINK1,ANKFY1,AP3M1,ATP13A2,VPS13D,GAK,VPS13C,AC138894.1,HOOK2,VIPAS39,STX8,SNAPIN,NPC1,LAMP2,CLEC16A,VPS53,MTM1,MGRN1,RILP,CHMP1A,AP1G1,VPS4A,CACNG7,AP3S2,SNX16,LEPROT,CACNG5	grey	VSMC_M10
GO:0090501	0.92	0.11	59	124	RNA phosphodiester bond hydrolysis	BP	1	PAN2,RPP21,CPSF6,CNOT2,CNOT6,RIDA,PNLDC1,UTP23,AGO2,EXOSC4,CPSF1,TSR1,EXOSC3,TSEN34,PNPT1,RNASEH1,PCF11,NUDT16,POLR2I,PAN3,BMS1,CSTF3,NUDT12,POP4,CNOT1,USB1,CNOT6L,RPP40,POP5,CPSF2,DIS3L2,YBEY,NOP9,ANGEL2,NYNRIN,NCBP2,KIAA0391,POP7,ZC3H12C,CPSF4,AP002990.1,MRPL44,EXD2,ISG20L2,ANGEL1,RNASEH2A,CSTF2,CNOT8,KRI1,ERI2,SLFN14,PARN,DROSHA,INTS11,NOL9,POLR3K,RPP38,RPP30,EXOSC5	grey	VSMC_M10
GO:0001832	0.92	0.17	7	18	blastocyst growth	BP	1	TAF8,NBN,ACVR1C,RTF1,SBDS,RAD51B,NDEL1	grey	VSMC_M10
GO:0009409	0.92	0.14	17	39	response to cold	BP	1	SLC25A27,UCP1,P2RX3,EIF2AK4,GMPR,TRPM8,SLC9A1,VGF,SLC27A1,ACADVL,THRA,FOS,ACOT11,CIRBP,ACADM,CASP8,PLAC8	grey	VSMC_M10
GO:0099084	0.92	0.15	11	27	postsynaptic specialization organization	BP	1	SYNGAP1,LRRC4,LRFN1,GAP43,DLG1,NRXN2,NLGN2,NTNG2,ZDHHC12,GRID2,LRRTM2	grey	VSMC_M10
GO:0034330	0.92	0.09	269	541	cell junction organization	BP	1	LRP1,PRRT1,SYNGAP1,MTSS1,PTK2,MAPK14,NTRK2,PICK1,MPDZ,TEK,LRRC4,LINGO2,ABHD17B,SRF,GABRA1,FZD1,SLC1A1,ADGRF1,TLN1,SEMA4D,ADGRL3,CLDN19,SHANK1,GJA10,LRRN3,EPHA7,WHRN,PTN,ITGB1BP1,GRHL1,ADD2,TNC,CTTNBP2,YWHAZ,DLGAP3,VPS35,SDCBP,NRCAM,SLC7A11,PPFIA3,WASF1,MTMR2,SLC8A2,C5AR1,VSTM5,IQSEC1,CACNB2,CLASP2,PCDH8,FBF1,PTPRF,NUMBL,POU4F1,WNT11,SLITRK5,IKBKB,LRFN1,FARP1,ACTG1,CACNB4,PRNP,PCDHGC5,ARHGEF7,P2RX2,NRG1,PTPRA,PKP3,LRFN3,RYK,EPHB1,NPHP1,LSR,FAM107A,PIK3R1,CLSTN2,CTNND1,CHMP2B,MARVELD2,ROBO2,ERC2,FMN1,SORBS1,PTPRJ,MEF2C,CUX2,KIFC3,PLEKHA7,SEPT11,PTK2B,RAPGEF2,TIAM1,SLIT1,HOMER1,OPA1,HDAC7,TBX5,AMIGO2,F2RL1,F2R,SPARCL1,ITPKA,DSP,CYFIP1,DMTN,TUBA1A,LDB1,BDNF,DOCK10,PPFIA4,INA,NEURL1,PKP2,SLK,DNM1L,PPFIA1,COL17A1,CAPRIN2,TRPV4,SEMA3F,TGFB2,GAP43,COL16A1,PPFIBP1,CAMKV,DAG1,AMIGO3,NLGN4Y,SSH1,AJUBA,CFL1,STAU1,CLDN34,CDH24,BSN,SNAI1,ADNP,ARHGAP6,HSPA8,DISC1,ANK2,GNPAT,AGT,WASF2,ACE2,SLC9A1,RAB17,SPTBN2,NFATC4,ACTN3,NPAS4,PTPRO,CDKL5,IL10RA,EPHB3,TANC2,NOS1AP,WHAMM,FZD9,LAMC1,DLG1,APOD,CAPZA1,FZD5,MAPT,RAP1B,SRGN,C1QL1,TRIP6,ARVCF,TNR,NRXN2,FN1,SPOCK2,DOK7,GPBAR1,WNT4,DNM3,CNTNAP1,RAB3A,RAMP2,SYN1,VCL,OBSL1,GRIPAP1,EPHA4,LRTM2,DLG4,ACTB,CLDN7,SDK1,NLGN2,GPHN,CHRNB1,LGI2,CACNB1,PSEN1,SEMA4A,ITGAM,TLN2,RAB8B,ITGA3,NLGN3,TAOK2,EFNA1,AC138894.1,CHRNB2,ZDHHC15,MYH10,SMAD3,NTN1,CORO2B,SNAPIN,DRP2,MYO9A,VMP1,BCAS3,GPRASP2,BHLHB9,ARHGAP44,DSG	grey	VSMC_M10
GO:0035357	0.92	0.17	7	18	peroxisome proliferator activated receptor signaling pathway	BP	1	ASXL1,PDK3,GPS2,MED1,ALOXE3,RXRA,FABP5	grey	VSMC_M10
GO:0045071	0.92	0.14	15	35	negative regulation of viral genome replication	BP	1	APOBEC3H,RSAD2,ZC3HAV1,EIF2AK2,MAVS,FAM208A,OAS3,IFIH1,OASL,TNIP1,CCL5,INPP5K,SETDB1,OAS1,FAM111A	grey	VSMC_M10
GO:0021761	0.92	0.12	34	75	limbic system development	BP	1	NME1,ATAT1,UQCRQ,SMO,SRF,CDK6,NDNF,EIF2B3,XRCC1,TSKU,ALK,MKKS,SEMA3A,CASP3,DCLK2,TENT2,SRD5A1,HDAC1,ALDH1A3,ATP1A2,DLX1,KCNA1,HAP1,KDM6B,CDK5R1,DAB1,LRP8,CRK,PLXNA3,TSC1,PHLPP2,UBB,POU3F2,CRH	grey	VSMC_M10
GO:0033145	0.92	0.21	4	11	positive regulation of intracellular steroid hormone receptor signaling pathway	BP	1	KMT2D,PARP1,MED1,PAGR1	grey	VSMC_M10
GO:0042693	0.92	0.21	4	11	muscle cell fate commitment	BP	1	MEF2C,TBX5,RBPJ,TBX2	grey	VSMC_M10
GO:0097091	0.92	0.21	4	11	synaptic vesicle clustering	BP	1	BRSK1,RAB3A,SYN1,NLGN2	grey	VSMC_M10
GO:1900274	0.92	0.14	13	31	regulation of phospholipase C activity	BP	1	ESR1,KIT,LPAR1,EGFR,C5AR1,PHB,RASGRP4,FLT1,ARHGAP6,AGT,ABL2,GNA15,HRAS	grey	VSMC_M10
GO:0032695	0.92	0.21	4	11	negative regulation of interleukin-12 production	BP	1	PIBF1,NOD2,CMKLR1,MIR21	grey	VSMC_M10

GO:0007589	0.92	0.12	31	68	body fluid secretion	BP	1	NME1,SLC22A4,GUCA1B,PPAT,PRKCE,AQP1,NR1H2,EGFR,ATG5,TRAF3IP2,USF2,NR1H3,VDR,CHRM3,NEURL1,SLC6A3,CCND1,COPA,CREB1,SERPINC1,CHRM1,STAT5B,MED1,ANXA2,ZBTB7B,UPRT,SCNN1B,CELSR2,CEL,CYBA,DHODH	grey	VSMC_M10
GO:0099175	0.92	0.12	33	73	regulation of postsynapse organization	BP	1	ABHD17B,EPHA7,VPS35,LRFN1,PRNP,CHMP2B,CUX2,TIAM1,HOMER1,OPA1,ITPKA,DNM1L,CAPRIN2,SEMA3F,CFL1,HSPA8,CDKL5,TANC2,SRGN,DNM3,EPHA4,EFNA1,ZDHHC15,GPRASP2,BHLHB9,ARHGAP44,CDK5R1,LRP8,ABHD17A,GRID2,ABHD17C,WNT5A,LRRTM2	grey	VSMC_M10
GO:0001824	0.92	0.11	40	86	blastocyst development	BP	1	CNOT2,PNLDC1,RRP7A,MFNG,TAF8,SRF,RTN4,CCNB1IP1,CCDC62,CNOT1,NBN,ACVR1C,RTF1,ZBED6,NPM2,ELF3,SBDS,DAD1,PLPP4,RPL7L1,SP3,TET1,BCOR,TTLL4,AKAP3,ARHGDIG,WDR74,SLC25A34,MFN2,RAD51B,NDEL1,PPP4R4,NLE1,XAB2,SUPT6H,CMTM3,PEMT,C6orf141,MED21,ST8SIA6	grey	VSMC_M10
GO:1901841	0.92	0.19	5	13	regulation of high voltage-gated calcium channel activity	BP	1	CACNB2,NOS1AP,CALM1,RRAD,GEM	grey	VSMC_M10
GO:0071496	0.92	0.10	131	267	cellular response to external stimulus	BP	1	MARS,MAP3K5,CYP27B1,SNW1,PPARA,BAK1,HABP4,ATF4,PICK1,PIM1,TXN2,TFEB,SLC39A4,SRF,NUAK1,BRSK1,ALB,AQP1,RRAGD,CASP8AP2,PTN,TNC,EGFR,TLR4,VPS41,IL15,ATG5,FOXO3,MKX,KPTN,SESN3,FOXA3,SOX9,NUDT15,DNAJC15,RALB,PRKAG2,MYD88,SZT2,WNT11,RPTOR,CNN2,EIF2AK2,WRN,GAS6,LARS,ULK1,NR1H4,USF2,FAM107A,PRKAG1,EIF2AK4,TMEM150C,VDR,NR4A2,SLC38A2,CD40,NUAK2,NUPR2,SRD5A1,DNM1L,CBSL,GLRX2,SIK1,KCNJ2,SLC38A3,DAG1,KCNB1,TLR5,ADNP,HSPA8,AGT,CBL,ATP1A2,BAG3,SLC9A1,MTMR3,UCN2,HDAC4,USF1,XPR1,TBL2,GLUL,NFE2L2,ITGA4,SIK2,COMT,KCNK4,WNT4,PRKAG3,CTSV,LTBR,MAPK1,BHLHA15,WIPI2,MAX,TNFRSF8,MED1,RRAGB,ZFYVE1,FOS,MAPK3,TNRC6A,SREBF1,LAMP2,NIM1K,PTGER4,STK26,JUN,CLEC16A,KIAA1324,PIEZO1,CYBA,TSC1,LCN2,WDR59,ENG,HSPA5,SH3GLB1,BCL10,RIPOR1,MIR125B1,TRIM24,FADD,CASP8,BGLAP,IMPACT,GADD45A,CRADD,UPP1,RNF152	grey	VSMC_M10
GO:0043949	0.92	0.17	7	18	regulation of cAMP-mediated signaling	BP	1	UBE2B,GIPR,RAPGEF2,PDE4A,MGRN1,CRH,RASD2	grey	VSMC_M10
GO:0046755	0.92	0.16	9	22	viral budding	BP	1	VPS4B,CHMP2A,CHMP2B,CHMP4C,CHMP7,VPS37D,CHMP1A,MVB12B,VPS4A	grey	VSMC_M10
GO:0034660	0.92	0.09	208	412	ncRNA metabolic process	BP	1	MARS,ADAT2,HELB,RPP21,TFB1M,MOV10L1,TRMU,UTP23,RRP7A,TRMT11,AGO2,TUT7,C9orf64,EXOSC4,NOL6,XPO5,TSR1,EXOSC3,RPS14,MTO1,TSEN34,ELP1,PNPT1,UTP3,PUS10,TRIT1,MDN1,AGO1,FCF1,QRSL1,TUT4,DUS4L,NSUN6,ERCC2,RPS8,DEDD2,RPL14,INTS10,THUMPD3,USP36,ESF1,KRR1,DPH3,SIRT7,HARS,HARS2,TRMT6,TRNT1,CARS2,NUDT16,LARS,THUMPD2,PRKDC,TRMT9B,DHX37,BMS1,DIMT1,ELP4,POP4,CLP1,ZCCHC8,ELP3,BCDIN3D,USB1,TPRKB,URB1,DDX54,NSUN3,RRP12,TENT2,HELQ,RPUSD2,OSGEPL1,INTS8,RPP40,EXD1,RIOK1,TENT4B,WARS2,CDKAL1,GATC,POP5,PDCD11,RPUSD4,YARS2,TRMT10A,ZBTB8OS,RPS17,QTRT2,SBDS,TYW1B,INTS12,HEATR1,TYW5,FAM207A,DIS3L2,MRPS11,GAR1,TRUB1,YTHDF2,RTRAF,TARS2,DALRD3,YBEY,LCMT2,NOP9,RPS27,WDR12,METTL8,RPL7L1,TDRKH,WBP11,ELP6,NSUN5,DDX47,RPL11,METTL2B,KIAA0391,RBM7,TRMT1L,MAPT,PRKRA,LARS2,POP7,DDX3X,DDX10,RC3H1,MEPCE,DDX49,DARS2,TRPT1,RPL27,ALKBH8,ZSWIM8,STAT3,WDR74,TRMT5,INTS5,AP002990.1,FARSB,MRPL44,HSD17B10,NVL,MRM2,TSR2,ZCCHC4,LAS1L,MTFMT,ALKBH1,UTP18,THG1L,SMAD3,QTRT1,EARS2,INTS2,KRI1,ZNHIT3,ELP2,ERI2,THUMPD1,RIOK3,SLFN14,METTL4,RNF113B,UTP6,METTL6,SNU13,UTP14A,PARN,DROSHA,MRM3,INTS11,PUSL1,METTL16,LRRC47,NOL9,RPUSD1,WDR18,POLR3K,KARS,ADAT1,AARS,RPL35,ZNHIT6,DUS2,METTL18,CTU1,AGO4,MARS2,RPP38,MPHOSPH6,TRMT10B,DTD1,TP53RK,TRMT61A,RPUSD3,NSA2,C1D,DTD2,HRAS,PIH1D2,TRMT10C,RPP30,TRMT61B,TYW3,RC3H2,EXOSC5,GTF2H5	grey	VSMC_M10
GO:0044406	0.92	0.21	4	11	adhesion of symbiont to host	BP	1	NECTIN2,GAS6,ACE2,LRRC15	grey	VSMC_M10
GO:1901216	0.92	0.12	36	78	positive regulation of neuron death	BP	1	MAP3K5,ATF4,TFAP2B,EPHA7,TLR4,FOXO3,ZNF746,GRIK5,PRNP,CASP3,FBXW7,NQO2,TFAP2A,TGFB2,SSH1,MCL1,HDAC4,BACE1,MAP3K11,MAPT,FIS1,PARP1,ITGAM,FOS,PPP1R13B,CDK5R1,JUN,LCN2,NQO1,MIR125B1,RHOA,CASP8,WNT5A,DDIT3,BCL2L11,PITX3	grey	VSMC_M10

GO:1903507	0.92	0.09	482	945	negative regulation of nucleic acid-templated transcription	BP	1	SMARCC2,ATP8B1,PLAGL1,ZBTB2,ESR1,CNOT2,OSR2,SNW1,ZNF706,ZBTB12,PRKN,PPARA,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,PTCH1,ATF4,CBX7,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,RPS14,ZNF550,BEND6,ZNF268,SCMH1,NFE2L3,HOXA2,HOXA7,JAZF1,XPO1,AKIRIN2,CASP8AP2,BACH2,ZNF692,NR1H2,ZNF350,FOXP2,MED25,KLF11,POU3F3,LANCL2,CREM,SDCBP,OSR1,FOXO3,BEND5,HDAC2,PHF10,DNMT3A,BMI1,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,SUV39H2,ZNF404,PLK3,GLI2,DEDD2,RSF1,KDM4A,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,SFMBT2,GZF1,POU4F1,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,TAF7,NRG1,GAS6,RYBP,FOXP1,MITF,MTA3,ARID5A,IRF7,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,NCOA2,DKK3,SAP30,ZNF366,ARNTL,GCFC2,HMBOX1,MEF2C,PEX2,PKIA,TMBIM6,CNOT1,SLA2,CUX2,MCPH1,SOX6,FNIP2,BACH1,SFMBT1,NR1H3,EAPP,SCAF4,LCOR,DDX54,RUNX1T1,VDR,NKX3-1,BAHD1,HDAC7,NKX6-1,LOXL2,NR4A2,PHF21A,CRY2,PRDM11,CDYL,RREB1,RTF1,ZBED6,SOX13,ZNF248,TFAP2A,RIPPLY3,HIF1AN,PAX2,SALL1,PPHLN1,PRICKLE1,HIVEP1,JARID2,ATXN1,SUDS3,ZNF423,LDB1,IGF2,MAGEL2,ELK4,NUPR2,DCAF1,SUFU,TAGLN3,PCGF6,IRX2,RPL23,HDAC1,ELF3,CCND1,SP100,TRPV4,PDCD4,ZBTB20,SATB2,TCF7L2,AJUBA,ZNF639,PIAS3,LHX9,HJV,FABP4,SNAI1,ZNF202,H	grey	VSMC_M10
GO:0032506	0.92	0.14	15	35	cytokinetic process	BP	1	VPS4B,MYH9,MITD1,CHMP2A,CHMP2B,CHMP4C,RTKN,CHMP7,BIN3,KLHDC8B,CNTROB,SPIRE2,CHMP1A,VPS4A,RHOA	grey	VSMC_M10
GO:0009163	0.92	0.19	5	13	nucleoside biosynthetic process	BP	1	MTAP,NT5E,PRTFDC1,DTYMK,ADK	grey	VSMC_M10
GO:0034404	0.92	0.19	5	13	nucleobase-containing small molecule biosynthetic process	BP	1	MTAP,NT5E,PRTFDC1,DTYMK,ADK	grey	VSMC_M10
GO:0051651	0.92	0.10	78	163	maintenance of location in cell	BP	1	TSPO,SKP1,SUN2,GPAA1,TAF8,PRKCE,IBTK,ALB,ATG5,ARHGAP21,ATP7B,GRIK5,TAF3,RYR1,DIAPH1,RASA3,RYR3,PTK2B,ARL2BP,TPCN1,SLC8B1,F2R,PKD2,MORC3,CASQ2,RYR2,LCK,SP100,UBASH3B,SORL1,ANK2,GPER1,ATP1A2,CASQ1,NTSR1,TBCCD1,SLC30A4,SRGN,CEMIP,HK1,PTPN6,HTT,PINK1,FTH1,HAP1,VPS13D,VPS13C,PSEN1,ATP2A1,CD19,CALM1,S100A8,RIT2,BDKRB1,SLC25A23,TRPV1,PDPK1,RER1,PARK7,GPSM2,CYBA,JPH3,SLC30A7,SPOUT1,LCN2,HSPA5,MCOLN3,DMD,NOL3,JPH2,THY1,SUPT7L,FTL,DDIT3,TXN,INSIG2,PFN4,POLR2M	grey	VSMC_M10
GO:1990090	0.92	0.13	20	46	cellular response to nerve growth factor stimulus	BP	1	ARPC3,NTRK2,MICALL1,FOXO3,NTF4,WASF1,RAPGEF2,BDNF,CIB1,CBL,CREB1,MAPT,EHD1,CSTF2,CRK,TRPV1,PDPK1,LCN2,HSPA5,DYNC1LI2	grey	VSMC_M10
GO:0048872	0.92	0.10	112	229	homeostasis of number of cells	BP	1	TNFAIP3,MPIG6B,HSPA1B,BRD1,BAK1,SMAD5,L3MBTL3,FANCC,MAPK14,SMO,ZNF16,RBFOX2,SRF,OCIAD1,CDK6,KIT,PRDX1,RPS14,SMAP1,EPAS1,PTBP3,SLC46A2,BPGM,SLC7A11,FOXO3,TRAF3IP2,NAPEPLD,FOXA3,SOX9,ERCC2,WDR48,SLC25A38,ACVR2A,RAC3,NCKAP1L,PRKDC,MFHAS1,GAPT,ZC3H8,ASXL1,GPI,ACVR1B,PIK3CB,CASP3,MEF2C,IL7,AP3B1,F2R,TMEM14C,DMTN,ALAS1,LDB1,DOCK10,PKNOX1,RPS17,GPAM,TCIRG1,SART3,ACIN1,KRAS,DYRK3,GIGYF2,HCLS1,ARNT,SP3,PPP2R3C,BCL6,LPCAT3,RC3H1,CXCR2,PPP3CB,STAT3,STAT5B,ILDR2,INHA,LIPA,FOXP3,THRA,CARD11,MED1,HOXB6,AHSP,KAT7,DNASE2,UBAP2L,LAT,SCNN1B,GPRASP2,RCOR1,CD74,NLE1,IL7R,PTPN2,DNAJA3,BCL10,MIR222,ANKRD54,ARID4A,ADGRG1,SOX4,MAFB,FADD,CXCL6,CAMLG,TSC22D3,BCL2L11,FAM210B,SH2B2,SLC39A3,TNFSF13B,XKR8,RC3H2	grey	VSMC_M10
GO:0009154	0.92	0.14	15	35	purine ribonucleotide catabolic process	BP	1	PDE7B,PDE10A,GDA,NT5E,NUDT16,AMPD3,ENTPD4,FITM2,NUDT18,PDE9A,PDE8A,PDE4A,MLYCD,NUDT19,HINT1	grey	VSMC_M10
GO:0043555	0.92	0.17	7	18	regulation of translation in response to stress	BP	1	NCK2,EIF2AK2,EIF2AK4,RPS6KA1,DDX3X,IMPACT,PPP1R15A	grey	VSMC_M10
GO:0071548	0.92	0.14	13	31	response to dexamethasone	BP	1	FECH,AQP1,EGFR,FOXO3,BMI1,DNMT3B,ABCC2,SRD5A1,CPS1,ASS1,SMYD3,CLDN1,CRH	grey	VSMC_M10
GO:0003085	0.92	0.21	4	11	negative regulation of systemic arterial blood pressure	BP	1	NTSR1,TRPV1,GPR37L1,CRH	grey	VSMC_M10
GO:0061744	0.92	0.21	4	11	motor behavior	BP	1	SLC1A1,ADARB1,ATP1B2,DPP4	grey	VSMC_M10
GO:0042303	0.92	0.12	34	75	molting cycle	BP	1	FZD6,SMO,ZDHHC21,SOSTDC1,CD109,EGFR,FUZ,INTU,HDAC2,SOX9,ERCC2,PTCH2,GLI2,TSKU,FERMT1,ACVR1B,TRPC4AP,ARNTL,FZD3,LDB1,HDAC1,TERT,TGFB2,SNAI1,LAMA5,FARP2,SAV1,GORAB,RBPJ,NGFR,TRPV3,EPS8L3,WNT5A,DNASE1L2	grey	VSMC_M10
GO:0042633	0.92	0.12	34	75	hair cycle	BP	1	FZD6,SMO,ZDHHC21,SOSTDC1,CD109,EGFR,FUZ,INTU,HDAC2,SOX9,ERCC2,PTCH2,GLI2,TSKU,FERMT1,ACVR1B,TRPC4AP,ARNTL,FZD3,LDB1,HDAC1,TERT,TGFB2,SNAI1,LAMA5,FARP2,SAV1,GORAB,RBPJ,NGFR,TRPV3,EPS8L3,WNT5A,DNASE1L2	grey	VSMC_M10
GO:0007063	0.92	0.17	7	18	regulation of sister chromatid cohesion	BP	1	SLF1,SLF2,AXIN2,DDX11,SFPQ,NAA10,CTCF	grey	VSMC_M10
GO:0072673	0.92	0.18	6	16	lamellipodium morphogenesis	BP	1	WASF1,ABI1,ARHGEF7,RREB1,WASF2,SNX1	grey	VSMC_M10

GO:0007159	0.92	0.10	115	234	leukocyte cell-cell adhesion	BP	1	AGER,PPARA,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,RAC2,ZDHHC21,TNFRSF21,NCK2,SEMA4D,NT5E,PELI1,ADD2,IL4I1,IL15,PODXL2,BMI1,GLI2,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,SOX12,ZC3H8,IL1A,CASP3,TMEM131L,IL7,PAG1,JAM2,RASGRP1,RIPK2,AP3B1,MARCH7,SOX13,ADTRP,NOD2,IGF2,LCK,ICOSLG,BTN2A2,GPAM,PRKAR1A,SELPLG,HLX,CD28,RUNX3,DLG1,ADAM8,OLR1,MIA3,DUSP10,BCL6,ITGA4,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,FERMT3,LAG3,STAT5B,SCGB1A1,FOXP3,RASAL3,ZBTB1,CARD11,TBX21,STK10,ZBTB7B,IL4R,S100A8,TNIP1,UMOD,CD74,CCL5,CCL2,CCL25,YES1,NKAP,VAV1,TWSG1,IL7R,PTPN2,SOCS1,DNAJA3,PRKCZ,ASS1,GLMN,BCL10,MIR21,MIR222,MIR27A,RHOA,SOX4,FADD,DPP4,CD46,FUT4,MIR125A,THY1,FGL2,CD70,TNFSF9,LAX1,EFNB3,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0006368	0.92	0.12	26	58	transcription elongation from RNA polymerase II promoter	BP	1	ARID1B,SOX10,ERCC3,GTF2F2,ZMYND11,POLR2I,ELP4,SMARCD1,EAPP,RTF1,LDB1,ARID1A,RNF168,SETD2,WDR61,ENY2,ELL,NELFA,LEO1,PADI2,CDK12,ELP2,SUPT6H,RF00100,SERTAD2,RNF8	grey	VSMC_M10
GO:0061450	0.92	0.20	4	11	trophoblast cell migration	BP	1	AGO2,ACVR1B,ACVR1C,SYDE1	grey	VSMC_M10
GO:0051293	0.92	0.13	19	44	establishment of spindle localization	BP	1	MYH9,NLRP5,CDK5RAP2,SPRY1,CLASP2,LLGL2,SPRY2,NSFL1C,MOS,MCPH1,CFL1,HTT,KPNB1,NDEL1,TLE6,SAPCD2,SPIRE2,GPSM2,OOEP	grey	VSMC_M10
GO:0007229	0.92	0.11	42	92	integrin-mediated signaling pathway	BP	1	ITGA7,MPIG6B,PTK2,MYH9,TEC,TLN1,PLEK,PTN,ITGB1BP1,FERMT1,PTPRA,HCK,ADAMTS1,PTK2B,CDH17,DMTN,ITGB6,SLC2A10,COL16A1,ITGA10,FGR,ITGB5,LAMA5,DOCK1,ITGA2B,ITGA4,FN1,FERMT3,COL3A1,BST1,ITGAM,ITGA3,LAT,ITGA11,LAMA3,PRAM1,VAV1,ADAMTS13,VAV3,FYB1,THY1,ZNF304	grey	VSMC_M10
GO:0060999	0.92	0.13	16	38	positive regulation of dendritic spine development	BP	1	SHANK1,CUX2,TIAM1,OPA1,ITPKA,NEURL1,DNM1L,CAPRIN2,CDKL5,PSEN1,GPRASP2,BHLHB9,FMR1,LRP8,LLPH,FOXO6	grey	VSMC_M10
GO:0003151	0.92	0.12	26	59	outflow tract morphogenesis	BP	1	FOXH1,WNT11,TGFBR2,JAG1,RYR1,HAND2,EYA1,PARVA,ROBO1,ROBO2,MEF2C,NPY1R,TGFB2,DVL2,BMPR1A,DHRS3,RBPJ,TBX2,GATA6,ISL1,ENG,NOG,WNT5A,SIX1,NKX2-5,HEY2	grey	VSMC_M10
GO:0042983	0.92	0.20	4	11	amyloid precursor protein biosynthetic process	BP	1	AGO2,PAWR,SOAT1,ABCA7	grey	VSMC_M10
GO:0042984	0.92	0.20	4	11	regulation of amyloid precursor protein biosynthetic process	BP	1	AGO2,PAWR,SOAT1,ABCA7	grey	VSMC_M10
GO:0007006	0.92	0.11	47	99	mitochondrial membrane organization	BP	1	HEBP2,HSPA4,BAK1,TOMM22,TMEM14A,AGK,CHCHD6,TIMM50,IMMT,HIP1R,MTX3,OPA1,AP3B1,OXA1L,MFN1,RCC1L,SLC9A1,THEM4,STPG1,FZD9,NMT1,BCS1L,PINK1,MUL1,STAT3,TMEM102,CLN8,MFN2,ADCK1,CALM1,TIMM29,CAMK2A,MAIP1,C19orf70,ACAA2,NAIF1,MIR29A,NOL3,MINOS1,BNIP3L,TIMM10B,BCL2L11,SLC35F6,BCL2L2,TIMM8B,PPIF,AC140504.1	grey	VSMC_M10
GO:0071295	0.92	0.14	12	29	cellular response to vitamin	BP	1	CYP27B1,SNW1,PIM1,PTN,TNC,IL15,GAS6,VDR,MED1,MIR125B1,TRIM24,BGLAP	grey	VSMC_M10
GO:0032481	0.92	0.13	21	48	positive regulation of type I interferon production	BP	1	IRF5,GAPDH,TLR4,MYD88,TMEM173,MAVS,IRF7,OAS3,RIPK2,POLR3D,IFIH1,POLR3C,SETD2,DDX3X,POLR3A,G3BP1,RIOK3,RNF135,TICAM1,OAS1,ZCCHC3	grey	VSMC_M10
GO:0050927	0.92	0.16	8	20	positive regulation of positive chemotaxis	BP	1	AGER,CXCL8,VEGFC,F2RL1,IL16,PGF,SMAD3,ARTN	grey	VSMC_M10
GO:2000641	0.92	0.17	7	18	regulation of early endosome to late endosome transport	BP	1	RAB21,MTMR2,DNAJC13,MAPK1,SNX12,MAPK3,MAP2K1	grey	VSMC_M10
GO:1900044	0.93	0.20	4	11	regulation of protein K63-linked ubiquitination	BP	1	NOD2,DDX3X,GPS2,OTUB2	grey	VSMC_M10
GO:0045738	0.93	0.14	13	31	negative regulation of DNA repair	BP	1	HELB,HSF1,CYREN,FBH1,RNF169,SHLD1,ERCC6,SHLD2,OTUB2,SMCHD1,RMI2,NUDT16L1,TERF2	grey	VSMC_M10
GO:0060420	0.93	0.12	26	58	regulation of heart growth	BP	1	GLI1,PPARA,MAPK14,PI16,PIM1,TGFBR2,DUSP6,MEF2C,TBX5,JARID2,KCNK2,SAV1,MAPK1,BMPR1A,RBPJ,TBX2,YY1,GATA6,MIR199A1,MIR222,MIR25,NOG,BASP1,RGS4,HEY2,WNT2	grey	VSMC_M10
GO:0007422	0.93	0.12	31	69	peripheral nervous system development	BP	1	ERBB3,ONECUT2,ADGRG6,GFRA3,PLXNA4,NTRK2,SOX10,ADAM22,ETV1,NTF4,POU4F1,PRX,AKT2,SIRT2,NRG1,LGI4,HAND2,BDNF,DAG1,RUNX3,SERPINI1,CNTNAP1,MPP5,ASIC2,ISL1,SKI,SOX8,ISL2,CLDN1,POU3F2,ARTN	grey	VSMC_M10
GO:0048144	0.93	0.12	30	66	fibroblast proliferation	BP	1	B4GALT7,ESR1,MYC,CDK6,AQP1,MED25,TRIM32,BMI1,DACH1,PAWR,GAS6,PRKDC,PEX2,TP53INP1,MORC3,AGT,CREB1,FN1,FTH1,ANXA2,NGFR,CTC1,CD74,SKI,DAB2IP,WNT5A,EREG,C1QL4,WNT2,PDGFD	grey	VSMC_M10
GO:0048145	0.93	0.12	30	66	regulation of fibroblast proliferation	BP	1	B4GALT7,ESR1,MYC,CDK6,AQP1,MED25,TRIM32,BMI1,DACH1,PAWR,GAS6,PRKDC,PEX2,TP53INP1,MORC3,AGT,CREB1,FN1,FTH1,ANXA2,NGFR,CTC1,CD74,SKI,DAB2IP,WNT5A,EREG,C1QL4,WNT2,PDGFD	grey	VSMC_M10
GO:1900271	0.93	0.14	14	33	regulation of long-term synaptic potentiation	BP	1	AGER,PTN,PRNP,FAM107A,MME,EIF2AK4,IGSF11,STAU1,YTHDF1,CREB1,CRTC1,NSG1,EPHA4,CYP46A1	grey	VSMC_M10
GO:2001238	0.93	0.13	16	37	positive regulation of extrinsic apoptotic signaling pathway	BP	1	STK3,FAF1,PDIA3,DEDD2,RET,HTRA2,RIPK1,STK4,BMPR1B,GPER1,AGT,PEA15,LTBR,TRAF2,BCL10,FADD	grey	VSMC_M10
GO:0002287	0.93	0.13	20	46	alpha-beta T cell activation involved in immune response	BP	1	HLA-DRA,EOMES,FOXP1,RIPK2,HLX,BCL6,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,PTGER4,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0002293	0.93	0.13	20	46	alpha-beta T cell differentiation involved in immune response	BP	1	HLA-DRA,EOMES,FOXP1,RIPK2,HLX,BCL6,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,PTGER4,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0043537	0.93	0.14	14	33	negative regulation of blood vessel endothelial cell migration	BP	1	MEOX2,ITGB1BP1,MEF2C,PDCD10,VASH1,MAP2K5,MECP2,MIR199A1,MIR22,MIR24-1,RHOA,ACVRL1,GADD45A,RGCC	grey	VSMC_M10
GO:0021871	0.93	0.20	4	11	forebrain regionalization	BP	1	PGAP1,TTC21B,LHX1,ADGRG1	grey	VSMC_M10

GO:0031929	0.93	0.11	49	105	TOR signaling	BP	1	EPM2A,ROS1,RRAGD,MFSD8,KPTN,SESN3,SZT2,PIP4P1,RPTOR,NCKAP1L,GAS6,LARS,TMEM127,SLC38A9,ARNTL,RHEBL1,MAPKAPK5,TTI1,TBCK,PDCD6,GPR137B,DYRK3,RPS6KB2,DISC1,SH3BP4,SYAP1,SIK3,EIF4EBP2,GPR137,PINK1,ARAF,TIPRL,OTUD5,CARD11,RRAGB,DGKQ,LARP1,SMCR8,CLEC16A,TNFAIP8L1,MLST8,TSC1,LAMTOR5,TLDC1,WDR59,MAPKAP1,MIR199A1,LAMTOR2,RNF152	grey	VSMC_M10
GO:0046641	0.93	0.20	4	11	positive regulation of alpha-beta T cell proliferation	BP	1	TGFBR2,RIPK2,CD28,RASAL3	grey	VSMC_M10
GO:0060571	0.93	0.17	7	18	morphogenesis of an epithelial fold	BP	1	SOSTDC1,GLI2,OVOL2,LUZP1,NOG,WNT5A,WNT2	grey	VSMC_M10
GO:0018206	0.93	0.20	4	11	peptidyl-methionine modification	BP	1	METAP1D,NAA30,NAA60,PDF	grey	VSMC_M10
GO:0007549	0.93	0.17	6	16	dosage compensation	BP	1	YTHDC1,CDYL,H2AFY2,UPF1,PCGF3,SMCHD1	grey	VSMC_M10
GO:0045932	0.93	0.17	7	18	negative regulation of muscle contraction	BP	1	GUCY1A1,DOCK5,GRK2,ATP1A2,ADRA2C,CALCRL,KCNMA1	grey	VSMC_M10
GO:0007202	0.93	0.16	8	20	activation of phospholipase C activity	BP	1	LPAR1,EGFR,C5AR1,PHB,RASGRP4,ARHGAP6,AGT,GNA15	grey	VSMC_M10
GO:0030308	0.93	0.10	73	153	negative regulation of cell growth	BP	1	SEMA6A,CYP27B1,HSPA1B,PPARA,GDF9,FSTL4,PI16,CDKN2A,SMARCA2,SEMA4D,SEMA4C,RTN4,PPP2R1A,PPT1,EPHA7,SPHK2,PHB,WNT11,SERTAD3,ING1,SEMA3D,BTG1,SPART,SEMA3A,ULK1,RYK,ACVR1B,CDKN2AIP,PTPRJ,SEMA4F,NDUFS3,PRDM11,SEMA3G,SPP1,SEMA4G,KIAA0319,HYAL1,CAPRIN2,SEMA3F,TGFB2,EI24,SH3BP4,AGT,IP6K2,CDKN1B,WNT3,BCL6,SEMA6D,DDX3X,TNR,MUL1,DNAJB2,TSPYL2,SEMA4A,TRIM46,SMAD3,NTN1,BDKRB1,DCUN1D3,YY1,CDK5R1,ARHGAP4,PLXNA3,PSRC1,NAIF1,MIR199A1,SERTAD2,ACVRL1,WNT5A,RGS4,DACT3,NME6,CGRRF1	grey	VSMC_M10
GO:1900024	0.93	0.13	19	44	regulation of substrate adhesion-dependent cell spreading	BP	1	FBLN1,PTK2,ITGB1BP1,UNC13D,RAC3,ARHGEF7,DOCK5,RREB1,DMTN,CARMIL1,AP1AR,CASS4,CIB1,DOCK1,MELTF,CSPG5,DNM2,CRK,FGA	grey	VSMC_M10
GO:0015031	0.93	0.08	670	1301	protein transport	BP	1	TIMM21,VPS4B,LRP1,STX7,AP3S1,KIF5A,PEX7,AGAP2,PEX3,CANX,TBC1D30,TBC1D9B,PPP1R10,RAB21,SNX24,SNX31,PHAX,ZDHHC14,SLC12A2,RIMS2,PRKN,TAP1,KIF3A,TSPO,GOPC,VPS52,HSPA4,DERL1,FAM91A1,WASHC5,FAM53C,TSNARE1,EXOC4,SIL1,SYNGR1,MAPK14,TOMM22,PLA2G6,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,SMO,ZDHHC21,TOMM6,MYH9,PEX6,FBXO7,XPO5,WASHC4,APBA1,PEX1,VPS50,SCFD2,RFX3,SLC1A1,TGFBRAP1,TFAP2B,TBC1D8,TRAM2,BICD2,CHMP2A,RAB23,SVBP,SEC61B,STX17,SIX2,DNAJA1,PRKCE,RIMS1,TMEM30A,SPTBN1,HMGN3,RUFY3,CYB5R4,PPT1,SNX14,XPO1,SNX30,BMP8A,EHBP1,AFTPH,PLEK,RSAD2,NR1H2,ITGB1BP1,YWHAZ,SEC61G,EGFR,FUZ,ARHGEF5,TLR4,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,TRPM4,SLC7A11,LIN7B,EPS15,APOB,AGK,BCAP29,TRAF3IP2,ANKRD50,TTC26,DNAJC27,NAPA,BBS7,RAB7A,AP2S1,RAB10,COPG1,KPNA3,GIPR,ARL5B,LCP1,SYTL2,COG1,DLG2,CUBN,RBSN,DNAJC15,PLK3,FRMD4A,OPTN,GOLGA4,LLGL2,IPO13,STEAP3,AQP11,CCDC93,RAF1,ZFAND6,TBC1D4,MYO7A,NAPB,GCKR,SEC62,SEC22C,KPNA2,AKT2,PITRM1,LRP1B,HOOK3,ARRB1,TIMM50,SNX5,USP36,TBC1D16,AP3M2,KIF5C,FCHSD2,RINL,ATG16L2,NPLOC4,ARL5A,UBAC2,RAB5A,LIN7A,APBB3,ASPSCR1,TMCO6,NUP98,DPH3,SIRT7,FERMT1,HACL1,HEATR5B,CEP290,PRNP,ING1,BAG4,MAVS,AP5S1,DNAJC13,FUT10,FAM160A2,GAS6,BET1L,TRIM3,SIRT3,ARFIP2,VPS16,COPZ1,ARL6IP5,STX2,SYT9,SRP14,NCOA4,NR1H4,WASHC2A,KCNIP3,LYPLA1,NUP58,MIPEP,TM9SF4,NDUFAF2,ZDHHC20,KIF3B,FAM3D,IPO11,IL1A,RILPL1,RILPL2,IMMP1L,ANKRD27,SNX25,OSBP,PIK3R1,ABCB9,VAMP5,CHMP2B,TBC1D12,TNPO1,ANKRD13C,SNX6,ATP6V1A,SNX2,ATP6V1B2,SNX1,AIG1,LTC4S,SLC27A6,QKI,ACSL6,PNPLA3,FAAH,ELOVL1,HACL1,ABHD6,PLA2G4B,ADTRP,CPT1A,ACSL5,CYP2U1,PLA2G4A,ACADL,ACSBG1,SLC27A1,DAGLB,EPHX1,ACOT2,ALOXE3,MAPK3,ACSBG2,CYP2J2,PTGES2,ABCD3,ACOT4,ELOVL3	grey	VSMC_M10
GO:0001676	0.93	0.11	30	66	long-chain fatty acid metabolic process	BP	1	ADTRP,FAP,TNFRSF1B,DPP4	grey	VSMC_M10
GO:1903054	0.93	0.20	4	11	negative regulation of extracellular matrix organization	BP	1	ADRA1D,ADRA2B,RAPGEF2,ADRA2A,ADRA2C,CHGA	grey	VSMC_M10
GO:0071880	0.93	0.17	6	16	adenylate cyclase-activating adrenergic receptor signaling pathway	BP	1	HSF1,ATR,MAPKAPK2,MAPT,DNAJB1,CREBBP	grey	VSMC_M10
GO:1900034	0.93	0.17	6	16	regulation of cellular response to heat	BP	1	HELB,HSF1,CYREN,FBH1,RNF169,SHLD1,ERCC6,SHLD2,OTUB2,SMCHD1,RMI2,NUDT16L1	grey	VSMC_M10
GO:2000780	0.93	0.14	12	29	negative regulation of double-strand break repair	BP	1	TNFAIP3,ENPP3,FBXO7,TNFRSF21,PELI1,IL4I1,CST7,CD300LF,PIBF1,FOXJ1,CYGB,THBD,C1QTNF1,PAWR,PRNP,NCKAP1L,ZC3H8,FER,CASP3,TMEM131L,PAG1,NR1H3,MARCH7,CD200,BANK1,BTN2A2,PRKAR1A,HLX,TBC1D10C,UBASH3B,GPER1,FGR,RUNX3,DLG1,BCL6,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,INHA,SCGB1A1,FOXP3,TBX21,SYT11,ZBTB7B,IL4R,LDLR,BTK,CD74,TWSG1,PTPN2,SOCS1,ABAT,FOXF1,GLMN,MIR21,MIR27A,LST1,MIR125A,FGL2,LAX1,CEBPB,HAVCR2,RC3H2	grey	VSMC_M10
GO:0050866	0.93	0.10	65	136	negative regulation of cell activation	BP	1	MPDZ,SRF,CLDN19,WNT11,IKBKB,ACTG1,NPHP1,LSR,MARVELD2,CLDN34,SNAI1,DLG1,FZD5,GPBAR1,RAMP2,CLDN7,MARVELD3,MICALL2,CLDN15,CLDN1,APC	grey	VSMC_M10
GO:0120192	0.93	0.12	21	48	tight junction assembly	BP	1	ACTN3,RFLNB,SNX10,CCDC154	grey	VSMC_M10
GO:0035630	0.93	0.20	4	11	bone mineralization involved in bone maturation	BP	1	FECH,CAT,DNMT3A,PPP2CB,BACE1,MAPT,CLDN1	grey	VSMC_M10
GO:0010288	0.93	0.16	7	18	response to lead ion	BP	1	RPP21,RIDA,UTP23,AGO2,TSR1,TSEN34,RNASEH1,NUDT16,BMS1,NUDT12,POP4,RPP40,POP5,YBEY,NOP9,NYNRIN,KIAA0391,POP7,ZC3H12C,MRPL44,RNASEH2A,KRI1,SLFN14,DROSHA,INTS11,NOL9,RPP38,RPP30	grey	VSMC_M10
GO:0090502	0.93	0.12	28	62	RNA phosphodiester bond hydrolysis, endonucleolytic	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,MAPK14,CRY1,BRSK1,MSH2,ETAA1,XPC,PLK3,NEK11,PRKDC,ERCC6,CEP63,STK33,PLK2,RAD17,ATR,RAD9B,EIF2AK4,NBN,ABRAXAS1,DONSON,PIDD1,TAOK3,CCND1,GIGYF2,CHEK2,ATRIP,SYF2,CDKN1B,TIPRL,RHNO1,PRPF19,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,FOXN3,TAOK1,FZR1,DOT1L,FBXO31,NAE1,RPA4,RPS27L,SOX4,BRCC3,CRADD	grey	VSMC_M10
GO:0031570	0.93	0.10	52	111	DNA integrity checkpoint signaling	BP	1		grey	VSMC_M10

GO:0042093	0.93	0.12	19	44	T-helper cell differentiation	BP	1	HLA-DRA,FOXP1,RIPK2,HLX,BCL6,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,PTGER4,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0033157	0.93	0.09	95	196	regulation of intracellular protein transport	BP	1	PRKN,MAPK14,RAC2,SMO,SLC1A1,RAB23,TMEM30A,RUFY3,XPO1,ITGB1BP1,TCAF2,DNAJC27,LCP1,PLK3,AKT2,USP36,UBAC2,SIRT7,FERMT1,CEP290,PRNP,BAG4,MAVS,GAS6,NUP58,TM9SF4,PIK3R1,FBXW7,PKIA,HTRA2,ZFAND1,CSNK2A2,NUP54,RAPGEF3,DMTN,SUFU,CABP1,SP100,TCF7L2,KCNB1,YOD1,HCLS1,HPS4,SORL1,C2CD5,ARIH2,CIB1,BAG3,SFN,UHMK1,APOD,CTDSPL2,FZD5,FIS1,CEMIP,NMT1,DERL3,SEC16B,C11orf65,PDCD10,PINK1,MAPK1,CHRM1,TMEM30B,GRIPAP1,ATP13A2,NPEPPS,TARDBP,PSEN1,ITGAM,NDEL1,HAX1,SMAD3,BCAS3,ARHGAP44,MIEF2,CDK5R1,SREBF1,EFCAB7,INPP5K,BCAP31,OAZ1,PARK7,SH3GLB1,RIPOR1,MICALL2,BNIP3L,TXN,HRAS,MIEF1,RHOU,LEPROT,UBE2G2,DERL2,ZIC1	grey	VSMC_M10
GO:2000377	0.93	0.10	57	120	regulation of reactive oxygen species metabolic process	BP	1	PRKN,PPARA,TSPO,MAPK14,RAC2,FPR2,EGFR,TLR4,UCP1,ATG5,MYCN,FOXO3,SPHK2,DHFR,WISP3,TGFBR2,SIRT2,SIRT3,HVCN1,PTK2B,F2RL1,NQO2,RIPK1,TFAP2A,PAX2,SIRT5,SLC30A10,FBLN5,AGT,ACE2,HDAC4,PDK3,NFE2L2,MAPT,PIKFYVE,BCO2,GCH1,PINK1,MMP3,STAT3,BST1,ITGAM,NOXA1,PARK7,SLC25A33,GNAI3,CYBA,LCN2,MIR21,MIR27B,MIR24-1,RHOA,TIGAR,GADD45A,GRB2,APOPT1,AC140504.1	grey	VSMC_M10
GO:0050667	0.93	0.20	4	11	homocysteine metabolic process	BP	1	MTRR,CBSL,CPS1,COMT	grey	VSMC_M10
GO:0048536	0.93	0.14	13	31	spleen development	BP	1	TRAF3IP2,PRKDC,CDH17,JARID2,NFKB2,PPP2R3C,RC3H1,NKX3-2,CTC1,FADD,BCL2L11,NKX2-5,RC3H2	grey	VSMC_M10
GO:1903800	0.93	0.20	4	11	positive regulation of production of miRNAs involved in gene silencing by miRNA	BP	1	EGFR,MYCN,RIPK1,MAP2K1	grey	VSMC_M10
GO:0042559	0.93	0.18	5	13	pteridine-containing compound biosynthetic process	BP	1	DHFR,SPR,MTHFS,GCH1,PCBD2	grey	VSMC_M10
GO:0006937	0.93	0.10	57	121	regulation of muscle contraction	BP	1	ZDHHC21,CHRNA3,SRF,KIT,TNNI3,ASB3,TRPM4,SCN5A,ADRA2B,NR4A1,PLCE1,GUCY1A1,DOCK5,STC1,F2R,TNNC1,DSP,CASQ2,CHRM3,RYR2,PKP2,KCNJ2,TNNI1,TRPV4,ADRA2A,MYH7,GRK2,ANK2,GPER1,ACE2,ATP1A2,SLC9A1,CASQ1,ACTN3,HDAC4,DLG1,ADRA2C,CALCRL,ATP1B1,KCNA1,KCNMA1,MYL5,ATP2A1,CALM1,NMUR2,SETD3,DSG2,ABAT,P2RX1,RNF207,MIR21,RHOA,DMD,CHGA,TNNC2,HCN4,NKX2-5	grey	VSMC_M10
GO:0021766	0.93	0.12	26	59	hippocampus development	BP	1	NME1,ATAT1,UQCRQ,SMO,SRF,CDK6,EIF2B3,XRCC1,TSKU,ALK,MKKS,CASP3,DCLK2,TENT2,SRD5A1,HDAC1,DLX1,KCNA1,KDM6B,CDK5R1,DAB1,LRP8,CRK,PLXNA3,TSC1,PHLPP2	grey	VSMC_M10
GO:1902679	0.93	0.08	482	946	negative regulation of RNA biosynthetic process	BP	1	SMARCC2,ATP8B1,PLAGL1,ZBTB2,ESR1,CNOT2,OSR2,SNW1,ZNF706,ZBTB12,PRKN,PPARA,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,PTCH1,ATF4,CBX7,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,RPS14,ZNF550,BEND6,ZNF268,SCMH1,NFE2L3,HOXA2,HOXA7,JAZF1,XPO1,AKIRIN2,CASP8AP2,BACH2,ZNF692,NR1H2,ZNF350,FOXP2,MED25,KLF11,POU3F3,LANCL2,CREM,SDCBP,OSR1,FOXO3,BEND5,HDAC2,PHF10,DNMT3A,BMI1,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,SUV39H2,ZNF404,PLK3,GLI2,DEDD2,RSF1,KDM4A,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,SFMBT2,GZF1,POU4F1,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,TAF7,NRG1,GAS6,RYBP,FOXP1,MITF,MTA3,ARID5A,IRF7,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,NCOA2,DKK3,SAP30,ZNF366,ARNTL,GCFC2,HMBOX1,MEF2C,PEX2,PKIA,TMBIM6,CNOT1,SLA2,CUX2,MCPH1,SOX6,FNIP2,BACH1,SFMBT1,NR1H3,EAPP,SCAF4,LCOR,DDX54,RUNX1T1,VDR,NKX3-1,BAHD1,HDAC7,NKX6-1,LOXL2,NR4A2,PHF21A,CRY2,PRDM11,CDYL,RREB1,RTF1,ZBED6,SOX13,ZNF248,TFAP2A,RIPPLY3,HIF1AN,PAX2,SALL1,PPHLN1,PRICKLE1,HIVEP1,JARID2,ATXN1,SUDS3,ZNF423,LDB1,IGF2,MAGEL2,ELK4,NUPR2,DCAF1,SUFU,TAGLN3,PCGF6,IRX2,RPL23,HDAC1,ELF3,CCND1,SP100,TRPV4,PDCD4,ZBTB20,SATB2,TCF7L2,AJUBA,ZNF639,PIAS3,LHX9,HJV,FABP4,SNAI1,ZNF202,H	grey	VSMC_M10

GO:1901137	0.93	0.08	249	494	carbohydrate derivative biosynthetic process	BP	1	NME1,TBPL1,B4GALT7,B4GALNT1,RXYLT1,ATP5MGL,GFPT2,ALG12,PPT2,PPARA,ACSL6,A4GALT,PMM1,AGO2,GPAA1,IMPDH1,MTAP,LARGE1,GNPDA2,SLC35B2,CWH43,ST6GAL2,SRD5A3,UXS1,SLC25A13,PPAT,C1GALT1,CHST10,ALG2,PPCS,TMEM246,PIGF,FKTN,HAS1,NT5E,PPT1,IL15,DLD,NANP,SPHK2,CMPK1,HS3ST5,ADCY3,ALG11,PRTFDC1,POMGNT1,AKR1A1,B4GALT2,CHPF2,AQP11,PRKAG2,GALNT11,ATP5F1C,XYLB,ST6GALNAC2,MGAT5B,ELOVL1,CSGALNACT1,UGGT2,HBEGF,PAWR,PLCB1,TMTC4,PGAP2,GALNT15,PANK2,PDK1,FUT10,GXYLT2,EOGT,PDHX,ELOVL7,PANK1,POFUT1,AMPD3,PIGU,ST8SIA4,GK5,ATP5F1A,B3GNT4,MOGS,GUCY1A1,GUCY1B1,RPN2,DGUOK,GMPS,ST3GAL6,GALNT5,CHST1,AMPD1,GCNT2,PIGT,ADCY7,FAM173B,BMPR1B,ADCY2,NME4,A3GALT2,ALG10,HYAL1,SLC2A10,PGAP1,TYW1B,TRIP11,ACSL5,POGLUT1,TYW5,TCF7L2,DAD1,ST8SIA2,EGF,PRPS2,B3GALT1,B3GNT5,PIGM,LCMT2,ABCC5,HACD2,GALNT2,ADCY4,PIGV,DPAGT1,CTPS2,ALG3,MAN1C1,MGAT1,DNAJC30,PIGX,GAL3ST3,DTYMK,PIGZ,XXYLT1,PDK3,EDEM3,SLC25A16,TET1,PLOD3,CEMIP,SOAT1,DERL3,ALG9,MGAT2,ACSBG1,ATP5S,B3GALNT1,KDELC2,CHST3,GAL3ST4,PYGL,PIGC,CHST7,COASY,DDOST,PINK1,AC022400.6,STAT3,NME7,GALNT8,ADK,MPC2,ADCY10,HS3ST1,SCCPDH,PARP1,SLC2A4,TECR,PGAP3,CHST12,PIGH,GALNT16,SLC26A1,PSEN1,GUCY2D,PKLR,PANK3,KRTCAP2,GCDH,OGT,POMT2,UPRT,GLCE,ST8SIA5,COG7,HEXA,GALNT1,TNIP1,MPI,ACACA,PIGL,NPC1,SLC26A2,PRPSAP2,ADSSL1,ALG6,ACSBG2,MPPE1,HS6ST2,PMM2,ALG1,B3GALT6,ATP6V0C,PANK4,NME3,ABCA7,ATP5PB,ABO,VPS9D1,ACSF3,GBGT1,UCK1,FOXL1,MLYCD,CHST5,ST6	grey	VSMC_M10
GO:1905906	0.93	0.18	5	13	regulation of amyloid fibril formation	BP	1	PFDN5,PFDN4,PSEN1,LDLR,VBP1	grey	VSMC_M10
GO:0042541	0.93	0.20	4	11	hemoglobin biosynthetic process	BP	1	SLC25A37,ALAS1,LDB1,INHA	grey	VSMC_M10
GO:0045834	0.93	0.10	51	109	positive regulation of lipid metabolic process	BP	1	AGAP2,PPARA,PTK2,PLA2G6,TEK,KIT,PRKCE,FPR2,NR1H2,FGF21,SPHK2,ABHD5,APOC1,AKT2,SIRT3,FLT1,NR1H4,CYP7A1,ABHD6,SORBS1,PTK2B,NR1H3,HSD17B13,NOD2,SIRT4,GPLD1,IRS1,CPT1A,ZBTB20,AGT,FGR,LPGAT1,MLXIPL,SCAP,POR,CREB1,WNT4,FGFR3,SLC27A1,DAGLB,CD19,LDLR,CD74,SREBF1,VAV3,MLYCD,LDLRAP1,CNEP1R1,STARD4,CCDC3,FGF1	grey	VSMC_M10
GO:0048704	0.93	0.11	38	83	embryonic skeletal system morphogenesis	BP	1	OSR2,MDFI,SIX2,HOXA2,HOXA4,HOXA6,HOXA7,FUZ,MYCN,OSR1,BMI1,MEGF8,WDR60,TGFBR2,ALX1,EYA1,TFAP2A,HYAL1,SATB2,DLG1,SETD2,HOXD4,HOXD3,TULP3,WDR19,HOXB5,HOXB6,HOXB8,HOXB9,SMAD3,GSC,LHX1,ALX3,HOXB3,NOG,SIX1,SLC39A3,HOXA3	grey	VSMC_M10
GO:0097709	0.93	0.19	4	11	connective tissue replacement	BP	1	IL1A,F2R,PPP3CA,MIR199A1	grey	VSMC_M10
GO:1902003	0.93	0.13	15	35	regulation of amyloid-beta formation	BP	1	NTRK2,RTN4,PRNP,CASP3,SLC2A13,SORL1,RTN1,HAP1,EPHA4,TMED10,EFNA1,ABCA7,MIR29A,MIR24-1,MIR339	grey	VSMC_M10
GO:0000729	0.93	0.17	6	16	DNA double-strand break processing	BP	1	HELB,SPO11,RAD52,EXD2,SLX4,UBE2N	grey	VSMC_M10
GO:0009126	0.93	0.12	17	39	purine nucleoside monophosphate metabolic process	BP	1	IMPDH1,GDA,PPAT,NT5E,DLG2,AMPD3,DGUOK,GMPS,AMPD1,MAGI3,DLG1,CASK,ADK,CARD11,ADSSL1,MPP1,NUDT2	grey	VSMC_M10
GO:0050872	0.93	0.19	4	11	white fat cell differentiation	BP	1	PNPLA3,CEBPA,FABP4,PER2	grey	VSMC_M10
GO:0061337	0.93	0.11	34	76	cardiac conduction	BP	1	TRPM4,SLC8A2,CACNB2,ATP1A3,SCN5A,KCNJ3,TBX5,KCNE2,DSP,CASQ2,RYR2,PKP2,KCNJ2,ANK2,AGT,ACE2,ATP1A2,SLC9A1,SCN4B,ATP1B1,SLC4A3,ATP1B2,CACNA1G,ATP2A1,CALM1,DSG2,ISL1,ATP2B3,RNF207,TMEM65,KCNH2,SCN2B,HCN4,NKX2-5	grey	VSMC_M10
GO:0071428	0.93	0.19	4	11	rRNA-containing ribonucleoprotein complex export from nucleus	BP	1	XPO1,SDAD1,NOP9,TSC1	grey	VSMC_M10
GO:0016446	0.93	0.19	4	11	somatic hypermutation of immunoglobulin genes	BP	1	MSH2,MLH1,POLL,PMS2	grey	VSMC_M10
GO:0055001	0.93	0.09	71	150	muscle cell development	BP	1	STAC3,MAML1,PPARA,OBSCN,PI16,SMO,FLNC,LMOD2,SRF,PGM5,FHL2,TMOD1,BVES,KEL,MYLK3,ATG5,KLHL40,ACTG1,RYR1,P2RX2,LMOD3,MYOF,DYSF,HOMER1,TBX5,BIN3,LMOD1,PPP3CA,PRKAR1A,ANK2,AGT,ACTC1,NFATC4,MYOZ2,CASQ1,ACTN3,TMOD4,HDAC4,ALPK3,EFEMP2,MYPN,TTN,MYOZ1,RAMP2,TMOD2,OBSL1,LDB3,BMPR1A,CHRNB1,TCAP,WFIKKN2,YY1,FBXO22,ISL1,MYH11,SKI,WFIKKN1,SYPL2,ENG,MIR199A1,MIR23A,MIR24-1,DMD,CSRP2,KRT19,SMYD3,SIX1,RGS4,MYORG,NKX2-5,HEY2	grey	VSMC_M10
GO:0022404	0.93	0.11	28	63	molting cycle process	BP	1	FZD6,SMO,ZDHHC21,SOSTDC1,CD109,EGFR,FUZ,INTU,HDAC2,SOX9,ERCC2,GLI2,FERMT1,ACVR1B,TRPC4AP,FZD3,LDB1,HDAC1,TGFB2,SNAI1,LAMA5,FARP2,SAV1,GORAB,RBPJ,NGFR,WNT5A,DNASE1L2	grey	VSMC_M10
GO:0022405	0.93	0.11	28	63	hair cycle process	BP	1	FZD6,SMO,ZDHHC21,SOSTDC1,CD109,EGFR,FUZ,INTU,HDAC2,SOX9,ERCC2,GLI2,FERMT1,ACVR1B,TRPC4AP,FZD3,LDB1,HDAC1,TGFB2,SNAI1,LAMA5,FARP2,SAV1,GORAB,RBPJ,NGFR,WNT5A,DNASE1L2	grey	VSMC_M10
GO:0009124	0.93	0.13	16	37	nucleoside monophosphate biosynthetic process	BP	1	IMPDH1,PPAT,CMPK1,AMPD3,DGUOK,GMPS,AMPD1,PRPS2,ADK,UPRT,ADSSL1,UCK1,DHODH,DCTD,NUDT2,UPP1	grey	VSMC_M10
GO:0001942	0.93	0.11	27	61	hair follicle development	BP	1	FZD6,SMO,ZDHHC21,SOSTDC1,CD109,EGFR,FUZ,INTU,HDAC2,SOX9,ERCC2,GLI2,FERMT1,ACVR1B,TRPC4AP,FZD3,LDB1,HDAC1,TGFB2,SNAI1,LAMA5,SAV1,GORAB,RBPJ,NGFR,WNT5A,DNASE1L2	grey	VSMC_M10
GO:0006334	0.93	0.11	31	68	nucleosome assembly	BP	1	BRD2,ASF1A,UBN2,SOX9,RSF1,SPTY2D1,NAP1L5,RBBP4,SART3,H2AFY2,HIRA,TSPYL2,NAP1L2,NAA60,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,TSPYL5	grey	VSMC_M10
GO:0045777	0.93	0.15	8	20	positive regulation of blood pressure	BP	1	TAC3,ADH5,ADRA1D,ADRA2B,AGT,CYBA,HSD11B2,RHOA	grey	VSMC_M10
GO:0048332	0.93	0.11	24	55	mesoderm morphogenesis	BP	1	EXOC4,SRF,TXNRD1,SIX2,WNT11,EOMES,GPI,EYA1,TLX2,PAX2,PRKAR1A,SNAI1,SETD2,WNT3,TBX19,BMPR1A,KDM6B,ITGA3,SMAD3,TWSG1,FOXF1,POFUT2,NOG,WNT5A	grey	VSMC_M10

GO:0010507	0.93	0.11	30	67	negative regulation of autophagy	BP	1	RNF5,TSPO,NRBP2,MET,KDM4A,USP36,SIRT2,FEZ2,MTMR9,LZTS1,SEC22B,TMEM39A,USP30,MCL1,RUBCN,IL10RA,TAB3,TBC1D14,PINK1,STAT3,PHF23,NPC1,SMCR8,LEPR,CLEC16A,MTM1,TSC1,MIR199A1,TIGAR,CPTP	grey	VSMC_M10
GO:0032570	0.93	0.13	12	29	response to progesterone	BP	1	TSPO,SOX10,PTN,GPI,NCOA2,NR1H3,TGFB2,ABHD2,RAMP2,CD38,FOS,SREBF1	grey	VSMC_M10
GO:0036314	0.93	0.14	10	25	response to sterol	BP	1	PTCH1,SMO,TGFBR2,CYP7A1,GPLD1,DAG1,GRAMD1B,OSBPL7,LRP8,INSIG2	grey	VSMC_M10
GO:0060445	0.93	0.16	7	18	branching involved in salivary gland morphogenesis	BP	1	PLXNA1,SEMA3A,DAG1,LAMA5,BTBD7,LAMA1,ESRP2	grey	VSMC_M10
GO:0050900	0.93	0.09	120	245	leukocyte migration	BP	1	SLC12A2,AGER,GPSM3,PTK2,RAC2,MYH9,CCL27,KIT,ROR2,NINJ1,FPR2,HOXA7,CXCL8,AKIRIN1,PTN,ADD2,TRPM4,PODXL2,C5AR2,C5AR1,MYD88,OXSR1,FOXJ1,PLCB1,AIMP1,NCKAP1L,GAS6,FAM19A4,FLT1,MTUS1,RET,HCK,CYP7B1,FER,VEGFC,JAM2,PTK2B,CCL17,SLC8B1,F2RL1,ANO6,ADTRP,NOD2,GBF1,CD200,DNM1L,LCK,TRPV4,SBDS,TGFB2,CD99,PRSS56,SELPLG,CMKLR1,SLAMF8,MOSPD2,EPS8,PTPRO,FCER1G,APOD,ADAM8,MIA3,PIKFYVE,IL16,ITGA2B,ITGA4,IL12A,MCU,TNFSF18,CXCR2,BST1,MAPK1,STAT5B,CH25H,PADI2,CXCL16,TMEM102,TBX21,STK10,PGF,DAPK2,MAPK3,IL6R,S100A14,S100A8,BDKRB1,UMOD,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,YES1,VAV1,PTGER4,CRK,PIP5K1C,MPP1,BSG,VAV3,MIR24-1,RHOA,CCL16,S100A12,CHGA,DEFB124,FADD,DPP4,CXCL6,FUT4,ZNF580,THY1,WNT5A,DUSP1,ARTN,GCSAM,CCL22,PDGFD	grey	VSMC_M10
GO:1901653	0.93	0.09	132	270	cellular response to peptide	BP	1	LRP1,AP3S1,MARS,PIP4K2C,AGER,PNPLA3,PTK2,AKR1B1,GKAP1,HSF1,CCND3,GPT,PPAT,PHIP,FPR2,NOD1,CRHR2,KLF11,GRB10,TLR4,GAB1,LPIN1,MGARP,FOXO3,FGF21,SESN3,PIP4K2A,RAB10,CYSLTR2,ECHDC3,ATP1A3,KLF5,TBC1D4,AKT2,SNX5,PRNP,KL,PTPRA,LEPROTL1,PRKDC,TRIB3,NR4A1,FER,IDE,PIK3R1,SORBS1,RIPK2,OPA1,LPIN3,NKX6-1,NR4A2,CYFIP1,NOD2,IGF2,PXN,GPLD1,SRD5A1,IRS1,RPL23,GRB14,SLC30A10,SORL1,C2CD5,GPER1,AGT,SLC9A1,SYAP1,USF1,BACE1,SNX6,POR,NFE2L2,CREB1,YWHAG,RAP1B,FIS1,CPS1,EIF4EBP2,ITGA4,MEN1,SIK2,ESRRA,FBN1,GDF15,STAT3,SLC27A1,STAT5B,DDX11,RAB8A,EPHA4,GPR173,PARP1,SLC2A4,RAB15,MAX,CACNB1,AGTRAP,PSEN1,CACNA1A,FOXO4,NGFR,PKLR,RAB8B,NDEL1,ZBTB7B,OGT,PRKCB,CAMK2A,INSR,SREBF1,LPIN2,GHR,PTPN2,SOCS1,CRK,INPP5K,PDPK1,PRKCZ,SLC25A33,CYBA,ASS1,LCN2,INSRR,CA2,BGLAP,GRB2,BCL2L11,INSIG2,APC,BCL2L2,SH2B2,LEPROT	grey	VSMC_M10
GO:0061045	0.93	0.11	23	52	negative regulation of wound healing	BP	1	SERPINB2,TSPAN8,SLC12A2,CLDN19,CD109,CLASP2,THBD,PLAT,C1QTNF1,ADTRP,FAP,UBASH3B,USF1,CASK,WNT4,MYOZ1,F12,ANXA2,SMAD3,ABAT,CRK,SERPINF2,FGA	grey	VSMC_M10
GO:0051647	0.93	0.15	8	21	nucleus localization	BP	1	SUN2,HOOK3,SLIT1,SYNE2,NTN1,CLMN,DOCK7,FHOD1	grey	VSMC_M10
GO:0002526	0.93	0.11	26	58	acute inflammatory response	BP	1	MYLK3,IL1A,ANO6,OSM,ADAM8,CD163,FN1,SERPINC1,CXCR2,STAT3,F12,IL6R,S100A8,BTK,C3,OSMR,CREB3L3,SERPINF2,DNASE1,TRPV1,PARK7,ASS1,LCN2,HPR,PTGES,CEBPB	grey	VSMC_M10
GO:0008284	0.93	0.08	345	681	positive regulation of cell population proliferation	BP	1	NME1,ERBB3,SHMT2,PGGT1B,GLI1,MAP3K5,TNFAIP3,TSPAN31,ESR1,CNOT6,OSR2,AGER,IL5,HLA-DPB1,TSPO,GDF9,TNFRSF13C,MYC,PTK2,AKR1B1,MAPK15,MAPK14,NTRK2,KDM4C,SOX10,PIM1,RAC2,SMO,HSF1,ZNF16,TEK,CNTFR,CDK6,SLC25A27,KIT,NCK2,TFAP2B,DLX5,S1PR3,TBC1D8,PDCL3,ZNF268,SIX2,IL11,EPCAM,RTN4,PHIP,EMC10,EPGN,AREG,AKIRIN2,AQP1,PELI1,TGFA,PTN,ITGB1BP1,TNC,POU3F3,EGFR,TLR4,EPHA1,IL15,SDCBP,MYCN,TRPM4,OSR1,FGF21,SPHK2,FOXE3,HDAC2,BMI1,C5AR2,C5AR1,PRKD2,CNBP,PHB,SOX9,GAB2,CDC123,GLI2,AQP11,MYD88,PRDX3,KLF5,SCN5A,WDR48,ACER3,AKT2,ARRB1,ABCC4,TGFBR2,RPTOR,PURA,HBEGF,CHTOP,ADRA1D,ASH2L,MAB21L1,NRG1,CCKBR,DDRGK1,NCKAP1L,GAS6,FOXP1,MTA3,PRKDC,SLC7A1,FLT1,CIAO1,TRAF6,PLAG1,HCK,TOX,IL1A,CYP7B1,NR4A1,FER,HPGD,EYA1,MAB21L2,FZD3,MEF2C,IL7,VEGFC,ADAMTS1,PTK2B,CNOT6L,KMT2D,RPRD1B,EAPP,TIAM1,FGF5,RIPK2,NKX3-1,TBX5,AGGF1,F2R,SRSF6,NQO2,MARCH7,RREB1,GCNT2,PAX2,NOD2,ZNF335,ZNF423,CD40,IGF2,IRS1,RPL23,HDAC1,HYAL1,SINHCAF,CCND1,ICOSLG,TERT,TGFB2,ADRA2A,GPAM,PTHLH,TCIRG1,TCF7L2,COX17,PDCD6,HLX,KRAS,EGF,HCLS1,DISC1,GPER1,CACUL1,AGT,CIB1,TRAF5,ARNT,TGM1,VASH2,FZD7,OSM,RPS4X,HDAC4,HTRA1,GID8,THPO,CHRD,CD28,SYF2,MAP3K3,MLXIPL,RTKN2,GLUL,FZD9,LAMC1,CDKN1B,DLG1,PTH1R,TET1,CCAR1,STOX1,BCL6,CTSH,DBF4B,ITGA4,IL12A,FN1,PTPN6,PDCD10,CXCR2,GPBAR1,CALCRL,SHC4,FGFR3,STAT3,PTPRN,CD38,BST1,MAPK1,STAT5B,FOXP3,RASAL3,BMPR1A,CARD11,RBPJ,MED1,ALDH1A2,MFN2,RAD51B,FGFR4,SOX15,ANXA2,CTF1,STX4,RAB	grey	VSMC_M10
GO:0009112	0.93	0.13	13	31	nucleobase metabolic process	BP	1	SHMT2,DPYS,GDA,PPAT,CMPK1,GMPS,GMPR,CTPS2,CPS1,MAPK1,ALDH6A1,SHMT1,DHODH	grey	VSMC_M10
GO:0035710	0.93	0.11	29	65	CD4-positive, alpha-beta T cell activation	BP	1	AGER,HLA-DRA,RSAD2,TGFBR2,NCKAP1L,FOXP1,TOX,RIPK2,TCIRG1,HLX,RUNX3,BCL6,VSIR,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,PTGER4,TWSG1,SOCS1,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0046627	0.93	0.14	10	25	negative regulation of insulin receptor signaling pathway	BP	1	PIP4K2C,GRB10,PIP4K2A,IRS1,GRB14,PRKCB,PTPN2,SOCS1,INPP5K,PRKCZ	grey	VSMC_M10

GO:0070085	0.93	0.09	94	194	glycosylation	BP	1	B4GALT7,B4GALNT1,RXYLT1,GFPT2,ALG12,PMM1,LARGE1,ST6GAL2,SRD5A3,C1GALT1,ALG2,FKTN,IL15,ALG11,POMGNT1,B4GALT2,AQP11,GALNT11,ST6GALNAC2,MGAT5B,UGGT2,TMTC4,GALNT15,FUT10,GXYLT2,EOGT,POFUT1,ST8SIA4,B3GNT4,MOGS,RPN2,ST3GAL6,GALNT5,GCNT2,A3GALT2,ALG10,TRIP11,POGLUT1,DAD1,ST8SIA2,B3GALT1,B3GNT5,PIGM,GALNT2,PIGV,DPAGT1,ALG3,MAN1C1,MGAT1,PIGZ,FUOM,XXYLT1,EDEM3,TET1,PLOD3,DERL3,ALG9,MGAT2,B3GALNT1,KDELC2,DDOST,GALNT8,GALNT16,PSEN1,KRTCAP2,OGT,POMT2,ST8SIA5,COG7,GALNT1,MPI,NPC1,ALG6,PMM2,ALG1,B3GALT6,ABO,GBGT1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,FUT4,ENTPD5,DHDDS,TMEM258,POFUT2,ACER2,POMK,POMGNT2,PIGB,B4GALT3,ISPD,SLC35C1,ST8SIA6	grey	VSMC_M10
GO:0050852	0.93	0.10	39	85	T cell receptor signaling pathway	BP	1	CD226,HLA-DPB1,TEC,TNFRSF21,PRKD2,NECTIN2,EIF2B3,IKBKB,PAWR,PRNP,TRAF6,PTPRJ,SLA2,RIPK2,SPPL3,LCK,ICOSLG,BTN2A2,DENND1B,THEMIS2,CD28,RC3H1,PTPN6,MAPK1,FOXP3,CARD11,PSEN1,LCP2,PRAM1,PTPN2,IKBKG,BCL10,FYB1,BTN1A1,CD247,THY1,UBE2N,HRAS,RC3H2	grey	VSMC_M10
GO:0045838	0.93	0.19	4	11	positive regulation of membrane potential	BP	1	AKT2,GLRX,MFN1,PIAS3	grey	VSMC_M10
GO:0060192	0.93	0.19	4	11	negative regulation of lipase activity	BP	1	APOC1,PLA2R1,POR,ANXA8	grey	VSMC_M10
GO:0035825	0.93	0.12	20	46	homologous recombination	BP	1	UBE2B,DMC1,KLHDC3,MLH1,CCNB1IP1,RAD54B,SYCP1,HSF2BP,SPO11,C11orf80,RAD51B,EME1,RAD51C,RAD51D,ERCC4,SLX4,MEIOB,MSH4,RNF212B,CENPX	grey	VSMC_M10
GO:0044793	0.93	0.19	4	11	negative regulation by host of viral process	BP	1	PRKN,EIF2AK4,PSMC3,MIR222	grey	VSMC_M10
GO:0006301	0.93	0.14	11	27	postreplication repair	BP	1	POLI,UBE2B,REV1,MSH2,REV3L,PRIMPOL,SPRTN,POLN,ZBTB1,NSMCE1,UBE2N	grey	VSMC_M10
GO:0031623	0.93	0.10	39	85	receptor internalization	BP	1	LRP1,PICK1,USP46,CXCL8,RSPO1,SFRP4,SDCBP,EPS15,MTMR2,ARRB1,RAB5A,WDR54,ANKRD13A,EGF,ANKRD13D,GRK2,SAG,AP2M1,FCER1G,CALY,LRPAP1,CXCR2,GRK4,CALCRL,DNM3,RAMP2,DLG4,SNX1,DNM2,INSR,AP2B1,FMR1,MIR199A1,CNTN2,LDLRAP1,CACNG7,GRB2,CACNG5,LRRTM2	grey	VSMC_M10
GO:0061036	0.93	0.14	10	25	positive regulation of cartilage development	BP	1	SOX9,ZNF219,SOX6,LOXL2,BMPR1B,POR,FGF18,SMAD3,ACVRL1,WNT5A	grey	VSMC_M10
GO:1903322	0.93	0.10	57	121	positive regulation of protein modification by small protein conjugation or removal	BP	1	PRKN,DERL1,SKP1,CRY1,RNF20,PELI1,BMI1,PAXIP1,WDR48,MYCBP2,KLHL40,ARRB1,NMI,TRAF6,TRIB3,FAM107A,SPSB4,FBXW7,RIPK2,MARCH7,PRICKLE1,NOD2,TOLLIP,NHLRC1,PEF1,PDCD6,PIAS3,SART3,SPRTN,ARNT,HDAC4,SENP2,FBXO33,DDX3X,PINK1,MUL1,BIRC3,PHF23,RNF111,DCUN1D3,TNIP1,PSMD10,TICAM1,PIAS4,FZR1,HSPA5,BCL10,UBB,RWDD3,INAVA,RASSF5,UBE2N,PTTG1IP,CENPX,UBE2D1,TSPYL5,RASD2	grey	VSMC_M10
GO:0045815	0.93	0.16	6	16	positive regulation of gene expression, epigenetic	BP	1	ARID1B,SPHK2,SMARCD1,ARID1A,PADI2,SERTAD2	grey	VSMC_M10
GO:0007032	0.93	0.11	32	71	endosome organization	BP	1	VPS4B,PRKN,WASHC5,WASHC4,CHMP2A,RAB7A,AQP11,HOOK3,DNAJC13,FAM160A2,TMEM127,CHMP2B,CHMP4C,SYNJ1,CHMP7,VPS18,TMEM9,RNF26,RAB22A,STX6,VPS37D,ALS2CL,ANXA8,PI4K2B,HOOK2,RAB11A,RILP,CHMP1A,VPS4A,PHETA1,SNX10,PLEKHJ1	grey	VSMC_M10
GO:0006692	0.93	0.13	12	29	prostanoid metabolic process	BP	1	AKR1B1,ACOX1,PIBF1,HPGD,PLA2G4A,DAGLB,AC005520.1,CD74,PTGES2,CES2,FABP5,PTGES	grey	VSMC_M10
GO:0006693	0.93	0.13	12	29	prostaglandin metabolic process	BP	1	AKR1B1,ACOX1,PIBF1,HPGD,PLA2G4A,DAGLB,AC005520.1,CD74,PTGES2,CES2,FABP5,PTGES	grey	VSMC_M10
GO:0051654	0.93	0.13	11	27	establishment of mitochondrion localization	BP	1	AGTPBP1,LRPPRC,MGARP,WASF1,NECTIN2,OPA1,MARK1,MAPT,UXT,HAP1,UBB	grey	VSMC_M10
GO:2000035	0.93	0.19	4	11	regulation of stem cell division	BP	1	PRDM15,ESRRB,NAP1L2,EVI2B	grey	VSMC_M10
GO:0071027	0.93	0.19	4	11	nuclear RNA surveillance	BP	1	DXO,EXOSC4,EXOSC3,EXOSC5	grey	VSMC_M10
GO:0071028	0.93	0.19	4	11	nuclear mRNA surveillance	BP	1	DXO,EXOSC4,EXOSC3,EXOSC5	grey	VSMC_M10
GO:0007565	0.93	0.09	66	139	female pregnancy	BP	1	TAC3,CYP27B1,ESR1,FBLN1,AGO2,H3F3C,AKR1B1,PLA2G6,CLIC5,RLN1,PPAT,PTN,SPHK2,PSG3,PRDX3,THBD,TGFBR2,IDO1,ADRA2B,ACVR1B,HPGD,VDR,STC1,SLC38A2,ACVR1C,SLC38A1,ABCC2,SPP1,ADCY7,SLC38A3,COL16A1,PTHLH,KRAS,AGT,DEDD,SP3,OVGP1,MEN1,COMT,ADRA2C,WNT4,RAMP2,CTSV,CD38,MAPK1,STAT5B,SCGB1A1,SYDE1,MED1,ITGA3,PGF,FOS,MAPK3,UBE2Q1,UPRT,EPOR,VMP1,TLE6,BSG,DHODH,HSD11B2,MIR21,CRH,TCF23,LIF,HAVCR2	grey	VSMC_M10
GO:0090075	0.93	0.14	10	25	relaxation of muscle	BP	1	GUCY1A1,P2RY1,KCNJ2,GRK2,ATP1A2,ACTN3,ATP1B1,KCNMA1,ATP2A1,CHGA	grey	VSMC_M10
GO:0006285	0.93	0.19	4	11	base-excision repair, AP site formation	BP	1	MBD4,NEIL1,NTHL1,MPG	grey	VSMC_M10
GO:2001022	0.93	0.10	44	95	positive regulation of response to DNA damage stimulus	BP	1	EYA4,MRNIP,MYC,EGFR,XRCC1,PAXIP1,WDR48,FBH1,FAM168A,SHLD1,PRKDC,ERCC6,ATR,EYA1,SLF1,NKX3-1,ABRAXAS1,SPIDR,PLA2R1,SLF2,EYA3,PARP9,DTX3L,RNF168,MGMT,ZCWPW1,WAS,DDX11,PARP1,SHLD2,UIMC1,FXR2,WRAP53,NSMCE1,SMCHD1,FMR1,PIAS4,SPIRE2,OOEP,TIGAR,RNF8,UBE2N,BRCC3,CBX8	grey	VSMC_M10
GO:0009226	0.93	0.15	7	18	nucleotide-sugar biosynthetic process	BP	1	GFPT2,PMM1,GNPDA2,UXS1,MPI,PMM2,FUK	grey	VSMC_M10
GO:0010559	0.93	0.13	13	31	regulation of glycoprotein biosynthetic process	BP	1	AGO2,FKTN,IL15,HBEGF,PAWR,PLCB1,SLC2A10,TCF7L2,SOAT1,POMT2,ABCA7,ACER2,IL33	grey	VSMC_M10
GO:0010952	0.93	0.09	68	142	positive regulation of peptidase activity	BP	1	MAP3K5,GRAMD4,AGER,FBLN1,BAK1,MYC,HSF1,TTBK1,SLC1A1,NOD1,AKIRIN2,CASP8AP2,TNFSF15,HSPE1,ARRB1,DDRGK1,ARL6IP5,ST18,ASPH,FOXL2,HIP1R,ROBO1,PCOLCE2,DIABLO,HTRA2,RIPK2,SENP1,NKX3-1,ACVR1C,F2R,PIDD1,LCK,PDCD6,GPER1,PSME1,CIDEB,EGLN3,MAPT,FIS1,CTSH,DDX3X,FN1,VSIR,PSME3,PINK1,MUL1,STAT3,EPHA4,BCL2L13,NGFR,EFNA1,SMAD3,S100A8,BCAP31,P2RX1,BCL10,MIR21,MIR27B,RHOA,RPS27L,FADD,CASP8,ACER2,BCL2L11,PERP,APH1B,PRR7,CRADD	grey	VSMC_M10
GO:0001516	0.93	0.15	7	18	prostaglandin biosynthetic process	BP	1	PIBF1,PLA2G4A,DAGLB,CD74,PTGES2,FABP5,PTGES	grey	VSMC_M10

GO:0046457	0.93	0.15	7	18	prostanoid biosynthetic process	BP	1	PIBF1,PLA2G4A,DAGLB,CD74,PTGES2,FABP5,PTGES	grey	VSMC_M10
GO:0051900	0.93	0.15	7	18	regulation of mitochondrial depolarization	BP	1	TSPO,DCN,IFI6,FZD9,PPP2R3C,PARP1,MLLT11	grey	VSMC_M10
GO:0001707	0.93	0.11	23	53	mesoderm formation	BP	1	EXOC4,SRF,TXNRD1,SIX2,WNT11,EOMES,GPI,EYA1,TLX2,PAX2,PRKAR1A,SNAI1,WNT3,TBX19,BMPR1A,KDM6B,ITGA3,SMAD3,TWSG1,FOXF1,POFUT2,NOG,WNT5A	grey	VSMC_M10
GO:1901722	0.93	0.19	4	11	regulation of cell proliferation involved in kidney development	BP	1	MYC,IL6R,MIR125A,PDGFD	grey	VSMC_M10
GO:0042790	0.93	0.15	7	18	nucleolar large rRNA transcription by RNA polymerase I	BP	1	MARS,IPPK,SIRT7,DEDD,H2AFY2,DDX11,TCOF1	grey	VSMC_M10
GO:0009746	0.93	0.09	76	159	response to hexose	BP	1	ZNF236,NME1,LRP1,APOM,AGER,PLA2G6,TXN2,SRF,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,GIPR,KHK,EIF2B3,GRIK5,RAF1,GCKR,TGFBR2,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,CASP3,PTK2B,KCNJ11,TIAM1,RAB11FIP5,OPA1,NKX6-1,ACVR1C,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,SLC9B2,ZBTB20,ADRA2A,GPAM,TCF7L2,KCNB1,PFKFB2,POLG,GPER1,RAB11FIP2,MLXIPL,GLUL,SIDT2,CDKN1B,PDK3,KLF7,FIS1,MEN1,ENY2,ABCA12,PPP3CB,CTSV,PTPRN,NDUFA9,MPC2,ILDR2,STX4,PKLR,GPR68,SIN3A,SREBF1,OXCT1,NADK,BAIAP3,CYBA,RHOA,SOX4,CRH	grey	VSMC_M10
GO:0051098	0.93	0.08	146	296	regulation of binding	BP	1	NME1,LRP1,STK3,EIF3E,PRKN,AGER,PPARA,DERL1,LRRC6,HABP4,C6orf106,CSNK1E,MFNG,SMO,HSF1,MDFI,TTBK1,MITD1,ZNF462,ZNF618,ITGB1BP1,MED25,MET,ADD2,MAPRE1,HDAC2,SYMPK,ERCC2,MAPRE3,RALB,RSF1,PTPRF,POU4F1,FBH1,SIRT2,TMEM173,EFHB,PLCL2,DPH3,ARHGEF7,DDRGK1,PPP2CB,TAF10,TRAF6,TRIB3,PLK2,BTAF1,IDE,HIP1R,HAND2,FBXW7,HMBOX1,TMBIM6,P2RY1,RAPGEF2,FAM192A,TIAM1,EBF2,RIPK2,AMFR,IFIT2,STK4,DTNBP1,BDNF,SPPL3,PPP3CA,CAPRIN2,SP100,TERT,TCF7L2,TTBK2,EGF,ADNP,EPB41,UBASH3B,DISC1,SORL1,PARP9,DTX3L,NFATC4,PER2,C4orf3,PEX19,HDAC4,BTBD1,RPL11,GEMIN2,ITGA4,MEN1,MEPCE,LRPAP1,RAP1GAP,MARK2,RAMP2,DNAJB2,GREM2,DDX11,CRMP1,EPHA4,ACTB,PARP1,NVL,GNL3L,NSD1,ANXA2,MSX2,PEX14,PSEN1,TAF1,MAPK3,EIF3C,WFIKKN2,SMAD3,CALM1,SNAPIN,LARP6,SIN3A,MARK3,ISL1,ERCC4,JUN,TICAM1,ZBTB7C,FMR1,CRK,SKI,DOT1L,PKD1,WFIKKN1,PARK7,GPSM1,LAMTOR5,PRMT7,MIR27B,MIR27A,BAG2,NOG,WNT5A,LDLRAP1,DDIT3,TXN,ZNF304,ZNF593,LIF,STYX,HEY2	grey	VSMC_M10
GO:0042116	0.93	0.10	31	69	macrophage activation	BP	1	AGER,TTBK1,PRKCE,FPR2,TLR4,C5AR1,CST7,NMI,FOXP1,MFHAS1,CEBPA,NR1H3,DYSF,IFNGR2,CD200,GPR137B,MAPT,PLA2G4A,SLC11A1,TNIP2,ITGAM,SYT11,IL4R,LDLR,CD74,TICAM1,TRPV1,KARS,WNT5A,IL33,HAVCR2	grey	VSMC_M10
GO:0030097	0.93	0.08	311	618	hemopoiesis	BP	1	NME1,STK3,MPIG6B,HSPA1B,BRD1,AGER,HLA-DRA,IL5,TCF7,CCDC134,BAK1,XRCC6,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,ATF4,MAPK14,PIM1,MFNG,HSF1,KCP,MYH9,ZNF16,RBFOX2,TEK,FBXO7,SRF,CDK6,KIT,ROR2,NFIL3,RPS14,TMEM190,IL11,SMAP1,EPAS1,MSH2,CD109,HOXA7,PTBP3,SLC46A2,MTURN,BPGM,CNOT4,PLEK,RSAD2,PTN,ADD2,IL4I1,TLR4,BVES,IL15,ATG5,OSTM1,FOXO3,ZBTB24,TRAF3IP2,BMI1,PIP4K2A,ABI1,ERCC1,ERCC2,CLPTM1,GAB2,GLI2,DHTKD1,PRDX3,FOXJ1,SLC25A38,POU4F1,IL15RA,KLF6,CMTM7,TGFBR2,ACVR2A,EOMES,JAG1,PLCL2,RASGRP4,CNN2,C12orf29,EIF2AK2,ASH2L,FUT10,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,MFHAS1,FLT1,TRAF6,TCF15,SOX12,TOX,ZC3H8,ASXL1,IL1A,ACVR1B,CAMK4,CEBPA,NCOA6,PIK3R1,CASP3,FBXW7,PTPRJ,MEF2C,TMEM131L,IL7,TPD52,PTK2B,RASGRP1,LMBR1L,CIAPIN1,RIPK2,TENT2,CDH17,AP3B1,F2RL1,TESC,RIPK1,SOX13,STK4,TMEM14C,TSPAN2,DMTN,ITGB6,ALAS1,LDB1,DCAF1,RAB7B,DOCK10,SH3PXD2A,PKNOX1,LRRK1,LCK,SBDS,SLC9B2,TGFB2,TCIRG1,ACP6,GPR137B,PRKX,RABL3,SELPLG,PIAS3,HLX,SART3,ACIN1,DYRK3,TCTA,HCLS1,YTHDF2,UBASH3B,SLAMF8,ARIH2,CIB1,WASF2,ARNT,FZD7,OSM,HDAC4,THPO,MMP21,CD28,FCER1G,RUNX3,FARP2,RTKN2,ZBTB46,PATZ1,FZD9,SP3,PPP2R3C,ETV6,ADAM8,NFE2L2,CREB1,NBEAL2,FZD5,DUSP10,BCL6,SYVN1,BATF2,ITGA4,WDR61,VSIR,XRCC5,ARMC6,RC3H1,ESRRA,PTPN6,GPR137,MEOX1,FBN1,TNFSF18,WNT4,LAG3,PPP3CB,PRRC2C,LTBR,STAT3,STAT5B,LEO1,INHA,TFE3,FOXP3,ZBTB1,PARP1,GPS2,THRA,CARD11,RBPJ,MED1,ANXA2,TBX21,SETD1A,PSEN1,SEMA4A,HOXB8,AHSP,KAT7,DOCK2,CTC1,FOS,BATF,DNASE	grey	VSMC_M10
GO:1904706	0.93	0.15	8	20	negative regulation of vascular associated smooth muscle cell proliferation	BP	1	MEF2C,PDCD4,GNA13,GPER1,EFEMP2,CDKN1B,RHOA,MIR339	grey	VSMC_M10
GO:0060352	0.93	0.18	4	11	cell adhesion molecule production	BP	1	CXCL8,COLEC12,MIR222,MIR27B	grey	VSMC_M10
GO:0050830	0.93	0.12	14	33	defense response to Gram-positive bacterium	BP	1	NOD1,C5AR1,MYD88,RIPK2,NOD2,FGR,IL12A,IL7R,DROSHA,HIST1H2BK,CHGA,HIST1H2BF,HIST1H2BJ,HAVCR2	grey	VSMC_M10
GO:0051340	0.93	0.18	4	11	regulation of ligase activity	BP	1	XRCC1,XRCC4,FAM173B,NHEJ1	grey	VSMC_M10
GO:0009048	0.93	0.17	5	14	dosage compensation by inactivation of X chromosome	BP	1	YTHDC1,CDYL,UPF1,PCGF3,SMCHD1	grey	VSMC_M10

GO:0048534	0.93	0.08	327	649	hematopoietic or lymphoid organ development	BP	1	NME1,STK3,MPIG6B,HSPA1B,BRD1,AGER,HLA-DRA,IL5,TCF7,CCDC134,BAK1,XRCC6,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,ATF4,MAPK14,PIM1,MFNG,HSF1,KCP,MYH9,ZNF16,RBFOX2,TEK,FBXO7,SRF,CDK6,KIT,ROR2,NFIL3,RPS14,TMEM190,IL11,SMAP1,EPAS1,MSH2,CD109,HOXA7,PTBP3,SLC46A2,MTURN,BPGM,CNOT4,PLEK,RSAD2,PTN,ADD2,IL4I1,TLR4,BVES,IL15,ATG5,OSTM1,FOXO3,ZBTB24,TRAF3IP2,BMI1,PIP4K2A,ABI1,ERCC1,ERCC2,CLPTM1,GAB2,GLI2,DHTKD1,RAF1,PRDX3,FOXJ1,SLC25A38,POU4F1,IL15RA,KLF6,CMTM7,TGFBR2,ACVR2A,EOMES,JAG1,PLCL2,RASGRP4,CNN2,C12orf29,EIF2AK2,ASH2L,FUT10,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,MFHAS1,FLT1,TRAF6,TCF15,SOX12,RET,TOX,ZC3H8,ASXL1,IL1A,ACVR1B,CAMK4,CEBPA,NCOA6,PIK3R1,CASP3,HAND2,FBXW7,PTPRJ,MEF2C,TMEM131L,IL7,TPD52,PTK2B,RASGRP1,LMBR1L,CIAPIN1,RIPK2,TENT2,CDH17,AP3B1,F2RL1,TESC,RIPK1,SOX13,STK4,TMEM14C,TSPAN2,DMTN,ITGB6,ALAS1,JARID2,LDB1,NFKB2,DCAF1,RAB7B,DOCK10,SH3PXD2A,PKNOX1,LRRK1,LCK,SBDS,SLC9B2,TGFB2,TCIRG1,ACP6,GPR137B,PRKX,RABL3,SELPLG,PIAS3,HLX,SART3,ACIN1,DYRK3,TCTA,HCLS1,YTHDF2,UBASH3B,SLAMF8,ARIH2,CIB1,WASF2,ARNT,FZD7,OSM,HDAC4,THPO,MMP21,CD28,FCER1G,RUNX3,FARP2,EPHB3,RTKN2,ZBTB46,PATZ1,FZD9,SP3,PPP2R3C,ETV6,ADAM8,NFE2L2,CREB1,NBEAL2,FZD5,DUSP10,BCL6,SYVN1,BATF2,ITGA4,WDR61,VSIR,XRCC5,ARMC6,RC3H1,ESRRA,PTPN6,GPR137,MEOX1,FBN1,TNFSF18,WNT4,LAG3,PPP3CB,PRRC2C,LTBR,STAT3,NKX3-2,MAPK1,STAT5B,LEO1,INHA,TFE3,FOXP3,ZBTB1,PARP1,GPS2,THRA,CARD11,RBPJ,MED1,ANXA2,TBX21,SE	grey	VSMC_M10
GO:1903672	0.93	0.16	6	16	positive regulation of sprouting angiogenesis	BP	1	BMPER,SLC39A12,JAK1,PDPK1,MIR125A,FGF1	grey	VSMC_M10
GO:0060349	0.93	0.10	34	76	bone morphogenesis	BP	1	OSR2,TEK,DLX5,RAB23,COL27A1,SFRP4,SOX9,MEGF8,TSKU,TGFBR2,RARB,MEF2C,STC1,TFAP2A,BMPR1B,TRPV4,TRIP11,AXIN2,ACTN3,POR,COL13A1,ALPL,FGFR3,MMP13,DHRS3,MSX2,FGF18,TMEM107,THBS3,FOXN3,CDX1,GHR,SKI,INSIG2	grey	VSMC_M10
GO:0014013	0.93	0.10	33	73	regulation of gliogenesis	BP	1	TSPO,SOX10,DAAM2,TTBK1,PTN,EGFR,MYCN,HDAC2,KDM4A,SIRT2,PLAG1,SYNJ1,NKX6-1,SPINT1,RNF10,HDAC1,DAG1,CERS2,DLX1,DUSP10,TNFRSF1B,PRPF19,LDLR,MBD1,DAB1,SKI,SOX8,MIR222,MIR125B1,GPR37L1,NOG,LIF,PITX3	grey	VSMC_M10
GO:0019932	0.93	0.08	105	218	second-messenger-mediated signaling	BP	1	NFATC1,PDE7B,ADGRG6,RIMS2,PDE10A,UBE2B,RCAN2,FHL2,TNNI3,PPP2R1A,FPR2,CXCL8,AQP1,PLEK,EGFR,TRPM4,GRIN2D,SLC8A2,NDNF,SOX9,GIPR,ACKR2,EFHB,PRNP,P2RX2,NRG1,P2RX3,PLCE1,PTPRJ,P2RX7,GUCY1A1,GUCY1B1,SLA2,PTK2B,RAPGEF2,RAPGEF3,PLA2G4B,DMTN,CASQ2,KSR2,CHRM3,CAP2,RYR2,ADCY2,SPPL3,PDE9A,PPP3CA,INPP5A,NR5A2,CMKLR1,ADNP,TBC1D10C,ANK2,DGKD,TRPM8,LAT2,AGT,CIB1,ATP1A2,SLC9A1,NFATC4,MYOZ2,CASQ1,ACTN3,HDAC4,RCAN3,NOS1AP,HOMER2,MAPT,FIS1,EIF4EBP2,MCU,CXCR2,HTT,PPP3CB,MYOZ1,ATP1B1,BST1,BHLHA15,DGKQ,LAT,TMEM100,CALM1,BTK,RIT2,PDE4A,NMUR2,MAPK7,RASD1,KSR1,NOS2,MGRN1,BCAP31,PDPK1,CAMTA1,NFATC3,PTGFR,CAP1,DMD,CCR10,PDZD3,IRGM,SAMD14,CRH,RASD2	grey	VSMC_M10
GO:0009615	0.93	0.08	124	253	response to virus	BP	1	TNFAIP3,USP15,C6orf106,APOBEC3H,MAPK14,EXOSC4,IRF5,CDK6,GSDME,ANKRD17,RSAD2,IL15,PUM2,APOB,TRAF3IP2,ZC3HAV1,PHB,UNC13D,MYD88,SEC14L1,IKBKB,NMI,ZMYND11,TMEM173,CLPB,NPLOC4,EIF2AK2,MAVS,AIMP1,IRF7,PCBP2,TRIM44,IRF2,AUP1,EIF2AK4,SERINC5,OAS3,NLRC5,IFNGR2,F2RL1,POLR3D,IFIT2,HERC5,ITGB6,CD40,GBF1,MX2,IFIH1,OASL,HYAL1,HYAL3,CRCP,GPAM,ADARB1,UNC93B1,POLR3C,CFL1,PARP9,DTX3L,IRF9,IFI6,RNF26,FGR,NLRX1,ABCF3,TRAF3IP1,HTRA1,TRIM52,XPR1,SETD2,IVNS1ABP,PRKRA,RTP4,IL12A,DDX3X,MUL1,BIRC3,POLR3A,PIM2,FOXP3,RNF216,TKFC,CCDC130,SPON2,TBX21,SMAD3,AKAP1,TSPAN6,STAT2,POLR3E,G3BP1,SIN3A,TRAF3,CCL5,RIOK3,RNF135,TICAM1,TTC4,FMR1,ATAD3A,NCBP3,IKBKG,POLR3K,LAMTOR5,IFI44L,ZDHHC1,MIR21,OAS1,RPS15A,ZDHHC11,FADD,TRIM34,BNIP3L,ZCCHC3,CREBZF,IFNLR1,IRGM,SAP30BP,FGL2,KCNJ8,IFIT3,BATF3,CCL22,EXOSC5	grey	VSMC_M10
GO:0046890	0.93	0.09	60	127	regulation of lipid biosynthetic process	BP	1	ORMDL2,CYP27B1,AVIL,PPARA,TSPO,PLA2G6,NR1H2,LPIN1,DKKL1,APOB,SPHK2,APOC1,PIBF1,SIRT3,NR1H4,TRIB3,CYP7A1,ASAH1,ABHD6,DKK3,FBXW7,SORBS1,NR1H3,FITM2,ORMDL1,HSD17B13,ERLIN1,PRMT3,SIRT4,GPLD1,LPCAT1,SIK1,ZBTB20,SNAI1,GPER1,LPGAT1,MLXIPL,SCAP,POR,CREB1,ACADL,LPCAT3,WNT4,SLC27A1,ACADVL,FGFR4,DGKQ,LDLR,ASXL3,CD74,SREBF1,C3,ABCA3,GFI1,FABP5,CNEP1R1,STARD4,INSIG2,CCDC3,FGF1	grey	VSMC_M10
GO:1903039	0.93	0.09	68	143	positive regulation of leukocyte cell-cell adhesion	BP	1	AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,NCK2,IL4I1,IL15,BMI1,GLI2,TGFBR2,NCKAP1L,SLC7A1,TRAF6,SOX12,IL1A,IL7,RASGRP1,RIPK2,AP3B1,SOX13,NOD2,IGF2,LCK,ICOSLG,GPAM,HLX,CD28,RUNX3,ADAM8,DUSP10,BCL6,ITGA4,IL12A,VSIR,PTPN6,STAT5B,FOXP3,RASAL3,ZBTB1,CARD11,ZBTB7B,IL4R,CD74,CCL5,CCL2,YES1,NKAP,VAV1,IL7R,SOCS1,DNAJA3,PRKCZ,BCL10,MIR21,RHOA,SOX4,FADD,DPP4,CD46,FUT4,THY1,CD70,TNFSF9,EFNB3,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0051280	0.93	0.18	4	11	negative regulation of release of sequestered calcium ion into cytosol	BP	1	PKD2,CASQ2,NTSR1,CALM1	grey	VSMC_M10

GO:0030307	0.94	0.09	63	134	positive regulation of cell growth	BP	1	ADNP2,NEDD4L,LRP1,RIMS2,PRKN,H3F3C,CPNE5,EXOSC4,SRF,SEMA4D,RIMS1,RUFY3,EGFR,TRIM32,SDCBP,GOLGA4,MEGF8,CPNE9,RPTOR,HBEGF,SYT1,SLC23A2,CDKN2AIP,PTK2B,ZFYVE27,CYFIP1,BDNF,HYAL1,TGFB2,ZNF639,ADNP,DISC1,CIB1,SLC9A1,SFN,RPS6KA1,CDKL5,WNT3,MAPT,SUPV3L1,DDX3X,FN1,DDX49,MUL1,CD38,CXCL16,NDEL1,RAB11A,TAF9B,NTN1,MAP2K5,S100A8,PSMD10,TRPV2,L1CAM,SLC25A33,CYBA,MIR199A1,RHOA,FXN,CACNG7,N6AMT1,DERL2	grey	VSMC_M10
GO:0042438	0.94	0.16	6	16	melanin biosynthetic process	BP	1	SLC7A11,RAPGEF2,OCA2,CITED1,SLC45A2,WNT5A	grey	VSMC_M10
GO:0007520	0.94	0.13	10	25	myoblast fusion	BP	1	MAPK14,MYH9,DYRK1B,MYOF,JAM2,ADAMTS15,EHD1,GDF15,IL4R,CACNA1H	grey	VSMC_M10
GO:1902751	0.94	0.13	11	27	positive regulation of cell cycle G2/M phase transition	BP	1	VPS4B,MTA3,CCND1,DYRK3,STOX1,DBF4B,RAD51B,RAB11A,RAD51C,SIN3A,MECP2	grey	VSMC_M10
GO:0032781	0.94	0.14	8	20	positive regulation of ATPase activity	BP	1	NAPA,CHTOP,TOR1AIP1,DNAJC10,DNAJB2,ATP1B1,DNAJB1,ATP1B2	grey	VSMC_M10
GO:0120033	0.94	0.13	10	25	negative regulation of plasma membrane bounded cell projection assembly	BP	1	TBC1D30,ARHGAP24,SRGAP2C,LIMK2,RAP1GAP,DNM2,ARHGAP44,EVL,CDK10,ODF2L	grey	VSMC_M10
GO:0030166	0.94	0.11	21	49	proteoglycan biosynthetic process	BP	1	B4GALT7,CHST10,HS3ST5,CHPF2,CSGALNACT1,BMPR1B,SLC2A10,TCF7L2,GAL3ST3,CHST3,GAL3ST4,CHST7,AC022400.6,CHST12,GLCE,HS6ST2,B3GALT6,FOXL1,HS6ST3,CHSY3,HS2ST1	grey	VSMC_M10
GO:0030575	0.94	0.16	5	14	nuclear body organization	BP	1	HABP4,DYRK3,CELF3,WRAP53,AFF2	grey	VSMC_M10
GO:0030837	0.94	0.11	23	53	negative regulation of actin filament polymerization	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,SPTBN1,ADD2,MKKS,LMOD3,HIP1R,DMTN,CARMIL1,LMOD1,ADD3,SSH1,SPTBN2,TMOD4,EPS8,CAPZA1,TMOD2,SPTB,SSH2,CARMIL2,PFN4	grey	VSMC_M10
GO:0000184	0.94	0.12	14	34	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	PABPC1,SKIV2L,EIF3E,PNLDC1,DHX34,UPF3A,NCBP2,UPF1,DCP1B,CASC3,SMG5,UPF3B,PARN,MAGOHB	grey	VSMC_M10
GO:0150146	0.94	0.16	5	14	cell junction disassembly	BP	1	IQSEC1,PIK3R1,EPHA4,ITGAM,C3	grey	VSMC_M10
GO:0003281	0.94	0.10	26	60	ventricular septum development	BP	1	FRS2,PTK7,HOXA13,CNTRL,WNT11,TGFBR2,PAX8,ROBO1,ROBO2,TBX5,SALL1,SUFU,TGFB2,TRIP11,LUZP1,SAV1,BMPR1A,RBPJ,DCTN5,STRA6,AP2B1,SOX4,NOG,WNT5A,NKX2-5,HEY2	grey	VSMC_M10
GO:0040013	0.94	0.08	127	261	negative regulation of locomotion	BP	1	LRP1,SEMA6A,SRGAP1,FBLN1,TRIB1,MAPK15,SRF,SEMA4D,SEMA4C,MEOX2,SVBP,CLDN19,RNF20,HAS1,HOXA7,PTN,ITGB1BP1,FUZ,EPHA1,FOXO3,C5AR2,CLASP2,DACH1,CYGB,WNT11,SRGAP3,JAG1,NAV3,PLCB1,SPINT2,CNN2,SEMA3D,DCN,SEMA3A,NRG1,MITF,DPYSL3,RYK,ABHD6,ROBO1,ROBO2,PTPRJ,MEF2C,SEMA4F,STC1,TBX5,ACVR1C,TP53INP1,SEMA3G,SEMA4G,ADTRP,SRGAP2C,CD200,SINHCAF,SP100,SEMA3F,ADARB1,GNA13,DAG1,ABHD2,AP1AR,SLAMF8,CERS2,PTPRO,CHRD,CLIC4,PATZ1,APOD,WNT3,FRMD5,NFE2L2,MIA3,DUSP10,SEMA6D,PDCD10,WNT4,COL3A1,STAT3,VCL,WAS,PADI2,EPHA4,BMPR1A,SYNJ2BP,ATP1B2,SEMA4A,NGFR,VASH1,MAP2K5,EVL,CD74,CCL2,CCL25,PTGER4,STK26,PTPN2,CRK,ARHGAP4,MECP2,PLXNA3,PIP5K1L,ENG,MARVELD3,SCAI,DAB2IP,WDR63,MIR29A,MIR199A1,MIR21,MIR22,MIR24-1,MIR491,RHOA,C5orf30,ADGRG1,DPP4,ACVRL1,NOG,THY1,WNT5A,GADD45A,DUSP1,RGCC,GCSAM,DUSP22,LDLRAD4,RAP2B	grey	VSMC_M10
GO:0051223	0.94	0.08	205	412	regulation of protein transport	BP	1	LRP1,SLC12A2,PRKN,GOPC,MAPK14,PLA2G6,PICK1,RAC2,SMO,RFX3,SLC1A1,TFAP2B,RAB23,DNAJA1,PRKCE,TMEM30A,HMGN3,RUFY3,XPO1,BMP8A,RSAD2,NR1H2,ITGB1BP1,EGFR,ARHGEF5,TLR4,TCAF2,TRPM4,SLC7A11,DNAJC27,GIPR,LCP1,PLK3,FRMD4A,LLGL2,AKT2,USP36,UBAC2,APBB3,DPH3,SIRT7,FERMT1,CEP290,PRNP,BAG4,MAVS,GAS6,SIRT3,SYT9,NR1H4,LYPLA1,NUP58,TM9SF4,NDUFAF2,FAM3D,IL1A,OSBP,PIK3R1,ARNTL,FBXW7,PKIA,HTRA2,VEGFC,ZFAND1,CSNK2A2,NUP54,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX6-1,RAPGEF3,ACVR1C,F2RL1,F2R,ZBED6,DMTN,ADTRP,SUFU,SIRT4,GPLD1,IRS1,CABP1,CD200,DNM1L,HDAC1,PPP3CA,SP100,CPT1A,SLC9B2,TGFB2,ADRA2A,TCIRG1,TCF7L2,KCNB1,YOD1,PFKFB2,HCLS1,HSPA8,HPS4,SORL1,C2CD5,GPER1,ARIH2,CIB1,BAG3,SFN,PER2,STX1A,UHMK1,GLUL,SIDT2,SLC16A1,APOD,ADAM8,KLF7,CTDSPL2,FZD5,FIS1,CEMIP,NMT1,TTN,DERL3,SEC16B,IL12A,ENY2,ABCA12,C11orf65,MCU,PDCD10,PPP3CB,PINK1,CD38,MPC2,MAPK1,CHRM1,TMEM30B,GRIPAP1,RAB8A,ATP13A2,CNST,SYT7,RSC1A1,NLGN2,NPEPPS,TARDBP,STX4,PSEN1,ITGAM,SNX12,TMED10,NDEL1,AC138894.1,HAX1,RAB11A,MYH10,SMAD3,SYTL4,GPR68,BCAS3,ARHGAP44,CCL5,MIEF2,CDK5R1,SREBF1,ISL1,OXCT1,NOS2,EFCAB7,ABAT,RPH3AL,INPP5K,NADK,BCAP31,PRKCZ,OAZ1,BAIAP3,PARK7,LRRC8A,GAPVD1,SH3GLB1,WWP2,RIPOR1,MIR199A1,MICALL2,FGA,CHGA,SOX4,DPP4,BNIP3L,CRH,TXN,DOC2B,HRAS,UQCC2,MIEF1,RHOU,LEPROT,PARD6A,UBE2G2,DERL2,ZIC1	grey	VSMC_M10
GO:0007519	0.94	0.09	57	122	skeletal muscle tissue development	BP	1	STAC3,VGLL2,PITX1,LEMD2,MAPK14,SMO,MEOX2,HIVEP3,MYH14,AKIRIN1,BVES,KEL,KLF5,KLHL40,NR1D2,RYR1,DCN,P2RX2,LMOD3,EPHB1,NR4A1,SMYD1,NLN,FOXL2,FLNB,VAMP5,SAP30,ARNTL,MEF2C,TLL2,HOMER1,BIN3,RBM24,IGF2,MYH15,NEURL1,PPP3CA,HLX,USP19,MYOZ2,CASQ1,ACTN3,HDAC4,YBX3,MYOZ1,MYLPF,ZNF689,FOS,FBXO22,SKI,SOX8,RHOA,DMD,SIX1,POPDC2,MYORG,UQCC2	grey	VSMC_M10
GO:0007040	0.94	0.10	27	61	lysosome organization	BP	1	WASHC5,TFEB,ACP4,PPT1,MFSD8,RAB7A,MYO7A,HOOK3,TMEM106B,FAM160A2,CHMP2B,ACP2,AP3B1,VPS18,RAB7B,TMEM9,HPS4,SPG11,PIKFYVE,SYT7,CLN8,AC138894.1,HOOK2,CLN6,SNAPIN,TMEM199,RAB39A	grey	VSMC_M10

GO:0080171	0.94	0.10	27	61	lytic vacuole organization	BP	1	WASHC5,TFEB,ACP4,PPT1,MFSD8,RAB7A,MYO7A,HOOK3,TMEM106B,FAM160A2,CHMP2B,ACP2,AP3B1,VPS18,RAB7B,TMEM9,HPS4,SPG11,PIKFYVE,SYT7,CLN8,AC138894.1,HOOK2,CLN6,SNAPIN,TMEM199,RAB39A	grey	VSMC_M10
GO:0050679	0.94	0.09	73	154	positive regulation of epithelial cell proliferation	BP	1	NME1,TNFAIP3,OSR2,MYC,SMO,TEK,DLX5,PDCL3,RTN4,EMC10,EPGN,AREG,TGFA,PTN,EGFR,OSR1,FOXE3,C5AR2,C5AR1,PRKD2,SOX9,SCN5A,WDR48,RPTOR,CYP7B1,NR4A1,EYA1,VEGFC,AGGF1,SRSF6,RREB1,PAX2,NOD2,IGF2,HYAL1,CCND1,TCF7L2,PDCD6,EGF,ARNT,TGM1,VASH2,FZD7,HTRA1,GLUL,LAMC1,STOX1,ITGA4,GPBAR1,STAT3,PTPRN,BMPR1A,MED1,PGF,MAP2K5,PDPK1,CYBA,ESRP2,MIR29A,MIR21,MIR23A,MIR27B,MIR27A,LAMB1,ACVRL1,ZNF580,NOG,CLDN1,WNT5A,ZNF304,HRAS,FGF1,WNT2	grey	VSMC_M10
GO:0071243	0.94	0.15	7	18	cellular response to arsenic-containing substance	BP	1	ATF4,MAPK13,HSF1,ZFAND1,SLC38A2,DDX3X,PPIF	grey	VSMC_M10
GO:0042098	0.94	0.09	60	127	T cell proliferation	BP	1	AGER,HLA-DPB1,TNFRSF13C,RAC2,CCND3,TNFRSF21,NCK2,PELI1,IL4I1,IL15,BMI1,FOXJ1,TGFBR2,PAWR,PRNP,NCKAP1L,SLC7A1,TRAF6,IL1A,CASP3,TMEM131L,RASGRP1,LMBR1L,RIPK2,MARCH7,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,CD28,DLG1,VSIR,RC3H1,PTPN6,TNFSF18,SLC11A1,WNT4,PPP3CB,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,DOCK2,ZBTB7B,CCL5,TWSG1,DNAJA3,GLMN,MIR21,FADD,CD46,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0034982	0.94	0.18	4	11	mitochondrial protein processing	BP	1	ATP23,MIPEP,IMMP1L,SIRT4	grey	VSMC_M10
GO:0000027	0.94	0.15	7	18	ribosomal large subunit assembly	BP	1	MDN1,RPL6,DHX30,RPL11,RPL10L,NLE1,RPL23A	grey	VSMC_M10
GO:0002065	0.94	0.10	27	61	columnar/cuboidal epithelial cell differentiation	BP	1	ROS1,SMO,CDK6,RFX3,KLF5,WNT11,RARB,CBFA2T2,ARNTL,NKX6-1,ZBED6,FAM20C,SIDT2,MEN1,PYY,SAV1,WNT4,NKX3-2,DLX3,GATA6,PDPK1,WDR77,TMEM231,SOX4,WNT5A,TIGAR,CEBPB	grey	VSMC_M10
GO:0034329	0.94	0.08	154	318	cell junction assembly	BP	1	LRP1,PTK2,NTRK2,MPDZ,TEK,LRRC4,LINGO2,SRF,GABRA1,FZD1,ADGRF1,TLN1,SEMA4D,ADGRL3,CLDN19,GJA10,LRRN3,EPHA7,ITGB1BP1,ADD2,VPS35,SDCBP,NRCAM,VSTM5,CLASP2,FBF1,POU4F1,WNT11,SLITRK5,IKBKB,LRFN1,FARP1,ACTG1,ARHGEF7,NRG1,PTPRA,PKP3,LRFN3,RYK,EPHB1,NPHP1,LSR,FAM107A,CLSTN2,CTNND1,MARVELD2,ROBO2,FMN1,SORBS1,PTPRJ,MEF2C,CUX2,PTK2B,RAPGEF2,SLIT1,HDAC7,TBX5,AMIGO2,DMTN,LDB1,BDNF,PKP2,SLK,COL17A1,TRPV4,GAP43,COL16A1,AMIGO3,NLGN4Y,AJUBA,CLDN34,CDH24,BSN,SNAI1,ADNP,ARHGAP6,ANK2,GNPAT,AGT,ACE2,SLC9A1,RAB17,SPTBN2,ACTN3,NPAS4,PTPRO,EPHB3,WHAMM,LAMC1,DLG1,APOD,CAPZA1,FZD5,RAP1B,TRIP6,ARVCF,NRXN2,FN1,SPOCK2,GPBAR1,WNT4,DNM3,CNTNAP1,RAMP2,VCL,OBSL1,LRTM2,ACTB,CLDN7,SDK1,NLGN2,LGI2,SEMA4A,TLN2,NLGN3,TAOK2,CHRNB2,SMAD3,NTN1,CORO2B,MYO9A,VMP1,BCAS3,GPRASP2,BHLHB9,CAMSAP3,ASIC2,EPB41L3,CDH6,CDH10,SLITRK2,PIP5K1C,PDPK1,MECP2,AMIGO1,CEL,TSC1,NTNG2,ZDHHC12,MARVELD3,ADGRL2,MICALL2,RHOA,CLDN15,GRID2,ACVRL1,PEAK1,THY1,CLDN1,WNT5A,SIX1,APC,DUSP22,LRRTM2	grey	VSMC_M10
GO:0045324	0.94	0.14	7	18	late endosome to vacuole transport	BP	1	CHMP2A,LEPROTL1,CHMP2B,CHMP4C,CHMP7,CHMP1A,LEPROT	grey	VSMC_M10
GO:0007143	0.94	0.13	10	25	female meiotic nuclear division	BP	1	WASHC5,MLH1,HSF2BP,PRKAR1A,SEPT1,RAD51C,MEIOB,SPIRE2,UBB,EREG	grey	VSMC_M10
GO:0034637	0.94	0.10	28	63	cellular carbohydrate biosynthetic process	BP	1	AKR1B1,HAS1,EPM2AIP1,PPP1CB,CSGALNACT1,AKT2,PPP1R3B,GBE1,B3GNT4,SORBS1,IGF2,NHLRC1,IRS1,PPP1R3E,PPP1R3D,PER2,PASK,PRKAG3,AC022400.6,PPP1R3F,INSR,IMPA2,INPP5K,AGL,HAS3,ACADM,FBP2,HS2ST1	grey	VSMC_M10
GO:1904376	0.94	0.13	10	25	negative regulation of protein localization to cell periphery	BP	1	GOPC,LYPLA1,PPFIA1,AP2M1,PPP2R5A,LRRC15,LZTFL1,RSC1A1,SAPCD2,MRAP2	grey	VSMC_M10
GO:0040029	0.94	0.09	39	86	regulation of gene expression, epigenetic	BP	1	BAZ2A,ARID1B,H3F3C,YTHDC1,SPHK2,DNMT3A,BMI1,SETDB2,SIRT2,FAM208A,SMARCD1,BAHD1,CDYL,PPHLN1,ZNF335,IGF2,HDAC1,ZNFX1,TFAP2C,ARID1A,HDAC4,TET1,H2AFY2,UPF1,PADI2,PHF8,PCGF3,NRDE2,SMCHD1,MECP2,GLMN,PRMT7,CTCF,SERTAD2,SETDB1,ARID4A,CREBZF,BEND3,ZNF304	grey	VSMC_M10
GO:0006305	0.94	0.10	23	53	DNA alkylation	BP	1	BAZ2A,MOV10L1,MYC,PICK1,STPG4,DNMT3A,BMI1,TEX15,DNMT3B,MTRR,HEMK1,TDRKH,MGMT,PARP1,FOS,METTL4,MBD1,MECP2,PRMT7,CTCF,MIR29A,BEND3,N6AMT1	grey	VSMC_M10
GO:0006306	0.94	0.10	23	53	DNA methylation	BP	1	BAZ2A,MOV10L1,MYC,PICK1,STPG4,DNMT3A,BMI1,TEX15,DNMT3B,MTRR,HEMK1,TDRKH,MGMT,PARP1,FOS,METTL4,MBD1,MECP2,PRMT7,CTCF,MIR29A,BEND3,N6AMT1	grey	VSMC_M10
GO:1900076	0.94	0.10	22	51	regulation of cellular response to insulin stimulus	BP	1	PIP4K2C,GKAP1,GRB10,PIP4K2A,ECHDC3,SNX5,SORBS1,OPA1,IGF2,GPLD1,IRS1,GRB14,SORL1,AGT,ESRRA,ZBTB7B,PRKCB,PTPN2,SOCS1,INPP5K,PRKCZ,BGLAP	grey	VSMC_M10
GO:0006448	0.94	0.15	6	16	regulation of translational elongation	BP	1	DPH2,DPH3,USP16,ALKBH1,DPH1,AARS	grey	VSMC_M10
GO:0042147	0.94	0.09	36	80	retrograde transport, endosome to Golgi	BP	1	PRKN,VPS52,RGP1,VPS35,RAB7A,RBSN,UBE2O,SNX5,HEATR5B,BET1L,WASHC2A,TMEM87B,GBF1,MAGEL2,RAB7B,VTI1A,TBC1D10C,STX6,SNX6,SNX32,PIKFYVE,VPS26A,TBC1D14,CLTCL1,ANKFY1,STX5,SNX12,TBC1D10B,SNX1,VPS53,BAIAP3,RNF126,PHETA1,RAB6B,VAMP3,PLEKHJ1	grey	VSMC_M10

GO:0018205	0.94	0.08	154	313	peptidyl-lysine modification	BP	1	ATAT1,YEATS4,SNW1,BRD1,PHF1,UHRF2,SUPT3H,HINT2,PHF14,LIPT1,KANSL3,CAMKMT,ING3,ATG5,SETD7,TRPM4,SPHK2,HDAC2,BMI1,SETDB2,EED,IWS1,SUV39H2,SUMO2,KDM4A,PAXIP1,TADA3,ARRB1,CBX4,SIRT2,DPY30,SIRT7,NSD3,TAF7,ASH2L,EP400,SIRT3,TAF10,SDR16C5,EEF1AKMT1,DNMT3B,SMYD1,TAF9,EYA1,PHF20,SETD6,KMT2D,NNAT,KANSL2,SENP1,HDAC7,LOXL2,LOXL4,RTF1,SIRT5,WDR82,ZNF335,JARID2,TOLLIP,RBBP5,LDB1,FAM173B,SIRT4,IFIH1,HDAC1,AUTS2,PIAS3,ARNT,HDAC4,STX1A,MRGBP,EEF1AKMT2,ING5,SENP5,SENP2,SETD2,POR,MBIP,PLOD3,BCOR,MEN1,WDR61,VCPKMT,TADA2B,NAA40,ING4,NELFA,MUL1,TADA1,DYDC1,P3H4,FOXP3,LIAS,MSL1,MED24,GNL3L,NSD1,SETD1A,KAT7,PAGR1,MUC1,TAF1,MAPK3,OGT,NAP1L2,VIPAS39,CRTC2,RPS6KA5,PIAS2,NDUFAB1,SETD3,SIN3A,ISL1,SUZ12,SUPT6H,CXXC1,GLYR1,PIAS4,DOHH,CREBBP,NAA60,DOT1L,HCFC1,MECP2,PRDM16,CHD5,PARK7,GTF3C4,GCSH,MTF2,GFI1,CTCF,PRMT6,METTL18,SETDB1,RNF212B,ARID4A,TAF12,SOX4,CPA4,RWDD3,BEND3,SMYD3,METTL21A,SUPT7L,SENP7,ZNF304,NNMT,LIF,N6AMT1,P3H3,RPS6KA4,HINT1,RASD2	grey	VSMC_M10
GO:0016331	0.94	0.09	59	127	morphogenesis of embryonic epithelium	BP	1	STK3,FZD6,BRD2,PTCH1,PTK7,SEMA4C,FUZ,TEAD2,OSR1,SOX9,GLI2,PCDH8,IFT172,OVOL2,SPINT2,TRAF6,RET,PAX8,CASP3,FZD3,VEGFC,OPA1,IFT52,SPINT1,STK4,TFAP2A,PAX2,PRICKLE1,SUFU,IRX2,ALDH1A3,TGFB2,DVL3,KDF1,LAMA5,GRHL3,LUZP1,SETD2,WNT4,TULP3,LIAS,DVL2,ALDH1A2,TGFB1I1,MKS1,MIB1,JAG2,SKI,SOX8,TSC1,GLMN,BCL10,VASP,SOX4,NOG,WNT5A,SIX1,RALA,WNT2	grey	VSMC_M10
GO:0044057	0.94	0.08	197	398	regulation of system process	BP	1	RIMS2,AGER,PPARA,GDF9,SOX10,PI16,ZDHHC21,CHRNA3,CRY1,SRF,KIT,SLC1A1,TNFRSF21,ABCG5,ABCG8,TNNI3,EPAS1,RIMS1,ASB3,SHANK1,AQP1,NR1H2,EGFR,BVES,DLGAP3,LPIN1,TRPM4,FOXO3,FIG4,GRIN2D,MTMR2,TRPC3,SLC8A2,CST7,CACNB2,ATP1A3,CELF2,SCN5A,GPD1L,SNX5,C1QTNF1,HBEGF,ADRA1D,SEMA3A,GAS6,FAM19A4,ADRA2B,NR4A1,HIP1R,HAND2,P2RX3,PLCE1,JAM2,DLGAP4,GUCY1A1,CUX2,PTK2B,NR1H3,DOCK5,HOMER1,STC1,NKX3-1,KCNJ3,TBX5,F2RL1,F2R,CRY2,TNNC1,FTO,GLS,KCNE2,DSP,CASQ2,JARID2,KCNIP2,CHRM3,RYR2,FAM173B,RNF10,PKP2,PDE9A,PPP3CA,KCNJ2,TNNI1,TRPV4,TGFB2,ADRA2A,IGSF11,DAG1,SSH1,MYH7,ZFHX2,EPB41,OPRD1,GRK2,GTF2IRD1,ANK2,GPER1,AGT,ACE2,ATP1A2,SLC9A1,PER2,CASQ1,ACTN3,HDAC4,MTG2,STX1A,TMEM25,NTSR1,PTPRO,SCN4B,CNIH2,NOS1AP,DLG1,COMT,TNR,LPCAT3,ADRA2C,PTGER2,CALCRL,ECE1,PRKAG3,GCH1,CAMK2G,ATP1B1,KCNA1,SMTNL2,CD38,NPTX2,KCNMA1,DES,INHA,SLC4A3,DLG4,PARP1,THRA,NLGN2,TNFRSF1B,ATP1B2,HRH2,MYL5,STX1B,RAB8B,NLGN3,CACNA1G,ATP2A1,TMEM100,SMAD3,CORO2B,CALM1,TBX2,NMUR2,SETD3,YY1,BEGAIN,DSG2,ASIC2,SREBF1,ISL1,DLGAP1,CYP2J2,ABAT,FMR1,INPP5K,ATP2B3,TRPV1,P2RX1,PRKCZ,MECP2,RNF207,CACNA1H,CYBA,MIR199A1,MIR21,MIR25,RHOA,FGA,DMD,GPR35,FABP5,NOL3,CHGA,SLC22A5,TMEM65,KCNH2,TNNC2,SCN2B,RGS4,CRH,POPDC2,CACNG5,HCN4,NKX2-5,KCNMB4,HEY2,KCNG2	grey	VSMC_M10
GO:0006509	0.94	0.11	15	36	membrane protein ectodomain proteolysis	BP	1	MYH9,TIMP4,ERAP1,SH3D19,GPLD1,ADRA2A,DAG1,BACE1,LRIG2,ADAM8,SPPL2A,PSEN2,TNFRSF1B,PSEN1,SPPL2B	grey	VSMC_M10
GO:0003206	0.94	0.09	46	101	cardiac chamber morphogenesis	BP	1	ADGRG6,LY6E,SMO,FOXH1,TEK,SRF,FHL2,TNNI3,DNAH11,POU4F1,WNT11,TGFBR2,OVOL2,JAG1,NRG1,HAND2,PARVA,ROBO1,ROBO2,MEF2C,ADAMTS1,TBX5,TNNC1,DSP,RYR2,PKP2,TNNI1,TGFB2,MYH7,SAV1,BMPR1A,DHRS3,RBPJ,MED1,MKS1,TBX2,GATA6,ISL1,FOXF1,ENG,SOX4,NOG,WNT5A,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0030183	0.94	0.09	44	96	B cell differentiation	BP	1	BAK1,MFNG,KIT,IL11,MSH2,IL4I1,TRAF3IP2,KLF6,CMTM7,PLCL2,NCKAP1L,PRKDC,PIK3R1,PTPRJ,IL7,TPD52,PTK2B,CDH17,DCAF1,DOCK10,TCIRG1,RABL3,SLAMF8,HDAC4,FZD9,SP3,PPP2R3C,BCL6,SYVN1,ITGA4,PTPN6,STAT5B,INHA,GPS2,CARD11,RBPJ,CD19,BTK,YY1,PTPN2,LRRC8A,NHEJ1,ZFP36L2,TNFSF13B	grey	VSMC_M10
GO:0061005	0.94	0.10	21	49	cell differentiation involved in kidney development	BP	1	MTSS1,PTCH1,PODXL,SMO,SIX2,POU3F3,OSR1,FOXJ1,JAG1,ASXL1,PAX8,MEF2C,PAX2,SALL1,PRKX,PTPRO,WNT4,CITED1,LHX1,BASP1,LIF	grey	VSMC_M10
GO:0072073	0.94	0.09	53	115	kidney epithelium development	BP	1	MTSS1,MYC,SMAD5,KLHL3,PTCH1,PODXL,SMO,TFAP2B,CAT,SIX2,EPCAM,BMPER,EPHA7,POU3F3,OSR1,SPRY1,SOX9,AQP11,FOXJ1,GZF1,WNT11,JAG1,RARB,RET,ASXL1,PAX8,EYA1,ROBO2,FMN1,MEF2C,PKD2,PAX2,SALL1,IRX2,AGT,LAMA5,PTPRO,DLG1,CXCR2,WNT4,EPHA4,MAGED1,CITED1,SMAD3,LHX1,GPC3,PKD1,SOX8,NOG,BASP1,SIX1,LIF,FGF1	grey	VSMC_M10
GO:0031643	0.94	0.16	5	14	positive regulation of myelination	BP	1	SOX10,CST7,RNF10,DAG1,TNFRSF1B	grey	VSMC_M10
GO:1990874	0.94	0.10	24	54	vascular associated smooth muscle cell proliferation	BP	1	MAP3K5,HPGD,MEF2C,ADAMTS1,NQO2,TERT,PDCD4,GNA13,GPER1,AGT,EFEMP2,CDKN1B,BMPR1A,MFN2,JUN,GNAI3,MIR21,MIR222,MIR27B,MIR27A,RHOA,FOXJ2,MIR339,LDLRAP1	grey	VSMC_M10
GO:0010633	0.94	0.10	26	59	negative regulation of epithelial cell migration	BP	1	MEOX2,SVBP,ITGB1BP1,DCN,SEMA3A,MEF2C,STC1,SP100,PATZ1,DUSP10,PDCD10,SYNJ2BP,VASH1,MAP2K5,EVL,MECP2,MARVELD3,DAB2IP,MIR199A1,MIR21,MIR22,MIR24-1,RHOA,ACVRL1,GADD45A,RGCC	grey	VSMC_M10
GO:0034205	0.94	0.11	19	44	amyloid-beta formation	BP	1	NTRK2,RTN4,PRNP,CASP3,SLC2A13,SORL1,BACE1,RTN1,HAP1,EPHA4,PSEN2,PSEN1,TMED10,EFNA1,ABCA7,MIR29A,MIR24-1,MIR339,APH1B	grey	VSMC_M10

GO:0044283	0.94	0.07	207	414	small molecule biosynthetic process	BP	1	GLS2,SHMT2,CYP27B1,LTC4S,QKI,PPARA,MCAT,HSD17B8,HSD17B3,AKR1B1,ATF4,PYCR3,PSAT1,GPT,HACD4,MTAP,GNMT,ALDH1A1,CRY1,PLPP6,SRD5A3,SPTLC1,SLC25A13,IPPK,HMGCLL1,PPP4R3B,NT5E,ZNF692,PLEK,NR1H2,FAM3C,DKKL1,MGST2,APOB,BCAT2,NANP,SPHK2,DHFR,PRTFDC1,EBP,AKR1A1,APOC1,PRKAG2,PIBF1,ITPKC,ACER3,ELOVL1,SPTLC3,ACSS3,SIRT7,NR1H4,APIP,TRIB3,CSAD,CYP7A1,ELOVL7,ASAH1,CYP7B1,GPI,THNSL2,NLN,CBR4,OSBP,DKK3,GPD1,CYP2R1,P2RY1,PTK2B,PRKAG1,NR1H3,SERINC5,SPR,ENOPH1,COQ2,SDSL,HOGA1,ASNSD1,GLS,ITPKA,ERLIN1,PRMT3,PLTP,SIRT5,PRKAB1,MTRR,ASL,COQ5,MTR,CBSL,SIK1,ALDH1A3,COQ10B,MST1,SNAI1,ABHD2,MSMO1,MECR,GPER1,SC5D,ABCB11,DHRS9,PC,HACD2,IP6K2,LPGAT1,SLC37A4,PER2,OSBPL2,NTSR1,OAT,MLXIPL,DTYMK,HMGCL,GLUL,SCAP,HSD17B7,POR,PTH1R,SORD,PLA2G4A,OSBPL6,UPB1,ACADL,PLOD3,GGT2,TM7SF2,CPS1,OSBPL1A,ACSBG1,PECR,LPCAT3,WNT4,AASDHPPT,CYP27A1,PRKAG3,GCH1,GGT6,NDUFA9,ADK,DAGLB,FADS3,LIAS,ACADVL,COQ8A,DDB1,TECR,HSD17B10,DEGS1,ALDH1A2,FGFR4,LIPC,DGKQ,OSBPL7,PNPO,ALOXE3,PKLR,OGT,AC138894.1,HACD3,CRTC2,MPO,NDUFAB1,CYP46A1,ACSM3,ACACA,CD74,ABHD3,SHMT1,SREBF1,LEPR,ACSBG2,IMPA2,PTPN2,ACAA2,ABAT,GAMT,CACNA1H,PARK7,DECR2,ACSF3,ASS1,MLYCD,COQ4,PTGES2,ABCD3,GFI1,ACADM,FBP2,ACOT4,FABP5,FADS6,TPK1,ELOVL3,DHDDS,MTHFD2L,AMACR,ACER2,GGT5,PDSS2,NNMT,STARD4,PTGES,INSIG2,PHGDH,FGF1,ARPP19,PCBD2	grey	VSMC_M10
GO:0042088	0.94	0.13	10	25	T-helper 1 type immune response	BP	1	TLR4,TRAF6,RIPK2,HLX,PLA2G4A,SLC11A1,SEMA4A,IL4R,HRAS,HAVCR2	grey	VSMC_M10
GO:0042249	0.94	0.16	5	14	establishment of planar polarity of embryonic epithelium	BP	1	PTK7,DVL3,GRHL3,DVL2,WNT5A	grey	VSMC_M10
GO:0048025	0.94	0.15	6	16	negative regulation of mRNA splicing, via spliceosome	BP	1	SRSF10,SRSF6,SRSF4,RBM10,SRSF12,SAP18	grey	VSMC_M10
GO:0033135	0.94	0.09	48	104	regulation of peptidyl-serine phosphorylation	BP	1	BAK1,NTRK2,NCK2,IL11,EGFR,NTF4,BRAF,PRKD2,RAF1,SPRY2,GPD1L,RPTOR,PLCL2,BAG4,GAS6,RET,FNIP2,PAQR3,RIPK2,RAPGEF3,STK4,DMTN,BDNF,CAPRIN2,HCLS1,OPRD1,OSM,INPP5J,MLXIPL,STOX1,PDCD10,PINK1,ARAF,NSD1,HAX1,SH2D3A,DOCK7,INPP5K,MTCP1,PARK7,MAPKAP1,DMD,IRGM,SMYD3,WNT5A,GADD45A,TXN,LIF	grey	VSMC_M10
GO:0006024	0.94	0.10	29	66	glycosaminoglycan biosynthetic process	BP	1	B4GALT7,HAS1,HS3ST5,CHPF2,CSGALNACT1,B3GNT4,ST3GAL6,GALNT5,CHST1,GCNT2,HYAL1,EGF,ABCC5,CEMIP,CHST3,CHST7,AC022400.6,HS3ST1,CHST12,GLCE,HEXA,HS6ST2,B3GALT6,CHST5,ST3GAL2,HAS3,HS3ST2,CHSY3,HS2ST1	grey	VSMC_M10
GO:0002068	0.94	0.13	9	23	glandular epithelial cell development	BP	1	SMO,CDK6,RFX3,RARB,ARNTL,NKX6-1,SIDT2,PDPK1,WNT5A	grey	VSMC_M10
GO:0070527	0.94	0.10	22	51	platelet aggregation	BP	1	MYH9,TLN1,PLEK,SLC7A11,MYL12A,C1QTNF1,ACTG1,CLIC1,PIK3CB,DMTN,UBASH3B,ITGA2B,FN1,PTPN6,FERMT3,VCL,ACTB,PEAR1,ABAT,STXBP1,FGA,RAP2B	grey	VSMC_M10
GO:0032609	0.94	0.10	26	59	interferon-gamma production	BP	1	CD226,HLA-DPB1,TLR4,PRNP,GAS6,NR1H4,RASGRP1,RIPK2,F2RL1,NOD2,CD96,FZD5,IL12A,VSIR,SLC11A1,INHA,SCGB1A1,FOXP3,ISL1,SLC7A5,MIR24-1,FADD,WNT5A,DDIT3,HRAS,HAVCR2	grey	VSMC_M10
GO:0032649	0.94	0.10	26	59	regulation of interferon-gamma production	BP	1	CD226,HLA-DPB1,TLR4,PRNP,GAS6,NR1H4,RASGRP1,RIPK2,F2RL1,NOD2,CD96,FZD5,IL12A,VSIR,SLC11A1,INHA,SCGB1A1,FOXP3,ISL1,SLC7A5,MIR24-1,FADD,WNT5A,DDIT3,HRAS,HAVCR2	grey	VSMC_M10
GO:0010971	0.94	0.12	10	25	positive regulation of G2/M transition of mitotic cell cycle	BP	1	VPS4B,MTA3,CCND1,STOX1,DBF4B,RAD51B,RAB11A,RAD51C,SIN3A,MECP2	grey	VSMC_M10
GO:0060008	0.94	0.15	5	14	Sertoli cell differentiation	BP	1	HSD17B4,SOX9,CTSV,SOX8,ARID4A	grey	VSMC_M10
GO:0010862	0.94	0.11	13	32	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	GDF9,BMP8A,SDCBP,ACVR2A,RBPMS,ACVR1B,TGFB2,GDF15,INHA,BMPR1A,TWSG1,ENG,ACVRL1	grey	VSMC_M10
GO:1902017	0.94	0.10	19	45	regulation of cilium assembly	BP	1	TBC1D30,MAPK15,DYNC2LI1,FUZ,ATG5,ZMYND10,CDKL5,LIMK2,HTT,SDCCAG8,HAP1,MNS1,CNTROB,CCDC151,DNM2,IFT20,WRAP73,CDK10,ODF2L	grey	VSMC_M10
GO:1902692	0.94	0.13	8	21	regulation of neuroblast proliferation	BP	1	SOX10,SMO,PTN,FZD3,VEGFC,ZNF335,DISC1,FOXG1	grey	VSMC_M10
GO:0051234	0.94	0.06	1789	3429	establishment of localization	BP	1	ATP9B,TIMM21,NME1,VPS4B,ERBB3,SLC39A5,NEDD4L,APOF,ATP8B1,MIP,STARD6,MYO1A,LRP1,STX7,SLC18B1,STAC3,AP3S1,SLC2A12,KIF5A,SLC26A10,PEX7,TNFAIP3,AGAP2,HEBP2,REPS1,CYP27B1,PEX3,SLC16A7,CANX,TBC1D30,ATP5MGL,TBC1D9B,PPP1R10,CPSF6,RAB21,NIPAL2,SNCAIP,SNX24,SNX31,MAPK8IP2,CPT1B,PHAX,MARCH3,APOM,ZDHHC14,SLC12A2,HSPA1B,SYNJ2,SERAC1,RIMS2,IGF2R,SLC27A6,EMC2,CDC42SE2,KCNV1,PRRT1,PRKN,QKI,RNF5,AGER,PPARA,TAP1,SLC22A4,CALHM4,KIF3A,SEPT8,TSPO,GDF9,GOPC,SLC35F1,VPS52,HSPA4,DERL1,SMDT1,UBE2B,BAK1,FAM91A1,CATSPER3,WASHC5,MYC,LRRC6,KLHL3,MCHR1,PKD2L2,KCNK9,GRM4,PTK2,FAM53C,SLC45A4,PTP4A3,PTCH1,TSNARE1,LY6E,ZC3H3,EXOC4,SIL1,SYNGR1,MAPK15,AGTPBP1,SUN2,MAPK14,NTRK2,TOMM22,NRBP2,KCNJ4,CSNK1E,TMEM184B,PLA2G6,COPG2,PICK1,MICALL1,PIM1,TBC1D22B,BTBD9,RAC2,SMO,ZDHHC21,TTC39B,HSF1,PLIN2,TOMM6,SLC39A4,ATP6V1F,MYH9,GUCA1B,MFSD3,APOL4,APOL6,IFT74,CHRNA3,CHRNA5,PEX6,TRPM6,POT1,FBXO7,CRY1,CROT,ABCB1,SLC25A40,ABCC10,NOL6,STEAP2,GABRA1,XPO5,WASHC4,APBA1,CNGA1,SLC41A2,TMEM63B,PEX1,SLC35B2,OCIAD1,USP46,CLIC5,VPS50,SLC25A27,SCFD2,RFX3,KIT,SLC1A1,CA9,TGFBRAP1,TFAP2B,SLC25A13,TBC1D8,TRAM2,PPAT,TMEM14A,RGP1,WNK2,BICD2,MFSD14C,CHMP2A,CNNM4,TSPAN13,RAB23,DYNC2LI1,NLRP5,ABCG5,SVBP,ABCG8,LRPPRC,SEC61B,SLC3A1,STX17,CLDN19,SIX2,DNAJA1,IL11,BRSK1,PRKCE,SMAP1,ATP6V1E2,RIMS1,ABCB5,TMC4,TMEM30A,DNAH11,SPTBN1,IGF2BP3,FPR2,HMGN3,KCNQ4,YTHDC1,RIMS3,IBTK,PNPT1,RUFY3,SHANK1,SLC4A4,CYB5R	grey	VSMC_M10

GO:0032733	0.94	0.12	10	25	positive regulation of interleukin-10 production	BP	1	TLR4,PIBF1,F2RL1,NOD2,CD28,STAT3,PRKCZ,CD46,INAVA,TSLP	grey	VSMC_M10
GO:0010934	0.94	0.15	5	14	macrophage cytokine production	BP	1	TLR4,TGFB2,SPON2,CD74,WNT5A	grey	VSMC_M10
GO:0010935	0.94	0.15	5	14	regulation of macrophage cytokine production	BP	1	TLR4,TGFB2,SPON2,CD74,WNT5A	grey	VSMC_M10
GO:0006739	0.94	0.12	11	27	NADP metabolic process	BP	1	ME1,TP53I3,RBKS,NUDT12,FMO5,NUDT17,RPE,NADK,NQO1,TIGAR,RPIA	grey	VSMC_M10
GO:0043217	0.94	0.15	5	14	myelin maintenance	BP	1	PRX,AKT2,MPP5,DEGS1,EPB41L3	grey	VSMC_M10
GO:0019953	0.94	0.07	284	565	sexual reproduction	BP	1	TBPL1,TRIM36,GLI1,YTHDC2,B4GALNT1,ATAT1,TSPAN8,MAPK8IP2,IGF2R,MOV10L1,PACRG,QKI,BRD2,GDF9,ROS1,MCM9,HSF2,UBE2B,CATSPER3,WASHC5,TOB2,SMAD5,H3F3C,FANCC,TUT7,DMC1,PICK1,SPATA31D3,MYH9,CFAP69,FANCG,SMARCA2,TDRD6,KIT,CCIN,TSGA10,TDRD7,NLRP5,DNAJA1,FOXJ3,SCMH1,RIMS1,MSH2,RAD23B,SPACA6,YTHDC1,KLK14,CABS1,FANCL,GJA10,HERPUD2,GMCL1,PTN,NOBOX,CCDC155,DKKL1,CREM,TUT4,FOXO3,ARMC2,DLD,DDO,TXNRD3,APOB,IZUMO1,SPATA6,SPATA5,HDAC2,ADCY3,TTC26,TRPC3,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,MLH1,ACOX1,FOXJ1,WDR48,TTC21A,PLAT,CCNB1IP1,ACVR2A,SIRT2,MKKS,SPATA24,ADAM18,PLCB1,MCM8,GOLGA3,PANK2,BTG1,SOHLH2,FUT10,TEX15,UBXN8,KATNAL1,STX2,NPHP1,ING2,HPGD,SPATA9,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,P2RY1,PTK2B,KMT2D,PRKAG1,SFMBT1,AP3B1,CDYL,SYCP1,DNAH1,NPM2,DPCD,OCA2,ROPN1L,SIAH1,BMPR1B,GAS2,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,HYAL3,TESMIN,SLC9B1,PRKAR1A,INTS13,SPATA2,RNF114,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,TSSK4,CIB1,CCDC87,DDX6,HDAC4,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,CLIC4,SEPT2,LIMK2,PATZ1,CATSPER2,OVOL1,ETV6,YBX3,LYZL6,WNT3,CADM1,OVGP1,SPATA32,GGT2,TTC12,BCL6,VGF,RPL10L,DDX3X,SPAG16,ZCWPW1,WNT4,PLCD4,RAB3A,CTSV,BIRC3,STAT3,AKAP3,ADCY10,PARP11,CALR3,KDM5A,ZMYND15,MNS1,YBX2,THRA,SPIN2A,SEPT1,ADAM21,ADAM20,MYCBPAP,UBE2Q1,VIPAS39,UBAP2L,SOX30,CCDC42,CREB3L4,IL4R,SPESP1,NOX5,PAQR5,RAD51C	grey	VSMC_M10
GO:0045920	0.94	0.13	9	23	negative regulation of exocytosis	BP	1	VPS4B,PRKN,RAB7A,NCKAP1L,ADRA2A,RAP1B,RSC1A1,FMR1,FOXF1	grey	VSMC_M10
GO:0050685	0.94	0.12	10	25	positive regulation of mRNA processing	BP	1	SNW1,HSF1,TRA2A,NUP98,HSPA8,CELF3,NCBP2,LEO1,PRPF19,CIRBP	grey	VSMC_M10
GO:0090224	0.94	0.11	14	34	regulation of spindle organization	BP	1	VPS4B,HSPA1B,MAPK15,CHMP2A,CHMP2B,CHMP4C,RNF4,FSD1,PKD1,CHMP1A,PSRC1,GPSM2,CCSAP,DRG1	grey	VSMC_M10
GO:1902742	0.94	0.11	13	32	apoptotic process involved in development	BP	1	BAK1,PAX8,HAND2,ROBO2,XKR6,VDR,PAX2,TGFB2,FZD5,TNFRSF1B,JAG2,BCL2L11,XKR8	grey	VSMC_M10
GO:0060389	0.94	0.10	20	47	pathway-restricted SMAD protein phosphorylation	BP	1	LRP1,USP15,GDF9,BMP8A,BMPER,SDCBP,TGFBR2,ACVR2A,RBPMS,ACVR1B,SNX25,TGFB2,GDF15,INHA,BMPR1A,TWSG1,ENG,ACVRL1,NOG,LDLRAD4	grey	VSMC_M10
GO:0010763	0.94	0.15	5	14	positive regulation of fibroblast migration	BP	1	PTK2,PRKCE,BAG4,ARHGEF7,DMTN	grey	VSMC_M10
GO:0010256	0.94	0.07	209	422	endomembrane system organization	BP	1	VPS4B,ATP8B1,NEMP1,TBPL1,EMC2,PRKN,A4GALT,FER1L6,MTSS1,WASHC5,ASAP1,LEMD2,SYNGR1,MAPK15,SUN2,BAIAP2L2,MICALL1,MYH9,TJAP1,WASHC4,TRAM2,CHMP2A,STX17,SPTBN1,RTN4,SPACA6,EMC10,TRAPPC12,YWHAZ,HACE1,LPIN1,IZUMO1,RAB7A,ARHGAP21,RAB10,COG1,CLASP2,RBSN,NECTIN2,PLK3,OPTN,AQP11,GRIK5,EMC3,PRX,AKT2,HOOK3,SIRT2,YIPF4,NPLOC4,SYT1,ARHGEF7,ATL2,DNAJC13,FAM160A2,STX2,SYT9,TMEM127,NSFL1C,ANO4,OSBP,MYOF,CHMP2B,TRAPPC11,EMC4,XKR6,PLSCR4,SPAG4,P2RX7,CHMP4C,KIFC3,SEC31A,DYSF,SYNJ1,AP3B1,CHMP7,ZFYVE27,BIN3,F2R,ANO6,VPS18,COL4A3BP,DOP1B,SEC31B,DTNBP1,ARMH3,GBF1,SEC22B,TGFB2,TMEM9,TRIP11,VTI1A,SNAP23,GET4,ANK2,GPER1,RNF26,COG2,RAB22A,SEC23IP,CASQ1,OSBPL2,GORASP2,STX1A,TOR1AIP1,STX6,VPS37D,WHAMM,LYZL6,NSF,CREB1,MIA3,ALS2CL,SRGN,SEC16B,MOSPD3,TANGO2,LPCAT3,ATL1,PDCD10,HTT,RAB3A,SMPD4,SNAP29,PTPRN,PARP11,MAPK1,BHLHA15,ARL6IP1,STX5,OBSL1,STX18,AKAP8L,SYT7,ANXA8,MPP5,DEGS1,PI4K2B,GAK,CPLX1,TARDBP,STX1B,STX4,BNIP1,SYT11,TMED10,NDEL1,MAPK3,AC138894.1,HOOK2,RAB11A,MAP2K1,SOX30,SPESP1,NOX5,SYTL4,SNAPIN,PRKCB,DNM2,VMP1,COG7,BCAS3,LMAN1L,CAMSAP3,CXorf56,EPB41L3,RILP,TLE6,EMC6,SGTA,BAIAP3,UBL4A,ABCA7,SEC16A,SURF4,CHMP1A,SYPL2,COL5A1,TOR1B,MFSD14A,GOLGA8M,STXBP1,FNBP1L,TMED5,COG4,MTSS1L,SH3GLB1,VPS4A,REEP6,PHETA1,LEMD3,PLK5,BLOC1S3,SNAP47,WDR83OS,SNX10,CAMLG,TLCD1,EMC7,HIKESHI,TRAM1L1,TBC1D20,FAM174B,TMED3,PLEKHJ1,POLR2M,XKR8,CAVIN2,ZFP69B	grey	VSMC_M10
GO:0033137	0.94	0.12	10	25	negative regulation of peptidyl-serine phosphorylation	BP	1	BAK1,NCK2,GPD1L,PAQR3,DMTN,INPP5J,MLXIPL,INPP5K,DMD,GADD45A	grey	VSMC_M10
GO:0002700	0.94	0.08	49	106	regulation of production of molecular mediator of immune response	BP	1	CD226,IL5,KIT,EXOSC3,MSH2,RSAD2,TLR4,ATG5,TRPM4,SPHK2,HMCES,PHB,LACC1,MLH1,PAXIP1,SHLD1,MAVS,HPX,PRKDC,TRAF6,GPI,TMBIM6,F2RL1,NOD2,CD40,CD96,TGFB2,DENND1B,CD28,FZD5,BCL6,HK1,FOXP3,SHLD2,TNFRSF1B,SPON2,TBX21,STX4,IL4R,BTK,CD74,SUPT6H,TICAM1,PRKCZ,TRAF2,SLC7A5,BCL10,WNT5A,INAVA	grey	VSMC_M10
GO:0050765	0.94	0.15	5	14	negative regulation of phagocytosis	BP	1	ATG5,CD300LF,CNN2,DYSF,SYT11	grey	VSMC_M10

GO:0003008	0.94	0.06	632	1240	system process	BP	1	RDH5,NEDD4L,ATP8B1,MIP,TAC3,MYO1A,LRP1,EYA4,LVRN,STAC3,SLC16A7,MAPK8IP2,ALDH7A1,ADM2,SLC12A2,RIMS2,PRRT1,PRKN,AGER,PPARA,HLA-DRA,COL11A2,GDF9,SNTB1,SYNGAP1,SMAD5,LRRC6,KLHL3,XPNPEP3,PTP4A3,AKR1B1,AGTPBP1,NTRK2,PLA2G6,SOX10,PI16,BTBD9,ZDHHC21,OPN1SW,GUCA1B,RBFOX2,CHRNA3,TEK,PRPH2,GRM8,CHRNA5,RORB,LMOD2,CRY1,ZFAND5,SRF,ABCB1,TTBK1,CFAP69,GABRA1,CNGA1,PHF24,CLIC5,KIT,SLC1A1,ADGRF1,TNFRSF21,TFAP2B,KIAA1211,TBC1D8,ADH5,CNNM4,MEOX2,TMOD1,ABCG5,ABCG8,CLDN19,PPCS,BRSK1,TNNI3,EPAS1,RIMS1,DNAH11,ASB3,KCNQ4,GSDME,SHANK1,SLC4A4,MYBPC2,PPT1,AQP1,GJA10,MYH14,SLC1A4,NR1H2,WHRN,PTN,ITGB1BP1,YWHAZ,POU3F3,EGFR,TLR4,GRIK2,BVES,DLGAP3,CLCN1,LPIN1,IL15,KEL,MYLK3,ATG5,SOBP,TRPM4,SLC7A11,FOXO3,NTF4,FIG4,TULP2,PRKAR2B,GRIN2D,HDAC2,ADCY3,MTMR2,TRPC3,BBS7,SLC8A2,C5AR1,SLC26A5,MYO3A,CST7,SOX9,MYO7B,EML2,OPA3,CACNB2,USH1G,ASIC3,XRCC1,STAC,B4GALT2,CRYGN,KDM4A,ZNF513,GRIK5,ATP1A3,CELF2,SCN5A,SCN1A,MYO7A,MYCBP2,METTL23,POU4F1,SPRY2,SLC24A3,GPD1L,ABCC4,CHRNA6,SNX5,C1QTNF1,CHD8,MKKS,NEK10,FSCN2,HBEGF,PDE6G,LRTOMT,AP000812.5,PLCB1,TMTC4,RYR1,RAC3,PRNP,ADRA1D,DDHD2,KERA,LUM,DIAPH1,SPART,SEMA3A,P2RX2,CCKBR,GAS6,LMOD3,ARL6IP5,FAM19A4,SLC7A1,ADRA2B,ATXN7,TUB,TCF15,EPHB1,PLK2,NPHP1,SOAT2,SGCG,ASPH,HTR7,FAM107A,GPI,FGFBP3,NR4A1,CAMK4,SLMAP,MYOF,CASP3,HIP1R,CHMP2B,MARVELD2,ERAP1,HAND2,EYA1,PLS1,P2RX3,PLCE1,CHRM5,CEP250,CCDC66,ADGRV1,LIMA1,PTPRJ,MEF2C,ASIC1	grey	VSMC_M10
GO:0043401	0.94	0.08	51	111	steroid hormone mediated signaling pathway	BP	1	ESR1,CNOT2,PPARA,RXRB,KDM4C,FOXH1,RBFOX2,CRY1,DNAJA1,PGRMC2,PHB,EGLN2,TADA3,TAF7,RNF14,DDRGK1,FOXP1,CALCOCO1,NCOA4,CYP7B1,UFSP2,ZNF366,ARNTL,CNOT1,KMT2D,DDX54,NKX3-1,CRY2,VPS18,HDAC1,ABHD2,GPER1,ARID1A,RXRG,ESRRA,PADI2,DNAAF4,PARP1,MED1,PAGR1,ESRRB,PIAS2,NCOR1,PPARGC1B,ISL1,RHOXF1,PARK7,RXRA,RHOA,TRIM68,YWHAH	grey	VSMC_M10
GO:0032507	0.94	0.10	24	55	maintenance of protein location in cell	BP	1	TSPO,SKP1,SUN2,GPAA1,TAF8,GRIK5,TAF3,ARL2BP,MORC3,SP100,SORL1,SRGN,HK1,PINK1,VPS13D,VPS13C,RIT2,RER1,PARK7,HSPA5,SUPT7L,TXN,INSIG2,PFN4	grey	VSMC_M10
GO:0097066	0.94	0.13	8	21	response to thyroid hormone	BP	1	AKR1B1,KIT,SLC26A5,CRLS1,LMO2,CTSH,MED1,ANXA2	grey	VSMC_M10
GO:0090305	0.94	0.07	103	213	nucleic acid phosphodiester bond hydrolysis	BP	1	PAN2,ENPP3,RPP21,CPSF6,CNOT2,CNOT6,RIDA,DXO,PNLDC1,UTP23,AGO2,EXOSC4,HSF1,CPSF1,TSR1,EXOSC3,TSEN34,PNPT1,RNASEH1,ENDOD1,ERCC1,XPC,ERCC2,ERCC3,PCF11,ZRANB3,FBH1,MGME1,ASTE1,NUDT16,WRN,POLR2I,PXDNL,PAN3,BMS1,CSTF3,NUDT12,FOXL2,POP4,CNOT1,USB1,CNOT6L,HARBI1,RPP40,FAN1,POP5,CPSF2,DIS3L2,AEN,CCDC36,POLG,YBEY,SPO11,PGBD5,NOP9,C11orf80,ANGEL2,NYNRIN,NCBP2,KIAA0391,POP7,ZC3H12C,APEX2,CPSF4,PMS2,AP002990.1,N4BP2,DCP1B,MRPL44,EXD2,LAS1L,ISG20L2,EME1,DNASE2,ANGEL1,RNASEH2A,TDP1,CSTF2,CNOT8,KRI1,G3BP1,ERI2,SLFN14,PLD4,PARN,ERCC4,DROSHA,TREX2,PAM16,DNASE1,INTS11,NTHL1,MEIOB,DFFB,DNASE1L1,NOL9,POLR3K,EDC4,RPP38,DNASE1L2,RPP30,NMNAT1,EXOSC5	grey	VSMC_M10
GO:0006195	0.94	0.10	16	38	purine nucleotide catabolic process	BP	1	PDE7B,PDE10A,GDA,NT5E,NUDT15,NUDT16,AMPD3,ENTPD4,FITM2,NUDT18,PDE9A,PDE8A,PDE4A,MLYCD,NUDT19,HINT1	grey	VSMC_M10
GO:0042063	0.94	0.07	111	230	gliogenesis	BP	1	ERBB3,LRP1,ADGRG6,SNW1,AGER,TSPO,SUN2,NTRK2,PICK1,SOX10,SMO,DAAM2,TTBK1,ADAM22,CDK6,TNFRSF21,ROR2,MBOAT7,RTN4,FPR2,AREG,PTN,EGFR,TLR4,MYCN,HDAC2,C5AR1,SOX9,HDAC11,ERCC2,EIF2B3,KDM4A,PRX,AKT2,SIRT2,NRG1,PLAG1,LGI4,SOX6,P2RY1,PTK2B,TIAM1,FGF5,SYNJ1,NKX6-1,SPINT1,SOX13,PAX2,TSPAN2,SRGAP2C,RNF10,HDAC1,TGFB2,GAP43,DAG1,KRAS,TTC21B,SOX2,DISC1,CERS2,NDUFS2,DLX1,CSPG5,NSUN5,CREB1,DUSP10,MAPT,CNTNAP1,STAT3,MAPK1,CHRM1,EPHA4,MPP5,TNFRSF1B,PRPF19,ATP1B2,PSEN1,MAPK3,MAP2K1,LDLR,S100A8,CCL2,CDK5R1,LEPR,MBD1,DAB1,LRP8,MXRA8,SKI,SOX8,GPR157,LAMC3,DAB2IP,MIR222,MIR125B1,RHOA,ADGRG1,CNTN2,FOXG1,SOX4,LAMB1,CNTF,GPR37L1,METTL14,NOG,POU3F2,CSPG4,NRROS,PHGDH,LIF,PITX3	grey	VSMC_M10
GO:0008286	0.94	0.08	42	93	insulin receptor signaling pathway	BP	1	AP3S1,PIP4K2C,GKAP1,CCND3,PHIP,GRB10,GAB1,SESN3,PIP4K2A,AKT2,SNX5,KL,PTPRA,FER,IDE,PIK3R1,SORBS1,OPA1,IGF2,GPLD1,IRS1,GRB14,SORL1,C2CD5,AGT,EIF4EBP2,SIK2,FOXO4,NDEL1,ZBTB7B,OGT,PRKCB,INSR,SREBF1,PTPN2,SOCS1,INPP5K,PRKCZ,INSRR,GRB2,APC,SH2B2	grey	VSMC_M10
GO:0046386	0.94	0.12	11	27	deoxyribose phosphate catabolic process	BP	1	DPYS,GDA,NUDT15,MBD4,NUDT16,NUDT18,UPB1,NEIL1,NT5M,NTHL1,UPP1	grey	VSMC_M10

GO:0034470	0.94	0.07	172	345	ncRNA processing	BP	1	ADAT2,HELB,RPP21,TFB1M,TRMU,UTP23,RRP7A,TRMT11,AGO2,TUT7,C9orf64,EXOSC4,NOL6,TSR1,EXOSC3,RPS14,MTO1,TSEN34,ELP1,UTP3,PUS10,TRIT1,MDN1,AGO1,FCF1,TUT4,DUS4L,NSUN6,ERCC2,RPS8,RPL14,INTS10,THUMPD3,USP36,ESF1,KRR1,DPH3,SIRT7,TRMT6,TRNT1,NUDT16,THUMPD2,PRKDC,TRMT9B,DHX37,BMS1,DIMT1,ELP4,POP4,CLP1,ZCCHC8,ELP3,BCDIN3D,USB1,TPRKB,URB1,DDX54,NSUN3,RRP12,HELQ,RPUSD2,OSGEPL1,INTS8,RPP40,RIOK1,TENT4B,CDKAL1,POP5,PDCD11,RPUSD4,TRMT10A,ZBTB8OS,RPS17,QTRT2,SBDS,TYW1B,INTS12,HEATR1,TYW5,FAM207A,MRPS11,GAR1,TRUB1,YTHDF2,RTRAF,DALRD3,YBEY,LCMT2,NOP9,RPS27,WDR12,METTL8,RPL7L1,WBP11,ELP6,NSUN5,DDX47,RPL11,METTL2B,KIAA0391,TRMT1L,PRKRA,POP7,DDX3X,DDX10,DDX49,TRPT1,RPL27,ALKBH8,STAT3,WDR74,TRMT5,INTS5,AP002990.1,HSD17B10,NVL,MRM2,TSR2,ZCCHC4,LAS1L,MTFMT,ALKBH1,UTP18,THG1L,SMAD3,QTRT1,INTS2,KRI1,ZNHIT3,ELP2,ERI2,THUMPD1,RIOK3,RNF113B,UTP6,METTL6,SNU13,UTP14A,PARN,DROSHA,MRM3,INTS11,PUSL1,METTL16,NOL9,RPUSD1,WDR18,POLR3K,KARS,ADAT1,AARS,RPL35,ZNHIT6,DUS2,METTL18,CTU1,AGO4,RPP38,MPHOSPH6,TRMT10B,TP53RK,TRMT61A,RPUSD3,NSA2,C1D,PIH1D2,TRMT10C,RPP30,TRMT61B,TYW3,EXOSC5,GTF2H5	grey	VSMC_M10
GO:0071375	0.94	0.07	105	219	cellular response to peptide hormone stimulus	BP	1	AP3S1,MARS,PIP4K2C,PNPLA3,PTK2,GKAP1,HSF1,CCND3,GPT,PPAT,PHIP,CRHR2,GRB10,GAB1,LPIN1,MGARP,FGF21,SESN3,PIP4K2A,RAB10,CYSLTR2,ECHDC3,TBC1D4,AKT2,SNX5,KL,PTPRA,LEPROTL1,PRKDC,TRIB3,NR4A1,FER,IDE,PIK3R1,SORBS1,OPA1,LPIN3,NKX6-1,NR4A2,CYFIP1,IGF2,PXN,GPLD1,SRD5A1,IRS1,GRB14,SLC30A10,SORL1,C2CD5,GPER1,AGT,SLC9A1,SYAP1,USF1,POR,NFE2L2,CREB1,YWHAG,RAP1B,CPS1,EIF4EBP2,MEN1,SIK2,ESRRA,FBN1,GDF15,STAT3,SLC27A1,STAT5B,RAB8A,GPR173,PARP1,SLC2A4,RAB15,MAX,AGTRAP,FOXO4,PKLR,RAB8B,NDEL1,ZBTB7B,OGT,PRKCB,CAMK2A,INSR,SREBF1,LPIN2,GHR,PTPN2,SOCS1,CRK,INPP5K,PDPK1,PRKCZ,SLC25A33,CYBA,ASS1,INSRR,CA2,BGLAP,GRB2,INSIG2,APC,SH2B2,LEPROT	grey	VSMC_M10
GO:1903306	0.94	0.15	5	14	negative regulation of regulated secretory pathway	BP	1	NCKAP1L,ADRA2A,RAP1B,FMR1,FOXF1	grey	VSMC_M10
GO:1902570	0.94	0.15	5	14	protein localization to nucleolus	BP	1	WRN,POLR1A,TERT,GLUL,NVL	grey	VSMC_M10
GO:0031589	0.94	0.07	142	294	cell-substrate adhesion	BP	1	ITGA7,ONECUT2,LRP1,TNXB,FBLN1,PARVG,PTK2,RAC2,CDKN2A,TEK,SRF,CDK6,SGCE,PRKCE,HOXA7,PTN,ITGB1BP1,EPHA1,BVES,NDNF,FBLN2,CLASP2,RSU1,BCAM,UNC13D,RIN2,JAG1,ACTG1,FERMT1,RAC3,ARHGEF7,RELL2,GAS6,PTPRA,EPHB1,AKIP1,FAM107A,FER,PIK3CB,PIK3R1,LPXN,PARVA,FMN1,SORBS1,PTPRJ,PTK2B,TIAM1,DOCK5,RREB1,STK4,GCNT2,DMTN,ITGB6,LDB1,PXN,CD96,SLK,CARMIL1,PPFIA1,COL17A1,FBLN5,COL16A1,PRKX,DAG1,AJUBA,ITGA10,ARHGAP6,AP1AR,DISC1,LAMB3,CASS4,CIB1,SLC9A1,FZD7,ITGB5,ACTN3,LAMA5,PTPRO,EPHB3,DOCK1,MELTF,WHAMM,CSPG5,STRC,EFEMP2,LAMC1,APOD,HOXD3,BCL6,COL13A1,TRIP6,ITGA2B,ITGA4,MEN1,FN1,CASK,SPOCK2,FERMT3,WNT4,NID2,COL3A1,TRPM7,VCL,BST1,MINK1,RADIL,ATP1B2,ITGA3,THBS3,TAOK2,EFNA1,SMAD3,ITGA11,CORO2B,DNM2,OTOA,BCAS3,CAMSAP3,CCL25,ADAMTS12,CRK,PDPK1,L1CAM,PRKCZ,PKD1,ADAMTS13,TSC1,NTNG2,FOXF1,LAMC3,MICALL2,RHOA,FGA,LAMB1,ACVRL1,PEAK1,THY1,TIMM10B,ACER2,BCL2L11,DUSP22,VAMP3	grey	VSMC_M10
GO:0007498	0.94	0.08	40	89	mesoderm development	BP	1	EXOC4,MEST,SMO,FOXH1,SRF,TXNRD1,SIX2,TEAD2,OSR1,POU4F1,WNT11,ACVR2A,EOMES,TCF15,HCK,GPI,EYA1,TLX2,PAX2,LDB1,POGLUT1,PRKAR1A,SNAI1,BMX,OVOL1,SETD2,WNT3,TBX19,BMPR1A,KDM6B,ITGA3,SMAD3,BTK,LHX1,TWSG1,FOXF1,POFUT2,NOG,WNT5A,MESD	grey	VSMC_M10
GO:0002902	0.94	0.15	5	14	regulation of B cell apoptotic process	BP	1	FOXP1,BCL6,BTK,CD74,BCL10	grey	VSMC_M10
GO:0014841	0.94	0.16	4	12	skeletal muscle satellite cell proliferation	BP	1	AKIRIN1,EPHB1,STAT3,SIX1	grey	VSMC_M10
GO:0014856	0.94	0.16	4	12	skeletal muscle cell proliferation	BP	1	AKIRIN1,EPHB1,STAT3,SIX1	grey	VSMC_M10

GO:0001934	0.94	0.07	271	543	positive regulation of protein phosphorylation	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,MAP3K4,AGER,IL5,GDF9,XRCC6,PTK2,TAB1,NTRK2,PLA2G6,HSF1,CCND3,CHRNA3,TEK,TTBK1,TEC,KIT,SLC1A1,ROR2,SEMA4D,CLDN19,IL11,FPR2,MOB1B,EPGN,AREG,BMP8A,ETAA1,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,EGFR,ARHGEF5,TLR4,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,HDAC2,SLC8A2,MOB3C,PRKD2,PHB,ABI1,SOX9,MAPRE3,RALB,PRKAG2,RAF1,PIBF1,FBH1,SPRY2,WNT11,AKT2,ARRB1,TGFBR2,ACVR2A,NEK10,RPTOR,TCIM,HBEGF,PRNP,BAG4,MAVS,NRG1,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,ERCC6,FLT1,ADRA2B,TRAF6,RET,ACVR1B,OSBP,ZFP91,ROBO1,FBXW7,PTPRJ,VEGFC,P2RY1,MADD,PTK2B,RASGRP1,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,FGF5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CDK2AP1,PKD2,STK4,ADTRP,NOD2,CNTN1,TAOK3,CD40,IGF2,BMPR1B,BDNF,NEURL1,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K6,TGFB2,ADRA2A,FAM20A,DAG1,AXIN2,SLCO3A1,AJUBA,NCF1,KRAS,EGF,HCLS1,ADNP,OPRD1,GPER1,CHEK2,CASS4,SPATC1L,PARP9,PARP14,CACUL1,AGT,CIB1,DVL3,STRADB,OSM,SYAP1,THPO,STRADA,PDE8A,LIMK2,GPRC5D,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,STOX1,CEMIP,DBF4B,IL12A,MAP4K2,DDX3X,XRCC5,DUSP19,PDCD10,TNFSF18,ADRA2C,DOK7,SLC11A1,GDF15,MARK2,FGFR3,PINK1,ARAF,SLC27A1,MAPK1,INHA,EPHA4,DLG4,MAGED1,DVL2,BMPR1A,WNK3,RPLP1,FXR2,ANXA2,DGKQ,CTF1,PSEN1,FGF18,LCP2,PGF,TAOK2,EFNA1,MAPK3,AC138894.1,IL6R,HAX1,MAP2K1,LAT,PIK3R5,MAP2K5,CALM1,RPS6KA5,PSMD10,CD74,INSR,CCL5,CSF1R,YES1,CDK5R1,ISL1,GHR,LEPR,SH2D3A,C3,TWSG1,RALBP1,UNC119,DOCK7,TAOK1,SOCS1	grey	VSMC_M10
GO:0035272	0.94	0.11	14	34	exocrine system development	BP	1	SOX10,PLXNA1,SOX9,SEMA3A,NKX3-1,IGF2,TGFB2,DAG1,LAMA5,BTBD7,LAMA1,TWSG1,RAB26,ESRP2	grey	VSMC_M10
GO:0003014	0.94	0.09	33	74	renal system process	BP	1	KLHL3,XPNPEP3,AKR1B1,CHRNA3,TFAP2B,AQP1,SNX5,GAS6,STC1,F2RL1,F2R,SULF2,AGT,MCAM,PTPRO,COMT,KCNMA1,ITGA3,AC138894.1,TMEM63C,CHRNB2,CORO2B,TBC1D8B,MYO5B,INPP5K,SERPINF2,TRPV1,CYBA,HSD11B2,RHOA,CHRNB4,JCHAIN,PRKRIP1	grey	VSMC_M10
GO:0002294	0.94	0.10	19	45	CD4-positive, alpha-beta T cell differentiation involved in immune response	BP	1	HLA-DRA,FOXP1,RIPK2,HLX,BCL6,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,PTGER4,PRKCZ,MIR21,RC3H2	grey	VSMC_M10
GO:0061430	0.95	0.16	4	12	bone trabecula morphogenesis	BP	1	SEMA4D,THBS3,CHAD,PPARGC1B	grey	VSMC_M10
GO:0050886	0.95	0.09	21	49	endocrine process	BP	1	GDF9,CRY1,C1QTNF1,MME,RAB11FIP5,NKX3-1,F2RL1,F2R,CRY2,KRAS,ENPEP,AGT,ACE2,ECE1,INHA,RAB8B,SERPINF2,CYBA,HSD11B2,RHOA,CRH	grey	VSMC_M10
GO:2000779	0.95	0.09	34	76	regulation of double-strand break repair	BP	1	MRNIP,HELB,HSF1,POT1,CYREN,WDR48,FBH1,RNF169,SIRT7,SHLD1,PPP4R2,TEX15,PRKDC,ERCC6,SLF1,SPIDR,SLF2,PARP9,DTX3L,RTEL1,MGMT,SETD2,ZCWPW1,WAS,DDX11,PARP1,SHLD2,WRAP53,OTUB2,SMCHD1,RMI2,NUDT16L1,SPIRE2,OOEP	grey	VSMC_M10
GO:0060572	0.95	0.14	5	14	morphogenesis of an epithelial bud	BP	1	SOSTDC1,GLI2,NOG,WNT5A,WNT2	grey	VSMC_M10
GO:0060669	0.95	0.12	8	21	embryonic placenta morphogenesis	BP	1	RSPO3,GJB5,SPINT2,SPINT1,IGF2,SETD2,FZD5,GRB2	grey	VSMC_M10
GO:0000380	0.95	0.09	29	66	alternative mRNA splicing, via spliceosome	BP	1	ZC3H10,PUF60,RBFOX2,SMU1,YTHDC1,CELF2,WTAP,CELF1,SRSF6,RBM24,RBM5,CELF3,RBM7,RBM10,FXR2,RBM25,SLU7,SFPQ,RAVER2,MBNL3,NSRP1,FMR1,CELF5,ESRP2,SRRM4,NOVA1,RBM11,SRSF12,SAP18	grey	VSMC_M10
GO:0045723	0.95	0.14	5	14	positive regulation of fatty acid biosynthetic process	BP	1	NR1H2,NR1H3,LPGAT1,MLXIPL,CD74	grey	VSMC_M10
GO:0035331	0.95	0.16	4	12	negative regulation of hippo signaling	BP	1	MAPK14,AJUBA,WWC1,MARK3	grey	VSMC_M10
GO:0001974	0.95	0.10	14	34	blood vessel remodeling	BP	1	BAK1,RSPO3,EPAS1,ATG5,ACVR2B,JAG1,MEF2C,AGT,RBPJ,MIR27B,NOL3,ACVRL1,LIF,HOXA3	grey	VSMC_M10
GO:0060143	0.95	0.14	5	14	positive regulation of syncytium formation by plasma membrane fusion	BP	1	MAPK14,RAPGEF3,EHD1,GDF15,IL4R	grey	VSMC_M10
GO:0034103	0.95	0.09	25	57	regulation of tissue remodeling	BP	1	TNFAIP3,TNFRSF11B,EGFR,IL15,HAND2,P2RX7,SPP1,PPP3CA,GPR137B,UBASH3B,AGT,ADAM8,GPR137,SUCO,CD38,SYT7,CSF1R,PPARGC1B,LEPR,ATP6AP1,DEF8,MIR199A1,MIR27B,CA2,BGLAP	grey	VSMC_M10
GO:0031668	0.95	0.07	98	205	cellular response to extracellular stimulus	BP	1	MARS,MAP3K5,CYP27B1,SNW1,PPARA,ATF4,PICK1,PIM1,TXN2,TFEB,SLC39A4,SRF,NUAK1,BRSK1,ALB,RRAGD,PTN,TNC,VPS41,IL15,ATG5,FOXO3,KPTN,SESN3,FOXA3,NUDT15,DNAJC15,RALB,PRKAG2,SZT2,RPTOR,EIF2AK2,WRN,GAS6,LARS,ULK1,NR1H4,USF2,FAM107A,PRKAG1,EIF2AK4,VDR,NR4A2,SLC38A2,NUAK2,NUPR2,SRD5A1,DNM1L,CBSL,GLRX2,SIK1,SLC38A3,KCNB1,ADNP,HSPA8,CBL,MTMR3,UCN2,USF1,XPR1,TBL2,GLUL,NFE2L2,ITGA4,SIK2,COMT,WNT4,PRKAG3,CTSV,MAPK1,BHLHA15,WIPI2,MAX,MED1,RRAGB,ZFYVE1,FOS,MAPK3,TNRC6A,SREBF1,LAMP2,NIM1K,STK26,JUN,CLEC16A,KIAA1324,TSC1,LCN2,WDR59,HSPA5,SH3GLB1,RIPOR1,MIR125B1,TRIM24,BGLAP,IMPACT,UPP1,RNF152	grey	VSMC_M10
GO:0032692	0.95	0.14	6	16	negative regulation of interleukin-1 production	BP	1	TNFAIP3,IL1R2,GAS6,SERPINB1,MIR27B,CPTP	grey	VSMC_M10
GO:0035136	0.95	0.11	12	30	forelimb morphogenesis	BP	1	OSR2,TFAP2B,HOXA13,OSR1,FMN1,TBX5,RPGRIP1L,TFAP2A,WNT3,ALDH1A2,RNF165,ALX3	grey	VSMC_M10
GO:2000379	0.95	0.09	25	57	positive regulation of reactive oxygen species metabolic process	BP	1	TSPO,MAPK14,FPR2,EGFR,TLR4,FOXO3,TGFBR2,HVCN1,PTK2B,F2RL1,NQO2,RIPK1,AGT,ACE2,HDAC4,NFE2L2,MAPT,ITGAM,PARK7,GNAI3,CYBA,LCN2,MIR24-1,GADD45A,GRB2	grey	VSMC_M10
GO:0033028	0.95	0.12	8	21	myeloid cell apoptotic process	BP	1	CDKN2A,SLC7A11,IRF7,PIK3CB,MEF2C,NOD2,CXCR2,THRA	grey	VSMC_M10
GO:0051131	0.95	0.14	6	16	chaperone-mediated protein complex assembly	BP	1	HSPA4,MKKS,LONP1,PSMG2,TMEM35A,BBS10	grey	VSMC_M10
GO:0032350	0.95	0.11	12	30	regulation of hormone metabolic process	BP	1	CYP27B1,PAX8,DKK3,PRMT3,TCF7L2,ARNT,SLCO1C1,POR,GNB3,WNT4,DGKQ,GFI1	grey	VSMC_M10
GO:0071875	0.95	0.13	7	19	adrenergic receptor signaling pathway	BP	1	ZDHHC21,ADRA1D,ADRA2B,RAPGEF2,ADRA2A,ADRA2C,CHGA	grey	VSMC_M10
GO:0051444	0.95	0.13	7	18	negative regulation of ubiquitin-protein transferase activity	BP	1	USP44,RPL23,DTX3L,RPL11,PSEN1,PARK7,BAG2	grey	VSMC_M10

GO:0007099	0.95	0.10	15	37	centriole replication	BP	1	VPS4B,MDM1,CHMP2A,CDK5RAP2,CEP295NL,CEP63,PLK2,CEP44,ALMS1,AC112128.1,CEP152,CNTROB,TRIM37,CEP192,C2CD3	grey	VSMC_M10
GO:0097345	0.95	0.11	10	25	mitochondrial outer membrane permeabilization	BP	1	TMEM14A,HIP1R,FZD9,NMT1,MUL1,TMEM102,ACAA2,BNIP3L,SLC35F6,AC140504.1	grey	VSMC_M10
GO:0061041	0.95	0.08	44	96	regulation of wound healing	BP	1	SERPINB2,TNFAIP3,TSPAN8,SLC12A2,PTK2,ENPP4,CLDN19,PRKCE,CD109,CLASP2,THBD,PLAT,C1QTNF1,ACTG1,HBEGF,FERMT1,F2RL1,F2R,SRSF6,ANO6,RREB1,DMTN,ADTRP,FAP,ADRA2A,UBASH3B,USF1,NFE2L2,DUOX1,CASK,SERPINC1,WNT4,MYOZ1,F12,ANXA2,SMAD3,ABAT,CRK,SERPINF2,MIR29A,FGA,CLDN1,HRAS,CADM4	grey	VSMC_M10
GO:0006978	0.95	0.14	5	14	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	BP	1	SP100,CHEK2,ING4,MUC1,RPS27L	grey	VSMC_M10
GO:0061684	0.95	0.14	5	14	chaperone-mediated autophagy	BP	1	PLK3,HSPA8,BAG3,ATP13A2,LAMP2	grey	VSMC_M10
GO:2000249	0.95	0.10	14	34	regulation of actin cytoskeleton reorganization	BP	1	BAIAP2L2,TEK,CCL27,HCK,PTK2B,RAPGEF3,IQGAP2,HCLS1,ABL2,HAX1,BCAS3,CSF1R,GMFG,HRAS	grey	VSMC_M10
GO:1904385	0.95	0.12	8	21	cellular response to angiotensin	BP	1	HSF1,SLC30A10,AGT,NFE2L2,AGTRAP,CAMK2A,CYBA,CA2	grey	VSMC_M10
GO:0006071	0.95	0.14	5	14	glycerol metabolic process	BP	1	GK5,COQ2,PLA2G4A,MOGAT3,TKFC	grey	VSMC_M10
GO:0030902	0.95	0.08	53	116	hindbrain development	BP	1	GLI1,UQCRQ,AGTPBP1,CKB,SMO,RBFOX2,SEMA4C,HOXA2,WHRN,PTN,C5AR1,XRCC1,GLI2,B4GALT2,SCN5A,POU4F1,CEP290,CLP1,FAIM2,RPGRIP1L,CNTN1,ZNF423,LDB1,TTBK2,EGF,TTC21B,GNPAT,GBX2,SPTBN2,HAP1,ALDH1A2,ATP1B2,PSEN1,MAP2K1,LHX1,CDK5R1,SEZ6,DAB1,ABAT,CRK,SDF4,MECP2,AARS,HSPA5,MAFB,GRID2,GPR37L1,NANOS1,HOXB3,NOG,CEND1,OTX1,PDSS2	grey	VSMC_M10
GO:0007043	0.95	0.08	45	99	cell-cell junction assembly	BP	1	MPDZ,SRF,TLN1,CLDN19,FBF1,WNT11,IKBKB,ACTG1,PKP3,NPHP1,LSR,CTNND1,MARVELD2,HDAC7,TBX5,PKP2,TRPV4,CLDN34,CDH24,SNAI1,ANK2,GNPAT,AGT,ACE2,PTPRO,DLG1,FZD5,ARVCF,GPBAR1,CNTNAP1,RAMP2,VCL,ACTB,CLDN7,TLN2,EPB41L3,CDH6,CDH10,PIP5K1C,MARVELD3,MICALL2,RHOA,CLDN15,CLDN1,APC	grey	VSMC_M10
GO:0006486	0.95	0.07	87	182	protein glycosylation	BP	1	B4GALT7,RXYLT1,GFPT2,ALG12,PMM1,LARGE1,ST6GAL2,SRD5A3,C1GALT1,ALG2,FKTN,IL15,ALG11,POMGNT1,B4GALT2,AQP11,GALNT11,ST6GALNAC2,MGAT5B,UGGT2,TMTC4,GALNT15,FUT10,GXYLT2,EOGT,POFUT1,ST8SIA4,B3GNT4,MOGS,RPN2,ST3GAL6,GALNT5,GCNT2,ALG10,TRIP11,POGLUT1,DAD1,ST8SIA2,B3GALT1,B3GNT5,GALNT2,DPAGT1,ALG3,MAN1C1,MGAT1,XXYLT1,EDEM3,TET1,PLOD3,DERL3,ALG9,MGAT2,B3GALNT1,KDELC2,DDOST,GALNT8,GALNT16,PSEN1,KRTCAP2,OGT,POMT2,ST8SIA5,COG7,GALNT1,MPI,NPC1,ALG6,PMM2,ALG1,B3GALT6,ABO,GBGT1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,FUT4,ENTPD5,DHDDS,TMEM258,POFUT2,ACER2,POMK,POMGNT2,B4GALT3,ISPD,SLC35C1,ST8SIA6	grey	VSMC_M10
GO:0043413	0.95	0.07	87	182	macromolecule glycosylation	BP	1	B4GALT7,RXYLT1,GFPT2,ALG12,PMM1,LARGE1,ST6GAL2,SRD5A3,C1GALT1,ALG2,FKTN,IL15,ALG11,POMGNT1,B4GALT2,AQP11,GALNT11,ST6GALNAC2,MGAT5B,UGGT2,TMTC4,GALNT15,FUT10,GXYLT2,EOGT,POFUT1,ST8SIA4,B3GNT4,MOGS,RPN2,ST3GAL6,GALNT5,GCNT2,ALG10,TRIP11,POGLUT1,DAD1,ST8SIA2,B3GALT1,B3GNT5,GALNT2,DPAGT1,ALG3,MAN1C1,MGAT1,XXYLT1,EDEM3,TET1,PLOD3,DERL3,ALG9,MGAT2,B3GALNT1,KDELC2,DDOST,GALNT8,GALNT16,PSEN1,KRTCAP2,OGT,POMT2,ST8SIA5,COG7,GALNT1,MPI,NPC1,ALG6,PMM2,ALG1,B3GALT6,ABO,GBGT1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,FUT4,ENTPD5,DHDDS,TMEM258,POFUT2,ACER2,POMK,POMGNT2,B4GALT3,ISPD,SLC35C1,ST8SIA6	grey	VSMC_M10
GO:0035162	0.95	0.12	7	19	embryonic hemopoiesis	BP	1	STK3,CCDC134,ATF4,KIT,TGFBR2,STK4,MED1	grey	VSMC_M10
GO:1901861	0.95	0.11	12	30	regulation of muscle tissue development	BP	1	SIRT2,LMOD3,MEF2C,IGF2,USP19,ACTN3,YBX3,CREB1,SOX15,SMAD3,MRTFB,JPH2	grey	VSMC_M10
GO:0007566	0.95	0.10	15	36	embryo implantation	BP	1	FBLN1,AGO2,H3F3C,TGFBR2,ACVR1B,STC1,ACVR1C,SPP1,SCGB1A1,SYDE1,UBE2Q1,VMP1,BSG,MIR21,LIF	grey	VSMC_M10
GO:0010573	0.95	0.11	12	30	vascular endothelial growth factor production	BP	1	ATF4,ADAMTS3,C5AR1,IL1A,SULF2,ARNT,IL6R,ISL1,C3,MIR199A1,ADGRG1,MIR125A	grey	VSMC_M10
GO:0010310	0.95	0.13	6	16	regulation of hydrogen peroxide metabolic process	BP	1	RAC2,PINK1,MMP3,STAT3,NOXA1,AC140504.1	grey	VSMC_M10
GO:0061180	0.95	0.09	25	58	mammary gland epithelium development	BP	1	ESR1,PTCH1,SMO,SOSTDC1,RTN4,AREG,GLI2,AKT2,ROBO1,ORAI1,VDR,RREB1,CCND1,MGMT,WNT3,WNT4,MAPK1,MED1,NTN1,CSF1R,FOXF1,ATP2C2,WNT5A,CEBPB,WNT2	grey	VSMC_M10
GO:0072578	0.95	0.15	4	12	neurotransmitter-gated ion channel clustering	BP	1	SLC7A11,SSH1,DLG4,GPHN	grey	VSMC_M10
GO:0048706	0.95	0.08	48	105	embryonic skeletal system development	BP	1	OSR2,MDFI,SIX2,HOXA2,HOXA4,HOXA6,HOXA7,FUZ,MYCN,OSR1,BMI1,KIAA1217,MEGF8,WDR60,WNT11,TGFBR2,ACVR2A,ALX1,EYA1,TFAP2A,HYAL1,SLC2A10,SULF2,SATB2,DLX1,SP3,DLG1,SETD2,HOXD4,HOXD3,NKX3-2,TULP3,WDR19,HOXB5,HOXB6,HOXB8,HOXB9,SMAD3,MKS1,GSC,LHX1,ALX3,HOXB3,NOG,WNT5A,SIX1,SLC39A3,HOXA3	grey	VSMC_M10

GO:0051604	0.95	0.07	112	230	protein maturation	BP	1	SEC11C,ATP23,CPM,MYRFL,BAK1,XPNPEP3,PTCH1,ISCA1,TSPAN33,MYH9,PLGRKT,IL1R2,LIPT1,ACP4,ADAMTS3,BCL2L12,KEL,CST7,IFT172,AANAT,PLAT,PITRM1,TASP1,PRNP,CPXM1,CIAO1,MIPEP,ASPH,IMMP1L,CASP3,PCSK1,SCG5,HTRA2,MME,NNAT,SPCS1,RIPK2,TESC,IFT52,PIDD1,CPN1,LONP2,SIRT4,RHBDD1,SPPL3,LTO1,HJV,ENPEP,SORL1,SPRTN,HSCB,GALNT2,ACE2,CIDEB,PRSS12,ECE2,CPXM2,BACE1,MELTF,PCSK7,PISD,ADAM8,SRGN,TYSND1,CTSH,VSIR,LPCAT3,CPZ,HGFAC,NAA40,ECE1,NAA30,LIAS,PSEN2,PARP1,DDI2,F12,TSPAN17,PSEN1,SNX12,OGT,AC138894.1,SNAPIN,NDUFAB1,DOHH,SERPINF2,CREBBP,NAA60,NAA10,LMF1,ADAMTS13,GCSH,HPR,TMEM208,CIAO2B,FGA,GLRX5,NOL3,CNTN2,SOX4,FADD,CASP8,BAG2,FXN,C2CD3,CISD3,PERP,APH1B,FAM111A,TMPRSS12,ISCA2,SPCS2	grey	VSMC_M10
GO:1904667	0.95	0.15	4	11	negative regulation of ubiquitin protein ligase activity	BP	1	USP44,RPL23,RPL11,BAG2	grey	VSMC_M10
GO:0099054	0.95	0.10	14	35	presynapse assembly	BP	1	FZD1,VPS35,SDCBP,SLITRK5,FARP1,LRFN3,NLGN4Y,BSN,NLGN2,NLGN3,SLITRK2,CEL,NTNG2,WNT5A	grey	VSMC_M10
GO:0098781	0.95	0.09	23	53	ncRNA transcription	BP	1	MARS,RPAP2,SNAPC3,IPPK,GTF3C6,TOPAZ1,SIRT7,ZC3H8,ZNF143,CDK7,GTF3C3,DEDD,CELF3,H2AFY2,MEPCE,ELL,DDX11,CC2D1A,ICE2,SNAPC5,TCOF1,SNAPC4,GTF3C4	grey	VSMC_M10
GO:0045005	0.95	0.09	17	41	DNA-dependent DNA replication maintenance of fidelity	BP	1	MCM9,ETAA1,ZRANB3,FBH1,WRN,PRIMPOL,ATR,DONSON,ZGRF1,RTEL1,DDX11,EXD2,EME1,TIPIN,OOEP,FAM111A,CENPX	grey	VSMC_M10
GO:0050926	0.95	0.12	8	21	regulation of positive chemotaxis	BP	1	AGER,CXCL8,VEGFC,F2RL1,IL16,PGF,SMAD3,ARTN	grey	VSMC_M10
GO:0032717	0.95	0.14	5	14	negative regulation of interleukin-8 production	BP	1	ANXA4,ARRB1,MAPKBP1,OTUD7B,MAP2K5	grey	VSMC_M10
GO:0036302	0.95	0.15	4	12	atrioventricular canal development	BP	1	RBPJ,TBX2,GATA6,ENG	grey	VSMC_M10
GO:1901800	0.95	0.08	48	104	positive regulation of proteasomal protein catabolic process	BP	1	HSPA1B,PRKN,RNF217,TRIB1,CSNK1E,ZYG11B,BBS7,PLK3,SUMO2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,TRIB3,PLK2,CEBPA,FBXW7,RNFT2,KCNE2,PRICKLE1,RNF144B,USP13,AC013489.1,ARIH2,RNF185,NFE2L2,COP1,SOCS4,DNAJB2,PSMC3,OSBPL7,PSEN1,TAF1,KEAP1,PSMD10,FBXO22,FMR1,FZR1,BCAP31,SGTA,TMEM259,ZER1,DAB2IP,PSMC1,BAG2,RNFT1,DDA1	grey	VSMC_M10
GO:0007162	0.95	0.07	103	215	negative regulation of cell adhesion	BP	1	ERBB3,LRP1,SEMA6A,PPARA,FBLN1,PTK2,PLXNA4,PODXL,CDKN2A,ADAM22,TNFRSF21,SEMA4D,EPCAM,HOXA7,PELI1,AKNA,ITGB1BP1,TNC,IL4I1,PLXNA1,CLASP2,FOXJ1,C1QTNF1,JAG1,PAWR,SPINT2,PRNP,PLXNC1,NCKAP1L,ZC3H8,FAM107A,PIK3R1,LPXN,CASP3,TMEM131L,PAG1,RND1,MARCH7,GCNT2,DMTN,ADTRP,TRPV4,BTN2A2,PRKAR1A,HLX,ARHGAP6,AP1AR,YTHDF2,UBASH3B,FZD7,PTPRO,RUNX3,MELTF,DLG1,APOD,MIA3,BCL6,MEN1,ABCA12,TNR,VSIR,CASK,RC3H1,PTPN6,TNFSF18,LAG3,ARHGDIG,SCGB1A1,FOXP3,TBX21,MUC1,ZBTB7B,IL4R,MAP2K5,CORO2B,BCAS3,CD74,MAPK7,CCL25,TWSG1,PTPN2,SOCS1,DAB1,ABAT,PLXNA3,ASS1,GLMN,MIR21,MIR222,MIR27A,RHOA,ACVRL1,MIR125A,ACER2,DUSP1,FGL2,RGCC,DUSP22,LAX1,CEBPB,CBLL1,HAVCR2,RC3H2	grey	VSMC_M10
GO:1902743	0.95	0.09	19	45	regulation of lamellipodium organization	BP	1	AVIL,RAC2,AKIRIN1,ARHGEF7,FER,PIK3R1,PLCE1,BIN3,RREB1,CYFIP1,DMTN,CARMIL1,AUTS2,WASF2,HDAC4,NCKAP1,WAS,DNM2,CARMIL2	grey	VSMC_M10
GO:0090042	0.95	0.15	4	12	tubulin deacetylation	BP	1	BEX4,TADA3,SIRT2,MAPT	grey	VSMC_M10
GO:0060039	0.95	0.13	6	17	pericardium development	BP	1	HAND2,TBX5,RPGRIP1L,SETD2,SMAD3,WNT5A	grey	VSMC_M10
GO:0044818	0.95	0.09	18	43	mitotic G2/M transition checkpoint	BP	1	MRNIP,TRIM39,BRSK1,RAD17,NBN,ABRAXAS1,DONSON,TAOK3,SYF2,UIMC1,FOXO4,TAOK2,FOXN3,TAOK1,FZR1,NAE1,BRCC3,NABP1	grey	VSMC_M10
GO:0051347	0.95	0.06	218	441	positive regulation of transferase activity	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,MAP3K4,AGER,ROS1,SKP1,XRCC6,MYC,PTK2,TAB1,MAPK15,NTRK2,CCND3,ZNF16,CHRNA3,TEK,POT1,TTBK1,KIT,SLC1A1,ROR2,FPR2,MOB1B,EPGN,AREG,ETAA1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,EGFR,ARHGEF5,TLR4,EPHA1,CCNY,SLC8A2,BMI1,PHB,ABI1,MAPRE3,EPM2AIP1,RALB,PRKAG2,PIBF1,SPRY2,WNT11,ALK,TGFBR2,NEK10,RPTOR,TCIM,HBEGF,PRNP,NRG1,NCKAP1L,GAS6,ERCC6,FLT1,RYK,ADRA2B,TRAF6,TRIB3,EPHB1,RET,ZFP91,ROBO1,FBXW7,HMBOX1,VEGFC,MADD,PTK2B,RASGRP1,RAPGEF2,MAPKAPK5,PRKAG1,TIAM1,SERINC5,NBN,PKD2,STK4,NOD2,TAOK3,CD40,DSTYK,IGF2,BMPR1B,IRS1,NEURL1,CD200,CCND1,MAP2K6,TGFB2,ADRA2A,FAM20A,DAG1,AJUBA,NCF1,KRAS,EGF,PFKFB2,ADNP,POLG2,SORL1,CASS4,SPATC1L,DTX3L,CACUL1,AGT,FGR,CIB1,DVL3,STRADB,SYAP1,STRADA,EPHB3,DUSP12,GPRC5D,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,MAPT,STOX1,CEMIP,DBF4B,EPHB4,MAP4K2,DDX3X,XRCC5,DUSP19,PDCD10,ADRA2C,DOK7,SLC11A1,MARK2,FGFR3,PINK1,SLC27A1,MAPK1,EPHA4,DLG4,MAGED1,DVL2,BMPR1A,NVL,FGFR4,RPLP1,DGKQ,WRAP53,PSEN1,FGF18,LCP2,TAOK2,EFNA1,MAPK3,IL6R,MAP2K1,CD19,LAT,PIK3R5,MAP2K5,CALM1,DCUN1D3,PSMD10,CD74,INSR,CCL5,CSF1R,CDK5R1,GHR,UNC119,PARN,TAOK1,SOCS1,DAB1,LRP8,FZR1,PDPK1,CAMKK1,PRKCZ,MLST8,PKD1,TRAF2,MTCP1,PARK7,PSRC1,VAV3,BCL10,DAB2IP,MIR21,MIR125B1,RHOA,S100A12,ZNF622,INSRR,IRGM,WNT5A,TIGAR,MMD,SPDYA,TXN,COPS8,RGCC,UBE2N,DAZAP2,HRAS,EREG,MAP2K7,C3orf58,FGF1,PIFO,PDGFD	grey	VSMC_M10
GO:0070979	0.95	0.11	10	25	protein K11-linked ubiquitination	BP	1	PRKN,UBE2B,UBE2E2,ANAPC5,ANAPC7,RNF26,RNF4,ANAPC4,FZR1,CDC26	grey	VSMC_M10
GO:0048260	0.95	0.09	17	41	positive regulation of receptor-mediated endocytosis	BP	1	RAB21,PICK1,PPT1,SFRP4,ARRB1,SYNJ1,EGF,DGKD,CBL,AP2M1,ANXA2,DNM2,INSR,SGIP1,C3,FMR1,LDLRAP1	grey	VSMC_M10
GO:1901660	0.95	0.15	4	12	calcium ion export	BP	1	SLC8A2,SLC8B1,CALM1,ATP2B3	grey	VSMC_M10
GO:0051497	0.95	0.11	10	26	negative regulation of stress fiber assembly	BP	1	MET,CLASP2,PIK3R1,PPFIA1,ARHGAP6,WASF2,WAS,CORO2B,INPP5K,MIR21	grey	VSMC_M10

GO:0030511	0.95	0.10	11	28	positive regulation of transforming growth factor beta receptor signaling pathway	BP	1	SNW1,SDCBP,FERMT1,ING2,SLC2A10,MEN1,RNF111,TGFB1I1,CITED1,CREBBP,MIR21	grey	VSMC_M10
GO:1903846	0.95	0.10	11	28	positive regulation of cellular response to transforming growth factor beta stimulus	BP	1	SNW1,SDCBP,FERMT1,ING2,SLC2A10,MEN1,RNF111,TGFB1I1,CITED1,CREBBP,MIR21	grey	VSMC_M10
GO:0002090	0.95	0.09	18	43	regulation of receptor internalization	BP	1	PICK1,USP46,RSPO1,SFRP4,SDCBP,MTMR2,ARRB1,WDR54,ANKRD13A,EGF,ANKRD13D,AP2M1,LRPAP1,DLG4,INSR,FMR1,MIR199A1,LRRTM2	grey	VSMC_M10
GO:1901224	0.95	0.09	22	51	positive regulation of NIK/NF-kappaB signaling	BP	1	AGER,PTP4A3,NOD1,EGFR,TLR4,PHB,NMI,TCIM,EIF2AK2,TRAF6,TRIM44,NOD2,PDCD4,EDARADD,RTKN2,TRIP6,DDX3X,RC3H1,RHOA,C1QTNF4,HAVCR2,RC3H2	grey	VSMC_M10
GO:0030810	0.95	0.14	5	14	positive regulation of nucleotide biosynthetic process	BP	1	PPARA,GUCA1B,PINK1,STAT3,NOS2	grey	VSMC_M10
GO:1900373	0.95	0.14	5	14	positive regulation of purine nucleotide biosynthetic process	BP	1	PPARA,GUCA1B,PINK1,STAT3,NOS2	grey	VSMC_M10
GO:0014075	0.95	0.10	15	36	response to amine	BP	1	NME1,SLC1A1,HDAC2,HNMT,NR4A1,ASIC1,NR4A2,HDAC1,PPP3CA,CPS1,CALM1,ADAMTS13,ASS1,NQO1,RGS4	grey	VSMC_M10
GO:0030948	0.95	0.15	4	12	negative regulation of vascular endothelial growth factor receptor signaling pathway	BP	1	PDCD6,TNMD,DAB2IP,CADM4	grey	VSMC_M10
GO:0000460	0.95	0.10	14	34	maturation of 5.8S rRNA	BP	1	EXOSC4,EXOSC3,PRKDC,URB1,RPP40,NOP9,WDR12,LAS1L,KRI1,ERI2,NOL9,MPHOSPH6,NSA2,C1D	grey	VSMC_M10
GO:0007517	0.95	0.06	125	259	muscle organ development	BP	1	ITGA7,STAC3,VGLL2,PITX1,LEMD2,LY6E,MAPK14,SMO,FOXH1,LARGE1,CNTFR,SGCE,ETV1,MEOX2,HIVEP3,TNNI3,FKTN,MYH14,AKIRIN1,BVES,KEL,MKX,KLF5,POU4F1,KLHL40,EID2,SIRT2,HBEGF,NR1D2,RYR1,DCN,P2RX2,NRG1,LMOD3,TCF15,EPHB1,SGCG,NR4A1,SMYD1,NLN,MRAS,FOXL2,FLNB,VAMP5,SAP30,ARNTL,MEF2C,SOX6,TLL2,SFMBT1,HOMER1,BIN3,TNNC1,DSP,RBM24,RYR2,IGF2,MYH15,NEURL1,PKP2,PPP3CA,TNNI1,TGFB2,ADARB1,DAG1,HLX,USP19,MYH7,USP2,UNC45A,ACTC1,COL6A3,MYOZ2,CASQ1,ACTN3,HDAC4,LAMA5,BTBD1,EFEMP2,YBX3,CREB1,TTN,MYOZ1,BMPR1A,TCAP,RBPJ,MED1,MYLPF,ZNF689,SOX15,CTF1,FOXO4,FOS,ZNF609,SMAD3,ITGA11,GSC,STRA6,FBXO22,UNC45B,ISL1,MRTFB,SKI,CACNA1H,SOX8,ASS1,ENG,ZFHX3,RHOA,DMD,CNTF,JPH2,NOG,LBX1,WNT5A,BASP1,SIX1,TCF23,LIF,POPDC2,MYORG,UQCC2,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0060326	0.95	0.07	99	206	cell chemotaxis	BP	1	SLC12A2,GPSM3,CXCL14,PTK2,RAC2,CCL27,KIT,NINJ1,FPR2,LPAR1,CXCL8,AKIRIN1,PTN,MET,GAB1,TRPM4,C5AR2,C5AR1,PRKD2,OXSR1,ACKR2,HBEGF,NCKAP1L,GAS6,FAM19A4,FLT1,EPHB1,MTUS1,CYP7B1,NR4A1,PARVA,VEGFC,PTK2B,CCL17,TIAM1,SLC8B1,F2RL1,ANO6,NOD2,GBF1,ELMO2,DNM1L,TRPV4,SBDS,TGFB2,PRSS56,CMKLR1,SLAMF8,MOSPD2,PTPRO,FCER1G,ADAM8,PIKFYVE,IL16,IL12A,MCU,TNFSF18,CXCR2,BST1,MAPK1,CH25H,PADI2,CXCL16,TMEM102,HOXB9,FGF18,PGF,DAPK2,MAPK3,IL6R,S100A14,S100A8,CD74,CCL14,CCL5,CSF1R,CCL7,CCL2,CCL25,VAV1,CRK,PIP5K1C,ARHGEF16,MPP1,BSG,VAV3,CCL16,S100A12,CHGA,DEFB124,CCR10,DPP4,CXCL6,ZNF580,WNT5A,DUSP1,FGF1,CCL22,PDGFD	grey	VSMC_M10
GO:0022604	0.95	0.06	125	261	regulation of cell morphogenesis	BP	1	ITGA7,NEDD4L,RAB21,RIMS2,CDC42SE2,PRKN,FBLN1,PTK2,PLXNA4,CPNE5,CDC42EP1,RAC2,STRIP2,MYH9,KIT,SEMA4D,FGD3,ZNF135,RIMS1,PHIP,LPAR1,MYH14,PTN,ITGB1BP1,ZMYM6,BVES,PLXNA1,SLC26A5,UNC13D,SS18L2,MYL12A,CPNE9,SYT1,RAC3,SLC23A2,ARHGEF7,DIAPH1,PLXNC1,FGD6,PRKDC,HCK,ANKRD27,PARVA,SH3D19,CUX2,P2RY1,PTK2B,RND1,TIAM1,DOCK5,OPA1,RHOBTB2,FITM2,RREB1,ITPKA,CYFIP1,DMTN,BRWD1,GAS2,DNM1L,CARMIL1,FGD4,CAPRIN2,DAG1,CFL1,AP1AR,EPB41,CASS4,PDZD8,FGR,CIB1,DVL3,SS18L1,EPS8,COCH,CDKL5,RHOBTB1,DOCK1,MELTF,CSPG5,DLG1,TBCCD1,CDC42EP2,FN1,MARK2,MUL1,OBSL1,RHOJ,EPHA4,DLG4,DVL2,FBLIM1,FGD1,SEMA4A,TAOK2,MYH10,BRWD3,MYO9A,DNM2,PARP6,GPRASP2,BHLHB9,CSF1R,CCL7,CCL2,EPB41L3,LRP8,CRK,PLXNA3,PALM,CAMSAP1,STRIP1,NTNG2,FBXO31,CFDP1,MIR21,RHOA,FGA,LST1,AGO4,CNTN2,RND3,WNT5A,CACNG7,RHOU	grey	VSMC_M10
GO:1901655	0.95	0.08	34	77	cellular response to ketone	BP	1	FECH,AKR1B1,SOX10,PRKCE,AQP1,TNC,EGFR,FOXO3,SPHK2,ADCY3,BMI1,MAP4K1,GAS6,NCOA4,DNMT3B,ABCC2,SPP1,ADCY2,SRD5A1,NPAS4,FDX1,PTGER2,AKAP8,LARP1,SCNN1B,ACACA,PTGER4,GNB1,PARK7,AS1,PTGFR,SMYD3,CRH,GNG2	grey	VSMC_M10
GO:0072311	0.95	0.12	6	17	glomerular epithelial cell differentiation	BP	1	PODXL,FOXJ1,JAG1,ASXL1,PTPRO,BASP1	grey	VSMC_M10
GO:0008356	0.95	0.14	4	12	asymmetric cell division	BP	1	RAB10,ING2,RGS14,DOCK7	grey	VSMC_M10
GO:0043367	0.95	0.08	24	56	CD4-positive, alpha-beta T cell differentiation	BP	1	HLA-DRA,RSAD2,NCKAP1L,FOXP1,TOX,RIPK2,HLX,RUNX3,BCL6,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,PTGER4,SOCS1,PRKCZ,MIR21,RC3H2	grey	VSMC_M10

GO:0030098	0.95	0.06	125	259	lymphocyte differentiation	BP	1	HLA-DRA,TCF7,BAK1,XRCC6,MFNG,FBXO7,SRF,KIT,NFIL3,IL11,MSH2,SLC46A2,RSAD2,IL4I1,IL15,ATG5,TRAF3IP2,BMI1,CLPTM1,GLI2,FOXJ1,IL15RA,KLF6,CMTM7,TGFBR2,EOMES,PLCL2,NCKAP1L,GAS6,FOXP1,PRKDC,SOX12,TOX,ZC3H8,IL1A,CAMK4,PIK3R1,PTPRJ,TMEM131L,IL7,TPD52,PTK2B,RASGRP1,LMBR1L,RIPK2,CDH17,AP3B1,SOX13,DCAF1,DOCK10,PKNOX1,LCK,TCIRG1,RABL3,HLX,SLAMF8,FZD7,HDAC4,CD28,FCER1G,RUNX3,PATZ1,FZD9,SP3,PPP2R3C,ADAM8,FZD5,DUSP10,BCL6,SYVN1,ITGA4,VSIR,RC3H1,PTPN6,TNFSF18,WNT4,LAG3,PPP3CB,STAT3,STAT5B,INHA,FOXP3,ZBTB1,GPS2,CARD11,RBPJ,TBX21,SEMA4A,KAT7,DOCK2,BATF,ZBTB7B,IL6R,CD19,IL4R,BTK,BCL11B,YY1,CD74,JAG2,NKAP,VAV1,LEPR,PTGER4,IL7R,PTPN2,SOCS1,DROSHA,DNAJA3,PRKCZ,TSC1,LRRC8A,MIR21,RHOA,SOX4,MAFB,FADD,CD46,FGL2,TNFSF9,NHEJ1,ZFP36L2,PRR7,TNFSF13B,RC3H2	grey	VSMC_M10
GO:0018130	0.95	0.05	1506	2900	heterocycle biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,SMARCC2,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,POLI,SHMT2,TBPL1,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ATP5MGL,HELB,ZBTB2,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,STK3,OSR2,SNW1,TFB1M,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,MAP3K4,PPT2,PRKN,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,RXRB,TSPO,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,PYCR3,MAPK15,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,MOCS1,PSAT1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,SLC35B2,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,UXS1,NCK2,FHL2,TGFBRAP1,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PPAT,REV1,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,SIX2,PPCS,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,ME1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,NT5E,ZNF483,JAZF1,PPT1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,DDC,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32	grey	VSMC_M10
GO:0001975	0.95	0.11	9	23	response to amphetamine	BP	1	SLC1A1,HDAC2,NR4A1,ASIC1,NR4A2,HDAC1,PPP3CA,CALM1,RGS4	grey	VSMC_M10
GO:0006047	0.95	0.14	4	12	UDP-N-acetylglucosamine metabolic process	BP	1	GFPT2,GNPDA2,DPAGT1,MGAT1	grey	VSMC_M10
GO:0045069	0.95	0.08	27	62	regulation of viral genome replication	BP	1	PABPC1,PPARA,APOBEC3H,CXCL8,RSAD2,ZC3HAV1,EIF2AK2,MAVS,FAM208A,OAS3,IFIH1,OASL,TMEM39A,ADARB1,NR5A2,STAU1,CD28,DDX3X,DDB1,HACD3,LARP1,TNIP1,CCL5,INPP5K,SETDB1,OAS1,FAM111A	grey	VSMC_M10
GO:0051495	0.95	0.07	92	194	positive regulation of cytoskeleton organization	BP	1	VPS4B,ARPC3,HSPA1B,MTSS1,WASHC5,MAPK15,BAIAP2L2,PICK1,CDC42EP1,TEK,LMOD2,CCL27,SLAIN2,NCK2,KIAA1211,PRKCE,LPAR1,PLEK,ITGB1BP1,MET,ARHGEF5,CDK5RAP2,EPHA1,MYLK3,MAPRE1,WASF1,SLAIN1,WNT11,FCHSD2,NAV3,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,CLIP1,KATNBL1,FMN1,P2RX7,KATNB1,PTK2B,RAPGEF3,F2RL1,IQGAP2,CYFIP1,MAGEL2,PXN,CARMIL1,LMOD1,TRPV4,HCLS1,AP1AR,WASF2,WHAMM,CDKN1B,DLG1,CDC42EP2,MAPT,TOGARAM1,NCKAP1,NIN,WNT4,ARPC1A,WAS,PFN3,HAX1,SMAD3,BCAS3,EVL,CDK5R1,SERPINF2,MLST8,MECP2,PLXNA3,SPIRE2,PSRC1,GPSM2,TSC1,WDR63,CARMIL2,FHOD1,RHOA,VASP,GMFG,GRB2,RGCC,HRAS,PDXP,DRG1	grey	VSMC_M10
GO:0006999	0.95	0.14	4	12	nuclear pore organization	BP	1	RTN4,NUP98,NUP54,AHCTF1	grey	VSMC_M10
GO:0010569	0.95	0.09	18	43	regulation of double-strand break repair via homologous recombination	BP	1	MRNIP,HELB,WDR48,FBH1,SHLD1,PPP4R2,TEX15,ERCC6,SPIDR,RTEL1,SETD2,WAS,PARP1,SHLD2,WRAP53,SMCHD1,RMI2,OOEP	grey	VSMC_M10
GO:0031331	0.95	0.06	180	366	positive regulation of cellular catabolic process	BP	1	PAN2,LRP1,PIP4K2C,TNFAIP3,EPM2A,CNOT2,CNOT6,RIDA,PABPC1,HSPA1B,DXO,PNLDC1,PRKN,PPARA,RNF217,TRIB1,AGO2,PRXL2C,PTK2,TNRC6B,TUT7,AGTPBP1,GTPBP1,CSNK1E,HSF1,TFEB,FBXO7,SPTLC1,EXOSC3,PNPT1,SLC4A4,NOD1,VPS35,SCOC,ZYG11B,TUT4,FOXO3,FAF1,FGF21,ZC3HAV1,SESN3,BBS7,PIP4K2A,ABHD5,PLK3,SUMO2,OPTN,MLH1,RALB,TNRC6C,KLHL40,AKT2,SIRT2,TMEM173,LSM1,DCN,RNF14,DDRGK1,SH3RF2,ULK1,PAN3,TRIB3,PLK2,CEBPA,PIK3CB,SH3D19,FBXW7,GPD1,P2RX7,CNOT1,CELF1,PTK2B,CNOT6L,RIPK2,TPCN1,RNFT2,TP53INP1,FTO,KCNE2,PRICKLE1,NOD2,TENT4B,RBM24,RNF144B,GPLD1,IRS1,CPT1A,ZBTB20,ADRA2A,DHRSX,DIS3L2,USP13,GIGYF2,AC013489.1,EGF,YTHDF2,DISC1,ATG16L1,DTX3L,SH3BP4,ARIH2,ARNT,BAG3,YTHDF1,MLXIPL,RNF185,EIF4ENIF1,ADAM8,NFE2L2,SUPV3L1,COP1,RC3H1,UPF1,HTT,SAMD4A,ZSWIM8,SOCS4,PINK1,DNAJB2,POLR2G,PIM2,DAGLB,NT5C3B,DCP1B,VPS13D,TNFRSF1B,PSMC3,TARDBP,OSBPL7,PSEN1,TAF1,MAPK3,TOB1,TNRC6A,LDLR,CNOT8,LARP1,KEAP1,RNF128,PSMD10,FBXO22,INSR,SMCR8,PARN,TICAM1,FMR1,FZR1,BCAP31,METTL16,PLEKHN1,SGTA,IKBKG,TMEM259,PARK7,GPSM1,GNAI3,KIAA1324,TSC1,ZER1,SH3GLB1,DAB2IP,TRIM68,TRIM34,BNIP3L,ENTPD5,METTL14,PSMC1,TRIM65,NANOS1,BAG2,RNFT1,IRGM,BCL2L11,HSPB8,PTTG1IP,ZFP36L2,DDA1,RNF152,RC3H2,EXOSC5	grey	VSMC_M10
GO:2000810	0.95	0.12	6	17	regulation of bicellular tight junction assembly	BP	1	IKBKB,NPHP1,SNAI1,FZD5,GPBAR1,CLDN1	grey	VSMC_M10

GO:0031115	0.95	0.14	4	12	negative regulation of microtubule polymerization	BP	1	MAPRE1,EML2,ARHGEF7,INPP5J	grey	VSMC_M10
GO:0048643	0.95	0.14	4	12	positive regulation of skeletal muscle tissue development	BP	1	LMOD3,MEF2C,IGF2,ACTN3	grey	VSMC_M10
GO:1901360	0.95	0.05	2406	4575	organic cyclic compound metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,RDH5,ZC3H10,SMARCC2,PAN2,APOF,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,RDH16,POLI,HSD17B4,RNMT,SHMT2,EYA4,TBPL1,ALDH8A1,GLI1,MARS,PDE7B,CLK4,MAP3K5,RPA3,TNFAIP3,CYP27B1,TSFM,HIVEP2,ADAT2,ATP23,PLAGL1,MAML1,MRNIP,ENPP3,ATP5MGL,HELB,RPP21,PPP1R10,ZBTB2,CPSF6,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,SNCAIP,PABPC1,SNW1,TFB1M,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,CYP21A2,ZBED4,PNLDC1,MAP3K4,PPT2,PRKN,QKI,AGER,TRMU,PPARA,PDE10A,ACSL6,UTP23,MED30,IL5,BRD2,TAF2,SULT4A1,RXRB,TSPO,VGLL2,HSD17B8,MCM9,ASF1A,RRP7A,HSF2,TCF7,PHF1,SMPDL3A,UBE2B,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PRXL2C,HABP4,HSD17B3,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,LY6E,AKR1B1,ZC3H3,ATF4,PYCR3,TUT7,MAPK15,RPAP2,CBX7,APOBEC3H,GTPBP1,MAPK14,UHRF2,CBY1,DMC1,PUF60,C9orf64,CSNK1E,PICK1,KDM4C,SOX10,PIM1,CMTR1,BTBD9,NRF1,TMPRSS6,EXOSC4,SMO,TTC39B,SNAPC3,BNC2,HSF1,MOCS1,PSAT1,OARD1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,RBM28,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,GNMT,POT1,GPR37,KLHDC3,RORB,ZNF300,PRDM4,CRY1,GDA,DMTF1,CROT,SRF,SMU1,ZNF318,NFX1,NOL6,GNPDA2,XPO5,CDK14,FZD1,MTERF1,NFXL1,GALT,SLC35B2,NFKBIE,FANCG,SUPT3H,SMARCA2,ENPP4,RFX3,KIT,SLC1A1,ADGRF1,PLPP6,SRD5A3,UXS1,NCK2,FHL2,TSR1,TGFBRAP1,TFAP2B,SLC25A	grey	VSMC_M10
GO:0010955	0.95	0.11	9	23	negative regulation of protein processing	BP	1	IL1R2,ACP4,BCL2L12,CST7,PRNP,SIRT4,SNX12,SERPINF2,NOL3	grey	VSMC_M10
GO:1903318	0.95	0.11	9	23	negative regulation of protein maturation	BP	1	IL1R2,ACP4,BCL2L12,CST7,PRNP,SIRT4,SNX12,SERPINF2,NOL3	grey	VSMC_M10
GO:0061024	0.95	0.06	300	599	membrane organization	BP	1	ATP9B,VPS4B,ATP8B1,NEMP1,STX7,HEBP2,SYNJ2,EMC2,PRKN,SEPT8,TSPO,A4GALT,HSPA4,BAK1,FER1L6,MTSS1,ASAP1,LEMD2,TSNARE1,SYNGR1,MAPK15,SUN2,TOMM22,BAIAP2L2,PICK1,MICALL1,RAC2,MYH9,LRRC4,ABCB1,TGFBRAP1,TRAM2,TMEM14A,MITD1,CHMP2A,ABCG5,ABCG8,STX17,RIMS1,TMEM30A,SPTBN1,RTN4,SPACA6,EMC10,PPT1,AAK1,PTN,EGFR,VPS41,HACE1,LPIN1,NRCAM,SLC7A11,APOB,AGK,IZUMO1,CHCHD6,ARHGAP12,NAPA,RAB7A,PIP4K2A,RUBCNL,NECTIN2,GRIK5,TBC1D4,EMC3,PRX,AKT2,TIMM50,FCHSD2,SIRT2,YIPF4,SYT1,ATL2,FCHSD1,NCKAP1L,GAS6,BET1L,STX2,SYT9,NSFL1C,ANO4,MAL,RILPL1,RILPL2,ANKRD27,IMMT,OSBP,PITPNM2,MYOF,HIP1R,CHMP2B,EMC4,XKR6,PLSCR4,FCHO2,SPAG4,P2RX7,CHMP4C,ARFGAP2,MTX3,SEC31A,DYSF,SYNJ1,OPA1,AP3B1,CHMP7,RHOBTB2,BIN3,F2RL1,ANO6,COL4A3BP,SEC31B,PLTP,KCNIP2,VPS39,GBF1,RAB7B,AZIN2,KLHL12,DNM1L,SEC22B,TGFB2,PEF1,VTI1A,PDCD6,SNAP23,OXA1L,NLGN4Y,SSH1,MFN1,GET4,RCC1L,PITPNM1,PITPNC1,GRAMD1B,HSPA8,ANK2,C2CD5,GPER1,GNPAT,SLC9A1,AP2M1,OSBPL2,STX1A,TOR1AIP1,STX6,THEM4,RHOBTB1,STPG1,DOCK1,WHAMM,FZD9,VPS8,SCAP,DLG1,LYZL6,NSF,MIA3,SPG11,PIKFYVE,BLOC1S6,STARD5,NMT1,RTP4,MOSPD3,ABCA12,NRXN2,LPCAT3,ATL1,ANXA7,SEC24C,BCS1L,RAB3A,PINK1,MUL1,PLA2G16,VAMP1,SNAP29,STAT3,ANKFY1,PI4KA,ATP1B1,GLDN,PARP11,ARL6IP1,STX5,TMEM30B,STX18,RAB8A,ATP13A2,CPLANE2,DLG4,AKAP8L,SYT7,SLC2A4,NLGN2,TMEM102,GPHN,CHRNB1,CLN8,MPP5,DEGS1,MFN2,ANXA2,GAK,CPLX1,TARDBP,STX1B,STX4,BNIP1,NAXE,ITGAM,SYT11,DOCK2,RAB8B,NLGN3,TMED10,NDEL1,AC1	grey	VSMC_M10
GO:0009411	0.95	0.07	59	127	response to UV	BP	1	MAP3K4,UBE2B,BAK1,MYC,ATF4,MAPK13,OPN1SW,REV1,CAT,BRSK1,MSH2,AQP1,PTN,EGFR,TRIM32,ERCC1,XPC,ERCC2,ERCC3,ZRANB3,WRN,ERCC6,ERCC8,PIK3R1,PRIMPOL,CASP3,ATR,SCARA3,MME,EIF2AK4,DDB2,TP53INP1,RHBDD1,HYAL1,HYAL3,CCND1,SPRTN,NFATC4,USF1,MEN1,IL12A,MMP3,RHNO1,ZBTB1,PARP1,DDB1,TAF1,TIPIN,DCUN1D3,YY1,CUL4B,ERCC4,TP53I13,FMR1,CREBBP,SDF4,CIRBP,IMPACT,MAP2K7	grey	VSMC_M10
GO:0048661	0.95	0.08	35	78	positive regulation of smooth muscle cell proliferation	BP	1	MAP3K5,AKR1B1,EGFR,TLR4,PHB,MYD88,ABCC4,TGFBR2,HBEGF,FOXP1,TRAF6,HPGD,ADAMTS1,NQO2,TERT,AGT,HDAC4,CALCRL,BMPR1A,MFN2,RBPMS2,IL6R,CCL5,JUN,SERPINF2,GNAI3,CYBA,MIR21,MIR222,MIR27B,MIR27A,FOXJ2,LDLRAP1,EREG,PDGFD	grey	VSMC_M10
GO:0050965	0.95	0.14	4	12	detection of temperature stimulus involved in sensory perception of pain	BP	1	ASIC3,EPHB1,NTSR1,TRPV1	grey	VSMC_M10
GO:0071392	0.95	0.10	11	28	cellular response to estradiol stimulus	BP	1	ESR1,HSF1,EGFR,POU4F1,CCDC62,LCOR,SRD5A1,GPER1,BCL2L11,FAM210B,BCL2L2	grey	VSMC_M10
GO:0044706	0.95	0.07	75	159	multi-multicellular organism process	BP	1	TAC3,CYP27B1,ESR1,FBLN1,AGO2,H3F3C,AKR1B1,PLA2G6,CLIC5,RLN1,PPAT,KLK14,PTN,DKKL1,DDO,SPHK2,PSG3,PRDX3,THBD,TGFBR2,ACVR2A,IDO1,ADRA2B,ACVR1B,HPGD,VDR,STC1,SLC38A2,ACVR1C,SLC38A1,ABCC2,SPP1,PLA2G4B,ADCY7,HYAL3,SLC38A3,COL16A1,PTHLH,KRAS,AGT,DEDD,SP3,OVGP1,MEN1,COMT,ADRA2C,WNT4,RAMP2,CTSV,CD38,MAPK1,STAT5B,SCGB1A1,SYDE1,MED1,ITGA3,PGF,FOS,MAPK3,UBE2Q1,UPRT,EPOR,VMP1,TEKT3,TLE6,P2RX1,BSG,DHODH,PTGFR,HSD11B2,MIR21,CRH,TCF23,LIF,HAVCR2	grey	VSMC_M10
GO:0019934	0.95	0.11	7	19	cGMP-mediated signaling	BP	1	PDE10A,AQP1,GUCY1B1,PTK2B,PDE9A,ADNP,PDZD3	grey	VSMC_M10
GO:0060252	0.95	0.13	5	14	positive regulation of glial cell proliferation	BP	1	TSPO,EGFR,PLAG1,MIR222,MIR125B1	grey	VSMC_M10

GO:0010810	0.95	0.07	82	175	regulation of cell-substrate adhesion	BP	1	ONECUT2,LRP1,FBLN1,PTK2,RAC2,CDKN2A,TEK,CDK6,PRKCE,HOXA7,PTN,ITGB1BP1,EPHA1,NDNF,FBLN2,CLASP2,RSU1,UNC13D,RIN2,JAG1,ACTG1,FERMT1,RAC3,ARHGEF7,RELL2,PTPRA,FAM107A,PIK3CB,PIK3R1,FMN1,PTPRJ,PTK2B,DOCK5,RREB1,STK4,GCNT2,DMTN,LDB1,SLK,CARMIL1,COL16A1,DAG1,ARHGAP6,AP1AR,DISC1,CASS4,CIB1,SLC9A1,FZD7,PTPRO,DOCK1,MELTF,CSPG5,EFEMP2,APOD,BCL6,MEN1,FN1,CASK,SPOCK2,WNT4,VCL,BST1,MINK1,ITGA3,SMAD3,CORO2B,DNM2,BCAS3,CAMSAP3,CCL25,CRK,PRKCZ,TSC1,FOXF1,RHOA,FGA,ACVRL1,PEAK1,THY1,ACER2,DUSP22	grey	VSMC_M10
GO:0032091	0.95	0.08	34	76	negative regulation of protein binding	BP	1	PPARA,CSNK1E,TTBK1,MITD1,ITGB1BP1,SYMPK,RALB,PTPRF,EFHB,TMBIM6,FAM192A,IFIT2,DTNBP1,TTBK2,ADNP,DISC1,SORL1,NFATC4,ITGA4,LRPAP1,DNAJB2,DDX11,CRMP1,ACTB,GNL3L,PEX14,MAPK3,WFIKKN2,WFIKKN1,PARK7,MIR27B,BAG2,NOG,STYX	grey	VSMC_M10
GO:0010824	0.95	0.09	16	39	regulation of centrosome duplication	BP	1	VPS4B,MDM1,CHMP2A,XPO1,CDK5RAP2,CEP295NL,PLK2,CHMP2B,CHMP4C,ALMS1,TMEM67,AC112128.1,CCDC84,TRIM37,NUBP1,CHMP1A	grey	VSMC_M10
GO:0006890	0.95	0.09	19	45	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	BP	1	ATP9B,COPG2,PICK1,BICD2,BET1L,COPZ1,GBF1,SEC22B,ERGIC2,COPA,HTT,KIF1C,STX18,BNIP1,TMED10,COG7,RER1,COG4,RAB6B	grey	VSMC_M10
GO:0031497	0.95	0.07	38	84	chromatin assembly	BP	1	BAZ2A,BRD2,ASF1A,H3F3C,UBN2,SOX9,RSF1,SIRT2,M1AP,SPTY2D1,NAP1L5,RBBP4,SART3,H2AFY2,HIRA,TSPYL2,PHF8,NAP1L2,NAA60,CTCF,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,BEND3,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,TSPYL5	grey	VSMC_M10
GO:0035924	0.95	0.08	27	62	cellular response to vascular endothelial growth factor stimulus	BP	1	SEMA6A,PTP4A3,MAPK14,ADAMTS3,ITGB1BP1,TSPAN12,GAB1,PRKD2,SPRY2,DCN,FLT1,NR4A1,PIK3CB,ROBO1,VEGFC,MAPKAPK2,IL12A,RAMP2,PGF,ADAMTS12,DAB2IP,MIR199A1,MIR21,MIR23A,MIR27B,MIR27A,CADM4	grey	VSMC_M10
GO:0042246	0.95	0.08	23	53	tissue regeneration	BP	1	LARGE1,TEC,NINJ1,AKIRIN1,PTN,KLF5,TGFBR2,BIN3,LGR6,PPP3CA,GAP43,DAG1,SOX2,FZD7,FZD9,CDKN1B,APOD,DUSP10,MYOZ1,NINJ2,ENO3,SOX15,MIR199A1	grey	VSMC_M10
GO:0002253	0.95	0.06	91	191	activation of immune response	BP	1	CD226,HLA-DPB1,XRCC6,PTK2,PLA2G6,TEC,TNFRSF21,PRKCE,FPR2,TLR4,C5AR2,C5AR1,PRKD2,PHB,NECTIN2,EIF2B3,IKBKB,TMEM173,PAWR,PLCL2,PRNP,MAVS,NCKAP1L,FOXP1,PRKDC,TRAF6,HCK,LPXN,PTPRJ,MEF2C,SLA2,RIPK2,NOD2,GPLD1,SPPL3,LCK,BANK1,ICOSLG,BTN2A2,DENND1B,CMKLR1,THEMIS2,LAT2,BMX,FGR,PLPP4,CD28,FCER1G,NONO,XRCC5,RC3H1,PTPN6,CFP,CD38,MAPK1,FOXP3,GPS2,CARD11,PSEN1,LCP2,CD19,SFPQ,PRKCB,BTK,SIN3A,YES1,PRAM1,VAV1,C7,C3,PTPN2,CREBBP,IKBKG,VAV3,BCL10,CMTM3,FYB1,BTN1A1,CD46,ZCCHC3,A2M,CFD,CD247,THY1,RGCC,UBE2N,GCSAM,HRAS,LAX1,SH2B2,RC3H2	grey	VSMC_M10
GO:0018196	0.95	0.11	8	21	peptidyl-asparagine modification	BP	1	UGGT2,RPN2,HIF1AN,DAD1,MGAT1,DERL3,MGAT2,DDOST	grey	VSMC_M10
GO:0055117	0.95	0.08	25	58	regulation of cardiac muscle contraction	BP	1	TNNI3,ASB3,TRPM4,SCN5A,STC1,DSP,CASQ2,RYR2,PKP2,KCNJ2,ANK2,ACE2,ATP1A2,SLC9A1,HDAC4,DLG1,ATP1B1,ATP2A1,CALM1,DSG2,RNF207,DMD,CHGA,HCN4,NKX2-5	grey	VSMC_M10
GO:0034616	0.95	0.14	4	12	response to laminar fluid shear stress	BP	1	NFE2L2,MAP2K5,MAPK7,ASS1	grey	VSMC_M10
GO:0051570	0.95	0.12	6	17	regulation of histone H3-K9 methylation	BP	1	SETD7,KDM4A,DNMT3B,JARID2,MECP2,ZNF304	grey	VSMC_M10
GO:0098609	0.95	0.06	294	592	cell-cell adhesion	BP	1	SERPINB8,ITGA7,TNXB,AGER,PPARA,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,COL14A1,TNFRSF13C,OBSCN,PTK2,MAPK14,PODXL,CDC42EP1,RAC2,ZDHHC21,MYH9,LRRC4,SRF,CLDN12,KIT,TNFRSF21,NCK2,TLN1,SEMA4D,NINJ1,ADGRL3,CLDN19,EPCAM,NT5E,PELI1,PLEK,EPHA7,AKNA,ADD2,IL4I1,EGFR,BVES,IL15,NRCAM,SLC7A11,PCDH10,IZUMO1,FAT4,PODXL2,BMI1,RAB10,SOX9,DLG2,NECTIN2,PVR,GLI2,PCDH8,FOXJ1,PTPRF,MYL12A,TGFBR2,C1QTNF1,JAG1,ACTG1,PAWR,SPINT2,PRNP,PCDHGC5,PCDH1,UNC5D,CLIC1,NCKAP1L,PKP3,SLC7A1,LRFN3,TRAF6,SOX12,NPHP1,RET,ZC3H8,IL1A,FER,PIK3CB,CLSTN2,CASP3,DENND6A,CTNND1,PARVA,ROBO1,ROBO2,TENM3,ADGRV1,TMEM131L,IL7,NCAM2,PAG1,JAM2,KIFC3,PLEKHA7,RASGRP1,RIPK2,CDH17,AP3B1,AMIGO2,MARCH7,SPARCL1,DSP,SOX13,GCNT2,ALCAM,DMTN,ADTRP,NOD2,VSIG10,IGF2,ELMO2,NECTIN3,CD200,PKP2,LCK,ICOSLG,TRPV4,TGFB2,BTN2A2,GPAM,IGSF11,PRKAR1A,CD99,AMIGO3,NLGN4Y,AJUBA,SELPLG,HLX,CDH24,KIRREL1,SOX2,YTHDF2,UBASH3B,ICAM2,ITGB5,LAMA5,NECTIN4,CD28,RUNX3,EPHB3,DLG1,ADAM8,CADM1,OLR1,MYPN,MIA3,DUSP10,HMCN1,BCL6,COL13A1,ITGA2B,ITGA4,IL12A,CDH23,ARVCF,ABCA12,TNR,NRXN2,FN1,VSIR,RC3H1,PTPN6,TNFSF18,FERMT3,WNT4,LAG3,PKD1L1,VCL,GLDN,STAT5B,OBSL1,MINK1,NINJ2,SCGB1A1,FOXP3,RASAL3,DLG4,ACTB,ZBTB1,CLDN7,FBLIM1,SDK1,CARD11,NLGN2,PCDH7,PEAR1,SYNJ2BP,ANXA2,ATP1B2,TBX21,PSEN1,STK10,ITGAM,TLN2,NLGN3,ZBTB7B,TENM2,MEGF11,NTN1,IL4R,MAP2K5,PCDH11X,PCDH19,S100A8,VMP1,ICAM5,TNIP1,UMOD,DSG2,DSC3,CD74,CCL5,LAMA3,MA	grey	VSMC_M10

GO:0042327	0.95	0.06	305	612	positive regulation of phosphorylation	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,MAP3K4,AGER,IL5,GDF9,ROS1,XRCC6,PRXL2C,PTK2,TAB1,NTRK2,PLA2G6,HSF1,CCND3,ZNF16,CHRNA3,TEK,TTBK1,TEC,KIT,SLC1A1,ROR2,SEMA4D,CLDN19,IL11,FPR2,MOB1B,SLC4A4,EPGN,AREG,BMP8A,ETAA1,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,HDAC2,SLC8A2,MOB3C,PRKD2,PHB,ABI1,SOX9,MAPRE3,RALB,PRKAG2,RAF1,PIBF1,FBH1,SPRY2,WNT11,ALK,AKT2,ARRB1,TGFBR2,ACVR2A,NEK10,RPTOR,TCIM,HBEGF,PRNP,BAG4,MAVS,NRG1,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,ERCC6,FLT1,RYK,ADRA2B,TRAF6,EPHB1,RET,ACVR1B,OSBP,ZFP91,ROBO1,FBXW7,PTPRJ,GPD1,P2RX7,VEGFC,P2RY1,MADD,PTK2B,RASGRP1,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,FGF5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CDK2AP1,PKD2,STK4,ADTRP,NOD2,CNTN1,TAOK3,CD40,DSTYK,IGF2,BMPR1B,BDNF,IRS1,NEURL1,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K6,TGFB2,ZBTB20,ADRA2A,FAM20A,DAG1,AXIN2,SLCO3A1,AJUBA,NCF1,KRAS,EGF,PFKFB2,HCLS1,ADNP,OPRD1,GPER1,CHEK2,CASS4,SPATC1L,PARP9,PARP14,CACUL1,AGT,FGR,CIB1,ARNT,DVL3,STRADB,FZD7,OSM,SYAP1,THPO,STRADA,MLXIPL,EPHB3,PDE8A,LIMK2,DUSP12,GPRC5D,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,MAPT,STOX1,CEMIP,DBF4B,EPHB4,IL12A,MAP4K2,DDX3X,XRCC5,DUSP19,PDCD10,TNFSF18,ADRA2C,DOK7,SLC11A1,GDF15,MARK2,FGFR3,PINK1,ARAF,SLC27A1,MAPK1,INHA,EPHA4,DLG4,MAGED1,DVL2,BMPR1A,WNK3,FGFR4,RPLP1,FXR2,ANXA2,DGKQ,CTF1,PSEN1,FGF18,LCP2,PGF,TAOK2,EFNA1,MAP	grey	VSMC_M10
GO:1903053	0.95	0.09	18	43	regulation of extracellular matrix organization	BP	1	LRP1,SOX9,CLASP2,TCF15,ADTRP,FAP,SLC2A10,DAG1,AGT,PHLDB1,MELTF,EFEMP2,TNFRSF1B,FGFR4,SMAD3,CARMIL2,DPP4,RGCC	grey	VSMC_M10
GO:0001710	0.95	0.14	4	12	mesodermal cell fate commitment	BP	1	SIX2,EYA1,PAX2,BMPR1A	grey	VSMC_M10
GO:0016482	0.95	0.06	71	153	cytosolic transport	BP	1	KIF5A,RAB21,PRKN,VPS52,RGP1,SRSF10,WDR91,VPS35,EPS15,MTMR2,RAB7A,PIP4K2A,RBSN,UBE2O,HOOK3,SNX5,RAB5A,HEATR5B,DNAJC13,FAM160A2,BET1L,WASHC2A,TMEM87B,ANKRD27,DOP1B,GBF1,MAGEL2,RAB7B,CCDC91,VTI1A,TBC1D10C,AP1AR,SORL1,STX6,TANC2,SNX6,SNX32,PIKFYVE,VPS26A,TBC1D14,KLHL20,AP4M1,CLTCL1,ANKFY1,MAPK1,STX5,KIF1C,SYT7,GAK,VPS13C,SNX12,TBC1D10B,SNX1,TRIM46,MAPK3,AC138894.1,HOOK2,MAP2K1,STX8,MYO1D,VPS53,RILP,CORO7,BAIAP3,RNF126,AP1G1,PHETA1,RAB6B,SNX16,VAMP3,PLEKHJ1	grey	VSMC_M10
GO:0051014	0.95	0.14	4	12	actin filament severing	BP	1	AVIL,MYH9,CFL1,GMFG	grey	VSMC_M10
GO:1905508	0.95	0.09	13	33	protein localization to microtubule organizing center	BP	1	MAPRE1,PIBF1,HOOK3,NSFL1C,CEP250,MCPH1,DISC1,CEP192,WRAP73,SNX10,C2CD3,APC,PARD6A	grey	VSMC_M10
GO:0006607	0.95	0.14	4	12	NLS-bearing protein import into nucleus	BP	1	KPNA3,KPNA2,NUP54,KPNB1	grey	VSMC_M10
GO:0046184	0.95	0.14	4	12	aldehyde biosynthetic process	BP	1	DKK3,WNT4,PNPO,CACNA1H	grey	VSMC_M10
GO:0033182	0.95	0.14	4	12	regulation of histone ubiquitination	BP	1	RNF20,OTUB2,PARK7,UBE2N	grey	VSMC_M10
GO:0014037	0.95	0.09	14	35	Schwann cell differentiation	BP	1	ERBB3,ADGRG6,NTRK2,ADAM22,PRX,AKT2,SIRT2,NRG1,LGI4,DAG1,CNTNAP1,MPP5,SKI,POU3F2	grey	VSMC_M10
GO:1901223	0.95	0.11	8	21	negative regulation of NIK/NF-kappaB signaling	BP	1	NMI,HDAC7,DDX3X,PPM1A,TSPAN6,LITAF,MIR21,MIR27B	grey	VSMC_M10
GO:0033212	0.95	0.14	4	12	iron import into cell	BP	1	STEAP2,ISCU,NOX5,LCN2	grey	VSMC_M10
GO:0008589	0.95	0.07	31	71	regulation of smoothened signaling pathway	BP	1	GLI1,PTCH1,SMO,FUZ,INTU,PTCH2,KCTD21,GLI2,MEGF8,IFT172,KCTD6,IFT81,RPGRIP1L,SUFU,TTC23,ARMC9,TTC21B,POR,STK36,GORAB,GPR161,TULP3,MKS1,TUBD1,MOSMO,GPC3,MGRN1,CREBBP,GPR37L1,C2CD3,ZIC1	grey	VSMC_M10
GO:0022412	0.95	0.06	119	247	cellular process involved in reproduction in multicellular organism	BP	1	TBPL1,YTHDC2,MOV10L1,PACRG,QKI,GDF9,UBE2B,CATSPER3,WASHC5,SMAD5,H3F3C,FANCC,TUT7,DMC1,PICK1,CFAP69,FANCG,SMARCA2,KIT,FOXJ3,MSH2,SPACA6,YTHDC1,GMCL1,PTN,NOBOX,CCDC155,TUT4,FOXO3,ARMC2,DLD,IZUMO1,TTC26,DNMT3A,PANX1,RSPH6A,TOPAZ1,ERCC1,NECTIN2,MLH1,TTC21A,CCNB1IP1,ARRB1,SIRT2,MKKS,PANK2,SOHLH2,TEX15,NPHP1,ING2,ROBO2,M1AP,CELF1,JAM2,PTK2B,KMT2D,CDYL,SYCP1,DNAH1,NPM2,OCA2,ROPN1L,BMPR1B,NECTIN3,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,PRKAR1A,ABHD2,CCDC36,YTHDF2,SPO11,TSSK4,CIB1,DDX6,OSBP2,TDRKH,CATSPER2,ETV6,LYZL6,TTC12,SPAG16,WNT4,ZMYND15,MNS1,YBX2,SEPT1,SOX30,CCDC42,SPESP1,NOX5,PAQR5,RAD51C,TAF4B,SPEF2,CATSPERD,ZNF449,MEIOB,CHD5,TPGS1,WDR77,SPIRE2,MFSD14A,STRBP,PRMT7,AURKC,UBB,SYCP3,AGO4,FOXJ2,NANOS1,ZSCAN21,SPDYA,RNF8,TBC1D20,EREG,ZGLP1	grey	VSMC_M10
GO:0050769	0.95	0.06	85	181	positive regulation of neurogenesis	BP	1	LRP1,RAB21,SNW1,TIAM2,TSPO,PLXNA4,NTRK2,SOX10,SMO,SRF,TTBK1,KIT,SEMA4D,RUFY3,PTN,EGFR,TRIM32,PLXNA1,HDAC2,GOLGA4,MEGF8,XRCC2,NUMBL,SS18L2,PLXNC1,PLAG1,ANKRD27,FAIM,ROBO1,ROBO2,FZD3,VEGFC,CUX2,MME,TIAM1,SYNJ1,OPA1,NKX6-1,ZFYVE27,SPINT1,ITPKA,CYFIP1,ZNF335,BDNF,NEURL1,DNM1L,HDAC1,CAPRIN2,DAG1,ADNP,DISC1,GPER1,SS18L1,CDKL5,WNT3,MAPT,FN1,XRCC5,NIN,OBSL1,HAP1,EPHA4,SPEN,TNFRSF1B,RGS14,PRPF19,NDEL1,RAB11A,MAP2K1,NTN1,PARP6,GPRASP2,BHLHB9,TRPV2,LRP8,L1CAM,PLXNA3,SOX8,AMIGO1,FBXO31,MIR222,MIR125B1,FOXG1,LIF,WNT2	grey	VSMC_M10
GO:0007632	0.95	0.09	14	35	visual behavior	BP	1	SYNGAP1,KIT,SLC7A11,B4GALT2,DDHD2,NPHP1,KRAS,ATP1A2,CREB1,RGS14,CHRNB2,IFT20,MECP2,ABCA7	grey	VSMC_M10

GO:0031347	0.95	0.06	196	397	regulation of defense response	BP	1	CD226,TNFAIP3,USP15,ENPP3,ESR1,AGER,PPARA,GPSM3,XRCC6,C6orf106,MAPK14,MAPK13,TEK,TTBK1,NINJ1,FPR2,NT5E,NOD1,AKIRIN2,NR1H2,AKNA,EGFR,TLR4,IL15,VPS35,MGST2,CDK19,TRAF3IP2,NAPEPLD,CST7,LACC1,NECTIN2,PVR,OPTN,MYD88,FNDC4,SEC14L1,IKBKB,SIRT2,NMI,TMEM173,NR1D2,NPLOC4,MAVS,HPX,FOXP1,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,PLK2,HCK,IL37,CEBPA,ERAP1,MEF2C,CELF1,SETD6,MCPH1,RASGRP1,EIF2AK4,NR1H3,TRAFD1,OAS3,NLRC5,RIPK2,OTULIN,F2RL1,RIPK1,POLR3D,MAPKBP1,HERC5,NOD2,CD96,CD200,CD200R1L,TRPV4,PDCD4,POLR3C,NCF1,FABP4,SPATA2,YTHDF2,GPER1,SLAMF8,PARP9,DTX3L,PARP14,RNF26,AGT,FGR,ACE2,NLRX1,TRAF3IP1,OSM,HTRA1,SNX4,COCH,CD28,ADAM8,CADM1,DUSP10,NONO,IL16,GGT2,BCL6,IL12A,XRCC5,LPCAT3,PTPN6,TNFSF18,LAG3,CALCRL,CASP12,MUL1,MMP3,BIRC3,BST1,STAT5B,DAGLB,SCGB1A1,FOXP3,RNF216,GPS2,TKFC,USP18,F12,TNFRSF1B,MED1,SYT11,AREL1,MAPK3,DCST1,SMAD3,TSPAN6,LDLR,S100A8,SFPQ,BTK,STAT2,TNIP1,SIN3A,TRAF3,CCL5,RIOK3,MAPK7,YES1,ISL1,RNF135,VAV1,PTGER4,C3,OSMR,ADAMTS12,PTPN2,SOCS1,DROSHA,CREB3L3,LRP8,CRK,CREBBP,DNASE1,PARK7,CYBA,FOXF1,KARS,AP1G1,ZDHHC1,MIR199A1,MIR21,MIR222,MIR22,S100A12,C5orf30,OAS1,ZDHHC11,FADD,CXCL6,CASP8,ZCCHC3,A2M,IFNLR1,IRGM,WNT5A,FGL2,IL33,CRH,SERPINB9,PTGES,TSLP,CEBPB,EREG,HAVCR2	grey	VSMC_M10
GO:0048193	0.95	0.06	125	259	Golgi vesicle transport	BP	1	ATP9B,AP3S1,GOPC,VPS52,EXOC4,MAPK15,NRBP2,COPG2,PICK1,STEAP2,BICD2,STX17,SPTBN1,TRAPPC12,TRAPPC3,EPS15,BCAP29,NAPA,RAB10,COPG1,COG1,RBSN,OPTN,GOLGA4,CCDC93,SEC22C,ANK1,YIPF4,BET1L,COPZ1,LYPLA1,VAMP5,TRAPPC11,ARFGAP2,EXOC6B,SEC31A,DOP1B,SEC31B,KIF13A,GBF1,RAB7B,KLHL12,SEC22B,PGAP1,ERGIC2,TRIP11,CCDC91,PEF1,VTI1A,PDCD6,SNAP23,AP1AR,SORL1,TRAPPC2,SEC22A,COG2,HYOU1,SEC23IP,TRAPPC4,COPA,BBS1,RNF215,STX6,RAB1B,WHAMM,SCAP,NSF,MIA3,TRAPPC6B,CTAGE9,SEC16B,SCAMP3,TBC1D14,KLHL20,AP4M1,HTT,SEC24C,ANKFY1,EXOC5,STX5,KIF1C,STX18,CYTH3,RAB8A,CNST,RSC1A1,CNIH4,GAK,VPS13C,BNIP1,SNX12,RAB8B,TMED10,SNX1,AC138894.1,DNM2,GGA2,COG7,LMAN1L,SCAMP2,VPS35L,CXorf56,PPP6C,NAPG,MPPE1,CORO7,BCAP31,RAB26,RER1,SEC16A,SPIRE2,TMED5,COG4,AP1G1,COG8,C16orf70,RAB6B,AP3S2,YIF1A,TBC1D20,RABIF,VAMP3,TMED3,TRAPPC6A,TRAPPC3L	grey	VSMC_M10
GO:0071277	0.95	0.08	27	63	cellular response to calcium ion	BP	1	CPNE5,BRAF,SCN5A,CPNE9,SYT1,RYR1,SYT9,RYR3,ADGRV1,MEF2C,CPNE2,PKD2,DMTN,SYT8,GPLD1,CARF,CLIC4,RASA4,RASGRP2,SYT7,SYT11,FOS,SLC25A23,CPNE7,HSPA5,WNT5A,PPIF	grey	VSMC_M10
GO:0007093	0.95	0.07	54	117	mitotic cell cycle checkpoint signaling	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,BRSK1,MSH2,CDK5RAP2,XPC,PLK3,DYNC1LI1,ANAPC15,IK,NEK11,USP44,PRKDC,STK33,PLK2,RAD17,RAD9B,CHMP4C,NBN,ABRAXAS1,DONSON,ZFYVE19,PIDD1,TAOK3,CCND1,GIGYF2,CHEK2,SYF2,CDKN1B,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,LCMT1,FOXN3,PSMG2,TAOK1,FZR1,FBXO31,VPS4A,NAE1,PLK5,RPS27L,SOX4,DUSP1,APC,BRCC3,CRADD,NABP1	grey	VSMC_M10
GO:0002520	0.95	0.05	348	694	immune system development	BP	1	NME1,PHLPP1,TNFAIP3,STK3,MPIG6B,HSPA1B,BRD1,AGER,HLA-DRA,IL5,TCF7,CCDC134,BAK1,XRCC6,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,ATF4,MAPK14,PIM1,MFNG,HSF1,KCP,MYH9,ZNF16,RBFOX2,TEK,FBXO7,SRF,CDK6,KIT,ROR2,NFIL3,EXOSC3,RPS14,TMEM190,IL11,SMAP1,EPAS1,MSH2,CD109,HOXA7,PTBP3,SLC46A2,MTURN,BPGM,CYREN,CNOT4,PLEK,RSAD2,PTN,ADD2,IL4I1,TLR4,BVES,IL15,ATG5,OSTM1,FOXO3,ZBTB24,TRAF3IP2,HMCES,BMI1,PIP4K2A,ABI1,ERCC1,ERCC2,CLPTM1,GAB2,MLH1,GLI2,DHTKD1,RAF1,PRDX3,FOXJ1,PAXIP1,SLC25A38,POU4F1,IL15RA,KLF6,CMTM7,TGFBR2,ACVR2A,EOMES,JAG1,PLCL2,RASGRP4,CNN2,SHLD1,C12orf29,EIF2AK2,ASH2L,FUT10,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,MFHAS1,FLT1,TRAF6,TCF15,SOX12,RET,TOX,ZC3H8,ASXL1,IL1A,ACVR1B,CAMK4,CEBPA,NCOA6,PIK3R1,CASP3,HAND2,FBXW7,PTPRJ,MEF2C,TMEM131L,IL7,TPD52,XRCC4,PTK2B,RASGRP1,LMBR1L,CIAPIN1,RIPK2,NBN,TENT2,CDH17,AP3B1,F2RL1,TESC,RIPK1,MARCH7,SOX13,STK4,TMEM14C,TSPAN2,DMTN,ITGB6,ALAS1,JARID2,POLL,CD40,LDB1,NFKB2,DCAF1,RAB7B,DOCK10,SH3PXD2A,PKNOX1,LRRK1,LCK,SBDS,SLC9B2,TGFB2,TCIRG1,ACP6,GPR137B,PRKX,RABL3,SELPLG,PIAS3,HLX,SART3,ACIN1,DYRK3,TCTA,HCLS1,YTHDF2,UBASH3B,SLAMF8,ARIH2,CIB1,WASF2,ARNT,FZD7,OSM,HDAC4,THPO,MMP21,CD28,FCER1G,RUNX3,FARP2,EPHB3,RNF168,RTKN2,ZBTB46,PATZ1,FZD9,SP3,PPP2R3C,ETV6,ADAM8,NFE2L2,CREB1,NBEAL2,FZD5,DUSP10,BCL6,SYVN1,BATF2,ITGA4,WDR61,VSIR,XRCC5,ARMC6,RC3H1,ESRRA,PTPN6,GPR137,MEOX1,FBN1,TNFSF18,WNT4,LAG3,PPP3CB,PRRC2C,LT	grey	VSMC_M10
GO:0055093	0.95	0.11	7	19	response to hyperoxia	BP	1	CAT,HDAC2,DNMT3B,HDAC1,POLG,MT-ATP6,MT-CYB	grey	VSMC_M10

GO:0007276	0.95	0.05	233	469	gamete generation	BP	1	TBPL1,GLI1,YTHDC2,B4GALNT1,ATAT1,TSPAN8,IGF2R,MOV10L1,PACRG,QKI,BRD2,GDF9,ROS1,MCM9,HSF2,UBE2B,CATSPER3,WASHC5,TOB2,SMAD5,H3F3C,FANCC,TUT7,DMC1,PICK1,SPATA31D3,CFAP69,FANCG,SMARCA2,TDRD6,KIT,CCIN,TSGA10,TDRD7,DNAJA1,FOXJ3,SCMH1,MSH2,RAD23B,YTHDC1,CABS1,FANCL,GJA10,HERPUD2,GMCL1,PTN,NOBOX,CCDC155,CREM,TUT4,FOXO3,ARMC2,DLD,TXNRD3,APOB,SPATA6,SPATA5,TTC26,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,MLH1,ACOX1,FOXJ1,WDR48,TTC21A,CCNB1IP1,ACVR2A,SIRT2,MKKS,SPATA24,ADAM18,MCM8,GOLGA3,PANK2,BTG1,SOHLH2,TEX15,KATNAL1,NPHP1,ING2,HPGD,SPATA9,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,PTK2B,KMT2D,PRKAG1,SFMBT1,AP3B1,CDYL,SYCP1,DNAH1,NPM2,DPCD,OCA2,ROPN1L,SIAH1,BMPR1B,GAS2,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,TESMIN,PRKAR1A,SPATA2,RNF114,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,TSSK4,CIB1,CCDC87,DDX6,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,SEPT2,LIMK2,PATZ1,CATSPER2,OVOL1,ETV6,YBX3,WNT3,CADM1,SPATA32,GGT2,TTC12,BCL6,RPL10L,DDX3X,SPAG16,ZCWPW1,WNT4,CTSV,BIRC3,ADCY10,PARP11,CALR3,KDM5A,ZMYND15,MNS1,YBX2,SPIN2A,SEPT1,MYCBPAP,VIPAS39,SOX30,CCDC42,CREB3L4,IL4R,PAQR5,RAD51C,DNM2,YY1,TAF4B,ALKBH5,JAG2,RHOXF1,IFT20,ACSBG2,TXNDC2,SPEF2,CATSPERD,PARN,ZNF449,HSPB11,BCAP31,RNF151,TMEM203,MEIOB,GAMT,CHD5,SOX8,TPGS1,WDR77,SPIRE2,MFSD14A,LRRC8A,NR6A1,STRBP,PRMT7,TSNAXIP1,MSH4,FSTL3,AURKC,UBB,SYCP3,ARID4A,AGO4,TCFL5,N	grey	VSMC_M10
GO:0019219	0.95	0.05	1478	2852	regulation of nucleobase-containing compound metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,EYA4,GLI1,MARS,CLK4,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,MRNIP,HELB,PPP1R10,ZBTB2,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PABPC1,SNW1,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DXO,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,MED30,IL5,BRD2,RXRB,VGLL2,HSF2,TCF7,PHF1,UBE2B,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PRXL2C,HABP4,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,ATF4,TUT7,MAPK15,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,PUF60,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,GUCA1B,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,STPG4,EPCAM,MSH2,SP4,IGF2BP3,PPP2R1A,ZNF462,TRA2A,PHIP,HMGN3,YTHDC1,NFYC,NFE2L3,PNPT1,SLC4A4,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,JAZF1,CREB5,PTBP3,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,CYREN,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRI	grey	VSMC_M10
GO:0045995	0.95	0.08	21	50	regulation of embryonic development	BP	1	NLRP5,OSR1,LAMA4,CLASP2,PLCB1,POGLUT1,DAG1,CFL1,PHLDB1,LAMA5,NFE2L2,WNT4,LHX1,INSR,LAMA3,AMOT,LAMA1,TLE6,CCSAP,TGIF2,WNT2	grey	VSMC_M10
GO:1903978	0.95	0.13	4	12	regulation of microglial cell activation	BP	1	TTBK1,CST7,SYT11,LDLR	grey	VSMC_M10
GO:0009143	0.95	0.13	4	12	nucleoside triphosphate catabolic process	BP	1	ENPP3,SMPDL3A,NUDT15,NUDT16	grey	VSMC_M10
GO:0015012	0.95	0.10	9	24	heparan sulfate proteoglycan biosynthetic process	BP	1	HS3ST5,CSGALNACT1,TCF7L2,AC022400.6,GLCE,HS6ST2,B3GALT6,HS6ST3,HS2ST1	grey	VSMC_M10
GO:0031297	0.96	0.09	14	35	replication fork processing	BP	1	ETAA1,ZRANB3,FBH1,WRN,PRIMPOL,ATR,ZGRF1,RTEL1,DDX11,EXD2,EME1,OOEP,FAM111A,CENPX	grey	VSMC_M10
GO:0030041	0.96	0.06	75	160	actin filament polymerization	BP	1	ARPC3,AVIL,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,NCK2,KIAA1211,TMOD1,PRKCE,SPTBN1,ADD2,FAM49A,WASF1,MSRB2,PLEKHG2,FCHSD2,MKKS,BAG4,DIAPH1,FCHSD1,NCKAP1L,ARFIP2,LMOD3,TTC17,HCK,FAM107A,FER,HIP1R,FMN1,PTK2B,IQGAP2,CYFIP1,DMTN,MAGEL2,CARMIL1,LMOD1,ADD3,SSH1,HCLS1,ARHGAP6,AP1AR,WASF2,SPTBN2,TMOD4,EPS8,WHAMM,DLG1,CAPZA1,CDC42EP2,NCKAP1,ARPC1A,WAS,TMOD2,SPTB,PFN3,WASHC3,HAX1,GAS7,EVL,PSTPIP1,SSH2,CORO7,MLST8,SPIRE2,WDR63,CARMIL2,MICALL2,RHOA,VASP,GMFG,GRB2,PFN4,COTL1	grey	VSMC_M10
GO:0070670	0.96	0.09	11	28	response to interleukin-4	BP	1	TCF7,NFIL3,CD300LF,PARP14,STAT5B,CITED1,IL4R,KEAP1,PTPN2,ADAMTS13,HSPA5	grey	VSMC_M10
GO:0042698	0.96	0.08	19	46	ovulation cycle	BP	1	ESR1,GDF9,PTN,EGFR,FOXO3,TIMP4,ARRB1,CASP3,ROBO2,ADAMTS1,BMPR1B,GAS2,MAP2K6,TGFB2,ADNP,PTPRN,STAT5B,HSPA5,EREG	grey	VSMC_M10

GO:0065008	0.96	0.05	1434	2770	regulation of biological quality	BP	1	ATP9B,ZNF236,NME1,SERPINB2,ITGA7,RDH5,ORMDL2,SLC39A5,NEDD4L,PAN2,ATP8B1,ARPC3,RDH16,TAC3,HSD17B4,LRP1,SEMA6A,LVRN,ALDH8A1,TNFAIP3,HEBP2,CYP27B1,AVIL,SERF2,TRIM39,ESR1,CNOT2,TSPAN8,RAB21,CNOT6,RIDA,STK3,ZNF207,PRR16,SNCAIP,PABPC1,MAPK8IP2,PHAX,APOM,ADM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,DXO,CYP21A2,BRD1,CDC42SE2,PNLDC1,PRRT1,PRKN,RNF5,AGER,PPARA,FBLN1,TNFRSF11B,SLC22A4,PNPLA3,PNPLA5,TSPO,GDF9,HSD17B8,FSTL4,DERL1,SMDT1,SYNGAP1,UBE2B,BAK1,CSDC2,WASHC5,MYC,SMAD5,L3MBTL3,KLHL3,MCHR1,KCNK9,AGO2,GRM4,PTK2,HSD17B3,GPR20,PTP4A3,PTCH1,TNRC6B,FANCC,AKR1B1,ATF4,TUT7,SYNGR1,AGTPBP1,PLXNA4,MAPK14,NTRK2,PLA2G6,BAIAP2L2,PICK1,PIM1,CKB,BTBD9,CDC42EP1,RAC2,TMPRSS6,STRIP2,SMO,ZDHHC21,TTC39B,TXN2,HSF1,SLC39A4,MYH9,GUCA1B,ZNF16,RBFOX2,CHRNA3,TEK,LINGO2,LARGE1,CHRNA5,PEX6,FBXO7,LMOD2,ALDH1A1,CRY1,ABHD17B,SRF,ABCB1,BAG1,ADAM22,STEAP2,GABRA1,CLDN12,APBA1,TEC,TXNRD1,OCIAD1,CDK6,USP46,ENPP4,SLC25A27,RFX3,KIT,SLC1A1,CDC37L1,SRD5A3,NCK2,TLN1,TFAP2B,GADD45G,SEMA4D,GAPDH,KIAA1211,S1PR3,PPAT,TMEM14A,PDCL3,WNK2,FGD3,PRDX1,ADH5,EXOSC3,SEMA4C,RPS14,CNNM4,TMOD1,PLEKHH2,ABCG5,ABCG8,CLDN19,ERP44,ISOC2,IL11,BRSK1,PRKCE,SMAP1,TNNI3,EPAS1,RDH13,RIMS1,ABCB5,TMEM30A,SPTBN1,RTN4,PHIP,FPR2,HMGN3,RIMS3,IBTK,PNPT1,RUFY3,ACP4,SHANK1,SLC4A4,CYB5R4,HOXA13,LPAR1,PPT1,PTBP3,ALB,SLC46A2,BMP8A,CRHR2,AQP1,MYH14,BPGM,SLC31A2,MTF1,PLEK,LRRN3,AAK1,EPHA7,NR1H2,WHRN,PTN,ITGB1BP1,DGKI,GRH	grey	VSMC_M10
GO:0019082	0.96	0.10	10	26	viral protein processing	BP	1	CANX,ST6GALNAC2,MOGS,SPCS1,PARP9,MGAT1,MGAT2,GALNT1,ST6GALNAC4,ST3GAL2	grey	VSMC_M10
GO:2001258	0.96	0.09	12	30	negative regulation of cation channel activity	BP	1	KCNRG,KCNE2,PKD2,CASQ2,GNB5,CALM1,FMR1,RRAD,MIR24-1,GPR35,CRBN,GEM	grey	VSMC_M10
GO:0045685	0.96	0.08	23	54	regulation of glial cell differentiation	BP	1	DAAM2,TTBK1,TNFRSF21,PTN,MYCN,HDAC2,KDM4A,NKX6-1,SPINT1,HDAC1,DAG1,DLX1,DUSP10,EPHA4,TNFRSF1B,PRPF19,LDLR,MBD1,DAB1,CNTN2,GPR37L1,NOG,LIF	grey	VSMC_M10
GO:2000178	0.96	0.11	6	17	negative regulation of neural precursor cell proliferation	BP	1	PTN,SIRT2,SPINT2,SPINT1,WNT5A,CEND1	grey	VSMC_M10
GO:0006677	0.96	0.13	4	12	glycosylceramide metabolic process	BP	1	B3GALT1,GALC,GLA,B4GALT3	grey	VSMC_M10
GO:0003044	0.96	0.09	12	30	regulation of systemic arterial blood pressure mediated by a chemical signal	BP	1	ADRA1D,MME,F2RL1,F2R,ENPEP,AGT,ACE2,ECE1,SERPINF2,CYBA,HSD11B2,RHOA	grey	VSMC_M10
GO:0072523	0.96	0.08	18	43	purine-containing compound catabolic process	BP	1	PDE7B,PDE10A,GDA,ENPP4,NT5E,NUDT15,NUDT16,AHCY,AMPD3,ENTPD4,FITM2,NUDT18,PDE9A,PDE8A,PDE4A,MLYCD,NUDT19,HINT1	grey	VSMC_M10
GO:0030518	0.96	0.07	43	96	intracellular steroid hormone receptor signaling pathway	BP	1	ESR1,CNOT2,KDM4C,FOXH1,RBFOX2,CRY1,DNAJA1,PHB,EGLN2,TADA3,TAF7,RNF14,DDRGK1,FOXP1,CALCOCO1,NCOA4,CYP7B1,UFSP2,ZNF366,ARNTL,CNOT1,KMT2D,DDX54,NKX3-1,CRY2,VPS18,HDAC1,GPER1,ARID1A,PADI2,DNAAF4,PARP1,MED1,PAGR1,PIAS2,NCOR1,PPARGC1B,ISL1,RHOXF1,PARK7,RHOA,TRIM68,YWHAH	grey	VSMC_M10
GO:0007405	0.96	0.08	17	42	neuroblast proliferation	BP	1	FRS2,SOX10,SMO,AKNA,PTN,RAB10,NUMBL,FZD3,VEGFC,ZNF335,DISC1,FZD9,KCNA1,DAGLB,DOCK7,FOXG1,ARTN	grey	VSMC_M10
GO:0006779	0.96	0.09	11	28	porphyrin-containing compound biosynthetic process	BP	1	FECH,TSPO,SLC25A38,CPOX,COX15,TMEM14C,ALAS1,ABCB6,COX10,NFE2L1,FXN	grey	VSMC_M10
GO:0033014	0.96	0.09	11	28	tetrapyrrole biosynthetic process	BP	1	FECH,TSPO,SLC25A38,CPOX,COX15,TMEM14C,ALAS1,ABCB6,COX10,NFE2L1,FXN	grey	VSMC_M10
GO:0090504	0.96	0.09	12	31	epiboly	BP	1	CLASP2,MEGF8,HBEGF,FERMT1,ARHGAP24,RREB1,AJUBA,PDCD10,COL5A1,CARMIL2,RHOA,ACVRL1	grey	VSMC_M10
GO:0048871	0.96	0.05	185	378	multicellular organismal homeostasis	BP	1	TNFAIP3,SLC12A2,TNFRSF11B,AKR1B1,ATF4,BTBD9,RAC2,SMO,HSF1,ALDH1A1,SRF,CLDN12,SLC1A1,TFAP2B,GADD45G,KIAA1211,PRDX1,EPAS1,HOXA13,ALB,BMP8A,AQP1,MTF1,NR1H2,WHRN,GRHL1,MET,GRB10,EGFR,USP45,TRIM32,TLR4,NCDN,LPIN1,IL15,UCP1,FGF21,LAMA4,NAPEPLD,SOX9,CUBN,USH1G,ACVR2B,TSKU,ELOVL1,ALK,MKKS,ACTG1,NR1D2,PLCL2,RAC3,ERCC6,TRAF6,TUB,LSR,IL1A,ABHD6,ARNTL,CCDC66,ADGRV1,IL7,P2RX7,JAM2,PTK2B,NR1H3,ALMS1,EBF2,USH1C,HOMER1,F2R,SLC40A1,FTO,SPP1,GCNT2,NOD2,KSR2,ITGB6,ZNF423,PRKAB1,LDB1,PM20D1,LPCAT1,LRRK1,MAP2K6,TRPV4,TCIRG1,GPR137B,CMKLR1,KRAS,FABP4,GIGYF2,UBASH3B,TRPM8,GPR3,KDF1,SFN,PER2,ACTN3,BBS1,NTSR1,PASK,MLXIPL,GRHL3,HOMER2,LAMC1,ADAM8,PTH1R,PBLD,ACADL,CTSH,CDH23,ABCA12,GPR137,SLC11A1,CRTC1,STAT3,VCL,CD38,SLC27A1,ILDR2,LIPA,TFE3,MFAP2,ACADVL,ACTB,YBX2,THRA,CLN8,RBPJ,WNK3,MFN2,ATP1B2,KDM6B,SLC25A44,ALOXE3,ZBTB7B,OGT,ESRRB,PCTP,RAB3D,IL4R,MKS1,SCNN1B,ACACA,TRPV2,CSF1R,PPARGC1B,SGIP1,LEPR,DOCK7,MYO5B,ACOT11,ABAT,INPP5K,TRPV1,ABCA3,PRDM16,ATP6AP1,DEF8,LCN2,UBB,OAS1,DMD,BSCL2,FABP5,SLC22A5,CA2,NANOS1,JCHAIN,ELOVL3,BGLAP,PEMT,SNX10,NOVA1,CLDN1,INAVA,PLAC8,DDIT3,DRAM2,PTGES,APC,CEBPB,BBS10,MRAP2,DIO2	grey	VSMC_M10
GO:2000042	0.96	0.11	6	17	negative regulation of double-strand break repair via homologous recombination	BP	1	HELB,FBH1,SHLD1,SHLD2,SMCHD1,RMI2	grey	VSMC_M10
GO:0048641	0.96	0.11	6	17	regulation of skeletal muscle tissue development	BP	1	LMOD3,MEF2C,IGF2,USP19,ACTN3,YBX3	grey	VSMC_M10

GO:0010720	0.96	0.06	110	231	positive regulation of cell development	BP	1	LRP1,RAB21,SNW1,TIAM2,IL5,TSPO,TRIB1,PLXNA4,NTRK2,SOX10,SMO,SRF,TTBK1,RFX3,KIT,SEMA4D,RUFY3,PTN,EGFR,TRIM32,PLXNA1,HDAC2,GOLGA4,MEGF8,UNC13D,XRCC2,NUMBL,SS18L2,SIRT2,RAC3,ARHGEF7,PLXNC1,LMOD3,PRKDC,PLAG1,RET,ANKRD27,FAIM,ROBO1,ROBO2,FZD3,VEGFC,CUX2,MME,TIAM1,DOCK5,SYNJ1,OPA1,NKX6-1,ZFYVE27,SPINT1,RREB1,ITPKA,CYFIP1,DMTN,ZNF335,BDNF,NEURL1,DNM1L,CARMIL1,HDAC1,CAPRIN2,SLC9B2,DAG1,ADNP,DISC1,GPER1,CASS4,CIB1,ACTN3,SS18L1,CDKL5,DOCK1,CSPG5,WNT3,MAPT,FN1,XRCC5,NIN,OBSL1,HAP1,EPHA4,SPEN,TNFRSF1B,RGS14,PRPF19,NDEL1,RAB11A,MAP2K1,NTN1,GPR68,DNM2,PARP6,GPRASP2,BHLHB9,TRPV2,LRP8,CRK,L1CAM,ATP6AP1,PLXNA3,SOX8,AMIGO1,FBXO31,MIR222,MIR125B1,FGA,FOXG1,LIF,WNT2	grey	VSMC_M10
GO:0002566	0.96	0.13	4	12	somatic diversification of immune receptors via somatic mutation	BP	1	MSH2,MLH1,POLL,PMS2	grey	VSMC_M10
GO:0006897	0.96	0.05	218	444	endocytosis	BP	1	ATP9B,NME1,NEDD4L,LRP1,REPS1,CANX,RAB21,MARCH3,SYNJ2,IGF2R,AGER,CSNK1E,PICK1,MICALL1,BTBD9,RAC2,MYH9,STEAP2,OCIAD1,USP46,SMAP1,FPR2,PPT1,CXCL8,EHBP1,FKBP15,RSPO1,AAK1,NR1H2,AMPH,SFRP4,SDCBP,WASF1,EPS15,ARHGAP12,MTMR2,RAB7A,AP2S1,CUBN,APOC1,RIN2,ACKR2,LRP1B,ARRB1,TGFBR2,NEU3,SNX5,AP3M2,FCHSD2,RINL,ACTG1,SYT1,RAB5A,HEATR5B,DNAJC13,NCKAP1L,TUB,ATP6V1H,PIK3CB,HIP1R,MTMR9,XKR6,FCHO2,SCARA3,WDR54,LMBR1L,DPYSL2,NR1H3,BMP2K,SYNJ1,TPCN1,LOXL2,RHOBTB2,BIN3,F2RL1,LOXL4,ANO6,PLA2R1,SYT8,MAPKAPK3,DNM1L,CARMIL1,ANKRD13A,PPP3CA,SLC9B2,NLGN4Y,DENND1B,MAPKAPK2,EGF,ANKRD13D,GRK2,SORL1,ANK2,SAG,DGKD,PGBD1,SH3BP4,CBL,RAB22A,WASF2,RAB4A,RAB17,AP2M1,PRSS12,STX1A,RUBCN,REPS2,RIN1,IL10RA,FCER1G,RHOBTB1,DOCK1,SH3GL3,CALY,OLR1,MIA3,RUFY2,PIKFYVE,PRG4,TMPRSS5,ABL2,NECAP1,CD163,EHD1,ITGA4,RABGAP1L,LRPAP1,CXCR2,GRK4,CLTCL1,CALCRL,HSPG2,DNM3,PPP3CB,RAMP2,ANKFY1,AP3M1,MAPK1,RAB5C,EPS15L1,RHOJ,CXCL16,NECAP2,DLG4,ACTB,SLC2A4,NLGN2,PDLIM7,PEAR1,ANXA2,SPON2,DGKQ,GAK,STX1B,NEURL1B,ITGAM,SYT11,SNX12,DOCK2,NLGN3,SNX1,CSNK1G1,EPN3,MAPK3,APOBR,AC138894.1,HOOK2,CALM1,LDLR,DNM2,RIT2,HHIPL1,SCAMP5,PSTPIP1,SYNRG,INSR,NPC1,MIB1,AP2B1,COLEC12,CD320,SGIP1,GHR,TRIP10,C3,RALBP1,UNC119,GPC3,FMR1,LRP8,PIP5K1C,SRL,ABCA7,CEL,GPR107,USP20,FNBP1L,BTBD8,GAPVD1,AP1G1,DENND1A,CAP1,MIR199A1,MIR27B,MIR27A,HAVCR1,CNTN2,SNX10,WNT5A,LDLRAP1,CACNG7,GRB2,HRAS,RHOU,CACNG5,CBLL1,XKR8,LRRTM2	grey	VSMC_M10
GO:0007435	0.96	0.09	10	26	salivary gland morphogenesis	BP	1	PLXNA1,SEMA3A,NKX3-1,TGFB2,DAG1,LAMA5,BTBD7,LAMA1,TWSG1,ESRP2	grey	VSMC_M10
GO:0042177	0.96	0.07	46	101	negative regulation of protein catabolic process	BP	1	AGAP2,TRIM39,RGP1,PDCL3,EGFR,SDCBP,PHB,AQP11,TIMP4,MYCBP2,KLHL40,SIRT2,NRG1,DDRGK1,RYBP,PSMF1,TAF9,USP25,CSNK2A2,FAM192A,MARCH7,SUFU,AZIN2,RPL23,USP19,DEDD,RPL11,LRIG2,ATP13A2,EPHA4,ANXA2,PSEN1,SNX12,EFNA1,TAF1,OGT,SMAD3,NOS2,RILP,SGTA,PARK7,BANP,DAB2IP,CAMLG,STYX,MAP1A	grey	VSMC_M10
GO:0002862	0.96	0.11	6	17	negative regulation of inflammatory response to antigenic stimulus	BP	1	MAPK14,PLK2,HCK,NOD2,FGR,YES1	grey	VSMC_M10
GO:0120255	0.96	0.11	6	17	olefinic compound biosynthetic process	BP	1	HSD17B3,DKKL1,DKK3,WNT4,DGKQ,CACNA1H	grey	VSMC_M10
GO:0048146	0.96	0.08	17	41	positive regulation of fibroblast proliferation	BP	1	ESR1,MYC,CDK6,AQP1,BMI1,GAS6,PRKDC,AGT,FN1,ANXA2,NGFR,CTC1,CD74,WNT5A,EREG,WNT2,PDGFD	grey	VSMC_M10
GO:0043403	0.96	0.09	11	28	skeletal muscle tissue regeneration	BP	1	LARGE1,AKIRIN1,KLF5,TGFBR2,BIN3,PPP3CA,DAG1,FZD7,MYOZ1,ENO3,SOX15	grey	VSMC_M10
GO:0006879	0.96	0.07	24	56	cellular iron ion homeostasis	BP	1	MYC,TMPRSS6,STEAP2,HEPHL1,HPX,NCOA4,SLC40A1,ISCU,HJV,SLC11A1,ABCB6,ATP13A2,FTH1,CYB561A3,NOX5,TMEM199,SLC46A1,NUBP1,ATP6AP1,FRRS1,LCN2,SLC22A17,FXN,FTL	grey	VSMC_M10
GO:0071539	0.96	0.09	12	31	protein localization to centrosome	BP	1	MAPRE1,PIBF1,HOOK3,NSFL1C,CEP250,MCPH1,DISC1,CEP192,SNX10,C2CD3,APC,PARD6A	grey	VSMC_M10
GO:0106027	0.96	0.07	34	78	neuron projection organization	BP	1	PICK1,ABHD17B,SHANK1,VPS35,MTMR2,ATP1A3,PRNP,EPHB1,PLS1,CUX2,TIAM1,HOMER1,OPA1,ITPKA,DOCK10,DNM1L,CAPRIN2,CFL1,EPHB3,TANC2,DNM3,EPHA4,DLG4,PSEN1,ITGA3,EFNA1,ZDHHC15,GPRASP2,BHLHB9,ARHGAP44,INSR,CDK5R1,LRP8,MAP1A	grey	VSMC_M10
GO:0055076	0.96	0.06	49	107	transition metal ion homeostasis	BP	1	SLC39A5,PRKN,MYC,BTBD9,TMPRSS6,SLC39A4,STEAP2,SLC1A1,EPAS1,SLC31A2,HEPHL1,ATP7B,SLC39A12,STEAP3,PRNP,HPX,NCOA4,SLC39A13,SLC25A37,AP3B1,SLC40A1,CUTC,LCK,BDH2,SLC30A10,ISCU,HJV,MELTF,SLC30A4,SLC11A1,ABCB6,ATP13A2,FTH1,CYB561A3,NOX5,S100A8,SLC39A6,TMEM199,SLC46A1,NUBP1,ATP6AP1,SLC30A7,FRRS1,LCN2,MT1X,SLC22A17,FXN,FTL,SCO1	grey	VSMC_M10

GO:0034654	0.96	0.05	1473	2841	nucleobase-containing compound biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,SMARCC2,ATP8B1,ONECUT2,BAZ2A,TCF4,POLI,TBPL1,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ATP5MGL,HELB,ZBTB2,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,CNOT6,STK3,OSR2,SNW1,TFB1M,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,MAP3K4,PPT2,PRKN,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,MAPK15,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,SLC35B2,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,UXS1,NCK2,FHL2,TGFBRAP1,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PPAT,REV1,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,SIX2,PPCS,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,ME1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,NT5E,ZNF483,JAZF1,PPT1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,TRAF1,BCL2L12,SCAF1,LPIN1,SF	grey	VSMC_M10
GO:0051926	0.96	0.08	16	39	negative regulation of calcium ion transport	BP	1	TMBIM6,STC1,PKD2,CASQ2,ADRA2A,ATP1A2,C4orf3,NTSR1,SESTD1,GNB5,CALM1,FMR1,INPP5K,RRAD,GPR35,GEM	grey	VSMC_M10
GO:0006582	0.96	0.11	6	17	melanin metabolic process	BP	1	SLC7A11,RAPGEF2,OCA2,CITED1,SLC45A2,WNT5A	grey	VSMC_M10
GO:0009887	0.96	0.05	392	784	animal organ morphogenesis	BP	1	ONECUT2,SEMA6A,GLI1,TNFAIP3,ADGRG6,ESR1,FRS2,OSR2,FZD6,PPARA,TNFRSF11B,BAK1,RSPO3,MYC,KLHL3,LEMD2,PTK2,PTCH1,FANCC,LY6E,EXOC4,ATF4,TAB1,AGTPBP1,MAPK14,NTRK2,PIM1,SMO,MDFI,FOXH1,TEK,RORB,ZFAND5,PTK7,SRF,SLC1A1,FHL2,TFAP2B,ROR2,DLX5,CNNM4,TDRD7,SOSTDC1,RAB23,SIX2,COL9A1,TNNI3,RDH13,DNAH11,RTN4,KCNQ4,KLK4,ACP4,HOXA2,HOXA4,HOXA6,HOXA7,HOXA13,AREG,AQP1,COL27A1,WHRN,TGFA,PTN,TNC,TSPAN12,FUZ,SFRP4,TEAD2,MYCN,SOBP,OSR1,FOXO3,NTF4,FGF21,BRAF,INTU,SPRY1,PLXNA1,FOXE3,HDAC2,BBS7,BMI1,MYO3A,SETDB2,SOX9,SLC4A2,USH1G,GLI2,MEGF8,IFT172,FOXJ1,SCN5A,WDR48,MYO7A,CSRNP1,GZF1,POU4F1,TSKU,WDR60,SPRY2,WNT11,DZANK1,TGFBR2,OVOL2,ACVR2A,RELT,JAG1,MKKS,RARB,FSCN2,RYR1,ALX1,CEP290,DCN,SPEF1,SEMA3A,NRG1,STX2,RYK,TRAF6,TCF15,EPHB1,PLAG1,ASXL1,CYP7B1,PAX8,HAND2,EYA1,PARVA,PLS1,ROBO1,ROBO2,TENM3,FBXW7,FMN1,FZD3,MEF2C,IL7,VEGFC,ADAMTS1,SOX6,FRAS1,ACTG2,NPY1R,TIAM1,FGF5,SLIT1,USH1C,VDR,STC1,NKX3-1,NKX6-1,TBX5,AP3B1,SRSF6,IFT52,TNNC1,COL4A3BP,RPGRIP1L,DSP,PKD2,TFAP2A,PAX2,SALL1,VANGL1,PRICKLE1,NKD1,ITGB6,ZNF335,RYR2,IGF2,BMPR1B,SUFU,SLC4A10,NECTIN3,IRX2,PKP2,HDAC1,HYAL1,ELF3,ALDH1A3,TNNI1,TRPV4,PDCD4,TGFB2,SULF2,TRIP11,SATB2,TCIRG1,FAM20A,ADARB1,NR5A2,FAM20C,PRKX,DAG1,AXIN2,LHX9,HLX,SHROOM2,KRAS,SNAI1,AMELX,MYH7,JHY,NRL,LAMB3,ZNRF3,AGT,FGR,GBX2,DVL3,ACTC1,FZD7,RPS6KA1,TREH,MYO3B,ACTN3,HTRA1,LAMA5,DLX1,GRHL3,SP3,STRC,EFEMP2,LAMC1,DLG1,SETD	grey	VSMC_M10
GO:0007178	0.96	0.05	130	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SLC39A5,ONECUT2,LRP1,USP15,SNW1,PPARA,GDF9,SMAD5,LEMD2,PTK2,ZC3H3,TAB1,MAPK14,KCP,FOXH1,TGFBRAP1,TFAP2B,ROR2,DLX5,SOSTDC1,CD109,SPTBN1,HOXA13,BMP8A,BMPER,SFRP4,SDCBP,SPRY1,MEGF8,ACVR2B,UBE2O,SPRY2,EID2,TGFBR2,OVOL2,ACVR2A,FERMT1,SPRED3,SPART,RBPMS,AMHR2,ACVR1B,SNX25,LPXN,DKK3,ING2,HPGD,IL17RD,SLC33A1,VEPH1,ACVR1C,GCNT2,HIVEP1,ITGB6,ZNF423,BMPR1B,FBXL15,PXN,KIAA0319,SLC2A10,PDCD4,TGFB2,HJV,SORL1,ITGB5,HTRA1,CHRD,DLX1,SNX6,CREB1,CTDSPL2,PBLD,MEN1,PPM1L,HTRA3,FBN1,FKBP8,COL3A1,GDF15,STAT3,AKAP3,PPM1A,GREM2,INHA,BMPR1A,PARP1,MPP5,RBPJ,RNF111,TGFB1I1,ITGA3,FOS,RBPMS2,MAPK3,CILP,TOB1,CITED1,SH2B1,WFIKKN2,TMEM100,SMAD3,RNF165,DNM2,CHRDL1,FAM83G,NLK,TWSG1,GPC3,JUN,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,MIR21,FSTL3,LEMD3,ACVRL1,NOG,WNT5A,NCEH1,NRROS,TGIF2,DUSP22,LDLRAD4,RGMB,UBE2D1,PEG10	grey	VSMC_M10
GO:0006098	0.96	0.13	4	12	pentose-phosphate shunt	BP	1	RBKS,RPE,TIGAR,RPIA	grey	VSMC_M10
GO:0050817	0.96	0.06	78	166	coagulation	BP	1	SERPINB2,TSPAN8,MPIG6B,FZD6,FBLN1,MAPK14,MYH9,SRF,TEC,ENPP4,TLN1,PLEK,DGKI,TLR4,SLC7A11,HS3ST5,THBD,PLAT,MYL12A,C1QTNF1,ACTG1,CLIC1,GAS6,ADRA2B,PIK3CB,P2RY1,HPS5,AP3B1,F2RL1,F2R,ANO6,DMTN,ADTRP,DTNBP1,CD40,FAP,LCK,ADRA2A,ITPK1,PRSS56,UBASH3B,HPS4,DGKD,USF1,PAFAH2,FCER1G,DGKG,NFE2L2,BLOC1S6,PLA2G4A,ITGA2B,FN1,PTPN6,SERPINC1,ADRA2C,FERMT3,HGFAC,COL3A1,VCL,WAS,ACTB,ANXA8,F12,PEAR1,ANXA2,DGKQ,PSEN1,DGKE,VAV1,ABAT,SERPINF2,P2RX1,ADAMTS13,VAV3,STXBP1,FGA,BLOC1S3,RAP2B	grey	VSMC_M10
GO:0014065	0.96	0.06	50	111	phosphatidylinositol 3-kinase signaling	BP	1	ERBB3,RGL2,PTK2,NTRK2,TEK,KIT,ROR2,SEMA4D,CAT,EGFR,SOX9,FBXL2,SIRT2,DCN,FLT1,PIK3CB,PREX2,PIK3R1,RASGRP1,NKX3-1,F2RL1,F2R,IRS1,TGFB2,NCF1,EGF,HCLS1,GPER1,AGT,FGR,CBL,OSM,CD28,PIK3IP1,FN1,NYAP1,PTPN6,PEAR1,HAX1,PIK3R5,INSR,CCL5,PIP5K1C,DAB2IP,MIR21,ENTPD5,STAMBP,C3orf58,HCST,PDGFD	grey	VSMC_M10

GO:0050728	0.96	0.06	41	91	negative regulation of inflammatory response	BP	1	TNFAIP3,ENPP3,PPARA,MAPK14,TEK,FPR2,NT5E,VPS35,CST7,FNDC4,NR1D2,MFHAS1,NR1H4,PLK2,HCK,NR1H3,OTULIN,NOD2,CD200,GPER1,SLAMF8,FGR,NLRX1,DUSP10,LPCAT3,CALCRL,FOXP3,GPS2,TNFRSF1B,SYT11,SMAD3,LDLR,MAPK7,YES1,ISL1,PTGER4,PTPN2,FOXF1,MIR199A1,MIR222,C5orf30	grey	VSMC_M10
GO:0043277	0.96	0.08	15	37	apoptotic cell clearance	BP	1	LRP1,RAC2,CD300LF,GAS6,XKR6,NR1H3,RHOBTB2,TXNDC5,RHOBTB1,SPG11,PEAR1,CCL2,C3,ABCA7,XKR8	grey	VSMC_M10
GO:0032469	0.96	0.09	9	24	endoplasmic reticulum calcium ion homeostasis	BP	1	BAK1,TMTC4,TMBIM6,RAP1GDS1,TMCO1,FIS1,PSEN1,ATP2A1,BCAP31	grey	VSMC_M10
GO:0007252	0.96	0.11	6	17	I-kappaB phosphorylation	BP	1	TLR4,IKBKB,DDRGK1,TRAF2,DAB2IP,MIR27B	grey	VSMC_M10
GO:0000423	0.96	0.09	9	24	mitophagy	BP	1	PRKN,OPTN,HTRA2,USP30,PINK1,VPS13D,MFN2,VPS13C,TIGAR	grey	VSMC_M10
GO:0006517	0.96	0.09	9	24	protein deglycosylation	BP	1	RNF5,UGGT2,AGA,AMFR,MAN1C1,RNF185,EDEM3,SYVN1,PARK7	grey	VSMC_M10
GO:0002067	0.96	0.08	14	35	glandular epithelial cell differentiation	BP	1	SMO,CDK6,RFX3,RARB,ARNTL,NKX6-1,ZBED6,SIDT2,MEN1,WNT4,GATA6,PDPK1,WDR77,WNT5A	grey	VSMC_M10
GO:0016570	0.96	0.05	195	399	histone modification	BP	1	BAZ2A,EYA4,USP15,YEATS4,SNW1,BRD1,SKP1,PHF1,UBE2B,KDM3B,C6orf89,KDM4C,USP49,PRDM4,SUPT3H,PHF14,KANSL3,RNF20,ING3,ATG5,SETD7,SPHK2,KDM7A,HDAC2,BMI1,PRKD2,SETDB2,PHB,HDAC11,EED,IWS1,SUV39H2,KDM4A,PAXIP1,UBE2E1,TADA3,ARRB1,USP36,SIRT2,DPY30,SIRT7,CHTOP,NSD3,NEK11,TAF7,ASH2L,EP400,RYBP,SIRT3,TAF10,MTA3,NR1H4,ATXN7,SDR16C5,ASXL1,DNMT3B,SMYD1,HPF1,TAF9,ING2,EYA1,PHF20,SETD6,USP16,KMT2D,DDB2,KANSL2,HDAC7,RTF1,WDR82,ZNF335,JARID2,SUDS3,RBBP5,LDB1,IGF2,ELK4,DCAF1,PCGF6,HDAC1,AUTS2,SART3,MST1,EYA3,DTX3L,RCOR3,PER2,HDAC4,MRGBP,USP21,RNF168,ING5,BAZ1B,SETD2,MBIP,TET1,PHC1,BCL6,BCOR,MEN1,WDR61,ENY2,ATXN7L3,TADA2B,NAA40,ING4,RCOR2,NELFA,PINK1,TBL1XR1,TADA1,LEO1,KDM5A,PADI2,DYDC1,FOXP3,AKAP8L,AKAP8,KDM5C,MSL1,MED24,DDB1,PRDM2,PHF8,NSD1,UIMC1,EPOP,SETD1A,PCGF3,KDM6B,RIOX1,KAT7,PAGR1,MUC1,JDP2,TAF1,MAPK3,ZBTB7B,OGT,NAP1L2,CRTC2,KDM8,RPS6KA5,TRIM37,SFPQ,OTUB2,PRKCB,SETD3,SIN3A,RCOR1,SREBF1,ISL1,SUZ12,CUL4B,SUPT6H,CXXC1,FMR1,GLYR1,CREBBP,NAA60,SKI,DOT1L,HCFC1,MECP2,PRDM16,CHD5,PARK7,MIER2,GTF3C4,MTF2,GFI1,PRMT7,CTCF,HSF4,PRMT6,AURKC,SETDB1,PRDM6,ARID4A,TAF12,CPA4,SAP30BP,BEND3,SMYD3,SUPT7L,RNF8,ZNF304,NNMT,UBE2N,UBE2U,LIF,N6AMT1,BRCC3,RPS6KA4,CBX8	grey	VSMC_M10
GO:0071786	0.96	0.11	6	17	endoplasmic reticulum tubular network organization	BP	1	RTN4,RAB10,ATL2,ZFYVE27,ATL1,ARL6IP1	grey	VSMC_M10
GO:0050921	0.96	0.06	50	109	positive regulation of chemotaxis	BP	1	AGER,GPSM3,PTK2,RAC2,CCL27,FPR2,CXCL8,AKIRIN1,PTN,MET,C5AR1,PRKD2,MEGF8,OXSR1,NCKAP1L,GAS6,VEGFC,PTK2B,TIAM1,F2RL1,ANO6,DNM1L,TRPV4,PRSS56,CMKLR1,MOSPD2,IL16,IL12A,MCU,TNFSF18,CXCR2,MAPK1,TMEM102,STX4,FGF18,PGF,DAPK2,MAPK3,IL6R,SMAD3,S100A14,CD74,CCL5,CSF1R,CCL7,DEFB124,ZNF580,WNT5A,ARTN,PDGFD	grey	VSMC_M10
GO:0070168	0.96	0.10	8	22	negative regulation of biomineral tissue development	BP	1	TRPM4,SOX9,GAS6,PTK2B,SRGN,BCOR,RFLNB,HEY2	grey	VSMC_M10
GO:0110150	0.96	0.10	8	22	negative regulation of biomineralization	BP	1	TRPM4,SOX9,GAS6,PTK2B,SRGN,BCOR,RFLNB,HEY2	grey	VSMC_M10
GO:0051962	0.96	0.05	102	216	positive regulation of nervous system development	BP	1	LRP1,RAB21,SNW1,TIAM2,TSPO,PLXNA4,NTRK2,SOX10,SMO,LINGO2,SRF,TTBK1,KIT,SEMA4D,RUFY3,LRRN3,PTN,EGFR,TRIM32,PLXNA1,HDAC2,VSTM5,GOLGA4,MEGF8,XRCC2,NUMBL,SS18L2,PLXNC1,EPHB1,PLAG1,ANKRD27,FAIM,CLSTN2,ROBO1,ROBO2,FZD3,VEGFC,CUX2,MME,TIAM1,SYNJ1,OPA1,NKX6-1,AMIGO2,ZFYVE27,SPINT1,ITPKA,CYFIP1,ZNF335,BDNF,NEURL1,DNM1L,HDAC1,CAPRIN2,DAG1,AMIGO3,ADNP,DISC1,GPER1,SS18L1,CDKL5,EPHB3,WNT3,MAPT,FN1,XRCC5,NIN,OBSL1,HAP1,EPHA4,LRTM2,SPEN,NLGN2,TNFRSF1B,RGS14,PRPF19,SEMA4A,NLGN3,NDEL1,RAB11A,MAP2K1,NTN1,PARP6,GPRASP2,BHLHB9,TRPV2,ASIC2,SLITRK2,LRP8,L1CAM,PLXNA3,SOX8,AMIGO1,FBXO31,ADGRL2,MIR222,MIR125B1,FOXG1,GRID2,LIF,WNT2,LRRTM2	grey	VSMC_M10
GO:0034284	0.96	0.06	77	164	response to monosaccharide	BP	1	ZNF236,NME1,LRP1,APOM,AGER,PLA2G6,TXN2,SRF,CAT,PRKCE,HMGN3,TRPM4,FOXO3,FGF21,GIPR,KHK,EIF2B3,GRIK5,RAF1,GCKR,TGFBR2,GAS6,NR1H4,CYP7A1,NDUFAF2,OSBP,CASP3,PTK2B,KCNJ11,TIAM1,RAB11FIP5,OPA1,NKX6-1,ACVR1C,ZBED6,PAX2,TWNK,GPLD1,PPP3CA,SLC9B2,ZBTB20,ADRA2A,GPAM,TCF7L2,KCNB1,PFKFB2,POLG,GPER1,RAB11FIP2,MLXIPL,GLUL,SIDT2,CDKN1B,PDK3,KLF7,FIS1,MEN1,ENY2,ABCA12,PPP3CB,CTSV,PTPRN,NDUFA9,MPC2,ILDR2,STX4,PKLR,GPR68,SIN3A,SREBF1,OXCT1,NADK,BAIAP3,CYBA,RHOA,SOX4,CRH	grey	VSMC_M10
GO:0070192	0.96	0.07	23	54	chromosome organization involved in meiotic cell cycle	BP	1	UBE2B,DMC1,CCDC155,MLH1,CCNB1IP1,SIRT7,TEX15,SYCP1,CCDC36,SPO11,HORMAD2,TEX12,MAJIN,ZCWPW1,STAG3,P3H4,SYCE2,RAD51C,MEIOB,MSH4,RNF212B,AGO4,SYCE1L	grey	VSMC_M10
GO:0061001	0.96	0.08	17	42	regulation of dendritic spine morphogenesis	BP	1	CUX2,TIAM1,OPA1,ITPKA,DNM1L,CAPRIN2,CFL1,TANC2,DNM3,EPHA4,EFNA1,ZDHHC15,GPRASP2,BHLHB9,ARHGAP44,CDK5R1,LRP8	grey	VSMC_M10
GO:0097421	0.96	0.09	11	28	liver regeneration	BP	1	GLI1,PTCH1,PNPT1,EGFR,CSNK2A2,CCND1,CPT1A,SULF2,RPL19,CLDN1,CEBPB	grey	VSMC_M10
GO:0006743	0.96	0.10	7	19	ubiquinone metabolic process	BP	1	COQ2,COQ5,COQ10B,NDUFA9,COQ8A,COQ4,PDSS2	grey	VSMC_M10
GO:0006783	0.96	0.09	10	26	heme biosynthetic process	BP	1	FECH,TSPO,SLC25A38,CPOX,COX15,TMEM14C,ALAS1,COX10,NFE2L1,FXN	grey	VSMC_M10

GO:0048598	0.96	0.05	230	469	embryonic morphogenesis	BP	1	ITGA7,GLI1,FRS2,STK3,OSR2,FZD6,BRD2,TBC1D32,PITX1,RSPO3,PTCH1,EXOC4,SMO,MDFI,FOXH1,PTK7,SRF,TXNRD1,C2orf49,ROR2,DLX5,SEMA4C,SIX2,KCNQ4,HOXA2,HOXA4,HOXA6,HOXA7,HOXA13,WHRN,FUZ,GJB5,TEAD2,MYCN,SOBP,OSR1,DLD,INTU,HDAC2,BBS7,BMI1,MYO3A,SETDB2,SOX9,CLASP2,USH1G,GLI2,MEGF8,PCDH8,IFT172,MYO7A,LMBR1,WDR60,SPRY2,WNT11,TGFBR2,OVOL2,ACVR2A,EOMES,MKKS,RARB,SPINT2,ALX1,FREM2,CEP290,FLT1,TRAF6,RET,GPI,PAX8,CASP3,HAND2,EYA1,PLS1,MAB21L2,FAM208A,FZD3,MEF2C,VEGFC,TLX2,MMP15,FRAS1,USH1C,OPA1,TBX5,IFT52,SPINT1,RPGRIP1L,RTF1,PKD2,STK4,TFAP2A,PAX2,SALL1,PRICKLE1,FBXW4,LDB1,RYR2,IGF2,SUFU,IRX2,CDON,HDAC1,HYAL1,ALDH1A3,TGFB2,POGLUT1,SATB2,PRKAR1A,DAG1,HLX,SNAI1,SOX2,YTHDF2,LAMB3,GBX2,DVL3,KDF1,COL7A1,FZD7,ITGB5,MYO3B,PHLDB1,LAMA5,SYF2,GRHL3,SP3,STRC,SP9,DLG1,LUZP1,SETD2,WNT3,HOXD4,HOXD3,FZD5,STOX1,PRKRA,ITGA4,FN1,FBN1,WNT4,COL5A2,ECE1,TBX19,NKX3-2,MAPK1,TULP3,LEO1,GREM2,MFAP2,LIAS,DVL2,BMPR1A,WDR19,TCAP,MED1,ALDH1A2,MSX2,PSEN1,KDM6B,HOXB5,HOXB6,HOXB8,HOXB9,TGFB1I1,ITGA3,TMEM107,EFNA1,RBPMS2,MAPK3,POU3F4,SMAD3,NTN1,MAP2K5,MKS1,GSC,TBX4,TBX2,LHX1,STRA6,LAMA3,MAPK7,AMOT,GATA6,MIB1,JAG2,TWSG1,GPC3,CREBBP,SKI,RNF207,SOX8,ALX3,COL5A1,TSC1,FOXF1,TMEM231,ENG,GLMN,BCL10,DUSP2,CHRNA10,VASP,FOXG1,SOX4,MAFB,LAMB1,HOXB3,POFUT2,NOG,LBX1,WNT5A,LBX2,OTX1,SIX1,DUSP1,C2CD3,DUSP4,GRB2,BCL2L11,TGIF2,YBX1,INSIG2,RALA,SLC39A3,NKX2-5,WNT2,HOXA3,ZIC1	grey	VSMC_M10
GO:0035456	0.96	0.10	7	19	response to interferon-beta	BP	1	PNPT1,TMEM173,HTRA2,OAS1,IRGM,XAF1,UBE2G2	grey	VSMC_M10
GO:0098534	0.96	0.08	16	40	centriole assembly	BP	1	VPS4B,MDM1,CHMP2A,CDK5RAP2,CCDC61,CEP295NL,CEP63,PLK2,CEP44,ALMS1,AC112128.1,CEP152,CNTROB,TRIM37,CEP192,C2CD3	grey	VSMC_M10
GO:0048667	0.96	0.05	217	446	cell morphogenesis involved in neuron differentiation	BP	1	NEDD4L,LRP1,SEMA6A,KIF5A,RAB21,MAPK8IP2,TIAM2,SULT4A1,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,RAC2,SMO,RBFOX2,CHRNA3,SRF,SEMA4D,DLX5,ETV1,SEMA4C,BRSK1,RTN4,RUFY3,SHANK1,HOXA2,EPHA7,WHRN,PTN,HECW1,EPHA1,KEL,NRCAM,PLXNA1,RAB10,ABI1,GOLGA4,GLI2,MEGF8,MYO7A,MYCBP2,NUMBL,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,FARP1,KIF5C,TMEM106B,FEZ2,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,ULK1,RYK,EPHB1,RET,TTL,ANKRD27,PREX2,PLS1,ROBO1,ROBO2,FZD3,MEF2C,SEMA4F,TLX2,CUX2,RAPGEF2,DPYSL2,TIAM1,SLIT1,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,C8orf37,SEMA3G,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,SEMA4G,DTNBP1,SIAH1,LZTS1,BMPR1B,BDNF,DOCK10,KIAA0319,LGR6,DNM1L,PPP3CA,HECW2,CAPRIN2,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,CFL1,ADNP,DISC1,GBX2,KALRN,NFATC4,SS18L1,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,TANC2,STRC,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,SEMA6D,EPHB4,ITGA4,TNR,FN1,ATL1,NIN,DNM3,PPP3CB,RAB3A,MARK2,VCL,OBSL1,MINK1,RAB8A,CRMP1,EPHA4,LRTM2,DLG4,ACTB,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,NTN1,RPS6KA5,RNF165,DNM2,PARP6,GPRASP2,BHLHB9,BCL11B,LHX1,ARHGAP44,SIN3A,TRPV2,LAMA3,CDK5R1,ISL1,EMB,LAMA1,DOCK7,SLC9A6,DAB1,SLITRK2,LRP8,L1CAM,NTN3,ARHGAP4,PLXNA3,BSG,TUBB3,AMIGO1,CELSR2,NTNG2,FBXO31,STXBP1,BARHL2,DPYSL5,EFNA4,CNTN2,VASP,FOXG1,ISL2,NOG,THY1,WNT5A,POU3F2,CHN1,ARTN,NRXN3,LYPLA2,BTBD3,YWHAH,EFNB3,ISPD,MAP1A,OLFM1	grey	VSMC_M10
GO:0002040	0.96	0.06	52	114	sprouting angiogenesis	BP	1	SEMA6A,RSPO3,TEK,CEMIP2,SRF,MEOX2,BMPER,ITGB1BP1,SLC39A12,PLK2,NR4A1,PIK3CB,PARVA,ROBO1,FBXW7,VEGFC,PTK2B,OTULIN,HDAC7,LOXL2,ADTRP,GPLD1,CIB1,MAP3K3,GLUL,E2F2,MIA3,EPHB4,IL12A,PDCD10,RAMP2,RHOJ,SYNJ2BP,NAXE,NGFR,PGF,MAP2K5,ESM1,JAK1,PDPK1,MIR199A1,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,ACVRL1,MIR125A,FGF1	grey	VSMC_M10
GO:0043281	0.96	0.06	72	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	TNFAIP8,MAP3K5,GRAMD4,BAK1,MYC,HSF1,SLC1A1,NOD1,AQP1,CASP8AP2,EPHA7,TNFSF15,BCL2L12,HSPE1,RAF1,PRDX3,ARRB1,GAS6,ARL6IP5,ST18,GPI,NR4A1,FOXL2,HIP1R,ROBO1,DIABLO,HTRA2,SENP1,NKX3-1,ACVR1C,F2R,PIDD1,PAX2,LCK,PDCD6,SOX2,GPER1,IFI6,SFN,RPS6KA1,EGLN3,MGMT,POR,MAPT,FIS1,CTSH,DDX3X,MUL1,BIRC3,ARL6IP1,BCL2L13,NGFR,SMAD3,MAP2K5,S100A8,NLE1,BCAP31,P2RX1,PARK7,LAMTOR5,BCL10,MIR27B,RHOA,RPS27L,NOL3,CASP8,ACER2,SERPINB9,BCL2L11,CAAP1,PRR7,CRADD	grey	VSMC_M10
GO:0044331	0.96	0.09	8	22	cell-cell adhesion mediated by cadherin	BP	1	EPCAM,FER,DENND6A,CTNND1,PLEKHA7,SERPINF2,WNT5A,RGCC	grey	VSMC_M10
GO:0032785	0.96	0.11	6	17	negative regulation of DNA-templated transcription, elongation	BP	1	POU4F1,EAPP,RNF168,NELFA,RF00100,RNF8	grey	VSMC_M10

GO:0000904	0.96	0.05	276	562	cell morphogenesis involved in differentiation	BP	1	NEDD4L,LRP1,SEMA6A,KIF5A,RAB21,MAPK8IP2,TIAM2,MPIG6B,FBLN1,PARVG,SULT4A1,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,ATF4,PLXNA4,NTRK2,RAC2,SMO,MYH9,RBFOX2,CHRNA3,TEK,SRF,SEMA4D,DLX5,ETV1,SEMA4C,BRSK1,RTN4,RUFY3,SHANK1,HOXA2,HOXA13,EPHA7,WHRN,PTN,ITGB1BP1,MET,HECW1,EPHA1,BVES,KEL,NRCAM,PLXNA1,RAB10,ABI1,GOLGA4,GLI2,MEGF8,UNC13D,MYO7A,MYCBP2,NUMBL,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,FARP1,KIF5C,TMEM106B,FEZ2,RAC3,SPINT2,ARHGEF7,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,ULK1,PRKDC,RYK,EPHB1,AKIP1,RET,TTL,FER,RILPL1,RILPL2,ANKRD27,FLNB,PREX2,PIK3R1,LPXN,CASP3,PARVA,PLS1,ROBO1,ROBO2,FZD3,MEF2C,SEMA4F,TLX2,CUX2,ARHGEF26,RAPGEF2,DPYSL2,TIAM1,SLIT1,DOCK5,STC1,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,C8orf37,SEMA3G,RREB1,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,DMTN,SEMA4G,DTNBP1,SIAH1,LZTS1,BMPR1B,BDNF,PXN,DOCK10,KIAA0319,LGR6,DNM1L,CARMIL1,PPP3CA,HECW2,CAPRIN2,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,CFL1,ADNP,AP1AR,YTHDF2,DISC1,LAMB3,CASS4,CIB1,GBX2,KALRN,NFATC4,FZD7,SS18L1,LAMA5,YTHDF1,PTPRO,CDKL5,CLIC4,EPHB3,TANC2,DOCK1,MELTF,CSPG5,STRC,LAMC1,WNT3,KLF7,CREB1,NBEAL2,MYPN,SPG11,MAPT,PLOD3,SEMA6D,EPHB4,ITGA4,TNR,FN1,ATL1,PTPN6,NIN,FERMT3,DNM3,PPP3CB,RAB3A,MARK2,VCL,OBSL1,MINK1,RAB8A,CRMP1,EPHA4,LRTM2,DLG4,ACTB,RADIL,UNC5A,PSEN1,SEMA4A,RAB25,NGFR,NLGN3,TAOK2,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,NTN1,TNMD,RPS6KA5,CCDC88C,RNF165,DNM2,PARP6,GPRASP2,BHLHB9,BCL11B,LHX1,ARH	grey	VSMC_M10
GO:0071887	0.96	0.06	35	79	leukocyte apoptotic process	BP	1	BAK1,CDKN2A,TNFRSF21,SLC46A2,SLC7A11,TRAF3IP2,IDO1,GAS6,FOXP1,IRF7,ZC3H8,PIK3CB,CASP3,MEF2C,LMBR1L,RAPGEF2,RIPK1,NOD2,GPAM,HCLS1,PDCD1,ADAM8,BCL6,CXCR2,EFNA1,BTK,CD74,CCL5,IL7R,DNAJA3,BCL10,FADD,WNT5A,TSC22D3,BCL2L11	grey	VSMC_M10
GO:0006282	0.96	0.06	54	118	regulation of DNA repair	BP	1	EYA4,MRNIP,HELB,HSF1,POT1,CYREN,EGFR,XRCC1,WDR48,FBH1,RNF169,FAM168A,SIRT7,SHLD1,PPP4R2,TEX15,PRKDC,ERCC6,ERCC8,EYA1,SLF1,ABRAXAS1,SPIDR,WRNIP1,SLF2,AXIN2,EYA3,PARP9,DTX3L,RNF168,RTEL1,MGMT,SETD2,ZCWPW1,WAS,DDX11,RAD52,PARP1,SHLD2,UIMC1,WRAP53,KAT7,OTUB2,SMCHD1,RMI2,NUDT16L1,SPIRE2,TERF2,OOEP,TIGAR,RNF8,UBE2N,BRCC3,CBX8	grey	VSMC_M10
GO:0006790	0.96	0.05	131	270	sulfur compound metabolic process	BP	1	SUOX,HSD17B4,PPT2,ACSL6,SULT4A1,ISCA1,MTAP,GNMT,SLC35B2,CLIC5,SLC1A1,PPCS,CHAC2,PPT1,MGST2,SLC7A11,DLD,HS3ST5,NDNF,AKR1A1,MMACHC,GSTK1,GLB1,CHPF2,ELOVL1,CSGALNACT1,BTD,DCN,PDK1,CLIC1,ARL6IP5,SUCLG2,CIAO1,PDHX,APIP,CSAD,ELOVL7,PAX8,AHCY,GSS,B3GNT4,MSRA,ACOT12,CIAPIN1,ENOPH1,ST3GAL6,FITM2,CHST1,ABCC2,MTRR,MCEE,MTR,CBSL,GLRX2,HYAL1,TPST1,GPAM,FAR2,ACSL5,ARSG,ISCU,THTPA,MCCC1,HSCB,HACD2,THEM5,GAL3ST3,HMGCL,NUBPL,SMS,ACOT9,PDK3,NFE2L2,SQOR,GGT2,CPS1,ACSBG1,COMT,CHST3,SPOCK2,GAL3ST4,CHST7,AC022400.6,GGT6,MPC2,STAT5B,MAT1A,LIAS,TECR,CHST12,IDUA,SLC26A1,ACOT2,GCDH,GSTZ1,GLCE,ACSM3,ACACA,SLC26A2,GHR,ACSBG2,PIPOX,NUBP1,ACOT11,METTL16,B3GALT6,TKTL1,CIAO3,PARK7,ACSF3,MLYCD,CHST5,PTGES2,ST3GAL2,CIAO2B,MIR21,SULT1C3,GLRX5,GSTT4,ACOT4,TPK1,ELOVL3,MTHFD2L,PEMT,GLO1,FXN,NUDT19,GGT5,CHSY3,PHGDH,ISCA2	grey	VSMC_M10
GO:2000116	0.96	0.06	79	167	regulation of cysteine-type endopeptidase activity	BP	1	TNFAIP8,MAP3K5,GRAMD4,BAK1,MYC,HSF1,TTBK1,SLC1A1,NOD1,AQP1,CASP8AP2,EPHA7,TNFSF15,BCL2L12,HSPE1,CST7,RAF1,PRDX3,ARRB1,GAS6,ARL6IP5,ST18,ASPH,GPI,NR4A1,FOXL2,HIP1R,ROBO1,DIABLO,HTRA2,RIPK2,SENP1,NKX3-1,ACVR1C,F2R,PIDD1,PAX2,LCK,PDCD6,SOX2,GPER1,IFI6,CIDEB,SFN,RPS6KA1,EGLN3,MGMT,POR,MAPT,FIS1,CTSH,DDX3X,MUL1,BIRC3,ARL6IP1,BCL2L13,NGFR,SMAD3,MAP2K5,S100A8,NLE1,BCAP31,P2RX1,PARK7,LAMTOR5,BCL10,MIR27B,RHOA,RPS27L,NOL3,FADD,CASP8,ACER2,SERPINB9,BCL2L11,PERP,CAAP1,PRR7,CRADD	grey	VSMC_M10
GO:2000113	0.96	0.05	581	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	SMARCC2,PAN2,ATP8B1,SHMT2,PLAGL1,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,ZBTB12,EIF3E,PNLDC1,PRKN,PPARA,MRPL13,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PTCH1,TNRC6B,ATF4,TUT7,CBX7,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SCMH1,IGF2BP3,NFE2L3,PNPT1,HOXA2,HOXA7,JAZF1,XPO1,AKIRIN2,CASP8AP2,BACH2,ZNF692,NR1H2,ZNF350,FOXP2,MED25,KLF11,AGO1,POU3F3,LANCL2,CREM,SDCBP,TUT4,OSR1,FOXO3,BEND5,DHFR,HDAC2,PHF10,DNMT3A,BMI1,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,SUV39H2,ZNF404,PLK3,MLH1,GLI2,DEDD2,RSF1,KDM4A,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,SFMBT2,GZF1,POU4F1,FBH1,TNRC6C,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,HBEGF,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,EIF2AK2,LSM1,TAF7,NRG1,GAS6,RYBP,FOXP1,MITF,MTA3,ARID5A,IRF7,PAN3,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,RAD17,NCOA2,DKK3,SAP30,ATR,ZNF366,ARNTL,GCFC2,HMBOX1,ENC1,MEF2C,PEX2,PKIA,TMBIM6,CNOT1,CELF1,SLA2,CUX2,MCPH1,SOX6,CNOT6L,FNIP2,BACH1,SFMBT1,EIF2AK4,NR1H3,EIF4E2,EAPP,SCAF4,LCOR,DDX54,RUNX1T1,PAIP2B,VDR,NKX3-1,BAHD1,HDAC7,NKX6-1,LOXL2,NR4A2,DONSON,PHF21A,CRY2,PRDM11,CDYL,FTO,RREB1,RTF1,ZBED6,SOX13,ZNF248,TFAP2A,RI	grey	VSMC_M10

GO:0042168	0.96	0.08	15	37	heme metabolic process	BP	1	FECH,TSPO,SLC25A38,HPX,CPOX,COX15,ABCC2,TMEM14C,ALAS1,BDH2,ABCB6,COX10,SLC46A1,NFE2L1,FXN	grey	VSMC_M10
GO:1902236	0.96	0.10	6	17	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	BP	1	PRKN,TMBIM6,OPA1,HYOU1,SYVN1,PARK7	grey	VSMC_M10
GO:0071230	0.96	0.07	25	59	cellular response to amino acid stimulus	BP	1	PNPLA3,NTRK2,HSF1,RRAGD,SESN3,DNMT3A,RPTOR,LARS,SLC38A9,OPA1,NEURL1,COL16A1,SH3BP4,COL5A2,RRAGB,SOCS1,AMIGO1,CYBA,LAMTOR5,ASS1,LAMTOR2,SIX1,BCL2L2,CEBPB,PDGFD	grey	VSMC_M10
GO:0003181	0.96	0.09	8	22	atrioventricular valve morphogenesis	BP	1	TGFBR2,TBX5,TGFB2,BMPR1A,EFNA1,SOX4,HEY2,OLFM1	grey	VSMC_M10
GO:0031294	0.96	0.08	11	28	lymphocyte costimulation	BP	1	TNFRSF13C,LCK,CD28,PTPN6,CARD11,YES1,CD320,VAV1,DPP4,EFNB3,TNFSF13B	grey	VSMC_M10
GO:0016339	0.96	0.09	8	22	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	BP	1	CDH17,AJUBA,CDH24,CDH23,ARVCF,CDH6,CDH10,CDH16	grey	VSMC_M10
GO:0046326	0.96	0.08	12	31	positive regulation of glucose import	BP	1	MAPK14,FGF21,AKT2,PIK3R1,SORBS1,IRS1,TERT,NFE2L2,CLTCL1,INSR,GPC3,ARPP19	grey	VSMC_M10
GO:0036498	0.96	0.10	6	17	IRE1-mediated unfolded protein response	BP	1	BAK1,DDRGK1,FICD,HSPA5,DAB2IP,BCL2L11	grey	VSMC_M10
GO:0003007	0.96	0.05	92	197	heart morphogenesis	BP	1	ADGRG6,LEMD2,PTK2,PTCH1,LY6E,TAB1,PIM1,SMO,FOXH1,TEK,SRF,FHL2,TNNI3,DNAH11,RTN4,TEAD2,SPRY1,BBS7,SETDB2,SOX9,MEGF8,IFT172,POU4F1,WNT11,TGFBR2,OVOL2,JAG1,MKKS,RYR1,NRG1,ASXL1,HAND2,EYA1,PARVA,ROBO1,ROBO2,MEF2C,ADAMTS1,NPY1R,TBX5,IFT52,TNNC1,COL4A3BP,DSP,PKD2,RYR2,SUFU,PKP2,TNNI1,PDCD4,TGFB2,AXIN2,SNAI1,MYH7,ACTC1,TTN,EPHB4,SAV1,TBX19,DVL2,BMPR1A,TCAP,DHRS3,RBPJ,MED1,ALDH1A2,PSEN1,EFNA1,TMEM100,SMAD3,MKS1,TBX2,INSR,GATA6,MIB1,ISL1,RNF207,COL5A1,FOXF1,ENG,MIR21,SOX4,ACVRL1,NOG,LBX1,WNT5A,SIX1,C2CD3,NKX2-5,HEY2,OLFM1,WNT2	grey	VSMC_M10
GO:0051494	0.96	0.06	63	138	negative regulation of cytoskeleton organization	BP	1	AVIL,MDM1,PRKN,PICK1,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,SHANK1,MET,ADD2,CDK5RAP2,MAPRE1,EML2,CLASP2,TRIM54,MKKS,NAV3,ARHGEF7,SPEF1,LMOD3,ATXN7,PIK3R1,HIP1R,LIMA1,KATNB1,TMEM67,DMTN,CARMIL1,PPFIA1,LMOD1,ADD3,TTBK2,SSH1,ARHGAP6,CIB1,WASF2,SPTBN2,CCDC84,TMOD4,EPS8,INPP5J,CAPZA1,WAS,TMOD2,SPTB,CORO2B,TRIM37,CAMSAP3,TAOK1,NUBP1,SSH2,INPP5K,APC2,CAMSAP1,WDR63,CARMIL2,MIR21,GMFG,APC,PFN4,MAP6D1	grey	VSMC_M10
GO:0051156	0.96	0.10	6	17	glucose 6-phosphate metabolic process	BP	1	RBKS,GPI,RPE,HK1,TIGAR,RPIA	grey	VSMC_M10
GO:0033619	0.96	0.07	20	48	membrane protein proteolysis	BP	1	TMPRSS6,MYH9,TIMP4,RET,ERAP1,SH3D19,GPLD1,RHBDD1,SPPL3,ADRA2A,DAG1,BACE1,LRIG2,ADAM8,CTSH,SPPL2A,PSEN2,TNFRSF1B,PSEN1,SPPL2B	grey	VSMC_M10
GO:0050810	0.96	0.07	21	50	regulation of steroid biosynthetic process	BP	1	CYP27B1,TSPO,DKKL1,APOB,NR1H4,CYP7A1,ASAH1,DKK3,ERLIN1,SNAI1,SCAP,POR,LPCAT3,WNT4,FGFR4,DGKQ,SREBF1,GFI1,STARD4,INSIG2,FGF1	grey	VSMC_M10
GO:0034643	0.96	0.09	9	24	establishment of mitochondrion localization, microtubule-mediated	BP	1	AGTPBP1,LRPPRC,MGARP,WASF1,OPA1,MAPT,UXT,HAP1,UBB	grey	VSMC_M10
GO:0047497	0.96	0.09	9	24	mitochondrion transport along microtubule	BP	1	AGTPBP1,LRPPRC,MGARP,WASF1,OPA1,MAPT,UXT,HAP1,UBB	grey	VSMC_M10
GO:0009162	0.96	0.10	7	19	deoxyribonucleoside monophosphate metabolic process	BP	1	DPYS,GDA,DGUOK,UPB1,NT5M,DCTD,UPP1	grey	VSMC_M10
GO:1902275	0.96	0.08	11	29	regulation of chromatin organization	BP	1	SETDB2,FAM208A,SPTY2D1,PPHLN1,TET1,PADI2,PHF8,SETD1A,METTL4,SETDB1,ZNF304	grey	VSMC_M10
GO:0031333	0.96	0.06	52	115	negative regulation of protein-containing complex assembly	BP	1	AVIL,HSF1,LMOD2,KIAA1211,TMOD1,SPTBN1,ADD2,MAPRE1,SOX9,EML2,DNAJC15,RAF1,MKKS,ARHGEF7,ULK1,LMOD3,ANKRD27,HIP1R,DMTN,CARMIL1,LMOD1,ADD3,SSH1,OPRD1,SORL1,SPTBN2,TRAF3IP1,TMOD4,EPS8,INPP5J,CAPZA1,AIDA,DDX3X,TMOD2,PPM1A,SPTB,THRA,LCMT1,RIOK3,ISL1,PTGER4,SSH2,PRKCZ,PARK7,STXBP1,HSPA5,CARMIL2,IMPACT,CRBN,CPTP,PFN4,LDLRAD4	grey	VSMC_M10
GO:0150117	0.96	0.08	11	29	positive regulation of cell-substrate junction organization	BP	1	TEK,ITGB1BP1,IQSEC1,PIK3R1,FMN1,PTPRJ,COL16A1,WNT4,SMAD3,TSC1,THY1	grey	VSMC_M10
GO:0046459	0.96	0.12	4	12	short-chain fatty acid metabolic process	BP	1	THNSL2,MCEE,PHYH,ACOT4	grey	VSMC_M10
GO:0031398	0.96	0.06	46	102	positive regulation of protein ubiquitination	BP	1	PRKN,DERL1,SKP1,CRY1,RNF20,PELI1,BMI1,PAXIP1,MYCBP2,KLHL40,ARRB1,NMI,TRAF6,TRIB3,FAM107A,SPSB4,FBXW7,RIPK2,MARCH7,PRICKLE1,NOD2,NHLRC1,PEF1,PDCD6,SPRTN,SENP2,FBXO33,DDX3X,PINK1,BIRC3,PHF23,RNF111,DCUN1D3,PSMD10,TICAM1,FZR1,HSPA5,BCL10,UBB,INAVA,RASSF5,UBE2N,PTTG1IP,CENPX,UBE2D1,TSPYL5	grey	VSMC_M10
GO:0071384	0.96	0.07	19	46	cellular response to corticosteroid stimulus	BP	1	FECH,AQP1,EGFR,FOXO3,BMI1,FAM107A,DNMT3B,STC1,ABCC2,SRD5A1,GPER1,NPAS4,SCNN1B,ISL1,ASS1,SMYD3,CRH,BCL2L11,ZFP36L2	grey	VSMC_M10
GO:0007224	0.96	0.06	54	119	smoothened signaling pathway	BP	1	GLI1,TBC1D32,PTCH1,SMO,ROR2,TMEM17,FUZ,IQUB,INTU,TTC26,BBS7,PTCH2,KCTD21,GLI2,MEGF8,IFT172,TGFBR2,KCTD6,TCTN3,IFT81,NKX6-1,IFT52,RPGRIP1L,ZNF423,SUFU,CDON,TTC23,ARMC9,TTBK2,TTC21B,HHAT,SEPT2,POR,FKBP8,STK36,GORAB,GPR161,TULP3,EVC2,WDR19,MKS1,TUBD1,MOSMO,IFT20,GPC3,HSPB11,MGRN1,CREBBP,FOXF1,TMEM231,TCTN2,GPR37L1,C2CD3,ZIC1	grey	VSMC_M10
GO:0003156	0.96	0.09	9	24	regulation of animal organ formation	BP	1	FRS2,SPRY1,WNT11,ROBO1,ROBO2,WNT5A,SIX1,FGF1,WNT2	grey	VSMC_M10
GO:1902235	0.96	0.09	10	26	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	BP	1	PRKN,NCK2,TMBIM6,OPA1,HYOU1,SYVN1,PTPN2,PARK7,DDIT3,BCL2L11	grey	VSMC_M10
GO:0033143	0.96	0.07	27	63	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	CNOT2,KDM4C,FOXH1,CRY1,PHB,RNF14,DDRGK1,FOXP1,CYP7B1,UFSP2,ZNF366,ARNTL,CNOT1,KMT2D,CRY2,VPS18,HDAC1,DNAAF4,PARP1,MED1,PAGR1,PIAS2,NCOR1,ISL1,PARK7,RHOA,TRIM68	grey	VSMC_M10
GO:1902991	0.96	0.07	16	39	regulation of amyloid precursor protein catabolic process	BP	1	AGER,NTRK2,RTN4,PRNP,CASP3,SLC2A13,SORL1,RTN1,HAP1,EPHA4,TMED10,EFNA1,ABCA7,MIR29A,MIR24-1,MIR339	grey	VSMC_M10
GO:0014912	0.96	0.09	9	24	negative regulation of smooth muscle cell migration	BP	1	LRP1,TRIB1,MEF2C,GNA13,NFE2L2,SEMA6D,BMPR1A,MIR21,RHOA	grey	VSMC_M10

GO:0060393	0.96	0.07	18	44	regulation of pathway-restricted SMAD protein phosphorylation	BP	1	LRP1,GDF9,BMP8A,BMPER,SDCBP,ACVR2A,RBPMS,ACVR1B,SNX25,TGFB2,GDF15,INHA,BMPR1A,TWSG1,ENG,ACVRL1,NOG,LDLRAD4	grey	VSMC_M10
GO:0046578	0.96	0.05	74	161	regulation of Ras protein signal transduction	BP	1	CDC42SE2,RGL2,SYNGAP1,GPR20,LRRD1,EPS8L1,LPAR1,MET,SPRY1,IQSEC1,KBTBD6,RAF1,SPRY2,PSD3,ARRB1,RASGRP4,NRG1,PPP2CB,RASA3,PIK3CB,RASA2,FBXO8,ROBO1,PLCE1,ARHGEF28,MADD,RASGRP1,F2RL1,F2R,ARHGAP24,GBF1,PSD,TGFB2,AUTS2,RABL3,KRAS,CBL,EPS8,RASA4,BCL6,ABL2,COL3A1,LZTR1,MYO9B,CYTH3,RASAL3,IQSEC2,MFN2,STARD8,ITGA3,KCTD13,OGT,DENND4A,DNM2,RIT2,ARHGAP44,TNFAIP1,RALBP1,CRK,EPS8L3,RALGPS1,MAPKAP1,SCAI,DENND1A,DAB2IP,GPR35,ADGRG1,EPS8L2,STAMBP,STK19,HRAS,CADM4,SH2B2,ARPP19	grey	VSMC_M10
GO:0048813	0.96	0.06	57	126	dendrite morphogenesis	BP	1	NEDD4L,RAB21,MAPK8IP2,SULT4A1,RBFOX2,CHRNA3,SEMA4D,SHANK1,PTN,HECW1,ABI1,SS18L2,FARP1,TMEM106B,SEMA3A,EPHB1,ANKRD27,PREX2,TLX2,CUX2,RAPGEF2,TIAM1,OPA1,ITPKA,DTNBP1,LZTS1,DOCK10,DNM1L,PPP3CA,HECW2,CAPRIN2,CFL1,NFATC4,SS18L1,CDKL5,EPHB3,TANC2,KLF7,DNM3,OBSL1,MINK1,EPHA4,DLG4,TAOK2,EFNA1,CHRNB2,ZDHHC15,PARP6,GPRASP2,BHLHB9,ARHGAP44,CDK5R1,LRP8,CELSR2,FBXO31,BTBD3,YWHAH	grey	VSMC_M10
GO:0045736	0.96	0.09	9	24	negative regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	TNFAIP3,CDKN2A,FBXO7,CEBPA,CASP3,CDKN1B,HEXIM2,MEN1,APC	grey	VSMC_M10
GO:1904030	0.96	0.09	9	24	negative regulation of cyclin-dependent protein kinase activity	BP	1	TNFAIP3,CDKN2A,FBXO7,CEBPA,CASP3,CDKN1B,HEXIM2,MEN1,APC	grey	VSMC_M10
GO:0097061	0.96	0.06	30	70	dendritic spine organization	BP	1	PICK1,ABHD17B,SHANK1,VPS35,MTMR2,PRNP,EPHB1,CUX2,TIAM1,HOMER1,OPA1,ITPKA,DOCK10,DNM1L,CAPRIN2,CFL1,EPHB3,TANC2,DNM3,EPHA4,DLG4,ITGA3,EFNA1,ZDHHC15,GPRASP2,BHLHB9,ARHGAP44,INSR,CDK5R1,LRP8	grey	VSMC_M10
GO:0001838	0.96	0.06	48	107	embryonic epithelial tube formation	BP	1	STK3,FZD6,BRD2,PTCH1,PTK7,SEMA4C,FUZ,TEAD2,OSR1,SOX9,IFT172,OVOL2,SPINT2,TRAF6,RET,PAX8,CASP3,FZD3,OPA1,IFT52,SPINT1,STK4,PAX2,PRICKLE1,SUFU,IRX2,TGFB2,DVL3,GRHL3,LUZP1,SETD2,WNT4,TULP3,LIAS,DVL2,MKS1,MIB1,SKI,SOX8,TSC1,GLMN,BCL10,VASP,SOX4,NOG,WNT5A,SIX1,RALA	grey	VSMC_M10
GO:0070059	0.96	0.07	21	50	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP	1	MAP3K5,PRKN,BAK1,ATF4,NCK2,TRIB3,TMBIM6,OPA1,QRICH1,HYOU1,SYVN1,DNAJC10,ATP2A1,PTPN2,TRAF2,PARK7,DAB2IP,DDIT3,BCL2L11,PPP1R15A,CEBPB	grey	VSMC_M10
GO:0060322	0.96	0.05	309	624	head development	BP	1	NME1,LRP1,GLI1,ATAT1,FRS2,RIDA,OSR2,SYNJ2,FZD6,UQCRQ,CCDC134,BAK1,XRCC6,PITX1,PTCH1,FANCC,AGTPBP1,PLXNA4,SUN2,NTRK2,CSNK1E,CKB,SMO,RBFOX2,ZFAND5,SRF,TTBK1,FZD1,CDK6,SLC1A1,DLX5,EFHC1,CCIN,ADGRL3,SEMA4C,MBOAT7,RTN4,UTP3,HOXA2,PPT1,AQP1,EPHA7,AKNA,WHRN,PTN,FOXP2,CTTNBP2,POU3F3,CDK5RAP2,SLC7A11,FOXO3,ARMC4,SPHK2,FAT4,SPATA5,KDM7A,GRIN2D,NAPA,BBS7,BMI1,NDNF,C5AR1,SOX9,EIF2B3,XRCC1,GLI2,B4GALT2,RAF1,IFT172,FOXJ1,SCN5A,CSRNP1,NUMBL,HNMT,POU4F1,TSKU,SZT2,ALK,HOOK3,TGFBR2,EOMES,CHD8,SIRT2,MKKS,AATK,RARB,SYT1,PLCB1,RAC3,CEP290,SEMA3A,NRG1,WRN,PRKDC,RYK,SNPH,DHX37,TOX,ZSWIM6,NCOA6,CASP3,CTNND1,CLP1,DCLK2,TRABD2A,ROBO1,ROBO2,CRISPLD1,FZD3,FAIM2,HTRA2,NDUFS3,CELF1,CSNK2A2,MCPH1,SOX6,RAPGEF2,DPYSL2,NNAT,SLIT1,SYNJ1,TENT2,NR4A2,AMIGO2,SLC38A2,RPGRIP1L,PAX2,TSPAN2,SALL1,DNAH5,CNTN1,ZNF335,DPCD,ATXN1,SUDS3,ZNF423,LDB1,COX6B1,SRGAP2C,SLC4A10,SRD5A1,INA,NEURL1,CFAP43,SLC6A3,HDAC1,ALDH1A3,PPP3CA,PGAP1,SLC38A3,SATB2,COX17,TTBK2,AMIGO3,SHROOM2,KRAS,PITPNM1,EGF,TTC21B,SOX2,ZFHX2,JHY,DISC1,GNPAT,B3GNT5,GBX2,ATP1A2,BAG3,SPTBN2,UFC1,MACO1,DLX1,DNAJC30,EPHB3,LIMK2,NSUN5,APOD,SETD2,WNT3,CREB1,SEMA6D,BCL2A1,H2AFY2,DIXDC1,MEN1,TNR,DDX10,XRCC5,NIN,CXCR2,WNT4,HSPG2,COL3A1,STK36,ABCB6,TBX19,KCNA1,MAPK1,TULP3,TTC25,PADI2,HAP1,ACTB,SHROOM4,BMPR1A,DNAJB1,MPP5,RBPJ,PHF8,MED1,ALDH1A2,ATP1B2,SETD1A,PSEN1,KDM6B,ITGAM,NDEL1,TAF1,MAPK3,CITED1,CHRNB2,MAP2K1,POU3F4,EPOR,	grey	VSMC_M10
GO:0006144	0.96	0.10	6	17	purine nucleobase metabolic process	BP	1	SHMT2,GDA,PPAT,GMPS,GMPR,SHMT1	grey	VSMC_M10
GO:0042552	0.96	0.06	49	109	myelination	BP	1	ADGRG6,QKI,NTRK2,SOX10,ADAM22,TNFRSF21,PTN,LPIN1,KEL,FIG4,MTMR2,CST7,ERCC2,ACER3,PRX,AKT2,CMTM8,SIRT2,RARB,NRG1,MAL,LGI4,SBF2,JAM2,PLLP,SERINC5,CYFIP1,TSPAN2,RNF10,SCN2A,DAG1,ANK2,GNPAT,NSUN5,DLG1,PIKFYVE,ACSBG1,CNTNAP1,MPP5,DEGS1,TNFRSF1B,GALC,EPB41L3,SKI,AMIGO1,TSC1,ZNF24,CNTN2,POU3F2	grey	VSMC_M10

GO:0051253	0.96	0.04	522	1032	negative regulation of RNA metabolic process	BP	1	ZC3H10,SMARCC2,ATP8B1,PLAGL1,ZBTB2,ESR1,CNOT2,OSR2,PABPC1,SNW1,ZNF706,PHAX,ZBTB12,PRKN,PPARA,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,PTCH1,ATF4,CBX7,MAPK14,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,RPS14,ZNF550,BEND6,ZNF268,LRPPRC,SCMH1,RNF20,NFE2L3,HOXA2,HOXA7,JAZF1,PTBP3,XPO1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,NR1H2,ZNF350,FOXP2,MED25,KLF11,POU3F3,LANCL2,CREM,SDCBP,OSR1,FOXO3,BEND5,TRAF3IP2,HDAC2,PHF10,DNMT3A,BMI1,DHX34,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,SUV39H2,ZNF404,PLK3,GLI2,DEDD2,RSF1,KDM4A,MYD88,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,SFMBT2,GZF1,POU4F1,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,BAG4,TAF7,NUDT16,NRG1,GAS6,RYBP,FOXP1,MITF,PKP3,MTA3,ARID5A,IRF7,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,NCOA2,DKK3,SAP30,ZNF366,ARNTL,GCFC2,HMBOX1,MEF2C,PEX2,PKIA,BCDIN3D,TMBIM6,CNOT1,SLA2,CUX2,MCPH1,SOX6,FNIP2,BACH1,SFMBT1,NR1H3,EAPP,SCAF4,LCOR,DDX54,TENT2,RUNX1T1,VDR,NKX3-1,BAHD1,HDAC7,NKX6-1,LOXL2,NR4A2,SRSF6,PHF21A,CRY2,PRDM11,CDYL,RREB1,RTF1,ZBED6,SOX13,ZNF248,TFAP2A,RIPPLY3,HIF1AN,PAX2,SALL1,PPHLN1,PRICKLE1,HIVEP1,TENT5C,JARID2,ATXN1,TENT4B,SUDS3,RBM24,ZNF423,LDB1,I	grey	VSMC_M10
GO:0055094	0.96	0.09	9	24	response to lipoprotein particle	BP	1	TLR4,FGF21,MYD88,ADTRP,FCER1G,MIA3,LDLR,NPC1,TICAM1	grey	VSMC_M10
GO:0046605	0.96	0.07	17	42	regulation of centrosome cycle	BP	1	VPS4B,MDM1,CHMP2A,XPO1,CDK5RAP2,CEP295NL,PLK2,CHMP2B,CHMP4C,MCPH1,ALMS1,TMEM67,AC112128.1,CCDC84,TRIM37,NUBP1,CHMP1A	grey	VSMC_M10
GO:0032330	0.96	0.07	19	46	regulation of chondrocyte differentiation	BP	1	SIX2,MBOAT2,MKX,SOX9,GLI2,ZNF219,RARB,SOX6,LOXL2,BMPR1B,PTHLH,AXIN2,POR,NKX3-2,FGF18,SMAD3,ADAMTS12,RFLNB,ACVRL1	grey	VSMC_M10
GO:0150076	0.96	0.09	9	24	neuroinflammatory response	BP	1	TTBK1,CST7,CD200,CD200R1L,MMP3,TNFRSF1B,SYT11,LDLR,IL33	grey	VSMC_M10
GO:0006268	0.96	0.10	5	15	DNA unwinding involved in DNA replication	BP	1	SSBP1,PURA,WRN,TWNK,RECQL	grey	VSMC_M10
GO:0051704	0.96	0.04	356	709	multi-organism process	BP	1	TAC3,TBPL1,TRIM36,GLI1,YTHDC2,B4GALNT1,CYP27B1,ATAT1,ESR1,TSPAN8,MAPK8IP2,IGF2R,MOV10L1,PACRG,QKI,FBLN1,BRD2,GDF9,ROS1,MCM9,HSF2,UBE2B,CATSPER3,WASHC5,TOB2,SMAD5,AGO2,H3F3C,FANCC,AKR1B1,TUT7,DMC1,PLA2G6,PICK1,SPATA31D3,MYH9,CFAP69,FANCG,SMARCA2,CLIC5,TDRD6,KIT,RLN1,PPAT,CCIN,TSGA10,TDRD7,NLRP5,DNAJA1,FOXJ3,SCMH1,RIMS1,MSH2,RAD23B,SPACA6,YTHDC1,KLK14,CABS1,FANCL,GJA10,HERPUD2,GMCL1,PTN,NOBOX,CCDC155,DKKL1,CREM,TUT4,FOXO3,ARMC2,DLD,EPS15,DDO,TXNRD3,APOB,IZUMO1,SPATA6,SPHK2,SPATA5,HDAC2,ADCY3,TTC26,TRPC3,RAB7A,DNMT3A,PANX1,KPNA3,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,PSG3,MLH1,ACOX1,PRDX3,FOXJ1,WDR48,TTC21A,THBD,PLAT,KPNA2,CCNB1IP1,TGFBR2,ACVR2A,FCHSD2,SIRT2,MKKS,SPATA24,IDO1,ADAM18,PLCB1,MCM8,GOLGA3,PANK2,BTG1,FCHSD1,SOHLH2,FUT10,GAS6,TEX15,UBXN8,KATNAL1,STX2,ADRA2B,NPHP1,ACVR1B,ING2,HPGD,SPATA9,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,P2RY1,PTK2B,KMT2D,PRKAG1,SFMBT1,TPCN1,VDR,STC1,AP3B1,SLC38A2,ACVR1C,SLC38A1,CDYL,ABCC2,SPP1,SYCP1,DNAH1,PLA2G4B,NPM2,DPCD,OCA2,ADCY7,ROPN1L,SIAH1,BMPR1B,GAS2,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,HYAL3,SLC38A3,TESMIN,SLC9B1,COL16A1,PTHLH,PRKAR1A,INTS13,KRAS,SPATA2,RNF114,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,AGT,TSSK4,CIB1,CCDC87,DDX6,HDAC4,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,CLIC4,SEPT2,LIMK2,PATZ1,SP3,CATSPER2,OVOL1,ETV6,YBX3,LYZL6,WNT3,CADM1,PIKFYVE,OVGP1,SPAT	grey	VSMC_M10
GO:0032984	0.96	0.05	91	195	protein-containing complex disassembly	BP	1	VPS4B,SMARCC2,AVIL,MYC,JMJD4,LMOD2,KIAA1211,CHMP2A,TMOD1,PLEKHH2,STX17,SPTBN1,SNX14,PLEK,ADD2,MFSD8,NAPA,RUBCNL,CLASP2,MTRF1,TRIM54,NCKAP5,NAPB,NAV3,SPEF1,LMOD3,VPS16,ATXN7,C12orf65,LIX1,CHMP2B,LIMA1,SMARCD1,NCKAP5L,ZFAND1,KATNB1,SCAF4,SYNJ1,CHMP7,F2RL1,DMTN,STMND1,RPL23,CARMIL1,LMOD1,ADD3,TRPV4,TMEM39A,TTBK2,CFL1,DYRK3,HSPA8,CIB1,SPTBN2,ARID1A,TMOD4,EPS8,RUBCN,CAPZA1,NSF,DHX8,UPF1,SNAP29,TBC1D25,TMOD2,PHF23,SPTB,GAK,PEX14,AC138894.1,CALM1,SNAPIN,VMP1,INSR,SMCR8,KLC1,CAMSAP3,LAMP2,TAOK1,CLEC16A,APC2,CAMSAP1,CHMP1A,VPS4A,CARMIL2,IRGM,CCSAP,APC,PDXP,MAP1A,MAP6D1	grey	VSMC_M10
GO:0035024	0.96	0.09	7	20	negative regulation of Rho protein signal transduction	BP	1	MET,BCL6,ABL2,ITGA3,KCTD13,TNFAIP1,SCAI	grey	VSMC_M10
GO:0061647	0.96	0.07	15	38	histone H3-K9 modification	BP	1	SETD7,SPHK2,SETDB2,SUV39H2,KDM4A,DNMT3B,JARID2,NAP1L2,CRTC2,MECP2,PRDM16,SETDB1,ARID4A,BEND3,ZNF304	grey	VSMC_M10
GO:0006023	0.96	0.06	29	68	aminoglycan biosynthetic process	BP	1	B4GALT7,HAS1,HS3ST5,CHPF2,CSGALNACT1,B3GNT4,ST3GAL6,GALNT5,CHST1,GCNT2,HYAL1,EGF,ABCC5,CEMIP,CHST3,CHST7,AC022400.6,HS3ST1,CHST12,GLCE,HEXA,HS6ST2,B3GALT6,CHST5,ST3GAL2,HAS3,HS3ST2,CHSY3,HS2ST1	grey	VSMC_M10

GO:0007033	0.96	0.05	73	157	vacuole organization	BP	1	ATG12,PIP4K2C,RNF5,WASHC5,TFEB,RAB23,STX17,ACP4,PPT1,ATG5,FIG4,MFSD8,RAB7A,PIP4K2A,RALB,MYO7A,HOOK3,ATG16L2,TMEM173,TMEM106B,RAB5A,FEZ2,FAM160A2,ULK1,VPS16,NSFL1C,CHMP2B,TBC1D12,ACP2,AP3B1,VPS18,TP53INP1,RAB7B,SEC22B,TMEM9,TMEM39A,TCIRG1,ADPRH,HPS4,ATG16L1,BAG3,MTMR3,RAB1B,SPG11,PIKFYVE,ATG2A,TBC1D14,PINK1,ATG9A,ATP13A2,WIPI2,PHF23,SYT7,CLN8,MFN2,ANXA2,PSEN1,AC138894.1,HOOK2,CLN6,SNAPIN,VMP1,ATG2B,SMCR8,IFT20,TMEM199,MTM1,EMC6,KIAA1324,SH3GLB1,VPS4A,IRGM,RAB39A	grey	VSMC_M10
GO:0046785	0.96	0.06	32	74	microtubule polymerization	BP	1	ZNF207,HSPA1B,TUBGCP6,SLAIN2,MET,CDK5RAP2,MAPRE1,EML2,SLC39A12,CLASP2,MAPRE3,SLAIN1,NAV3,ARHGEF7,CLIP1,TUBGCP5,TRPV4,TUBGCP4,INPP5J,CDKN1B,MAPT,TOGARAM1,NIN,TUBG1,NDEL1,CAMSAP3,CDK5R1,CEP192,MECP2,CAMSAP1,PSRC1,DRG1	grey	VSMC_M10
GO:0090307	0.96	0.06	24	57	mitotic spindle assembly	BP	1	VPS4B,ZNF207,HSPA1B,CHMP2A,CCDC61,CLASP2,PIBF1,KIF3B,CHMP2B,CHMP4C,ABRAXAS1,AC112128.1,CHEK2,ABRAXAS2,TOGARAM1,KPNB1,RAB11A,CEP192,WRAP73,CHMP1A,RHOA,AURKC,CCSAP,DRG1	grey	VSMC_M10
GO:1990000	0.96	0.08	10	26	amyloid fibril formation	BP	1	PRKN,PFDN5,RIPK1,SIAH1,BACE1,MAPT,PFDN4,PSEN1,LDLR,VBP1	grey	VSMC_M10
GO:0010755	0.96	0.11	4	12	regulation of plasminogen activation	BP	1	PLGRKT,MELTF,F12,SERPINF2	grey	VSMC_M10
GO:0006694	0.96	0.05	58	126	steroid biosynthetic process	BP	1	CYP27B1,CYP21A2,TSPO,HSD17B8,HSD17B3,AKR1B1,PLPP6,SRD5A3,HINT2,DKKL1,APOB,EBP,PRKAG2,NR1H4,CYP7A1,ASAH1,CYP7B1,OSBP,DKK3,CYP2R1,ERLIN1,SRD5A1,CYB5R1,SNAI1,MSMO1,SC5D,ABCB11,OSBPL2,SCAP,HSD17B7,POR,OSBPL6,TM7SF2,OSBPL1A,FDX1,LPCAT3,WNT4,CYP27A1,CH25H,HSD17B10,MED1,FGFR4,DGKQ,OSBPL7,ERG28,CYP46A1,DHRS11,SREBF1,ACAA2,CACNA1H,ABCD3,GFI1,HSD11B2,SDR42E1,AMACR,STARD4,INSIG2,FGF1	grey	VSMC_M10
GO:0070830	0.96	0.07	18	44	bicellular tight junction assembly	BP	1	SRF,CLDN19,WNT11,IKBKB,NPHP1,MARVELD2,CLDN34,SNAI1,DLG1,FZD5,GPBAR1,RAMP2,CLDN7,MARVELD3,MICALL2,CLDN15,CLDN1,APC	grey	VSMC_M10
GO:0046165	0.96	0.05	49	108	alcohol biosynthetic process	BP	1	CYP27B1,AKR1B1,PLPP6,SRD5A3,SPTLC1,IPPK,PLEK,APOB,SPHK2,DHFR,EBP,ITPKC,ACER3,SPTLC3,CYP7A1,ASAH1,DKK3,CYP2R1,P2RY1,PTK2B,SPR,ITPKA,ERLIN1,MSMO1,GPER1,SC5D,IP6K2,NTSR1,SCAP,HSD17B7,POR,PTH1R,TM7SF2,LPCAT3,WNT4,CYP27A1,GCH1,DGKQ,SREBF1,IMPA2,ACAA2,CACNA1H,PARK7,GFI1,DHDDS,ACER2,INSIG2,FGF1,PCBD2	grey	VSMC_M10
GO:0044703	0.96	0.04	345	688	multi-organism reproductive process	BP	1	TAC3,TBPL1,TRIM36,GLI1,YTHDC2,B4GALNT1,CYP27B1,ATAT1,ESR1,TSPAN8,MAPK8IP2,IGF2R,MOV10L1,PACRG,QKI,FBLN1,BRD2,GDF9,ROS1,MCM9,HSF2,UBE2B,CATSPER3,WASHC5,TOB2,SMAD5,AGO2,H3F3C,FANCC,AKR1B1,TUT7,DMC1,PLA2G6,PICK1,SPATA31D3,MYH9,CFAP69,FANCG,SMARCA2,CLIC5,TDRD6,KIT,RLN1,PPAT,CCIN,TSGA10,TDRD7,NLRP5,DNAJA1,FOXJ3,SCMH1,RIMS1,MSH2,RAD23B,SPACA6,YTHDC1,KLK14,CABS1,FANCL,GJA10,HERPUD2,GMCL1,PTN,NOBOX,CCDC155,DKKL1,CREM,TUT4,FOXO3,ARMC2,DLD,DDO,TXNRD3,APOB,IZUMO1,SPATA6,SPHK2,SPATA5,HDAC2,ADCY3,TTC26,TRPC3,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,PSG3,MLH1,ACOX1,PRDX3,FOXJ1,WDR48,TTC21A,THBD,PLAT,CCNB1IP1,TGFBR2,ACVR2A,SIRT2,MKKS,SPATA24,IDO1,ADAM18,PLCB1,MCM8,GOLGA3,PANK2,BTG1,SOHLH2,FUT10,TEX15,UBXN8,KATNAL1,STX2,ADRA2B,NPHP1,ACVR1B,ING2,HPGD,SPATA9,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,P2RY1,PTK2B,KMT2D,PRKAG1,SFMBT1,VDR,STC1,AP3B1,SLC38A2,ACVR1C,SLC38A1,CDYL,ABCC2,SPP1,SYCP1,DNAH1,PLA2G4B,NPM2,DPCD,OCA2,ADCY7,ROPN1L,SIAH1,BMPR1B,GAS2,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,HYAL3,SLC38A3,TESMIN,SLC9B1,COL16A1,PTHLH,PRKAR1A,INTS13,KRAS,SPATA2,RNF114,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,AGT,TSSK4,CIB1,CCDC87,DDX6,HDAC4,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,CLIC4,SEPT2,LIMK2,PATZ1,SP3,CATSPER2,OVOL1,ETV6,YBX3,LYZL6,WNT3,CADM1,OVGP1,SPATA32,GGT2,TTC12,BCL6,VGF,RPL10L,MEN1,DDX3X,COMT,SPAG16,ZCW	grey	VSMC_M10

GO:0050865	0.96	0.05	189	385	regulation of cell activation	BP	1	CD226,TNFAIP3,ENPP3,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,XRCC6,RAC2,FBXO7,TTBK1,TEC,TNFRSF21,NCK2,EXOSC3,MSH2,SLC46A2,PELI1,PLEK,IL4I1,TLR4,IL15,SPHK2,HMCES,BMI1,CST7,CD300LF,CLPTM1,NECTIN2,GAB2,MLH1,GLI2,UNC13D,MYD88,PIBF1,FOXJ1,PAXIP1,CYGB,THBD,IL15RA,TGFBR2,C1QTNF1,PAWR,SHLD1,PRNP,NCKAP1L,GAS6,PRKDC,SLC7A1,MFHAS1,TRAF6,SOX12,TOX,ZC3H8,IL1A,CAMK4,CEBPA,FER,CASP3,MEF2C,TMEM131L,IL7,PAG1,RASGRP1,NR1H3,RIPK2,AP3B1,F2RL1,MARCH7,SOX13,DMTN,NOD2,ZNF335,CD40,IGF2,CD200,LCK,BANK1,ICOSLG,BTN2A2,GPAM,PRKAR1A,GPR137B,HLX,TBC1D10C,UBASH3B,GPER1,SLAMF8,THEMIS2,FGR,RPS6KA1,SNX4,CD28,FCER1G,RUNX3,DLG1,PPP2R3C,ADAM8,DUSP10,BLOC1S6,PLA2G4A,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,LAG3,TNIP2,CD38,BST1,C12orf4,STAT5B,INHA,SCGB1A1,FOXP3,RASAL3,ZBTB1,SHLD2,CARD11,TNFRSF1B,SOX15,TBX21,STX4,ITGAM,SYT11,ZBTB7B,CHRNB2,CD19,LAT,IL4R,LDLR,BTK,CD74,CCL5,STXBP2,CCL2,YES1,NKAP,CD320,PRAM1,VAV1,TWSG1,IL7R,SUPT6H,PTPN2,SOCS1,DROSHA,TICAM1,ABAT,DNAJA3,PDPK1,PRKCZ,FOXF1,VAV3,KARS,STXBP1,GLMN,AP1G1,BCL10,MIR21,MIR27A,RHOA,HAVCR1,LST1,BLOC1S3,SOX4,FADD,DPP4,CD46,MIR125A,THY1,WNT5A,FGL2,IL33,CD70,TNFSF9,TSLP,ZFP36L2,LAX1,EFNB3,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0032006	0.96	0.06	37	84	regulation of TOR signaling	BP	1	EPM2A,ROS1,RRAGD,KPTN,SESN3,SZT2,PIP4P1,RPTOR,NCKAP1L,GAS6,LARS,TMEM127,SLC38A9,ARNTL,MAPKAPK5,TTI1,TBCK,PDCD6,GPR137B,DYRK3,SH3BP4,SIK3,GPR137,ARAF,OTUD5,RRAGB,DGKQ,SMCR8,CLEC16A,TNFAIP8L1,MLST8,TSC1,LAMTOR5,WDR59,MIR199A1,LAMTOR2,RNF152	grey	VSMC_M10
GO:0060236	0.96	0.08	12	31	regulation of mitotic spindle organization	BP	1	VPS4B,HSPA1B,CHMP2A,CHMP2B,CHMP4C,FSD1,PKD1,CHMP1A,PSRC1,GPSM2,CCSAP,DRG1	grey	VSMC_M10
GO:0002063	0.96	0.08	10	27	chondrocyte development	BP	1	COL27A1,SOX9,TSKU,TGFBR2,BMPR1B,SULF2,PTHLH,AXIN2,FGF18,RFLNB	grey	VSMC_M10
GO:0050435	0.96	0.07	21	50	amyloid-beta metabolic process	BP	1	NTRK2,RTN4,PRNP,IDE,CASP3,MME,SLC2A13,SORL1,BACE1,RTN1,HAP1,EPHA4,PSEN2,PSEN1,TMED10,EFNA1,ABCA7,MIR29A,MIR24-1,MIR339,APH1B	grey	VSMC_M10
GO:0008543	0.96	0.06	25	59	fibroblast growth factor receptor signaling pathway	BP	1	FRS2,FUZ,FGF21,SPRY1,PRKD2,SPRY2,KL,FGFBP3,FGF5,DSTYK,SULF2,LRIT3,WNT4,FLRT1,FGFR3,CHURC1,FGFR4,FGF18,NGFR,FGF22,NOG,WNT5A,SHISA2,FGF1,FRS3	grey	VSMC_M10
GO:1904996	0.96	0.10	5	15	positive regulation of leukocyte adhesion to vascular endothelial cell	BP	1	TRAF6,ITGA4,MIR21,RHOA,FUT4	grey	VSMC_M10
GO:0009988	0.96	0.07	14	35	cell-cell recognition	BP	1	NCK2,IZUMO1,ADAM18,EPHB1,DLG1,OVGP1,DOCK2,UBAP2L,SPESP1,ZP2,GLIPR1L2,HAVCR2,SPA17,TMPRSS12	grey	VSMC_M10
GO:1904356	0.96	0.06	24	57	regulation of telomere maintenance via telomere lengthening	BP	1	MAP3K4,MAPK15,POT1,ATR,HMBOX1,MAPKAPK5,TENT4B,STN1,RTEL1,XRCC5,MAPK1,PARP1,GNL3L,SMG5,CTC1,PIF1,MAPK3,PARN,ERCC4,SLX4,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0031670	0.96	0.07	16	40	cellular response to nutrient	BP	1	CYP27B1,SNW1,PIM1,SRF,PTN,TNC,IL15,GAS6,NR1H4,USF2,VDR,USF1,MED1,MIR125B1,TRIM24,BGLAP	grey	VSMC_M10
GO:0016236	0.96	0.05	127	265	macroautophagy	BP	1	VPS4B,ATG12,PIP4K2C,EPM2A,TMEM74,PRKN,RNF5,KLHL3,C6orf106,EXOC4,NRBP2,SPTLC1,GAPDH,CHMP2A,RAB23,STX17,ATP6V1E2,SNX14,NOD1,ATP6V1C2,VPS41,VPS35,SCOC,ATG5,MFSD8,SESN3,RAB7A,PIP4K2A,RUBCNL,ATP6V0E2,OPTN,RALB,ATP6V0B,MTMR14,SNX5,USP36,ATG16L2,TMEM173,RAB5A,FEZ2,DCN,DDRGK1,ULK1,VPS16,NSFL1C,ATP6V1H,CASP3,LIX1,CHMP2B,TBC1D12,HTRA2,AUP1,CHMP4C,ATG10,RIPK2,TP53INP1,NOD2,VPS39,LZTS1,ATP6V1B2,TEX264,SEC22B,EI24,TMEM39A,TCIRG1,VTI1A,ADPRH,USP30,YOD1,ATG16L1,BAG3,MTMR3,UFC1,RUBCN,RAB1B,VPS37D,SNX6,SNX32,PIKFYVE,VPS26A,ATG2A,TBC1D14,HTT,RETREG3,ATP6V0A1,PINK1,ATG9A,SNAP29,TBC1D25,ATP13A2,WIPI2,PHF23,ATP6V1D,VPS13D,MFN2,VPS13C,ZFYVE1,PSEN1,MAPK3,AC138894.1,CALM1,SNAPIN,LARP1,VMP1,ATG2B,NPC1,SMCR8,CDK5R1,LAMP2,IFT20,CLEC16A,MTM1,EMC6,ATP6V0C,IKBKG,GPSM1,GNAI3,KIAA1324,TSC1,SH3GLB1,VPS4A,PJVK,BNIP3L,IRGM,TIGAR,HSPB8,CAPNS1	grey	VSMC_M10
GO:0034976	0.96	0.05	106	222	response to endoplasmic reticulum stress	BP	1	MAP3K5,CANX,PRKN,RNF5,DERL1,BAK1,ATF4,PLA2G6,FOXRED2,NCK2,ERMP1,SEC61B,ERP44,ECPAS,CXCL8,HERPUD2,NR1H2,FGF21,PDIA3,AQP11,UBXN4,UGGT2,FBXO17,DNAJC18,NPLOC4,UBAC2,TMTC4,EIF2AK2,DDRGK1,PPP2CB,UBXN8,TRIB3,PIK3R1,USP25,TMBIM6,AUP1,ATG10,EIF2AK4,NR1H3,TMEM67,OPA1,AMFR,RNFT2,COL4A3BP,ERLIN1,NHLRC1,RHBDD1,CCND1,GET4,FICD,USP13,YOD1,USP19,QRICH1,HYOU1,GORASP2,UFC1,RNF185,TBL2,RHBDD2,TMCO1,EDEM3,NFE2L2,SYVN1,DERL3,DDX3X,TMUB2,DNAJC10,LPCAT3,DNAJB12,TMEM129,ANKZF1,DNAJB2,SDF2L1,BHLHA15,CALR3,FBXO2,TARDBP,ATP2A1,SEL1L,CREB3L4,ANKS4B,SCAMP5,TTC23L,PTPN2,JUN,CREB3L3,BCAP31,SGTA,TRAF2,ABCA7,TMEM259,SEC16A,PARK7,HSPA5,DAB2IP,MIR199A1,RNFT1,FAM8A1,DDIT3,BCL2L11,PPP1R15A,CEBPB,UBE2G2,NRBF2,DERL2	grey	VSMC_M10

GO:0016051	0.96	0.05	72	155	carbohydrate biosynthetic process	BP	1	PPARA,AKR1B1,ATF4,GPT,GNMT,CRY1,SLC25A13,CHST10,HAS1,PPP4R3B,ZNF692,PLEK,FAM3C,AKR1A1,EPM2AIP1,PPP1CB,CSGALNACT1,AKT2,SIRT7,PPP1R3B,GPI,NLN,GBE1,B3GNT4,SORBS1,GPD1,P2RY1,PTK2B,ST3GAL6,IGF2,NHLRC1,IRS1,SIK1,MST1,PPP1R3E,EGF,B3GALT1,GPER1,PC,PPP1R3D,SLC37A4,PER2,NTSR1,PASK,PTH1R,SORD,MGAT2,B3GALNT1,PRKAG3,AC022400.6,PPP1R3F,DDB1,CHST12,DGKQ,OGT,CRTC2,INSR,LEPR,IMPA2,PTPN2,INPP5K,AGL,ST3GAL2,HAS3,ST6GALNAC5,ACADM,FBP2,FUT4,NNMT,HS2ST1,ARPP19,ST8SIA6	grey	VSMC_M10
GO:0034349	0.96	0.10	5	15	glial cell apoptotic process	BP	1	TNFRSF21,GAS6,CASP3,CCL2,TRAF2	grey	VSMC_M10
GO:0032456	0.96	0.06	30	70	endocytic recycling	BP	1	VPS52,MICALL1,VPS50,BVES,VPS35,EPS15,ANKRD50,RAB7A,CCDC93,ANKRD27,VPS26C,VPS39,DENND1B,SORL1,RAB17,SNX4,SNX27,STX6,VPS26A,EHD1,NSG1,GRIPAP1,RAB8A,SNX12,RAB11A,ARHGAP44,VPS35L,VPS53,DENND1A,MICALL2	grey	VSMC_M10
GO:0006658	0.96	0.08	8	22	phosphatidylserine metabolic process	BP	1	ABHD16A,MBOAT2,SERINC5,PLA1A,LPCAT3,ABHD12B,SLC27A1,PLA2G15	grey	VSMC_M10
GO:0050818	0.96	0.06	23	54	regulation of coagulation	BP	1	SERPINB2,TSPAN8,ENPP4,HS3ST5,THBD,PLAT,C1QTNF1,F2RL1,F2R,ANO6,DMTN,ADTRP,FAP,UBASH3B,USF1,NFE2L2,SERPINC1,F12,ANXA2,PSEN1,ABAT,SERPINF2,FGA	grey	VSMC_M10
GO:0060412	0.96	0.07	13	34	ventricular septum morphogenesis	BP	1	WNT11,TGFBR2,ROBO1,ROBO2,TGFB2,SAV1,BMPR1A,RBPJ,SOX4,NOG,WNT5A,NKX2-5,HEY2	grey	VSMC_M10
GO:0032331	0.96	0.08	8	22	negative regulation of chondrocyte differentiation	BP	1	MKX,SOX9,GLI2,RARB,PTHLH,NKX3-2,ADAMTS12,RFLNB	grey	VSMC_M10
GO:0010566	0.96	0.10	5	15	regulation of ketone biosynthetic process	BP	1	DKKL1,DKK3,SIRT5,WNT4,DGKQ	grey	VSMC_M10
GO:0002719	0.97	0.10	5	15	negative regulation of cytokine production involved in immune response	BP	1	CD96,TGFB2,BCL6,FOXP3,TBX21	grey	VSMC_M10
GO:0043968	0.97	0.10	5	15	histone H2A acetylation	BP	1	YEATS4,ING3,SPHK2,EP400,NAA40	grey	VSMC_M10
GO:0006356	0.97	0.07	12	31	regulation of transcription by RNA polymerase I	BP	1	MARS,ATF4,IPPK,POU4F1,SIRT7,RASL11A,HEATR1,DEDD,H2AFY2,DDX11,PHF8,POLR2K	grey	VSMC_M10
GO:0006656	0.97	0.08	9	24	phosphatidylcholine biosynthetic process	BP	1	CDS1,LPCAT1,CHKA,PCYT1A,LPCAT3,SLC27A1,ABHD3,FABP5,PEMT	grey	VSMC_M10
GO:1903018	0.97	0.07	14	35	regulation of glycoprotein metabolic process	BP	1	AGO2,FKTN,IL15,HBEGF,PAWR,PLCB1,SLC2A10,TCF7L2,RAB1B,SOAT1,POMT2,ABCA7,ACER2,IL33	grey	VSMC_M10
GO:0009225	0.97	0.07	13	33	nucleotide-sugar metabolic process	BP	1	GFPT2,PMM1,GNPDA2,GALT,UXS1,TGDS,CSGALNACT1,UGGT2,DPAGT1,MGAT1,MPI,PMM2,FUK	grey	VSMC_M10
GO:0010737	0.97	0.09	7	20	protein kinase A signaling	BP	1	AKAP7,LCP1,TCIM,ADGRV1,SPATC1L,TTN,PDE4A	grey	VSMC_M10
GO:0032504	0.97	0.04	284	571	multicellular organism reproduction	BP	1	TBPL1,GLI1,YTHDC2,B4GALNT1,CYP27B1,ATAT1,ESR1,TSPAN8,MAPK8IP2,IGF2R,MOV10L1,PACRG,QKI,BRD2,GDF9,ROS1,MCM9,HSF2,UBE2B,CATSPER3,WASHC5,TOB2,SMAD5,H3F3C,FANCC,AKR1B1,TUT7,DMC1,PLA2G6,PICK1,SPATA31D3,CFAP69,FANCG,SMARCA2,TDRD6,KIT,PPAT,CCIN,TSGA10,TDRD7,DNAJA1,FOXJ3,SCMH1,MSH2,RAD23B,SPACA6,YTHDC1,KLK14,CABS1,FANCL,GJA10,HERPUD2,GMCL1,PTN,EGFR,NOBOX,CCDC155,DKKL1,CREM,TUT4,FOXO3,ARMC2,DLD,DDO,TXNRD3,APOB,IZUMO1,SPATA6,SPATA5,HDAC2,TTC26,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,MLH1,ACOX1,PRDX3,TIMP4,FOXJ1,WDR48,TTC21A,CCNB1IP1,ARRB1,ACVR2A,SIRT2,MKKS,SPATA24,ADAM18,MCM8,GOLGA3,PANK2,BTG1,SOHLH2,TEX15,KATNAL1,NPHP1,CASP3,ING2,HPGD,SPATA9,ROBO2,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,P2RY1,PTK2B,KMT2D,PRKAG1,SFMBT1,VDR,STC1,AP3B1,CDYL,SPP1,SYCP1,DNAH1,NPM2,DPCD,OCA2,ADCY7,ROPN1L,SIAH1,BMPR1B,GAS2,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,HYAL3,MAP2K6,TESMIN,TGFB2,PRKAR1A,SPATA2,RNF114,ADNP,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,TSSK4,CIB1,CCDC87,DDX6,HDAC4,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,SEPT2,LIMK2,PATZ1,SP3,CATSPER2,OVOL1,ETV6,YBX3,LYZL6,WNT3,CADM1,SPATA32,GGT2,TTC12,BCL6,RPL10L,MEN1,DDX3X,COMT,SPAG16,ZCWPW1,WNT4,CTSV,BIRC3,PTPRN,ADCY10,PARP11,MAPK1,STAT5B,CALR3,KDM5A,ZMYND15,MNS1,YBX2,THRA,MED1,SPIN2A,SEPT1,ITGA3,MYCBPAP,MAPK3,UBE2Q1,VIPAS39,SOX30,CCDC42,CREB3L4,EPOR,IL4R,SPES	grey	VSMC_M10
GO:0051092	0.97	0.05	54	119	positive regulation of NF-kappaB transcription factor activity	BP	1	HSPA1B,AGER,CAT,NOD1,TRIM32,TLR4,TRAF1,PRKD2,MYD88,PRDX3,IRAK2,ALK,IKBKB,EIF2AK2,DDRGK1,TRAF6,FER,RHEBL1,RIPK2,RIPK1,PIDD1,NOD2,CD40,RAB7B,SLCO3A1,KRAS,AGT,CIB1,TRAF5,TRIM52,RTKN2,ADAM8,TNFSF18,RNF25,STAT3,CARD11,RPS6KA5,S100A8,TRIM37,PRKCB,BTK,CAMK2A,TICAM1,PRKCZ,TRAF2,IKBKG,LAMTOR5,BCL10,S100A12,TRIM68,TRIM34,WNT5A,UBE2N,RPS6KA4	grey	VSMC_M10
GO:0051090	0.97	0.04	159	328	regulation of DNA-binding transcription factor activity	BP	1	TNFAIP3,ESR1,STK3,HSPA1B,FZD6,AGER,IL5,TRIB1,PTCH1,PIM1,SMO,HSF1,MDFI,FOXH1,LRRC14,CDKN2A,SRF,FZD1,NFKBIE,KIT,ADGRF1,CAT,MTURN,NOD1,PELI1,ANXA4,ARHGEF5,TRIM32,TLR4,TRAF1,SFRP4,FAF1,HDAC2,PRKD2,MYD88,PRDX3,TAF3,FOXJ1,PAXIP1,IRAK2,POU4F1,ALK,ARRB1,EOMES,IKBKB,BHLHE40,NFKBIB,TMEM173,PURA,EIF2AK2,PRNP,MAVS,TFDP1,DDRGK1,GAS6,TRAF6,HCK,FER,HAND2,SETD6,RHEBL1,EIF2AK4,NLRC5,RIPK2,OTULIN,NKX3-1,NKX6-1,RIPK1,PIDD1,PKD2,NOD2,CD40,RAB7B,SUFU,CD200,SIK1,PPP3CA,SP100,TCF7L2,SLCO3A1,CMKLR1,KRAS,HCLS1,OPRD1,AGT,TSSK4,CIB1,TRAF5,HES6,CARF,HDAC4,TRIM52,RTKN2,ADAM8,PPP2R5B,MEN1,SAV1,TNFSF18,CRTC1,RNF25,STK36,PINK1,STAT3,NWD1,KDM5A,FOXP3,DVL2,CARD11,PEX14,PYDC1,TAF1,MAPK3,SMAD3,CRTC2,MAP2K5,RPS6KA5,S100A8,TRIM37,PRKCB,BTK,KEAP1,BEX1,PSMD10,TRAF3,CAMK2A,PPARGC1B,TICAM1,LRP8,PIAS4,PRKCZ,PKD1,TRAF2,IKBKG,PARK7,LAMTOR5,GFI1,WWP2,BCL10,DAB2IP,MIR199A1,MIR21,MIR27A,S100A12,TAF12,TRIM68,TRIM34,CREBZF,MIR125A,RWDD3,WNT5A,COMMD6,DDIT3,COMMD7,RGCC,UBE2N,C3orf33,RPS6KA4,HAVCR2,WNT2	grey	VSMC_M10

GO:0019098	0.97	0.10	5	15	reproductive behavior	BP	1	MAPK8IP2,HDAC2,HDAC4,THRA,UBE2Q1	grey	VSMC_M10
GO:0032986	0.97	0.10	5	15	protein-DNA complex disassembly	BP	1	SMARCC2,MYC,SMARCD1,RPL23,ARID1A	grey	VSMC_M10
GO:0002009	0.97	0.04	200	412	morphogenesis of an epithelium	BP	1	ESR1,FRS2,STK3,FZD6,BRD2,MTSS1,RSPO3,MYC,KLHL3,PTCH1,PODXL,SOX10,SMO,FOXH1,PTK7,SRF,CA9,ROR2,SEMA4C,SOSTDC1,SIX2,BRSK1,KLK14,HOXA13,AREG,EPHA7,MET,TNC,FUZ,TEAD2,MYCN,OSR1,INTU,SPRY1,PLXNA1,ARHGAP12,BBS7,RAB10,PRKD2,SETDB2,SOX9,CLASP2,GLI2,MEGF8,PCDH8,IFT172,GZF1,SPRY2,WNT11,TGFBR2,OVOL2,JAG1,MKKS,ACTG1,HBEGF,FERMT1,SPINT2,FREM2,CEP290,SPEF1,SEMA3A,FOXP1,SYNE4,RYK,TRAF6,TCF15,NPHP1,RET,CYP7B1,PAX8,CASP3,HAND2,EYA1,FMN1,FZD3,MEF2C,VEGFC,FRAS1,TIAM1,VDR,NKX3-1,OPA1,TBX5,IFT52,ARHGAP24,SPINT1,RPGRIP1L,RREB1,PKD2,STK4,TFAP2A,PAX2,SALL1,VANGL1,PRICKLE1,NKD1,RYR2,SUFU,IRX2,ALDH1A3,TGFB2,PRKX,DAG1,AJUBA,KRAS,SNAI1,EGF,JHY,ZNRF3,AGT,GBX2,DVL3,KDF1,NFATC4,FZD7,TRAF3IP1,LAMA5,CLIC4,GRHL3,DLG1,LUZP1,SETD2,FZD5,STOX1,PLOD3,CTSH,PDCD10,CXCR2,WNT4,GORAB,EXOC5,VCL,DAAM1,TULP3,EPHA4,ARHGEF19,LIAS,ACTB,MAGED1,DVL2,MPP5,TCAP,RBPJ,MED1,ALDH1A2,PSEN1,TGFB1I1,NGFR,CITED1,SMAD3,NTN1,MKS1,BTBD7,MYO9A,TBX4,TBX2,LHX1,LAMA3,CSF1R,MIB1,CAMSAP3,JAG2,LAMA1,IFT20,ADAMTS12,GPC3,SKI,PKD1,SAPCD2,RNF207,SOX8,CELSR2,COL5A1,TSC1,FOXF1,LCN2,ENG,GLMN,BCL10,ESRP2,CARMIL2,MIR21,RHOA,VASP,SERPINB5,SOX4,ACVRL1,NOG,LBX1,WNT5A,LBX2,SIX1,CELSR3,C2CD3,GRB2,RALA,LIF,NKX2-5,FGF1,WNT2	grey	VSMC_M10
GO:0051043	0.97	0.09	7	20	regulation of membrane protein ectodomain proteolysis	BP	1	TIMP4,SH3D19,GPLD1,ADRA2A,LRIG2,ADAM8,TNFRSF1B	grey	VSMC_M10
GO:1904666	0.97	0.09	7	19	regulation of ubiquitin protein ligase activity	BP	1	SKP1,USP44,RPL23,DNM1L,RPL11,FZR1,BAG2	grey	VSMC_M10
GO:0060048	0.97	0.05	46	103	cardiac muscle contraction	BP	1	NEDD4L,SMAD5,TNNI3,ASB3,TRPM4,CACNB2,SCN5A,SCN1A,GPD1L,STC1,KCNJ3,TNNC1,KCNE2,DSP,CASQ2,RYR2,PKP2,KCNJ2,MAP2K6,TNNI1,MYH7,GRK2,ANK2,ACE2,ATP1A2,ACTC1,SLC9A1,HDAC4,SCN4B,NOS1AP,DLG1,TTN,ATP1B1,TCAP,CACNA1G,ATP2A1,CALM1,DSG2,RNF207,DMD,CHGA,KCNH2,SCN2B,KCNJ8,HCN4,NKX2-5	grey	VSMC_M10
GO:0008016	0.97	0.05	66	144	regulation of heart contraction	BP	1	SLC1A1,TNNI3,EPAS1,ASB3,BVES,TRPM4,SLC8A2,CACNB2,ATP1A3,CELF2,SCN5A,GPD1L,HBEGF,ADRA1D,SEMA3A,STC1,KCNJ3,TBX5,KCNE2,DSP,CASQ2,KCNIP2,RYR2,PKP2,KCNJ2,TGFB2,MYH7,GRK2,ANK2,AGT,ACE2,ATP1A2,SLC9A1,HDAC4,SCN4B,NOS1AP,DLG1,GCH1,ATP1B1,DES,SLC4A3,THRA,ATP1B2,CACNA1G,ATP2A1,CALM1,TBX2,DSG2,SREBF1,ISL1,CYP2J2,ATP2B3,TRPV1,RNF207,CACNA1H,DMD,CHGA,TMEM65,KCNH2,SCN2B,RGS4,POPDC2,HCN4,NKX2-5,HEY2,KCNG2	grey	VSMC_M10
GO:0006828	0.97	0.11	4	13	manganese ion transport	BP	1	TRPC3,SLC30A10,SLC11A1,ATP2C2	grey	VSMC_M10
GO:0043500	0.97	0.05	39	88	muscle adaptation	BP	1	PPARA,PI16,IL15,FOXO3,TRPC3,KDM4A,SCN5A,HAND2,TNNC1,JARID2,PDE9A,PPP3CA,TNNI1,DAG1,MYH7,GTF2IRD1,AGT,SLC9A1,MYOZ2,CASQ1,ACTN3,HDAC4,MYOZ1,PRKAG3,CAMK2G,CAMTA2,PARP1,TCAP,TNFRSF1B,SMAD3,YY1,GATA6,CYBA,MIR199A1,MIR21,MIR25,NOL3,RGS4,HEY2	grey	VSMC_M10
GO:0060284	0.97	0.04	186	384	regulation of cell development	BP	1	LRP1,SEMA6A,RAB21,SNW1,TIAM2,FBLN1,IL5,TSPO,FSTL4,SYNGAP1,TRIB1,PLXNA4,NTRK2,SOX10,SMO,ZDHHC21,DAAM2,SRF,TTBK1,RFX3,KIT,SEMA4D,S1PR3,SEMA4C,RTN4,RUFY3,EPHA7,PTN,ITGB1BP1,EGFR,TRIM32,MYCN,PLXNA1,HDAC2,GOLGA4,MEGF8,KDM4A,UNC13D,XRCC2,NUMBL,POU4F1,SS18L2,HOOK3,IKBKB,BHLHE40,SIRT2,PLCB1,RAC3,ARHGEF7,SEMA3D,SPART,PLXNC1,SEMA3A,ULK1,LMOD3,PRKDC,RYK,PLAG1,RET,ANKRD27,FAIM,ROBO1,ROBO2,ARNTL,FBXW7,FZD3,SEMA4F,VEGFC,TLX2,CUX2,MME,RAPGEF2,TIAM1,DOCK5,SYNJ1,OPA1,NKX6-1,ZFYVE27,SPINT1,SEMA3G,RREB1,ITPKA,SPP1,CYFIP1,DMTN,SEMA4G,ZNF335,BDNF,RNF10,KIAA0319,NEURL1,DNM1L,CARMIL1,HDAC1,PPP3CA,CAPRIN2,SLC9B2,SEMA3F,PTHLH,DAG1,AXIN2,ADNP,AP1AR,YTHDF2,DISC1,SORL1,GPER1,SLAMF8,CASS4,CIB1,CERS2,NFATC4,HES6,PER2,ACTN3,HDAC4,SS18L1,CDKL5,DLX1,DOCK1,MELTF,CSPG5,WNT3,DUSP10,MAPT,SEMA6D,TNR,FN1,XRCC5,FBN1,NIN,VCL,OBSL1,HAP1,EPHA4,BMPR1A,SPEN,TNFRSF1B,RGS14,PRPF19,PSEN1,SEMA4A,TRIM46,NDEL1,RAB11A,MAP2K1,NTN1,LDLR,GPR68,DNM2,PARP6,GPRASP2,BHLHB9,TRPV2,FBXO22,CDK5R1,DOCK7,MBD1,DAB1,RFLNB,LRP8,CRK,TRPV1,L1CAM,SKI,ARHGAP4,ATP6AP1,PLXNA3,SOX8,AMIGO1,FBXO31,MIR222,MIR125B1,FGA,FOXG1,GPR37L1,HOXB3,NOG,THY1,WNT5A,LIF,YWHAH,EFNB3,PITX3,HEY2,WNT2	grey	VSMC_M10
GO:0010171	0.97	0.07	15	38	body morphogenesis	BP	1	DLX5,FUZ,CLASP2,CSRNP1,MAB21L2,CRISPLD1,DAG1,PHLDB1,WNT3,GREM2,STRA6,GPC3,SKI,ANKRD11,NOG	grey	VSMC_M10
GO:1901292	0.97	0.06	30	69	nucleoside phosphate catabolic process	BP	1	PDE7B,ENPP3,DPYS,PDE10A,SMPDL3A,GDA,NT5E,ENTPD6,NUDT15,NUDT5,MBD4,NUDT16,NUDT12,AMPD3,ENTPD4,FITM2,NUDT18,PDE9A,NUDT17,PDE8A,UPB1,PDE4A,NEIL1,NT5M,NTHL1,MLYCD,ENTPD5,NUDT19,HINT1,UPP1	grey	VSMC_M10
GO:0030195	0.97	0.07	14	35	negative regulation of blood coagulation	BP	1	SERPINB2,TSPAN8,THBD,PLAT,C1QTNF1,ADTRP,FAP,UBASH3B,USF1,F12,ANXA2,ABAT,SERPINF2,FGA	grey	VSMC_M10

GO:0034614	0.97	0.05	57	124	cellular response to reactive oxygen species	BP	1	MAP3K5,TNFAIP3,ERCC6L2,FANCC,MAPK13,HSF1,GPR37,PRDX1,AQP1,ZNF277,MET,EGFR,UCP1,FOXO3,DHFR,HDAC2,PRDX3,PAWR,FER,RIPK1,PKD2,PAX2,PXN,GLRX2,FBLN5,NCF1,PDE8A,NFE2L2,MAPT,PDCD10,GCH1,PINK1,ANKZF1,MAPK1,SOD3,KDM6B,FOS,MAPK3,MPO,BTK,MAPK7,PPARGC1B,STK26,JUN,PARK7,LCN2,NQO1,MIR21,PJVK,GPR37L1,ZNF580,IMPACT,FXN,TXN,CBX8,PPIF,PDGFD	grey	VSMC_M10
GO:0008037	0.97	0.05	43	97	cell recognition	BP	1	CD226,TNFRSF21,NCK2,CNTNAP3,RTN4,YWHAZ,NRCAM,IZUMO1,MEGF8,ADAM18,SEMA3A,TUB,EPHB1,CASP3,ROBO1,ROBO2,NCAM2,CRTAC1,GAP43,EPHB3,DLG1,CADM1,MYPN,OVGP1,EPHA4,PEAR1,SPON2,DOCK2,UBAP2L,SPESP1,ZP2,COLEC12,CDK5R1,EMB,BSG,AMIGO1,CNTN2,FOXG1,GLIPR1L2,EFNB3,HAVCR2,SPA17,TMPRSS12	grey	VSMC_M10
GO:0032963	0.97	0.05	34	78	collagen metabolic process	BP	1	TNXB,TMPRSS6,TRAM2,ADAMTS3,HDAC2,CYGB,CYP7A1,MMP15,F2R,FAP,AMELX,MMP21,PLOD3,P3H2,MMP11,VSIR,WNT4,SUCO,MMP13,MMP3,P3H4,VIPAS39,LARP6,CIITA,MMP23B,SERPINF2,MMP25,COL5A1,ENG,MIR29A,MIR21,RGCC,P3H3,CBX8	grey	VSMC_M10
GO:0001819	0.97	0.04	147	304	positive regulation of cytokine production	BP	1	CD226,LRP1,HSPA1B,AGPAT1,AGER,GPSM3,HLA-DPB1,ATF4,MAPK14,MAPK13,IRF5,KIT,GAPDH,SPTBN1,NOD1,AKIRIN2,PELI1,RSAD2,TRIM32,TLR4,IL15,SPHK2,HDAC2,C5AR1,PANX1,PRKD2,PHB,LACC1,MYD88,PIBF1,WNT11,TMEM173,PLCB1,FERMT1,EIF2AK2,LUM,MAVS,FOXP1,IRF7,TRAF6,NR1H4,IL1A,PIK3R1,PTPRJ,IL7,P2RX7,RASGRP1,OAS3,RIPK2,F2RL1,F2R,RIPK1,POLR3D,PLA2R1,NOD2,CD40,RAB7B,IFIH1,CD200,HDAC1,TRPV4,ADRA2A,SULF2,POLR3C,DENND1B,TLR5,MAPKAPK2,SORL1,AGT,FGR,ARNT,NFATC4,OSM,CD28,FCER1G,SETD2,ADAM8,CADM1,CREB1,FZD5,IL16,HK1,IL12A,DDX3X,SLC11A1,STAT3,STAT5B,POLR3A,FOXP3,BMPR1A,CARD11,TNFRSF8,SPON2,PSEN1,PYDC1,TMED10,BATF,ZBTB7B,IL6R,SMAD3,IL4R,NOX5,S100A13,G3BP1,SCAMP5,CD74,RIOK3,CSF1R,GATA6,ISL1,RNF135,PTGER4,C3,NOS2,TICAM1,SERPINF2,PRKCZ,TRAF2,AGPAT2,PARK7,CYBA,SLC7A5,LAMTOR5,GLMN,BCL10,MIR21,MIR27B,OAS1,DEFB124,FADD,CD46,CASP8,ZCCHC3,ZNF580,WNT5A,INAVA,IL33,DDIT3,RGCC,C1QTNF4,TSLP,HRAS,CEBPB,EREG,HAVCR2,IL17D,IL17B	grey	VSMC_M10
GO:0048524	0.97	0.06	23	55	positive regulation of viral process	BP	1	PABPC1,PPARA,CHMP2A,RAB7A,RSF1,KPNA2,CHMP2B,TMEM39A,ADARB1,NR5A2,STAU1,PC,CD28,DDX3X,DDB1,HACD3,LARP1,CD74,CCL5,FMR1,VPS4A,TBC1D20,ZNF502	grey	VSMC_M10
GO:0046885	0.97	0.08	7	20	regulation of hormone biosynthetic process	BP	1	CYP27B1,DKK3,ARNT,POR,WNT4,DGKQ,GFI1	grey	VSMC_M10
GO:0070897	0.97	0.07	12	31	transcription preinitiation complex assembly	BP	1	BAZ2A,ESR1,TAF7,BRF2,TAF9,CREB1,TAF6,THRA,TAF1,RRN3,TAF1C,TAF12	grey	VSMC_M10
GO:0051653	0.97	0.06	20	49	spindle localization	BP	1	MYH9,NLRP5,CDK5RAP2,CCDC155,SPRY1,CLASP2,LLGL2,SPRY2,NSFL1C,MOS,MCPH1,CFL1,HTT,KPNB1,NDEL1,TLE6,SAPCD2,SPIRE2,GPSM2,OOEP	grey	VSMC_M10
GO:0072175	0.97	0.05	52	116	epithelial tube formation	BP	1	STK3,FZD6,BRD2,PTCH1,PODXL,PTK7,SEMA4C,FUZ,TEAD2,OSR1,SOX9,IFT172,OVOL2,SPINT2,CEP290,TRAF6,RET,PAX8,CASP3,FZD3,OPA1,IFT52,SPINT1,STK4,PAX2,PRICKLE1,SUFU,IRX2,TGFB2,EGF,DVL3,GRHL3,LUZP1,SETD2,WNT4,TULP3,LIAS,DVL2,TCAP,MKS1,MIB1,SKI,SOX8,TSC1,GLMN,BCL10,VASP,SOX4,NOG,WNT5A,SIX1,RALA	grey	VSMC_M10
GO:0048015	0.97	0.05	60	133	phosphatidylinositol-mediated signaling	BP	1	ERBB3,RGL2,PTK2,NTRK2,TEK,KIT,ROR2,SEMA4D,CAT,EGFR,SOX9,FBXL2,GAB2,SIRT2,PLCB1,PLCL2,DCN,FLT1,PIK3CB,PITPNM2,PREX2,PIK3R1,PLCE1,RASGRP1,PLCH1,NKX3-1,F2RL1,F2R,IRS1,TGFB2,NCF1,EGF,HCLS1,GPER1,AGT,FGR,CBL,OSM,CD28,PIK3IP1,FN1,NYAP1,PTPN6,PLCD4,PI4KA,PEAR1,OGT,HAX1,PIK3R5,INSR,CCL5,CSF1R,PIP5K1C,DAB2IP,MIR21,ENTPD5,STAMBP,C3orf58,HCST,PDGFD	grey	VSMC_M10
GO:1900077	0.97	0.07	10	27	negative regulation of cellular response to insulin stimulus	BP	1	PIP4K2C,GRB10,PIP4K2A,IRS1,GRB14,PRKCB,PTPN2,SOCS1,INPP5K,PRKCZ	grey	VSMC_M10
GO:0015931	0.97	0.05	85	181	nucleobase-containing compound transport	BP	1	CPSF6,PHAX,QKI,ZC3H3,HSF1,NOL6,XPO5,SLC35B2,BICD2,LRPPRC,IGF2BP3,YTHDC1,PNPT1,XPO1,SLC35A1,IWS1,ABCC4,TGFBR2,KIF5C,NUP98,CHTOP,UPF3A,THOC7,NUP58,SLC35A4,CETN3,NUP54,SLC33A1,RIPK1,MX2,CALHM1,SLC35A5,DDX25,RFTN2,RTRAF,ABCC5,SLC29A2,NCBP2,SIDT2,POM121,SENP2,IGF2BP2,SETD2,ENY2,SLC29A3,SLC25A42,UPF1,PARP11,NXF1,SLC35A2,AHCTF1,AKAP8L,SLC29A4,CASC3,RSC1A1,FYTTD1,SMG5,RANBP17,SLC35B1,NRDE2,ALKBH5,LRRC8E,UPF3B,THOC2,SLC25A23,SLC25A41,SUPT6H,FMR1,NCBP3,SLC25A33,TSC1,NUP214,LRRC8A,SLC25A25,DDX19A,SLC35E3,SARNP,DDX19B,NXT2,SLC25A32,NUPL2,YBX1,MRPL18,SLC35C1,MAGOHB	grey	VSMC_M10
GO:0060986	0.97	0.07	10	27	endocrine hormone secretion	BP	1	GDF9,CRY1,C1QTNF1,RAB11FIP5,NKX3-1,CRY2,AGT,INHA,RAB8B,CRH	grey	VSMC_M10
GO:0097150	0.97	0.09	6	18	neuronal stem cell population maintenance	BP	1	FANCC,FOXO3,HOOK3,JAG1,MCPH1,SOX2	grey	VSMC_M10
GO:0018210	0.97	0.05	46	104	peptidyl-threonine modification	BP	1	TTBK1,PRKD2,PRKAG2,GALNT11,OXSR1,SPRY2,DYRK1B,TGFBR2,SIRT2,RPTOR,ULK1,PRKDC,EOGT,ACVR1B,CSNK2A2,RIPK2,DMTN,DCAF1,DYRK3,EGF,GRK2,TSSK4,GALNT2,STOX1,CEMIP,MARK2,MAPK1,WNK3,GALNT16,DGKQ,TAF1,MAP2K1,SBK1,CALM1,PRKCB,GALNT1,CDC42BPB,CAMK2A,CDK5R1,NLK,INPP5K,PDPK1,CDK10,IRGM,WNT5A,CADM4	grey	VSMC_M10
GO:0030193	0.97	0.06	21	50	regulation of blood coagulation	BP	1	SERPINB2,TSPAN8,ENPP4,THBD,PLAT,C1QTNF1,F2RL1,F2R,ANO6,DMTN,ADTRP,FAP,UBASH3B,USF1,NFE2L2,SERPINC1,F12,ANXA2,ABAT,SERPINF2,FGA	grey	VSMC_M10
GO:0035036	0.97	0.08	9	24	sperm-egg recognition	BP	1	IZUMO1,ADAM18,OVGP1,UBAP2L,SPESP1,ZP2,GLIPR1L2,SPA17,TMPRSS12	grey	VSMC_M10

GO:0016358	0.97	0.04	95	204	dendrite development	BP	1	NEDD4L,RAB21,MAPK8IP2,SULT4A1,FSTL4,SYNGAP1,ASAP1,RBFOX2,CHRNA3,NCK2,SEMA4D,SHANK1,PTN,HECW1,RTN4IP1,HDAC2,IQSEC1,ABI1,SS18L2,ALK,FARP1,TMEM106B,SEMA3A,EPHB1,PLK2,ANKRD27,PREX2,MEF2C,TLX2,CUX2,RAPGEF2,TIAM1,OPA1,ITPKA,CYFIP1,DTNBP1,SLC12A5,LZTS1,SRGAP2C,DOCK10,KIAA0319,NEURL1,DNM1L,PPP3CA,HECW2,CAPRIN2,MARK1,CFL1,DISC1,RAB17,NFATC4,TRAPPC4,SS18L1,CDKL5,EPHB3,TANC2,KLF7,DGKG,CRTC1,FLRT1,DNM3,OBSL1,MINK1,EPHA4,DLG4,SDK1,PSEN1,TAOK2,EFNA1,CHRNB2,ZDHHC15,NTN1,PARP6,GPRASP2,BHLHB9,ARHGAP44,CAMK2A,CDK5R1,SEZ6,DAB1,FMR1,LRP8,CRK,NTN3,MECP2,CELSR2,FBXO31,DAB2IP,RHOA,LST1,LLPH,BTBD3,YWHAH,MAP1A,FOXO6	grey	VSMC_M10
GO:0034244	0.97	0.09	5	15	negative regulation of transcription elongation from RNA polymerase II promoter	BP	1	EAPP,RNF168,NELFA,RF00100,RNF8	grey	VSMC_M10
GO:0046483	0.97	0.04	2295	4376	heterocycle metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,ZC3H10,SMARCC2,PAN2,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,POLI,HSD17B4,RNMT,SHMT2,EYA4,TBPL1,GLI1,MARS,PDE7B,CLK4,MAP3K5,RPA3,TNFAIP3,TSFM,HIVEP2,ADAT2,ATP23,PLAGL1,MAML1,MRNIP,ENPP3,ATP5MGL,HELB,RPP21,PPP1R10,ZBTB2,CPSF6,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,PABPC1,SNW1,TFB1M,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,MAP3K4,PPT2,PRKN,QKI,AGER,TRMU,PPARA,PDE10A,ACSL6,UTP23,MED30,IL5,BRD2,TAF2,RXRB,TSPO,VGLL2,MCM9,ASF1A,RRP7A,HSF2,TCF7,PHF1,SMPDL3A,UBE2B,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PRXL2C,HABP4,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,ZC3H3,ATF4,PYCR3,TUT7,MAPK15,RPAP2,CBX7,APOBEC3H,GTPBP1,MAPK14,UHRF2,CBY1,DMC1,PUF60,C9orf64,CSNK1E,PICK1,KDM4C,SOX10,PIM1,CMTR1,BTBD9,NRF1,TMPRSS6,EXOSC4,SMO,SNAPC3,BNC2,HSF1,MOCS1,PSAT1,OARD1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,RBM28,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,GNMT,POT1,KLHDC3,RORB,ZNF300,PRDM4,CRY1,GDA,DMTF1,CROT,SRF,SMU1,ZNF318,NFX1,NOL6,GNPDA2,XPO5,CDK14,FZD1,MTERF1,NFXL1,GALT,SLC35B2,NFKBIE,FANCG,SUPT3H,SMARCA2,ENPP4,RFX3,KIT,ADGRF1,UXS1,NCK2,FHL2,TSR1,TGFBRAP1,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,PPAT,REV1,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,	grey	VSMC_M10
GO:2000146	0.97	0.04	111	234	negative regulation of cell motility	BP	1	LRP1,SRGAP1,FBLN1,TRIB1,MAPK15,SRF,MEOX2,SVEP,CLDN19,RNF20,HAS1,HOXA7,PTN,ITGB1BP1,FUZ,EPHA1,FOXO3,C5AR2,CLASP2,DACH1,CYGB,WNT11,SRGAP3,JAG1,NAV3,PLCB1,SPINT2,CNN2,DCN,SEMA3A,NRG1,MITF,DPYSL3,ABHD6,ROBO1,PTPRJ,MEF2C,STC1,TBX5,ACVR1C,TP53INP1,ADTRP,SRGAP2C,CD200,SINHCAF,SP100,ADARB1,GNA13,DAG1,ABHD2,AP1AR,SLAMF8,CERS2,CHRD,CLIC4,PATZ1,APOD,FRMD5,NFE2L2,MIA3,DUSP10,SEMA6D,PDCD10,WNT4,COL3A1,STAT3,VCL,WAS,PADI2,EPHA4,BMPR1A,SYNJ2BP,ATP1B2,NGFR,VASH1,MAP2K5,EVL,CD74,CCL2,CCL25,PTGER4,STK26,CRK,ARHGAP4,MECP2,PIP5KL1,ENG,MARVELD3,SCAI,DAB2IP,WDR63,MIR29A,MIR199A1,MIR21,MIR22,MIR24-1,MIR491,RHOA,C5orf30,ADGRG1,DPP4,ACVRL1,NOG,THY1,GADD45A,DUSP1,RGCC,GCSAM,DUSP22,LDLRAD4,RAP2B	grey	VSMC_M10
GO:0060841	0.97	0.10	4	13	venous blood vessel development	BP	1	ACVR2B,FOXF1,ENG,ACVRL1	grey	VSMC_M10
GO:0010644	0.97	0.07	10	27	cell communication by electrical coupling	BP	1	ATP1A3,TBX5,CASQ2,RYR2,PKP2,ATP1A2,ATP1B1,KCNA1,ATP1B2,CALM1	grey	VSMC_M10
GO:0014072	0.97	0.08	8	22	response to isoquinoline alkaloid	BP	1	SLC1A1,PRKCE,GPI,PEA15,GHR,FADD,RGS4,PITX3	grey	VSMC_M10
GO:0043278	0.97	0.08	8	22	response to morphine	BP	1	SLC1A1,PRKCE,GPI,PEA15,GHR,FADD,RGS4,PITX3	grey	VSMC_M10
GO:0051972	0.97	0.06	17	42	regulation of telomerase activity	BP	1	MAP3K4,MYC,MAPK15,POT1,PARP4,HMBOX1,MAPKAPK5,MEN1,XRCC5,MAPK1,NVL,WRAP53,PIF1,MAPK3,PARN,TEN1,MAP2K7	grey	VSMC_M10
GO:0042772	0.97	0.09	5	15	DNA damage response, signal transduction resulting in transcription	BP	1	SP100,CHEK2,ING4,MUC1,RPS27L	grey	VSMC_M10
GO:0090199	0.97	0.06	16	39	regulation of release of cytochrome c from mitochondria	BP	1	PRKN,BAK1,PLA2G6,OPA1,DNM1L,GPER1,CIDEB,PINK1,PSMD10,PAM16,MLLT11,NOL3,FXN,BCL2L11,BCL2L2,PPIF	grey	VSMC_M10
GO:0042273	0.97	0.06	24	56	ribosomal large subunit biogenesis	BP	1	MDN1,RPL14,RPL6,SDAD1,URB1,LTO1,WDR12,RPL7L1,DHX30,RPL11,RPL10L,WDR74,RSL24D1,NVL,LAS1L,ZNHIT3,NLE1,SNU13,RPL23A,NOL9,RPL35,ZNHIT6,ZNF622,NSA2	grey	VSMC_M10
GO:1904424	0.97	0.09	5	15	regulation of GTP binding	BP	1	MET,ARHGEF7,RAP1GAP,EPHA4,GPSM1	grey	VSMC_M10
GO:1902806	0.97	0.05	52	115	regulation of cell cycle G1/S phase transition	BP	1	GLI1,TRIM39,CCND3,FBXO7,ANKRD17,LSM10,EGFR,PLK3,UBE2E2,RPTOR,TCIM,PLCB1,TFDP1,DDRGK1,PRKDC,PLK2,FAM107A,FBXW7,ADAMTS1,PIDD1,PKD2,HYAL1,CCND1,TERT,GIGYF2,CHEK2,PSME1,CDKN1B,DLG1,SUSD2,MEN1,DDX3X,MEPCE,PTPN6,ECD,PSME3,PAGR1,MUC1,TAF1,DCUN1D3,CCL2,PKD1,CDK10,FBXO31,MIR29A,MIR222,PLK5,RPS27L,SOX4,RGCC,APC,CRADD	grey	VSMC_M10
GO:0032615	0.97	0.06	15	38	interleukin-12 production	BP	1	AGER,MAPK14,IRF5,TLR4,PIBF1,PLCB1,FOXP1,TRAF6,RIPK2,NOD2,CD40,CMKLR1,IL16,ISL1,MIR21	grey	VSMC_M10
GO:0032655	0.97	0.06	15	38	regulation of interleukin-12 production	BP	1	AGER,MAPK14,IRF5,TLR4,PIBF1,PLCB1,FOXP1,TRAF6,RIPK2,NOD2,CD40,CMKLR1,IL16,ISL1,MIR21	grey	VSMC_M10
GO:0034243	0.97	0.07	11	29	regulation of transcription elongation from RNA polymerase II promoter	BP	1	ZMYND11,EAPP,LDB1,RNF168,ELL,NELFA,LEO1,CDK12,SUPT6H,RF00100,RNF8	grey	VSMC_M10
GO:0050901	0.97	0.08	7	20	leukocyte tethering or rolling	BP	1	ADD2,PODXL2,JAM2,SELPLG,ITGA4,CCL25,FUT4	grey	VSMC_M10
GO:0097106	0.97	0.07	9	25	postsynaptic density organization	BP	1	SYNGAP1,LRRC4,LRFN1,DLG1,NRXN2,NLGN2,ZDHHC12,GRID2,LRRTM2	grey	VSMC_M10
GO:0048546	0.97	0.06	14	36	digestive tract morphogenesis	BP	1	GLI1,SOX10,SIX2,BBS7,GLI2,WNT11,OVOL2,HLX,EPHB3,RBPMS2,SMAD3,STRA6,FOXF1,WNT5A	grey	VSMC_M10
GO:2000765	0.97	0.10	4	13	regulation of cytoplasmic translation	BP	1	CNBP,RBM24,YBX3,FMR1	grey	VSMC_M10

GO:0061037	0.97	0.07	11	29	negative regulation of cartilage development	BP	1	MKX,SOX9,GLI2,WNT11,RARB,PTHLH,NKX3-2,ADAMTS12,RFLNB,MIR21,NOG	grey	VSMC_M10
GO:0006986	0.97	0.05	57	124	response to unfolded protein	BP	1	HSPA1B,PRKN,PACRG,HSPA4,DERL1,BAK1,ATF4,HSF1,NCK2,ERMP1,ERP44,DNAJA1,HERPUD2,FGF21,HSPE1,OPTN,KBTBD6,UBXN4,TMTC4,EIF2AK2,DDRGK1,PIK3R1,TMBIM6,AMFR,RHBDD1,CCND1,FICD,YOD1,HSPA8,QRICH1,BAG3,TBL2,RHBDD2,EDEM3,NFE2L2,DERL3,DNAJC4,TMEM129,DNAJB2,BHLHA15,DNAJB1,MFN2,CREBRF,CREB3L4,PTPN2,CREB3L3,ABCA7,TOR1B,HSPA5,DAB2IP,MIR199A1,HSPB2,DDIT3,BCL2L11,HSPB8,PPP1R15A,DERL2	grey	VSMC_M10
GO:0001774	0.97	0.07	11	29	microglial cell activation	BP	1	AGER,TTBK1,FPR2,C5AR1,CST7,IFNGR2,MAPT,ITGAM,SYT11,LDLR,TRPV1	grey	VSMC_M10
GO:0060973	0.97	0.10	4	13	cell migration involved in heart development	BP	1	BVES,HAND2,TBX5,ENG	grey	VSMC_M10
GO:0046651	0.97	0.04	83	177	lymphocyte proliferation	BP	1	AGER,IL5,HLA-DPB1,TNFRSF13C,RAC2,CCND3,TNFRSF21,NCK2,PELI1,IL4I1,TLR4,IL15,BMI1,MYD88,FOXJ1,TGFBR2,PURA,PAWR,PLCL2,PRNP,NCKAP1L,SLC7A1,TRAF6,GAPT,IL1A,CASP3,MEF2C,TMEM131L,IL7,RASGRP1,LMBR1L,RIPK2,MARCH7,ZNF335,CD40,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,CD28,DLG1,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,SLC11A1,WNT4,PPP3CB,CD38,BST1,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,DOCK2,ZBTB7B,CHRNB2,CD19,BTK,CD74,CCL5,CD320,TWSG1,IL7R,TICAM1,DNAJA3,VAV3,GLMN,MIR21,LST1,FADD,CD46,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0010972	0.97	0.06	21	51	negative regulation of G2/M transition of mitotic cell cycle	BP	1	MRNIP,TRIM39,BRSK1,RAD17,CHMP4C,NBN,ABRAXAS1,DONSON,ZFYVE19,TAOK3,SYF2,UIMC1,FOXO4,TAOK2,FOXN3,TAOK1,FZR1,VPS4A,NAE1,BRCC3,NABP1	grey	VSMC_M10
GO:0019438	0.97	0.03	1502	2902	aromatic compound biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,SMARCC2,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,POLI,SHMT2,TBPL1,GLI1,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ATP5MGL,HELB,ZBTB2,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,STK3,OSR2,SNW1,TFB1M,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,ZBED4,MAP3K4,PPT2,PRKN,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,RXRB,TSPO,VGLL2,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,KDM3B,PTP4A3,PTCH1,ATF4,MAPK15,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,PSAT1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,POT1,GPR37,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,SLC35B2,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,UXS1,NCK2,FHL2,TGFBRAP1,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PPAT,REV1,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,SIX2,PPCS,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,ME1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,NT5E,ZNF483,JAZF1,PPT1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,DDC,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNG,CDKERAP2,TRAF1,PCL2L12,CCAF1,LPIN1,CEBP	grey	VSMC_M10
GO:0007272	0.97	0.05	49	110	ensheathment of neurons	BP	1	ADGRG6,QKI,NTRK2,SOX10,ADAM22,TNFRSF21,PTN,LPIN1,KEL,FIG4,MTMR2,CST7,ERCC2,ACER3,PRX,AKT2,CMTM8,SIRT2,RARB,NRG1,MAL,LGI4,SBF2,JAM2,PLLP,SERINC5,CYFIP1,TSPAN2,RNF10,SCN2A,DAG1,ANK2,GNPAT,NSUN5,DLG1,PIKFYVE,ACSBG1,CNTNAP1,MPP5,DEGS1,TNFRSF1B,GALC,EPB41L3,SKI,AMIGO1,TSC1,ZNF24,CNTN2,POU3F2	grey	VSMC_M10
GO:0008366	0.97	0.05	49	110	axon ensheathment	BP	1	ADGRG6,QKI,NTRK2,SOX10,ADAM22,TNFRSF21,PTN,LPIN1,KEL,FIG4,MTMR2,CST7,ERCC2,ACER3,PRX,AKT2,CMTM8,SIRT2,RARB,NRG1,MAL,LGI4,SBF2,JAM2,PLLP,SERINC5,CYFIP1,TSPAN2,RNF10,SCN2A,DAG1,ANK2,GNPAT,NSUN5,DLG1,PIKFYVE,ACSBG1,CNTNAP1,MPP5,DEGS1,TNFRSF1B,GALC,EPB41L3,SKI,AMIGO1,TSC1,ZNF24,CNTN2,POU3F2	grey	VSMC_M10
GO:0015909	0.97	0.06	19	46	long-chain fatty acid transport	BP	1	CPT1B,SLC27A6,PLA2G6,PLIN2,AKT2,PLA2R1,CPT1A,ACSL5,FABP4,SLC25A20,NTSR1,PLA2G4A,SLC27A1,ABCD4,NMUR2,PROCA1,ABCD3,FABP5,PLA2G2C	grey	VSMC_M10

GO:0031667	0.97	0.04	176	362	response to nutrient levels	BP	1	MARS,MAP3K5,CYP27B1,TPH2,SNW1,PPARA,TNFRSF11B,TSPO,ATF4,PICK1,PIM1,TXN2,HSF1,TFEB,SLC39A4,GPT,SRF,NUAK1,ABCG5,CAT,ABCG8,BRSK1,ALB,BMP8A,RRAGD,NR1H2,PTN,TNC,EGFR,VPS41,IL15,UCP1,ATG5,FOXO3,FGF21,KPTN,SESN3,DNMT3A,FOXA3,GIPR,ERCC1,DNAJC15,RALB,KDM4A,PRKAG2,SZT2,WNT11,TGFBR2,SIRT2,MKKS,RPTOR,EIF2AK2,WRN,GAS6,LARS,ULK1,NR1H4,USF2,FAM107A,DNMT3B,AHCY,GSS,PRKAG1,EIF2AK4,VDR,STC1,OPA1,SLC38A2,ACVR1C,SPP1,PAX2,NOD2,SIRT5,CD40,NUAK2,NUPR2,SRD5A1,DNM1L,SIK1,CCND1,SLC38A3,CPT1A,TRPV4,DAD1,KCNB1,AMELX,HSPA8,SORL1,GNPAT,CBL,CIDEB,MTMR3,UCN2,USF1,XPR1,TBL2,HMGCL,GLUL,MGMT,SLC16A1,POR,NFE2L2,SORD,FIS1,VGF,CPS1,SIK2,COMT,SERPINC1,BCHE,WNT4,ALPL,GDF15,PRKAG3,CTSV,MAPK1,BHLHA15,WIPI2,MAX,MED1,ALDH1A2,RRAGB,BNIP1,ZFYVE1,FOXO4,PKLR,MAPK3,OGT,MPO,TNRC6A,LDLR,LARP1,SCNN1B,BCAS3,NMUR2,ADSSL1,SREBF1,LAMP2,SGIP1,NIM1K,GHR,OXCT1,STK26,JUN,CLEC16A,MBD1,TRPV1,KIAA1324,CYBA,TSC1,ASS1,TLDC1,AGL,LCN2,SLC25A25,WDR59,HSPA5,DHODH,SH3GLB1,NQO1,BCL10,RIPOR1,HSD11B2,ACADM,MIR125B1,MT-CYB,SETDB1,TRIM24,SLC6A19,BGLAP,PEMT,IMPACT,DDIT3,LRAT,UPP1,RNF152	grey	VSMC_M10
GO:0051546	0.97	0.10	4	13	keratinocyte migration	BP	1	EPB41L4B,IQSEC1,HBEGF,FERMT1	grey	VSMC_M10
GO:0051153	0.97	0.05	31	72	regulation of striated muscle cell differentiation	BP	1	MAML1,FRS2,PPARA,MAPK14,PI16,TRIM32,MYLK3,MAMSTR,NRG1,LMOD3,SMYD1,NLN,MEF2C,SOX6,RBM24,BDNF,SIK1,FZD7,ACTN3,HDAC4,BHLHA15,YY1,FBXO22,PIEZO1,PLPP7,MIR199A1,MIR222,RGS4,YBX1,NKX2-5,RBM38	grey	VSMC_M10
GO:0022010	0.97	0.10	4	13	central nervous system myelination	BP	1	SOX10,ERCC2,CNTNAP1,CNTN2	grey	VSMC_M10
GO:0032291	0.97	0.10	4	13	axon ensheathment in central nervous system	BP	1	SOX10,ERCC2,CNTNAP1,CNTN2	grey	VSMC_M10
GO:0051894	0.97	0.07	9	25	positive regulation of focal adhesion assembly	BP	1	TEK,ITGB1BP1,FMN1,PTPRJ,COL16A1,WNT4,SMAD3,TSC1,THY1	grey	VSMC_M10
GO:0006725	0.97	0.03	2312	4410	cellular aromatic compound metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,ZC3H10,SMARCC2,PAN2,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,POLI,HSD17B4,RNMT,SHMT2,EYA4,TBPL1,ALDH8A1,GLI1,MARS,PDE7B,CLK4,MAP3K5,RPA3,TNFAIP3,TSFM,HIVEP2,ADAT2,ATP23,PLAGL1,MAML1,MRNIP,ENPP3,ATP5MGL,HELB,RPP21,PPP1R10,ZBTB2,CPSF6,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,SNCAIP,PABPC1,SNW1,TFB1M,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,MAP3K4,PPT2,PRKN,QKI,AGER,TRMU,PPARA,PDE10A,ACSL6,UTP23,MED30,IL5,BRD2,TAF2,RXRB,TSPO,VGLL2,MCM9,ASF1A,RRP7A,HSF2,TCF7,PHF1,SMPDL3A,UBE2B,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PRXL2C,HABP4,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,LY6E,AKR1B1,ZC3H3,ATF4,TUT7,MAPK15,RPAP2,CBX7,APOBEC3H,GTPBP1,MAPK14,UHRF2,CBY1,DMC1,PUF60,C9orf64,CSNK1E,PICK1,KDM4C,SOX10,PIM1,CMTR1,BTBD9,NRF1,TMPRSS6,EXOSC4,SMO,SNAPC3,BNC2,HSF1,PSAT1,OARD1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,RBM28,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,GNMT,POT1,GPR37,KLHDC3,RORB,ZNF300,PRDM4,CRY1,GDA,DMTF1,CROT,SRF,SMU1,ZNF318,NFX1,NOL6,GNPDA2,XPO5,CDK14,FZD1,MTERF1,NFXL1,GALT,SLC35B2,NFKBIE,FANCG,SUPT3H,SMARCA2,ENPP4,RFX3,KIT,SLC1A1,ADGRF1,UXS1,NCK2,FHL2,TSR1,TGFBRAP1,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,PPAT,REV1,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,	grey	VSMC_M10
GO:0050850	0.97	0.08	7	20	positive regulation of calcium-mediated signaling	BP	1	P2RX2,NRG1,P2RX3,SPPL3,CIB1,SLC9A1,CAMTA1	grey	VSMC_M10
GO:0016572	0.97	0.06	13	34	histone phosphorylation	BP	1	UBE2B,NEK11,DCAF1,MST1,BAZ1B,AKAP8L,AKAP8,MAPK3,RPS6KA5,PRKCB,FMR1,AURKC,RPS6KA4	grey	VSMC_M10
GO:0072224	0.97	0.10	4	13	metanephric glomerulus development	BP	1	OSR1,RET,PAX2,LHX1	grey	VSMC_M10
GO:0007599	0.97	0.04	77	166	hemostasis	BP	1	SERPINB2,TSPAN8,MPIG6B,FZD6,FBLN1,MAPK14,MYH9,SRF,TEC,ENPP4,TLN1,PLEK,DGKI,TLR4,SLC7A11,THBD,PLAT,MYL12A,C1QTNF1,ACTG1,CLIC1,GAS6,ADRA2B,GPI,PIK3CB,P2RY1,HPS5,AP3B1,F2RL1,F2R,ANO6,DMTN,ADTRP,DTNBP1,CD40,FAP,LCK,ADRA2A,ITPK1,PRSS56,UBASH3B,HPS4,DGKD,USF1,PAFAH2,FCER1G,DGKG,NFE2L2,BLOC1S6,PLA2G4A,ITGA2B,FN1,PTPN6,SERPINC1,ADRA2C,FERMT3,HGFAC,COL3A1,VCL,WAS,ACTB,ANXA8,F12,PEAR1,ANXA2,DGKQ,DGKE,VAV1,ABAT,SERPINF2,P2RX1,ADAMTS13,VAV3,STXBP1,FGA,BLOC1S3,RAP2B	grey	VSMC_M10

GO:0010558	0.97	0.03	582	1150	negative regulation of macromolecule biosynthetic process	BP	1	SMARCC2,PAN2,ATP8B1,SHMT2,PGGT1B,PLAGL1,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,ZBTB12,EIF3E,PNLDC1,PRKN,PPARA,MRPL13,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PTCH1,TNRC6B,ATF4,TUT7,CBX7,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SCMH1,IGF2BP3,NFE2L3,PNPT1,HOXA2,HOXA7,JAZF1,XPO1,AKIRIN2,CASP8AP2,BACH2,ZNF692,NR1H2,ZNF350,FOXP2,MED25,KLF11,AGO1,POU3F3,LANCL2,CREM,SDCBP,TUT4,OSR1,FOXO3,BEND5,DHFR,HDAC2,PHF10,DNMT3A,BMI1,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,SUV39H2,ZNF404,PLK3,MLH1,GLI2,DEDD2,RSF1,KDM4A,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,SFMBT2,GZF1,POU4F1,FBH1,TNRC6C,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,HBEGF,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,EIF2AK2,LSM1,TAF7,NRG1,GAS6,RYBP,FOXP1,MITF,MTA3,ARID5A,IRF7,PAN3,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,RAD17,NCOA2,DKK3,SAP30,ATR,ZNF366,ARNTL,GCFC2,HMBOX1,ENC1,MEF2C,PEX2,PKIA,TMBIM6,CNOT1,CELF1,SLA2,CUX2,MCPH1,SOX6,CNOT6L,FNIP2,BACH1,SFMBT1,EIF2AK4,NR1H3,EIF4E2,EAPP,SCAF4,LCOR,DDX54,RUNX1T1,PAIP2B,VDR,NKX3-1,BAHD1,HDAC7,NKX6-1,LOXL2,NR4A2,DONSON,PHF21A,CRY2,PRDM11,CDYL,FTO,RREB1,RTF1,ZBED6,SOX13,ZNF248,TFAP2A,RI	grey	VSMC_M10
GO:0007596	0.97	0.04	76	164	blood coagulation	BP	1	SERPINB2,TSPAN8,MPIG6B,FZD6,FBLN1,MAPK14,MYH9,SRF,TEC,ENPP4,TLN1,PLEK,DGKI,TLR4,SLC7A11,THBD,PLAT,MYL12A,C1QTNF1,ACTG1,CLIC1,GAS6,ADRA2B,PIK3CB,P2RY1,HPS5,AP3B1,F2RL1,F2R,ANO6,DMTN,ADTRP,DTNBP1,CD40,FAP,LCK,ADRA2A,ITPK1,PRSS56,UBASH3B,HPS4,DGKD,USF1,PAFAH2,FCER1G,DGKG,NFE2L2,BLOC1S6,PLA2G4A,ITGA2B,FN1,PTPN6,SERPINC1,ADRA2C,FERMT3,HGFAC,COL3A1,VCL,WAS,ACTB,ANXA8,F12,PEAR1,ANXA2,DGKQ,DGKE,VAV1,ABAT,SERPINF2,P2RX1,ADAMTS13,VAV3,STXBP1,FGA,BLOC1S3,RAP2B	grey	VSMC_M10
GO:0048469	0.97	0.04	52	116	cell maturation	BP	1	BRD1,CATSPER3,WASHC5,L3MBTL3,ANKS1A,AKR1B1,TUT7,DMC1,PICK1,SOX10,RFX3,EPAS1,PTBP3,IL15,NRCAM,TUT4,FOXO3,DLD,ERCC2,BFSP1,SIRT2,RAC3,RET,LGI4,CEBPA,PTK2B,RND1,OPA1,NKX6-1,NR4A2,KCNIP2,ROPN1L,ABHD2,YTHDF2,FARP2,CATSPER2,FZD5,PTH1R,C1QL1,GLDN,BHLHA15,BTK,SLFN14,C3,CATSPERD,MECP2,SOX8,WDR77,SRRM4,CNTN2,FAM210B,EREG	grey	VSMC_M10
GO:0009895	0.97	0.04	121	254	negative regulation of catabolic process	BP	1	AGAP2,TRIM39,PABPC1,PHAX,RNF5,PPARA,TSPO,MAPK14,NRBP2,RGP1,PDCL3,LRPPRC,MET,EGFR,SDCBP,TRAF3IP2,MTMR2,DHX34,PHB,APOC1,KDM4A,AQP11,MYD88,TIMP4,MYCBP2,ALK,KLHL40,USP36,SIRT2,FEZ2,NRG1,DDRGK1,RYBP,PKP3,PSMF1,TAF9,MTMR9,USP25,CSNK2A2,FAM192A,TENT2,MARCH7,TENT5C,TENT4B,RBM24,LZTS1,SUFU,GPLD1,AZIN2,RPL23,SEC22B,ADRA2A,TMEM39A,USP30,AXIN2,MAPKAPK2,USP19,SORL1,MCL1,TRAF5,ANGEL2,ACTN3,HDAC4,DEDD,RUBCN,IL10RA,EIF4ENIF1,RPL11,LRIG2,YBX3,TAB3,TBC1D14,SLC11A1,RBM10,PINK1,STAT3,ATP13A2,EPHA4,PHF23,ANXA2,TARDBP,PSEN1,SNX12,EFNA1,TAF1,OGT,TOB1,TENT5D,SMAD3,NRDE2,LARP1,NCOR1,NPC1,SMCR8,LEPR,NOS2,PARN,CLEC16A,FMR1,MTM1,RILP,PAM16,METTL16,SGTA,CIRBP,TRAF2,PARK7,TSC1,BANP,DAB2IP,MIR199A1,MIR21,BSCL2,TIGAR,CAMLG,CPTP,YBX1,STYX,TENT5A,MAP1A,NMNAT1	grey	VSMC_M10
GO:0072698	0.97	0.05	21	52	protein localization to microtubule cytoskeleton	BP	1	ABHD17B,MAPRE1,MAPRE3,PIBF1,HOOK3,DIAPH1,CHAMP1,NSFL1C,CEP250,MCPH1,TTBK2,DISC1,CEP192,ABHD17A,WRAP73,SNX10,ABHD17C,C2CD3,APC,PARD6A,MAP1A	grey	VSMC_M10
GO:0002042	0.97	0.05	23	55	cell migration involved in sprouting angiogenesis	BP	1	SRF,MEOX2,ITGB1BP1,PLK2,NR4A1,ROBO1,FBXW7,HDAC7,ADTRP,GPLD1,CIB1,MAP3K3,MIA3,EPHB4,PDCD10,RHOJ,MAP2K5,MIR199A1,MIR23A,MIR22,MIR27B,MIR27A,RHOA	grey	VSMC_M10

GO:0048609	0.97	0.04	279	563	multicellular organismal reproductive process	BP	1	TBPL1,GLI1,YTHDC2,B4GALNT1,CYP27B1,ATAT1,ESR1,TSPAN8,MAPK8IP2,IGF2R,MOV10L1,PACRG,QKI,BRD2,GDF9,ROS1,MCM9,HSF2,UBE2B,CATSPER3,WASHC5,TOB2,SMAD5,H3F3C,FANCC,AKR1B1,TUT7,DMC1,PLA2G6,PICK1,SPATA31D3,CFAP69,FANCG,SMARCA2,TDRD6,KIT,PPAT,CCIN,TSGA10,TDRD7,DNAJA1,FOXJ3,SCMH1,MSH2,RAD23B,YTHDC1,KLK14,CABS1,FANCL,GJA10,HERPUD2,GMCL1,PTN,EGFR,NOBOX,CCDC155,DKKL1,CREM,TUT4,FOXO3,ARMC2,DLD,DDO,TXNRD3,APOB,SPATA6,SPATA5,HDAC2,TTC26,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,MLH1,ACOX1,PRDX3,TIMP4,FOXJ1,WDR48,TTC21A,CCNB1IP1,ARRB1,ACVR2A,SIRT2,MKKS,SPATA24,ADAM18,MCM8,GOLGA3,PANK2,BTG1,SOHLH2,TEX15,KATNAL1,NPHP1,CASP3,ING2,HPGD,SPATA9,ROBO2,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,P2RY1,PTK2B,KMT2D,PRKAG1,SFMBT1,VDR,STC1,AP3B1,CDYL,SPP1,SYCP1,DNAH1,NPM2,DPCD,OCA2,ADCY7,ROPN1L,SIAH1,BMPR1B,GAS2,ACTR1A,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,HYAL3,MAP2K6,TESMIN,TGFB2,PRKAR1A,SPATA2,RNF114,ADNP,ABHD2,CCDC36,YTHDF2,SPATC1L,SPO11,TSSK4,CIB1,CCDC87,DDX6,HDAC4,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,SEPT2,LIMK2,PATZ1,SP3,CATSPER2,OVOL1,ETV6,YBX3,WNT3,CADM1,SPATA32,GGT2,TTC12,BCL6,RPL10L,MEN1,DDX3X,COMT,SPAG16,ZCWPW1,WNT4,CTSV,BIRC3,PTPRN,ADCY10,PARP11,MAPK1,STAT5B,CALR3,KDM5A,ZMYND15,MNS1,YBX2,THRA,MED1,SPIN2A,SEPT1,ITGA3,MYCBPAP,MAPK3,UBE2Q1,VIPAS39,SOX30,CCDC42,CREB3L4,EPOR,IL4R,PAQR5,RAD51C,DNM2,YY1,	grey	VSMC_M10
GO:0008340	0.97	0.09	4	13	determination of adult lifespan	BP	1	MSH2,IDE,RAD54B,PRDM2	grey	VSMC_M10
GO:0001954	0.97	0.05	20	49	positive regulation of cell-matrix adhesion	BP	1	TEK,CDK6,ITGB1BP1,EPHA1,RIN2,FERMT1,FMN1,PTPRJ,PTK2B,COL16A1,DAG1,DISC1,CIB1,EFEMP2,WNT4,SMAD3,CCL25,PRKCZ,TSC1,THY1	grey	VSMC_M10
GO:0007431	0.97	0.07	10	27	salivary gland development	BP	1	PLXNA1,SEMA3A,NKX3-1,TGFB2,DAG1,LAMA5,BTBD7,LAMA1,TWSG1,ESRP2	grey	VSMC_M10
GO:0042407	0.97	0.09	5	15	cristae formation	BP	1	CHCHD6,IMMT,PINK1,ADCK1,C19orf70	grey	VSMC_M10
GO:0042311	0.97	0.06	12	31	vasodilation	BP	1	PLA2G6,EGFR,ATG5,MKKS,GUCY1A1,F2RL1,GPER1,AGT,PLOD3,CPS1,GCH1,KCNMA1	grey	VSMC_M10
GO:0060444	0.97	0.08	6	18	branching involved in mammary gland duct morphogenesis	BP	1	ESR1,AREG,VDR,WNT4,MED1,WNT5A	grey	VSMC_M10
GO:0034605	0.97	0.05	22	53	cellular response to heat	BP	1	HSPA1B,HSF1,PDCL3,HDAC2,STAC,CLPB,TCIM,IL1A,ATR,HTRA2,TRPV4,PDCD6,MAPKAPK2,BAG3,MAPT,DNAJB1,SLU7,CREBBP,TRPV1,HIKESHI,HSBP1L1,FGF1	grey	VSMC_M10
GO:0034204	0.97	0.06	15	39	lipid translocation	BP	1	ATP9B,ATP8B1,ABCB1,TMEM30A,ANO4,XKR6,PLSCR4,P2RX7,ANO6,ABCA12,TMEM30B,ATP11C,ABCA3,ABCA7,XKR8	grey	VSMC_M10
GO:0006491	0.97	0.08	6	18	N-glycan processing	BP	1	ST8SIA4,GANC,ST8SIA2,MAN1C1,ST8SIA5,ST8SIA6	grey	VSMC_M10
GO:0060997	0.97	0.05	22	54	dendritic spine morphogenesis	BP	1	SHANK1,EPHB1,CUX2,TIAM1,OPA1,ITPKA,DOCK10,DNM1L,CAPRIN2,CFL1,EPHB3,TANC2,DNM3,EPHA4,DLG4,EFNA1,ZDHHC15,GPRASP2,BHLHB9,ARHGAP44,CDK5R1,LRP8	grey	VSMC_M10
GO:0030336	0.97	0.04	105	223	negative regulation of cell migration	BP	1	LRP1,SRGAP1,TRIB1,MAPK15,SRF,MEOX2,SVBP,CLDN19,RNF20,HAS1,HOXA7,PTN,ITGB1BP1,FUZ,EPHA1,FOXO3,C5AR2,CLASP2,DACH1,CYGB,WNT11,SRGAP3,JAG1,NAV3,PLCB1,CNN2,DCN,SEMA3A,NRG1,MITF,DPYSL3,ABHD6,ROBO1,PTPRJ,MEF2C,STC1,TBX5,ACVR1C,TP53INP1,ADTRP,SRGAP2C,CD200,SINHCAF,SP100,ADARB1,GNA13,DAG1,ABHD2,SLAMF8,CERS2,CHRD,CLIC4,PATZ1,APOD,NFE2L2,MIA3,DUSP10,SEMA6D,PDCD10,WNT4,COL3A1,STAT3,VCL,PADI2,EPHA4,BMPR1A,SYNJ2BP,ATP1B2,NGFR,VASH1,MAP2K5,EVL,CD74,CCL2,CCL25,PTGER4,STK26,ARHGAP4,MECP2,PIP5KL1,ENG,MARVELD3,SCAI,DAB2IP,WDR63,MIR29A,MIR199A1,MIR21,MIR22,MIR24-1,MIR491,RHOA,C5orf30,ADGRG1,DPP4,ACVRL1,NOG,THY1,GADD45A,DUSP1,RGCC,GCSAM,DUSP22,LDLRAD4,RAP2B	grey	VSMC_M10
GO:0043407	0.97	0.05	19	47	negative regulation of MAP kinase activity	BP	1	STK38,DNAJA1,SPRY1,SPRY2,PIK3CB,PTPRJ,PAQR3,PDCD4,SORL1,AGT,AIDA,DUSP10,DUSP19,PTPN6,RGS14,INPP5K,DAB2IP,DUSP1,LAX1	grey	VSMC_M10
GO:2000045	0.97	0.05	43	97	regulation of G1/S transition of mitotic cell cycle	BP	1	CCND3,FBXO7,ANKRD17,LSM10,EGFR,PLK3,UBE2E2,RPTOR,PLCB1,TFDP1,PRKDC,PLK2,FAM107A,ADAMTS1,PIDD1,PKD2,HYAL1,CCND1,TERT,GIGYF2,CHEK2,PSME1,CDKN1B,DLG1,DDX3X,MEPCE,PTPN6,ECD,PSME3,MUC1,DCUN1D3,CCL2,PKD1,CDK10,FBXO31,MIR29A,MIR222,PLK5,RPS27L,SOX4,RGCC,APC,CRADD	grey	VSMC_M10
GO:0002026	0.97	0.08	6	18	regulation of the force of heart contraction	BP	1	RYR2,MYH7,GRK2,ATP1A2,SLC9A1,CHGA	grey	VSMC_M10
GO:0001780	0.97	0.09	4	13	neutrophil homeostasis	BP	1	SLC7A11,PIK3CB,CXCR2,XKR8	grey	VSMC_M10

GO:0031327	0.97	0.03	607	1198	negative regulation of cellular biosynthetic process	BP	1	ORMDL2,SMARCC2,PAN2,ATP8B1,SHMT2,CYP27B1,PLAGL1,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,ZBTB12,EIF3E,PNLDC1,PRKN,PPARA,TSPO,MRPL13,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PTCH1,TNRC6B,ATF4,TUT7,CBX7,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SCMH1,IGF2BP3,NFE2L3,PNPT1,HOXA2,HOXA7,JAZF1,XPO1,AKIRIN2,CASP8AP2,BACH2,ZNF692,PLEK,NR1H2,ZNF350,FOXP2,MED25,KLF11,AGO1,POU3F3,LANCL2,FAM3C,DKKL1,CREM,SDCBP,TUT4,OSR1,FOXO3,BEND5,DHFR,HDAC2,PHF10,DNMT3A,BMI1,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,APOC1,SUV39H2,ZNF404,PLK3,MLH1,GLI2,DEDD2,RSF1,KDM4A,DACH1,TAF3,PIBF1,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,SFMBT2,GZF1,POU4F1,FBH1,TNRC6C,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,HBEGF,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,EIF2AK2,LSM1,TAF7,NRG1,GAS6,RYBP,FOXP1,MITF,MTA3,ARID5A,IRF7,PAN3,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,CYP7A1,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,RAD17,NCOA2,DKK3,SAP30,ATR,ZNF366,ARNTL,FBXW7,GCFC2,HMBOX1,ENC1,MEF2C,PEX2,PKIA,TMBIM6,CNOT1,CELF1,SLA2,CUX2,MCPH1,SOX6,CNOT6L,FNIP2,RAPGEF2,BACH1,SFMBT1,EIF2AK4,NR1H3,EIF4E2,EAPP,SCAF4,LCOR,DDX54,RUNX1T1,PAIP2B,VDR,NKX3-1,BAHD1,HDAC7,NKX6-	grey	VSMC_M10
GO:0034332	0.97	0.06	15	39	adherens junction organization	BP	1	MTSS1,NUMBL,KIFC3,PLEKHA7,DSP,CDH24,RAMP2,VCL,EPHA4,ACTB,CAMSAP3,CDH6,CDH10,PIP5K1C,INAVA	grey	VSMC_M10
GO:2001021	0.97	0.05	31	72	negative regulation of response to DNA damage stimulus	BP	1	HELB,PPP1R10,HSF1,CYREN,TRIM32,ERCC1,DDIAS,XRCC1,FBH1,RNF169,SHLD1,ERCC6,TAF9,ING2,MARCH7,DYRK3,SNAI1,CHEK2,RTEL1,SHLD2,MUC1,TAF9B,OTUB2,PSMD10,CD74,SMCHD1,ERCC4,RMI2,NUDT16L1,TERF2,PTTG1IP	grey	VSMC_M10
GO:0006029	0.97	0.05	28	67	proteoglycan metabolic process	BP	1	B4GALT7,CHST10,HS3ST5,NDNF,CHPF2,CSGALNACT1,DCN,BMPR1B,HYAL1,SLC2A10,SULF2,TCF7L2,GAL3ST3,CHST3,SPOCK2,GAL3ST4,CHST7,AC022400.6,CHST12,IDUA,GLCE,ADAMTS12,HS6ST2,B3GALT6,FOXL1,HS6ST3,CHSY3,HS2ST1	grey	VSMC_M10
GO:0051222	0.97	0.04	114	241	positive regulation of protein transport	BP	1	LRP1,MAPK14,PLA2G6,RAC2,SMO,PRKCE,TMEM30A,RUFY3,NR1H2,ITGB1BP1,EGFR,ARHGEF5,TLR4,TCAF2,TRPM4,GIPR,PLK3,FRMD4A,AKT2,USP36,APBB3,CEP290,PRNP,MAVS,GAS6,SIRT3,TM9SF4,IL1A,OSBP,PIK3R1,FBXW7,HTRA2,VEGFC,ZFAND1,CSNK2A2,NNAT,PFKM,NKX6-1,RAPGEF3,F2RL1,GPLD1,DNM1L,TGFB2,TCF7L2,KCNB1,PFKFB2,HCLS1,HPS4,SORL1,C2CD5,GPER1,ARIH2,CIB1,BAG3,SFN,GLUL,ADAM8,CTDSPL2,FZD5,FIS1,CEMIP,NMT1,TTN,SEC16B,MCU,PDCD10,PPP3CB,PINK1,CD38,MPC2,MAPK1,CHRM1,TMEM30B,ATP13A2,CNST,NLGN2,NPEPPS,TARDBP,STX4,PSEN1,ITGAM,TMED10,AC138894.1,MYH10,SMAD3,SYTL4,GPR68,BCAS3,MIEF2,CDK5R1,ISL1,OXCT1,EFCAB7,ABAT,RPH3AL,NADK,BCAP31,PRKCZ,OAZ1,BAIAP3,LRRC8A,SH3GLB1,RIPOR1,MICALL2,FGA,SOX4,CRH,DOC2B,HRAS,MIEF1,RHOU,LEPROT,PARD6A,ZIC1	grey	VSMC_M10
GO:0048024	0.97	0.05	37	85	regulation of mRNA splicing, via spliceosome	BP	1	ZC3H10,SNW1,QKI,PUF60,RBFOX2,SMU1,TRA2A,YTHDC1,SRSF10,CELF2,NUP98,WTAP,RBM39,CELF1,SRSF6,RBM24,RBM5,HSPA8,SRSF4,CELF3,RBM7,RBM10,PRPF19,FXR2,RBM25,RAVER2,MBNL3,NSRP1,FMR1,CELF5,METTL16,CIRBP,SRRM4,NOVA1,RBM11,SRSF12,SAP18	grey	VSMC_M10
GO:0016311	0.97	0.04	165	342	dephosphorylation	BP	1	PHLPP1,EYA4,ARMT1,SYNJ2,PTP4A3,RPAP2,PPP1R16A,NUAK1,PLPP6,SEMA4D,PTPDC1,INPP4A,PLPPR1,PPP2R1A,PPP4R3B,ACP4,NT5E,RNGTT,PLEK,VRK3,LPIN1,INPP4B,FIG4,NANP,MTMR2,ENTPD6,SYMPK,PPM1N,PTPRF,PPP1CB,PIP4P1,TIMM50,MTMR14,IKBKB,PTPRQ,PLPP5,DUSP6,BAG4,NUDT16,NCKAP1L,PPP4R2,PPP2CB,PTPRA,PPP1R3B,MFHAS1,MTMR7,NT5DC3,THNSL2,EYA1,FRA10AC1,CHRM5,MTMR9,PTPRJ,MEF2C,EPHX2,RPRD1B,ACP2,ENOPH1,SYNJ1,LPIN3,CRY2,PTPN5,PPM1K,DUSP8,GPLD1,SPPL3,LRRK1,LCK,PPP3CA,TGFB2,PPP2R2D,PPA2,ACP6,INPP5A,ALPG,SSH1,PUDP,PPP1R3E,PFKFB2,THTPA,MTMR11,UBASH3B,EYA3,ATP1A2,PPP2R5A,PLPP4,PPP1R3D,ILKAP,MTMR3,PFKFB4,LHPP,PTPRO,DUSP18,INPP5J,DUSP12,DUSP16,DLG1,PPP2R3C,PPM1J,CTDSPL2,DUSP10,CTTNBP2NL,SACM1L,PPP2R5B,PPM1L,DUSP19,PPP1R2C,PTPN6,HTT,PPP3CB,ALPL,PINK1,CAMK2G,TIPRL,PPM1A,PPP2R5E,NT5C3B,BOD1L2,SMG5,UBLCP1,PTPN21,SMAD3,PLPPR2,CALM1,PPP4R4,RPRD1A,PPP2R5C,DUSP14,PPARGC1B,LPIN2,NT5M,PPP6C,IMPA2,PTPN2,MTMR12,SSH2,MTM1,MTMR1,INPP5K,CAMTA1,TSC1,PLPP7,CDC14A,LRRC39,PHLPP2,LRRC40,FBP2,PHOSPHO2,MINPP1,NCEH1,TIGAR,CNEP1R1,DUSP26,DUSP1,DUSP4,SDHAF2,PPP1R15A,DUSP22,STYX,INPP1,PDXP,SGPP1,TMEM225B,PTPMT1,ARPP19	grey	VSMC_M10
GO:0046685	0.97	0.06	11	29	response to arsenic-containing substance	BP	1	FECH,TNFRSF11B,ATF4,MAPK13,HSF1,ZFAND1,SLC38A2,ABCC2,DDX3X,RNF4,PPIF	grey	VSMC_M10
GO:0010614	0.97	0.06	10	27	negative regulation of cardiac muscle hypertrophy	BP	1	PPARA,PI16,JARID2,TNFRSF1B,SMAD3,YY1,MIR199A1,MIR21,MIR25,RGS4	grey	VSMC_M10
GO:0002244	0.97	0.04	42	96	hematopoietic progenitor cell differentiation	BP	1	KCP,SRF,KIT,TMEM190,PLEK,BVES,ZBTB24,ERCC2,DHTKD1,C12orf29,EIF2AK2,PRKDC,FLT1,TCF15,LMBR1L,TENT2,AP3B1,SBDS,ACP6,YTHDF2,OSM,MMP21,NFE2L2,XRCC5,ARMC6,PTPN6,MEOX1,PRRC2C,ZBTB1,SETD1A,PSEN1,BATF,SIN3A,CSF1R,PLD4,CIAO3,SLC7A6OS,FSTL3,SOX4,METTL14,SP7,HOXB3	grey	VSMC_M10

GO:0006401	0.97	0.04	112	237	RNA catabolic process	BP	1	PAN2,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,SKIV2L,DXO,EIF3E,PNLDC1,CSDC2,AGO2,TNRC6B,TUT7,GTPBP1,MAPK14,EXOSC4,CNOT11,EXOSC3,LRPPRC,PNPT1,RNASEH1,AGO1,TUT4,PUM2,TRAF3IP2,MTPAP,ZC3HAV1,DHX34,FASTK,MLH1,DEDD2,MYD88,TNRC6C,LSM1,NUDT16,PKP3,UPF3A,PAN3,NUDT12,ZCCHC8,TTC37,CNOT1,CELF1,CNOT6L,TENT2,FTO,TENT5C,TENT4B,RBM24,DIS3L2,AXIN2,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,NCBP2,EIF4ENIF1,SIDT2,YBX3,RBM7,SUPV3L1,RC3H1,DDX49,UPF1,SLC11A1,RBM10,SAMD4A,ZSWIM8,POLR2G,SCGB1A1,NT5C3B,DCP1B,CASC3,MRPL44,TNFRSF1B,FXR2,TARDBP,SMG5,TOB1,RNASEH2A,TENT5D,NRDE2,TNRC6A,CNOT8,LARP1,SLFN14,ALKBH5,UPF3B,PARN,DROSHA,FMR1,METTL16,PLEKHN1,LSM7,CIRBP,TRAF2,EDC4,AGO4,METTL14,NANOS1,CACNG7,YBX1,ZFP36L2,TENT5A,MAGOHB,RC3H2,EXOSC5	grey	VSMC_M10
GO:0001829	0.97	0.09	4	13	trophectodermal cell differentiation	BP	1	CNOT2,SRF,CNOT1,SP3	grey	VSMC_M10
GO:0006022	0.97	0.04	43	98	aminoglycan metabolic process	BP	1	B4GALT7,PIM1,CEMIP2,HAS1,IL15,HS3ST5,NDNF,GLB1,CHPF2,CSGALNACT1,DCN,B3GNT4,ST3GAL6,GALNT5,CHST1,GCNT2,HYAL1,HYAL3,EGF,ABCC5,GAL3ST3,OVGP1,CEMIP,CHST3,SPOCK2,CHST7,AC022400.6,HS3ST1,CHST12,IDUA,CLN6,GLCE,HEXA,HS6ST2,IDS,B3GALT6,CHST5,ST3GAL2,HAS3,CTBS,HS3ST2,CHSY3,HS2ST1	grey	VSMC_M10
GO:0007528	0.97	0.06	15	39	neuromuscular junction development	BP	1	PTN,TNC,CACNB2,CACNB4,P2RX2,F2R,PPFIBP1,FZD9,DOK7,GPHN,CACNB1,DNAJA3,RER1,SIX1,MESD	grey	VSMC_M10
GO:0035148	0.97	0.04	58	129	tube formation	BP	1	STK3,FZD6,BRD2,PTCH1,PODXL,PTK7,SEMA4C,ITGB1BP1,YWHAZ,FUZ,TEAD2,OSR1,SOX9,IFT172,OVOL2,SPINT2,CEP290,TRAF6,RET,PAX8,CASP3,FZD3,OPA1,IFT52,SPINT1,STK4,PAX2,PRICKLE1,SUFU,IRX2,TGFB2,EGF,DVL3,GRHL3,LUZP1,SETD2,WNT4,TULP3,SDCCAG8,LIAS,DVL2,TCAP,MKS1,BCAS3,MIB1,SKI,SOX8,TSC1,GLMN,BCL10,DAB2IP,VASP,SOX4,NOG,WNT5A,SIX1,BCL2L11,RALA	grey	VSMC_M10
GO:1902101	0.97	0.09	4	13	positive regulation of metaphase/anaphase transition of cell cycle	BP	1	MAPK15,ANAPC5,ANAPC7,ANAPC4	grey	VSMC_M10
GO:0001841	0.97	0.04	40	92	neural tube formation	BP	1	STK3,FZD6,BRD2,PTCH1,PTK7,SEMA4C,FUZ,TEAD2,IFT172,OVOL2,SPINT2,TRAF6,CASP3,FZD3,OPA1,IFT52,SPINT1,STK4,PAX2,PRICKLE1,SUFU,TGFB2,DVL3,GRHL3,LUZP1,SETD2,TULP3,LIAS,DVL2,MKS1,MIB1,SKI,TSC1,GLMN,BCL10,VASP,SOX4,NOG,WNT5A,RALA	grey	VSMC_M10
GO:0002093	0.97	0.09	4	13	auditory receptor cell morphogenesis	BP	1	WHRN,MYO7A,PLS1,STRC	grey	VSMC_M10
GO:0002011	0.97	0.05	20	50	morphogenesis of an epithelial sheet	BP	1	SRF,ARHGAP12,CLASP2,MEGF8,JAG1,HBEGF,FERMT1,ARHGAP24,RREB1,DAG1,AJUBA,PDCD10,DVL2,MPP5,LAMA1,COL5A1,CARMIL2,RHOA,ACVRL1,WNT5A	grey	VSMC_M10
GO:0051271	0.97	0.04	114	241	negative regulation of cellular component movement	BP	1	LRP1,SRGAP1,FBLN1,TRIB1,MAPK15,SRF,MEOX2,SVBP,CLDN19,RNF20,HAS1,HOXA7,PTN,ITGB1BP1,FUZ,EPHA1,FOXO3,C5AR2,CLASP2,DACH1,CYGB,WNT11,SRGAP3,JAG1,NAV3,PLCB1,SPINT2,CNN2,DCN,SEMA3A,NRG1,MITF,DPYSL3,ABHD6,ROBO1,PTPRJ,MEF2C,STC1,TBX5,ACVR1C,TP53INP1,ADTRP,SRGAP2C,CD200,SINHCAF,SP100,ADARB1,GNA13,DAG1,ABHD2,AP1AR,SLAMF8,CERS2,PTPRO,CNIH2,CHRD,CLIC4,PATZ1,CDKN1B,APOD,FRMD5,NFE2L2,MIA3,DUSP10,SEMA6D,PDCD10,WNT4,COL3A1,STAT3,VCL,WAS,PADI2,EPHA4,BMPR1A,SYNJ2BP,ATP1B2,NGFR,VASH1,MAP2K5,EVL,CD74,CCL2,CCL25,PTGER4,STK26,CRK,ARHGAP4,MECP2,PIP5KL1,ENG,MARVELD3,SCAI,DAB2IP,WDR63,MIR29A,MIR199A1,MIR21,MIR22,MIR24-1,MIR491,RHOA,C5orf30,ADGRG1,DPP4,ACVRL1,NOG,THY1,GADD45A,DUSP1,RGCC,GCSAM,DUSP22,LDLRAD4,RAP2B	grey	VSMC_M10
GO:1901532	0.97	0.07	9	25	regulation of hematopoietic progenitor cell differentiation	BP	1	EIF2AK2,PRKDC,TCF15,YTHDF2,OSM,NFE2L2,ZBTB1,SETD1A,METTL14	grey	VSMC_M10
GO:0007096	0.97	0.08	5	15	regulation of exit from mitosis	BP	1	SIRT2,NPM2,CDKN1B,CDC14A,RGCC	grey	VSMC_M10
GO:1904262	0.97	0.09	4	13	negative regulation of TORC1 signaling	BP	1	KPTN,SESN3,SZT2,RNF152	grey	VSMC_M10
GO:0043388	0.97	0.06	16	40	positive regulation of DNA binding	BP	1	NME1,PRKN,ERCC2,POU4F1,SIRT2,DDRGK1,TRAF6,HAND2,EGF,PARP1,CALM1,ISL1,SKI,PARK7,LAMTOR5,TXN	grey	VSMC_M10
GO:0043154	0.97	0.05	23	55	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	TNFAIP8,AQP1,BCL2L12,RAF1,PRDX3,GAS6,GPI,NR4A1,PAX2,IFI6,SFN,RPS6KA1,POR,DDX3X,BIRC3,ARL6IP1,MAP2K5,NLE1,PARK7,LAMTOR5,NOL3,SERPINB9,CAP1	grey	VSMC_M10
GO:0035115	0.97	0.07	9	25	embryonic forelimb morphogenesis	BP	1	OSR2,HOXA13,OSR1,TBX5,RPGRIP1L,TFAP2A,WNT3,ALDH1A2,ALX3	grey	VSMC_M10
GO:0006287	0.97	0.09	4	13	base-excision repair, gap-filling	BP	1	POLL,POLG,NEIL1,LIG3	grey	VSMC_M10
GO:0046323	0.97	0.05	22	54	glucose import	BP	1	MAPK14,SLC25A27,GRB10,FGF21,PRKAG2,AKT2,ASPSCR1,PIK3R1,SORBS1,IRS1,SLC2A10,TERT,PEA15,NFE2L2,CLTCL1,SLC27A1,SLC2A4,SLC5A2,INSR,GPC3,TSC1,ARPP19	grey	VSMC_M10
GO:0035268	0.97	0.07	7	20	protein mannosylation	BP	1	RXYLT1,LARGE1,FKTN,TMTC4,POMT2,POMGNT2,ISPD	grey	VSMC_M10

GO:0048812	0.97	0.03	244	503	neuron projection morphogenesis	BP	1	NEDD4L,LRP1,SEMA6A,KIF5A,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,SULT4A1,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,CPNE5,RAC2,SMO,RBFOX2,CHRNA3,SRF,SEMA4D,DLX5,ETV1,SEMA4C,BRSK1,RIMS1,RTN4,RUFY3,SHANK1,HOXA2,EPHA7,PTN,EGFR,HECW1,EPHA1,KEL,NRCAM,NTF4,WASF1,PLXNA1,RAB10,ABI1,GOLGA4,GLI2,MEGF8,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,CPNE9,FARP1,KIF5C,SYT1,TMEM106B,FEZ2,SLC23A2,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NCKAP1L,ULK1,RYK,EPHB1,RET,TTL,ANKRD27,PREX2,ROBO1,ROBO2,FZD3,SEMA4F,TLX2,CUX2,RAPGEF2,DPYSL2,EIF2AK4,TIAM1,SLIT1,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,SEMA3G,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,SEMA4G,ZNF335,DTNBP1,TAOK3,SIAH1,LZTS1,BMPR1B,BDNF,DOCK10,KIAA0319,LGR6,DNM1L,PPP3CA,HECW2,CAPRIN2,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,CFL1,ADNP,DISC1,GBX2,DVL3,KALRN,NFATC4,SS18L1,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,TANC2,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,SEMA6D,EPHB4,ITGA4,TNR,FN1,NCKAP1,NYAP1,ATL1,NIN,FLRT1,DNM3,PPP3CB,CNTNAP1,RAB3A,MARK2,MUL1,VCL,OBSL1,MINK1,RAB8A,CRMP1,EPHA4,LRTM2,DLG4,ACTB,DVL2,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,NTN1,GAS7,RPS6KA5,RNF165,MYO9A,DNM2,PARP6,GPRASP2,BHLHB9,BCL11B,LHX1,ARHGAP44,SIN3A,TRPV2,LAMA3,CDK5R1,ISL1,EMB,EPB41L3,LAMA1,DOCK7,TAOK1,SLC9A6,DAB1,SLITRK2,LRP8,L1CAM,NTN3,PRKCZ,ARHGAP4,PLXNA3,BSG,TUBB3,AMIGO1,CELSR2,NTNG2,FBXO31,STXBP1,B	grey	VSMC_M10
GO:0010811	0.97	0.04	44	100	positive regulation of cell-substrate adhesion	BP	1	TEK,CDK6,PRKCE,PTN,ITGB1BP1,EPHA1,NDNF,FBLN2,RSU1,UNC13D,RIN2,FERMT1,RAC3,ARHGEF7,RELL2,FMN1,PTPRJ,PTK2B,DOCK5,RREB1,STK4,DMTN,CARMIL1,COL16A1,DAG1,DISC1,CASS4,CIB1,DOCK1,CSPG5,EFEMP2,FN1,SPOCK2,WNT4,ITGA3,SMAD3,DNM2,CCL25,CRK,PRKCZ,TSC1,FOXF1,FGA,THY1	grey	VSMC_M10
GO:0017145	0.97	0.06	10	27	stem cell division	BP	1	KIT,BMI1,ING2,PRDM15,TGFB2,FZD7,ESRRB,NAP1L2,EVI2B,ZFP36L2	grey	VSMC_M10
GO:0001837	0.97	0.04	59	131	epithelial to mesenchymal transition	BP	1	RTN4,AKNA,FUZ,SDCBP,SPRY1,HDAC2,SOX9,CLASP2,SPRY2,WNT11,TGFBR2,OVOL2,EOMES,JAG1,SPRED3,ALX1,KBTBD8,IL17RD,FAM208A,TIAM1,LOXL2,TBX5,GCNT2,KLHL12,USF3,PDCD4,TGFB2,PEF1,TCF7L2,PDCD6,DAG1,AXIN2,SNAI1,AMELX,PHLDB1,WNT4,RBPJ,TGFB1I1,EFNA1,TMEM100,SMAD3,GSC,TCOF1,ISL1,RFLNB,ENG,DAB2IP,MIR21,MIR222,POFUT2,NOG,WNT5A,DACT3,SDHAF2,RGCC,LDLRAD4,HEY2,OLFM1,WNT2	grey	VSMC_M10
GO:0044319	0.97	0.06	11	30	wound healing, spreading of cells	BP	1	CLASP2,HBEGF,FERMT1,ARHGAP24,RREB1,AJUBA,PDCD10,COL5A1,CARMIL2,RHOA,ACVRL1	grey	VSMC_M10
GO:0090505	0.97	0.06	11	30	epiboly involved in wound healing	BP	1	CLASP2,HBEGF,FERMT1,ARHGAP24,RREB1,AJUBA,PDCD10,COL5A1,CARMIL2,RHOA,ACVRL1	grey	VSMC_M10
GO:0035729	0.97	0.09	4	13	cellular response to hepatocyte growth factor stimulus	BP	1	SIRT2,CREB1,MED1,ADAMTS12	grey	VSMC_M10
GO:0001958	0.97	0.07	8	23	endochondral ossification	BP	1	TEK,DLX5,MEF2C,COL13A1,ALPL,FGFR3,MMP13,FGF18	grey	VSMC_M10
GO:0036075	0.97	0.07	8	23	replacement ossification	BP	1	TEK,DLX5,MEF2C,COL13A1,ALPL,FGFR3,MMP13,FGF18	grey	VSMC_M10
GO:0009314	0.97	0.03	174	359	response to radiation	BP	1	FECH,MRNIP,CPT1B,MAP3K4,SYNGAP1,UBE2B,BAK1,XRCC6,MYC,ATF4,MAPK14,MAPK13,HSF1,FBXL6,OPN1SW,PRPH2,CRY1,FANCG,KIT,REV1,ABCG5,CAT,CAMKMT,BRSK1,RDH13,MSH2,AQP1,GJA10,PTN,EGFR,TRIM32,SLC7A11,TRPC3,DNMT3A,ERCC1,XPC,ERCC2,ERCC3,PLK3,B4GALT2,XRCC2,ZRANB3,PAXIP1,AANAT,THBD,PPP1CB,AKT2,XRRA1,PLEKHB1,BHLHE40,DDHD2,WRN,PRKDC,ERCC6,NPHP1,ERCC8,DNMT3B,PIK3R1,PRIMPOL,CASP3,ATR,EYA1,CEP250,CCDC66,SCARA3,RAD9B,CYP2R1,XRCC4,MME,EIF2AK4,DDB2,TENT2,ABRAXAS1,SPIDR,CDS1,RAD54B,CRY2,TP53INP1,ITGB6,SLC4A10,TRPM1,RHBDD1,SIK1,HYAL1,HYAL3,CCND1,KRAS,PITPNM1,RRH,AEN,POLG,SPRTN,SAG,CHEK2,EYA3,USP2,CBL,ATP1A2,NFATC4,PER2,USF1,RNF168,BACE1,MGMT,CREB1,NMT1,MEN1,IL12A,COP1,XRCC5,CRTC1,GRK4,COL3A1,MMP3,RHNO1,GNB5,ROM1,FOXP3,ZBTB1,PARP1,DDB1,RGS14,UIMC1,GUCY2D,FBXL22,FOS,TAF1,CHRNB2,TIPIN,DNM2,DCUN1D3,YY1,CCL7,ASIC2,CUL4B,IFT20,UNC119,ERCC4,JUN,TP53I13,FMR1,CREBBP,SDF4,MECP2,CIRBP,ABCA7,PER3,GNAT2,CYBA,KARS,LCN2,HSPA5,FBXL8,MIR21,FBXL12,SWI5,REEP6,IMPACT,TIGAR,GADD45A,DUSP1,TXN,RNF8,GRB2,GPR88,LZIC,NHEJ1,HRAS,TMEM109,BRCC3,MAP2K7,TSPYL5,GTF2H5,NABP1	grey	VSMC_M10

GO:0090304	0.97	0.03	2047	3916	nucleic acid metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,POLI,RNMT,EYA4,TBPL1,GLI1,MARS,CLK4,MAP3K5,RPA3,TNFAIP3,TSFM,HIVEP2,ADAT2,ATP23,PLAGL1,MAML1,MRNIP,ENPP3,HELB,RPP21,PPP1R10,ZBTB2,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,MDC1,ZFC3H1,CNOT6,RIDA,STK3,OSR2,PABPC1,SNW1,TFB1M,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,TRMU,PPARA,PDE10A,UTP23,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,MCM9,ASF1A,RRP7A,HSF2,TCF7,PHF1,UBE2B,XRCC6,NCOA7,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,HABP4,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,ZC3H3,ATF4,TUT7,MAPK15,RPAP2,CBX7,APOBEC3H,GTPBP1,MAPK14,UHRF2,CBY1,DMC1,PUF60,C9orf64,CSNK1E,PICK1,KDM4C,SOX10,PIM1,CMTR1,NRF1,TMPRSS6,EXOSC4,SMO,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,FOXH1,LRRC14,RBM28,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,POT1,KLHDC3,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,ZNF318,NFX1,NOL6,XPO5,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,FANCG,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TSR1,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,RFX8,DLX5,CNOT11,REV1,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,STPG4,EPCAM,MTO1,MSH2,SP4,TSEN34,PRPF31,TFPT,IGF2BP3,PPP2R1A,ZNF462,TRA2A,RAD23B,PHIP,HMGN3,ELP1,YT	grey	VSMC_M10
GO:0006446	0.97	0.05	28	66	regulation of translational initiation	BP	1	EIF3E,AGO2,HABP4,ATF4,NCK2,MTIF2,CDC123,EIF2AK2,EIF2AK4,PAIP2B,BANK1,KLHL25,RPS6KB2,YTHDF2,YTHDF1,UHMK1,NCBP2,EIF4EBP2,DDX3X,POLR2G,ALKBH1,LARP1,CCL5,FMR1,IMPACT,EIF1B,EIF1,PPP1R15A	grey	VSMC_M10
GO:0097284	0.97	0.09	4	13	hepatocyte apoptotic process	BP	1	STK3,PPARA,DNMT3A,STK4	grey	VSMC_M10
GO:0036296	0.97	0.06	10	27	response to increased oxygen levels	BP	1	CAT,HDAC2,DNMT3B,HDAC1,POLG,TMEM199,ATP6AP1,LCN2,MT-ATP6,MT-CYB	grey	VSMC_M10
GO:0043651	0.97	0.09	4	13	linoleic acid metabolic process	BP	1	ELOVL1,ALOXE3,CYP2J2,ELOVL3	grey	VSMC_M10
GO:0031532	0.97	0.04	41	94	actin cytoskeleton reorganization	BP	1	PARVG,BAIAP2L2,MYH9,TEK,PTK7,CCL27,KIT,CLDN19,PLEK,GAB1,HCK,FER,PARVA,PTK2B,RAPGEF3,IQGAP2,DMTN,DTNBP1,TRPV4,AUTS2,HCLS1,CASS4,EPS8,FARP2,WHAMM,ABL2,MCU,MINK1,SYDE1,PLEK2,HAX1,BCAS3,CDC42BPB,CSF1R,MICALL2,RHOA,INSRR,GMFG,GRB2,RALA,HRAS	grey	VSMC_M10
GO:0000018	0.97	0.04	36	83	regulation of DNA recombination	BP	1	MRNIP,HELB,UBE2B,EXOSC3,MSH2,HMCES,ERCC2,MLH1,ZRANB3,PAXIP1,WDR48,FBH1,KPNA2,SHLD1,PPP4R2,TEX15,ERCC6,SPIDR,CD40,CD28,RTEL1,SETD2,BCL6,ZCWPW1,WAS,FOXP3,PARP1,SHLD2,TBX21,WRAP53,SMCHD1,IL7R,SUPT6H,RMI2,TERF2,OOEP	grey	VSMC_M10
GO:0051882	0.97	0.07	7	20	mitochondrial depolarization	BP	1	TSPO,DCN,IFI6,FZD9,PPP2R3C,PARP1,MLLT11	grey	VSMC_M10
GO:0002320	0.97	0.08	5	16	lymphoid progenitor cell differentiation	BP	1	KIT,PRKDC,ZBTB1,BATF,SOX4	grey	VSMC_M10
GO:0060713	0.97	0.07	6	18	labyrinthine layer morphogenesis	BP	1	RSPO3,GJB5,SPINT2,SPINT1,FZD5,GRB2	grey	VSMC_M10
GO:0032801	0.97	0.07	8	23	receptor catabolic process	BP	1	MTMR2,SNX25,MYLIP,DTX3L,ZNRF3,ANXA2,AC004687.2,SH3GLB1	grey	VSMC_M10
GO:0045063	0.97	0.09	4	13	T-helper 1 cell differentiation	BP	1	RIPK2,HLX,SEMA4A,IL4R	grey	VSMC_M10
GO:0035051	0.97	0.04	53	119	cardiocyte differentiation	BP	1	MAML1,FRS2,PPARA,CBY1,PI16,SRF,FHL2,EGFR,BVES,MYLK3,ATG5,SPRY1,JAG1,RARB,NRG1,HAND2,MEF2C,SOX6,TBX5,PRICKLE1,SIK1,PDCD4,TGFB2,GPER1,AGT,ACTC1,SLC9A1,FZD7,ALPK3,TTN,MAPK1,OBSL1,BMPR1A,TCAP,RBPJ,KDM6B,MAPK3,TBX2,YY1,GATA6,ISL1,MYH11,IFT20,TSC1,ACADM,MIR199A1,MIR21,MIR222,MIR23A,MIR24-1,RGS4,NKX2-5,HEY2	grey	VSMC_M10
GO:0034599	0.97	0.04	111	234	cellular response to oxidative stress	BP	1	ADNP2,MAP3K5,TNFAIP3,HSPA1B,PRKN,NCOA7,ERCC6L2,FANCC,ATF4,MAPK13,HSF1,GPR37,FBXO7,SLC1A1,ERMP1,PRDX1,EPAS1,PNPT1,VRK2,AQP1,ZNF277,MET,EGFR,TLR4,UCP1,SLC7A11,FOXO3,DHFR,HDAC2,PRDX3,SIRT2,PAWR,BRF2,PDK1,ARL6IP5,STX2,FER,DIABLO,ARNTL,FBXW7,MSRA,HTRA2,GPX8,NR4A2,RIPK1,TP53INP1,PKD2,PLA2R1,PAX2,PXN,GLRX2,HDAC1,FBLN5,STAU1,NCF1,MCL1,ARNT,PYROXD1,PDE8A,MGMT,NFE2L2,MAPT,NONO,PRKRA,PRODH,PDCD10,GCH1,PINK1,MMP3,ANKZF1,MAPK1,RAD52,ATP13A2,PARP1,SOD3,STX4,KDM6B,FOS,MAPK3,MPO,SFPQ,BTK,KEAP1,SIN3A,MAPK7,PPARGC1B,LONP1,STK26,JUN,PARK7,TSC1,TLDC1,LCN2,MAPKAP1,NQO1,MIR21,NFE2L1,ZNF622,PJVK,NOL3,GPR37L1,DHRS2,ZNF580,IMPACT,FXN,TXN,RBM11,NUDT2,CBX8,PPIF,PDGFD	grey	VSMC_M10
GO:0046633	0.97	0.06	9	25	alpha-beta T cell proliferation	BP	1	IL15,TGFBR2,RIPK2,CD28,VSIR,RASAL3,DOCK2,ZBTB7B,TWSG1	grey	VSMC_M10
GO:0035633	0.97	0.06	12	32	maintenance of blood-brain barrier	BP	1	SLC12A2,CLDN12,SLC1A1,ACTG1,LSR,JAM2,LAMC1,VCL,ACTB,WNK3,DMD,CLDN1	grey	VSMC_M10
GO:0018279	0.97	0.07	7	20	protein N-linked glycosylation via asparagine	BP	1	UGGT2,RPN2,DAD1,MGAT1,DERL3,MGAT2,DDOST	grey	VSMC_M10
GO:0022617	0.97	0.05	19	47	extracellular matrix disassembly	BP	1	LRP1,TMPRSS6,KLK4,LCP1,CLASP2,MMP15,ADAMTS15,FAP,MELTF,LAMC1,KIF9,ADAM8,MMP11,CTSV,MMP13,MMP3,FGFR4,CARMIL2,DPP4	grey	VSMC_M10
GO:0007339	0.97	0.07	7	20	binding of sperm to zona pellucida	BP	1	ADAM18,OVGP1,UBAP2L,ZP2,GLIPR1L2,SPA17,TMPRSS12	grey	VSMC_M10

GO:0060562	0.97	0.03	127	269	epithelial tube morphogenesis	BP	1	ESR1,STK3,FZD6,BRD2,MTSS1,MYC,KLHL3,PTCH1,PODXL,SMO,FOXH1,PTK7,SRF,SEMA4C,SOSTDC1,SIX2,AREG,EPHA7,MET,TNC,FUZ,TEAD2,MYCN,OSR1,SPRY1,BBS7,PRKD2,SETDB2,SOX9,GLI2,MEGF8,IFT172,GZF1,SPRY2,WNT11,TGFBR2,OVOL2,MKKS,SPINT2,CEP290,FOXP1,TRAF6,RET,PAX8,CASP3,HAND2,EYA1,FMN1,FZD3,MEF2C,VDR,NKX3-1,OPA1,IFT52,SPINT1,PKD2,STK4,PAX2,SALL1,PRICKLE1,RYR2,SUFU,IRX2,TGFB2,PRKX,DAG1,KRAS,EGF,AGT,GBX2,DVL3,NFATC4,LAMA5,CLIC4,GRHL3,DLG1,LUZP1,SETD2,STOX1,CTSH,CXCR2,WNT4,TULP3,EPHA4,LIAS,MAGED1,DVL2,TCAP,RBPJ,MED1,PSEN1,CITED1,SMAD3,NTN1,MKS1,TBX2,LHX1,CSF1R,MIB1,LAMA1,ADAMTS12,GPC3,SKI,PKD1,RNF207,SOX8,TSC1,FOXF1,LCN2,ENG,GLMN,BCL10,ESRP2,MIR21,RHOA,VASP,SOX4,ACVRL1,NOG,LBX1,WNT5A,SIX1,C2CD3,RALA,NKX2-5,FGF1,WNT2	grey	VSMC_M10
GO:0042771	0.97	0.06	13	34	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	BP	1	SNW1,MSH2,TAF9,ING2,MARCH7,AEN,CHEK2,MUC1,TAF9B,CD74,CDIP1,RPS27L,TMEM109	grey	VSMC_M10
GO:0061318	0.97	0.08	5	16	renal filtration cell differentiation	BP	1	PODXL,JAG1,ASXL1,PTPRO,BASP1	grey	VSMC_M10
GO:0072112	0.97	0.08	5	16	glomerular visceral epithelial cell differentiation	BP	1	PODXL,JAG1,ASXL1,PTPRO,BASP1	grey	VSMC_M10
GO:0071385	0.97	0.05	17	43	cellular response to glucocorticoid stimulus	BP	1	FECH,AQP1,EGFR,FOXO3,BMI1,FAM107A,DNMT3B,STC1,ABCC2,SRD5A1,NPAS4,ISL1,ASS1,SMYD3,CRH,BCL2L11,ZFP36L2	grey	VSMC_M10
GO:0060411	0.97	0.05	24	59	cardiac septum morphogenesis	BP	1	SMO,DNAH11,WNT11,TGFBR2,JAG1,PARVA,ROBO1,ROBO2,TBX5,TGFB2,SAV1,BMPR1A,DHRS3,RBPJ,MKS1,TBX2,GATA6,ISL1,ENG,SOX4,NOG,WNT5A,NKX2-5,HEY2	grey	VSMC_M10
GO:0072350	0.97	0.08	4	13	tricarboxylic acid metabolic process	BP	1	ACO2,SIRT4,IDH3A,ASS1	grey	VSMC_M10
GO:0035966	0.97	0.04	66	143	response to topologically incorrect protein	BP	1	HSPA1B,PRKN,PACRG,RNF5,HSPA4,DERL1,BAK1,ATF4,HSF1,NCK2,ERMP1,ERP44,DNAJA1,HERPUD2,FGF21,HSPE1,OPTN,KBTBD6,UBXN4,UGGT2,DNAJC18,TMTC4,EIF2AK2,DDRGK1,PIK3R1,TMBIM6,AUP1,AMFR,RHBDD1,CCND1,FICD,YOD1,HSPA8,QRICH1,BAG3,RNF185,TBL2,RHBDD2,EDEM3,NFE2L2,DERL3,DNAJB12,DNAJC4,TMEM129,DNAJB2,SDF2L1,BHLHA15,F12,DNAJB1,MFN2,CREBRF,CREB3L4,PTPN2,CREB3L3,ABCA7,RNF126,TOR1B,HSPA5,DAB2IP,MIR199A1,HSPB2,DDIT3,BCL2L11,HSPB8,PPP1R15A,DERL2	grey	VSMC_M10
GO:0003171	0.97	0.06	8	23	atrioventricular valve development	BP	1	TGFBR2,TBX5,TGFB2,BMPR1A,EFNA1,SOX4,HEY2,OLFM1	grey	VSMC_M10
GO:0031099	0.97	0.04	69	150	regeneration	BP	1	LRP1,GLI1,IGF2R,TSPO,BAK1,PTCH1,LARGE1,TEC,PPAT,NINJ1,PNPT1,AKIRIN1,PTN,TNC,EGFR,LPIN1,DHFR,C5AR1,LCP1,KLF5,PTPRF,TGFBR2,CHL1,GAS6,ULK1,CSNK2A2,BIN3,SPP1,KIAA0319,MTR,LGR6,PPP3CA,CCND1,CPT1A,GAP43,SULF2,DAG1,SOX2,KREMEN1,CERS2,FZD7,FZD9,CDKN1B,LRIG2,APOD,DUSP10,TNR,MYOZ1,NINJ2,ENO3,EPHA4,MED1,RPL19,SOX15,PGF,NDEL1,MAP2K1,ISL1,OMG,MAPK8IP3,MIR199A1,MIR222,MT-CYB,CNTF,RTN4RL1,THY1,CLDN1,NNMT,CEBPB	grey	VSMC_M10
GO:0050729	0.97	0.04	41	93	positive regulation of inflammatory response	BP	1	GPSM3,MAPK13,TTBK1,NINJ1,EGFR,TLR4,IL15,MGST2,CDK19,NAPEPLD,NMI,CEBPA,RIPK1,TRPV4,PDCD4,FABP4,AGT,OSM,SNX4,CD28,ADAM8,IL16,TNFSF18,STAT5B,LDLR,S100A8,BTK,TNIP1,PTGER4,C3,OSMR,CREB3L3,PARK7,KARS,MIR21,MIR22,S100A12,WNT5A,IL33,TSLP,CEBPB	grey	VSMC_M10
GO:0006740	0.97	0.08	4	13	NADPH regeneration	BP	1	RBKS,RPE,TIGAR,RPIA	grey	VSMC_M10
GO:0045910	0.97	0.05	13	34	negative regulation of DNA recombination	BP	1	HELB,MSH2,MLH1,ZRANB3,FBH1,SHLD1,RTEL1,BCL6,FOXP3,SHLD2,SMCHD1,RMI2,TERF2	grey	VSMC_M10
GO:0043112	0.97	0.04	59	131	receptor metabolic process	BP	1	LRP1,PICK1,USP46,CXCL8,RSPO1,BVES,SFRP4,SDCBP,EPS15,MTMR2,OPTN,ARRB1,TBC1D16,RAB5A,NRG1,SNX25,WDR54,MYLIP,ANKRD13A,EGF,AP1AR,ANKRD13D,GRK2,SORL1,SAG,DTX3L,ZNRF3,AP2M1,FCER1G,CALY,NSF,LRPAP1,CXCR2,GRK4,CALCRL,DNM3,ECE1,RAMP2,NSG1,DLG4,ANXA2,PSEN1,SNX1,AC004687.2,DNM2,INSR,AP2B1,FMR1,SH3GLB1,MIR199A1,PHETA1,CNTN2,LDLRAP1,CACNG7,GRB2,VAMP3,PLEKHJ1,CACNG5,LRRTM2	grey	VSMC_M10
GO:0016126	0.97	0.05	20	49	sterol biosynthetic process	BP	1	PLPP6,APOB,EBP,PRKAG2,CYP7A1,ERLIN1,CYB5R1,MSMO1,SC5D,SCAP,HSD17B7,POR,TM7SF2,LPCAT3,CH25H,ERG28,SREBF1,ACAA2,INSIG2,FGF1	grey	VSMC_M10
GO:0036295	0.97	0.08	4	13	cellular response to increased oxygen levels	BP	1	DNMT3B,TMEM199,ATP6AP1,LCN2	grey	VSMC_M10
GO:0042181	0.97	0.05	14	36	ketone biosynthetic process	BP	1	HSD17B3,DKKL1,DKK3,COQ2,SIRT5,COQ5,COQ10B,WNT4,NDUFA9,COQ8A,DGKQ,CACNA1H,COQ4,PDSS2	grey	VSMC_M10
GO:0010881	0.97	0.07	6	18	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	BP	1	CASQ2,RYR2,ANK2,ATP1A2,CALM1,DMD	grey	VSMC_M10
GO:0031295	0.97	0.06	10	27	T cell costimulation	BP	1	TNFRSF13C,LCK,CD28,PTPN6,CARD11,YES1,VAV1,DPP4,EFNB3,TNFSF13B	grey	VSMC_M10
GO:0001946	0.97	0.07	5	16	lymphangiogenesis	BP	1	ACVR2B,VEGFC,PPP3CB,VASH1,ACVRL1	grey	VSMC_M10
GO:0050819	0.97	0.05	15	38	negative regulation of coagulation	BP	1	SERPINB2,TSPAN8,HS3ST5,THBD,PLAT,C1QTNF1,ADTRP,FAP,UBASH3B,USF1,F12,ANXA2,ABAT,SERPINF2,FGA	grey	VSMC_M10
GO:0060047	0.98	0.04	79	172	heart contraction	BP	1	NEDD4L,SMAD5,SLC1A1,TNNI3,EPAS1,ASB3,BVES,ATG5,TRPM4,SLC8A2,CACNB2,ATP1A3,CELF2,SCN5A,SCN1A,GPD1L,HBEGF,ADRA1D,SEMA3A,SGCG,STC1,KCNJ3,TBX5,TNNC1,KCNE2,DSP,CASQ2,KCNIP2,RYR2,PKP2,DNM1L,KCNJ2,MAP2K6,TNNI1,TGFB2,MYH7,GRK2,ANK2,AGT,ACE2,ATP1A2,ACTC1,SLC9A1,HDAC4,SCN4B,NOS1AP,DLG1,TTN,GCH1,ATP1B1,DES,SLC4A3,THRA,TCAP,ATP1B2,CACNA1G,ATP2A1,CALM1,TBX2,DSG2,SREBF1,ISL1,CYP2J2,ATP2B3,TRPV1,RNF207,CACNA1H,DMD,CHGA,TMEM65,KCNH2,SCN2B,RGS4,POPDC2,KCNJ8,HCN4,NKX2-5,HEY2,KCNG2	grey	VSMC_M10

GO:0035150	0.98	0.04	44	100	regulation of tube size	BP	1	PLA2G6,ZDHHC21,ITGB1BP1,EGFR,KEL,ATG5,TRPM4,MKKS,ADRA1D,ADRA2B,HTR7,GUCY1A1,P2RY1,DOCK5,F2RL1,F2R,CHRM3,RAP1GDS1,ADRA2A,GPER1,AGT,ACE2,ATP1A2,PER2,PLOD3,CPS1,ADRA2C,ECE1,GCH1,SMTNL2,CD38,KCNMA1,SOD3,HRH2,SCPEP1,SCNN1B,ASIC2,SERPINF2,P2RX1,MIR21,RHOA,HTR1D,FGA,KCNMB4	grey	VSMC_M10
GO:0035296	0.98	0.04	44	100	regulation of tube diameter	BP	1	PLA2G6,ZDHHC21,ITGB1BP1,EGFR,KEL,ATG5,TRPM4,MKKS,ADRA1D,ADRA2B,HTR7,GUCY1A1,P2RY1,DOCK5,F2RL1,F2R,CHRM3,RAP1GDS1,ADRA2A,GPER1,AGT,ACE2,ATP1A2,PER2,PLOD3,CPS1,ADRA2C,ECE1,GCH1,SMTNL2,CD38,KCNMA1,SOD3,HRH2,SCPEP1,SCNN1B,ASIC2,SERPINF2,P2RX1,MIR21,RHOA,HTR1D,FGA,KCNMB4	grey	VSMC_M10
GO:0097746	0.98	0.04	44	100	blood vessel diameter maintenance	BP	1	PLA2G6,ZDHHC21,ITGB1BP1,EGFR,KEL,ATG5,TRPM4,MKKS,ADRA1D,ADRA2B,HTR7,GUCY1A1,P2RY1,DOCK5,F2RL1,F2R,CHRM3,RAP1GDS1,ADRA2A,GPER1,AGT,ACE2,ATP1A2,PER2,PLOD3,CPS1,ADRA2C,ECE1,GCH1,SMTNL2,CD38,KCNMA1,SOD3,HRH2,SCPEP1,SCNN1B,ASIC2,SERPINF2,P2RX1,MIR21,RHOA,HTR1D,FGA,KCNMB4	grey	VSMC_M10
GO:0006936	0.98	0.03	121	256	muscle contraction	BP	1	NEDD4L,STAC3,SNTB1,SMAD5,PLA2G6,ZDHHC21,CHRNA3,LMOD2,SRF,KIT,TMOD1,TNNI3,ASB3,MYBPC2,MYH14,CLCN1,TRPM4,CACNB2,STAC,SCN5A,SCN1A,GPD1L,MKKS,RYR1,P2RX2,LMOD3,ADRA2B,ASPH,HTR7,NR4A1,SLMAP,MYOF,P2RX3,PLCE1,GUCY1A1,CKMT2,DOCK5,HOMER1,STC1,KCNJ3,F2R,TNNC1,COL4A3BP,KCNE2,DSP,CASQ2,KCNIP2,CHRM3,RYR2,RAP1GDS1,PKP2,LMOD1,KCNJ2,MAP2K6,TNNI1,TRPV4,ADRA2A,SYNM,SULF2,MYH7,SCN7A,GRK2,ANK2,GPER1,AGT,ACE2,ATP1A2,ACTC1,SLC9A1,CASQ1,ACTN3,TMOD4,HDAC4,SCN4B,MYOM3,NOS1AP,DLG1,TTN,ADRA2C,CALCRL,ATP1B1,KCNA1,CD38,KCNMA1,DES,TMOD2,TPM4,CHRNB1,TCAP,STAC2,ARHGEF11,MYL5,CACNA1G,CHRNB2,ATP2A1,CALM1,SCNN1B,TBX2,NMUR2,SETD3,DTNA,DSG2,MYH11,ABAT,TRPV1,P2RX1,GAMT,RNF207,CACNA1H,MIR21,RHOA,HTR1D,DMD,CHRNG,CHGA,KCNH2,TNNC2,SCN2B,KCNJ8,HCN4,NKX2-5	grey	VSMC_M10
GO:1901362	0.98	0.03	1558	3012	organic cyclic compound biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,SMARCC2,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,POLI,SHMT2,TBPL1,GLI1,MARS,MAP3K5,TNFAIP3,CYP27B1,TSFM,HIVEP2,PLAGL1,MAML1,ATP5MGL,HELB,ZBTB2,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,STK3,OSR2,SNW1,TFB1M,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,CYP21A2,ZBED4,MAP3K4,PPT2,PRKN,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,RXRB,TSPO,VGLL2,HSD17B8,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,HSD17B3,KDM3B,PTP4A3,PTCH1,AKR1B1,ATF4,PYCR3,MAPK15,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,MOCS1,PSAT1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,POT1,GPR37,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,SLC35B2,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,PLPP6,SRD5A3,UXS1,NCK2,FHL2,TGFBRAP1,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,RFX8,DLX5,PPAT,HINT2,REV1,PHF14,IPPK,ETV1,ZNF135,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,SIX2,PPCS,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,NFE2L3,ME1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,NT5E,ZNF483,JAZF1,PPT1,CREB5,MYCL,XPO1,MTURN,NOD1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,DDC,KLF	grey	VSMC_M10
GO:0086064	0.98	0.06	8	23	cell communication by electrical coupling involved in cardiac conduction	BP	1	ATP1A3,TBX5,RYR2,PKP2,ATP1A2,ATP1B1,ATP1B2,CALM1	grey	VSMC_M10
GO:0060828	0.98	0.03	98	210	regulation of canonical Wnt signaling pathway	BP	1	RPS12,GLI1,STK3,FZD6,PRKN,UBE2B,RSPO3,RNF146,MAPK14,CSNK1E,SOX10,DAAM2,PTK7,CDK14,ROR2,DLX5,WNK2,SOSTDC1,RSPO1,EGFR,HECW1,FUZ,SFRP4,CCNY,DKKL1,TRPM4,FOXO3,SOX9,PPM1N,SCEL,WNT11,RBMS3,CHD8,UBAC2,FERMT1,PFDN5,CTNND1,DKK3,ARNTL,TMEM131L,LMBR1L,OTULIN,AMFR,SOX13,STK4,PRICKLE1,NKD1,PRDM15,LGR6,LRRK1,HDAC1,CAPRIN2,TMEM9,SULF2,TCF7L2,DKK2,AXIN2,EGF,TTC21B,SOX2,ZNRF3,KREMEN1,BICC1,FZD7,GID8,PTPRO,FZD9,CCNYL1,DDX3X,TBL1XR1,PPM1A,OTUD5,IGFBP4,RBPJ,PSEN1,TMEM88,CSNK1G1,SMAD3,MKS1,CCDC88C,G3BP1,NLE1,ISL1,IFT20,GPC3,TLE6,APC2,DAB2IP,MIR199A1,MIR222,SOX4,NOG,WNT5A,DDIT3,DACT3,SDHAF2,APC,NKX2-5	grey	VSMC_M10
GO:0006911	0.98	0.05	15	39	phagocytosis, engulfment	BP	1	RAC2,MYH9,ARHGAP12,NCKAP1L,XKR6,RHOBTB2,F2RL1,ANO6,RHOBTB1,DOCK1,ITGAM,C3,ABCA7,HAVCR1,XKR8	grey	VSMC_M10
GO:0061756	0.98	0.05	13	34	leukocyte adhesion to vascular endothelial cell	BP	1	ZDHHC21,ADD2,PODXL2,TRAF6,JAM2,SELPLG,ITGA4,CCL25,MIR21,MIR222,RHOA,FUT4,MIR125A	grey	VSMC_M10
GO:0051450	0.98	0.08	4	13	myoblast proliferation	BP	1	SOX15,ZNF609,GATA6,MIR199A1	grey	VSMC_M10
GO:1900046	0.98	0.05	21	51	regulation of hemostasis	BP	1	SERPINB2,TSPAN8,ENPP4,THBD,PLAT,C1QTNF1,F2RL1,F2R,ANO6,DMTN,ADTRP,FAP,UBASH3B,USF1,NFE2L2,SERPINC1,F12,ANXA2,ABAT,SERPINF2,FGA	grey	VSMC_M10
GO:1900363	0.98	0.07	5	16	regulation of mRNA polyadenylation	BP	1	CPSF6,ZC3H3,HSF1,RNF20,YTHDC1	grey	VSMC_M10
GO:1901739	0.98	0.08	4	13	regulation of myoblast fusion	BP	1	MAPK14,EHD1,GDF15,IL4R	grey	VSMC_M10
GO:0051053	0.98	0.04	41	94	negative regulation of DNA metabolic process	BP	1	HELB,HSF1,POT1,MSH2,CYREN,ERCC1,XRCC1,MLH1,DACH1,ZRANB3,FBH1,RNF169,SHLD1,ERCC6,NBN,TENT4B,STN1,KCNK2,RTEL1,BCL6,MEN1,XRCC5,FOXP3,PARP1,SHLD2,GNL3L,CTC1,PIF1,OTUB2,SMCHD1,ERCC4,RMI2,NUDT16L1,PAM16,SLX4,TERF2,ACVRL1,TINF2,TEN1,DUSP1,NMNAT1	grey	VSMC_M10

GO:0045332	0.98	0.05	13	35	phospholipid translocation	BP	1	ATP9B,ATP8B1,ABCB1,TMEM30A,ANO4,XKR6,PLSCR4,P2RX7,ANO6,TMEM30B,ATP11C,ABCA7,XKR8	grey	VSMC_M10
GO:1902230	0.98	0.06	9	25	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	TRIM32,DDIAS,TAF9,ING2,MARCH7,SNAI1,MUC1,TAF9B,CD74	grey	VSMC_M10
GO:0030155	0.98	0.03	265	541	regulation of cell adhesion	BP	1	ERBB3,ONECUT2,MIP,LRP1,SEMA6A,AGER,PPARA,HLA-DRA,FBLN1,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,PTK2,PLXNA4,MAPK14,PODXL,RAC2,ZDHHC21,CDKN2A,IFT74,TEK,SRF,ADAM22,NUAK1,CDK6,TNFRSF21,NCK2,SEMA4D,PRKCE,EPCAM,PPP2R1A,EPB41L4B,HOXA7,CXCL8,PELI1,EPHA7,AKNA,PTN,ITGB1BP1,TNC,IL4I1,EPHA1,IL15,FAF1,PLXNA1,LAMA4,BMI1,NDNF,PRKD2,SOX9,FBLN2,CLASP2,RSU1,GLI2,PCDH8,UNC13D,FOXJ1,PPP1CB,RIN2,TGFBR2,C1QTNF1,JAG1,ACTG1,PAWR,FERMT1,RAC3,SPINT2,PRNP,BAG4,ARHGEF7,RELL2,PLXNC1,NCKAP1L,PTPRA,SLC7A1,LRFN3,TRAF6,SOX12,RET,ZC3H8,FAM107A,IL1A,PIK3CB,PIK3R1,LPXN,CASP3,DENND6A,TENM3,FMN1,PTPRJ,TMEM131L,IL7,PAG1,PTK2B,RASGRP1,RND1,RIPK2,DOCK5,AP3B1,CYTIP,TESC,MARCH7,RREB1,SOX13,STK4,GCNT2,DMTN,ADTRP,NOD2,LDB1,JGF2,SLK,CARMIL1,HYAL1,LCK,PPP3CA,ICOSLG,TRPV4,TGFB2,BTN2A2,GPAM,COL16A1,PRKAR1A,PRKX,DAG1,HLX,ARHGAP6,SOX2,AP1AR,YTHDF2,UBASH3B,DISC1,CASS4,CIB1,SLC9A1,FZD7,LAMA5,PTPRO,CHRD,CD28,RUNX3,EPHB3,DOCK1,MELTF,CSPG5,EFEMP2,DLG1,APOD,ADAM8,FRMD5,MIA3,DUSP10,BCL6,ABL2,ITGA4,MEN1,IL12A,ABCA12,TNR,FN1,VSIR,CASK,SPOCK2,RC3H1,PTPN6,SERPINI1,TNFSF18,FERMT3,WNT4,LAG3,VCL,BST1,ARHGDIG,STAT5B,CYTH3,MINK1,TFE3,SCGB1A1,FOXP3,EPHA4,RASAL3,ZBTB1,CARD11,TMEM102,TBX21,STX4,ITGA3,MUC1,EFNA1,ZBTB7B,SMAD3,IL4R,MAP2K5,CORO2B,DNM2,BCAS3,CD74,CCL5,LAMA3,MAPK7,CAMSAP3,CCL2,CCL25,YES1,JAG2,NKAP,VAV1,LAMA1,JAK1,TWSG1,IL7R,PTPN2,SOCS1,DAB1,ABAT,CRK,DNAJA3,SERPINF2,PRKCZ,PKD1,PLXNA3,CELSR2,PIEZO	grey	VSMC_M10
GO:2000047	0.98	0.07	5	16	regulation of cell-cell adhesion mediated by cadherin	BP	1	EPCAM,DENND6A,SERPINF2,WNT5A,RGCC	grey	VSMC_M10
GO:1903052	0.98	0.04	53	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,ZYG11B,BBS7,PLK3,SUMO2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,TRIB3,PLK2,CEBPA,FBXW7,PTK2B,RNFT2,KCNE2,PRICKLE1,RNF144B,USP13,AC013489.1,EGFL,DISC1,ARIH2,RNF185,NFE2L2,COP1,SOCS4,DNAJB2,PSMC3,OSBPL7,PSEN1,TAF1,KEAP1,PSMD10,FBXO22,FMR1,FZR1,BCAP31,SGTA,TMEM259,ZER1,DAB2IP,PSMC1,BAG2,RNFT1,DDA1	grey	VSMC_M10
GO:0044380	0.98	0.04	22	55	protein localization to cytoskeleton	BP	1	ABHD17B,MAPRE1,MAPRE3,PIBF1,HOOK3,DIAPH1,CHAMP1,NSFL1C,CEP250,MCPH1,TTBK2,DISC1,CEP192,ABHD17A,WRAP73,KLHL21,SNX10,ABHD17C,C2CD3,APC,PARD6A,MAP1A	grey	VSMC_M10
GO:1900047	0.98	0.05	14	36	negative regulation of hemostasis	BP	1	SERPINB2,TSPAN8,THBD,PLAT,C1QTNF1,ADTRP,FAP,UBASH3B,USF1,F12,ANXA2,ABAT,SERPINF2,FGA	grey	VSMC_M10
GO:0010212	0.98	0.03	62	137	response to ionizing radiation	BP	1	MRNIP,BAK1,XRCC6,MYC,MAPK14,HSF1,ABCG5,MSH2,DNMT3A,ERCC1,XRCC2,PAXIP1,THBD,XRRA1,WRN,PRKDC,ERCC6,DNMT3B,CASP3,ATR,EYA1,RAD9B,CYP2R1,XRCC4,ABRAXAS1,SPIDR,RAD54B,ITGB6,CCND1,AEN,POLG,CHEK2,EYA3,CBL,RNF168,MGMT,MEN1,COP1,XRCC5,RHNO1,PARP1,UIMC1,DNM2,DCUN1D3,CCL7,CYBA,KARS,HSPA5,MIR21,SWI5,TIGAR,GADD45A,RNF8,GRB2,LZIC,NHEJ1,HRAS,TMEM109,BRCC3,TSPYL5,GTF2H5,NABP1	grey	VSMC_M10
GO:0120032	0.98	0.03	72	158	regulation of plasma membrane bounded cell projection assembly	BP	1	ATP8B1,AVIL,TBC1D30,MAPK15,PODXL,CDC42EP1,RAC2,SRF,KIT,DYNC2LI1,EPS8L1,AKIRIN1,FUZ,ATG5,KLF5,RAB5A,DPYSL3,FER,PIK3R1,PLCE1,P2RX7,BIN3,F2RL1,ARHGAP24,CYFIP1,DMTN,SRGAP2C,NEURL1,ZMYND10,GAP43,AUTS2,WASF2,RAB17,HDAC4,EPS8,CDKL5,LIMK2,CDC42EP2,NCKAP1,HTT,DNM3,RAP1GAP,WAS,SDCCAG8,HAP1,MNS1,MIEN1,PLEK2,FXR2,CNTROB,NDEL1,TENM2,AC138894.1,CCDC151,DNM2,BCAS3,ARHGAP44,EVL,IFT20,FMR1,WRAP73,PALM,EPS8L3,DEF8,CDK10,FNBP1L,ODF2L,CARMIL2,EPS8L2,APC,RALA,HRAS	grey	VSMC_M10
GO:1902750	0.98	0.04	21	52	negative regulation of cell cycle G2/M phase transition	BP	1	MRNIP,TRIM39,BRSK1,RAD17,CHMP4C,NBN,ABRAXAS1,DONSON,ZFYVE19,TAOK3,SYF2,UIMC1,FOXO4,TAOK2,FOXN3,TAOK1,FZR1,VPS4A,NAE1,BRCC3,NABP1	grey	VSMC_M10
GO:0032210	0.98	0.04	20	50	regulation of telomere maintenance via telomerase	BP	1	MAP3K4,MAPK15,POT1,ATR,HMBOX1,MAPKAPK5,TENT4B,STN1,XRCC5,MAPK1,GNL3L,SMG5,CTC1,PIF1,MAPK3,PARN,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0090287	0.98	0.03	107	230	regulation of cellular response to growth factor stimulus	BP	1	ONECUT2,SEMA6A,SNW1,PPARA,LEMD2,PTP4A3,KCP,TFAP2B,SOSTDC1,CD109,ADAMTS3,HOXA13,BMPER,GRB10,TSPAN12,FUZ,SFRP4,SDCBP,WASF1,SPRY1,PRKD2,UBE2O,SPRY2,EID2,FERMT1,SPRED3,DCN,SPART,FGFBP3,PIK3CB,SNX25,DKK3,ING2,ROBO1,IL17RD,VEGFC,VEPH1,CYFIP1,ZNF423,DSTYK,FBXL15,SLC2A10,SULF2,PDCD6,LRIT3,SORL1,DOK5,AGT,ARNT,HTRA1,CHRD,DLX1,SNX6,CTDSPL2,PBLD,PPP2R5B,MEN1,IL12A,CASK,HTRA3,FBN1,WNT4,FKBP8,PPM1A,GREM2,MPP5,RBPJ,RNF111,TGFB1I1,FGF18,NGFR,ITGA3,RBPMS2,TOB1,CITED1,WFIKKN2,SMAD3,TNMD,PRKCB,RNF165,DNM2,CHRDL1,TWSG1,ADAMTS12,GPC3,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,DAB2IP,MIR199A1,MIR21,FSTL3,LEMD3,ACVRL1,NOG,WNT5A,NRROS,SHISA2,CADM4,LDLRAD4,FGF1,UBE2D1,PEG10	grey	VSMC_M10
GO:2000725	0.98	0.07	5	16	regulation of cardiac muscle cell differentiation	BP	1	FRS2,MEF2C,SOX6,FZD7,MIR222	grey	VSMC_M10
GO:0090329	0.98	0.05	16	41	regulation of DNA-dependent DNA replication	BP	1	SSBP1,DACH1,ZRANB3,FBH1,NUGGC,NBN,WRNIP1,DONSON,POLG2,BCL6,DBF4B,KAT7,TIPIN,LIG3,METTL4,WDR18	grey	VSMC_M10

GO:0032496	0.98	0.03	106	225	response to lipopolysaccharide	BP	1	TNFAIP3,CYP27B1,TSPO,TRIB1,MAPK14,HSF1,ADH5,PRKCE,CXCL8,AKIRIN2,PELI1,TLR4,MGST2,APOB,CDK19,HDAC2,C5AR1,PTGIR,MYD88,PRDX3,TIMP4,IRAK2,THBD,NFKBIB,DCN,FOXP1,TRAF6,HCK,IL1A,IL37,NR4A1,FER,CASP3,HPGD,PLSCR4,MEF2C,NUGGC,NR1H3,RIPK2,F2R,ABCC2,NOD2,CD40,NFKB2,MAPKAPK3,CD96,HDAC1,PDCD4,MAPKAPK2,IL10RA,DUSP10,GGT2,CPS1,IL12A,COMT,UPF1,SLC11A1,TNIP2,ALPL,GCH1,MAPK1,SGMS1,OTUD5,SCGB1A1,FOXP3,LIAS,AKAP8,TNFRSF1B,SPON2,FOS,MAPK3,CITED1,MPO,S100A14,S100A8,BDKRB1,TNIP1,CCL5,CCL2,LITAF,PTGER4,NOS2,JUN,TICAM1,ADAMTS13,ASS1,LCN2,GFI1,BCL10,DAB2IP,PTGFR,MIR21,RHOA,CXCL6,CASP8,GNG12,IRGM,CMPK2,IL36G,CLDN1,WNT5A,GGT5,PTGES,KCNJ8,CEBPB,HAVCR2	grey	VSMC_M10
GO:0032511	0.98	0.08	4	13	late endosome to vacuole transport via multivesicular body sorting pathway	BP	1	LEPROTL1,CHMP4C,CHMP7,LEPROT	grey	VSMC_M10
GO:0036258	0.98	0.06	9	25	multivesicular body assembly	BP	1	VPS4B,CHMP2A,CHMP2B,CHMP4C,CHMP7,VPS37D,RAB11A,CHMP1A,VPS4A	grey	VSMC_M10
GO:0071900	0.98	0.03	143	300	regulation of protein serine/threonine kinase activity	BP	1	MAP3K5,TNFAIP3,STK3,TNXB,MAP3K4,AGER,TRIB1,TAB1,STK38,CCND3,CDKN2A,FBXO7,KIT,ROR2,DNAJA1,EPGN,ETAA1,TGFA,EGFR,ARHGEF5,TLR4,CCNY,PRKAR2B,SPRY1,SLC8A2,MAPRE3,RALB,PRKAG2,SPRY2,NEK10,RPTOR,TCIM,FLT1,TRAF6,TRIB3,CEBPA,PIK3CB,CDK7,CASP3,ROBO1,PTPRJ,PKIA,CCNH,CCNJ,PTK2B,RASGRP1,CCNG2,RAPGEF2,PRKAG1,TIAM1,PAQR3,CCNJL,PKD2,STK4,HERC5,NOD2,DTNBP1,TAOK3,CD40,IGF2,BMPR1B,CCND1,MAP2K6,PDCD4,ADRA2A,FAM20A,PRKAR1A,AJUBA,MST1,KRAS,EGF,SORL1,SPATC1L,AGT,CIB1,DVL3,SFN,SYAP1,STRADA,CDKN1B,MAP3K11,ADAM8,AIDA,FZD5,DUSP10,HEXIM2,CEMIP,DBF4B,MEN1,MAP4K2,DDX3X,DUSP19,PTPN6,PDCD10,HTT,PRKAG3,SLC27A1,EPHA4,ACTB,MAGED1,DVL2,BMPR1A,CDK12,RGS14,PSEN1,FGF18,MAP2K1,PIK3R5,MAP2K5,CALM1,PSMD10,INSR,CSF1R,CDK5R1,GHR,KSR1,TAOK1,INPP5K,MLST8,PKD1,TRAF2,MTCP1,PSRC1,DAB2IP,MIR24-1,RHOA,S100A12,CNPPD1,IRGM,THY1,WNT5A,GADD45A,DUSP1,SPDYA,RGCC,APC,DAZAP2,HRAS,LAX1,MAP2K7,C3orf58,FGF1,PDGFD	grey	VSMC_M10
GO:0032103	0.98	0.03	137	286	positive regulation of response to external stimulus	BP	1	CD226,LRP1,USP15,AGER,GPSM3,XRCC6,PTK2,MAPK13,RAC2,TTBK1,CCL27,NINJ1,FPR2,ANKRD17,CXCL8,NOD1,AKIRIN2,AKIRIN1,PTN,MET,EGFR,TLR4,IL15,MGST2,PUM2,CDK19,C5AR1,NAPEPLD,PRKD2,NECTIN2,PVR,OPTN,MEGF8,OXSR1,THBD,IKBKB,NMI,TMEM173,MAVS,NCKAP1L,GAS6,HPX,PRKDC,IRF7,TRAF6,HCK,CEBPA,VEGFC,PTK2B,RASGRP1,TIAM1,NLRC5,RIPK2,F2RL1,RIPK1,ANO6,POLR3D,NOD2,OASL,DNM1L,TRPV4,PDCD4,PRSS56,POLR3C,CMKLR1,FABP4,MOSPD2,PARP9,AGT,OSM,SNX4,USF1,COCH,CD28,ADAM8,CADM1,NONO,IL16,IL12A,XRCC5,MCU,TNFSF18,CXCR2,LAG3,MAPK1,STAT5B,TMEM102,MED1,STX4,FGF18,PGF,DAPK2,NDEL1,MAPK3,IL6R,SMAD3,LDLR,S100A14,S100A8,SFPQ,BTK,TNIP1,SIN3A,CD74,CCL5,RIOK3,CSF1R,CCL7,VAV1,PTGER4,C3,OSMR,CREB3L3,SERPINF2,CREBBP,PARK7,CYBA,KARS,AP1G1,MIR21,MIR222,MIR22,S100A12,DEFB124,FADD,CNTF,ZCCHC3,ZNF580,IRGM,WNT5A,IL33,ARTN,TSLP,CEBPB,EREG,HAVCR2,PDGFD	grey	VSMC_M10
GO:0043502	0.98	0.04	30	71	regulation of muscle adaptation	BP	1	PPARA,PI16,FOXO3,TRPC3,SCN5A,HAND2,TNNC1,JARID2,PDE9A,PPP3CA,TNNI1,DAG1,MYH7,GTF2IRD1,AGT,SLC9A1,CASQ1,ACTN3,HDAC4,PRKAG3,CAMK2G,PARP1,TNFRSF1B,SMAD3,YY1,MIR199A1,MIR21,MIR25,NOL3,RGS4	grey	VSMC_M10
GO:0032990	0.98	0.03	260	536	cell part morphogenesis	BP	1	NEDD4L,LRP1,SEMA6A,KIF5A,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,SULT4A1,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,CPNE5,RAC2,SMO,RBFOX2,CHRNA3,SRF,SEMA4D,DLX5,ETV1,SEMA4C,BRSK1,RIMS1,RTN4,PNPT1,RUFY3,SHANK1,HOXA2,MYH14,EPHA7,PTN,EGFR,HECW1,EPHA1,KEL,NRCAM,NTF4,WASF1,SSBP1,PLXNA1,RAB10,ABI1,NECTIN2,GOLGA4,GLI2,MEGF8,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,CPNE9,FARP1,KIF5C,SYT1,TMEM106B,FEZ2,SLC23A2,ARHGEF7,SEMA3D,PANK2,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NCKAP1L,ULK1,RYK,EPHB1,RET,TTL,ANKRD27,PREX2,ROBO1,ROBO2,FZD3,SEMA4F,TLX2,CUX2,RAPGEF2,DPYSL2,EIF2AK4,TIAM1,SLIT1,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,COL4A3BP,SEMA3G,RREB1,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,SEMA4G,ZNF335,DTNBP1,TAOK3,SIAH1,LZTS1,BMPR1B,BDNF,DOCK10,KIAA0319,LGR6,DNM1L,PPP3CA,HECW2,CAPRIN2,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,CFL1,ADNP,POLG2,DISC1,WASF2,GBX2,DVL3,KALRN,NFATC4,SS18L1,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,TANC2,NUBPL,CSPG5,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,FIS1,SUPV3L1,SEMA6D,EPHB4,ITGA4,TNR,FN1,NCKAP1,NYAP1,ATL1,NIN,FLRT1,DNM3,PPP3CB,CNTNAP1,RAB3A,MARK2,MUL1,VCL,OBSL1,MINK1,RAB8A,CRMP1,EPHA4,LRTM2,DLG4,ACTB,DVL2,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,SNX1,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,NTN1,GAS7,RPS6KA5,RNF165,MYO9A,DNM2,PARP6,GPRASP2,BHLHB9,BCL11B,LHX1,ARHGAP44,SIN3A,TRPV2,LAMA3,CDK5R1,ISL1,EMB,EPB41L3,LAMA1,DOCK7,TAOK1,SLC9A6,	grey	VSMC_M10
GO:1903077	0.98	0.06	8	23	negative regulation of protein localization to plasma membrane	BP	1	GOPC,LYPLA1,PPFIA1,AP2M1,PPP2R5A,LRRC15,RSC1A1,MRAP2	grey	VSMC_M10
GO:0097194	0.98	0.04	25	60	execution phase of apoptosis	BP	1	HSF1,DEDD2,CIDEC,SIRT2,FOXL2,CASP3,XKR6,FZD3,HTRA2,MADD,ACVR1C,FAP,ACIN1,GPER1,CIDEB,BNIP1,DNASE2,TAOK1,PAM16,DFFB,CASP8,AIFM3,BLCAP,NMNAT1,XKR8	grey	VSMC_M10
GO:0002335	0.98	0.06	8	23	mature B cell differentiation	BP	1	MFNG,CMTM7,PLCL2,PTK2B,CDH17,DOCK10,SLAMF8,CD19	grey	VSMC_M10

GO:0048017	0.98	0.03	61	137	inositol lipid-mediated signaling	BP	1	ERBB3,RGL2,PTK2,NTRK2,TEK,KIT,ROR2,SEMA4D,CAT,EGFR,SOX9,FBXL2,GAB2,SIRT2,PLCB1,PLCL2,DCN,FLT1,PIK3CB,PITPNM2,PREX2,PIK3R1,PLCE1,RASGRP1,PLCH1,NKX3-1,F2RL1,F2R,IRS1,TGFB2,NCF1,EGF,HCLS1,GPER1,AGT,FGR,CBL,OSM,CD28,PIK3IP1,FN1,NYAP1,PTPN6,PLCD4,PI4KA,PEAR1,OGT,HAX1,PIK3R5,INSR,CCL5,CSF1R,ADAP2,PIP5K1C,DAB2IP,MIR21,ENTPD5,STAMBP,C3orf58,HCST,PDGFD	grey	VSMC_M10
GO:0043297	0.98	0.04	21	52	apical junction assembly	BP	1	SRF,CLDN19,FBF1,WNT11,IKBKB,NPHP1,MARVELD2,CLDN34,SNAI1,DLG1,FZD5,GPBAR1,RAMP2,VCL,CLDN7,MARVELD3,MICALL2,RHOA,CLDN15,CLDN1,APC	grey	VSMC_M10
GO:0001885	0.98	0.04	21	53	endothelial cell development	BP	1	ZDHHC21,S1PR3,HOXA13,MET,MYD88,IKBKB,PLCB1,MARVELD2,ARHGEF26,RAPGEF2,STC1,RAPGEF3,F2RL1,CLIC4,RAP1B,PLOD3,VCL,FOXP3,VEZF1,TNMD,CLDN1	grey	VSMC_M10
GO:0032943	0.98	0.03	83	179	mononuclear cell proliferation	BP	1	AGER,IL5,HLA-DPB1,TNFRSF13C,RAC2,CCND3,TNFRSF21,NCK2,PELI1,IL4I1,TLR4,IL15,BMI1,MYD88,FOXJ1,TGFBR2,PURA,PAWR,PLCL2,PRNP,NCKAP1L,SLC7A1,TRAF6,GAPT,IL1A,CASP3,MEF2C,TMEM131L,IL7,RASGRP1,LMBR1L,RIPK2,MARCH7,ZNF335,CD40,IGF2,ICOSLG,BTN2A2,GPAM,PRKAR1A,CD28,DLG1,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,SLC11A1,WNT4,PPP3CB,CD38,BST1,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,DOCK2,ZBTB7B,CHRNB2,CD19,BTK,CD74,CCL5,CD320,TWSG1,IL7R,TICAM1,DNAJA3,VAV3,GLMN,MIR21,LST1,FADD,CD46,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0031145	0.98	0.06	6	18	anaphase-promoting complex-dependent catabolic process	BP	1	ANAPC5,ANAPC7,ANAPC4,FZR1,FBXO31,CDC26	grey	VSMC_M10
GO:0140058	0.98	0.05	10	28	neuron projection arborization	BP	1	SULT4A1,PTN,SEMA3A,DVL3,DLG4,DVL2,TAOK2,MYO9A,NTNG2,WNT5A	grey	VSMC_M10
GO:1903649	0.98	0.05	10	28	regulation of cytoplasmic transport	BP	1	RAB21,PRKN,MTMR2,DNAJC13,SORL1,MAPK1,SNX12,TRIM46,MAPK3,MAP2K1	grey	VSMC_M10
GO:0043065	0.98	0.03	200	410	positive regulation of apoptotic process	BP	1	MTCH2,TNFAIP8,MAP3K5,TRIM39,STK3,IGF2R,TSPO,BAK1,ATF4,TOMM22,IRF5,CDKN2A,NCK2,TFAP2B,GADD45G,ZNF268,DNAJA1,TFPT,GSDME,HOXA13,EPHA7,PTN,KLF11,ING3,SFRP4,DKKL1,FOXO3,CDK19,FAF1,SPHK2,SPRY1,ERCC3,PDIA3,DEDD2,GRIK5,POU4F1,FBH1,WNT11,ARRB1,SIRT2,RARB,IDO1,PAWR,PRNP,DUSP6,ARHGEF7,BTG1,RNF122,RYBP,ARL6IP5,PRKDC,RET,NSMAF,ZC3H8,NR4A1,PIK3CB,FOXL2,CASP3,HIP1R,HPGD,DIABLO,FBXW7,MEF2C,HTRA2,TCTN3,C3orf38,RAPGEF2,PNMA2,RIPK2,VDR,NKX3-1,ACVR1C,NQO2,RIPK1,ANO6,PRDM11,TP53INP1,PIDD1,PLA2R1,IFIT2,STK4,TFAP2A,SUDS3,CD40,SIAH1,BMPR1B,GPLD1,FAP,CALHM2,NEURL1,DNM1L,SIK1,HDAC1,ALDH1A3,LCK,STK17B,MAP2K6,PDCD4,TGFB2,RBM5,GPER1,QRICH1,CHEK2,ADAMTSL4,MCL1,AGT,IP6K2,SLC9A1,NFATC4,PEA15,HDAC4,NTSR1,STPG1,BACE1,ING5,FZD9,PDCD1,RPL11,MAP3K11,ADAM8,CREB1,CCAR1,FIS1,PRKRA,BCL6,CTSH,ITGA4,IL12A,DDX3X,SAV1,CXCR2,HTT,ING4,RBM10,LTBR,ADCY10,KCNMA1,MAGED1,TNFRSF1B,TNFRSF8,ALDH1A2,MFN2,MAP3K9,PSEN1,PNMA1,ITGAM,NGFR,DAPK2,S100A8,SFPQ,DNM2,DCUN1D3,CAMK2A,CCL5,CCL2,CDK5R1,PTPN2,JUN,PIAS4,BCAP31,TRPV1,PLEKHN1,TRAF2,PARK7,LCN2,PIP5KL1,DHODH,NQO1,BCL10,DAB2IP,MIR29A,MIR21,MIR23A,MIR125B1,MIR27B,MIR24-1,RHOA,UBB,ZNF622,MLLT11,SOX4,FADD,BNIP3L,CASP8,MIR125A,CD248,WNT5A,TIGAR,GADD45A,DUSP1,DDIT3,BCL2L11,RGCC,APC,PLAGL2,PRR7,CRADD,PITX3,SAP18,OLFM1	grey	VSMC_M10
GO:0030521	0.98	0.05	14	37	androgen receptor signaling pathway	BP	1	KDM4C,FOXH1,DNAJA1,PHB,RNF14,FOXP1,NKX3-1,HDAC1,ARID1A,PIAS2,NCOR1,PARK7,RHOA,TRIM68	grey	VSMC_M10
GO:0060443	0.98	0.05	14	37	mammary gland morphogenesis	BP	1	ESR1,PTCH1,SOSTDC1,AREG,GLI2,TGFBR2,VDR,ELF3,WNT4,MED1,NTN1,TBX2,CSF1R,WNT5A	grey	VSMC_M10
GO:0045132	0.98	0.04	31	73	meiotic chromosome segregation	BP	1	UBE2B,MAPK15,DMC1,CCDC155,MLH1,CCNB1IP1,SIRT7,TEX15,MOS,M1AP,SYCP1,CCDC36,SPO11,HORMAD2,TEX12,MAJIN,ZCWPW1,STAG3,P3H4,SEPT1,EME1,SYCE2,RAD51C,ERCC4,SLX4,MEIOB,MSH4,RNF212B,AGO4,SYCE1L,CENPX	grey	VSMC_M10
GO:0019896	0.98	0.07	5	16	axonal transport of mitochondrion	BP	1	AGTPBP1,MGARP,OPA1,MAPT,HAP1	grey	VSMC_M10
GO:0007595	0.98	0.05	14	37	lactation	BP	1	NME1,PPAT,USF2,VDR,NEURL1,SLC6A3,CCND1,CREB1,SERPINC1,STAT5B,MED1,ZBTB7B,UPRT,DHODH	grey	VSMC_M10
GO:0002446	0.98	0.06	8	23	neutrophil mediated immunity	BP	1	MYD88,F2RL1,ITGAM,SCNN1B,STXBP2,PRAM1,DNASE1,CXCL6	grey	VSMC_M10
GO:0019081	0.98	0.07	5	16	viral translation	BP	1	EIF3L,PCBP2,EIF2AK4,EIF2D,MCTS1	grey	VSMC_M10
GO:0007568	0.98	0.03	119	252	aging	BP	1	LRP1,MAP3K5,CANX,SLC12A2,AGER,TSPO,BAK1,MAPK14,CDKN2A,SRF,NUAK1,CDK6,CAT,MSH2,PNPT1,ZNF277,DDC,IL15,FOXO3,DLD,TPRA1,DNMT3A,NAPEPLD,ERCC1,ERCC2,TGFBR2,PAWR,PRNP,DCN,KL,WRN,SIRT3,PRKDC,PLK2,IDE,GSS,ATR,ING2,ARNTL,HTRA2,P2RY1,MME,RPN2,MAPKAPK5,OPA1,AMFR,RAD54B,LOXL2,PRELP,KCNE2,PLA2R1,MORC3,PAX2,NFKB2,GLRX2,SLC6A3,PPP3CA,TERT,MAP2K6,CISD2,PDCD4,SLC30A10,DAG1,KRAS,POLG,CHEK2,AGT,MAP3K3,SCAP,CDKN1B,APOD,NFE2L2,CREB1,PTH1R,BCL6,BCL2A1,CTSV,STAT3,MAPK1,ENO3,BMPR1A,CLN8,PRDM2,TNFRSF1B,PSEN1,FOXO4,CTC1,FOS,YPEL3,MAPK3,VASH1,MAP2K1,MPO,RNF165,TBX2,SIN3A,LITAF,SREBF1,LONP1,JUN,MBD1,ABAT,DNAJA3,FZR1,ASS1,NQO1,TERF2,MIR21,MIR22,MT-ATP6,PRMT6,FOXG1,BGLAP,CLDN1,GRB2,YBX1,HRAS,MAP2K7,PITX3	grey	VSMC_M10

GO:1902905	0.98	0.03	82	179	positive regulation of supramolecular fiber organization	BP	1	ARPC3,HSPA1B,MTSS1,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,SLAIN2,NCK2,KIAA1211,PRKCE,LPAR1,PLEK,ITGB1BP1,MET,ARHGEF5,CDK5RAP2,EPHA1,MYLK3,MAPRE1,WASF1,SLAIN1,WNT11,FCHSD2,NAV3,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,CLIP1,FMN1,KATNB1,PTK2B,RAPGEF3,F2RL1,IQGAP2,CYFIP1,MAGEL2,PXN,CARMIL1,LMOD1,TRPV4,AP1AR,WASF2,WHAMM,EFEMP2,CDKN1B,DLG1,CDC42EP2,MAPT,TOGARAM1,NCKAP1,NIN,WNT4,ARPC1A,WAS,PFN3,PSEN1,SMAD3,EVL,CDK5R1,SERPINF2,MLST8,MECP2,SPIRE2,PSRC1,TSC1,WDR63,CARMIL2,FHOD1,RHOA,VASP,GMFG,GRB2,RGCC,PDXP,DRG1	grey	VSMC_M10
GO:0032869	0.98	0.03	73	161	cellular response to insulin stimulus	BP	1	AP3S1,MARS,PIP4K2C,PNPLA3,GKAP1,CCND3,GPT,PPAT,PHIP,GRB10,GAB1,LPIN1,SESN3,PIP4K2A,RAB10,ECHDC3,TBC1D4,AKT2,SNX5,KL,PTPRA,PRKDC,TRIB3,FER,IDE,PIK3R1,SORBS1,OPA1,LPIN3,CYFIP1,IGF2,GPLD1,SRD5A1,IRS1,GRB14,SORL1,C2CD5,AGT,SLC9A1,SYAP1,USF1,YWHAG,EIF4EBP2,SIK2,ESRRA,SLC27A1,RAB8A,PARP1,SLC2A4,RAB15,FOXO4,PKLR,RAB8B,NDEL1,ZBTB7B,OGT,PRKCB,INSR,SREBF1,LPIN2,GHR,PTPN2,SOCS1,INPP5K,PDPK1,PRKCZ,SLC25A33,INSRR,BGLAP,GRB2,INSIG2,APC,SH2B2	grey	VSMC_M10
GO:0006596	0.98	0.07	4	13	polyamine biosynthetic process	BP	1	AZIN2,SMS,OAZ1,NNMT	grey	VSMC_M10
GO:0035914	0.98	0.04	19	48	skeletal muscle cell differentiation	BP	1	LEMD2,HIVEP3,AKIRIN1,KLF5,KLHL40,NR1D2,EPHB1,NR4A1,SMYD1,NLN,SAP30,ARNTL,MEF2C,RBM24,ZNF689,FOS,SOX8,SIX1,UQCC2	grey	VSMC_M10
GO:0046822	0.98	0.03	41	94	regulation of nucleocytoplasmic transport	BP	1	CPSF6,MAPK14,SMO,RAB23,XPO1,DNAJC27,IWS1,SIRT7,FERMT1,MAVS,GAS6,NUP58,PIK3R1,PKIA,NUP54,RAPGEF3,MX2,SUFU,CABP1,SP100,TCF7L2,HCLS1,BAG3,SFN,UHMK1,NCBP2,APOD,SETD2,CTDSPL2,MAPK1,AKAP8L,TARDBP,PSEN1,SMAD3,NRDE2,EFCAB7,SUPT6H,PARK7,NUP214,TXN,ZIC1	grey	VSMC_M10
GO:0070507	0.98	0.03	60	135	regulation of microtubule cytoskeleton organization	BP	1	VPS4B,TRIM36,ATAT1,HSPA1B,MAPK15,MPDZ,SLAIN2,BICD2,CHMP2A,MET,CDK5RAP2,MAPRE1,EML2,SLC39A12,CLASP2,MAPRE3,TRIM54,SLAIN1,NAV3,ARHGEF7,SPEF1,RASSF7,ATXN7,FAM107A,CEP70,CHMP2B,CLIP1,CHMP4C,KATNB1,STMND1,TRPV4,TTBK2,CIB1,TRAF3IP1,PHLDB1,INPP5J,CDKN1B,MAPT,TOGARAM1,DIXDC1,NIN,RNF4,MARK2,CAMSAP3,CDK5R1,TAOK1,FSD1,PKD1,MECP2,APC2,CAMSAP1,CHMP1A,PSRC1,GPSM2,RHOA,CCSAP,APC,MAP1A,DRG1,MAP6D1	grey	VSMC_M10
GO:0030203	0.98	0.03	40	93	glycosaminoglycan metabolic process	BP	1	B4GALT7,PIM1,CEMIP2,HAS1,IL15,HS3ST5,NDNF,GLB1,CHPF2,CSGALNACT1,DCN,B3GNT4,ST3GAL6,GALNT5,CHST1,GCNT2,HYAL1,HYAL3,EGF,ABCC5,CEMIP,CHST3,SPOCK2,CHST7,AC022400.6,HS3ST1,CHST12,IDUA,CLN6,GLCE,HEXA,HS6ST2,IDS,B3GALT6,CHST5,ST3GAL2,HAS3,HS3ST2,CHSY3,HS2ST1	grey	VSMC_M10
GO:0090100	0.98	0.03	36	85	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SNW1,GDF9,ZC3H3,KCP,BMP8A,SDCBP,ACVR2B,UBE2O,ACVR2A,FERMT1,RBPMS,ACVR1B,ING2,ZNF423,FBXL15,KIAA0319,SLC2A10,TGFB2,MEN1,FKBP8,GDF15,INHA,BMPR1A,PARP1,RBPJ,RNF111,TGFB1I1,CITED1,SH2B1,RNF165,TWSG1,GPC3,CREBBP,ENG,MIR21,ACVRL1	grey	VSMC_M10
GO:0046632	0.98	0.04	31	74	alpha-beta T cell differentiation	BP	1	HLA-DRA,RSAD2,TGFBR2,EOMES,NCKAP1L,FOXP1,TOX,RIPK2,AP3B1,HLX,RUNX3,BCL6,RC3H1,TNFSF18,STAT3,FOXP3,TBX21,SEMA4A,BATF,ZBTB7B,IL6R,IL4R,BCL11B,NKAP,PTGER4,SOCS1,PRKCZ,MIR21,RHOA,PRR7,RC3H2	grey	VSMC_M10
GO:0071695	0.98	0.03	74	163	anatomical structure maturation	BP	1	BRD1,CATSPER3,WASHC5,L3MBTL3,ANKS1A,AKR1B1,TUT7,DMC1,PICK1,SOX10,RFX3,SEMA4D,EPAS1,ANKRD17,PTBP3,IL15,NRCAM,TUT4,FOXO3,DLD,ERCC2,BFSP1,SIRT2,RYR1,FERMT1,RAC3,RET,LGI4,CEBPA,TRPC4AP,PTK2B,RND1,OPA1,NKX6-1,NR4A2,PAX2,KCNIP2,ROPN1L,TGFB2,DAG1,ABHD2,YTHDF2,ACTN3,FARP2,CATSPER2,FZD5,PTH1R,C1QL1,FGFR3,GLDN,BHLHA15,RBPJ,ALDH1A2,THBS3,BTK,SLFN14,CDK5R1,C3,CATSPERD,RFLNB,MECP2,SOX8,WDR77,RHOA,SRRM4,CNTN2,ACVRL1,SNX10,WNT5A,CEND1,DDIT3,CCDC154,FAM210B,EREG	grey	VSMC_M10
GO:0007179	0.98	0.03	70	156	transforming growth factor beta receptor signaling pathway	BP	1	ONECUT2,USP15,SNW1,PPARA,GDF9,SMAD5,PTK2,TAB1,FOXH1,TGFBRAP1,CD109,SDCBP,SPRY1,SPRY2,EID2,TGFBR2,FERMT1,SPRED3,SNX25,LPXN,DKK3,ING2,HPGD,IL17RD,VEPH1,GCNT2,ITGB6,PXN,SLC2A10,TGFB2,ITGB5,HTRA1,SNX6,CREB1,PBLD,MEN1,HTRA3,FBN1,COL3A1,GDF15,STAT3,PPM1A,BMPR1A,PARP1,MPP5,RNF111,TGFB1I1,ITGA3,FOS,CITED1,WFIKKN2,SMAD3,DNM2,NLK,TWSG1,JUN,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,MIR21,LEMD3,ACVRL1,NRROS,DUSP22,LDLRAD4,PEG10	grey	VSMC_M10
GO:0051443	0.98	0.05	8	23	positive regulation of ubiquitin-protein transferase activity	BP	1	SKP1,BMI1,TRIB3,FBXW7,PINK1,DCUN1D3,FZR1,UBE2N	grey	VSMC_M10
GO:0007127	0.98	0.03	41	94	meiosis I	BP	1	MOV10L1,UBE2B,DMC1,KLHDC3,FOXJ3,CCDC155,MLH1,CCNB1IP1,SIRT7,TEX15,ING2,M1AP,RAD54B,SYCP1,HSF2BP,CCDC36,SPO11,C11orf80,TEX12,MAJIN,ZCWPW1,STAG3,P3H4,RAD51B,EME1,SYCE2,RAD51C,RAD51D,ERCC4,SLX4,MEIOB,MSH4,UBB,SYCP3,RNF212B,AGO4,FOXJ2,ZSCAN21,SYCE1L,BCL2L11,CENPX	grey	VSMC_M10
GO:0032204	0.98	0.04	31	74	regulation of telomere maintenance	BP	1	PPP1R10,MAP3K4,MYC,MAPK15,POT1,ERCC1,XRCC1,ATR,HMBOX1,MAPKAPK5,NBN,TENT4B,STN1,RTEL1,XRCC5,UPF1,MAPK1,PARP1,GNL3L,SMG5,YLPM1,CTC1,PIF1,MAPK3,PARN,ERCC4,SLX4,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0015908	0.98	0.04	25	60	fatty acid transport	BP	1	CPT1B,SLC27A6,PPARA,PLA2G6,PLIN2,CROT,AKT2,SLC5A8,PLA2R1,CPT1A,MAP2K6,ACSL5,FABP4,SLC25A20,NTSR1,PLA2G4A,FIS1,SLC27A1,ABCD4,NMUR2,PROCA1,ABCD3,FABP5,PLA2G2C,PTGES	grey	VSMC_M10

GO:0045597	0.98	0.02	315	639	positive regulation of cell differentiation	BP	1	TCF4,LRP1,CYP27B1,MAML1,RAB21,STK3,SNW1,TIAM2,HSPA1B,BRD1,AGER,HLA-DRA,IL5,TSPO,XRCC6,TRIB1,SMAD5,PTCH1,PLXNA4,MAPK14,NTRK2,CSNK1E,KDM4C,SOX10,PIM1,SMO,HSF1,ZNF16,SRF,TTBK1,RFX3,KIT,ROR2,SEMA4D,BEND6,ZNF268,SMAP1,RUFY3,MTURN,AKIRIN1,PTN,IL4I1,EGFR,TRIM32,IL15,SFRP4,MYLK3,DKKL1,SDCBP,NRCAM,TRPM4,FOXO3,APOB,MAMSTR,PLXNA1,HDAC2,NAPEPLD,SOX9,PTCH2,GOLGA4,GLI2,MEGF8,AAMDC,KDM4A,UNC13D,XRCC2,ACVR2B,KLF5,FOXJ1,NUMBL,POU4F1,IL15RA,SS18L2,RIN2,TGFBR2,OVOL2,ZNF219,ACVR2A,JAG1,SIRT2,PLCB1,RAC3,ALX1,ARHGEF7,BTG1,PLXNC1,CLIC1,NRG1,NCKAP1L,GAS6,LMOD3,PRKDC,ADRA2B,TRAF6,TCF15,SOX12,PLAG1,RET,TOX,DNMT3B,PAX8,ACVR1B,CEBPA,SMYD1,ANKRD27,FAIM,ROBO1,ROBO2,ARNTL,FZD3,MEF2C,IL7,VEGFC,CUX2,SOX6,RASGRP1,MME,RAPGEF2,TIAM1,RIPK2,DOCK5,SYNJ1,VDR,OPA1,NKX6-1,CDS1,LOXL2,TBX5,AP3B1,ZFYVE27,TESC,RIPK1,SPINT1,RREB1,ITPKA,SOX13,STK4,GCNT2,HIF1AN,PAX2,CYFIP1,DMTN,ADAMTS20,ZNF335,RBM24,BMPR1B,RAB7B,BDNF,NEURL1,CDON,DNM1L,CARMIL1,HDAC1,CAPRIN2,TERT,SLC9B2,TGFB2,TCF7L2,DAG1,AXIN2,HLX,CMKLR1,ACIN1,SNAI1,HCLS1,ADNP,SOX2,DISC1,GPER1,CASS4,AGT,CIB1,ARNT,KDF1,SFN,RPS6KA1,ACTN3,SS18L1,SYAP1,CDKL5,THPO,RUNX3,DLX1,DOCK1,ZBTB46,CSPG5,EFEMP2,SH3GL3,PPP2R3C,ADAM8,WNT3,HOXD3,POR,CREB1,DUSP10,MAPT,BLOC1S6,BCL6,H2AFY2,BRINP2,FN1,VSIR,XRCC5,SAV1,NIN,ADRA2C,WNT4,SUCO,RAMP2,STAT3,CYB5D2,STAT5B,OBSL1,TFE3,HAP1,FOXP3,EPHA4,ZBTB1,BMPR1A,PARP1,SPEN,P	grey	VSMC_M10
GO:0071383	0.98	0.03	74	163	cellular response to steroid hormone stimulus	BP	1	FECH,ESR1,CNOT2,PPARA,RXRB,KDM4C,SOX10,FOXH1,RBFOX2,CRY1,DNAJA1,AQP1,EGFR,MGARP,FOXO3,PGRMC2,BMI1,PHB,ATP1A3,EGLN2,TADA3,TAF7,RNF14,DDRGK1,FOXP1,CALCOCO1,NCOA4,FAM107A,CYP7B1,DNMT3B,UFSP2,ZNF366,ARNTL,CNOT1,KMT2D,DDX54,STC1,NKX3-1,CRY2,VPS18,ABCC2,ADTRP,SRD5A1,HDAC1,ABHD2,GPER1,ATP1A2,ARID1A,NPAS4,RXRG,ESRRA,PADI2,DNAAF4,PARP1,MED1,PAGR1,ESRRB,PIAS2,SCNN1B,NCOR1,NPC1,PPARGC1B,ISL1,RHOXF1,PARK7,RXRA,ASS1,RHOA,TRIM68,SMYD3,CRH,BCL2L11,YWHAH,ZFP36L2	grey	VSMC_M10
GO:0022612	0.98	0.03	41	95	gland morphogenesis	BP	1	GLI1,TNFAIP3,ESR1,FRS2,PTCH1,SOSTDC1,HOXA13,AREG,TGFA,PTN,TNC,PLXNA1,SOX9,GLI2,TGFBR2,SEMA3A,PLAG1,CYP7B1,FBXW7,VDR,NKX3-1,ELF3,TGFB2,SULF2,DAG1,RPS6KA1,LAMA5,WNT4,MED1,NTN1,BTBD7,TBX2,CSF1R,LAMA1,TWSG1,ESRP2,SERPINB5,NOG,WNT5A,CEBPB,FGF1	grey	VSMC_M10
GO:0031960	0.98	0.03	52	117	response to corticosteroid	BP	1	FECH,TPH2,AREG,AQP1,EGFR,FOXO3,BMI1,GLB1,AANAT,HNMT,FAM107A,DNMT3B,CASP3,STC1,ABCC2,CPN1,SRD5A1,CCND1,KRAS,GPER1,NPAS4,CPS1,ACSBG1,BCHE,RPL27,ALPL,CTSV,SCGB1A1,PARP1,FOS,SOX30,CALM1,SCNN1B,PPARGC1B,ISL1,GHR,ABCA3,CYBA,ASS1,AGL,ENG,HSD11B2,RHOA,BGLAP,SMYD3,CLDN1,DUSP1,CRH,BCL2L11,ZFP36L2,GPR83,PDCD7	grey	VSMC_M10
GO:0006139	0.98	0.02	2235	4274	nucleobase-containing compound metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,POLI,HSD17B4,RNMT,SHMT2,EYA4,TBPL1,GLI1,MARS,PDE7B,CLK4,MAP3K5,RPA3,TNFAIP3,TSFM,HIVEP2,ADAT2,ATP23,PLAGL1,MAML1,MRNIP,ENPP3,ATP5MGL,HELB,RPP21,PPP1R10,ZBTB2,CPSF6,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,CNOT6,RIDA,STK3,OSR2,PABPC1,SNW1,TFB1M,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,MAP3K4,PPT2,PRKN,QKI,AGER,TRMU,PPARA,PDE10A,ACSL6,UTP23,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,MCM9,ASF1A,RRP7A,HSF2,TCF7,PHF1,SMPDL3A,UBE2B,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PRXL2C,HABP4,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,ZC3H3,ATF4,TUT7,MAPK15,RPAP2,CBX7,APOBEC3H,GTPBP1,MAPK14,UHRF2,CBY1,DMC1,PUF60,C9orf64,CSNK1E,PICK1,KDM4C,SOX10,PIM1,CMTR1,NRF1,TMPRSS6,EXOSC4,SMO,SNAPC3,BNC2,HSF1,OARD1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,RBM28,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,GNMT,POT1,KLHDC3,RORB,ZNF300,PRDM4,CRY1,GDA,DMTF1,CROT,SRF,SMU1,ZNF318,NFX1,NOL6,GNPDA2,XPO5,CDK14,FZD1,MTERF1,NFXL1,GALT,SLC35B2,NFKBIE,FANCG,SUPT3H,SMARCA2,ENPP4,RFX3,KIT,ADGRF1,UXS1,NCK2,FHL2,TSR1,TGFBRAP1,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,PPAT,REV1,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,RAB23,ZNF667,ZNF787,PHF3,	grey	VSMC_M10
GO:0018027	0.98	0.05	7	21	peptidyl-lysine dimethylation	BP	1	SETD7,SUV39H2,KMT2D,EEF1AKMT2,SETD2,SETD1A,SETD3	grey	VSMC_M10
GO:0006475	0.98	0.03	61	136	internal protein amino acid acetylation	BP	1	ATAT1,YEATS4,BRD1,SUPT3H,PHF14,KANSL3,ING3,ATG5,SPHK2,BMI1,IWS1,PAXIP1,TADA3,ARRB1,TAF7,EP400,TAF10,SDR16C5,TAF9,PHF20,KANSL2,LDB1,AUTS2,MRGBP,ING5,POR,MAPT,MBIP,TADA2B,NAA40,ING4,TADA1,FOXP3,MSL1,MED24,KAT7,MUC1,TAF1,MAPK3,OGT,NAP1L2,CRTC2,RPS6KA5,SIN3A,ISL1,GLYR1,CREBBP,NAA60,NAA10,HCFC1,MECP2,CHD5,PARK7,GTF3C4,CTCF,TAF12,CPA4,BEND3,SUPT7L,LIF,RPS6KA4	grey	VSMC_M10
GO:0002066	0.98	0.04	13	35	columnar/cuboidal epithelial cell development	BP	1	ROS1,SMO,CDK6,RFX3,KLF5,RARB,ARNTL,NKX6-1,SIDT2,NKX3-2,PDPK1,WNT5A,TIGAR	grey	VSMC_M10
GO:0048714	0.98	0.06	5	16	positive regulation of oligodendrocyte differentiation	BP	1	PTN,HDAC2,HDAC1,DAG1,TNFRSF1B	grey	VSMC_M10

GO:0030111	0.98	0.03	131	277	regulation of Wnt signaling pathway	BP	1	NFATC1,LRP1,RPS12,GLI1,TNFAIP3,STK3,FZD6,PRKN,UBE2B,RSPO3,RNF146,MAPK14,CBY1,CSNK1E,SOX10,DAAM2,MDFI,PTK7,CDK14,ROR2,DLX5,WNK2,SOSTDC1,PPP2R1A,RSPO1,GRB10,ATP6V1C2,EGFR,HECW1,FUZ,SFRP4,CCNY,DKKL1,TRPM4,FOXO3,SOX9,PPM1N,SCEL,TSKU,WNT11,RBMS3,CHD8,UBAC2,FERMT1,SPEF1,PFDN5,CTNND1,DKK3,TRABD2A,ARNTL,TMEM131L,LMBR1L,TIAM1,OTULIN,AMFR,SOX13,STK4,SALL1,PRICKLE1,NKD1,PRDM15,LGR6,LRRK1,HDAC1,CAPRIN2,TERT,TMEM9,SULF2,TCF7L2,DKK2,AXIN2,EGF,TTC21B,SOX2,DISC1,ZNRF3,KREMEN1,TMEM237,BICC1,NFATC4,FZD7,GID8,PTPRO,FZD9,SENP2,WNT3,CCNYL1,DIXDC1,DDX3X,TBL1XR1,PPM1A,OTUD5,IGFBP4,RBPJ,PSEN1,TMEM88,ITGA3,CSNK1G1,CITED1,SOX30,SMAD3,MKS1,AC004687.2,CCDC88C,GSC,G3BP1,NLE1,ISL1,NLK,IFT20,GPC3,TLE6,TAX1BP3,ATP6V0C,SKI,APC2,FOXL1,DAB2IP,MIR199A1,MIR222,TRABD2B,SOX4,NOG,WNT5A,LBX2,DDIT3,DACT3,SDHAF2,SHISA2,APC,NKX2-5	grey	VSMC_M10
GO:0046324	0.98	0.04	17	44	regulation of glucose import	BP	1	MAPK14,SLC25A27,GRB10,FGF21,PRKAG2,AKT2,ASPSCR1,PIK3R1,SORBS1,IRS1,TERT,PEA15,NFE2L2,CLTCL1,INSR,GPC3,ARPP19	grey	VSMC_M10
GO:0034629	0.98	0.05	7	21	cellular protein-containing complex localization	BP	1	WASHC5,RALB,DLG1,SNAPIN,TNFAIP2,KLHL21,EXOC3L4	grey	VSMC_M10
GO:0032720	0.98	0.04	16	41	negative regulation of tumor necrosis factor production	BP	1	TNFAIP3,TSPO,C6orf106,TLR4,C5AR2,GAS6,NR1H4,IL37,NOD2,VSIR,PTPN6,FOXP3,AKAP8,SYT11,MIR125B1,HAVCR2	grey	VSMC_M10
GO:0090316	0.98	0.03	61	136	positive regulation of intracellular protein transport	BP	1	MAPK14,RAC2,SMO,TMEM30A,RUFY3,ITGB1BP1,TCAF2,PLK3,AKT2,USP36,CEP290,PRNP,MAVS,GAS6,TM9SF4,PIK3R1,FBXW7,HTRA2,ZFAND1,CSNK2A2,RAPGEF3,TCF7L2,KCNB1,HCLS1,HPS4,SORL1,C2CD5,ARIH2,CIB1,BAG3,SFN,CTDSPL2,FZD5,FIS1,CEMIP,NMT1,SEC16B,PDCD10,PINK1,MAPK1,CHRM1,TMEM30B,NPEPPS,TARDBP,PSEN1,ITGAM,SMAD3,BCAS3,MIEF2,CDK5R1,EFCAB7,BCAP31,OAZ1,SH3GLB1,RIPOR1,MICALL2,HRAS,MIEF1,RHOU,LEPROT,ZIC1	grey	VSMC_M10
GO:0003018	0.98	0.03	92	200	vascular process in circulatory system	BP	1	LRP1,SLC16A7,SLC12A2,AGER,PTP4A3,PLA2G6,ZDHHC21,TEK,ABCB1,SLC1A1,SLC4A4,SLC1A4,ITGB1BP1,EGFR,KEL,MYLK3,ATG5,TRPM4,SLC8A2,SLC24A3,ABCC4,MKKS,ADRA1D,SLC7A1,ADRA2B,HTR7,FGFBP3,PTPRJ,GUCY1A1,P2RY1,DOCK5,SLC38A2,F2RL1,F2R,SLC38A1,ABCC2,ABCG2,CHRM3,SLC2A13,RAP1GDS1,SLC2A10,SLC38A3,TRPV4,ADRA2A,SLCO3A1,GPER1,AGT,ABCC5,ACE2,ATP1A2,SLCO1C1,PER2,SLC29A2,SLC16A1,PLOD3,CPS1,ADRA2C,CXCR2,ECE1,GCH1,RAMP2,SMTNL2,CD38,SLC27A1,SLC38A5,KCNMA1,SLC4A3,SLC29A4,SLC2A4,SOD3,ATP1B2,HRH2,SLC7A3,ABCC3,SCPEP1,SCNN1B,INSR,ASIC2,YES1,LEPR,SERPINF2,P2RX1,SLC7A5,MIR21,MIR23A,RHOA,HTR1D,FGA,FABP5,SLC22A5,KCNJ8,KCNMB4	grey	VSMC_M10
GO:0038083	0.98	0.06	6	19	peptidyl-tyrosine autophosphorylation	BP	1	TEC,EGFR,AATK,PTK2B,BMX,MAPK3	grey	VSMC_M10
GO:0010922	0.98	0.05	9	26	positive regulation of phosphatase activity	BP	1	PLEK,VRK3,MTMR9,MEF2C,GPLD1,SMAD3,CALM1,PPARGC1B,PPP1R15A	grey	VSMC_M10
GO:0046634	0.98	0.04	26	63	regulation of alpha-beta T cell activation	BP	1	AGER,HLA-DRA,TGFBR2,NCKAP1L,RIPK2,AP3B1,HLX,CD28,RUNX3,BCL6,IL12A,VSIR,RC3H1,TNFSF18,FOXP3,RASAL3,TBX21,ZBTB7B,IL4R,NKAP,TWSG1,SOCS1,PRKCZ,MIR21,RHOA,RC3H2	grey	VSMC_M10
GO:0002092	0.98	0.05	7	21	positive regulation of receptor internalization	BP	1	PICK1,SFRP4,ARRB1,EGF,AP2M1,INSR,FMR1	grey	VSMC_M10
GO:0000725	0.98	0.03	56	126	recombinational repair	BP	1	RPA3,MRNIP,HELB,MCM9,DMC1,CCDC155,REV3L,XRCC1,XRCC2,WDR48,FBH1,MCM8,SHLD1,APS1,WRN,PPP4R2,TEX15,ERCC6,NBN,HELQ,SPIDR,RAD54B,POLL,FAN1,RECQL,RTEL1,SETD2,POLN,WAS,RHNO1,RAD52,PARP1,SHLD2,AP5Z1,RAD51B,EXD2,WRAP53,SWSAP1,NSMCE1,RAD51C,SFPQ,YY1,RAD51D,LIG3,SMCHD1,ERCC4,RMI2,SLX4,MEIOB,GINS2,RPA4,SWI5,OOEP,UBE2N,SFR1,NABP1	grey	VSMC_M10
GO:0009890	0.98	0.02	617	1222	negative regulation of biosynthetic process	BP	1	ORMDL2,SMARCC2,PAN2,ATP8B1,SHMT2,PGGT1B,CYP27B1,PLAGL1,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,ZBTB12,EIF3E,PNLDC1,PRKN,PPARA,TSPO,MRPL13,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PTCH1,TNRC6B,ATF4,TUT7,CBX7,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SCMH1,IGF2BP3,NFE2L3,PNPT1,HOXA2,HOXA7,JAZF1,XPO1,AKIRIN2,CASP8AP2,BACH2,ZNF692,PLEK,NR1H2,ZNF350,FOXP2,MED25,KLF11,AGO1,POU3F3,LANCL2,FAM3C,DKKL1,CREM,SDCBP,TUT4,OSR1,FOXO3,BEND5,DHFR,HDAC2,PHF10,DNMT3A,BMI1,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,EED,APOC1,SUV39H2,ZNF404,PLK3,MLH1,GLI2,DEDD2,RSF1,KDM4A,DACH1,TAF3,PIBF1,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,CYGB,SFMBT2,GZF1,POU4F1,FBH1,TNRC6C,WNT11,THAP1,EID2,OVOL2,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,HBEGF,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,EIF2AK2,LSM1,TAF7,NRG1,GAS6,RYBP,FOXP1,MITF,MTA3,ARID5A,IRF7,PAN3,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,CYP7A1,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,RAD17,NCOA2,DKK3,SAP30,ATR,ZNF366,ARNTL,FBXW7,GCFC2,HMBOX1,ENC1,MEF2C,PEX2,PKIA,TMBIM6,CNOT1,CELF1,SLA2,CUX2,MCPH1,SOX6,CNOT6L,FNIP2,RAPGEF2,BACH1,SFMBT1,EIF2AK4,NR1H3,EIF4E2,EAPP,SCAF4,LCOR,DDX54,RUNX1T1,PAIP2B,VDR,NKX3-1,BAHD1,HDAC7,NKX6-	grey	VSMC_M10

GO:1902904	0.98	0.03	62	139	negative regulation of supramolecular fiber organization	BP	1	AVIL,PRKN,PICK1,LMOD2,KIAA1211,TMOD1,PLEKHH2,SPTBN1,SHANK1,MET,ADD2,MAPRE1,EML2,CLASP2,TRIM54,MKKS,NAV3,ARHGEF7,SPEF1,LMOD3,ATXN7,PFDN5,PIK3R1,HIP1R,LIMA1,KATNB1,DMTN,CARMIL1,PPFIA1,LMOD1,ADD3,TTBK2,SSH1,ARHGAP6,HSPA8,CIB1,WASF2,SPTBN2,TMOD4,EPS8,INPP5J,CAPZA1,WAS,TMOD2,SPTB,PFDN4,CORO2B,LDLR,CAMSAP3,TAOK1,SSH2,INPP5K,APC2,VBP1,CAMSAP1,WDR63,CARMIL2,MIR21,GMFG,APC,PFN4,MAP6D1	grey	VSMC_M10
GO:0000724	0.98	0.03	55	124	double-strand break repair via homologous recombination	BP	1	RPA3,MRNIP,HELB,MCM9,DMC1,CCDC155,REV3L,XRCC1,XRCC2,WDR48,FBH1,MCM8,SHLD1,AP5S1,WRN,PPP4R2,TEX15,ERCC6,NBN,HELQ,SPIDR,RAD54B,POLL,FAN1,RECQL,RTEL1,SETD2,POLN,WAS,RAD52,PARP1,SHLD2,AP5Z1,RAD51B,EXD2,WRAP53,SWSAP1,NSMCE1,RAD51C,SFPQ,YY1,RAD51D,LIG3,SMCHD1,ERCC4,RMI2,SLX4,MEIOB,GINS2,RPA4,SWI5,OOEP,UBE2N,SFR1,NABP1	grey	VSMC_M10
GO:0072010	0.98	0.06	6	19	glomerular epithelium development	BP	1	PODXL,FOXJ1,JAG1,ASXL1,PTPRO,BASP1	grey	VSMC_M10
GO:0021700	0.98	0.03	94	204	developmental maturation	BP	1	BRD1,CATSPER3,WASHC5,L3MBTL3,ANKS1A,AKR1B1,TUT7,DMC1,PICK1,SOX10,RFX3,SEMA4D,EPAS1,SHANK1,ANKRD17,PTBP3,YWHAZ,IL15,NRCAM,TUT4,FOXO3,DLD,ERCC2,BFSP1,SIRT2,RYR1,FERMT1,RAC3,RET,LGI4,CEBPA,ANKRD27,TRPC4AP,PTK2B,RND1,OPA1,NKX6-1,NR4A2,PAX2,KCNIP2,ROPN1L,NEURL1,TGFB2,DAG1,ABHD2,YTHDF2,DISC1,NFATC4,ACTN3,FARP2,CATSPER2,FZD5,PTH1R,BLOC1S6,C1QL1,RAB3A,FGFR3,PTPRN,GLDN,BHLHA15,DLG4,RBPJ,ALDH1A2,THBS3,ZDHHC15,SNAPIN,BTK,SLFN14,CDK5R1,C3,CATSPERD,SEZ6,RFLNB,MECP2,BAIAP3,SOX8,PALM,WDR77,STXBP1,AP1G1,DAB2IP,RHOA,SRRM4,BLOC1S3,CNTN2,ACVRL1,SNX10,WNT5A,CEND1,DDIT3,CCDC154,RAB32,FAM210B,EREG	grey	VSMC_M10
GO:0043604	0.98	0.02	337	672	amide biosynthetic process	BP	1	ORMDL2,PAN2,RPS12,SHMT2,HBS1L,MARS,B4GALNT1,TSFM,RMND1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,EIF3E,PNLDC1,PPT2,QKI,ACSL6,MRPL13,RPS18,MRPL55,JMJD4,AGO2,HABP4,RPS10,TNRC6B,ATF4,TUT7,GTPBP1,PLA2G6,EIF3L,GTPBP2,SLC1A1,NCK2,MRPS9,SPTLC1,GAPDH,CNOT11,AASDH,EXOSC3,RPS14,LRPPRC,PPCS,SRBD1,CHAC2,IGF2BP3,MTIF2,PNPT1,PPT1,AGO1,EGFR,ASCC3,MGST2,QRSL1,C6orf203,TUT4,SLC7A11,FOXO3,SMPD2,DLD,PUM2,AGK,NANP,SPHK2,DHFR,EEFSEC,MKNK1,CNBP,EIF2B3,RPS8,MLH1,CDC123,MTRF1,DPH2,AANAT,RPSA,RPL14,MRPL33,TNRC6C,ELOVL1,AKT2,METTL17,SPTLC3,MRPS12,PURA,DPH3,HARS,HARS2,SLC25A15,EIF2AK2,CARS2,LSM1,MRPL3,AIMP1,PDK1,RPL31,LARS,EIF4E3,SIRT3,UPF3A,PRKDC,MRPL17,KBTBD8,PAN3,PDHX,MRPL15,ELOVL7,ASAH1,CEBPA,C12orf65,MRPL35,ST8SIA4,GSS,RPL6,PCSK1,MRPS27,MRPL19,ENC1,MRPS28,CNOT1,CELF1,USP16,PTK2B,CNOT6L,MAPKAPK5,EIF2AK4,EIF4E2,NSUN3,PAIP2B,ORMDL1,FTO,CYFIP1,NOD2,TENT4B,RBM24,WARS2,MRPS17,PM20D1,CDKAL1,EIF2D,GATC,ASL,NEURL1,RPUSD4,YARS2,RPL23,DDX25,RPL4,RPS17,BANK1,LTO1,CAPRIN2,IGHMBP2,BDH2,RPL27A,ACSL5,MRPS35,DIS3L2,MRPL52,ST8SIA2,SGMS2,RCC1L,KLHL25,GIGYF2,MRPS11,RPS6KB2,YTHDF2,B3GALT1,TRNAU1AP,MRPS21,CERS6,TARS2,DALRD3,HACD2,RPS27,CERS2,RPS6KA1,PER2,DDX6,RPS4X,MTG2,YTHDF1,PASK,CD28,UHMK1,NCBP2,EIF4ENIF1,NSUN5,RPL11,IGF2BP2,YBX3,PDK3,NFE2L2,EFL1,GGT2,CPS1,LARS2,EIF4EBP2,RPL10L,ACSBG1,DDX3X,RC3H1,DARS2,UPF1,RPL27,UBA52,MRPS36,COA3,SAMD4A,SMPD4,PINK1,STAT3,GGT6,MPC2,MAPK1,POLR2G,SGMS1,N	grey	VSMC_M10
GO:0006909	0.98	0.03	74	163	phagocytosis	BP	1	LRP1,CDC42SE2,PTK2,PLA2G6,RAC2,MYH9,PRKCE,FPR2,MET,TLR4,IL15,ATG5,ARHGAP12,RAB7A,CD300LF,UNC13D,MYD88,MYO7A,IL15RA,RAB5A,CNN2,NCKAP1L,GAS6,FAM19A4,TUB,HCK,TM9SF4,XKR6,PTPRJ,NR1H3,DYSF,RHOBTB2,F2RL1,ANO6,TXNDC5,NOD2,RAB7B,ELMO2,RAB11FIP2,FGR,PLPP4,RUBCN,FCER1G,RHOBTB1,DOCK1,NCF2,SPG11,PIKFYVE,SLC11A1,SYT7,PEAR1,SPON2,ITGAM,SYT11,DOCK2,AC138894.1,LDLR,DNM2,ICAM5,COLEC12,CCL2,YES1,PLD4,VAV1,LEPR,C3,PIP5K1C,ABCA7,CYBA,VAV3,HAVCR1,RAB39A,MESD,XKR8	grey	VSMC_M10
GO:0042987	0.98	0.04	21	52	amyloid precursor protein catabolic process	BP	1	AGER,NTRK2,RTN4,PRNP,CASP3,SLC2A13,SORL1,BACE1,RTN1,HAP1,EPHA4,PSEN2,PSEN1,TMED10,EFNA1,AC138894.1,ABCA7,MIR29A,MIR24-1,MIR339,APH1B	grey	VSMC_M10
GO:0010001	0.98	0.03	79	173	glial cell differentiation	BP	1	ERBB3,LRP1,ADGRG6,AGER,NTRK2,PICK1,SOX10,SMO,DAAM2,TTBK1,ADAM22,CDK6,TNFRSF21,ROR2,FPR2,PTN,EGFR,TLR4,MYCN,HDAC2,C5AR1,SOX9,HDAC11,ERCC2,EIF2B3,KDM4A,PRX,AKT2,SIRT2,NRG1,LGI4,SOX6,FGF5,NKX6-1,SPINT1,SOX13,PAX2,TSPAN2,HDAC1,GAP43,DAG1,KRAS,TTC21B,SOX2,DLX1,CSPG5,NSUN5,DUSP10,MAPT,CNTNAP1,STAT3,MAPK1,EPHA4,MPP5,TNFRSF1B,PRPF19,PSEN1,MAPK3,MAP2K1,LDLR,S100A8,MBD1,DAB1,MXRA8,SKI,SOX8,GPR157,LAMC3,RHOA,CNTN2,SOX4,CNTF,GPR37L1,METTL14,NOG,POU3F2,NRROS,PHGDH,LIF	grey	VSMC_M10
GO:0060491	0.98	0.03	72	159	regulation of cell projection assembly	BP	1	ATP8B1,AVIL,TBC1D30,MAPK15,PODXL,CDC42EP1,RAC2,SRF,KIT,DYNC2LI1,EPS8L1,AKIRIN1,FUZ,ATG5,KLF5,RAB5A,DPYSL3,FER,PIK3R1,PLCE1,P2RX7,BIN3,F2RL1,ARHGAP24,CYFIP1,DMTN,SRGAP2C,NEURL1,ZMYND10,GAP43,AUTS2,WASF2,RAB17,HDAC4,EPS8,CDKL5,LIMK2,CDC42EP2,NCKAP1,HTT,DNM3,RAP1GAP,WAS,SDCCAG8,HAP1,MNS1,MIEN1,PLEK2,FXR2,CNTROB,NDEL1,TENM2,AC138894.1,CCDC151,DNM2,BCAS3,ARHGAP44,EVL,IFT20,FMR1,WRAP73,PALM,EPS8L3,DEF8,CDK10,FNBP1L,ODF2L,CARMIL2,EPS8L2,APC,RALA,HRAS	grey	VSMC_M10

GO:0090049	0.98	0.04	16	41	regulation of cell migration involved in sprouting angiogenesis	BP	1	MEOX2,ITGB1BP1,PLK2,FBXW7,HDAC7,CIB1,MAP3K3,PDCD10,RHOJ,MAP2K5,MIR199A1,MIR23A,MIR22,MIR27B,MIR27A,RHOA	grey	VSMC_M10
GO:0042752	0.98	0.03	38	89	regulation of circadian rhythm	BP	1	PHLPP1,PPARA,CSNK1E,FBXL6,RORB,CRY1,SUV39H2,PPP1CB,BHLHE40,NR1D2,PRKDC,SPSB4,ARNTL,FBXW7,NR1H3,CRY2,MAGEL2,SIK1,ARNTL2,USP2,PER2,CREB1,NONO,CRTC1,MAGED1,DDB1,TARDBP,FBXL22,CIPC,CHRNB2,SFPQ,SIN3A,PER3,ZFHX3,FBXL8,FBXL12,CRH,PASD1	grey	VSMC_M10
GO:0014741	0.98	0.05	10	28	negative regulation of muscle hypertrophy	BP	1	PPARA,PI16,JARID2,TNFRSF1B,SMAD3,YY1,MIR199A1,MIR21,MIR25,RGS4	grey	VSMC_M10
GO:0002237	0.98	0.03	111	236	response to molecule of bacterial origin	BP	1	TNFAIP3,CYP27B1,TSPO,TRIB1,MAPK14,HSF1,IRF5,ADH5,PRKCE,CXCL8,AKIRIN2,PELI1,TLR4,MGST2,APOB,CDK19,HDAC2,C5AR1,PTGIR,MYD88,PRDX3,TIMP4,IRAK2,THBD,NFKBIB,SIRT2,DCN,FOXP1,TRAF6,HCK,IL1A,IL37,NR4A1,FER,CASP3,HPGD,PLSCR4,MEF2C,NUGGC,NR1H3,RIPK2,F2R,ABCC2,NOD2,CD40,NFKB2,MAPKAPK3,CD96,HDAC1,PDCD4,MAPKAPK2,IL10RA,FZD5,DUSP10,GGT2,CPS1,IL12A,COMT,UPF1,SLC11A1,TNIP2,ALPL,GCH1,MAPK1,SGMS1,OTUD5,SCGB1A1,FOXP3,LIAS,AKAP8,TNFRSF1B,SPON2,FOS,MAPK3,CITED1,MPO,S100A14,S100A8,BDKRB1,TNIP1,CCL5,CCL2,LITAF,PTGER4,NOS2,JUN,TICAM1,ADAMTS13,ASS1,LCN2,GFI1,BCL10,DAB2IP,PTGFR,MIR21,RHOA,DEFB124,CXCL6,CASP8,GNG12,IRGM,CMPK2,IL36G,CLDN1,WNT5A,INAVA,GGT5,PTGES,KCNJ8,CEBPB,HAVCR2	grey	VSMC_M10
GO:0071826	0.98	0.03	79	170	ribonucleoprotein complex subunit organization	BP	1	CPSF6,SF3A3,EIF3E,RRP7A,AGO2,PUF60,EIF3L,C12orf45,RPS14,PRPF31,YTHDC1,SRSF10,MDN1,AGO1,CLNS1A,CELF2,RPSA,CRNKL1,PRKDC,TGS1,USP39,TAF9,CLP1,RPL6,ATR,GCFC2,AAR2,CELF1,ZFAND1,SRSF6,SCAF11,EIF2D,RBM5,SART3,DYRK3,MRPS11,ZRSR2,RPS27,CELF3,DHX30,RPL11,GEMIN2,SNRPD3,PRPF39,RPL10L,XRCC5,DHX8,PRPF19,KHDC4,EIF3C,LUC7L3,SLU7,COIL,ZNHIT3,KLC1,NLE1,XAB2,MCTS1,SNU13,RPL23A,ERAL1,CELF5,LUC7L,ZNHIT6,PRMT7,RNVU1-6,RNU5E-1,RNU5B-1,AGO4,RPS27L,NOL3,RNU4ATAC,RF00003,SNRPC,RNU2-1,RNU4-2,SRSF12,RNU4-1,PIH1D2	grey	VSMC_M10
GO:0051781	0.98	0.03	26	63	positive regulation of cell division	BP	1	ZNF16,CAT,MACC1,PRKCE,TGFA,PTN,ITGB1BP1,SIRT2,KIF3B,IL1A,CSPP1,VEGFC,FGF5,NKX3-1,IGF2,TGFB2,OSM,PGF,GAREM1,CDC14A,RHOA,AURKC,YBX1,EREG,FGF1,PDGFD	grey	VSMC_M10
GO:0032868	0.98	0.03	95	206	response to insulin	BP	1	AP3S1,MARS,PIP4K2C,PPARA,PNPLA3,GKAP1,CCND3,GPT,CRY1,PPAT,CAT,PHIP,GRB10,GAB1,LPIN1,SESN3,PIP4K2A,RAB10,HADHA,KHK,EPM2AIP1,ECHDC3,TBC1D4,AANAT,AKT2,SNX5,KL,PTPRA,PRKDC,TRIB3,FER,IDE,PIK3R1,SORBS1,OPA1,LPIN3,ACVR1C,SRSF6,CRY2,CYFIP1,IGF2,GPLD1,SRD5A1,IRS1,GRB14,TRPV4,SRSF4,SORL1,C2CD5,AGT,SLC9A1,SYAP1,USF1,SCAP,YWHAG,VGF,EIF4EBP2,SIK2,ESRRA,PTPRN,SLC27A1,RAB8A,PARP1,SLC2A4,RAB15,MAX,VPS13C,FOXO4,PKLR,RAB8B,NDEL1,ZBTB7B,OGT,CITED1,UPRT,PRKCB,INSR,SREBF1,LPIN2,GHR,PTPN2,SOCS1,INPP5K,PDPK1,PRKCZ,SLC25A33,TSC1,TLDC1,HSD11B2,INSRR,BGLAP,GRB2,INSIG2,APC,SH2B2	grey	VSMC_M10
GO:0034698	0.98	0.05	6	19	response to gonadotropin	BP	1	PAX8,SRD5A1,POR,CTSV,ITGA3,GATA6	grey	VSMC_M10
GO:0006354	0.98	0.03	34	80	DNA-templated transcription, elongation	BP	1	TSFM,ARID1B,SOX10,ERCC2,ERCC3,GTF2F2,POU4F1,ZMYND11,POLR2I,ERCC6,ELP4,SMARCD1,EAPP,RTF1,LDB1,ARID1A,RNF168,SETD2,WDR61,ENY2,ELL,NELFA,LEO1,PADI2,CDK12,KAT7,ELP2,TEFM,SUPT6H,RF00100,SERTAD2,HTATSF1,RNF8,GTF2H5	grey	VSMC_M10
GO:0031639	0.98	0.05	6	18	plasminogen activation	BP	1	PLGRKT,PLAT,MELTF,F12,SERPINF2,FGA	grey	VSMC_M10
GO:0042982	0.98	0.03	27	65	amyloid precursor protein metabolic process	BP	1	AGER,AGO2,NTRK2,RTN4,PAWR,PRNP,CASP3,SLC2A13,SORL1,BACE1,DLG1,SOAT1,RTN1,NSG1,HAP1,EPHA4,PSEN2,PSEN1,TMED10,EFNA1,AC138894.1,ABCA7,MIR29A,MIR24-1,MIR339,LDLRAP1,APH1B	grey	VSMC_M10
GO:0032508	0.98	0.03	31	75	DNA duplex unwinding	BP	1	HELB,MCM9,XRCC6,POT1,ASCC3,SSBP1,ERCC2,ERCC3,GTF2F2,FBH1,CHD8,PURA,MCM8,WRN,DQX1,NBN,HELQ,RAD54B,WRNIP1,TWNK,RAD54L2,IGHMBP2,RECQL,RTEL1,SUPV3L1,DDX3X,XRCC5,DDX11,PIF1,G3BP1,CHD5	grey	VSMC_M10
GO:0032007	0.98	0.04	12	33	negative regulation of TOR signaling	BP	1	EPM2A,KPTN,SESN3,SZT2,TMEM127,ARNTL,MAPKAPK5,PDCD6,SH3BP4,TNFAIP8L1,TSC1,RNF152	grey	VSMC_M10
GO:0032272	0.98	0.03	27	66	negative regulation of protein polymerization	BP	1	AVIL,LMOD2,KIAA1211,TMOD1,SPTBN1,ADD2,MAPRE1,EML2,MKKS,ARHGEF7,LMOD3,HIP1R,DMTN,CARMIL1,LMOD1,ADD3,SSH1,SPTBN2,TMOD4,EPS8,INPP5J,CAPZA1,TMOD2,SPTB,SSH2,CARMIL2,PFN4	grey	VSMC_M10
GO:0090092	0.98	0.03	88	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ONECUT2,LRP1,SNW1,PPARA,GDF9,LEMD2,ZC3H3,KCP,TFAP2B,SOSTDC1,CD109,HOXA13,BMP8A,BMPER,SFRP4,SDCBP,SPRY1,ACVR2B,UBE2O,SPRY2,EID2,ACVR2A,FERMT1,SPRED3,SPART,RBPMS,ACVR1B,SNX25,DKK3,ING2,IL17RD,VEPH1,ZNF423,FBXL15,KIAA0319,SLC2A10,TGFB2,SORL1,HTRA1,CHRD,DLX1,SNX6,CTDSPL2,PBLD,MEN1,HTRA3,FBN1,FKBP8,GDF15,PPM1A,GREM2,INHA,BMPR1A,PARP1,MPP5,RBPJ,RNF111,TGFB1I1,ITGA3,RBPMS2,CILP,TOB1,CITED1,SH2B1,WFIKKN2,SMAD3,RNF165,DNM2,CHRDL1,TWSG1,GPC3,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,MIR21,FSTL3,LEMD3,ACVRL1,NOG,WNT5A,NRROS,LDLRAD4,UBE2D1,PEG10	grey	VSMC_M10
GO:0009791	0.98	0.03	28	68	post-embryonic development	BP	1	IGF2R,BAK1,AGO2,APOB,ERCC1,ERCC2,MYO7A,CSRNP1,SZT2,NR4A2,MORC3,SLC4A10,ALDH5A1,GIGYF2,FZD5,FBN1,STK36,RAB3A,MFAP2,PSEN1,BCL11B,LHX1,MECP2,ACADM,BCL2L11,PLAGL2,TAL2,RC3H2	grey	VSMC_M10
GO:0000132	0.98	0.05	9	26	establishment of mitotic spindle orientation	BP	1	CDK5RAP2,SPRY1,SPRY2,NSFL1C,MCPH1,HTT,NDEL1,SAPCD2,GPSM2	grey	VSMC_M10

GO:0009408	0.98	0.03	36	84	response to heat	BP	1	HSPA1B,HSF1,PDCL3,DNAJA1,HDAC2,EIF2B3,ASIC3,STAC,CLPB,TCIM,IL1A,ATR,P2RX3,HTRA2,TP53INP1,ABCC2,TRPV4,PDCD6,MAPKAPK2,BAG3,CASQ1,MAPT,DNAJB1,TGFB1I1,PKLR,SLU7,TRPV2,DNAJA3,CREBBP,TRPV3,TRPV1,MT-CYB,HIKESHI,HSBP1L1,MAP2K7,FGF1	grey	VSMC_M10
GO:0044839	0.98	0.03	59	132	cell cycle G2/M phase transition	BP	1	VPS4B,MRNIP,TRIM39,TAF2,FBXL6,ABCB1,CDK14,BRSK1,CCNY,PLK3,PAXIP1,PPME1,NEK10,PLCB1,MTA3,RAD17,PKIA,CHMP4C,BACH1,NBN,USH1C,ABRAXAS1,DONSON,ZFYVE19,TAOK3,FBXL15,CCND1,DYRK3,CHEK2,SYF2,STOX1,DBF4B,AKAP8L,AKAP8,RAD51B,UIMC1,FOXO4,FBXL22,CTC1,TAOK2,ESRRB,RAB11A,KDM8,LCMT1,FOXN3,CALM1,RAD51C,DNM2,SIN3A,TAOK1,FZR1,MECP2,VPS4A,FBXL8,NAE1,FBXL12,BRCC3,ARPP19,NABP1	grey	VSMC_M10
GO:0060485	0.98	0.02	109	235	mesenchyme development	BP	1	SEMA6A,MYC,EXOC4,SOX10,SMO,BNC2,FOXH1,PTK7,SEMA4D,SEMA4C,SIX2,RTN4,AKNA,FUZ,TEAD2,SDCBP,OSR1,SPRY1,HDAC2,SOX9,CLASP2,SPRY2,WNT11,TGFBR2,OVOL2,EOMES,JAG1,SPRED3,ALX1,SEMA3D,SEMA3A,NRG1,KBTBD8,TCF15,RET,HAND2,ROBO1,ROBO2,IL17RD,FAM208A,MEF2C,SEMA4F,ACTG2,TIAM1,LOXL2,TBX5,SEMA3G,PKD2,GCNT2,PAX2,SEMA4G,RBM24,KLHL12,USF3,SEMA3F,PDCD4,TGFB2,POGLUT1,PEF1,TCF7L2,PDCD6,DAG1,AXIN2,SNAI1,AMELX,GBX2,ACTC1,PHLDB1,LAMA5,SEMA6D,FN1,MEOX1,WNT4,MAPK1,BMPR1A,RADIL,RBPJ,ALDH1A2,SEMA4A,TGFB1I1,EFNA1,MAPK3,TMEM100,SMAD3,GSC,TBX2,TCOF1,ISL1,RANBP3L,RFLNB,SOX8,FOXF1,ENG,DAB2IP,MIR21,MIR222,ACVRL1,POFUT2,NOG,WNT5A,BASP1,SIX1,DACT3,SDHAF2,RGCC,LDLRAD4,HEY2,OLFM1,WNT2	grey	VSMC_M10
GO:0045861	0.98	0.03	100	213	negative regulation of proteolysis	BP	1	SERPINB8,SERPINB2,TNFAIP8,LRP1,TRIM39,PI16,IL1R2,GAPDH,PDCL3,CD109,ACP4,AQP1,NR1H2,BCL2L12,SDCBP,CST7,AQP11,RAF1,PRDX3,TIMP4,UBE2O,PLAT,KLHL40,SPINT2,PRNP,DDRGK1,GAS6,RYBP,PSMF1,GPI,NR4A1,IDE,TAF9,USP25,CSNK2A2,FAM192A,NR1H3,SERPINB1,SPINT1,MARCH7,PAX2,APLP2,SUFU,SIRT4,TM4SF20,RPL23,USP19,SORL1,IFI6,AGT,COL6A3,SFN,COL7A1,RPS6KA1,CST6,RPL11,LRIG2,POR,DDX3X,SPOCK2,SERPINC1,SERPINI1,BIRC3,ARL6IP1,EPHA4,ANXA8,CLN8,ANXA2,SIMC1,PSEN1,PAPLN,SNX12,TMED10,EFNA1,TAF1,OGT,AC138894.1,WFIKKN2,MAP2K5,NLE1,C3,GPC3,SERPINF2,SGTA,WFIKKN1,PARK7,LAMTOR5,MIR199A1,MIR24-1,NOL3,SERPINB5,A2M,MIR339,SERPINE3,CAMLG,SERPINB9,CAAP1,STYX,MAP1A,RARRES1	grey	VSMC_M10
GO:0097067	0.98	0.06	4	14	cellular response to thyroid hormone stimulus	BP	1	KIT,LMO2,CTSH,MED1	grey	VSMC_M10
GO:0043162	0.98	0.05	7	21	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	BP	1	VPS4B,RNF115,VPS37D,RNF126,MVB12B,VPS4A,UBAP1L	grey	VSMC_M10
GO:0014808	0.98	0.04	9	26	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	1	RYR1,CASQ2,RYR2,ANK2,ATP1A2,CASQ1,CALM1,DMD,NOL3	grey	VSMC_M10
GO:1903514	0.98	0.04	9	26	release of sequestered calcium ion into cytosol by endoplasmic reticulum	BP	1	RYR1,CASQ2,RYR2,ANK2,ATP1A2,CASQ1,CALM1,DMD,NOL3	grey	VSMC_M10
GO:0090050	0.98	0.05	8	23	positive regulation of cell migration involved in sprouting angiogenesis	BP	1	PLK2,HDAC7,CIB1,MAP3K3,RHOJ,MIR23A,MIR27B,MIR27A	grey	VSMC_M10
GO:0018209	0.98	0.02	125	267	peptidyl-serine modification	BP	1	BAK1,MAPK14,NTRK2,MAPK13,STK38,CSNK1E,TTBK1,SLC1A1,NCK2,IL11,BRSK1,PRKCE,VRK2,VRK3,EGFR,NTF4,BRAF,NDNF,MKNK1,PRKD2,RAF1,MGAT5B,SPRY2,AKT2,GPD1L,DYRK1B,TGFBR2,IKBKB,RPTOR,PLCL2,MAP4K1,BAG4,DCN,GAS6,ULK1,PRKDC,PLK2,RET,CAMK4,MAST4,HPF1,ATR,DCLK2,CSNK2A2,FNIP2,MAPKAPK5,PAQR3,RIPK2,TOP1,RAPGEF3,RIPK1,STK4,MORC3,DMTN,BDNF,MAPKAPK3,CAPRIN2,POGLUT1,CAMKV,PRKX,TTBK2,MARK1,MST1,DYRK3,MAPKAPK2,HCLS1,RPS6KB2,OPRD1,GRK2,CHEK2,TSSK4,GALNT2,RPS6KA1,OSM,INPP5J,MLXIPL,UHMK1,PDK3,PIKFYVE,STOX1,KDELC2,SPOCK2,PDCD10,MARK2,MAST3,PINK1,ARAF,MAPK1,STK32B,PARP1,NSD1,GALNT16,DGKQ,CSNK1G1,TAF1,MAPK3,HAX1,SBK1,RPS6KA5,PRKCB,GALNT1,CAMK2A,MAPK7,MARK3,CDK5R1,SH2D3A,NLK,DOCK7,INPP5K,PDPK1,PRKCZ,NAA10,PKD1,MTCP1,PARK7,MAPKAP1,AURKC,DMD,IRGM,SMYD3,WNT5A,GADD45A,TXN,LIF,RPS6KA4	grey	VSMC_M10
GO:0015748	0.98	0.03	44	102	organophosphate ester transport	BP	1	ATP9B,ATP8B1,ABCB1,SLC35B2,ABCG8,TMEM30A,APOC1,ABCC4,ANO4,PITPNM2,XKR6,PLSCR4,P2RX7,SLC33A1,ANO6,COL4A3BP,PLTP,SLC37A1,CALHM1,SLC37A2,PITPNM1,PITPNC1,ABCC5,SLC37A4,OSBPL2,ABCA12,SLC25A42,TMEM30B,PCTP,LDLR,LRRC8E,SLC25A23,SLC25A41,PRELID3A,ATP11C,PITPNA,ABCA3,ABCA7,SLC25A33,LRRC8A,SLC25A25,SLC25A32,CPTP,XKR8	grey	VSMC_M10
GO:0006414	0.98	0.03	20	50	translational elongation	BP	1	HBS1L,TSFM,GTPBP1,GTPBP2,ASCC3,C6orf203,EEFSEC,DPH2,DPH3,C12orf65,USP16,TRNAU1AP,EFL1,MRPL44,RPLP1,ALKBH1,DPH1,AARS,EEF1B2,DIO2	grey	VSMC_M10
GO:2000177	0.98	0.03	25	62	regulation of neural precursor cell proliferation	BP	1	GLI1,SOX10,SMO,PTN,FOXO3,GLI2,SIRT2,SPINT2,TOX,FZD3,VEGFC,SPINT1,ZNF335,ZNF423,EGF,DISC1,FZD9,LHX1,RHOA,ADGRG1,FOXG1,GPR37L1,WNT5A,CEND1,PITX3	grey	VSMC_M10
GO:1901654	0.98	0.03	68	151	response to ketone	BP	1	NME1,FECH,TSPO,AKR1B1,SOX10,HSF1,MTAP,CA9,PRKCE,AQP1,PTN,FOXP2,TNC,EGFR,FOXO3,SPHK2,ADCY3,BMI1,GLB1,AANAT,MAP4K1,GAS6,NCOA4,DNMT3B,GPI,NCOA2,KCNJ11,NR1H3,NKX3-1,OPA1,ABCC2,SPP1,ADCY2,SRD5A1,CCND1,TGFB2,ABHD2,CBL,NPAS4,CPS1,FDX1,RPL27,PTGER2,RAMP2,CD38,FOXP3,AKAP8,PARP1,FOS,CALM1,LARP1,SCNN1B,ACACA,SIN3A,SREBF1,PTGER4,GNB1,PARK7,CYBA,ASS1,NQO1,PTGFR,BGLAP,SMYD3,CLDN1,DUSP1,CRH,GNG2	grey	VSMC_M10

GO:0061351	0.98	0.03	48	111	neural precursor cell proliferation	BP	1	SLC39A5,GLI1,FRS2,FZD6,SOX10,SMO,ORC3,AKNA,PTN,POU3F3,FOXO3,C5AR1,RAB10,GLI2,NUMBL,HOOK3,SIRT2,RARB,SPINT2,RYK,EPHB1,TOX,FZD3,VEGFC,SPINT1,ZNF335,ZNF423,EGF,DISC1,GBX2,NDUFS2,FZD9,DIXDC1,KCNA1,DAGLB,LHX1,IFT20,DOCK7,RHOA,ADGRG1,FOXG1,GPR37L1,WNT5A,CEND1,POU3F2,ARTN,PITX3,WNT2	grey	VSMC_M10
GO:0061050	0.98	0.06	5	16	regulation of cell growth involved in cardiac muscle cell development	BP	1	PPARA,PI16,YY1,MIR199A1,RGS4	grey	VSMC_M10
GO:0034728	0.98	0.03	42	97	nucleosome organization	BP	1	SMARCC2,BRD2,ASF1A,UBN2,SOX9,RSF1,ACTR6,SMARCD1,SPTY2D1,NAP1L5,RBBP4,SART3,ARID1A,VPS72,SETD2,H2AFY2,HIRA,TSPYL2,NAP1L2,SUPT6H,NAA60,CHD5,CTCF,SYCP3,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,RNF8,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,TSPYL5	grey	VSMC_M10
GO:0051258	0.98	0.02	117	250	protein polymerization	BP	1	ARPC3,AVIL,ZNF207,HSPA1B,TUBGCP6,PRKN,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,TTBK1,SLAIN2,NCK2,KIAA1211,CHMP2A,TMOD1,PRKCE,SPTBN1,MET,ADD2,CDK5RAP2,FAM49A,MAPRE1,WASF1,MSRB2,EML2,SLC39A12,CLASP2,MAPRE3,SLAIN1,PLEKHG2,FCHSD2,MKKS,NAV3,BAG4,ARHGEF7,DIAPH1,FCHSD1,NCKAP1L,ARFIP2,LMOD3,TTC17,HCK,FAM107A,FER,HIP1R,CLIP1,FMN1,PTK2B,IQGAP2,TUBGCP5,CYFIP1,DMTN,CASQ2,MAGEL2,DNM1L,CARMIL1,LMOD1,ADD3,TRPV4,SSH1,HCLS1,ARHGAP6,AP1AR,TUBGCP4,WASF2,SPTBN2,CASQ1,TMOD4,EPS8,INPP5J,WHAMM,CDKN1B,DLG1,CAPZA1,CDC42EP2,MAPT,TOGARAM1,NCKAP1,NIN,TUBG1,PINK1,ARPC1A,WAS,TMOD2,SPTB,PFN3,WASHC3,NDEL1,HAX1,GAS7,EVL,PSTPIP1,MIEF2,CAMSAP3,CDK5R1,RNF135,CEP192,SSH2,CORO7,MLST8,MECP2,CAMSAP1,SPIRE2,PSRC1,WDR63,CARMIL2,MICALL2,RHOA,FGA,VASP,GMFG,GRB2,PFN4,COTL1,DRG1	grey	VSMC_M10
GO:0008625	0.98	0.03	28	67	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	TNFAIP3,STK3,CASP8AP2,FAF1,DEDD2,RAF1,FAIM,PIK3R1,DIABLO,FAIM2,MADD,PIDD1,STK4,BMPR1B,SP100,BAG3,PEA15,DEDD,DDX47,DDX3X,STX4,PARK7,DAB2IP,MIR222,FGA,FADD,CASP8,CRADD	grey	VSMC_M10
GO:1900273	0.98	0.05	6	19	positive regulation of long-term synaptic potentiation	BP	1	MME,EIF2AK4,IGSF11,STAU1,CREB1,CRTC1	grey	VSMC_M10
GO:0006914	0.98	0.02	218	450	autophagy	BP	1	VPS4B,ATG12,PIP4K2C,EPM2A,TMEM74,PRKN,RNF5,TSPO,AL096711.2,KLHL3,C6orf106,EXOC4,MAPK15,NRBP2,TFEB,FBXO7,DCAF12,TGFBRAP1,SPTLC1,GAPDH,CHMP2A,RAB23,STX17,ATP6V1E2,SNX14,NOD1,RRAGD,MET,ATP6V1C2,VPS41,VPS35,SCOC,ATG5,FOXO3,MFSD8,SESN3,RAB7A,PIP4K2A,RUBCNL,ATP6V0E2,FBXL2,PLK3,OPTN,RALB,ATP6V0B,KDM4A,MTMR14,SNX5,USP36,SIRT2,ATG16L2,RPTOR,TMEM173,RAB5A,FEZ2,DCN,DDRGK1,ULK1,ARFIP2,VPS16,NSFL1C,ATP6V1H,TRIB3,PLK2,DEPP1,DRAM1,SBF2,PIK3CB,C19orf12,CASP3,LIX1,CHMP2B,MTMR9,TBC1D12,FBXW7,HTRA2,TMBIM6,AUP1,CHMP4C,CSNK2A2,ATG10,RIPK2,TPCN1,WDR41,VPS18,TP53INP1,NOD2,TOLLIP,VPS39,LZTS1,ATP6V1B2,TEX264,NHLRC1,DNM1L,SEC22B,CISD2,EI24,TMEM39A,TCIRG1,VTI1A,ADPRH,DHRSX,GPR137B,USP30,USP13,YOD1,HSPA8,ATG16L1,SH3BP4,MCL1,BAG3,CISD1,TRAPPC4,MTMR3,UFC1,RUBCN,IL10RA,RAB1B,VPS37D,RNF185,SNX6,SNX32,FZD5,MAPT,PIKFYVE,TAB3,FIS1,VPS26A,ABL2,ATG2A,SEC16B,TBC1D14,GPR137,FUNDC1,HTT,ANXA7,RETREG3,MARK2,ATP6V0A1,PINK1,MUL1,ATG9A,SNAP29,STAT3,TBC1D25,PIM2,RAB8A,ATP13A2,HAP1,WIPI2,PHF23,ATP6V1D,VPS13D,MFN2,RRAGB,OSBPL7,VPS13C,ZFYVE1,PSEN1,SYT11,DAPK2,MAPK3,AC138894.1,HAX1,CALM1,SNAPIN,S100A8,LARP1,VMP1,ATG2B,BCAS3,KEAP1,TECPR2,NPC1,RMC1,SMCR8,CDK5R1,SREBF1,LAMP2,LEPR,IFT20,ATG4C,ERCC4,CLEC16A,TICAM1,MTM1,EMC6,ATP6V0C,IKBKG,FUNDC2,SEC16A,PARK7,GPSM1,GNAI3,KIAA1324,TSC1,FNBP1L,SH3GLB1,VPS4A,TMEM208,MIR199A1,PJVK,TRIM68,TRIM34,BNIP3L,TRIM65,IRGM,TIGAR,ACER2,DDIT3,DRAM2,CPTP,BCL2L	grey	VSMC_M10
GO:0061919	0.98	0.02	218	450	process utilizing autophagic mechanism	BP	1	VPS4B,ATG12,PIP4K2C,EPM2A,TMEM74,PRKN,RNF5,TSPO,AL096711.2,KLHL3,C6orf106,EXOC4,MAPK15,NRBP2,TFEB,FBXO7,DCAF12,TGFBRAP1,SPTLC1,GAPDH,CHMP2A,RAB23,STX17,ATP6V1E2,SNX14,NOD1,RRAGD,MET,ATP6V1C2,VPS41,VPS35,SCOC,ATG5,FOXO3,MFSD8,SESN3,RAB7A,PIP4K2A,RUBCNL,ATP6V0E2,FBXL2,PLK3,OPTN,RALB,ATP6V0B,KDM4A,MTMR14,SNX5,USP36,SIRT2,ATG16L2,RPTOR,TMEM173,RAB5A,FEZ2,DCN,DDRGK1,ULK1,ARFIP2,VPS16,NSFL1C,ATP6V1H,TRIB3,PLK2,DEPP1,DRAM1,SBF2,PIK3CB,C19orf12,CASP3,LIX1,CHMP2B,MTMR9,TBC1D12,FBXW7,HTRA2,TMBIM6,AUP1,CHMP4C,CSNK2A2,ATG10,RIPK2,TPCN1,WDR41,VPS18,TP53INP1,NOD2,TOLLIP,VPS39,LZTS1,ATP6V1B2,TEX264,NHLRC1,DNM1L,SEC22B,CISD2,EI24,TMEM39A,TCIRG1,VTI1A,ADPRH,DHRSX,GPR137B,USP30,USP13,YOD1,HSPA8,ATG16L1,SH3BP4,MCL1,BAG3,CISD1,TRAPPC4,MTMR3,UFC1,RUBCN,IL10RA,RAB1B,VPS37D,RNF185,SNX6,SNX32,FZD5,MAPT,PIKFYVE,TAB3,FIS1,VPS26A,ABL2,ATG2A,SEC16B,TBC1D14,GPR137,FUNDC1,HTT,ANXA7,RETREG3,MARK2,ATP6V0A1,PINK1,MUL1,ATG9A,SNAP29,STAT3,TBC1D25,PIM2,RAB8A,ATP13A2,HAP1,WIPI2,PHF23,ATP6V1D,VPS13D,MFN2,RRAGB,OSBPL7,VPS13C,ZFYVE1,PSEN1,SYT11,DAPK2,MAPK3,AC138894.1,HAX1,CALM1,SNAPIN,S100A8,LARP1,VMP1,ATG2B,BCAS3,KEAP1,TECPR2,NPC1,RMC1,SMCR8,CDK5R1,SREBF1,LAMP2,LEPR,IFT20,ATG4C,ERCC4,CLEC16A,TICAM1,MTM1,EMC6,ATP6V0C,IKBKG,FUNDC2,SEC16A,PARK7,GPSM1,GNAI3,KIAA1324,TSC1,FNBP1L,SH3GLB1,VPS4A,TMEM208,MIR199A1,PJVK,TRIM68,TRIM34,BNIP3L,TRIM65,IRGM,TIGAR,ACER2,DDIT3,DRAM2,CPTP,BCL2L	grey	VSMC_M10

GO:0055017	0.98	0.03	30	72	cardiac muscle tissue growth	BP	1	GLI1,PPARA,MAPK14,PI16,PIM1,TGFBR2,MEF2C,TBX5,JARID2,TGFB2,PRKAR1A,AGT,KCNK2,SAV1,MAPK1,BMPR1A,RBPJ,TBX2,YY1,GATA6,MIR199A1,MIR222,MIR23A,MIR24-1,MIR25,NOG,RGS4,C3orf58,HEY2,WNT2	grey	VSMC_M10
GO:0061099	0.98	0.04	9	26	negative regulation of protein tyrosine kinase activity	BP	1	IBTK,CBL,SNX6,ZFYVE28,SOCS4,PSEN1,PTPN2,THY1,DUSP22	grey	VSMC_M10
GO:2000060	0.98	0.03	41	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,ZYG11B,BBS7,PLK3,SUMO2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,TRIB3,PLK2,CEBPA,FBXW7,PTK2B,PRICKLE1,RNF144B,AC013489.1,EGF,DISC1,ARIH2,NFE2L2,COP1,SOCS4,DNAJB2,PSEN1,TAF1,KEAP1,PSMD10,FBXO22,FZR1,BCAP31,SGTA,ZER1,DDA1	grey	VSMC_M10
GO:0043543	0.98	0.02	93	202	protein acylation	BP	1	ATAT1,YEATS4,ZDHHC14,BRD1,ZDHHC21,SUPT3H,HINT2,PHF14,KANSL3,ING3,ATG5,DLD,SPHK2,HDAC2,BMI1,IWS1,PAXIP1,AANAT,TADA3,ARRB1,TAF7,EP400,TAF10,SDR16C5,ZDHHC20,TAF9,ARNTL,PHF20,KANSL2,RAPGEF3,GOLGA7B,ZDHHC13,CDYL,LDB1,HDAC1,ZDHHC23,ZDHHC6,AUTS2,HHAT,ZDHHC18,ZDHHC24,MRGBP,ING5,GLUL,POR,MAPT,MBIP,NMT1,ZDHHC8,DDX3X,TADA2B,NAA40,ING4,NAA30,PPM1A,TADA1,ZDHHC4,FOXP3,MSL1,MED24,KAT7,MUC1,TAF1,MAPK3,OGT,NAP1L2,ZDHHC15,CRTC2,RPS6KA5,SIN3A,ISL1,TAOK1,GLYR1,CREBBP,NAA60,NAA10,HCFC1,MECP2,CHD5,PARK7,GTF3C4,ZDHHC12,CTCF,ZDHHC1,TAF12,ZDHHC11,SOX4,CPA4,BEND3,SUPT7L,LIF,RPS6KA4,MAP6D1	grey	VSMC_M10
GO:0040001	0.98	0.04	11	31	establishment of mitotic spindle localization	BP	1	CDK5RAP2,SPRY1,CLASP2,SPRY2,NSFL1C,MCPH1,HTT,KPNB1,NDEL1,SAPCD2,GPSM2	grey	VSMC_M10
GO:0071353	0.98	0.04	9	26	cellular response to interleukin-4	BP	1	TCF7,NFIL3,CD300LF,PARP14,IL4R,KEAP1,PTPN2,ADAMTS13,HSPA5	grey	VSMC_M10
GO:0043254	0.98	0.02	173	361	regulation of protein-containing complex assembly	BP	1	ARPC3,AVIL,ATAT1,ESR1,HSPA1B,IL5,SEPT8,BAK1,WASHC5,ASAP1,H3F3C,MAPK15,BAIAP2L2,PICK1,CDC42EP1,HSF1,LMOD2,TTBK1,SLAIN2,NCK2,KIAA1211,TMOD1,PRKCE,SPTBN1,TRAPPC12,PLEK,NR1H2,MED25,MET,ADD2,TLR4,CDK5RAP2,FAM49A,MAPRE1,WASF1,FAF1,NAPA,SOX9,EML2,SLC39A12,LCP1,MAPRE3,DNAJC15,RALB,RAF1,MYD88,NAPB,SLAIN1,PLEKHG2,FCHSD2,MKKS,NAV3,FERMT1,EIF2AK2,BAG4,ARHGEF7,FCHSD1,NRG1,NCKAP1L,ULK1,ARFIP2,LMOD3,HCK,FER,ANKRD27,HIP1R,ATR,TRABD2A,CLIP1,SLF1,FMN1,ANKRA2,PTK2B,FNIP2,SPIDR,CDH17,IQGAP2,CYFIP1,SLF2,DMTN,MAGEL2,CARMIL1,LMOD1,ADD3,SSH1,AJUBA,HCLS1,AP1AR,HSPA8,OPRD1,SORL1,WASF2,SPTBN2,TRAF3IP1,TMOD4,STX1A,EPS8,INPP5J,FARP2,WHAMM,CDKN1B,DLG1,KIF9,CALY,CAPZA1,CREB1,AIDA,CDC42EP2,MAPT,RAP1B,TOGARAM1,PPP2R5B,DDX3X,NCKAP1,NIN,TNFSF18,RNF4,RAB3A,PINK1,MMP3,ARPC1A,WAS,TMOD2,PPM1A,PARP1,SPTB,FBLIM1,THRA,PFN3,GNL3L,STX1B,HAX1,LCMT1,EVL,RIOK3,CAMSAP3,CDK5R1,ISL1,PTGER4,TICAM1,SSH2,ABCA3,PRKCZ,MLST8,HCFC1,MECP2,TRAF2,PARK7,CAMSAP1,SPIRE2,PSRC1,PIEZO1,STXBP1,HSPA5,SH3GLB1,DAB2IP,WDR63,CARMIL2,RHOA,TRABD2B,VASP,GMFG,IRGM,IMPACT,CRBN,GRB2,CPTP,BCL2L11,PFN4,LDLRAD4,BBS10,COTL1,DRG1	grey	VSMC_M10
GO:0048568	0.98	0.02	162	341	embryonic organ development	BP	1	GLI1,FRS2,STK3,OSR2,FZD6,VPS52,CCDC134,RSPO3,PTCH1,ATF4,SMO,MDFI,TFEB,FOXH1,PTK7,SRF,KIT,ROR2,DLX5,SIX2,EPAS1,RAD23B,KCNQ4,HOXA2,HOXA4,HOXA6,HOXA7,CXCL8,WHRN,FUZ,GJB5,TEAD2,MYCN,SOBP,OSR1,BBS7,BMI1,MYO3A,SETDB2,SOX9,ERCC1,ERCC2,ERCC3,USH1G,GLI2,MEGF8,IFT172,WDR48,MYO7A,WDR60,SPRY2,WNT11,TGFBR2,OVOL2,EOMES,MKKS,RARB,SPINT2,ALX1,CEP290,PAX8,CEBPA,HAND2,EYA1,PLS1,FZD3,MEF2C,USH1C,IFT52,SPINT1,PKD2,STK4,TFAP2A,PAX2,SALL1,RYR2,IGF2,SUFU,HYAL1,ALDH1A3,TGFB2,SATB2,HLX,SNAI1,GBX2,ARNT,VASH2,MYO3B,SYF2,GRHL3,SP3,STRC,DLG1,SETD2,HOXD4,HOXD3,FZD5,STOX1,PRKRA,COL13A1,FBN1,NKX3-2,MAPK1,TULP3,MFAP2,DVL2,BMPR1A,WDR19,TCAP,RBPJ,MED1,ALDH1A2,SOX15,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,EFNA1,RBPMS2,MAPK3,VASH1,CITED1,MAP2K1,POU3F4,SMAD3,NTN1,MKS1,GSC,TBX4,TBX2,LHX1,STRA6,MIB1,PKD1,RNF207,ALX3,FOXF1,ENG,KRT19,CHRNA10,FOXG1,MAFB,CASP8,HOXB3,NOG,LBX1,WNT5A,OTX1,SIX1,C2CD3,GRB2,INSIG2,LIF,CEBPB,SLC39A3,NKX2-5,PIFO,HEY2,WNT2,HOXA3,ZIC1	grey	VSMC_M10
GO:0071402	0.98	0.04	9	26	cellular response to lipoprotein particle stimulus	BP	1	TLR4,FGF21,MYD88,ADTRP,FCER1G,MIA3,LDLR,NPC1,TICAM1	grey	VSMC_M10
GO:0030833	0.98	0.03	65	145	regulation of actin filament polymerization	BP	1	ARPC3,AVIL,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,NCK2,KIAA1211,TMOD1,PRKCE,SPTBN1,ADD2,FAM49A,WASF1,PLEKHG2,FCHSD2,MKKS,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,FMN1,PTK2B,IQGAP2,CYFIP1,DMTN,MAGEL2,CARMIL1,LMOD1,ADD3,SSH1,HCLS1,AP1AR,WASF2,SPTBN2,TMOD4,EPS8,WHAMM,DLG1,CAPZA1,CDC42EP2,NCKAP1,ARPC1A,WAS,TMOD2,SPTB,PFN3,HAX1,EVL,SSH2,MLST8,SPIRE2,WDR63,CARMIL2,RHOA,VASP,GMFG,GRB2,PFN4,COTL1	grey	VSMC_M10
GO:0051299	0.98	0.06	4	14	centrosome separation	BP	1	NSFL1C,KIF3B,CNTROB,NDEL1	grey	VSMC_M10
GO:0055007	0.98	0.03	41	96	cardiac muscle cell differentiation	BP	1	MAML1,FRS2,PPARA,CBY1,PI16,SRF,FHL2,BVES,MYLK3,ATG5,RARB,NRG1,MEF2C,SOX6,TBX5,SIK1,AGT,ACTC1,SLC9A1,FZD7,ALPK3,TTN,OBSL1,BMPR1A,TCAP,RBPJ,KDM6B,YY1,GATA6,ISL1,MYH11,IFT20,TSC1,ACADM,MIR199A1,MIR222,MIR23A,MIR24-1,RGS4,NKX2-5,HEY2	grey	VSMC_M10

GO:0032101	0.98	0.02	319	646	regulation of response to external stimulus	BP	1	CD226,SERPINB2,LRP1,SEMA6A,TNFAIP3,CYP27B1,USP15,ENPP3,ESR1,TSPAN8,SNW1,SLC12A2,AGER,PPARA,GPSM3,XRCC6,TRIB1,PTK2,C6orf106,PLXNA4,MAPK14,MAPK13,RAC2,TEK,TTBK1,CCL27,ENPP4,SEMA4D,NINJ1,SEMA4C,CLDN19,CAMKMT,CD109,FPR2,NT5E,ANKRD17,CXCL8,NOD1,AKIRIN2,AKIRIN1,NR1H2,AKNA,PTN,MET,EGFR,TLR4,IL15,VPS35,MGST2,PUM2,CDK19,TRAF3IP2,C5AR2,C5AR1,NAPEPLD,PRKD2,CST7,CLASP2,LACC1,NECTIN2,PVR,OPTN,MEGF8,MYD88,OXSR1,PTPRF,MYCBP2,FNDC4,THBD,SEC14L1,PLAT,TGFBR2,IKBKB,C1QTNF1,CHD8,SIRT2,MKKS,NMI,TMEM173,NR1D2,NPLOC4,SEMA3D,MAVS,SEMA3A,NCKAP1L,GAS6,HPX,FOXP1,PRKDC,IRF7,MFHAS1,RYK,TRAF6,PCBP2,NR1H4,TRIM44,PLK2,MTUS1,HCK,IL37,CEBPA,ERAP1,ROBO1,ROBO2,SEMA4F,VEGFC,CELF1,SETD6,MCPH1,PTK2B,RASGRP1,EIF2AK4,NR1H3,TRAFD1,TIAM1,OAS3,NLRC5,RIPK2,OTULIN,SLC8B1,F2RL1,F2R,RIPK1,ANO6,POLR3D,SEMA3G,SPP1,MAPKBP1,DMTN,SEMA4G,ADTRP,HERC5,NOD2,CD96,FAP,KIAA0319,CD200,OASL,DNM1L,CD200R1L,SLC6A3,TRPV4,SEMA3F,PDCD4,PRSS56,POLR3C,CMKLR1,NCF1,FABP4,SPATA2,YTHDF2,UBASH3B,GPER1,SLAMF8,MOSPD2,PARP9,DTX3L,PARP14,KREMEN1,RNF26,AGT,FGR,ACE2,NLRX1,CERS2,TRAF3IP1,OSM,HTRA1,SNX4,USF1,COCH,YTHDF1,PTPRO,CD28,BACE1,LRIG2,PPP2R3C,ADAM8,WNT3,CADM1,NFE2L2,DUSP10,NONO,IL16,NMT1,GGT2,BCL6,SEMA6D,IL12A,TNR,CASK,XRCC5,LPCAT3,PTPN6,SERPINC1,MCU,TNFSF18,CXCR2,WNT4,LAG3,GRK4,CALCRL,MYOZ1,CASP12,MUL1,MMP3,BIRC3,BST1,MAPK1,STAT5B,DAGLB,PADI2,SCGB1A1,FOXP3,EPHA4,RNF216,GPS2,TKFC,USP18,F12,TMEM102,TNFRSF1	grey	VSMC_M10
GO:1902893	0.98	0.03	18	47	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	PPARA,SRF,FOXO3,SOX9,KLF5,TERT,TGFB2,NFATC4,HDAC4,STAT3,BMPR1A,NGFR,FOS,SMAD3,YY1,MRTFB,JUN,NFATC3	grey	VSMC_M10
GO:0009166	0.98	0.03	25	61	nucleotide catabolic process	BP	1	PDE7B,DPYS,PDE10A,GDA,NT5E,NUDT15,MBD4,NUDT16,NUDT12,AMPD3,ENTPD4,FITM2,NUDT18,PDE9A,NUDT17,PDE8A,UPB1,PDE4A,NEIL1,NT5M,NTHL1,MLYCD,NUDT19,HINT1,UPP1	grey	VSMC_M10
GO:0007265	0.98	0.02	139	296	Ras protein signal transduction	BP	1	RAB21,CDC42SE2,RGL2,SYNGAP1,GPR20,GRAP2,CDC42EP1,RAC2,CDKN2A,LRRD1,EPS8L1,CTNNAL1,LPAR1,MET,HACE1,SDCBP,WASF1,SPRY1,IQSEC1,KBTBD6,RALB,RAF1,SPRY2,PSD3,ARRB1,RASGRP4,NRG1,PPP2CB,RASA3,PLK2,MRAS,PIK3CB,RASA2,FBXO8,ROBO1,PLCE1,ARHGEF28,RTKN,MADD,RASGRP1,RAPGEF2,MAPKAPK5,TIAM1,RAPGEF3,F2RL1,F2R,ARHGAP24,RREB1,CYFIP1,KSR2,DOK2,GBF1,PSD,TGFB2,ADRA2A,GNA13,AUTS2,RABL3,CFL1,KRAS,ARHGAP6,RAB42,CBL,WASF2,RAB4A,CNKSR1,EPS8,FARP2,CDC42EP2,RASA4,RAP1B,BCL6,ABL2,RASGRP2,RFXANK,NCKAP1,COL3A1,LZTR1,ARHGDIG,WAS,MYO9B,CYTH3,RHOJ,RASAL3,RAB15,IQSEC2,DOK3,MFN2,ARHGEF11,KPNB1,STARD8,RIT1,NGFR,ITGA3,KCTD13,OGT,HACD3,DENND4A,LAT,NTN1,DNM2,RIT2,G3BP1,ARHGAP44,KSR1,TNFAIP1,RALBP1,RAB33A,JUN,CRK,GNB1,TAX1BP3,ARHGAP4,PARK7,EPS8L3,GPSM2,RALGPS1,MAPKAP1,SCAI,DENND1A,DAB2IP,RIPOR1,RHOA,SETDB1,GPR35,ADGRG1,EPS8L2,STAMBP,ZNF304,GRB2,RALA,STK19,HRAS,CADM4,SH2B2,RHOU,RAP2B,RAB39A,ARPP19	grey	VSMC_M10
GO:1901361	0.98	0.02	191	395	organic cyclic compound catabolic process	BP	1	PAN2,ALDH8A1,PDE7B,CYP27B1,ENPP3,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,DPYS,SKIV2L,DXO,EIF3E,PNLDC1,PDE10A,SMPDL3A,CSDC2,AGO2,TNRC6B,TUT7,APOBEC3H,GTPBP1,MAPK14,EXOSC4,HSF1,GDA,GALT,ENPP4,CNOT11,EXOSC3,LRPPRC,PNPT1,NT5E,RNASEH1,IL4I1,AGO1,TUT4,PUM2,HSD17B14,TRAF3IP2,MTPAP,ZC3HAV1,DHX34,ENTPD6,CDADC1,NUDT15,FASTK,MLH1,NUDT5,MBD4,DEDD2,MYD88,HNMT,FBH1,TNRC6C,IDO2,IDO1,LRTOMT,AP000812.5,LSM1,NUDT16,PKP3,UPF3A,PAN3,CYP7A1,NUDT12,AHCY,AMPD3,FOXL2,ZCCHC8,TTC37,CNOT1,EPHX2,CELF1,CNOT6L,TENT2,ENTPD4,FITM2,FTO,ABCC2,SPP1,NUDT18,TENT5C,TENT4B,RBM24,SRD5A1,PDE9A,SLC6A3,DIS3L2,AXIN2,HGD,NUDT17,MAPKAPK2,GIGYF2,YTHDF2,HSD11B1,TRAF5,FASTKD1,ANGEL2,YTHDF1,MGAT1,PDE8A,NCBP2,EIF4ENIF1,SIDT2,YBX3,NFE2L2,RBM7,TET1,SUPV3L1,UPB1,FAH,MTHFS,COMT,RC3H1,DDX49,UPF1,SLC11A1,RBM10,SAMD4A,CYP27A1,ZSWIM8,POLR2G,SCGB1A1,NT5C3B,DCP1B,CASC3,MRPL44,TNFRSF1B,FXR2,TARDBP,SMG5,ALDH6A1,DNASE2,TOB1,RNASEH2A,GSTZ1,TENT5D,NRDE2,TNRC6A,CNOT8,LARP1,PDE4A,CYP46A1,NEIL1,SLFN14,ALKBH5,UPF3B,NT5M,PARN,DROSHA,FMR1,TREX2,PAM16,DNASE1,METTL16,PLEKHN1,LSM7,NTHL1,DFFB,CIRBP,TRAF2,DNASE1L1,CEL,MLYCD,KYAT1,KYAT3,EDC4,AGO4,ENTPD5,METTL14,NANOS1,DIO3,DNASE1L2,NUDT19,CACNG7,ALDH1L1,YBX1,YWHAH,ZFP36L2,TENT5A,PDXP,MAGOHB,HINT1,UPP1,DIO2,NMNAT1,RC3H2,EXOSC5	grey	VSMC_M10
GO:0046579	0.98	0.03	19	49	positive regulation of Ras protein signal transduction	BP	1	GPR20,LRRD1,LPAR1,ARRB1,RASGRP4,NRG1,PIK3CB,ROBO1,RASGRP1,F2RL1,F2R,AUTS2,KRAS,COL3A1,GPR35,ADGRG1,STK19,HRAS,ARPP19	grey	VSMC_M10
GO:0060688	0.98	0.03	16	42	regulation of morphogenesis of a branching structure	BP	1	ESR1,SMO,SIX2,RTN4,SOX9,PAX8,PAX2,AGT,MAGED1,BTBD7,LHX1,SOX8,NOG,WNT5A,SIX1,WNT2	grey	VSMC_M10
GO:0061982	0.98	0.03	43	99	meiosis I cell cycle process	BP	1	MOV10L1,UBE2B,MAPK15,DMC1,KLHDC3,FOXJ3,CCDC155,ERCC1,MLH1,CCNB1IP1,SIRT7,TEX15,ING2,M1AP,RAD54B,SYCP1,HSF2BP,CCDC36,SPO11,C11orf80,TEX12,MAJIN,ZCWPW1,STAG3,P3H4,RAD51B,EME1,SYCE2,RAD51C,RAD51D,ERCC4,SLX4,MEIOB,MSH4,UBB,SYCP3,RNF212B,AGO4,FOXJ2,ZSCAN21,SYCE1L,BCL2L11,CENPX	grey	VSMC_M10
GO:0051294	0.98	0.04	11	31	establishment of spindle orientation	BP	1	CDK5RAP2,SPRY1,LLGL2,SPRY2,NSFL1C,MOS,MCPH1,HTT,NDEL1,SAPCD2,GPSM2	grey	VSMC_M10

GO:0002285	0.98	0.02	56	127	lymphocyte activation involved in immune response	BP	1	HLA-DRA,MFNG,EXOSC3,MSH2,TLR4,HMCES,ERCC1,LCP1,MLH1,UNC13D,PAXIP1,EOMES,PLCL2,SHLD1,NCKAP1L,FOXP1,GAPT,PTK2B,EIF2AK4,RIPK2,NBN,CDH17,F2RL1,CD40,DOCK10,HLX,CD28,FCER1G,RNF168,BCL6,RC3H1,TNFSF18,SLC11A1,STAT3,FOXP3,SHLD2,TBX21,PSEN1,SEMA4A,BATF,ZBTB7B,IL6R,CD19,IL4R,CD74,PTGER4,SUPT6H,PRKCZ,TSC1,AP1G1,MIR21,CD46,FGL2,RNF8,HAVCR2,RC3H2	grey	VSMC_M10
GO:0048729	0.98	0.02	236	490	tissue morphogenesis	BP	1	ESR1,FRS2,STK3,FZD6,BRD2,VPS52,MTSS1,RSPO3,MYC,KLHL3,PTCH1,LY6E,EXOC4,PODXL,SOX10,SMO,FOXH1,PTK7,SRF,TXNRD1,CA9,ROR2,SEMA4C,SOSTDC1,SIX2,BRSK1,TNNI3,KLK14,HOXA13,AREG,EPHA7,MET,TNC,FUZ,TEAD2,MYCN,OSR1,INTU,SPRY1,PLXNA1,ARHGAP12,BBS7,RAB10,PRKD2,SETDB2,SOX9,CLASP2,GLI2,MEGF8,PCDH8,IFT172,GZF1,POU4F1,SPRY2,WNT11,TGFBR2,OVOL2,EOMES,JAG1,MKKS,ACTG1,HBEGF,FERMT1,SPINT2,FREM2,CEP290,SPEF1,SEMA3A,NRG1,FOXP1,SYNE4,RYK,TRAF6,TCF15,NPHP1,RET,CYP7B1,GPI,PAX8,CASP3,HAND2,EYA1,ROBO1,ROBO2,FMN1,FZD3,MEF2C,VEGFC,TLX2,FRAS1,ACTG2,TIAM1,VDR,STC1,NKX3-1,OPA1,TBX5,IFT52,ARHGAP24,SPINT1,TNNC1,RPGRIP1L,RREB1,DSP,PKD2,STK4,TFAP2A,PAX2,SALL1,VANGL1,PRICKLE1,NKD1,RYR2,SUFU,IRX2,PKP2,ALDH1A3,TNNI1,TGFB2,PRKAR1A,ADARB1,PRKX,DAG1,AJUBA,KRAS,SNAI1,EGF,MYH7,JHY,ZNRF3,AGT,GBX2,DVL3,ACTC1,KDF1,NFATC4,FZD7,TRAF3IP1,LAMA5,CLIC4,GRHL3,EFEMP2,DLG1,LUZP1,SETD2,WNT3,FZD5,STOX1,PLOD3,TTN,CTSH,PDCD10,CXCR2,WNT4,GORAB,EXOC5,VCL,TBX19,DAAM1,TULP3,EPHA4,ARHGEF19,LIAS,ACTB,MAGED1,DVL2,BMPR1A,MPP5,TCAP,RBPJ,MED1,ALDH1A2,PSEN1,KDM6B,TGFB1I1,NGFR,ITGA3,CITED1,TMEM100,SMAD3,NTN1,MKS1,BTBD7,MYO9A,TBX4,TBX2,LHX1,LAMA3,CSF1R,MIB1,CAMSAP3,JAG2,ISL1,LAMA1,IFT20,TWSG1,ADAMTS12,GPC3,SKI,PKD1,SAPCD2,RNF207,SOX8,CELSR2,COL5A1,TSC1,FOXL1,FOXF1,LCN2,ENG,GLMN,BCL10,ESRP2,CARMIL2,MIR21,RHOA,VASP,SERPINB5,SOX4,ACVRL1,POFUT2,NOG,LBX1,WNT5A,LBX2,SIX1,CELSR3,C2CD3,ARTN,GRB2,R	grey	VSMC_M10
GO:0070201	0.98	0.02	211	436	regulation of establishment of protein localization	BP	1	LRP1,SLC12A2,PRKN,GOPC,PTP4A3,MAPK14,PLA2G6,PICK1,RAC2,SMO,RFX3,SLC1A1,TFAP2B,RAB23,DNAJA1,PRKCE,TMEM30A,HMGN3,RUFY3,XPO1,BMP8A,RSAD2,NR1H2,ITGB1BP1,EGFR,ARHGEF5,TLR4,TCAF2,TRPM4,SLC7A11,DNAJC27,GIPR,LCP1,PLK3,FRMD4A,LLGL2,AKT2,USP36,UBAC2,APBB3,DPH3,SIRT7,FERMT1,CEP290,PRNP,BAG4,MAVS,GAS6,SIRT3,SYT9,NR1H4,LYPLA1,NUP58,TM9SF4,NDUFAF2,FAM3D,IL1A,OSBP,PIK3R1,ARNTL,FBXW7,PKIA,HTRA2,VEGFC,ZFAND1,CSNK2A2,NUP54,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,SPIDR,NKX6-1,RAPGEF3,ACVR1C,F2RL1,F2R,ZBED6,DMTN,ADTRP,SUFU,SIRT4,GPLD1,IRS1,CABP1,CD200,DNM1L,HDAC1,PPP3CA,SP100,CPT1A,SLC9B2,TGFB2,ADRA2A,TCIRG1,TCF7L2,KCNB1,YOD1,PFKFB2,HCLS1,HSPA8,HPS4,SORL1,C2CD5,GPER1,ARIH2,CIB1,BAG3,SFN,PER2,STX1A,UHMK1,GLUL,SIDT2,SLC16A1,APOD,ADAM8,KLF7,CTDSPL2,FZD5,MAPT,FIS1,CEMIP,NMT1,TTN,DERL3,SEC16B,IL12A,ENY2,ABCA12,C11orf65,MCU,PDCD10,PPP3CB,PINK1,CD38,MPC2,MAPK1,CHRM1,TMEM30B,GRIPAP1,RAB8A,ATP13A2,CNST,SYT7,RSC1A1,NLGN2,NPEPPS,WRAP53,TARDBP,STX4,PSEN1,ITGAM,SNX12,TMED10,NDEL1,AC138894.1,HAX1,RAB11A,MYH10,SMAD3,CORO2B,SYTL4,GPR68,BCAS3,ARHGAP44,CCL5,MIEF2,CDK5R1,SREBF1,ISL1,OXCT1,NOS2,EFCAB7,ABAT,RPH3AL,INPP5K,NADK,BCAP31,PRKCZ,OAZ1,BAIAP3,PARK7,LRRC8A,GAPVD1,SH3GLB1,WWP2,RIPOR1,MIR199A1,MICALL2,FGA,OOEP,CHGA,SOX4,DPP4,BNIP3L,CRH,TXN,DOC2B,HRAS,UQCC2,MIEF1,RHOU,LEPROT,PARD6A,UBE2G2,DERL2,ZIC1	grey	VSMC_M10
GO:0006275	0.98	0.03	39	92	regulation of DNA replication	BP	1	GLI1,PPP2R1A,ANKRD17,ORC3,EGFR,SSBP1,FAF1,ORC5,GLI2,DACH1,ZRANB3,FBH1,RAD17,ATR,NUGGC,NBN,WRNIP1,DONSON,NPM2,STN1,EGF,POLG2,BCL6,DBF4B,USP37,TSPYL2,KAT7,KCTD13,CTC1,TIPIN,LIG3,METTL4,TNFAIP1,JUN,WDR18,TTF1,ACVRL1,HRAS,EREG	grey	VSMC_M10
GO:0055072	0.98	0.03	30	72	iron ion homeostasis	BP	1	MYC,BTBD9,TMPRSS6,STEAP2,EPAS1,HEPHL1,STEAP3,HPX,NCOA4,SLC25A37,SLC40A1,BDH2,ISCU,HJV,MELTF,SLC11A1,ABCB6,ATP13A2,FTH1,CYB561A3,NOX5,TMEM199,SLC46A1,NUBP1,ATP6AP1,FRRS1,LCN2,SLC22A17,FXN,FTL	grey	VSMC_M10
GO:0006353	0.98	0.05	6	19	DNA-templated transcription, termination	BP	1	MTERF1,PCF11,SCAF4,POLR3K,TTF1,MED18	grey	VSMC_M10
GO:0070661	0.98	0.02	93	201	leukocyte proliferation	BP	1	TNFAIP3,ENPP3,AGER,IL5,HLA-DPB1,TNFRSF13C,PTK2,RAC2,CCND3,KIT,TNFRSF21,NCK2,PELI1,IL4I1,TLR4,IL15,BMI1,MYD88,FOXJ1,TGFBR2,PURA,PAWR,PLCL2,PRNP,NCKAP1L,SLC7A1,TRAF6,GAPT,IL1A,CASP3,MEF2C,TMEM131L,IL7,RASGRP1,LMBR1L,RIPK2,F2RL1,MARCH7,ZNF335,CD40,IGF2,ICOSLG,BTN2A2,GPAM,TCIRG1,PRKAR1A,CD28,DLG1,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,SLC11A1,WNT4,PPP3CB,CD38,BST1,MAPK1,STAT5B,SCGB1A1,FOXP3,RASAL3,CARD11,TNFRSF1B,DOCK2,MAPK3,ZBTB7B,CHRNB2,CD19,BTK,CD74,CCL5,CSF1R,CD320,TWSG1,IL7R,TICAM1,DNAJA3,VAV3,GLMN,MIR21,LST1,FADD,CD46,IL33,CD70,TNFSF9,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10

GO:0022411	0.98	0.02	179	375	cellular component disassembly	BP	1	VPS4B,SMARCC2,LRP1,ATG12,AVIL,PRKN,TSPO,MYC,JMJD4,TMPRSS6,HSF1,FBXO7,LMOD2,KIAA1211,CHMP2A,TMOD1,PLEKHH2,STX17,SPTBN1,MTIF2,KLK4,SNX14,PLEK,ADD2,LPIN1,ATG5,MFSD8,NAPA,IQSEC1,RSPH6A,RUBCNL,LCP1,CLASP2,PLK3,OPTN,MTRF1,TRIM54,DEDD2,NCKAP5,NAPB,USP36,TMEM173,NAV3,SPEF1,DDRGK1,ULK1,LMOD3,VPS16,ATXN7,C12orf65,FOXL2,PIK3R1,LIX1,CHMP2B,FBXW7,LIMA1,SMARCD1,HTRA2,NCKAP5L,ZFAND1,CSNK2A2,MMP15,KATNB1,SCAF4,SYNJ1,CHMP7,ACVR1C,F2RL1,DMTN,STMND1,ADAMTS15,TEX264,GBF1,EIF2D,FAP,RPL23,DNM1L,CARMIL1,LMOD1,ADD3,CISD2,TRPV4,TMEM39A,USP30,TTBK2,CFL1,ACIN1,DYRK3,HSPA8,GPER1,CIB1,SPTBN2,ARID1A,TMOD4,EPS8,UFC1,RUBCN,MELTF,LAMC1,KIF9,ADAM8,CAPZA1,NSF,FZD5,FIS1,ATG2A,MMP11,FUNDC1,DHX8,UPF1,HTT,RETREG3,MARK2,CTSV,MMP13,PINK1,MUL1,MMP3,ATG9A,PLA2G16,SNAP29,TBC1D25,TMOD2,STX5,PADI2,ATP13A2,EPHA4,AKAP8L,WIPI2,PHF23,SPTB,VPS13D,MFN2,FGFR4,GAK,VPS13C,PEX14,ITGAM,NDEL1,DNASE2,AC138894.1,HAX1,CALM1,SNAPIN,PRKCB,VMP1,ATG2B,INSR,SMCR8,KLC1,CAMSAP3,SREBF1,LAMP2,MCTS1,C3,TAOK1,CLEC16A,PAM16,DFFB,APC2,FUNDC2,PARK7,CAMSAP1,CHMP1A,VPS4A,CARMIL2,PLK5,DPP4,BNIP3L,IRGM,TIGAR,CCSAP,APC,PDXP,BLCAP,MAP1A,NMNAT1,MRRF,MAP6D1	grey	VSMC_M10
GO:0030574	0.98	0.04	11	31	collagen catabolic process	BP	1	TMPRSS6,ADAMTS3,MMP15,FAP,MMP21,MMP11,VSIR,MMP13,MMP3,MMP23B,MMP25	grey	VSMC_M10
GO:0031109	0.98	0.03	47	109	microtubule polymerization or depolymerization	BP	1	ZNF207,HSPA1B,TUBGCP6,SLAIN2,MET,CDK5RAP2,MAPRE1,EML2,SLC39A12,CLASP2,MAPRE3,TRIM54,NCKAP5,SLAIN1,NAV3,ARHGEF7,SPEF1,ATXN7,CLIP1,NCKAP5L,KATNB1,TUBGCP5,STMND1,TRPV4,TTBK2,TUBGCP4,CIB1,INPP5J,CDKN1B,MAPT,TOGARAM1,NIN,TUBG1,NDEL1,CAMSAP3,CDK5R1,CEP192,TAOK1,MECP2,APC2,CAMSAP1,PSRC1,CCSAP,APC,MAP1A,DRG1,MAP6D1	grey	VSMC_M10
GO:0010613	0.98	0.04	9	26	positive regulation of cardiac muscle hypertrophy	BP	1	TRPC3,HAND2,PDE9A,PPP3CA,AGT,SLC9A1,PARP1,MIR199A1,MIR21	grey	VSMC_M10
GO:0014742	0.98	0.04	9	26	positive regulation of muscle hypertrophy	BP	1	TRPC3,HAND2,PDE9A,PPP3CA,AGT,SLC9A1,PARP1,MIR199A1,MIR21	grey	VSMC_M10
GO:0055006	0.98	0.03	29	71	cardiac cell development	BP	1	MAML1,PPARA,PI16,SRF,FHL2,BVES,MYLK3,ATG5,SPRY1,JAG1,TBX5,PDCD4,AGT,ACTC1,ALPK3,TTN,OBSL1,BMPR1A,TCAP,YY1,ISL1,MYH11,MIR199A1,MIR21,MIR23A,MIR24-1,RGS4,NKX2-5,HEY2	grey	VSMC_M10
GO:1990776	0.98	0.04	8	24	response to angiotensin	BP	1	HSF1,SLC30A10,AGT,NFE2L2,AGTRAP,CAMK2A,CYBA,CA2	grey	VSMC_M10
GO:0042044	0.98	0.05	6	19	fluid transport	BP	1	MIP,AQP1,AQP11,SCNN1B,INPP5K,PDZD3	grey	VSMC_M10
GO:1903510	0.98	0.03	29	71	mucopolysaccharide metabolic process	BP	1	PIM1,CEMIP2,HAS1,IL15,NDNF,GLB1,CHPF2,CSGALNACT1,DCN,B3GNT4,ST3GAL6,CHST1,HYAL1,HYAL3,EGF,ABCC5,CEMIP,CHST3,SPOCK2,CHST7,AC022400.6,CHST12,IDUA,GLCE,B3GALT6,CHST5,ST3GAL2,HAS3,CHSY3	grey	VSMC_M10
GO:0022618	0.98	0.02	75	163	ribonucleoprotein complex assembly	BP	1	CPSF6,SF3A3,EIF3E,RRP7A,AGO2,PUF60,EIF3L,C12orf45,RPS14,PRPF31,YTHDC1,SRSF10,MDN1,AGO1,CLNS1A,CELF2,RPSA,CRNKL1,PRKDC,TGS1,USP39,TAF9,CLP1,RPL6,ATR,GCFC2,AAR2,CELF1,SRSF6,SCAF11,EIF2D,RBM5,SART3,MRPS11,ZRSR2,RPS27,CELF3,DHX30,RPL11,GEMIN2,SNRPD3,PRPF39,RPL10L,XRCC5,PRPF19,KHDC4,EIF3C,LUC7L3,SLU7,COIL,ZNHIT3,NLE1,XAB2,MCTS1,SNU13,RPL23A,ERAL1,CELF5,LUC7L,ZNHIT6,PRMT7,RNVU1-6,RNU5E-1,RNU5B-1,AGO4,RPS27L,NOL3,RNU4ATAC,RF00003,SNRPC,RNU2-1,RNU4-2,SRSF12,RNU4-1,PIH1D2	grey	VSMC_M10
GO:1904589	0.98	0.03	22	55	regulation of protein import	BP	1	MAPK14,SMO,RAB23,ARHGEF5,FERMT1,MAVS,NUP58,PIK3R1,PKIA,NUP54,SUFU,CABP1,HCLS1,HSPA8,BAG3,APOD,MAPK1,TARDBP,PSEN1,SMAD3,EFCAB7,ZIC1	grey	VSMC_M10
GO:0051492	0.98	0.03	33	80	regulation of stress fiber assembly	BP	1	LPAR1,ITGB1BP1,MET,ARHGEF5,EPHA1,CLASP2,WNT11,MKKS,ACTG1,BAG4,PIK3R1,ALMS1,RAPGEF3,PXN,CARMIL1,PPFIA1,ARHGAP6,WASF2,SLC9A1,WNT4,WAS,SMAD3,CORO2B,EVL,PTGER4,INPP5K,SERPINF2,TSC1,FHOD1,MIR21,RHOA,ASAP3,RGCC	grey	VSMC_M10

GO:0045934	0.98	0.02	559	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	ZC3H10,SMARCC2,ATP8B1,PLAGL1,HELB,ZBTB2,ESR1,CNOT2,OSR2,PABPC1,SNW1,ZNF706,PHAX,ZBTB12,PRKN,PPARA,TCF7,XRCC6,PITX1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,PTCH1,ATF4,CBX7,MAPK14,CBY1,SOX10,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,TFAP2B,NFIL3,SEMA4D,RPS14,ZNF550,BEND6,ZNF268,LRPPRC,SCMH1,RNF20,MSH2,NFE2L3,HOXA2,HOXA7,JAZF1,PTBP3,XPO1,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,CYREN,NR1H2,ZNF350,FOXP2,MED25,KLF11,POU3F3,LANCL2,CREM,SDCBP,OSR1,FOXO3,BEND5,TRAF3IP2,HDAC2,PHF10,DNMT3A,BMI1,DHX34,ZC3H4,CNBP,SETDB2,PHB,SOX9,ZNF746,ERCC1,EED,SUV39H2,ZNF404,PLK3,XRCC1,MLH1,GLI2,DEDD2,RSF1,KDM4A,MYD88,DACH1,TAF3,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,SFMBT2,GZF1,POU4F1,FBH1,WNT11,THAP1,EID2,OVOL2,RNF169,ZNF219,EOMES,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,NR1D2,PAWR,PLCB1,SIRT7,DPF1,ALX1,SHLD1,BAG4,TAF7,NUDT16,NRG1,GAS6,RYBP,FOXP1,MITF,PKP3,MTA3,ARID5A,IRF7,ERCC6,TRAF6,LIN37,NR1H4,KCNIP3,TRIB3,PFDN5,SDR16C5,ZC3H8,DNMT3B,BTAF1,CEBPA,CBFA2T2,SMYD1,FOXL2,ZNF536,TFDP2,IRF2,NCOA2,DKK3,SAP30,ZNF366,ARNTL,GCFC2,HMBOX1,MEF2C,PEX2,PKIA,BCDIN3D,TMBIM6,CNOT1,SLA2,CUX2,MCPH1,SOX6,FNIP2,BACH1,SFMBT1,NR1H3,EAPP,SCAF4,LCOR,NBN,DDX54,TENT2,RUNX1T1,VDR,NKX3-1,BAHD1,HDAC7,NKX6-1,LOXL2,NR4A2,SRSF6,PHF21A,CRY2,PRDM11,CDYL,RREB1,RTF1,ZBED6,SOX13,ZNF248,TFAP2A,RIPPLY3,HIF1AN,PAX2,SALL1,PPHLN1,PRICKLE1,HIVEP1,TENT5C,	grey	VSMC_M10
GO:1990830	0.98	0.03	32	77	cellular response to leukemia inhibitory factor	BP	1	RNMT,GFPT2,PMM1,PTP4A3,SYNGR1,BSPRY,BCAT2,KLF5,SPRY2,PFKP,MRPL15,MRAS,PCOLCE2,VEGFC,JARID2,INA,NR5A2,ABCG4,EPS8,CREB1,XRCC5,SPOCK2,EFHC2,PDCD10,PADI2,ABCD4,SHMT1,MTF2,SNX10,NFYB,LRAT,PIGA	grey	VSMC_M10
GO:0002312	0.98	0.03	26	64	B cell activation involved in immune response	BP	1	MFNG,EXOSC3,MSH2,TLR4,HMCES,ERCC1,MLH1,PAXIP1,PLCL2,SHLD1,GAPT,PTK2B,NBN,CDH17,CD40,DOCK10,CD28,RNF168,BCL6,FOXP3,SHLD2,TBX21,BATF,CD19,SUPT6H,RNF8	grey	VSMC_M10
GO:0030199	0.98	0.03	22	56	collagen fibril organization	BP	1	TNXB,COL11A2,COL14A1,ADAMTS3,PXDN,CRTAP,LUM,TLL2,LOXL2,LOXL4,TGFB2,EFEMP2,PLOD3,COL13A1,MMP11,COL3A1,COL5A2,P3H4,ANXA2,VIPAS39,SERPINF2,COL5A1	grey	VSMC_M10
GO:2001044	0.98	0.05	4	14	regulation of integrin-mediated signaling pathway	BP	1	ITGB1BP1,DMTN,SLC2A10,BST1	grey	VSMC_M10
GO:0072678	0.98	0.03	16	42	T cell migration	BP	1	SLC12A2,CCL27,OXSR1,CD200,CD99,APOD,ADAM8,ITGA4,CXCL16,TMEM102,CCL5,CCL2,CRK,RHOA,FADD,WNT5A	grey	VSMC_M10
GO:1903311	0.98	0.02	115	247	regulation of mRNA metabolic process	BP	1	ZC3H10,PAN2,CPSF6,CNOT2,CNOT6,RIDA,PABPC1,SNW1,PNLDC1,QKI,CSDC2,AGO2,TNRC6B,ZC3H3,TUT7,GTPBP1,MAPK14,PUF60,HSF1,RBFOX2,SMU1,EXOSC3,RNF20,TRA2A,YTHDC1,PNPT1,SRSF10,TUT4,PUM2,TRAF3IP2,ZC3HAV1,DHX34,IWS1,FASTK,MLH1,MYD88,CELF2,TNRC6C,NUP98,BAG4,LSM1,WTAP,PKP3,PAN3,RBM39,CNOT1,CELF1,CNOT6L,SRSF6,FTO,TENT5C,TENT4B,RBM24,RBM5,DIS3L2,AXIN2,MAPKAPK2,GIGYF2,HSPA8,SRSF4,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,CELF3,NCBP2,EIF4ENIF1,YBX3,RBM7,RC3H1,UPF1,SLC11A1,RBM10,SAMD4A,POLR2G,LEO1,SCGB1A1,NT5C3B,DCP1B,PRPF19,FXR2,TARDBP,RBM25,TOB1,TENT5D,TNRC6A,CNOT8,LARP1,PAPOLA,ALKBH5,RAVER2,SUPT6H,PARN,MBNL3,NSRP1,FMR1,CELF5,METTL16,PLEKHN1,CIRBP,TRAF2,SRRM4,METTL14,NANOS1,NOVA1,CACNG7,RBM11,SRSF12,YBX1,ZFP36L2,TENT5A,SAP18,RC3H2,EXOSC5	grey	VSMC_M10
GO:0000469	0.98	0.04	9	26	cleavage involved in rRNA processing	BP	1	UTP23,TSR1,EXOSC3,BMS1,RPP40,NOP9,KRI1,ERI2,NOL9	grey	VSMC_M10
GO:0031401	0.98	0.02	369	747	positive regulation of protein modification process	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,SNW1,MAP3K4,PRKN,AGER,IL5,GDF9,DERL1,SKP1,PHF1,XRCC6,PTK2,TAB1,NTRK2,PLA2G6,C6orf89,HSF1,CCND3,CHRNA3,TEK,CRY1,TTBK1,TEC,KIT,SLC1A1,ROR2,SEMA4D,CLDN19,IL11,RNF20,FPR2,MOB1B,EPGN,AREG,BMP8A,PELI1,ETAA1,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,VRK3,EGFR,ARHGEF5,TLR4,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,SPHK2,HDAC2,SLC8A2,BMI1,MOB3C,PRKD2,PHB,ABI1,SOX9,SYMPK,MAPRE3,RALB,PRKAG2,RAF1,PIBF1,PAXIP1,WDR48,MYCBP2,FBH1,SPRY2,WNT11,KLHL40,AKT2,ARRB1,TGFBR2,ACVR2A,NMI,NEK10,RPTOR,TCIM,HBEGF,ASPSCR1,CHTOP,NSD3,PRNP,BAG4,MAVS,NRG1,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,ERCC6,FLT1,ADRA2B,TRAF6,TRIB3,SDR16C5,RET,FAM107A,DNMT3B,ACVR1B,OSBP,SPSB4,ZFP91,TRABD2A,ING2,ROBO1,ARNTL,FBXW7,PTPRJ,VEGFC,P2RY1,ATG10,MADD,PTK2B,RASGRP1,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,FGF5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,MARCH7,CDK2AP1,RTF1,PKD2,STK4,PRICKLE1,ADTRP,NOD2,CNTN1,JARID2,TAOK3,TOLLIP,CD40,IGF2,BMPR1B,NHLRC1,BDNF,NEURL1,SPPL3,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K6,TGFB2,ADRA2A,PEF1,FAM20A,PDCD6,DAG1,AUTS2,AXIN2,SLCO3A1,AJUBA,PIAS3,SART3,NCF1,KRAS,EGF,HCLS1,ADNP,OPRD1,GPER1,SPRTN,CHEK2,CASS4,SPATC1L,PARP9,PARP14,CACUL1,AGT,CIB1,ARNT,DVL3,STRADB,PPP2R5A,OSM,HDAC4,SYAP1,THPO,STRADA,PDE8A,LIMK2,NOS1AP,GPRC5D,CDKN1B,SENP2,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,TET1,STOX1,CEMIP,BCL6,FBXO33,DBF4B,IL12A,MAP4K2,WDR61,DDX3X,TAD	grey	VSMC_M10

GO:0030030	0.98	0.02	613	1226	cell projection organization	BP	1	NME1,NEDD4L,ATP8B1,ONECUT2,MYO1A,LRP1,SEMA6A,KIF5A,AVIL,TBC1D30,ATAT1,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,AGER,PARVG,KIF3A,SULT4A1,TSPO,TBC1D32,FSTL4,SYNGAP1,UBE2B,MTSS1,WASHC5,ASAP1,LRRC6,GFRA3,PTK2,PTCH1,MAPK15,PLXNA4,NTRK2,CBY1,PODXL,CPNE5,PICK1,MICALL1,CDC42EP1,RAC2,SMO,MYH9,RBFOX2,IFT74,CHRNA3,FBXO7,PTK7,ABHD17B,SRF,CFAP69,FZD1,RFX3,KIT,ADGRF1,TNFRSF21,NCK2,ROR2,SEMA4D,DLX5,PTPDC1,FGD3,ETV1,SEMA4C,RAB23,DYNC2LI1,SVBP,BRSK1,EPS8L1,RIMS1,TMEM30A,RTN4,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,CEP162,AREG,TMEM17,AKIRIN1,WDR92,PLEK,EPHA7,WHRN,PTN,TNC,EGFR,HECW1,FUZ,TRIM32,NCDN,EPHA1,IQUB,KEL,VPS35,ATG5,SDCBP,RTN4IP1,NRCAM,ARMC2,MAPRE1,NTF4,FIG4,WASF1,ARMC4,INTU,SPATA6,DHFR,PLXNA1,HDAC2,MTMR2,TTC26,BBS7,NDNF,VSTM5,ARHGEF4,RAB10,DRC1,CCDC61,IQSEC1,ABI1,RSPH6A,SLC39A12,NECTIN2,USH1G,CDNF,GOLGA4,GLI2,MEGF8,GALNT11,ATP1A3,FBF1,PIBF1,KLF5,IFT172,FOXJ1,PTPRF,MYO7A,TTC21A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,WDR60,SPRY2,CFAP61,SS18L2,SLITRK5,ALK,TTLL3,CCDC13,CPNE9,ABCC4,FARP1,KIF5C,MKKS,SYT1,TMEM106B,RAB5A,FEZ2,RAC3,CEP290,SLC23A2,PRNP,BAG4,ARHGEF7,SEMA3D,SPART,SPEF1,PLXNC1,SEMA3A,CHL1,UNC5D,FGD6,NCKAP1L,ULK1,ARFIP2,LRRC56,TMEM80,DPYSL3,ERCC6,RYK,TTC17,TUB,EPHB1,PLK2,NPHP1,RET,AL359736.1,TOX,TTL,KIF3B,CBFA2T2,FER,RILPL1,RILPL2,ANKRD27,CEP70,PREX2,PIK3R1,CASP3,PARVA,PLS1,ROBO1,ROBO2,PLCE1,CEP250,CCDC66,TENM3,ADGRV1,LIMA1,ENC1,FZD3,MEF2C,SEMA4F,P2RX7,TCTN3,NCAM2,IFT81	grey	VSMC_M10
GO:1901989	0.98	0.03	39	91	positive regulation of cell cycle phase transition	BP	1	VPS4B,GLI1,PPP1R10,MAPK15,CCND3,ZNF16,ANKRD17,LSM10,EGFR,TOPAZ1,UBE2E2,RPTOR,PLCB1,TFDP1,DDRGK1,MTA3,ANAPC5,ANAPC7,ADAMTS1,HYAL1,CCND1,TERT,DYRK3,CHEK2,STOX1,DBF4B,DDX3X,MEPCE,ANAPC4,RAD51B,PAGR1,RAB11A,RAD51C,SIN3A,MECP2,CDK10,MIR29A,MIR222,RGCC	grey	VSMC_M10
GO:0030201	0.98	0.04	10	29	heparan sulfate proteoglycan metabolic process	BP	1	HS3ST5,CSGALNACT1,SULF2,TCF7L2,AC022400.6,GLCE,HS6ST2,B3GALT6,HS6ST3,HS2ST1	grey	VSMC_M10
GO:0046545	0.98	0.03	31	75	development of primary female sexual characteristics	BP	1	ESR1,GDF9,DMC1,FANCG,KIT,FOXO3,DACH1,ARRB1,ACVR1B,FOXL2,CASP3,ROBO2,ADAMTS1,BMPR1B,GAS2,HYAL3,LHX9,SPO11,TAF4,VGF,WNT4,PTPRN,STAT5B,INHA,HSPA5,MSH4,LHX8,UBB,CEBPB,EREG,LHFPL2	grey	VSMC_M10
GO:0045880	0.98	0.04	11	31	positive regulation of smoothened signaling pathway	BP	1	GLI1,SMO,INTU,IFT172,TTC23,ARMC9,POR,STK36,GORAB,TUBD1,GPC3	grey	VSMC_M10
GO:0036257	0.98	0.04	9	26	multivesicular body organization	BP	1	VPS4B,CHMP2A,CHMP2B,CHMP4C,CHMP7,VPS37D,RAB11A,CHMP1A,VPS4A	grey	VSMC_M10
GO:0032835	0.99	0.03	20	52	glomerulus development	BP	1	MTSS1,PODXL,TEK,OSR1,FOXJ1,JAG1,RET,ASXL1,PLCE1,MEF2C,PAX2,SULF2,ENPEP,PTPRO,IL6R,LHX1,MIR125A,NOG,BASP1,PDGFD	grey	VSMC_M10
GO:0097035	0.99	0.03	16	43	regulation of membrane lipid distribution	BP	1	ATP9B,ATP8B1,ABCB1,TMEM30A,ANO4,XKR6,PLSCR4,P2RX7,ANO6,ABCA12,TMEM30B,ATP11C,ABCA3,ABCA7,TLCD1,XKR8	grey	VSMC_M10
GO:0042110	0.99	0.02	147	310	T cell activation	BP	1	AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TCF7,TNFRSF13C,RAC2,CCND3,MYH9,SRF,KIT,TNFRSF21,NCK2,SLC46A2,PELI1,RSAD2,IL4I1,IL15,ATG5,TRAF3IP2,BMI1,LCP1,CLPTM1,GLI2,FOXJ1,TGFBR2,EOMES,PAWR,PRNP,NCKAP1L,FOXP1,PRKDC,SLC7A1,TRAF6,SOX12,TOX,ZC3H8,IL1A,CAMK4,CASP3,TMEM131L,IL7,PAG1,SLA2,RASGRP1,LMBR1L,EIF2AK4,RIPK2,AP3B1,F2RL1,MARCH7,SOX13,NOD2,IGF2,PKNOX1,LCK,PPP3CA,ICOSLG,BTN2A2,GPAM,TCIRG1,PRKAR1A,RABL3,HLX,FZD7,CD28,FCER1G,RUNX3,PATZ1,SP3,DLG1,ADAM8,FZD5,DUSP10,BCL6,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,SLC11A1,WNT4,LAG3,PPP3CB,DDOST,STAT3,STAT5B,WAS,SCGB1A1,FOXP3,RASAL3,ZBTB1,CARD11,TNFRSF1B,TBX21,PSEN1,SEMA4A,DOCK2,BATF,ZBTB7B,IL6R,LAT,SMAD3,IL4R,BCL11B,CD74,CCL5,CCL2,YES1,JAG2,NKAP,VAV1,LEPR,PTGER4,TWSG1,IL7R,PTPN2,SOCS1,DROSHA,DNAJA3,PRKCZ,TSC1,GLMN,BCL10,MIR21,MIR27A,RHOA,SOX4,MAFB,FADD,DPP4,CD46,CASP8,THY1,FGL2,CD70,TNFSF9,NHEJ1,ZFP36L2,LAX1,EFNB3,CEBPB,PRR7,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0030038	0.99	0.02	40	95	contractile actin filament bundle assembly	BP	1	SRF,LPAR1,ITGB1BP1,MET,ARHGEF5,EPHA1,CLASP2,WNT11,ARRB1,MKKS,ACTG1,BAG4,PIK3R1,SORBS1,PTK2B,ALMS1,RAPGEF3,PXN,CARMIL1,PPFIA1,ARHGAP6,WASF2,SLC9A1,ITGB5,WNT4,WAS,KCTD13,SMAD3,CORO2B,EVL,PTGER4,TNFAIP1,INPP5K,SERPINF2,TSC1,FHOD1,MIR21,RHOA,ASAP3,RGCC	grey	VSMC_M10
GO:0043149	0.99	0.02	40	95	stress fiber assembly	BP	1	SRF,LPAR1,ITGB1BP1,MET,ARHGEF5,EPHA1,CLASP2,WNT11,ARRB1,MKKS,ACTG1,BAG4,PIK3R1,SORBS1,PTK2B,ALMS1,RAPGEF3,PXN,CARMIL1,PPFIA1,ARHGAP6,WASF2,SLC9A1,ITGB5,WNT4,WAS,KCTD13,SMAD3,CORO2B,EVL,PTGER4,TNFAIP1,INPP5K,SERPINF2,TSC1,FHOD1,MIR21,RHOA,ASAP3,RGCC	grey	VSMC_M10

GO:0065003	0.99	0.02	613	1210	protein-containing complex assembly	BP	1	TIMM21,MIP,ARPC3,BAZ2A,TCF4,SHMT2,AVIL,ATP23,ATAT1,CPSF6,ESR1,STK3,ZNF207,MAPK8IP2,APOM,HSPA1B,SF3A3,TUBGCP6,EIF3E,LYRM7,KCNV1,PRKN,HLA-DRA,HLA-DOB,HLA-DMA,IL5,BRD2,HLA-DPB1,SEPT8,HSD17B8,ASF1A,HSPA4,RRP7A,NDUFA6,BAK1,WASHC5,ASAP1,LRRC6,AGO2,H3F3C,PTK2,FANCC,MAPK15,CBY1,DMC1,PUF60,PSMD5,BAIAP2L2,PICK1,EIF3L,CDC42EP1,GPAA1,TSPAN33,HSF1,CHRNA3,PRPH2,GNMT,TRPM6,LMOD2,TTBK1,APBA1,C12orf45,SLAIN2,NCK2,TLN1,KIAA1211,NINJ1,COA5,CHMP2A,RPS14,TMOD1,SDHAF4,PRKCE,RIMS1,PRPF31,SPTBN1,RTN4,PPP2R1A,MPP6,YTHDC1,PNPT1,SKAP2,SHANK1,ECPAS,SRSF10,MDN1,WDR92,TRAPPC12,PLEK,NR1H2,ITGB1BP1,MED25,MET,ADD2,AGO1,TLR4,CDK5RAP2,TRAF1,TEAD2,FAM49A,TRPM4,MAPRE1,WASF1,ARMC4,EPS15,SSBP1,APOB,FAF1,NDUFB2,HIGD1A,UBN2,NAPA,AP2S1,VSTM5,MSRB2,ATPAF1,KCNRG,KPNA3,DRC1,SOX9,EML2,NDUFB6,SLC39A12,LCP1,TMEM126B,CLASP2,APOC1,MAPRE3,DNAJC15,KCTD2,CDC123,KCTD21,NDUFC2,RALB,RSF1,CLNS1A,CAND2,AQP11,RAF1,MYD88,CELF2,DMAC2,RPSA,NAPB,SLAIN1,CRNKL1,HGSNAT,PIP4P1,EID2,PLEKHG2,FCHSD2,MKKS,TMEM173,NAV3,SYT1,LIN7A,NUP98,RYR1,FERMT1,NDUFS8,EIF2AK2,PRNP,NDUFAF7,BAG4,TAF7,ARHGEF7,DIAPH1,ATL2,BRF2,FCHSD1,NDUFA12,NRG1,NCKAP1L,ULK1,ARFIP2,MITF,TAF10,LMOD3,PRKDC,COX7A1,TTC17,APIP,TGS1,SOAT2,HCK,TM9SF4,NDUFAF2,FAM107A,KCTD6,KCTD15,FER,CBR4,ANKRD27,USP39,LPXN,HIP1R,TAF9,CLP1,RPL6,ATR,TRABD2A,CLIP1,P2RX3,UQCC1,SLF1,RYR3,ERC2,GCFC2,FCHO2,FMN1,TMEM120B,ANKRA2,ASIC1,P2RX7,NDUFS3,AAR2,CELF	grey	VSMC_M10
GO:0051384	0.99	0.02	45	104	response to glucocorticoid	BP	1	FECH,TPH2,AREG,AQP1,EGFR,FOXO3,BMI1,GLB1,AANAT,HNMT,FAM107A,DNMT3B,CASP3,STC1,ABCC2,CPN1,SRD5A1,CCND1,KRAS,NPAS4,CPS1,ACSBG1,BCHE,ALPL,CTSV,SCGB1A1,FOS,CALM1,PPARGC1B,ISL1,GHR,ABCA3,ASS1,AGL,HSD11B2,RHOA,BGLAP,SMYD3,CLDN1,DUSP1,CRH,BCL2L11,ZFP36L2,GPR83,PDCD7	grey	VSMC_M10
GO:0035791	0.99	0.05	4	14	platelet-derived growth factor receptor-beta signaling pathway	BP	1	LRP1,PDGFRL,HIP1R,PTPN2	grey	VSMC_M10
GO:0060391	0.99	0.05	5	17	positive regulation of SMAD protein signal transduction	BP	1	RBPMS,KIAA0319,BMPR1A,PARP1,SH2B1	grey	VSMC_M10
GO:0051149	0.99	0.03	21	53	positive regulation of muscle cell differentiation	BP	1	MAML1,MAPK14,KIT,TRIM32,MYLK3,MAMSTR,NRG1,LMOD3,SMYD1,MEF2C,RBM24,GPER1,ACTN3,EFEMP2,SETD3,PIEZO1,ENG,MIR199A1,MIR21,MIR125B1,MIR22	grey	VSMC_M10
GO:0032509	0.99	0.04	9	26	endosome transport via multivesicular body sorting pathway	BP	1	VPS4B,CHMP2A,LEPROTL1,CHMP2B,CHMP4C,CHMP7,RILP,CHMP1A,LEPROT	grey	VSMC_M10
GO:0002252	0.99	0.02	172	360	immune effector process	BP	1	CD226,LRP1,STX7,ENPP3,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,PTK2,PLA2G6,MFNG,RAC2,KIT,PRDX1,EXOSC3,PRKCE,MSH2,ANKRD17,RSAD2,IL4I1,TLR4,ATG5,TRPM4,TRAF3IP2,SPHK2,HMCES,PHB,ERCC1,LCP1,LACC1,NECTIN2,PVR,GAB2,MLH1,UNC13D,MYD88,SLC22A13,FOXJ1,PAXIP1,EOMES,JAG1,NMI,TCIM,PLCL2,SHLD1,MAVS,NCKAP1L,HPX,FOXP1,PRKDC,IRF7,TRAF6,GAPT,HCK,GPI,FER,PTPRJ,TMBIM6,SLA2,PTK2B,RASGRP1,EIF2AK4,RIPK2,NBN,DYSF,CDH17,F2RL1,NOD2,CD40,GBF1,DOCK10,CD96,TGFB2,TCIRG1,SNAP23,HLX,DENND1B,NCF1,SLAMF8,LAT2,FGR,CBL,PLPP4,SNX4,CD28,FCER1G,RNF168,CADM1,FZD5,DUSP10,BCL6,HK1,CTSH,IL12A,RC3H1,PTPN6,TNFSF18,SLC11A1,LAG3,PTGDR,PPP3CB,CFP,STAT3,C12orf4,STAT5B,WAS,FOXP3,ZBTB1,SHLD2,TNFRSF1B,SPON2,TBX21,STX4,PSEN1,SEMA4A,ITGAM,DOCK2,BATF,ZBTB7B,IL6R,CD19,LAT,IL4R,MPO,S100A13,BTK,SCNN1B,CD74,STXBP2,FBXO38,YES1,PRAM1,VAV1,C7,PTGER4,C3,NOS2,IL7R,SUPT6H,TICAM1,CRK,DNASE1,PDPK1,PRKCZ,TRAF2,TSC1,SLC7A5,FOXF1,VAV3,KARS,STXBP1,AP1G1,BCL10,MIR21,CHGA,FADD,CXCL6,CD46,A2M,CFD,WNT5A,INAVA,FGL2,FCER2,RNF8,CD70,SERPINB9,RGCC,HAVCR2,RC3H2	grey	VSMC_M10
GO:0062197	0.99	0.02	133	282	cellular response to chemical stress	BP	1	ADNP2,MAP3K5,TNFAIP3,HSPA1B,PRKN,TSPO,XRCC6,NCOA7,ERCC6L2,FANCC,AKR1B1,ATF4,MAPK13,HSF1,GPR37,FBXO7,SLC1A1,ERMP1,PRDX1,DNAJA1,EPAS1,PNPT1,VRK2,AQP1,ZNF277,MET,EGFR,TLR4,UCP1,ATG5,SLC7A11,FOXO3,DHFR,HDAC2,OXSR1,PRDX3,SIRT2,PAWR,BRF2,PDK1,ARL6IP5,STX2,DNMT3B,FER,CASP3,DIABLO,ARNTL,FBXW7,MSRA,HTRA2,GPX8,NR4A2,RIPK1,TP53INP1,PKD2,PLA2R1,PAX2,PXN,GLRX2,HDAC1,TRPV4,FBLN5,SCN2A,STAU1,NCF1,MCL1,ARNT,PYROXD1,PDE8A,MGMT,YBX3,NFE2L2,MAPT,NONO,STOX1,PRKRA,PRODH,DDX3X,XRCC5,MICU1,PDCD10,GCH1,PINK1,MMP3,ANKZF1,MAPK1,RAD52,ATP13A2,PARP1,SLC2A4,WNK3,SOD3,STX4,KDM6B,FOS,MAPK3,AC138894.1,MPO,SFPQ,BTK,KEAP1,SIN3A,MAPK7,PPARGC1B,LRRC8E,SLC25A23,LONP1,STK26,JUN,PARK7,TSC1,TLDC1,LCN2,MAPKAP1,NQO1,MIR21,NFE2L1,ZNF622,LRRC8D,PJVK,NOL3,GPR37L1,DHRS2,ZNF580,IMPACT,FXN,DDIT3,TXN,RBM11,NUDT2,CBX8,PPIF,PDGFD	grey	VSMC_M10
GO:1902004	0.99	0.05	4	14	positive regulation of amyloid-beta formation	BP	1	CASP3,SLC2A13,EPHA4,EFNA1	grey	VSMC_M10
GO:0043967	0.99	0.03	23	58	histone H4 acetylation	BP	1	YEATS4,KANSL3,ING3,ATG5,IWS1,TADA3,ARRB1,TAF7,EP400,PHF20,KANSL2,AUTS2,ING5,NAA40,ING4,MSL1,KAT7,MUC1,OGT,NAA60,HCFC1,CHD5,BEND3	grey	VSMC_M10

GO:0140013	0.99	0.02	62	139	meiotic nuclear division	BP	1	FBXO43,MOV10L1,UBE2B,WASHC5,MAPK15,DMC1,KLHDC3,FOXJ3,CCDC155,MLH1,CCNB1IP1,SIRT2,PLCB1,SIRT7,TEX15,MOS,ING2,M1AP,RAD54B,SYCP1,SYCP2L,NPM2,HSF2BP,PRKAR1A,CCDC36,SPO11,GPR3,C11orf80,HORMAD2,TDRKH,TEX12,MAJIN,ZCWPW1,STAG3,WNT4,P3H4,RAD51B,SEPT1,EME1,SYCE2,RAD51C,RAD51D,ERCC4,FZR1,SLX4,MEIOB,SPIRE2,MSH4,UBB,SYCP3,RNF212B,AGO4,OOEP,FOXJ2,ZSCAN21,SYCE1L,WNT5A,SPDYA,BCL2L11,LIF,CENPX,EREG	grey	VSMC_M10
GO:2000181	0.99	0.02	35	83	negative regulation of blood vessel morphogenesis	BP	1	SEMA6A,SLC12A2,TEK,PTN,AGO1,WISP3,SPRY2,ISM1,DCN,PLK2,PIK3CB,ADAMTS1,TGFB2,AGT,E2F2,WNT4,HSPG2,SYNJ2BP,NAXE,SEMA4A,FOXO4,VASH1,TNMD,AMOT,MECP2,DAB2IP,MIR29A,MIR21,MIR222,MIR125B1,MIR24-1,FOXJ2,MIR125A,GADD45A,RGCC	grey	VSMC_M10
GO:0032392	0.99	0.03	33	80	DNA geometric change	BP	1	HELB,MCM9,XRCC6,POT1,MTERF1,ASCC3,SSBP1,ERCC2,ERCC3,GTF2F2,ZRANB3,FBH1,CHD8,PURA,MCM8,WRN,DQX1,NBN,HELQ,RAD54B,WRNIP1,TWNK,RAD54L2,IGHMBP2,RECQL,RTEL1,SUPV3L1,DDX3X,XRCC5,DDX11,PIF1,G3BP1,CHD5	grey	VSMC_M10
GO:0034109	0.99	0.03	29	71	homotypic cell-cell adhesion	BP	1	MYH9,TLN1,PLEK,SLC7A11,MYL12A,C1QTNF1,ACTG1,CLIC1,PIK3CB,DSP,DMTN,PKP2,CD99,UBASH3B,ITGA2B,FN1,PTPN6,FERMT3,VCL,ACTB,PEAR1,MEGF11,DSG2,CCL5,JAK1,ABAT,STXBP1,FGA,RAP2B	grey	VSMC_M10
GO:0070647	0.99	0.02	400	806	protein modification by small protein conjugation or removal	BP	1	NEDD4L,SHMT2,FEM1C,TRIM36,RMND5B,TNFAIP3,USP15,FBXO30,TRIM39,FBXO43,MARCH3,HSPA1B,TULP4,PRKN,RNF5,MED30,TSPO,DERL1,SKP1,UBE2B,RNF217,RNF146,KLHL3,JOSD1,UHRF2,ZC3HC1,FBXL6,USP49,FBXO7,KLHDC3,ASB15,CRY1,NFX1,DCAF12,SUPT3H,USP46,LNX1,FBXO10,DCAF10,SVBP,DNAJA1,RNF20,PRKCE,EPAS1,ASB3,UBE3D,FANCL,MINDY4,PELI1,CNOT4,BSPRY,HECW1,USP45,TRIM32,FBXW2,TRAF1,HACE1,NOSIP,USP38,ATG5,TRPM4,TRAF3IP2,BMI1,OTUD1,LRRC41,FBXL2,SUMO2,USP35,KBTBD6,KCTD21,TRIM54,CAND2,UBE2E2,PAXIP1,WDR48,UBE2O,MYCBP2,UBE3C,SPOPL,FBH1,ASB13,MED8,SPRY2,UBE2E1,KLHL40,CCNB1IP1,ARRB1,RNF169,USP36,CBX4,FBXO17,NMI,SIRT7,GPS1,TPP2,NHLRC3,RNF24,RNF14,RNF122,USP44,DDRGK1,SH3RF2,UBOX5,RYBP,TRIM3,TAF10,KBTBD8,LNX2,TRAF6,TRIM44,ATXN7,MARCH8,TRIB3,ERCC8,ASXL1,FAM107A,HECTD2,KCTD6,OTUD4,DTX4,SPSB4,USP39,ZFP91,RNF181,RNF7,UBE2L6,EYA1,TRPC4AP,FBXW7,USP25,TRIM2,HLTF,ENC1,ANAPC5,ANAPC7,USP16,ATG10,KLHL2,DDB2,RIPK2,OTULIN,ASB8,SENP1,ABRAXAS1,HDAC7,AMFR,RNFT2,FBXO21,WDSUB1,VPS18,MARCH7,TTC3,NEURL2,HERC6,PRICKLE1,HERC5,NOD2,PRMT3,TRIM45,HERC2,WSB2,MYLIP,TOLLIP,SIAH1,MAGEL2,NHLRC1,FBXL15,DCAF1,RNF144B,FBXO25,DZIP3,OTUD7A,MED10,RNF10,PCGF6,KLHL12,IFIH1,NEURL1,RPL23,HECW2,PEF1,KLHL42,PDCD6,COPS7B,USP30,RNF115,RNF123,PIAS3,SART3,KLHL25,USP13,SPATA2,RNF114,AC013489.1,YOD1,USP19,OTUD7B,SPRTN,KLHL24,ASB11,DTX3L,ZNRF3,ABCB11,ARIH2,USP2,RNF26,NEDD8,CBL,TRAF5,ARNT,PER2,ASB1,HDAC4,STX1A,PELI3,RNF215,TRIM52,UFC1,AB	grey	VSMC_M10
GO:0010942	0.99	0.02	229	470	positive regulation of cell death	BP	1	MTCH2,TNFAIP8,LRP1,MAP3K5,HEBP2,TRIM39,STK3,IGF2R,TSPO,BAK1,ATF4,TOMM22,IRF5,CDKN2A,NCK2,TFAP2B,GADD45G,ZNF268,DNAJA1,TFPT,GSDME,HOXA13,NOD1,EPHA7,PTN,KLF11,ING3,TLR4,SFRP4,DKKL1,MYCN,FOXO3,CDK19,FAF1,SPHK2,SPRY1,DNMT3A,PHB,ZNF746,ERCC3,PDIA3,DEDD2,GRIK5,POU4F1,FBH1,WNT11,ARRB1,SIRT2,RARB,IDO1,PAWR,PRNP,DUSP6,ARHGEF7,BTG1,RNF122,RYBP,ARL6IP5,PRKDC,RET,NSMAF,ZC3H8,ACOX2,NR4A1,PIK3CB,FOXL2,CASP3,HIP1R,HPGD,DIABLO,FBXW7,MEF2C,HTRA2,TCTN3,C3orf38,CELF1,KATNB1,RAPGEF2,PNMA2,RIPK2,VDR,NKX3-1,ACVR1C,F2RL1,NQO2,RIPK1,ANO6,PRDM11,TP53INP1,PIDD1,PLA2R1,IFIT2,STK4,TFAP2A,SUDS3,CD40,SIAH1,BMPR1B,GPLD1,FAP,CALHM2,NEURL1,DNM1L,SIK1,HDAC1,ALDH1A3,LCK,STK17B,MAP2K6,PDCD4,TGFB2,RBM5,AXIN2,SSH1,GPER1,QRICH1,CHEK2,ADAMTSL4,MCL1,AGT,IP6K2,SLC9A1,CIDEB,NFATC4,PEA15,HDAC4,KCNK2,NTSR1,STPG1,BACE1,ING5,FZD9,PDCD1,RPL11,CDKN1B,MAP3K11,ADAM8,CREB1,MAPT,CCAR1,FIS1,PRKRA,BCL6,CTSH,PRODH,ITGA4,IL12A,DDX3X,SAV1,CXCR2,HTT,ING4,RBM10,MMP3,LTBR,ADCY10,KCNMA1,MAGED1,PARP1,TNFRSF1B,TNFRSF8,ALDH1A2,MFN2,MAP3K9,PSEN1,PNMA1,ITGAM,NGFR,DAPK2,FOS,S100A8,SFPQ,DNM2,DCUN1D3,CAMK2A,CCL5,PPP1R13B,CCL2,CDK5R1,NOS2,PTPN2,JUN,PIAS4,BCAP31,TRPV1,PLEKHN1,TRAF2,PARK7,LCN2,PIP5KL1,DHODH,HPR,NQO1,BCL10,DAB2IP,MIR29A,MIR21,MIR23A,MIR125B1,MIR27B,MIR24-1,RHOA,UBB,ZNF622,MLLT11,SOX4,FADD,BNIP3L,CASP8,MIR125A,CD248,WNT5A,TIGAR,GADD45A,ACER	grey	VSMC_M10
GO:0048662	0.99	0.03	17	44	negative regulation of smooth muscle cell proliferation	BP	1	TNFAIP3,TRIB1,OGN,IL15,PTGIR,MEF2C,PDCD4,GNA13,GPER1,EFEMP2,CDKN1B,APOD,IL12A,COMT,MFN2,RHOA,MIR339	grey	VSMC_M10
GO:0071229	0.99	0.03	26	65	cellular response to acid chemical	BP	1	PNPLA3,NTRK2,HSF1,RRAGD,SESN3,DNMT3A,RPTOR,LARS,SLC38A9,OPA1,PKD2,NEURL1,COL16A1,SH3BP4,COL5A2,RRAGB,SOCS1,AMIGO1,CYBA,LAMTOR5,ASS1,LAMTOR2,SIX1,BCL2L2,CEBPB,PDGFD	grey	VSMC_M10

GO:0120039	0.99	0.02	248	517	plasma membrane bounded cell projection morphogenesis	BP	1	NEDD4L,LRP1,SEMA6A,KIF5A,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,SULT4A1,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,CPNE5,RAC2,SMO,RBFOX2,CHRNA3,SRF,SEMA4D,DLX5,ETV1,SEMA4C,BRSK1,RIMS1,RTN4,RUFY3,SHANK1,HOXA2,EPHA7,PTN,EGFR,HECW1,EPHA1,KEL,NRCAM,NTF4,WASF1,PLXNA1,RAB10,ABI1,GOLGA4,GLI2,MEGF8,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,CPNE9,FARP1,KIF5C,SYT1,TMEM106B,FEZ2,SLC23A2,ARHGEF7,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NCKAP1L,ULK1,RYK,EPHB1,RET,TTL,ANKRD27,PREX2,ROBO1,ROBO2,FZD3,SEMA4F,TLX2,CUX2,RAPGEF2,DPYSL2,EIF2AK4,TIAM1,SLIT1,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,SEMA3G,RREB1,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,SEMA4G,ZNF335,DTNBP1,TAOK3,SIAH1,LZTS1,BMPR1B,BDNF,DOCK10,KIAA0319,LGR6,DNM1L,PPP3CA,HECW2,CAPRIN2,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,CFL1,ADNP,DISC1,WASF2,GBX2,DVL3,KALRN,NFATC4,SS18L1,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,TANC2,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,SEMA6D,EPHB4,ITGA4,TNR,FN1,NCKAP1,NYAP1,ATL1,NIN,FLRT1,DNM3,PPP3CB,CNTNAP1,RAB3A,MARK2,MUL1,VCL,OBSL1,MINK1,RAB8A,CRMP1,EPHA4,LRTM2,DLG4,ACTB,DVL2,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,SNX1,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,NTN1,GAS7,RPS6KA5,RNF165,MYO9A,DNM2,PARP6,GPRASP2,BHLHB9,BCL11B,LHX1,ARHGAP44,SIN3A,TRPV2,LAMA3,CDK5R1,ISL1,EMB,EPB41L3,LAMA1,DOCK7,TAOK1,SLC9A6,DAB1,SLITRK2,LRP8,L1CAM,NTN3,PRKCZ,ARHGAP4,PLXNA3,BSG,TUBB3,AMIGO1,CELSR2,NTN	grey	VSMC_M10
GO:0050657	0.99	0.02	60	135	nucleic acid transport	BP	1	CPSF6,PHAX,QKI,ZC3H3,HSF1,NOL6,XPO5,BICD2,LRPPRC,IGF2BP3,YTHDC1,PNPT1,XPO1,IWS1,TGFBR2,KIF5C,NUP98,CHTOP,UPF3A,THOC7,NUP58,CETN3,NUP54,MX2,DDX25,RFTN2,RTRAF,NCBP2,SIDT2,POM121,SENP2,IGF2BP2,SETD2,ENY2,UPF1,PARP11,NXF1,AHCTF1,AKAP8L,CASC3,FYTTD1,SMG5,RANBP17,NRDE2,ALKBH5,UPF3B,THOC2,SUPT6H,FMR1,NCBP3,TSC1,NUP214,DDX19A,SARNP,DDX19B,NXT2,NUPL2,YBX1,MRPL18,MAGOHB	grey	VSMC_M10
GO:0050658	0.99	0.02	60	135	RNA transport	BP	1	CPSF6,PHAX,QKI,ZC3H3,HSF1,NOL6,XPO5,BICD2,LRPPRC,IGF2BP3,YTHDC1,PNPT1,XPO1,IWS1,TGFBR2,KIF5C,NUP98,CHTOP,UPF3A,THOC7,NUP58,CETN3,NUP54,MX2,DDX25,RFTN2,RTRAF,NCBP2,SIDT2,POM121,SENP2,IGF2BP2,SETD2,ENY2,UPF1,PARP11,NXF1,AHCTF1,AKAP8L,CASC3,FYTTD1,SMG5,RANBP17,NRDE2,ALKBH5,UPF3B,THOC2,SUPT6H,FMR1,NCBP3,TSC1,NUP214,DDX19A,SARNP,DDX19B,NXT2,NUPL2,YBX1,MRPL18,MAGOHB	grey	VSMC_M10
GO:0070296	0.99	0.03	10	29	sarcoplasmic reticulum calcium ion transport	BP	1	RYR1,CASQ2,RYR2,ANK2,ATP1A2,CASQ1,ATP2A1,CALM1,DMD,NOL3	grey	VSMC_M10
GO:0060419	0.99	0.02	32	77	heart growth	BP	1	GLI1,PPARA,MAPK14,PI16,PIM1,TGFBR2,DUSP6,MEF2C,TBX5,JARID2,TGFB2,PRKAR1A,AGT,KCNK2,SAV1,MAPK1,BMPR1A,RBPJ,TBX2,YY1,GATA6,MIR199A1,MIR222,MIR23A,MIR24-1,MIR25,NOG,BASP1,RGS4,C3orf58,HEY2,WNT2	grey	VSMC_M10
GO:1902807	0.99	0.03	24	60	negative regulation of cell cycle G1/S phase transition	BP	1	FBXO7,PLK3,PRKDC,PLK2,FAM107A,PIDD1,PKD2,CCND1,GIGYF2,CHEK2,CDKN1B,DLG1,SUSD2,MEN1,MUC1,DCUN1D3,CCL2,FBXO31,MIR29A,PLK5,RPS27L,SOX4,APC,CRADD	grey	VSMC_M10
GO:0071312	0.99	0.03	10	29	cellular response to alkaloid	BP	1	SLC1A1,DDC,RYR1,CASP3,RYR3,SPIDR,CASQ2,RYR2,TRPV1,CRH	grey	VSMC_M10
GO:0019076	0.99	0.03	10	29	viral release from host cell	BP	1	VPS4B,CHMP2A,TRIM32,RAB7A,CHMP2B,CHMP4C,PC,DDB1,VPS4A,ZNF502	grey	VSMC_M10
GO:0035890	0.99	0.03	10	29	exit from host	BP	1	VPS4B,CHMP2A,TRIM32,RAB7A,CHMP2B,CHMP4C,PC,DDB1,VPS4A,ZNF502	grey	VSMC_M10
GO:0035891	0.99	0.03	10	29	exit from host cell	BP	1	VPS4B,CHMP2A,TRIM32,RAB7A,CHMP2B,CHMP4C,PC,DDB1,VPS4A,ZNF502	grey	VSMC_M10
GO:0022407	0.99	0.02	138	293	regulation of cell-cell adhesion	BP	1	AGER,PPARA,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,PTK2,MAPK14,PODXL,ZDHHC21,TNFRSF21,NCK2,EPCAM,PELI1,EPHA7,AKNA,IL4I1,IL15,BMI1,GLI2,PCDH8,FOXJ1,TGFBR2,C1QTNF1,JAG1,PAWR,SPINT2,PRNP,NCKAP1L,SLC7A1,LRFN3,TRAF6,SOX12,ZC3H8,IL1A,CASP3,DENND6A,TENM3,TMEM131L,IL7,PAG1,RASGRP1,RIPK2,AP3B1,MARCH7,SOX13,GCNT2,DMTN,ADTRP,NOD2,IGF2,LCK,ICOSLG,TRPV4,BTN2A2,GPAM,PRKAR1A,HLX,SOX2,YTHDF2,UBASH3B,CD28,RUNX3,EPHB3,DLG1,ADAM8,MIA3,DUSP10,BCL6,ITGA4,IL12A,ABCA12,TNR,VSIR,RC3H1,PTPN6,TNFSF18,FERMT3,WNT4,LAG3,STAT5B,MINK1,SCGB1A1,FOXP3,RASAL3,ZBTB1,CARD11,TBX21,ZBTB7B,IL4R,MAP2K5,CD74,CCL5,MAPK7,CCL2,CCL25,YES1,NKAP,VAV1,JAK1,TWSG1,IL7R,PTPN2,SOCS1,ABAT,DNAJA3,SERPINF2,PRKCZ,CELSR2,PIEZO1,ASS1,GLMN,BCL10,MIR21,MIR222,MIR27A,RHOA,FGA,FSTL3,SOX4,FADD,DPP4,CD46,FUT4,MIR125A,THY1,WNT5A,FGL2,CD70,TNFSF9,RGCC,LAX1,EFNB3,CEBPB,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0008154	0.99	0.02	83	183	actin polymerization or depolymerization	BP	1	ARPC3,AVIL,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,NCK2,KIAA1211,TMOD1,PLEKHH2,PRKCE,SPTBN1,PLEK,ADD2,FAM49A,WASF1,MSRB2,ABI1,PLEKHG2,FCHSD2,MKKS,BAG4,DIAPH1,FCHSD1,NCKAP1L,ARFIP2,LMOD3,TTC17,HCK,FAM107A,FER,HIP1R,FMN1,LIMA1,PTK2B,F2RL1,IQGAP2,CYFIP1,DMTN,MAGEL2,CARMIL1,LMOD1,ADD3,SSH1,CFL1,HCLS1,ARHGAP6,AP1AR,SPATC1L,WASF2,SPTBN2,TMOD4,EPS8,WHAMM,DLG1,CAPZA1,CDC42EP2,NCKAP1,ARPC1A,WAS,TMOD2,SPTB,PFN3,WASHC3,HAX1,GAS7,EVL,PSTPIP1,SSH2,CORO7,MLST8,SPIRE2,WDR63,CARMIL2,MICALL2,RHOA,VASP,GMFG,GRB2,PFN4,PDXP,COTL1	grey	VSMC_M10

GO:0048666	0.99	0.02	432	877	neuron development	BP	1	NME1,NEDD4L,ATP8B1,ONECUT2,LRP1,SEMA6A,KIF5A,AVIL,ATAT1,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,AGER,SULT4A1,TSPO,UQCRQ,FSTL4,SYNGAP1,WASHC5,ASAP1,GFRA3,PTK2,PTCH1,ANKS1A,AGTPBP1,PLXNA4,NTRK2,CPNE5,PICK1,MICALL1,RAC2,SMO,RBFOX2,CHRNA3,PRPH2,FBXO7,RORB,PTK7,SRF,FZD1,ADGRF1,TNFRSF21,NCK2,ROR2,SEMA4D,DLX5,ETV1,SEMA4C,SVBP,BRSK1,RDH13,RIMS1,TMEM30A,RTN4,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,PPT1,AREG,EPHA7,WHRN,PTN,TNC,YWHAZ,EGFR,HECW1,TRIM32,NCDN,EPHA1,KEL,RTN4IP1,NRCAM,NTF4,FIG4,WASF1,MFSD8,DHFR,PLXNA1,HDAC2,MTMR2,NDNF,RAB10,IQSEC1,ABI1,SLC39A12,USH1G,CDNF,GOLGA4,GLI2,MEGF8,PTPRF,MYO7A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,ALK,DZANK1,CPNE9,FARP1,KIF5C,SLC4A7,FSCN2,SYT1,TMEM106B,LRTOMT,AP000812.5,FEZ2,RAC3,CEP290,SLC23A2,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NCKAP1L,ULK1,DPYSL3,ERCC6,RYK,EPHB1,PLK2,RET,LGI4,TOX,TTL,CBFA2T2,ANKRD27,PREX2,CASP3,HAND2,DCLK2,PLS1,ROBO1,ROBO2,TENM3,ADGRV1,ENC1,FZD3,MEF2C,SEMA4F,HTRA2,NCAM2,TLX2,CUX2,KATNB1,PTK2B,RAPGEF2,DGUOK,DPYSL2,EIF2AK4,RND1,TIAM1,PAQR3,SLIT1,USH1C,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,CRTAC1,C8orf37,SEMA3G,RPGRIP1L,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,TSPAN2,SEMA4G,CNTN1,ZNF335,DTNBP1,MYLIP,TAOK3,SLC12A5,STMND1,KCNIP2,SIAH1,LZTS1,BMPR1B,BICDL1,PSD,BDNF,SRGAP2C,SLC4A10,DOCK10,KIAA0319,NEURL1,MTR,LGR6,DNM1L,PPP3CA,HECW2,CAPRIN2,TRPV4,SEMA3F,TGFB2,GAP43,TRIP11,ADARB1,DAG1,AUTS2,	grey	VSMC_M10
GO:0032436	0.99	0.02	35	83	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	HSPA1B,PRKN,RNF217,TRIB1,CSNK1E,ZYG11B,BBS7,PLK3,SUMO2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,TRIB3,PLK2,CEBPA,PRICKLE1,RNF144B,AC013489.1,ARIH2,NFE2L2,COP1,SOCS4,DNAJB2,PSEN1,TAF1,KEAP1,PSMD10,FBXO22,FZR1,BCAP31,SGTA,ZER1,DDA1	grey	VSMC_M10
GO:0033559	0.99	0.03	26	64	unsaturated fatty acid metabolic process	BP	1	AKR1B1,FAAH,ACOX1,PIBF1,ELOVL1,ELOVL7,ABHD6,HPGD,PLA2G4B,CYP2U1,PLA2G4A,DAGLB,FADS3,EPHX1,DEGS1,AC005520.1,ALOXE3,MAPK3,CD74,CYP2J2,DECR2,PTGES2,CES2,FABP5,ELOVL3,PTGES	grey	VSMC_M10
GO:0044062	0.99	0.05	4	14	regulation of excretion	BP	1	SNX5,STC1,AGT,COMT	grey	VSMC_M10
GO:0048660	0.99	0.02	55	124	regulation of smooth muscle cell proliferation	BP	1	MAP3K5,TNFAIP3,XRCC6,TRIB1,AKR1B1,OGN,EGFR,TLR4,IL15,PTGIR,PHB,MYD88,ABCC4,TGFBR2,HBEGF,FOXP1,PRKDC,TRAF6,HPGD,MEF2C,ADAMTS1,NQO2,TERT,PDCD4,TCF7L2,GNA13,GPER1,AGT,HDAC4,EFEMP2,CDKN1B,APOD,IL12A,COMT,XRCC5,CALCRL,BMPR1A,MFN2,RBPMS2,IL6R,CCL5,JUN,SERPINF2,GNAI3,CYBA,MIR21,MIR222,MIR27B,MIR27A,RHOA,FOXJ2,MIR339,LDLRAP1,EREG,PDGFD	grey	VSMC_M10
GO:0071985	0.99	0.03	11	31	multivesicular body sorting pathway	BP	1	VPS4B,CHMP2A,LEPROTL1,CHMP2B,CHMP4C,CHMP7,RUBCN,SYTL4,RILP,CHMP1A,LEPROT	grey	VSMC_M10
GO:0010324	0.99	0.03	21	54	membrane invagination	BP	1	RAC2,MYH9,CHMP2A,ARHGAP12,NCKAP1L,XKR6,FCHO2,RHOBTB2,F2RL1,ANO6,RHOBTB1,DOCK1,ITGAM,SYT11,C3,ABCA7,SPIRE2,FNBP1L,RHOA,HAVCR1,XKR8	grey	VSMC_M10
GO:0120036	0.99	0.02	595	1193	plasma membrane bounded cell projection organization	BP	1	NME1,NEDD4L,ATP8B1,ONECUT2,MYO1A,LRP1,SEMA6A,KIF5A,AVIL,TBC1D30,ATAT1,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,AGER,KIF3A,SULT4A1,TSPO,TBC1D32,FSTL4,SYNGAP1,UBE2B,MTSS1,WASHC5,ASAP1,LRRC6,GFRA3,PTK2,PTCH1,MAPK15,PLXNA4,NTRK2,PODXL,CPNE5,PICK1,MICALL1,CDC42EP1,RAC2,SMO,MYH9,RBFOX2,IFT74,CHRNA3,FBXO7,PTK7,ABHD17B,SRF,CFAP69,FZD1,RFX3,KIT,ADGRF1,TNFRSF21,NCK2,ROR2,SEMA4D,DLX5,PTPDC1,FGD3,ETV1,SEMA4C,RAB23,DYNC2LI1,SVBP,BRSK1,EPS8L1,RIMS1,TMEM30A,RTN4,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,CEP162,AREG,TMEM17,AKIRIN1,WDR92,PLEK,EPHA7,WHRN,PTN,TNC,EGFR,HECW1,FUZ,TRIM32,NCDN,EPHA1,IQUB,KEL,VPS35,ATG5,SDCBP,RTN4IP1,NRCAM,ARMC2,MAPRE1,NTF4,FIG4,WASF1,ARMC4,INTU,SPATA6,DHFR,PLXNA1,HDAC2,MTMR2,TTC26,BBS7,NDNF,VSTM5,ARHGEF4,RAB10,DRC1,IQSEC1,ABI1,RSPH6A,SLC39A12,NECTIN2,USH1G,CDNF,GOLGA4,GLI2,MEGF8,GALNT11,ATP1A3,FBF1,PIBF1,KLF5,IFT172,FOXJ1,PTPRF,MYO7A,TTC21A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,WDR60,CFAP61,SS18L2,SLITRK5,ALK,TTLL3,CDC13,CPNE9,ABCC4,FARP1,KIF5C,MKKS,SYT1,TMEM106B,RAB5A,FEZ2,RAC3,CEP290,SLC23A2,PRNP,BAG4,ARHGEF7,SEMA3D,SPART,SPEF1,PLXNC1,SEMA3A,CHL1,UNC5D,FGD6,NCKAP1L,ULK1,ARFIP2,TMEM80,DPYSL3,ERCC6,RYK,TTC17,TUB,EPHB1,PLK2,RET,AL359736.1,TOX,TTL,KIF3B,CBFA2T2,FER,RILPL1,RILPL2,ANKRD27,CEP70,PREX2,PIK3R1,CASP3,PARVA,PLS1,ROBO1,ROBO2,PLCE1,CEP250,CCDC66,TENM3,ADGRV1,LIMA1,ENC1,FZD3,MEF2C,SEMA4F,P2RX7,TCTN3,NCAM2,IFT81,TLX2,CCDC113,CFAP20,CUX2,ARHGEF26,	grey	VSMC_M10

GO:0019439	0.99	0.02	180	375	aromatic compound catabolic process	BP	1	PAN2,ALDH8A1,PDE7B,ENPP3,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,DPYS,SKIV2L,DXO,EIF3E,PNLDC1,PDE10A,SMPDL3A,CSDC2,AGO2,TNRC6B,TUT7,APOBEC3H,GTPBP1,MAPK14,EXOSC4,HSF1,GDA,GALT,ENPP4,CNOT11,EXOSC3,LRPPRC,PNPT1,NT5E,RNASEH1,IL4I1,AGO1,TUT4,PUM2,TRAF3IP2,MTPAP,ZC3HAV1,DHX34,ENTPD6,CDADC1,NUDT15,FASTK,MLH1,NUDT5,MBD4,DEDD2,MYD88,HNMT,FBH1,TNRC6C,IDO2,IDO1,LRTOMT,AP000812.5,LSM1,NUDT16,PKP3,UPF3A,PAN3,NUDT12,AHCY,AMPD3,FOXL2,ZCCHC8,TTC37,CNOT1,EPHX2,CELF1,CNOT6L,TENT2,ENTPD4,FITM2,FTO,ABCC2,NUDT18,TENT5C,TENT4B,RBM24,PDE9A,SLC6A3,DIS3L2,AXIN2,HGD,NUDT17,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,MGAT1,PDE8A,NCBP2,EIF4ENIF1,SIDT2,YBX3,RBM7,TET1,SUPV3L1,UPB1,FAH,MTHFS,COMT,RC3H1,DDX49,UPF1,SLC11A1,RBM10,SAMD4A,ZSWIM8,POLR2G,SCGB1A1,NT5C3B,DCP1B,CASC3,EPHX1,MRPL44,TNFRSF1B,FXR2,TARDBP,SMG5,DNASE2,TOB1,RNASEH2A,GSTZ1,TENT5D,NRDE2,TNRC6A,CNOT8,LARP1,PDE4A,NEIL1,SLFN14,ALKBH5,UPF3B,NT5M,PARN,DROSHA,FMR1,TREX2,PAM16,DNASE1,METTL16,PLEKHN1,LSM7,NTHL1,DFFB,CIRBP,TRAF2,DNASE1L1,MLYCD,KYAT1,KYAT3,EDC4,AGO4,ENTPD5,METTL14,NANOS1,DIO3,DNASE1L2,NUDT19,CACNG7,ALDH1L1,YBX1,ZFP36L2,TENT5A,PDXP,MAGOHB,HINT1,UPP1,DIO2,NMNAT1,RC3H2,EXOSC5	grey	VSMC_M10
GO:0032388	0.99	0.02	78	173	positive regulation of intracellular transport	BP	1	CPSF6,RAB21,PRKN,MAPK14,RAC2,SMO,TMEM30A,RUFY3,ITGB1BP1,TCAF2,MTMR2,PLK3,AKT2,USP36,CEP290,PRNP,MAVS,GAS6,TM9SF4,PIK3R1,FBXW7,HTRA2,ZFAND1,CSNK2A2,RAPGEF3,PGAP1,TCF7L2,KCNB1,HCLS1,HPS4,SORL1,C2CD5,ARIH2,CIB1,BAG3,SFN,NCBP2,CALY,CTDSPL2,FZD5,FIS1,CEMIP,NMT1,SEC16B,EHD1,ABCA12,PDCD10,PINK1,MAPK1,CHRM1,TMEM30B,STX18,NPEPPS,ANXA2,TARDBP,PSEN1,ITGAM,TRIM46,ATP2A1,SMAD3,NRDE2,BCAS3,MIEF2,CDK5R1,EFCAB7,BCAP31,OAZ1,SH3GLB1,RIPOR1,MICALL2,LDLRAP1,BORCS5,TBC1D20,HRAS,MIEF1,RHOU,LEPROT,ZIC1	grey	VSMC_M10
GO:1902186	0.99	0.04	7	22	regulation of viral release from host cell	BP	1	CHMP2A,TRIM32,CHMP2B,PC,DDB1,VPS4A,ZNF502	grey	VSMC_M10
GO:0009101	0.99	0.02	114	245	glycoprotein biosynthetic process	BP	1	B4GALT7,RXYLT1,GFPT2,ALG12,PMM1,AGO2,LARGE1,ST6GAL2,SRD5A3,C1GALT1,CHST10,ALG2,FKTN,IL15,HS3ST5,ALG11,POMGNT1,B4GALT2,CHPF2,AQP11,GALNT11,ST6GALNAC2,MGAT5B,CSGALNACT1,UGGT2,HBEGF,PAWR,PLCB1,TMTC4,GALNT15,FUT10,GXYLT2,EOGT,POFUT1,ST8SIA4,B3GNT4,MOGS,RPN2,ST3GAL6,GALNT5,GCNT2,BMPR1B,ALG10,SLC2A10,TRIP11,POGLUT1,TCF7L2,DAD1,ST8SIA2,B3GALT1,B3GNT5,GALNT2,DPAGT1,ALG3,MAN1C1,MGAT1,GAL3ST3,XXYLT1,EDEM3,TET1,PLOD3,SOAT1,DERL3,ALG9,MGAT2,B3GALNT1,KDELC2,CHST3,GAL3ST4,CHST7,DDOST,AC022400.6,GALNT8,CHST12,GALNT16,PSEN1,KRTCAP2,OGT,POMT2,GLCE,ST8SIA5,COG7,GALNT1,TNIP1,MPI,NPC1,ALG6,HS6ST2,PMM2,ALG1,B3GALT6,ABCA7,ABO,GBGT1,FOXL1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,FUT4,ENTPD5,DHDDS,TMEM258,POFUT2,ACER2,HS6ST3,IL33,POMK,CHSY3,POMGNT2,B4GALT3,ISPD,SLC35C1,HS2ST1,ST8SIA6	grey	VSMC_M10
GO:2000026	0.99	0.02	505	1014	regulation of multicellular organismal development	BP	1	NME1,LRP1,SEMA6A,GLI1,TNFAIP3,CYP27B1,RAB21,OSR2,SNW1,TIAM2,ADM2,SLC12A2,HSPA1B,BRD1,AGER,PPARA,HLA-DRA,IL5,TSPO,GDF9,FSTL4,TCF7,SYNGAP1,XRCC6,TRIB1,MYC,TOB2,AGO2,PTCH1,PLXNA4,MAPK14,NTRK2,SOX10,PI16,PIM1,SMO,ZDHHC21,HSF1,DAAM2,ZNF16,RBFOX2,TEK,LINGO2,FBXO7,CEMIP2,SRF,TTBK1,CDK6,RFX3,KIT,TNFRSF21,ROR2,SEMA4D,S1PR3,PDCL3,NINJ1,OMD,SEMA4C,NLRP5,SIX2,SMAP1,CD109,RTN4,RUFY3,HOXA7,EMC10,MYCL,CXCL8,SLC46A2,MTURN,AQP1,BMPER,CNOT4,LRRN3,EPHA7,MBOAT2,PTN,GRHL1,IL4I1,AGO1,EGFR,TSPAN12,TRIM32,TLR4,EPHA1,GAB1,LPIN1,IL15,SFRP4,MYCN,TRPM4,OSR1,FOXO3,FIG4,MKX,SPRY1,PLXNA1,WISP3,FOXE3,LAMA4,HDAC2,MTMR2,CSAR1,VSTM5,PRKD2,CST7,SOX9,SLC39A12,CLASP2,CLPTM1,SLC4A2,PTCH2,GOLGA4,GLI2,MEGF8,KDM4A,XRCC2,ACVR2B,FOXJ1,NUMBL,POU4F1,IL15RA,SPRY2,SS18L2,WNT11,HOOK3,TGFBR2,OVOL2,ZNF219,ACVR2A,IKBKB,ISM1,BHLHE40,JAG1,SIRT2,RARB,PLCB1,MAFG,FERMT1,SPRED3,DUSP6,SEMA3D,DCN,BTG1,SPART,PLXNC1,SEMA3A,KL,NCKAP1L,GAS6,ULK1,FOXP1,MITF,PRKDC,IRF7,FLT1,RYK,TRAF6,EPHB1,SOX12,PLK2,PLAG1,LGI4,TOX,ZC3H8,IL1A,PAX8,ACVR1B,CAMK4,ANKRD27,FAIM,PIK3CB,PIK3R1,CLSTN2,ERAP1,ROBO1,ROBO2,ARNTL,FBXW7,ADGRV1,FZD3,MEF2C,TMEM131L,SEMA4F,IL7,P2RX7,VEGFC,TLX2,JAM2,CUX2,ADAMTS1,SOX6,PTK2B,RASGRP1,MME,RAPGEF2,TIAM1,BMP2K,SLIT1,RIPK2,SYNJ1,VDR,OPA1,NKX6-1,RAPGEF3,LOXL2,TBX5,AP3B1,AMIGO2,ZFYVE27,AGGF1,SRSF6,TESC,RIPK1,ANO6,SPINT1,SEMA3G,ITPKA,	grey	VSMC_M10
GO:0006778	0.99	0.03	15	40	porphyrin-containing compound metabolic process	BP	1	FECH,TSPO,SLC25A38,HPX,CPOX,COX15,ABCC2,TMEM14C,ALAS1,BDH2,ABCB6,COX10,SLC46A1,NFE2L1,FXN	grey	VSMC_M10
GO:1902041	0.99	0.03	16	42	regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	1	TNFAIP3,STK3,FAF1,RAF1,FAIM,FAIM2,MADD,STK4,BMPR1B,SP100,PEA15,DDX3X,STX4,PARK7,MIR222,FGA	grey	VSMC_M10

GO:0071706	0.99	0.02	50	115	tumor necrosis factor superfamily cytokine production	BP	1	TNFAIP3,AGER,TSPO,C6orf106,NOD1,TLR4,SPHK2,HDAC2,CSAR2,MYD88,MAVS,GAS6,FOXP1,NR1H4,IL1A,IL37,PIK3R1,PTPRJ,RASGRP1,OAS3,RIPK2,RIPK1,NOD2,IFIH1,HDAC1,MAPKAPK2,NFATC4,ADAM8,FZD5,VSIR,PTPN6,STAT3,FOXP3,AKAP8,TNFRSF8,SPON2,PSEN1,SYT11,ISL1,TICAM1,CYBA,BCL10,MIR125B1,MIR27B,OAS1,FADD,WNT5A,IL33,C1QTNF4,HAVCR2	grey	VSMC_M10
GO:1903555	0.99	0.02	50	115	regulation of tumor necrosis factor superfamily cytokine production	BP	1	TNFAIP3,AGER,TSPO,C6orf106,NOD1,TLR4,SPHK2,HDAC2,CSAR2,MYD88,MAVS,GAS6,FOXP1,NR1H4,IL1A,IL37,PIK3R1,PTPRJ,RASGRP1,OAS3,RIPK2,RIPK1,NOD2,IFIH1,HDAC1,MAPKAPK2,NFATC4,ADAM8,FZD5,VSIR,PTPN6,STAT3,FOXP3,AKAP8,TNFRSF8,SPON2,PSEN1,SYT11,ISL1,TICAM1,CYBA,BCL10,MIR125B1,MIR27B,OAS1,FADD,WNT5A,IL33,C1QTNF4,HAVCR2	grey	VSMC_M10
GO:0051129	0.99	0.02	277	569	negative regulation of cellular component organization	BP	1	LRP1,SEMA6A,AVIL,TBC1D30,MDM1,ZNF207,FBXO43,APOM,HSPA1B,PRKN,TSPO,FSTL4,SYNGAP1,H3F3C,PICK1,HSF1,POT1,LMOD2,SEMA4D,KIAA1211,TMEM14A,SEMA4C,TMOD1,PLEKHH2,SPTBN1,RTN4,RUFY3,ACP4,SHANK1,LPAR1,EPHA7,NR1H2,PTN,ITGB1BP1,MET,ADD2,CDK5RAP2,SDCBP,MAPRE1,HDAC2,MTMR2,RAB7A,SOX9,EML2,ERCC1,CLASP2,APOC1,DNAJC15,XRCC1,TRIM54,RAF1,TBC1D4,TSKU,SPRY2,DYNC1LI1,NEU3,IKBKB,MKKS,NAV3,ANAPC15,IK,FEZ2,PRNP,ARHGEF7,SEMA3D,SPART,SPEF1,SEMA3A,USP44,ULK1,LMOD3,DPYSL3,RYK,NR1H4,ATXN7,PFDN5,FAM107A,CBFA2T2,ANKRD27,PIK3R1,HIP1R,ROBO2,LIMA1,SEMA4F,TLX2,WDR54,KATNB1,RAPGEF2,DGUOK,NR1H3,PAQR3,SCAF4,SLIT1,NBN,TMEM67,OPA1,RAPGEF3,ARHGAP24,SEMA3G,SPP1,DMTN,SEMA4G,ADTRP,MYLIP,TENT4B,SRGAP2C,FAP,KIAA0319,STN1,DNM1L,CARMIL1,PPFIA1,LMOD1,ANKRD13A,PPP3CA,ADD3,SEC22B,TRPV4,SEMA3F,TMEM39A,PRKAR1A,USP30,TTBK2,SSH1,ARHGAP6,HSPA8,ANKRD13D,OPRD1,SORL1,KREMEN1,CIB1,WASF2,CERS2,SPTBN2,NFATC4,CCDC84,TRAF3IP1,TMOD4,EPS8,RUBCN,PTPRO,INPP5J,RTEL1,LIMK2,FZD9,SH3GL3,LRIG2,APOD,WNT3,CAPZA1,AIDA,MAPT,TET1,SEMA6D,DDX3X,TNR,XRCC5,C11orf65,LRPAP1,DNM3,RAP1GAP,PINK1,MUL1,DNAJB2,CD38,WAS,TMOD2,PPM1A,CRMP1,EPHA4,DLG4,PARP1,PHF23,SPTB,THRA,DNAJB1,PHF8,TNFRSF1B,GNL3L,PFDN4,GAK,STX1B,PSEN1,SEMA4A,SYT11,ITGA3,CTC1,TRIM46,EFNA1,PIF1,ADCK1,NTN1,LCMT1,CORO2B,SNAPIN,LDLR,TRIM37,DNM2,RIT2,BCAS3,ARHGAP44,EVL,SCAMP5,PSMD10,RIOK3,SMCR8,CAMSAP3,CDK5R1,TOM1L2,ISL1,THOC2,PTGER4,UNC119,ERCC4,PSMG	grey	VSMC_M10
GO:0120193	0.99	0.03	21	54	tight junction organization	BP	1	MPDZ,SRF,CLDN19,WNT11,IKBKB,ACTG1,NPHP1,LSR,MARVELD2,CLDN34,SNAI1,DLG1,FZD5,GPBAR1,RAMP2,CLDN7,MARVELD3,MICALL2,CLDN15,CLDN1,APC	grey	VSMC_M10
GO:0000466	0.99	0.04	8	24	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	1	EXOSC3,URB1,RPP40,NOP9,WDR12,KRI1,ERI2,NOL9	grey	VSMC_M10
GO:0007155	0.99	0.02	518	1044	cell adhesion	BP	1	CD226,SERPINB8,ITGA7,ERBB3,ONECUT2,MIP,LRP1,SEMA6A,TNXB,AGER,PPARA,HLA-DRA,FBLN1,HLA-DOB,HLA-DMA,PARVG,HLA-DPB1,COL14A1,TNFRSF13C,MTSS1,OBSCN,PTK2,PLXNA4,MAPK14,PODXL,CDC42EP1,RAC2,ZDHHC21,MYH9,CDKN2A,IFT74,TEK,LRRC4,PRPH2,PTK7,SRF,ADAM22,NUAK1,CLDN12,APBA1,PGM5,CDK6,CD72,KIT,TNFRSF21,NCK2,SGCE,TLN1,CNTNAP3,SEMA4D,CHST10,NINJ1,OMD,ADGRL3,CLDN19,PRKCE,EPCAM,PPP2R1A,FPR2,HAS1,CTNNAL1,EPB41L4B,HOXA7,MYBPC2,NT5E,CXCL8,PELI1,PLEK,EPHA7,AKNA,PTN,ITGB1BP1,ADD2,TNC,IL4I1,EGFR,EPHA1,BVES,IL15,NRCAM,SLC7A11,PCDH10,FAF1,IZUMO1,FAT4,PLXNA1,WISP3,LAMA4,PODXL2,BMI1,NDNF,RAB10,PRKD2,SOX9,SYMPK,FBLN2,SSPO,CLASP2,DLG2,RSU1,NECTIN2,BCAM,PVR,CNTNAP5,GLI2,PCDH8,UNC13D,FOXJ1,PTPRF,RPSA,PPP1CB,MYL12A,RIN2,TGFBR2,C1QTNF1,JAG1,LGALS4,ACTG1,ADAM18,PAWR,FERMT1,RAC3,SPINT2,FREM2,COL6A6,COL6A5,PRNP,PCDHGC5,BAG4,ARHGEF7,RELL2,PLXNC1,PCDH1,CHL1,UNC5D,CLIC1,NCKAP1L,GAS6,PTPRA,PKP3,SLC7A1,LRFN3,TRAF6,EPHB1,SOX12,AKIP1,NPHP1,RET,HCK,TM9SF4,ZC3H8,FAM107A,IL1A,FER,PIK3CB,PIK3R1,CLSTN2,LPXN,CASP3,DENND6A,CTNND1,PARVA,ROBO1,ROBO2,TENM3,FMN1,ADGRV1,SORBS1,PTPRJ,TMEM131L,IL7,NCAM2,PAG1,JAM2,KIFC3,PLEKHA7,PTK2B,RASGRP1,RND1,TIAM1,RIPK2,DOCK5,CDH17,LOXL2,AP3B1,AMIGO2,CYTIP,AGGF1,TESC,MARCH7,WISP2,RREB1,SPARCL1,SPP1,DSP,SOX13,STK4,LRRN2,GCNT2,ALCAM,DMTN,ADTRP,NOD2,IGSF9B,CNTN1,ITGB6,VSIG10,LDB1,IGF2,PXN,ELMO2,NECTIN3,CD96,FAP,CD200,PKP2,CDON,SLK,CARMIL1	grey	VSMC_M10
GO:0045667	0.99	0.02	47	109	regulation of osteoblast differentiation	BP	1	GLI1,SMAD5,PTK2,PTCH1,ATF4,RORB,CDK6,SEMA4D,HOXA2,AREG,TRPM4,SOX9,ACVR2B,ACVR2A,JAG1,CLIC1,CEBPA,HAND2,MEF2C,VEGFC,HDAC7,BMPR1B,SUFU,TCIRG1,AXIN2,HDAC4,CHRD,MEN1,ESRRA,WNT4,SUCO,BMPR1A,PDLIM7,RIOX1,TOB1,CITED1,IL6R,SMAD3,TWSG1,RANBP3L,SKI,ATP6AP1,WDR63,MIR21,MIR27A,NOG,CEBPB	grey	VSMC_M10
GO:0002455	0.99	0.04	8	24	humoral immune response mediated by circulating immunoglobulin	BP	1	FOXJ1,HPX,NOD2,PTPN6,C7,C3,CD46,FCER2	grey	VSMC_M10
GO:0018393	0.99	0.02	59	134	internal peptidyl-lysine acetylation	BP	1	ATAT1,YEATS4,BRD1,SUPT3H,PHF14,KANSL3,ING3,ATG5,SPHK2,BMI1,IWS1,PAXIP1,TADA3,ARRB1,TAF7,EP400,TAF10,SDR16C5,TAF9,PHF20,KANSL2,LDB1,AUTS2,MRGBP,ING5,POR,MBIP,TADA2B,NAA40,ING4,TADA1,FOXP3,MSL1,MED24,KAT7,MUC1,TAF1,MAPK3,OGT,NAP1L2,CRTC2,RPS6KA5,SIN3A,JSL1,GLYR1,CREBBP,NAA60,HCFC1,MECP2,CHD5,PARK7,GTF3C4,CTCF,TAF12,CPA4,BEND3,SUPT7L,LIF,RPS6KA4	grey	VSMC_M10
GO:1902229	0.99	0.03	11	31	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	TRIM32,DDIAS,FBH1,TAF9,ING2,MARCH7,SNAI1,MUC1,TAF9B,CD74,PIAS4	grey	VSMC_M10

GO:0032640	0.99	0.02	48	111	tumor necrosis factor production	BP	1	TNFAIP3,AGER,TSPO,C6orf106,NOD1,TLR4,SPHK2,HDAC2,CSAR2,MYD88,MAVS,GAS6,FOXP1,NR1H4,IL1A,IL37,PIK3R1,PTPRJ,RASGRP1,OAS3,RIPK2,RIPK1,NOD2,IFIH1,HDAC1,MAPKAPK2,NFATC4,FZD5,VSIR,PTPN6,STAT3,FOXP3,AKAP8,TNFRSF8,SPON2,PSEN1,SYT11,ISL1,TICAM1,CYBA,MIR125B1,MIR27B,OAS1,FADD,WNT5A,IL33,C1QTNF4,HAVCR2	grey	VSMC_M10
GO:0032680	0.99	0.02	48	111	regulation of tumor necrosis factor production	BP	1	TNFAIP3,AGER,TSPO,C6orf106,NOD1,TLR4,SPHK2,HDAC2,CSAR2,MYD88,MAVS,GAS6,FOXP1,NR1H4,IL1A,IL37,PIK3R1,PTPRJ,RASGRP1,OAS3,RIPK2,RIPK1,NOD2,IFIH1,HDAC1,MAPKAPK2,NFATC4,FZD5,VSIR,PTPN6,STAT3,FOXP3,AKAP8,TNFRSF8,SPON2,PSEN1,SYT11,ISL1,TICAM1,CYBA,MIR125B1,MIR27B,OAS1,FADD,WNT5A,IL33,C1QTNF4,HAVCR2	grey	VSMC_M10
GO:1902042	0.99	0.03	9	26	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	1	TNFAIP3,RAF1,FAIM,FAIM2,PEA15,DDX3X,PARK7,MIR222,FGA	grey	VSMC_M10
GO:0051649	0.99	0.01	852	1679	establishment of localization in cell	BP	1	TIMM21,VPS4B,MYO1A,LRP1,STX7,AP3S1,KIF5A,PEX7,AGAP2,REPS1,PEX3,CANX,TBC1D30,TBC1D9B,PPP1R10,CPSF6,RAB21,SNCAIP,SNX31,CPT1B,PHAX,ZDHHC14,SYNJ2,SERAC1,RIMS2,PRKN,TAP1,KIF3A,TSPO,GOPC,VPS52,HSPA4,DERL1,UBE2B,BAK1,FAM91A1,WASHC5,LRRC6,GRM4,FAM53C,TSNARE1,EXOC4,SIL1,SYNGR1,MAPK15,AGTPBP1,SUN2,MAPK14,TOMM22,NRBP2,PLA2G6,COPG2,PICK1,MICALL1,TBC1D22B,BTBD9,RAC2,SMO,ZDHHC21,MYH9,IFT74,CHRNA3,CHRNA5,PEX6,FBXO7,NOL6,STEAP2,XPO5,WASHC4,APBA1,PEX1,USP46,VPS50,SCFD2,KIT,SLC1A1,TGFBRAP1,TBC1D8,TRAM2,RGP1,BICD2,CHMP2A,RAB23,DYNC2LI1,NLRP5,LRPPRC,SEC61B,STX17,SIX2,BRSK1,PRKCE,RIMS1,TMEM30A,HMGN3,YTHDC1,RIMS3,IBTK,RUFY3,PPT1,XPO1,SRSF10,BACH2,AFTPH,WDR91,TRAPPC12,PLEK,ITGB1BP1,DDC,YWHAZ,SEC61G,TRAPPC3,TCAF2,CDK5RAP2,VPS41,BVES,AMPH,STARD3NL,TBC1D9,CCDC155,VPS35,ATG5,SDCBP,MGARP,TRPM4,PPFIA3,LIN7B,WASF1,EPS15,AGK,BCAP29,TRAF3IP2,SPHK2,ANKRD50,SPRY1,GRIN2D,MTMR2,TTC26,DNAJC27,TRPC3,NAPA,BBS7,SLC8A2,RAB7A,PIP4K2A,AP2S1,KIF3C,ARHGAP21,RAB10,COPG1,KPNA3,MYO7B,ARL5B,CACNB2,IWS1,LCP1,SYTL2,KLC3,CLASP2,DLG2,RBSN,DNAJC15,PLK3,GAB2,MLH1,LLGL2,IPO13,AQP11,CCDC93,GRIK5,UNC13D,RAF1,ZFAND6,ATP5F1C,PIBF1,TBC1D4,IFT172,SCN5A,MYO7A,UBE2O,TTC21A,NAPB,GCKR,WDR60,SPRY2,SEC62,SEC22C,KPNA2,AKT2,PITRM1,HOOK3,ABCC4,TIMM50,SNX5,USP36,TBC1D16,AP3M2,KIF5C,MKKS,ANK1,DPY30,ACTG1,PURA,YIPF4,NPLOC4,ARL5A,SYT1,UBAC2,RAB5A,LIN7A,ASPSCR1,TMCO6,NUP98,SIRT7,RYR1,FERMT1,CHTOP,HACL1,HEATR5B,CE	grey	VSMC_M10
GO:0017038	0.99	0.02	79	174	protein import	BP	1	TIMM21,PEX7,PEX3,PPP1R10,HSPA4,FAM53C,MAPK14,TOMM22,SMO,PEX6,PEX1,RAB23,SIX2,ARHGEF5,TRAF3IP2,KPNA3,DNAJC15,IPO13,GCKR,KPNA2,TIMM50,TMCO6,NUP98,FERMT1,ING1,MAVS,NUP58,IPO11,PIK3R1,TNPO1,PEX2,PKIA,NUP54,PEX16,CRY2,PRICKLE1,LONP2,SUFU,CABP1,RPL23,PPP3CA,IPO9,HCLS1,HSPA8,AGT,BAG3,PEX19,TOMM40L,EIF4ENIF1,POM121,APOD,GRPEL1,FAM53A,STAT3,MAPK1,TIMM17B,PEX26,MED1,KPNB1,TARDBP,PEX14,PSEN1,RANBP17,RAB8B,TNPO2,SMAD3,LAMP2,EFCAB7,PAM16,PEX10,NUP214,NXT2,TIMM23B,HIKESHI,PTTG1IP,GRPEL2,ZIC1,PEX12,DNAJC19	grey	VSMC_M10
GO:0032691	0.99	0.05	4	14	negative regulation of interleukin-1 beta production	BP	1	TNFAIP3,SERPINB1,MIR27B,CPTP	grey	VSMC_M10
GO:0044344	0.99	0.02	36	86	cellular response to fibroblast growth factor stimulus	BP	1	FRS2,CXCL8,ITGB1BP1,FUZ,FGF21,SPRY1,NDNF,PRKD2,SPRY2,KL,FGFBP3,NR4A1,FGF5,DSTYK,HYAL1,SULF2,LRIT3,CPS1,WNT4,FLRT1,FGFR3,CHURC1,FGFR4,FGF18,NGFR,LHX1,CCL5,CCL2,FGF22,MIR339,NOG,WNT5A,SHISA2,ZFP36L2,FGF1,FRS3	grey	VSMC_M10
GO:0016567	0.99	0.02	322	656	protein ubiquitination	BP	1	NEDD4L,FEM1C,TRIM36,RMND5B,TNFAIP3,FBXO30,TRIM39,FBXO43,MARCH3,HSPA1B,TULP4,PRKN,RNF5,MED30,TSPO,DERL1,SKP1,UBE2B,RNF217,RNF146,KLHL3,UHRF2,ZC3HC1,FBXL6,FBXO7,KLHDC3,ASB15,CRY1,NFX1,DCAF12,LNX1,FBXO10,DCAF10,SVBP,DNAJA1,RNF20,PRKCE,ASB3,UBE3D,FANCL,PELI1,CNOT4,BSPRY,HECW1,TRIM32,FBXW2,TRAF1,HACE1,NOSIP,ATG5,TRAF3IP2,BMI1,LRRC41,FBXL2,KBTBD6,KCTD21,TRIM54,CAND2,UBE2E2,PAXIP1,WDR48,UBE2O,MYCBP2,UBE3C,SPOPL,FBH1,ASB13,MED8,SPRY2,UBE2E1,KLHL40,CCNB1IP1,ARRB1,RNF169,FBXO17,NMI,SIRT7,TPP2,NHLRC3,RNF24,RNF14,RNF122,USP44,SH3RF2,UBOX5,RYBP,TRIM3,KBTBD8,LNX2,TRAF6,TRIM44,MARCH8,TRIB3,ERCC8,FAM107A,HECTD2,KCTD6,DTX4,SPSB4,ZFP91,RNF181,RNF7,UBE2L6,TRPC4AP,FBXW7,TRIM2,HLTF,ENC1,ANAPC5,ANAPC7,KLHL2,DDB2,RIPK2,OTULIN,ASB8,AMFR,RNFT2,FBXO21,WDSUB1,VPS18,MARCH7,TTC3,NEURL2,HERC6,PRICKLE1,HERC5,NOD2,PRMT3,TRIM45,HERC2,WSB2,MYLIP,SIAH1,MAGEL2,NHLRC1,FBXL15,DCAF1,RNF144B,FBXO25,DZIP3,MED10,RNF10,PCGF6,KLHL12,NEURL1,RPL23,HECW2,PEF1,KLHL42,PDCD6,RNF115,RNF123,KLHL25,RNF114,AC013489.1,SPRTN,KLHL24,ASB11,DTX3L,ZNRF3,ABCB11,ARIH2,RNF26,CBL,TRAF5,PER2,ASB1,PELI3,RNF215,TRIM52,DCAF7,RNF185,RNF168,RNF214,BTBD1,RPL11,SENP2,NFE2L2,IVNS1ABP,PHC1,SYVN1,FBXO33,BCOR,KLHDC1,DDX3X,COP1,FBXO24,ATXN7L3,ASB16,RC3H1,SPSB2,KLHL20,TRIM9,UBAS2,RNF4,RNF25,ZSWIM8,SOCS4,TMEM129,PINK1,MUL1,BIRC3,LZTR1,DNAJB2,DCAF6,PPIL2,LEO1,RNF167,FBXL14,RNF216,PHF23,GPS2,NEURL4,MED24,DDB1,PRPF19,ANA	grey	VSMC_M10
GO:2000134	0.99	0.02	22	56	negative regulation of G1/S transition of mitotic cell cycle	BP	1	FBXO7,PLK3,PRKDC,PLK2,FAM107A,PIDD1,PKD2,CCND1,GIGYF2,CHEK2,CDKN1B,DLG1,MUC1,DCUN1D3,CCL2,FBXO31,MIR29A,PLK5,RPS27L,SOX4,APC,CRADD	grey	VSMC_M10

GO:0007417	0.99	0.02	391	795	central nervous system development	BP	1	NME1,LRP1,GLI1,ATAT1,FRS2,RIDA,STK3,SYNJ2,FZD6,PRKN,AGER,UQCRQ,CCDC134,BAK1,XRCC6,PITX1,PTCH1,FANCC,AGTPBP1,PLXNA4,SUN2,NTRK2,CSNK1E,SOX10,CKB,SMO,DAAM2,RBFOX2,SRF,TTBK1,ADAM22,FZD1,CDK6,SLC1A1,TNFRSF21,ROR2,DLX5,EFHC1,CCIN,ADGRL3,SEMA4C,MBOAT7,RTN4,FPR2,UTP3,HOXA2,PPT1,AQP1,MTF1,EPHA7,AKNA,WHRN,PTN,FOXP2,CTTNBP2,POU3F3,EGFR,TLR4,CDK5RAP2,MYCN,NRCAM,SLC7A11,FOXO3,ARMC4,INTU,SPHK2,FAT4,SPATA5,KDM7A,GRIN2D,HDAC2,NAPA,BBS7,BMI1,NDNF,C5AR1,VSTM5,SOX9,HDAC11,EED,ERCC2,EIF2B3,XRCC1,GLI2,B4GALT2,KDM4A,TIMP4,IFT172,FOXJ1,SCN5A,MYCBP2,NUMBL,MNX1,HNMT,POU4F1,TSKU,SZT2,ALK,HOOK3,TGFBR2,EOMES,CHD8,SIRT2,MKKS,AATK,RARB,SYT1,ZIC5,PLCB1,RAC3,BTD,CEP290,SEMA3A,NRG1,WRN,PRKDC,RYK,SNPH,DHX37,EPHB1,SOX12,MAL,LSR,TOX,ZSWIM6,PAX8,ACVR1B,NCOA6,CASP3,CTND1,CLP1,DCLK2,ROBO1,ROBO2,ZIC4,FZD3,ELP3,FAIM2,HTRA2,NDUFS3,CELF1,CSNK2A2,MCPH1,SOX6,RAPGEF2,DPYSL2,NNAT,SLIT1,SYNJ1,TENT2,NKX6-1,TRIO,NR4A2,AMIGO2,SLC38A2,RPGRIP1L,PKD2,SOX13,STK4,TFAP2A,PAX2,TSPAN2,SALL1,DNAH5,CNTN1,ZNF335,JARID2,DPCD,ATXN1,SUDS3,ZNF423,LDB1,COX6B1,SUFU,SRGAP2C,SLC4A10,SRD5A1,ALDH5A1,INA,TAGLN3,NEURL1,CFAP43,SLC6A3,HDAC1,ALDH1A3,PPP3CA,PGAP1,SLC38A3,SEMA3F,SATB2,COX17,ADARB1,DAG1,TTBK2,AMIGO3,SHROOM2,KRAS,PITPNM1,GIGYF2,EGF,HAPLN3,TTC21B,SOX2,ZFHX2,JHY,DISC1,GNPAT,B3GNT5,GBX2,ATP1A2,BAG3,KALRN,SPTBN2,UFC1,MACO1,CHRD,DLX1,DNAJC30,GRHL3,EPHB3,DHX30,NSUN5,SH3GL3,APOD,SETD2,WNT3,CREB	grey	VSMC_M10
GO:2000209	0.99	0.04	6	20	regulation of anoikis	BP	1	PTK2,NTRK2,SIK1,CHEK2,MCL1,ZNF304	grey	VSMC_M10
GO:0048858	0.99	0.02	249	520	cell projection morphogenesis	BP	1	NEDD4L,LRP1,SEMA6A,KIF5A,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,SULT4A1,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,CPNE5,RAC2,SMO,RBFOX2,CHRNA3,SRF,SEMA4D,DLX5,ETV1,SEMA4C,BRSK1,RIMS1,RTN4,RUFY3,SHANK1,HOXA2,EPHA7,PTN,EGFR,HECW1,EPHA1,KEL,NRCAM,NTF4,WASF1,PLXNA1,RAB10,ABI1,GOLGA4,GLI2,MEGF8,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,CPNE9,FARP1,KIF5C,SYT1,TMEM106B,FEZ2,SLC23A2,ARHGEF7,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NCKAP1L,ULK1,RYK,EPHB1,RET,TTL,ANKRD27,PREX2,ROBO1,ROBO2,FZD3,SEMA4F,TLX2,CUX2,RAPGEF2,DPYSL2,EIF2AK4,TIAM1,SLIT1,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,SEMA3G,RREB1,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,SEMA4G,ZNF335,DTNBP1,TAOK3,SIAH1,LZTS1,BMPR1B,BDNF,DOCK10,KIAA0319,LGR6,DNM1L,PPP3CA,HECW2,CAPRIN2,SEMA3F,GAP43,ADARB1,DAG1,AUTS2,LHX9,CFL1,ADNP,DISC1,WASF2,GBX2,DVL3,KALRN,NFATC4,SS18L1,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,TANC2,CSPG5,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,SEMA6D,EPHB4,ITGA4,TNR,FN1,NCKAP1,NYAP1,ATL1,NIN,FLRT1,DNM3,PPP3CB,CNTNAP1,RAB3A,MARK2,MUL1,VCL,OBSL1,MINK1,RAB8A,CRMP1,EPHA4,LRTM2,DLG4,ACTB,DVL2,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,SNX1,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,NTN1,GAS7,RPS6KA5,RNF165,MYO9A,DNM2,PARP6,GPRASP2,BHLHB9,BCL11B,LHX1,ARHGAP44,SIN3A,TRPV2,LAMA3,CDK5R1,ISL1,EMB,EPB41L3,LAMA1,DOCK7,TAOK1,SLC9A6,DAB1,SLITRK2,LRP8,L1CAM,NTN3,PRKCZ,ARHGAP4,PLXNA3,BSG,TUBB3,AMIGO1,CELSR2,	grey	VSMC_M10
GO:1903844	0.99	0.02	44	104	regulation of cellular response to transforming growth factor beta stimulus	BP	1	ONECUT2,SNW1,PPARA,CD109,SDCBP,SPRY1,SPRY2,EID2,FERMT1,SPRED3,SNX25,DKK3,ING2,IL17RD,VEPH1,SLC2A10,HTRA1,DLX1,SNX6,PBLD,MEN1,HTRA3,FBN1,PPM1A,MPP5,RNF111,TGFB1I1,ITGA3,CITED1,WFIKKN2,SMAD3,DNM2,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,MIR21,LEMD3,NRROS,LDLRAD4,PEG10	grey	VSMC_M10
GO:0045943	0.99	0.04	7	22	positive regulation of transcription by RNA polymerase I	BP	1	MARS,ATF4,IPPK,RASL11A,HEATR1,DDX11,PHF8	grey	VSMC_M10
GO:0045732	0.99	0.02	93	203	positive regulation of protein catabolic process	BP	1	NEDD4L,LRP1,TNFAIP3,HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,HECW1,TRIM32,HACE1,VPS35,ZYG11B,FAF1,BBS7,RAB7A,SOX9,PLK3,SUMO2,EGLN2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,TRIB3,PLK2,CEBPA,IDE,SH3D19,FBXW7,PTK2B,RNFT2,KCNE2,PRICKLE1,NKD1,MYLIP,RNF144B,GPLD1,LPCAT1,HECW2,SEC22B,ADRA2A,USP13,AC013489.1,EGF,DISC1,SORL1,ASB11,ARIH2,RNF185,CDKN1B,ADAM8,NSF,NFE2L2,COP1,SOCS4,DNAJB2,STX5,DDB1,TNFRSF1B,PSMC3,OSBPL7,PSEN1,AREL1,SNX1,TAF1,LDLR,KEAP1,RNF128,PSMD10,FBXO22,GPC3,FMR1,RILP,FZR1,BCAP31,SGTA,OAZ1,APC2,TMEM259,ZER1,WWP2,DAB2IP,PSMC1,BAG2,RNFT1,WNT5A,APC,PTTG1IP,DDA1	grey	VSMC_M10
GO:0007163	0.99	0.02	85	189	establishment or maintenance of cell polarity	BP	1	MAP7,PARVG,PTK2,RAC2,MYH9,TEK,PTK7,BRSK1,RUFY3,AQP1,CDK5RAP2,LIN7B,TRAF3IP2,SPRY1,RAB10,CLASP2,DLG2,FRMD4A,LLGL2,FBF1,FOXJ1,SPRY2,WNT11,ANK1,FSCN2,LIN7A,FERMT1,RAC3,SPINT2,NCKAP1L,FRMD4B,SYNE4,NSFL1C,TCF15,EPHB1,MOS,PARVA,MCPH1,PTK2B,RND1,RHOBTB2,RPGRIP1L,CAP2,GBF1,TCIRG1,RAB11FIP2,SLC9A1,SNX27,KIAA1614,CLIC4,RHOBTB1,DLG1,RAP1B,HTT,MARK2,CYTH3,SDCCAG8,ACTB,ARHGEF11,SYNJ2BP,DOCK2,NDEL1,WWC1,MYO9A,BCAS3,CDC42BPB,AMOT,CAMSAP3,LAMA1,IFT20,DOCK7,CRK,PRKCZ,PKD1,SAPCD2,GPSM2,FOXF1,CARMIL2,CAP1,RHOA,OOEP,PDZD11,RND3,WNT5A,PARD6A	grey	VSMC_M10
GO:0017015	0.99	0.02	43	102	regulation of transforming growth factor beta receptor signaling pathway	BP	1	ONECUT2,SNW1,PPARA,CD109,SDCBP,SPRY1,SPRY2,EID2,FERMT1,SPRED3,SNX25,DKK3,ING2,IL17RD,VEPH1,SLC2A10,HTRA1,SNX6,PBLD,MEN1,HTRA3,FBN1,PPM1A,MPP5,RNF111,TGFB1I1,ITGA3,CITED1,WFIKKN2,SMAD3,DNM2,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,MIR21,LEMD3,NRROS,LDLRAD4,PEG10	grey	VSMC_M10

GO:0007007	0.99	0.03	13	35	inner mitochondrial membrane organization	BP	1	AGK,CHCHD6,IMMT,MTX3,OPA1,PINK1,ADCK1,TIMM29,MAIP1,C19orf70,MINOS1,TIMM10B,TIMM8B	grey	VSMC_M10
GO:0031329	0.99	0.02	339	689	regulation of cellular catabolic process	BP	1	PAN2,LRP1,PIP4K2C,TNFAIP3,EPM2A,TRIM39,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,DXO,PNLDC1,PRKN,RNF5,PPARA,TSPO,RNF217,CSDC2,AL096711.2,TRIB1,AGO2,PRXL2C,PTK2,TNRC6B,EXOC4,TUT7,MAPK15,AGTPBP1,GTPBP1,MAPK14,NRBP2,CSNK1E,HSF1,TFEB,FBXO7,DCAF12,SPTLC1,GAPDH,RGP1,PDCL3,EXOSC3,LRPPRC,ATP6V1E2,RAD23B,PNPT1,SLC4A4,XPO1,NOD1,RRAGD,WDR91,MET,ATP6V1C2,VPS35,SCOC,ZYG11B,SDCBP,TUT4,FOXO3,PUM2,MFSD8,FAF1,FGF21,TRAF3IP2,MTMR2,ZC3HAV1,SESN3,BBS7,DHX34,PIP4K2A,NUDT15,ABHD5,ATP6V0E2,APOC1,FBXL2,PLK3,SUMO2,FASTK,OPTN,MLH1,RALB,ATP6V0B,KDM4A,AQP11,MYD88,TIMP4,TNRC6C,PPP1CB,KLHL40,AKT2,SNX5,USP36,SIRT2,RPTOR,TMEM173,FEZ2,LSM1,DCN,RNF14,DDRGK1,SH3RF2,RYBP,ULK1,PKP3,PPP1R3B,PAN3,PSMF1,ATP6V1H,TRIB3,PLK2,DEPP1,DRAM1,CEBPA,PIK3CB,CASP3,TAF9,SH3D19,MTMR9,FBXW7,USP25,GPD1,HTRA2,P2RX7,CNOT1,CELF1,CSNK2A2,PTK2B,CNOT6L,FAM192A,RIPK2,TPCN1,TENT2,WDR41,RNFT2,TP53INP1,FTO,MARCH7,KCNE2,PRICKLE1,NOD2,TENT5C,MYLIP,TENT4B,RBM24,LONP2,LZTS1,ATP6V1B2,RNF144B,SUFU,GPLD1,IRS1,RPL23,DNM1L,SEC22B,CPT1A,CISD2,ZBTB20,ADRA2A,TMEM39A,DHRSX,GPR137B,USP30,DIS3L2,AXIN2,MAPKAPK2,USP13,GIGYF2,AC013489.1,EGF,USP19,YTHDF2,DISC1,SORL1,ATG16L1,PSME1,DTX3L,ABCB11,SH3BP4,ARIH2,MCL1,TRAF5,ARNT,BAG3,CISD1,PPP1R3D,FASTKD1,ANGEL2,MTMR3,RUBCN,YTHDF1,IL10RA,MLXIPL,RNF185,EIF4ENIF1,RPL11,SNX6,SNX32,LRIG2,YBX3,ADAM8,NFE2L2,FZD5,MAPT,TAB3,VPS26A,SUPV3L1,ABL2,TYSND1,COP1,TBC1D14,RC3H1,GPR137,DDX49,UPF1,SLC1	grey	VSMC_M10
GO:0061077	0.99	0.02	22	55	chaperone-mediated protein folding	BP	1	HSPA1B,BAG1,PDCL3,HSPE1,CRTAP,DNAJC18,HSPA8,UNC45A,PEX19,DNAJC5,DNAJB12,DNAJB2,SDF2L1,DNAJB1,GAK,CD74,UNC45B,SGTA,TOR1B,TOR2A,HSPA5,SDF2	grey	VSMC_M10
GO:0051028	0.99	0.02	47	109	mRNA transport	BP	1	QKI,ZC3H3,HSF1,BICD2,LRPPRC,IGF2BP3,YTHDC1,XPO1,IWS1,KIF5C,NUP98,CHTOP,UPF3A,THOC7,NUP58,CETN3,NUP54,MX2,DDX25,NCBP2,POM121,SENP2,IGF2BP2,SETD2,ENY2,UPF1,PARP11,NXF1,AHCTF1,AKAP8L,CASC3,FYTTD1,SMG5,RANBP17,ALKBH5,UPF3B,THOC2,SUPT6H,FMR1,NCBP3,NUP214,DDX19A,SARNP,DDX19B,NXT2,NUPL2,MAGOHB	grey	VSMC_M10
GO:0046640	0.99	0.04	7	22	regulation of alpha-beta T cell proliferation	BP	1	TGFBR2,RIPK2,CD28,VSIR,RASAL3,ZBTB7B,TWSG1	grey	VSMC_M10
GO:0070301	0.99	0.02	33	79	cellular response to hydrogen peroxide	BP	1	MAP3K5,TNFAIP3,MAPK13,HSF1,GPR37,AQP1,ZNF277,MET,FOXO3,HDAC2,PAWR,RIPK1,PAX2,PDE8A,NFE2L2,PDCD10,PINK1,ANKZF1,KDM6B,MAPK7,STK26,PARK7,LCN2,NQO1,MIR21,GPR37L1,ZNF580,IMPACT,FXN,TXN,CBX8,PPIF,PDGFD	grey	VSMC_M10
GO:0032989	0.99	0.02	294	609	cellular component morphogenesis	BP	1	NEDD4L,LRP1,SEMA6A,TBPL1,KIF5A,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,SULT4A1,FSTL4,SYNGAP1,OBSCN,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,CPNE5,RAC2,SMO,RBFOX2,CHRNA3,LMOD2,SRF,PGM5,SEMA4D,DLX5,ETV1,SEMA4C,TMOD1,BRSK1,RIMS1,RTN4,PNPT1,RUFY3,SHANK1,HOXA2,MYH14,EPHA7,PTN,EGFR,HECW1,EPHA1,KEL,MYLK3,NRCAM,NTF4,FIG4,WASF1,SSBP1,PLXNA1,MTMR2,RAB10,ABI1,ERCC2,CLASP2,NECTIN2,GOLGA4,GLI2,MEGF8,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,CPNE9,FARP1,KIF5C,ACTG1,SYT1,TMEM106B,FEZ2,SLC23A2,ARHGEF7,SEMA3D,PANK2,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NCKAP1L,ULK1,LMOD3,RYK,EPHB1,RET,TTL,ANKRD27,PREX2,ROBO1,ROBO2,FZD3,SEMA4F,TLX2,CUX2,RAPGEF2,DPYSL2,EIF2AK4,TIAM1,SLIT1,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,COL4A3BP,SEMA3G,RREB1,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,SEMA4G,ZNF335,DTNBP1,TAOK3,SIAH1,LZTS1,BMPR1B,BDNF,DOCK10,KIAA0319,LGR6,DNM1L,LMOD1,PPP3CA,HECW2,CAPRIN2,SEMA3F,GAP43,PRKAR1A,ADARB1,DAG1,AUTS2,LHX9,CFL1,ADNP,POLG2,DISC1,ANK2,GNPAT,WASF2,GBX2,DVL3,ACTC1,KALRN,NFATC4,MYOZ2,CASQ1,TMOD4,PHLDB1,SS18L1,LAMA5,YTHDF1,PTPRO,CDKL5,EPHB3,TANC2,NUBPL,CSPG5,WNT3,KLF7,CREB1,MYPN,SPG11,MAPT,PIKFYVE,FIS1,SUPV3L1,SEMA6D,TTN,EPHB4,ITGA4,TNR,FN1,NCKAP1,NYAP1,ATL1,NIN,FLRT1,DNM3,PPP3CB,MYOZ1,CNTNAP1,RAB3A,MARK2,MUL1,VCL,TMOD2,OBSL1,MINK1,RAB8A,CRMP1,EPHA4,LRTM2,DLG4,ACTB,LDB3,DVL2,MPP5,TCAP,UNC5A,PSEN1,SEMA4A,NGFR,NLGN3,TAOK2,SNX1,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,SOX	grey	VSMC_M10
GO:0031503	0.99	0.02	84	186	protein-containing complex localization	BP	1	STX7,KIF5A,WASHC5,IFT74,ADAM22,NOL6,USP46,SLC1A1,DYNC2LI1,YTHDC1,XPO1,VPS35,EPS15,TTC26,IWS1,DLG2,RALB,IFT172,TTC21A,WDR60,KIF5C,PURA,CHTOP,ANKS1B,THOC7,TUB,KIF3B,ATR,IFT81,SDAD1,IFT52,DDX25,DAG1,TTC21B,NOP9,AP2M1,TRAF3IP1,CNIH2,DLG1,SETD2,CALY,TTC30A,ENY2,UPF1,DNM3,KIF17,NXF1,NSG1,GRIPAP1,RAB8A,DLG4,AKAP8L,WDR19,IQSEC2,FYTTD1,GPHN,SYNJ2BP,CPLX1,STX1B,SMG5,RAB11A,SNAPIN,SFPQ,ARHGAP44,TNFAIP2,AP2B1,ALKBH5,THOC2,IFT20,SUPT6H,HSPB11,PRKCZ,KLHL21,TSC1,NUP214,DDX19A,TERF2,SARNP,DDX19B,CEP112,CACNG7,HRAS,CACNG5,EXOC3L4	grey	VSMC_M10
GO:0006997	0.99	0.02	48	112	nucleus organization	BP	1	VPS4B,BAZ2A,NEMP1,TBPL1,LEMD2,HABP4,H3F3C,GOLM1,SUN2,CHMP2A,RTN4,LPIN1,NECTIN2,USP36,SIRT2,NUP98,NSFL1C,ATXN7,CHMP2B,SPAG4,CHMP4C,NUP54,CHMP7,SYCP1,DYRK3,GPER1,TOR1AIP1,CELF3,WDR73,PARP11,DDX11,AHCTF1,AKAP8L,PHF8,WRAP53,TARDBP,NDEL1,PRKCB,AFF2,CHD5,CHMP1A,TOR1B,MFSD14A,VPS4A,SYCP3,LEMD3,BEND3,RNF8	grey	VSMC_M10

GO:0018107	0.99	0.02	41	98	peptidyl-threonine phosphorylation	BP	1	TTBK1,PRKD2,PRKAG2,OXSR1,SPRY2,DYRK1B,TGFBR2,SIRT2,RPTOR,ULK1,PRKDC,ACVR1B,CSNK2A2,RIPK2,DMTN,DCAF1,DYRK3,EGF,GRK2,TSSK4,STOX1,CEMIP,MARK2,MAPK1,WNK3,DGKQ,TAF1,MAP2K1,SBK1,CALM1,PRKCB,CDC42BPB,CAMK2A,CDK5R1,NLK,INPP5K,PDPK1,CDK10,IRGM,WNT5A,CADM4	grey	VSMC_M10
GO:0002701	0.99	0.04	7	22	negative regulation of production of molecular mediator of immune response	BP	1	PRKDC,TMBIM6,CD96,TGFB2,BCL6,FOXP3,TBX21	grey	VSMC_M10
GO:0006979	0.99	0.02	171	357	response to oxidative stress	BP	1	ADNP2,MAP3K5,TNFAIP3,HSPA1B,PRKN,NDUFA6,BAK1,NCOA7,ERCC6L2,FANCC,ATF4,MAPK13,TXN2,HSF1,GPR37,FBXO7,SLC1A1,ERMP1,PRDX1,CAT,EPAS1,PNPT1,VRK2,AREG,AQP1,PXDN,MTF1,ZNF277,MET,EGFR,TLR4,UCP1,SLC7A11,FOXO3,DHFR,HDAC2,SESN3,MSRB2,ERCC1,NUDT15,ERCC2,ERCC3,PLK3,XRCC1,OXSR1,PRDX3,CYGB,SIRT2,PAWR,NDUFS8,SLC23A2,PRNP,BTG1,BRF2,NDUFA12,PDK1,WRN,PPP2CB,RBPMS,ARL6IP5,ERCC6,STX2,PXDNL,ERCC8,ACOX2,FER,C19orf12,GSS,CASP3,DIABLO,ARNTL,FBXW7,MSRA,HTRA2,SCARA3,TLDC2,PTK2B,ETFDH,GPX8,NR4A2,RIPK1,TP53INP1,ABCC2,PKD2,PLA2R1,PAX2,PXN,GLRX2,HDAC1,HYAL1,FBLN5,NDUFB4,PSMB5,STAU1,NCF1,MCL1,ARNT,PYROXD1,NDUFS2,PDE8A,MGMT,APOD,NFE2L2,MAPT,DUOX1,NONO,STOX1,PRKRA,PRODH,PDCD10,GCH1,PINK1,MMP3,ANKZF1,PTPRN,CD38,MAPK1,RAD52,ATP13A2,SCGB1A1,LIAS,PARP1,CLN8,RGS14,SOD3,STX4,PSEN1,KDM6B,FOS,MAPK3,THG1L,MPO,SFPQ,BTK,KEAP1,NEIL1,SIN3A,MAPK7,PPARGC1B,LONP1,STK26,JUN,CRK,PARK7,TSC1,TLDC1,LCN2,MAPKAP1,NQO1,MIR21,MT-ND1,MT-ND6,NFE2L1,ZNF622,PJVK,NOL3,GPR37L1,DHRS2,ZNF580,IMPACT,FXN,DUSP1,HBA2,TXN,RBM11,APOPT1,NUDT2,NAPRT,CBX8,PPIF,PDGFD	grey	VSMC_M10
GO:0150105	0.99	0.04	6	20	protein localization to cell-cell junction	BP	1	ACTG1,LSR,DSP,VCL,ACTB,JAK1	grey	VSMC_M10
GO:0031100	0.99	0.02	23	58	animal organ regeneration	BP	1	GLI1,IGF2R,BAK1,PTCH1,PPAT,PNPT1,EGFR,LPIN1,C5AR1,LCP1,TGFBR2,GAS6,CSNK2A2,CCND1,CPT1A,SULF2,MED1,RPL19,PGF,MT-CYB,CLDN1,NNMT,CEBPB	grey	VSMC_M10
GO:0009991	0.99	0.02	184	385	response to extracellular stimulus	BP	1	MARS,MAP3K5,CYP27B1,TPH2,SNW1,PPARA,TNFRSF11B,TSPO,ATF4,PICK1,PIM1,TXN2,HSF1,TFEB,SLC39A4,GPT,SRF,NUAK1,ABCG5,CAT,ABCG8,BRSK1,ALB,BMP8A,RRAGD,NR1H2,PTN,TNC,EGFR,VPS41,IL15,UCP1,ATG5,FOXO3,FGF21,KPTN,SESN3,DNMT3A,FOXA3,GIPR,ERCC1,NUDT15,DNAJC15,RALB,KDM4A,PRKAG2,SZT2,WNT11,TGFBR2,SIRT2,MKKS,RPTOR,RASGRP4,EIF2AK2,WRN,GAS6,LARS,ULK1,NR1H4,USF2,FAM107A,DNMT3B,AHCY,GSS,PRKAG1,EIF2AK4,VDR,STC1,OPA1,NR4A2,SLC38A2,ACVR1C,SPP1,PAX2,NOD2,SIRT5,CD40,NUAK2,NUPR2,SRD5A1,DNM1L,CBSL,GLRX2,SIK1,CCND1,SLC38A3,CPT1A,TRPV4,DAD1,KCNB1,ADNP,AMELX,HSPA8,SORL1,GNPAT,CBL,CIDEB,MTMR3,UCN2,USF1,XPR1,TBL2,HMGCL,GLUL,MGMT,SLC16A1,POR,NFE2L2,SORD,FIS1,VGF,CPS1,ITGA4,SIK2,COMT,SERPINC1,BCHE,WNT4,ALPL,GDF15,PRKAG3,CTSV,MAPK1,BHLHA15,WIPI2,MAX,MED1,ALDH1A2,RRAGB,BNIP1,ZFYVE1,FOXO4,PKLR,FOS,MAPK3,OGT,MPO,TNRC6A,LDLR,LARP1,SCNN1B,BCAS3,NMUR2,ADSSL1,SREBF1,LAMP2,SGIP1,NIM1K,GHR,OXCT1,STK26,JUN,CLEC16A,MBD1,TRPV1,KIAA1324,CYBA,TSC1,ASS1,TLDC1,AGL,LCN2,SLC25A25,WDR59,HSPA5,DHODH,SH3GLB1,NQO1,BCL10,RIPOR1,HSD11B2,ACADM,MIR125B1,MT-CYB,SETDB1,TRIM24,SLC6A19,BGLAP,PEMT,IMPACT,DDIT3,LRAT,UPP1,RNF152	grey	VSMC_M10
GO:0051236	0.99	0.02	61	138	establishment of RNA localization	BP	1	CPSF6,PHAX,QKI,ZC3H3,HSF1,NOL6,XPO5,BICD2,LRPPRC,IGF2BP3,YTHDC1,PNPT1,XPO1,IWS1,TGFBR2,KIF5C,NUP98,CHTOP,UPF3A,THOC7,NUP58,ATR,CETN3,NUP54,MX2,DDX25,RFTN2,RTRAF,NCBP2,SIDT2,POM121,SENP2,IGF2BP2,SETD2,ENY2,UPF1,PARP11,NXF1,AHCTF1,AKAP8L,CASC3,FYTTD1,SMG5,RANBP17,NRDE2,ALKBH5,UPF3B,THOC2,SUPT6H,FMR1,NCBP3,TSC1,NUP214,DDX19A,SARNP,DDX19B,NXT2,NUPL2,YBX1,MRPL18,MAGOHB	grey	VSMC_M10

GO:0010608	0.99	0.02	234	480	posttranscriptional regulation of gene expression	BP	1	ZC3H10,PAN2,SHMT2,HBS1L,TSFM,RMND1,ESR1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,PHAX,DXO,MOV10L1,EIF3E,PNLDC1,QKI,MRPL13,CSDC2,JMJD4,AGO2,HABP4,TNRC6B,ATF4,TUT7,MAPK14,XPO5,NCK2,GAPDH,CNOT11,EXOSC3,RPS14,TDRD7,LRPPRC,IGF2BP3,YTHDC1,MTIF2,PNPT1,PUS10,SNIP1,AGO1,EGFR,ASCC3,MYCN,C6orf203,TUT4,FOXO3,PUM2,TRAF3IP2,DHFR,EEFSEC,MKNK1,CNBP,FASTK,MLH1,CDC123,MTRF1,DPH2,MYD88,TNRC6C,AKT2,PURA,DPH3,EIF2AK2,LSM1,EIF4E3,UPF3A,PRKDC,KBTBD8,PAN3,C12orf65,CLP1,MRPS27,ENC1,BCDIN3D,CNOT1,CELF1,USP16,PTK2B,CNOT6L,MAPKAPK5,EIF2AK4,EIF4E2,NSUN3,TENT2,PAIP2B,RIPK1,FTO,GCNT2,CYFIP1,TENT5C,TENT4B,RBM24,NEURL1,RPUSD4,DDX25,PPP3CA,BANK1,CAPRIN2,TERT,DIS3L2,AXIN2,AJUBA,RCC1L,KLHL25,MAPKAPK2,GIGYF2,RPS6KB2,YTHDF2,TRNAU1AP,PARP9,TRAF5,FASTKD1,ANGEL2,RPS6KA1,PER2,DDX6,RPS4X,MTG2,YTHDF1,PASK,CD28,UHMK1,NCBP2,EIF4ENIF1,NSUN5,IGF2BP2,YBX3,PRKRA,EIF4EBP2,DDX3X,RC3H1,DDX49,UPF1,SLC11A1,COA3,RBM10,SAMD4A,PINK1,STAT3,MAPK1,POLR2G,SCGB1A1,NT5C3B,DCP1B,YBX2,CASC3,TNFRSF1B,ZCCHC4,FXR2,TARDBP,MAPK3,TOB1,EIF3C,ALKBH1,MAP2K1,TENT5D,SMAD3,NRDE2,TNRC6A,LARP6,CNOT8,LARP1,NCOR1,TCOF1,CCL5,SHMT1,ALKBH5,UPF3B,PARN,DROSHA,FMR1,DPH1,METTL16,PLEKHN1,CIRBP,TRAF2,TSC1,SPOUT1,AARS,BARHL2,MIRLET7A2,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR425,MIR125B1,MIR32,MIR22,MIR27B,MIR24-1,MIR7-1,MIR199A2,MIRLET7D,MIR27A,MIR23B,MIR365B,MIR25,MIR491,MIR24-	grey	VSMC_M10
GO:0030539	0.99	0.04	5	17	male genitalia development	BP	1	HSD17B3,ROR2,HOXA13,SRD5A1,ASB1	grey	VSMC_M10
GO:0061614	0.99	0.02	18	48	pri-miRNA transcription by RNA polymerase II	BP	1	PPARA,SRF,FOXO3,SOX9,KLF5,TERT,TGFB2,NFATC4,HDAC4,STAT3,BMPR1A,NGFR,FOS,SMAD3,YY1,MRTFB,JUN,NFATC3	grey	VSMC_M10
GO:0006084	0.99	0.03	10	29	acetyl-CoA metabolic process	BP	1	PPCS,DLD,PDK1,PDHX,ACOT12,PDK3,MPC2,ACACA,PIPOX,MLYCD	grey	VSMC_M10
GO:0045184	0.99	0.01	705	1395	establishment of protein localization	BP	1	TIMM21,VPS4B,LRP1,STX7,AP3S1,KIF5A,PEX7,TNFAIP3,AGAP2,PEX3,CANX,TBC1D30,TBC1D9B,PPP1R10,RAB21,SNX24,SNX31,PHAX,ZDHHC14,SLC12A2,RIMS2,EMC2,PRKN,TAP1,KIF3A,TSPO,GOPC,VPS52,HSPA4,DERL1,FAM91A1,WASHC5,FAM53C,PTP4A3,TSNARE1,EXOC4,SIL1,SYNGR1,MAPK14,TOMM22,PLA2G6,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,SMO,ZDHHC21,TOMM6,MYH9,PEX6,POT1,FBXO7,XPO5,WASHC4,APBA1,PEX1,VPS50,SCFD2,RFX3,SLC1A1,TGFBRAP1,TFAP2B,TBC1D8,TRAM2,BICD2,CHMP2A,RAB23,SVBP,SEC61B,STX17,SIX2,DNAJA1,PRKCE,RIMS1,TMEM30A,SPTBN1,HMGN3,RUFY3,CYB5R4,EMC10,PPT1,SNX14,XPO1,SNX30,BMP8A,EHBP1,AFTPH,PLEK,RSAD2,NR1H2,WHRN,ITGB1BP1,YWHAZ,SEC61G,EGFR,FUZ,ARHGEF5,TLR4,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,TRPM4,SLC7A11,LIN7B,EPS15,APOB,AGK,BRAF,BCAP29,TRAF3IP2,ANKRD50,TTC26,DNAJC27,NAPA,BBS7,RAB7A,AP2S1,RAB10,COPG1,KPNA3,GIPR,ARL5B,LCP1,SYTL2,COG1,DLG2,CUBN,RBSN,DNAJC15,PLK3,FRMD4A,OPTN,GOLGA4,LLGL2,IPO13,STEAP3,AQP11,CCDC93,RAF1,ZFAND6,TBC1D4,MYO7A,NAPB,GCKR,EMC3,SEC62,SEC22C,KPNA2,AKT2,PITRM1,LRP1B,HOOK3,ARRB1,TIMM50,SNX5,USP36,TBC1D16,AP3M2,KIF5C,FCHSD2,RINL,ATG16L2,NPLOC4,ARL5A,UBAC2,RAB5A,LIN7A,APBB3,ASPSCR1,TMCO6,NUP98,DPH3,SIRT7,FERMT1,HACL1,HEATR5B,CEP290,PRNP,ING1,BAG4,MAVS,AP5S1,DNAJC13,FUT10,FAM160A2,GAS6,BET1L,TRIM3,SIRT3,ARFIP2,VPS16,COPZ1,ARL6IP5,STX2,SYT9,SRP14,NCOA4,NR1H4,WASHC2A,KCNIP3,LYPLA1,NUP58,MIPEP,TM9SF4,NDUFAF2,ZDHHC20,KIF3B,FAM3D,IPO11,IL1A,RILPL1,RILPL2,IMMP1L,ANKRD27,SNX	grey	VSMC_M10
GO:0048010	0.99	0.02	18	48	vascular endothelial growth factor receptor signaling pathway	BP	1	PTK2,MAPK14,GRB10,PRKD2,FLT1,VEGFC,PTK2B,MAPKAPK3,PDCD6,MAPKAPK2,ARNT,FGF18,PGF,TNMD,PRKCB,VAV1,DAB2IP,CADM4	grey	VSMC_M10
GO:0098876	0.99	0.02	56	129	vesicle-mediated transport to the plasma membrane	BP	1	GOPC,VPS52,EXOC4,MICALL1,STEAP2,VPS50,SLC1A1,SPTBN1,BVES,VPS35,EPS15,ANKRD50,RAB7A,RAB10,OPTN,GOLGA4,CCDC93,LYPLA1,ANKRD27,VAMP5,EXOC6B,VPS26C,VPS39,KIF13A,DENND1B,SORL1,RAB17,BBS1,SNX4,SNX27,STX6,NSF,VPS26A,EHD1,EXOC5,NSG1,GRIPAP1,RAB8A,CNST,RSC1A1,CPLX1,STX1B,SNX12,AC138894.1,RAB11A,DNM2,GGA2,ARHGAP44,VPS35L,VPS53,RAB26,SEC16A,DENND1A,C16orf70,MICALL2,VAMP3	grey	VSMC_M10
GO:2000811	0.99	0.04	4	15	negative regulation of anoikis	BP	1	PTK2,NTRK2,MCL1,ZNF304	grey	VSMC_M10
GO:0048713	0.99	0.03	9	27	regulation of oligodendrocyte differentiation	BP	1	DAAM2,TNFRSF21,PTN,HDAC2,HDAC1,DAG1,DLX1,DUSP10,TNFRSF1B	grey	VSMC_M10
GO:0015914	0.99	0.02	28	70	phospholipid transport	BP	1	ATP9B,ATP8B1,ABCB1,ABCG8,TMEM30A,APOC1,ANO4,PITPNM2,XKR6,PLSCR4,P2RX7,ANO6,COL4A3BP,PLTP,PITPNM1,PITPNC1,OSBPL2,ABCA12,TMEM30B,PCTP,LDLR,PRELID3A,ATP11C,PITPNA,ABCA3,ABCA7,CPTP,XKR8	grey	VSMC_M10
GO:0006636	0.99	0.03	13	36	unsaturated fatty acid biosynthetic process	BP	1	PIBF1,ELOVL1,ELOVL7,PLA2G4A,DAGLB,FADS3,DEGS1,CD74,DECR2,PTGES2,FABP5,ELOVL3,PTGES	grey	VSMC_M10
GO:0061136	0.99	0.02	75	166	regulation of proteasomal protein catabolic process	BP	1	TRIM39,HSPA1B,PRKN,RNF217,TRIB1,CSNK1E,RAD23B,XPO1,ZYG11B,SDCBP,BBS7,NUDT15,PLK3,SUMO2,AQP11,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,RYBP,PSMF1,TRIB3,PLK2,CEBPA,TAF9,FBXW7,USP25,FAM192A,RNFT2,MARCH7,KCNE2,PRICKLE1,RNF144B,USP13,AC013489.1,USP19,PSME1,ARIH2,RNF185,RPL11,NFE2L2,COP1,PSME3,SOCS4,PINK1,ARAF,DNAJB2,DNAAF4,PSMC3,OSBPL7,PSEN1,TAF1,OGT,KEAP1,PSMD10,FBXO22,FMR1,FZR1,BCAP31,SGTA,PKD1,TMEM259,PARK7,ZER1,GLMN,DAB2IP,UBB,PSMC1,BAG2,RNFT1,CAMLG,DDA1,STYX,MAP1A	grey	VSMC_M10
GO:1990823	0.99	0.02	32	78	response to leukemia inhibitory factor	BP	1	RNMT,GFPT2,PMM1,PTP4A3,SYNGR1,BSPRY,BCAT2,KLF5,SPRY2,PFKP,MRPL15,MRAS,PCOLCE2,VEGFC,JARID2,INA,NR5A2,ABCG4,EPS8,CREB1,XRCC5,SPOCK2,EFHC2,PDCD10,PADI2,ABCD4,SHMT1,MTF2,SNX10,NFYB,LRAT,PIGA	grey	VSMC_M10

GO:0048806	0.99	0.03	12	34	genitalia development	BP	1	ESR1,BAK1,HSD17B3,ROR2,HOXA13,SRD5A1,ASB1,LHX1,STRA6,PKD1,WNT5A,DNAJC19	grey	VSMC_M10
GO:2000117	0.99	0.02	24	60	negative regulation of cysteine-type endopeptidase activity	BP	1	TNFAIP8,AQP1,BCL2L12,CST7,RAF1,PRDX3,GAS6,GPI,NR4A1,PAX2,IFI6,SFN,RPS6KA1,POR,DDX3X,BIRC3,ARL6IP1,MAP2K5,NLE1,PARK7,LAMTOR5,NOL3,SERPINB9,CAAP1	grey	VSMC_M10
GO:0018394	0.99	0.02	63	143	peptidyl-lysine acetylation	BP	1	ATAT1,YEATS4,BRD1,SUPT3H,HINT2,PHF14,KANSL3,ING3,ATG5,SPHK2,HDAC2,BMI1,IWS1,PAXIP1,TADA3,ARRB1,TAF7,EP400,TAF10,SDR16C5,TAF9,PHF20,KANSL2,LDB1,HDAC1,AUTS2,MRGBP,ING5,POR,MBIP,TADA2B,NAA40,ING4,TADA1,FOXP3,MSL1,MED24,KAT7,MUC1,TAF1,MAPK3,OGT,NAP1L2,CRTC2,RPS6KA5,SIN3A,ISL1,GLYR1,CREBBP,NAA60,HCFC1,MECP2,CHD5,PARK7,GTF3C4,CTCF,TAF12,SOX4,CPA4,BEND3,SUPT7L,LIF,RPS6KA4	grey	VSMC_M10
GO:0045216	0.99	0.02	64	146	cell-cell junction organization	BP	1	MTSS1,MPDZ,SRF,TLN1,CLDN19,WHRN,GRHL1,FBF1,NUMBL,WNT11,IKBKB,ACTG1,PKP3,NPHP1,LSR,CTNND1,MARVELD2,KIFC3,PLEKHA7,HDAC7,TBX5,F2RL1,F2R,DSP,PKP2,TRPV4,TGFB2,CLDN34,CDH24,SNAI1,ANK2,GNPAT,AGT,ACE2,PTPRO,DLG1,FZD5,ARVCF,GPBAR1,CNTNAP1,RAMP2,VCL,EPHA4,ACTB,CLDN7,NLGN2,TLN2,SMAD3,DSG2,CSF1R,CAMSAP3,EPB41L3,CDH6,CDH10,PIP5K1C,MARVELD3,MICALL2,RHOA,CLDN15,CLDN1,INAVA,APC,PERP,PARD6A	grey	VSMC_M10
GO:0048754	0.99	0.02	52	121	branching morphogenesis of an epithelial tube	BP	1	ESR1,MYC,PTCH1,SMO,SRF,SIX2,AREG,MET,TNC,MYCN,SPRY1,SOX9,GLI2,GZF1,SPRY2,TGFBR2,PAX8,EYA1,VDR,NKX3-1,PKD2,STK4,PAX2,SALL1,DAG1,KRAS,EGF,AGT,GBX2,NFATC4,LAMA5,CLIC4,DLG1,CTSH,WNT4,MAGED1,MED1,CITED1,MKS1,LHX1,LAMA1,GPC3,PKD1,SOX8,FOXF1,ENG,ESRP2,NOG,WNT5A,SIX1,FGF1,WNT2	grey	VSMC_M10
GO:1901222	0.99	0.02	31	75	regulation of NIK/NF-kappaB signaling	BP	1	AGER,PTP4A3,PRDX1,NOD1,EGFR,TLR4,PHB,NMI,TCIM,EIF2AK2,TRAF6,TRIM44,AKIP1,HDAC7,NOD2,PDCD4,EDARADD,RTKN2,TRIP6,DDX3X,RC3H1,PPM1A,TSPAN6,LITAF,MIR21,MIR27B,RHOA,NOL3,C1QTNF4,HAVCR2,RC3H2	grey	VSMC_M10
GO:0060142	0.99	0.04	5	17	regulation of syncytium formation by plasma membrane fusion	BP	1	MAPK14,RAPGEF3,EHD1,GDF15,IL4R	grey	VSMC_M10
GO:1901992	0.99	0.02	30	73	positive regulation of mitotic cell cycle phase transition	BP	1	VPS4B,CCND3,ANKRD17,LSM10,EGFR,UBE2E2,RPTOR,PLCB1,TFDP1,MTA3,ANAPC5,ANAPC7,ADAMTS1,HYAL1,CCND1,TERT,STOX1,DBF4B,DDX3X,MEPCE,ANAPC4,RAD51B,RAB11A,RAD51C,SIN3A,MECP2,CDK10,MIR29A,MIR222,RGCC	grey	VSMC_M10
GO:0042692	0.99	0.02	142	303	muscle cell differentiation	BP	1	NFATC1,STAC3,MAML1,FRS2,QKI,PPARA,ASF1A,OBSCN,H3F3C,MAPK14,CBY1,PI16,SMO,FLNC,MYH9,LMOD2,SRF,PGM5,KIT,FHL2,NINJ1,SEMA4C,TMOD1,ANKRD17,TRIM32,BVES,KEL,MYLK3,ATG5,MAMSTR,SOX9,KLF5,KLHL40,DYRK1B,RARB,ACTG1,RYR1,P2RX2,NRG1,LMOD3,SMYD1,NLN,MYOF,CASP3,MEF2C,JAM2,SOX6,DYSF,HOMER1,TBX5,BIN3,ZBED6,RBM24,ADAMTS15,IGF2,BDNF,SIK1,LMOD1,PPP3CA,PDCD4,PRKAR1A,KRAS,ANK2,GPER1,AGT,ACTC1,SLC9A1,NFATC4,FZD7,MYOZ2,CASQ1,ACTN3,TMOD4,HDAC4,ALPK3,EFEMP2,MYPN,TTN,EHD1,WNT4,MYOZ1,GDF15,RAMP2,BHLHA15,TMOD2,OBSL1,LDB3,BMPR1A,CHRNB1,TCAP,RBPJ,KDM6B,FOXO4,RBPMS2,WFIKKN2,IL4R,TBX2,SETD3,YY1,FBXO22,GATA6,JSL1,MYH11,IFT20,SUPT6H,MRTFB,SKI,MECP2,CACNA1H,WFIKKN1,SYPL2,PIEZO1,TSC1,PLPP7,FOXF1,ENG,GLMN,NFATC3,ACADM,MIR199A1,MIR21,MIR222,MIR23A,MIR125B1,MIR22,MIR24-1,DMD,CSRP2,KRT19,PRDM6,SMYD3,LBX2,SIX1,RGS4,TCF23,YBX1,POPDC2,MYORG,EREG,NKX2-5,RBM38,HEY2	grey	VSMC_M10
GO:0010574	0.99	0.03	9	27	regulation of vascular endothelial growth factor production	BP	1	ATF4,C5AR1,IL1A,SULF2,ARNT,ISL1,C3,MIR199A1,MIR125A	grey	VSMC_M10
GO:0050727	0.99	0.02	111	239	regulation of inflammatory response	BP	1	TNFAIP3,ENPP3,ESR1,AGER,PPARA,GPSM3,MAPK14,MAPK13,TEK,TTBK1,NINJ1,FPR2,NT5E,AKNA,EGFR,TLR4,IL15,VPS35,MGST2,CDK19,NAPEPLD,CST7,LACC1,MYD88,FNDC4,NMI,TMEM173,NR1D2,FOXP1,MFHAS1,NR1H4,PLK2,HCK,IL37,CEBPA,CELF1,SETD6,MCPH1,NR1H3,OTULIN,RIPK1,NOD2,CD200,CD200R1L,TRPV4,PDCD4,NCF1,FABP4,SPATA2,GPER1,SLAMF8,AGT,FGR,ACE2,NLRX1,OSM,SNX4,CD28,ADAM8,DUSP10,IL16,GGT2,BCL6,LPCAT3,TNFSF18,CALCRL,CASP12,MMP3,BIRC3,BST1,STAT5B,DAGLB,SCGB1A1,FOXP3,GPS2,USP18,F12,TNFRSF1B,SYT11,AREL1,SMAD3,LDLR,S100A8,BTK,TNIP1,CCL5,MAPK7,YES1,ISL1,PTGER4,C3,OSMR,ADAMTS12,PTPN2,DROSHA,CREB3L3,DNASE1,PARK7,FOXF1,KARS,MIR199A1,MIR21,MIR222,MIR22,S100A12,C5orf30,WNT5A,IL33,PTGES,TSLP,CEBPB	grey	VSMC_M10
GO:0043200	0.99	0.02	39	93	response to amino acid	BP	1	PNPLA3,NTRK2,HSF1,RRAGD,PTN,FGF21,SESN3,DNMT3A,RPTOR,CRLS1,LARS,SLC38A9,GSS,CASP3,TMBIM6,OPA1,NEURL1,COL16A1,SH3BP4,CDKN1B,CREB1,CPS1,COL5A2,RRAGB,SOCS1,AMIGO1,CYBA,LAMTOR5,ASS1,TLDC1,DHODH,NQO1,RHOA,PEMT,LAMTOR2,SIX1,BCL2L2,CEBPB,PDGFD	grey	VSMC_M10

GO:0043632	0.99	0.01	273	561	modification-dependent macromolecule catabolic process	BP	1	VPS4B,NEDD4L,FEM1C,RMND5B,TNFAIP3,USP15,CANX,TRIM39,HSPA1B,PRKN,RNF5,DERL1,SKP1,UBE2B,RNF217,RNF146,TRIB1,KLHL3,PTK2,TUT7,AGTPBP1,CSNK1E,FOXRED2,FBXL6,USP49,FBXO7,KLHDC3,DCAF12,USP46,LNX1,PDCL3,FBXO10,EXOSC3,SEC61B,RNF20,RAD23B,UBE3D,PNPT1,ECPAS,XPO1,PELI1,CNOT4,FBXO48,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,ZYG11B,SDCBP,TUT4,FAF1,BBS7,FBXL13,FBXL2,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,DMAC2,UBXN4,UBE3C,SPOPL,UBE2E1,KLHL40,ARRB1,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,NHLRC3,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,KCTD6,CEBPA,ARMC8,SPSB4,RNF7,TAF9,UBE2L6,FBXO8,TRPC4AP,ARNTL,FBXW7,USP25,TRIM2,ANAPC5,AUP1,ANAPC7,CSNK2A2,USP16,PTK2B,TMEM67,AMFR,FBXO21,ERLIN1,TTC3,PRICKLE1,MYLIP,FBXW4,TENT4B,TOLLIP,SIAH1,NHLRC1,FBXL15,RNF144B,SUFU,OTUD7A,RPL23,AMN1,HECW2,PSMD1,KLHL42,USP30,DIS3L2,RNF115,PSMB5,KLHL25,USP13,RNF114,AC013489.1,YOD1,EGF,USP19,OTUD7B,DISC1,DTX3L,ZNRF3,CACUL1,ARIH2,USP2,RNF26,NEDD8,CBL,ATE1,UBXN11,PSMD2,RNF215,GID8,USP21,VPS37D,RNF185,RNF168,RPL11,RHBDD2,EDEM3,NFE2L2,SYVN1,FBXO33,DERL3,KLHDC1,COP1,TMUB2,DNAJC10,RC3H1,DNAJB12,SPSB2,KLHL20,TRIM9,UBA52,USP37,USP48,RNF4,ZSWIM8,SOCS4,TMEM129,PINK1,ZFAND2B,ARAF,ANKZF1,DNAJB2,PSMA3,TBL1XR1,CALR3,RNF167,FBXL14,RNF216,FBXL18,USP18,DDB1,ANAPC4,FBXO2,RNF111,PSMC3,TBX21,PSEN1,TGFB1I1,AREL1,FBXL22,KCTD13,TAF1,DCST1,OGT,SEL1L,AC004687.2,USP31,KEAP1,UBL7,	grey	VSMC_M10
GO:0045137	0.99	0.02	76	170	development of primary sexual characteristics	BP	1	HSD17B4,ESR1,GDF9,LRRC6,H3F3C,DMC1,FANCG,KIT,MSH2,OSR1,FOXO3,SOX9,ERCC1,UTF1,DACH1,WDR48,ARRB1,ACVR2A,MKKS,SEMA3A,NCOA4,DHX37,ACVR1B,FOXL2,CASP3,ING2,ROBO2,ADAMTS1,NKX3-1,TESC,SALL1,BMPR1B,GAS2,SRD5A1,HYAL3,CCND1,TGFB2,LHX9,SPATA2,TFAP2C,SPO11,CBL,TAF4,PATZ1,YBX3,VGF,WNT4,CTSV,PTPRN,STAT5B,INHA,KDM5A,WDR19,SOX15,ADAM21,ADAM20,GATA6,MAMLD1,SOX8,HSPA5,MSH4,LHX8,FSTL3,UBB,ARID4A,AGO4,ADGRG1,WNT5A,BASP1,BCL2L11,TBC1D20,BCL2L2,CEBPB,EREG,CBX2,LHFPL2	grey	VSMC_M10
GO:0070593	0.99	0.04	4	15	dendrite self-avoidance	BP	1	MYPN,EMB,BSG,CNTN2	grey	VSMC_M10
GO:0003298	0.99	0.03	8	24	physiological muscle hypertrophy	BP	1	PPARA,PI16,AGT,YY1,MIR199A1,MIR23A,MIR24-1,RGS4	grey	VSMC_M10
GO:0003301	0.99	0.03	8	24	physiological cardiac muscle hypertrophy	BP	1	PPARA,PI16,AGT,YY1,MIR199A1,MIR23A,MIR24-1,RGS4	grey	VSMC_M10
GO:0061049	0.99	0.03	8	24	cell growth involved in cardiac muscle cell development	BP	1	PPARA,PI16,AGT,YY1,MIR199A1,MIR23A,MIR24-1,RGS4	grey	VSMC_M10
GO:0022610	0.99	0.01	520	1050	biological adhesion	BP	1	CD226,SERPINB8,ITGA7,ERBB3,ONECUT2,MIP,LRP1,SEMA6A,TNXB,AGER,PPARA,HLA-DRA,FBLN1,HLA-DOB,HLA-DMA,PARVG,HLA-DPB1,COL14A1,TNFRSF13C,MTSS1,OBSCN,PTK2,PLXNA4,MAPK14,PODXL,CDC42EP1,RAC2,ZDHHC21,MYH9,CDKN2A,IFT74,TEK,LRRC4,PRPH2,PTK7,SRF,ADAM22,NUAK1,CLDN12,APBA1,PGM5,CDK6,CD72,KIT,TNFRSF21,NCK2,SGCE,TLN1,CNTNAP3,SEMA4D,CHST10,NINJ1,OMD,ADGRL3,CLDN19,PRKCE,EPCAM,PPP2R1A,FPR2,HAS1,CTNNAL1,EPB41L4B,HOXA7,MYBPC2,NT5E,CXCL8,PELI1,PLEK,EPHA7,AKNA,PTN,ITGB1BP1,ADD2,TNC,IL4I1,EGFR,EPHA1,BVES,IL15,NRCAM,SLC7A11,PCDH10,FAF1,IZUMO1,FAT4,PLXNA1,WISP3,LAMA4,PODXL2,BMI1,NDNF,RAB10,PRKD2,SOX9,SYMPK,FBLN2,SSPO,CLASP2,DLG2,RSU1,NECTIN2,BCAM,PVR,CNTNAP5,GLI2,PCDH8,UNC13D,FOXJ1,PTPRF,RPSA,PPP1CB,MYL12A,RIN2,TGFBR2,C1QTNF1,JAG1,LGALS4,ACTG1,ADAM18,PAWR,FERMT1,RAC3,SPINT2,FREM2,COL6A6,COL6A5,PRNP,PCDHGC5,BAG4,ARHGEF7,RELL2,PLXNC1,PCDH1,CHL1,UNC5D,CLIC1,NCKAP1L,GAS6,PTPRA,PKP3,SLC7A1,LRFN3,TRAF6,EPHB1,SOX12,AKIP1,NPHP1,RET,HCK,TM9SF4,ZC3H8,FAM107A,IL1A,FER,PIK3CB,PIK3R1,CLSTN2,LPXN,CASP3,DENND6A,CTNND1,PARVA,ROBO1,ROBO2,TENM3,FMN1,ADGRV1,SORBS1,PTPRJ,TMEM131L,IL7,NCAM2,PAG1,JAM2,KIFC3,PLEKHA7,PTK2B,RASGRP1,RND1,TIAM1,RIPK2,DOCK5,CDH17,LOXL2,AP3B1,AMIGO2,CYTIP,AGGF1,TESC,MARCH7,WISP2,RREB1,SPARCL1,SPP1,DSP,SOX13,STK4,LRRN2,GCNT2,ALCAM,DMTN,ADTRP,NOD2,IGSF9B,CNTN1,ITGB6,VSIG10,LDB1,IGF2,PXN,ELMO2,NECTIN3,CD96,FAP,CD200,PKP2,CDON,SLK,CARMIL1	grey	VSMC_M10
GO:1901343	0.99	0.02	35	84	negative regulation of vasculature development	BP	1	SEMA6A,SLC12A2,TEK,PTN,AGO1,WISP3,SPRY2,ISM1,DCN,PLK2,PIK3CB,ADAMTS1,TGFB2,AGT,E2F2,WNT4,HSPG2,SYNJ2BP,NAXE,SEMA4A,FOXO4,VASH1,TNMD,AMOT,MECP2,DAB2IP,MIR29A,MIR21,MIR222,MIR125B1,MIR24-1,FOXJ2,MIR125A,GADD45A,RGCC	grey	VSMC_M10
GO:0032231	0.99	0.02	38	92	regulation of actin filament bundle assembly	BP	1	PRKN,MTSS1,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ARHGEF5,EPHA1,CLASP2,WNT11,MKKS,ACTG1,BAG4,PIK3R1,ALMS1,RAPGEF3,PXN,CARMIL1,PPFIA1,ARHGAP6,WASF2,SLC9A1,WNT4,WAS,PFN3,SMAD3,CORO2B,EVL,PTGER4,INPP5K,SERPINF2,TSC1,FHOD1,MIR21,RHOA,ASAP3,RGCC	grey	VSMC_M10
GO:0016525	0.99	0.02	34	82	negative regulation of angiogenesis	BP	1	SEMA6A,SLC12A2,TEK,PTN,AGO1,WISP3,SPRY2,ISM1,DCN,PLK2,PIK3CB,ADAMTS1,TGFB2,AGT,E2F2,HSPG2,SYNJ2BP,NAXE,SEMA4A,FOXO4,VASH1,TNMD,AMOT,MECP2,DAB2IP,MIR29A,MIR21,MIR222,MIR125B1,MIR24-1,FOXJ2,MIR125A,GADD45A,RGCC	grey	VSMC_M10

GO:0051216	0.99	0.02	68	154	cartilage development	BP	1	OSR2,COL11A2,PITX1,SMAD5,MAPK14,SRF,ROR2,SIX2,BMP8A,COL27A1,MBOAT2,MYCN,OSR1,MATN3,MKX,SOX9,GLI2,TSKU,WNT11,TGFBR2,CHRDL2,ZNF219,MKKS,RARB,LUM,DDRGK1,HAND2,MEF2C,SOX6,STC1,LOXL2,BMPR1B,GPLD1,HYAL1,HYAL3,TRPV4,SULF2,TRIP11,PTHLH,SATB2,AXIN2,SNAI1,AMELX,RUNX3,HOXD3,POR,PTH1R,ESRRA,FGFR3,MMP13,NKX3-2,BMPR1A,THRA,FGF18,THBS3,MAPK3,SMAD3,GHR,ADAMTS12,RFLNB,PKD1,MIR21,ACVRL1,HOXB3,NOG,WNT5A,OTOR,HOXA3	grey	VSMC_M10
GO:0000086	0.99	0.02	54	124	G2/M transition of mitotic cell cycle	BP	1	VPS4B,MRNIP,TRIM39,TAF2,FBXL6,ABCB1,CDK14,BRSK1,CCNY,PLK3,PPME1,PLCB1,MTA3,RAD17,PKIA,CHMP4C,BACH1,NBN,USH1C,ABRAXAS1,DONSON,ZFYVE19,TAOK3,FBXL15,CCND1,CHEK2,SYF2,STOX1,DBF4B,RAD51B,UIMC1,FOXO4,FBXL22,CTC1,TAOK2,ESRRB,RAB11A,KDM8,LCMT1,FOXN3,CALM1,RAD51C,DNM2,SIN3A,TAOK1,FZR1,MECP2,VPS4A,FBXL8,NAE1,FBXL12,BRCC3,ARPP19,NABP1	grey	VSMC_M10
GO:0002758	0.99	0.04	4	15	innate immune response-activating signal transduction	BP	1	IKBKB,TRAF6,HCK,CREBBP	grey	VSMC_M10
GO:1905314	0.99	0.02	13	37	semi-lunar valve development	BP	1	NFATC1,SOX9,JAG1,ROBO1,ROBO2,TGFB2,SNAI1,RBPJ,TNFRSF1B,EFNA1,STRA6,NKX2-5,HEY2	grey	VSMC_M10
GO:0010976	0.99	0.02	61	140	positive regulation of neuron projection development	BP	1	NME1,LRP1,AVIL,WASHC5,NTRK2,PTK7,FZD1,ROR2,TMEM30A,PTN,FIG4,NDNF,ALK,TMEM106B,DPYSL3,RET,TOX,CBFA2T2,ANKRD27,TENM3,ENC1,CUX2,KATNB1,PTK2B,RAPGEF2,TIAM1,OPA1,ITPKA,CYFIP1,CNTN1,BDNF,DNM1L,CAPRIN2,ADNP,DISC1,AGT,NFE2L2,ABL2,PPP2R5B,EHD1,SERPINI1,CRTC1,RETREG3,MARK2,ATP1B2,ITGA3,NDEL1,ZDHHC15,RIT2,GPRASP2,BHLHB9,FBXO38,RRN3,LRP8,AMIGO1,HSPA5,DAB2IP,MIR222,PLK5,CNTF,WNT5A	grey	VSMC_M10
GO:0035988	0.99	0.03	6	20	chondrocyte proliferation	BP	1	SIX2,SOX9,STC1,BMPR1B,FGFR3,MIR21	grey	VSMC_M10
GO:0006417	0.99	0.01	162	341	regulation of translation	BP	1	PAN2,SHMT2,HBS1L,TSFM,RMND1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,EIF3E,PNLDC1,QKI,MRPL13,JMJD4,AGO2,HABP4,TNRC6B,ATF4,TUT7,NCK2,GAPDH,CNOT11,EXOSC3,RPS14,LRPPRC,IGF2BP3,MTIF2,PNPT1,AGO1,ASCC3,C6orf203,TUT4,FOXO3,PUM2,DHFR,EEFSEC,MKNK1,CNBP,MLH1,CDC123,MTRF1,DPH2,TNRC6C,AKT2,PURA,DPH3,EIF2AK2,LSM1,EIF4E3,UPF3A,PRKDC,KBTBD8,PAN3,C12orf65,MRPS27,ENC1,CNOT1,CELF1,USP16,PTK2B,CNOT6L,MAPKAPK5,EIF2AK4,EIF4E2,NSUN3,PAIP2B,FTO,CYFIP1,TENT4B,RBM24,NEURL1,RPUSD4,DDX25,BANK1,CAPRIN2,DIS3L2,RCC1L,KLHL25,GIGYF2,RPS6KB2,YTHDF2,TRNAU1AP,RPS6KA1,PER2,DDX6,RPS4X,MTG2,YTHDF1,PASK,CD28,UHMK1,NCBP2,EIF4ENIF1,NSUN5,IGF2BP2,YBX3,EIF4EBP2,DDX3X,RC3H1,UPF1,COA3,SAMD4A,PINK1,STAT3,MAPK1,POLR2G,NT5C3B,DCP1B,YBX2,CASC3,ZCCHC4,FXR2,TARDBP,MAPK3,TOB1,EIF3C,ALKBH1,TNRC6A,LARP6,CNOT8,LARP1,TCOF1,CCL5,SHMT1,UPF3B,PARN,FMR1,DPH1,METTL16,PLEKHN1,CIRBP,TSC1,AARS,BARHL2,MIR29A,MIR21,MIR222,MIR125B1,MIR27B,MIR27A,RHOA,METTL18,SARNP,AGO4,RPS27L,SOX4,METTL14,NANOS1,IMPACT,EIF1B,EIF1,RPUSD3,PPP1R15A,YBX1,ZFP36L2,UQCC2,TRMT10C,DIO2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0046907	0.99	0.01	634	1261	intracellular transport	BP	1	TIMM21,VPS4B,MYO1A,STX7,AP3S1,KIF5A,PEX7,AGAP2,REPS1,PEX3,TBC1D30,TBC1D9B,PPP1R10,CPSF6,RAB21,SNX31,CPT1B,PHAX,ZDHHC14,SERAC1,RIMS2,PRKN,TAP1,KIF3A,TSPO,GOPC,VPS52,HSPA4,DERL1,FAM91A1,WASHC5,FAM53C,TSNARE1,SIL1,SYNGR1,MAPK15,AGTPBP1,SUN2,MAPK14,TOMM22,NRBP2,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,SMO,ZDHHC21,IFT74,PEX6,FBXO7,NOL6,XPO5,WASHC4,APBA1,PEX1,VPS50,SCFD2,SLC1A1,TGFBRAP1,TBC1D8,TRAM2,RGP1,BICD2,CHMP2A,RAB23,DYNC2LI1,LRPPRC,SEC61B,STX17,SIX2,RIMS1,TMEM30A,YTHDC1,RUFY3,XPO1,SRSF10,BACH2,AFTPH,WDR91,TRAPPC12,ITGB1BP1,YWHAZ,SEC61G,TRAPPC3,TCAF2,VPS41,BVES,TBC1D9,VPS35,SDCBP,MGARP,WASF1,EPS15,AGK,BCAP29,TRAF3IP2,ANKRD50,MTMR2,TTC26,DNAJC27,NAPA,BBS7,RAB7A,PIP4K2A,AP2S1,KIF3C,ARHGAP21,RAB10,COPG1,KPNA3,MYO7B,ARL5B,IWS1,LCP1,SYTL2,KLC3,DLG2,RBSN,DNAJC15,PLK3,IPO13,AQP11,CCDC93,ZFAND6,ATP5F1C,TBC1D4,IFT172,MYO7A,UBE2O,TTC21A,NAPB,GCKR,WDR60,SEC62,SEC22C,KPNA2,AKT2,PITRM1,HOOK3,TIMM50,SNX5,USP36,TBC1D16,AP3M2,KIF5C,MKKS,ANK1,DPY30,PURA,YIPF4,NPLOC4,ARL5A,UBAC2,RAB5A,ASPSCR1,TMCO6,NUP98,SIRT7,FERMT1,CHTOP,HACL1,HEATR5B,CEP290,PRNP,ING1,BAG4,MAVS,AP5S1,DNAJC13,FUT10,FAM160A2,GAS6,BET1L,ARFIP2,UPF3A,LEPROTL1,VPS16,COPZ1,STX2,SRP14,NCOA4,SDCBP2,WASHC2A,THOC7,TUB,KCNIP3,NUP58,MIPEP,TMEM87B,TM9SF4,ZDHHC20,KIF3B,IPO11,RILPL1,RILPL2,IMMP1L,ANKRD27,OSBP,PIK3R1,CHMP2B,TRAPPC11,ATP5F1A,TBC1D12,TNPO1,FBXW7,SCG5,PEX2,PKIA,HTRA2,AUP1,IFT81,ZFAND1,CHMP4C,C	grey	VSMC_M10
GO:0031954	0.99	0.03	8	25	positive regulation of protein autophosphorylation	BP	1	NEK10,VEGFC,NBN,DDX3X,TAOK2,CALM1,RAP2B,PDGFD	grey	VSMC_M10

GO:0051049	0.99	0.01	641	1276	regulation of transport	BP	1	VPS4B,ERBB3,NEDD4L,ATP8B1,LRP1,STAC3,CPSF6,RAB21,SNCAIP,MAPK8IP2,SLC12A2,RIMS2,KCNV1,PRRT1,PRKN,PPARA,TSPO,GDF9,GOPC,BAK1,CATSPER3,MCHR1,PTCH1,MAPK15,MAPK14,KCNJ4,PLA2G6,PICK1,PIM1,BTBD9,RAC2,SMO,TTC39B,CHRNA3,CHRNA5,CRY1,ABCB1,APBA1,USP46,CLIC5,SLC25A27,RFX3,SLC1A1,TFAP2B,TMEM14A,WNK2,CHMP2A,TSPAN13,RAB23,ABCG5,ABCG8,CLDN19,DNAJA1,IL11,PRKCE,SMAP1,RIMS1,TMEM30A,FPR2,HMGN3,KCNQ4,RIMS3,RUFY3,SHANK1,PPT1,XPO1,BMP8A,AQP1,SLC31A2,RSPO1,RSAD2,AAK1,NR1H2,ITGB1BP1,GRB10,EGFR,HECW1,ARHGEF5,TLR4,TCAF2,BVES,CLCN1,IL15,SFRP4,KEL,VPS35,ATG5,SDCBP,TRPM4,SLC7A11,OSR1,FGF21,BRAF,SPHK2,KCNJ14,MTMR2,DNAJC27,TRPC3,RAB7A,SLC26A5,AP2S1,RAB10,KCNRG,GIPR,CACNB2,IWS1,LCP1,CLASP2,CD300LF,APOC1,PLK3,FRMD4A,STAC,GAB2,LGL2,PRKAG2,GRIK5,UNC13D,OXSR1,TBC1D4,SCN5A,SCN1A,IL15RA,AKT2,GPD1L,ARRB1,NEU3,SNX5,USP36,C1QTNF1,ACTG1,SYT1,CACNB4,UBAC2,RAB5A,EFHB,APBB3,ASPSCR1,DPH3,SIRT7,NALCN,FERMT1,CNN2,CEP290,PRNP,BAG4,DIAPH1,MAVS,DNAJC13,P2RX2,AIMP1,CLIC1,NRG1,NCKAP1L,GAS6,BET1L,SIRT3,ARL6IP5,SYT9,ADRA2B,NR1H4,TUB,KCNIP3,TRIB3,LYPLA1,NUP58,HCK,TM9SF4,NDUFAF2,FAM3D,IL1A,PAX8,PXK,FER,ANKRD27,PIK3CB,OSBP,PIK3R1,SLMAP,HIP1R,SLC43A1,GLRX,P2RX3,ARNTL,FBXW7,SCG5,ORAI1,SORBS1,PTPRJ,MEF2C,ASIC1,PKIA,HTRA2,TMBIM6,P2RX7,VEGFC,ZFAND1,HVCN1,CSNK2A2,WDR54,KCNH3,NUP54,P2RY1,PTK2B,KCNJ11,NNAT,NR1H3,TIAM1,BMP2K,RAB11FIP5,DYSF,PFKM,SYNJ1,TPCN1,SLC8B1,HOMER1,IFNGR2,STC1,NKX3-1,NKX6-	grey	VSMC_M10
GO:0045859	0.99	0.01	248	513	regulation of protein kinase activity	BP	1	ERBB3,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,TNXB,MAP3K4,AGER,XRCC6,TRIB1,PTK2,TAB1,STK38,CCND3,CDKN2A,CHRNA3,FBXO7,TTBK1,KIT,SLC1A1,NCK2,ROR2,DNAJA1,IBTK,ACP4,EPGN,AREG,ETAA1,TNFSF15,TGFA,ITGB1BP1,EGFR,ARHGEF5,TLR4,EPHA1,CCNY,PRKAR2B,SPRY1,SLC8A2,C5AR1,PHB,ABI1,MAPRE3,RALB,PRKAG2,PIBF1,SPRY2,WNT11,TGFBR2,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,PRNP,TAF7,NRG1,NCKAP1L,GAS6,ERCC6,FLT1,ADRA2B,TRAF6,TRIB3,CEBPA,PIK3CB,ZFP91,CDK7,CASP3,ROBO1,PLCE1,FBXW7,PTPRJ,PKIA,CCNH,VEGFC,CCNJ,MADD,PTK2B,RASGRP1,CCNG2,RAPGEF2,PRKAG1,TIAM1,PAQR3,CCNJL,PKD2,STK4,DBNDD2,HERC5,NOD2,DTNBP1,TAOK3,CD40,IGF2,BMPR1B,NHLRC1,NEURL1,CCND1,MAP2K6,PDCD4,TGFB2,ADRA2A,FAM20A,PRKAR1A,ADARB1,DAG1,AJUBA,NCF1,MST1,KRAS,FABP4,EGF,ADNP,UBASH3B,SORL1,RTRAF,CASS4,SPATC1L,CACUL1,AGT,FGR,CIB1,CBL,DVL3,STRADB,SFN,CAMK2N2,SYAP1,PTPRO,STRADA,GPRC5D,SNX6,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,CCNYL1,AIDA,FZD5,YWHAG,DUSP10,STOX1,HEXIM2,CEMIP,TTN,DBF4B,MEN1,MAP4K2,DDX3X,XRCC5,DUSP19,PTPN6,PDCD10,TRPT1,ADRA2C,DOK7,SLC11A1,HTT,ZFYVE28,PRKAG3,MARK2,SOCS4,PINK1,SLC27A1,EPHA4,DLG4,ACTB,MAGED1,DVL2,BMPR1A,TSPYL2,CDK12,RGS14,RPLP1,DGKQ,PSEN1,PYDC1,FGF18,LCP2,TAOK2,EFNA1,IL6R,MAP2K1,LAT,PIK3R5,MAP2K5,CALM1,PSMD10,INSR,CCL5,CSF1R,SMCR8,CDK5R1,GHR,KSR1,UNC119,PTPN2,TAOK1,SOCS1,DAB1,LRP8,INPP5K,PDPK1,CAMKK1,PRKCZ,MLST8,PKD1,TRAF2,MTCP1,PARK7,DBNDD1,PSRC1,TSC1,DAB2IP,MIR21,MIR125B1,MIR24-	grey	VSMC_M10
GO:0006511	0.99	0.01	263	542	ubiquitin-dependent protein catabolic process	BP	1	VPS4B,NEDD4L,FEM1C,RMND5B,TNFAIP3,USP15,CANX,TRIM39,HSPA1B,PRKN,RNF5,DERL1,SKP1,UBE2B,RNF217,RNF146,TRIB1,KLHL3,PTK2,AGTPBP1,CSNK1E,FOXRED2,FBXL6,USP49,FBXO7,KLHDC3,DCAF12,USP46,LNX1,PDCL3,FBXO10,SEC61B,RNF20,RAD23B,UBE3D,ECPAS,XPO1,PELI1,CNOT4,FBXO48,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,ZYG11B,SDCBP,FAF1,BBS7,FBXL13,FBXL2,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,DMAC2,UBXN4,UBE3C,SPOPL,UBE2E1,KLHL40,ARRB1,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,NHLRC3,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,KCTD6,CEBPA,ARMC8,SPSB4,RNF7,TAF9,UBE2L6,FBXO8,TRPC4AP,ARNTL,FBXW7,USP25,TRIM2,ANAPC5,AUP1,ANAPC7,CSNK2A2,USP16,PTK2B,TMEM67,AMFR,FBXO21,ERLIN1,TTC3,PRICKLE1,MYLIP,FBXW4,TOLLIP,SIAH1,NHLRC1,FBXL15,RNF144B,SUFU,OTUD7A,RPL23,AMN1,HECW2,PSMD1,KLHL42,USP30,RNF115,PSMB5,KLHL25,USP13,RNF114,AC013489.1,YOD1,EGF,USP19,OTUD7B,DISC1,DTX3L,ZNRF3,CACUL1,ARIH2,USP2,RNF26,NEDD8,CBL,ATE1,UBXN11,PSMD2,RNF215,GID8,USP21,VPS37D,RNF185,RNF168,RPL11,RHBDD2,EDEM3,NFE2L2,SYVN1,FBXO33,DERL3,KLHDC1,COP1,TMUB2,DNAJC10,RC3H1,DNAJB12,SPSB2,KLHL20,TRIM9,USP37,USP48,RNF4,ZSWIM8,SOCS4,TMEM129,PINK1,ZFAND2B,ARAF,ANKZF1,DNAJB2,PSMA3,TBL1XR1,CALR3,RNF167,FBXL14,RNF216,FBXL18,USP18,DDB1,ANAPC4,FBXO2,RNF111,PSMC3,TBX21,PSEN1,TGFB1I1,AREL1,FBXL22,KCTD13,TAF1,DCST1,OGT,SEL1L,AC004687.2,USP31,KEAP1,UBL7,RNF128,PPP2R5C,PSMD10,FBXO22,MIB1,FBXO3	grey	VSMC_M10
GO:0031952	0.99	0.02	13	37	regulation of protein autophosphorylation	BP	1	MOB1B,EPHA7,NEK10,VEGFC,NBN,PPP2R5B,DDX3X,TAOK2,CALM1,ENG,IMPACT,RAP2B,PDGFD	grey	VSMC_M10
GO:0031032	0.99	0.02	76	172	actomyosin structure organization	BP	1	EPB41L2,OBSCN,MYH9,LMOD2,SRF,PGM5,TMOD1,EPB41L4B,LPAR1,MYH14,ITGB1BP1,MET,ARHGEF5,EPHA1,MYLK3,CLASP2,WNT11,ARRB1,MKKS,ACTG1,CNN2,BAG4,LMOD3,PIK3R1,SORBS1,EPB41L1,RTKN,PTK2B,ALMS1,RAPGEF3,PXN,CARMIL1,PPFIA1,LMOD1,PRKAR1A,ARHGAP6,EPB41,WASF2,ACTC1,SLC9A1,MYOZ2,CASQ1,ITGB5,TMOD4,FRMD5,MYPN,TTN,WNT4,MYOZ1,TRPM7,WAS,TMOD2,OBSL1,LDB3,TCAP,KCTD13,MYH10,SMAD3,CORO2B,EVL,CDC42BPB,MYH11,EPB41L3,PTGER4,TNFAIP1,INPP5K,SERPINF2,TSC1,VPS4A,FHOD1,MIR21,RHOA,CSRP2,KRT19,ASAP3,RGCC	grey	VSMC_M10

GO:0097305	0.99	0.02	78	174	response to alcohol	BP	1	FECH,PPARA,TSPO,BAK1,PTCH1,SMO,USP46,CAT,PRKCE,TNC,LANCL2,SETD7,FOXO3,SPHK2,HDAC2,ADCY3,DNMT3A,GLB1,AANAT,TGFBR2,MAP4K1,SLC23A2,CYP7A1,HPGD,PTK2B,SPIDR,TP53INP1,ADCY7,ADCY2,GPLD1,SLC6A3,CCND1,CPT1A,DAG1,GRAMD1B,CBL,ACTC1,NPAS4,EPS8,MGMT,FDX1,RPL27,PTGER2,STAT3,FOXP3,AKAP8,PARP1,SLC2A4,OSBPL7,FOS,CHRNB2,CALM1,S100A8,LARP1,SCNN1B,ACACA,CCL7,SREBF1,OXCT1,PTGER4,ABAT,LRP8,GNB1,SDF4,CYBA,NQO1,PTGFR,MT-CYB,RHOA,SETDB1,CASP8,BGLAP,PEMT,CLDN1,EEF1B2,RGS4,CRH,GNG2	grey	VSMC_M10
GO:0016573	0.99	0.02	57	131	histone acetylation	BP	1	YEATS4,BRD1,SUPT3H,PHF14,KANSL3,ING3,ATG5,SPHK2,BMI1,IWS1,PAXIP1,TADA3,ARRB1,TAF7,EP400,TAF10,SDR16C5,TAF9,PHF20,KANSL2,LDB1,AUTS2,MRGBP,ING5,MBIP,TADA2B,NAA40,ING4,TADA1,FOXP3,MSL1,MED24,KAT7,MUC1,TAF1,MAPK3,OGT,NAP1L2,CRTC2,RPS6KA5,SIN3A,ISL1,GLYR1,CREBBP,NAA60,HCFC1,MECP2,CHD5,PARK7,GTF3C4,CTCF,TAF12,CPA4,BEND3,SUPT7L,LIF,RPS6KA4	grey	VSMC_M10
GO:0097191	0.99	0.02	78	173	extrinsic apoptotic signaling pathway	BP	1	ERBB3,EYA4,TNFAIP3,STK3,HSPA1B,BAK1,ZC3HC1,PHIP,CASP8AP2,TRAF1,BCL2L12,FOXO3,FAF1,PDIA3,DEDD2,RAF1,ZMYND11,RET,IL1A,ACVR1B,FAIM,PIK3R1,EYA1,DIABLO,IL7,FAIM2,HTRA2,P2RX7,MADD,RIPK1,PIDD1,STK4,BMPR1B,SP100,TERT,TGFB2,TCF7L2,GPER1,EYA3,IFI6,MCL1,AGT,CIB1,BAG3,STRADB,PEA15,PELI3,DEDD,DDX47,BCL2A1,IL12A,DDX3X,HTT,PSME3,FGFR3,LTBR,TNFRSF1B,STX4,IL6R,SMAD3,MAP2K5,MAPK7,PDPK1,TRAF2,PARK7,BCL10,DAB2IP,MIR222,FGA,MLLT11,NOL3,FADD,CASP8,CD70,BCL2L11,BCL2L2,CRADD,SGPP1	grey	VSMC_M10
GO:0055119	0.99	0.04	4	15	relaxation of cardiac muscle	BP	1	KCNJ2,ATP1A2,ATP1B1,CHGA	grey	VSMC_M10
GO:0035329	0.99	0.02	12	35	hippo signaling	BP	1	STK3,MAPK14,MOB1B,TEAD2,FAT4,MOB1A,STK4,AJUBA,SAV1,WWC1,AMOT,MARK3	grey	VSMC_M10
GO:0045123	0.99	0.02	19	50	cellular extravasation	BP	1	AGER,ADD2,PODXL2,PLCB1,FER,JAM2,CD99,SELPLG,ADAM8,ITGA4,BST1,CCL2,CCL25,PTGER4,CRK,FADD,FUT4,THY1,PDGFD	grey	VSMC_M10
GO:0019941	0.99	0.01	267	550	modification-dependent protein catabolic process	BP	1	VPS4B,NEDD4L,FEM1C,RMND5B,TNFAIP3,USP15,CANX,TRIM39,HSPA1B,PRKN,RNF5,DERL1,SKP1,UBE2B,RNF217,RNF146,TRIB1,KLHL3,PTK2,AGTPBP1,CSNK1E,FOXRED2,FBXL6,USP49,FBXO7,KLHDC3,DCAF12,USP46,LNX1,PDCL3,FBXO10,SEC61B,RNF20,RAD23B,UBE3D,ECPAS,XPO1,PELI1,CNOT4,FBXO48,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,ZYG11B,SDCBP,FAF1,BBS7,FBXL13,FBXL2,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,DMAC2,UBXN4,UBE3C,SPOPL,UBE2E1,KLHL40,ARRB1,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,NHLRC3,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,KCTD6,CEBPA,ARMC8,SPSB4,RNF7,TAF9,UBE2L6,FBXO8,TRPC4AP,ARNTL,FBXW7,USP25,TRIM2,ANAPC5,AUP1,ANAPC7,CSNK2A2,USP16,PTK2B,TMEM67,AMFR,FBXO21,ERLIN1,TTC3,PRICKLE1,MYLIP,FBXW4,TOLLIP,SIAH1,NHLRC1,FBXL15,RNF144B,SUFU,OTUD7A,RPL23,AMN1,HECW2,PSMD1,KLHL42,USP30,RNF115,PSMB5,KLHL25,USP13,RNF114,AC013489.1,YOD1,EGF,USP19,OTUD7B,DISC1,DTX3L,ZNRF3,CACUL1,ARIH2,USP2,RNF26,NEDD8,CBL,ATE1,UBXN11,PSMD2,RNF215,GID8,USP21,VPS37D,RNF185,RNF168,RPL11,RHBDD2,EDEM3,NFE2L2,SYVN1,FBXO33,DERL3,KLHDC1,COP1,TMUB2,DNAJC10,RC3H1,DNAJB12,SPSB2,KLHL20,TRIM9,UBA52,USP37,USP48,RNF4,ZSWIM8,SOCS4,TMEM129,PINK1,ZFAND2B,ARAF,ANKZF1,DNAJB2,PSMA3,TBL1XR1,CALR3,RNF167,FBXL14,RNF216,FBXL18,USP18,DDB1,ANAPC4,FBXO2,RNF111,PSMC3,TBX21,PSEN1,TGFB1I1,AREL1,FBXL22,KCTD13,TAF1,DCST1,OGT,SEL1L,AC004687.2,USP31,KEAP1,UBL7,RNF128,PPP2R5C,PSMD10,FBXO22,MIB	grey	VSMC_M10
GO:0052548	0.99	0.01	127	270	regulation of endopeptidase activity	BP	1	SERPINB8,SERPINB2,TNFAIP8,MAP3K5,GRAMD4,AGER,PSMB8,BAK1,MYC,HSF1,TTBK1,SLC1A1,GAPDH,CD109,NOD1,AKIRIN2,AQP1,CASP8AP2,EPHA7,TNFSF15,BCL2L12,HSPE1,CST7,RAF1,PRDX3,TIMP4,UBE2O,ARRB1,SPINT2,PRNP,GAS6,ARL6IP5,ST18,PSMF1,ASPH,GPI,NR4A1,FOXL2,HIP1R,ROBO1,DIABLO,HTRA2,RIPK2,SENP1,NKX3-1,ACVR1C,SERPINB1,F2R,SPINT1,PIDD1,PAX2,APLP2,HDAC1,LCK,PDCD6,SOX2,SORL1,GPER1,PSME1,IFI6,AGT,COL6A3,CIDEB,SFN,COL7A1,RPS6KA1,CST6,EGLN3,MGMT,POR,MAPT,FIS1,CTSH,DDX3X,VSIR,SPOCK2,SERPINC1,SERPINI1,PSME3,MUL1,BIRC3,STAT3,PSMA3,ARL6IP1,ATP13A2,EPHA4,ANXA8,BCL2L13,ANXA2,PAPLN,NGFR,TMED10,EFNA1,WFIKKN2,SMAD3,MAP2K5,S100A8,NLE1,C3,SERPINF2,BCAP31,P2RX1,WFIKKN1,PARK7,LAMTOR5,BCL10,MIR21,MIR27B,MIR24-1,RHOA,RPS27L,NOL3,SERPINB5,FADD,CASP8,A2M,MIR339,SERPINE3,ACER2,SERPINB9,BCL2L11,PERP,APH1B,CAAP1,PRR7,CRADD,RARRES1	grey	VSMC_M10
GO:0031498	0.99	0.04	4	15	chromatin disassembly	BP	1	SMARCC2,SMARCD1,ARID1A,PADI2	grey	VSMC_M10

GO:0006954	0.99	0.01	241	497	inflammatory response	BP	1	TNFAIP3,ENPP3,ESR1,AGER,PPARA,GPSM3,IL5,MAPK14,MAPK13,IRF5,TEK,TTBK1,NFX1,KIT,PLGRKT,IL1R2,S1PR3,NINJ1,FPR2,REL,NT5E,CXCL8,NOD1,AKNA,PTN,EGFR,TLR4,IL15,MYLK3,VPS35,MGST2,CDK19,TRAF3IP2,C5AR2,C5AR1,NAPEPLD,PTGIR,CST7,LACC1,UNC13D,MYD88,IRAK2,FNDC4,ACER3,IL17RE,ACKR2,IKBKB,NMI,TMEM173,NR1D2,AIMP1,FOXP1,MFHAS1,NR1H4,PLK2,HCK,IL1A,IL37,PXK,PARP4,CAMK4,CEBPA,AHCY,CELF1,SETD6,MCPH1,RASGRP1,CCL17,NR1H3,RIPK2,OTULIN,AP3B1,F2RL1,F2R,RIPK1,ANO6,CHST1,ABCC2,SPP1,CHID1,TSPAN2,PLA2G4B,NOD2,ITGB6,ADCY7,TOLLIP,CD40,BMPR1B,CD96,CD200,CD200R1L,HYAL1,ELF3,HYAL3,TPST1,TRPV4,PDCD4,TCIRG1,SNAP23,TLR5,CMKLR1,NCF1,MAPKAPK2,FABP4,SPATA2,GPER1,SLAMF8,CERS6,THEMIS2,AGT,FGR,ACE2,NLRX1,NFATC4,OSM,HDAC4,SNX4,CD28,APOD,ADAM8,OLR1,NFE2L2,DUSP10,IL16,GGT2,BCL6,HK1,CD163,FN1,LPCAT3,SERPINC1,TNFSF18,CXCR2,SLC11A1,PTGDR,PTGER2,CALCRL,HSPG2,TNIP2,CASP12,MMP3,BIRC3,SCYL3,STAT3,BST1,STAT5B,SGMS1,LIPA,DAGLB,SCGB1A1,FOXP3,LIAS,IGFBP4,GPS2,USP18,F12,ADGRE5,RBPJ,TNFRSF1B,KDM6B,PNMA1,SYT11,AREL1,FOS,IL6R,LAT,SMAD3,IL4R,LDLR,RPS6KA5,GPR68,S100A8,BTK,SCNN1B,BDKRB1,TNIP1,PSTPIP1,HRH4,CCL14,CCL5,MAPK7,CSF1R,CCL7,CCL2,CCL25,YES1,PLD4,ISL1,PTGER4,C3,NOS2,OSMR,ADAMTS12,PTPN2,CIITA,DROSHA,TICAM1,CREB3L3,SERPINF2,DNASE1,MMP25,TRPV1,P2RX1,PRKCZ,IKBKG,PARK7,CYBA,FOXF1,ASS1,KARS,LCN2,HPR,DAB2IP,NFATC3,PTGFR,MIR199A1,MIR21,MIR222,MIR22,CCL16,S100A12,C5orf30,CXCL6,MIR125A,ZNF580,KLRG1,IRGM,IL36G,WNT5A,GGT5,IL33,CRH	grey	VSMC_M10
GO:1903046	0.99	0.02	68	153	meiotic cell cycle process	BP	1	FBXO43,MOV10L1,UBE2B,WASHC5,MAPK15,DMC1,MYH9,KLHDC3,FOXJ3,CCDC155,TOPAZ1,ERCC1,MLH1,CCNB1IP1,SIRT2,PLCB1,SIRT7,TEX15,MOS,ING2,M1AP,RAD54B,SYCP1,SYCP2L,NPM2,HSF2BP,PRKAR1A,CCDC36,YTHDF2,SPO11,GPR3,C11orf80,HORMAD2,TDRKH,OVOL1,TEX12,MAJIN,ZCWPW1,STAG3,WNT4,TUBG1,P3H4,RAD51B,SEPT1,EME1,SYCE2,RAD51C,RAD51D,ERCC4,FZR1,SLX4,MEIOB,SPIRE2,MSH4,UBB,SYCP3,RNF212B,AGO4,OOEP,FOXJ2,ZSCAN21,SYCE1L,WNT5A,SPDYA,BCL2L11,LIF,CENPX,EREG	grey	VSMC_M10
GO:0043068	0.99	0.01	203	422	positive regulation of programmed cell death	BP	1	MTCH2,TNFAIP8,MAP3K5,TRIM39,STK3,IGF2R,TSPO,BAK1,ATF4,TOMM22,IRF5,CDKN2A,NCK2,TFAP2B,GADD45G,ZNF268,DNAJA1,TFPT,GSDME,HOXA13,EPHA7,PTN,KLF11,ING3,SFRP4,DKKL1,FOXO3,CDK19,FAF1,SPHK2,SPRY1,ERCC3,PDIA3,DEDD2,GRIK5,POU4F1,FBH1,WNT11,ARRB1,SIRT2,RARB,IDO1,PAWR,PRNP,DUSP6,ARHGEF7,BTG1,RNF122,RYBP,ARL6IP5,PRKDC,RET,NSMAF,ZC3H8,NR4A1,PIK3CB,FOXL2,CASP3,HIP1R,HPGD,DIABLO,FBXW7,MEF2C,HTRA2,TCTN3,C3orf38,RAPGEF2,PNMA2,RIPK2,VDR,NKX3-1,ACVR1C,F2RL1,NQO2,RIPK1,ANO6,PRDM11,TP53INP1,PIDD1,PLA2R1,IFIT2,STK4,TFAP2A,SUDS3,CD40,SIAH1,BMPR1B,GPLD1,FAP,CALHM2,NEURL1,DNM1L,SIK1,HDAC1,ALDH1A3,LCK,STK17B,MAP2K6,PDCD4,TGFB2,RBM5,GPER1,QRICH1,CHEK2,ADAMTSL4,MCL1,AGT,IP6K2,SLC9A1,NFATC4,PEA15,HDAC4,NTSR1,STPG1,BACE1,ING5,FZD9,PDCD1,RPL11,MAP3K11,ADAM8,CREB1,CCAR1,FIS1,PRKRA,BCL6,CTSH,ITGA4,IL12A,DDX3X,SAV1,CXCR2,HTT,ING4,RBM10,LTBR,ADCY10,KCNMA1,MAGED1,TNFRSF1B,TNFRSF8,ALDH1A2,MFN2,MAP3K9,PSEN1,PNMA1,ITGAM,NGFR,DAPK2,S100A8,SFPQ,DNM2,DCUN1D3,CAMK2A,CCL5,CCL2,CDK5R1,NOS2,PTPN2,JUN,PIAS4,BCAP31,TRPV1,PLEKHN1,TRAF2,PARK7,LCN2,PIP5KL1,DHODH,NQO1,BCL10,DAB2IP,MIR29A,MIR21,MIR23A,MIR125B1,MIR27B,MIR24-1,RHOA,UBB,ZNF622,MLLT11,SOX4,FADD,BNIP3L,CASP8,MIR125A,CD248,WNT5A,TIGAR,GADD45A,DUSP1,FCER2,DDIT3,BCL2L11,RGCC,APC,PLAGL2,PRR7,CRADD,PITX3,SAP18,OLFM1	grey	VSMC_M10
GO:0071774	0.99	0.02	38	91	response to fibroblast growth factor	BP	1	FRS2,CXCL8,ITGB1BP1,TNC,FUZ,FGF21,SPRY1,NDNF,PRKD2,SPRY2,KL,FGFBP3,NR4A1,FGF5,DSTYK,HYAL1,SULF2,LRIT3,CPS1,WNT4,FLRT1,FGFR3,SCGB1A1,CHURC1,FGFR4,FGF18,NGFR,LHX1,CCL5,CCL2,FGF22,MIR339,NOG,WNT5A,SHISA2,ZFP36L2,FGF1,FRS3	grey	VSMC_M10
GO:0042306	0.99	0.02	20	52	regulation of protein import into nucleus	BP	1	MAPK14,SMO,RAB23,FERMT1,MAVS,NUP58,PIK3R1,PKIA,NUP54,SUFU,CABP1,HCLS1,BAG3,APOD,MAPK1,TARDBP,PSEN1,SMAD3,EFCAB7,ZIC1	grey	VSMC_M10

GO:0061061	0.99	0.01	243	504	muscle structure development	BP	1	NFATC1,ITGA7,STAC3,MAML1,FRS2,QKI,PPARA,VGLL2,ASF1A,PITX1,OBSCN,LEMD2,H3F3C,LY6E,MAPK14,CBY1,PI16,SMO,FLNC,MYH9,FOXH1,LARGE1,LMOD2,SRF,PGM5,CNTFR,KIT,SGCE,FHL2,NINJ1,ETV1,SEMA4C,MEOX2,SOSTDC1,TMOD1,HIVEP3,TNNI3,EPAS1,FKTN,ANKRD17,MYH14,AKIRIN1,TRIM32,BVES,KEL,MYLK3,ATG5,MKX,MAMSTR,SOX9,KLF5,POU4F1,KLHL40,DYRK1B,EID2,JAG1,SIRT2,RARB,ACTG1,HBEGF,NR1D2,SRA1,PLCB1,RYR1,DCN,BTG1,P2RX2,NRG1,LMOD3,TCF15,EPHB1,SGCG,NR4A1,SMYD1,NLN,MRAS,FOXL2,FLNB,VAMP5,MYOF,CASP3,SAP30,ARNTL,MEF2C,JAM2,SOX6,TLL2,CCL17,SFMBT1,DYSF,HOMER1,TBX5,BIN3,TNNC1,DSP,ZBED6,HIF1AN,PRICKLE1,NKD1,RBM24,ADAMTS15,RYR2,IGF2,MYH15,BDNF,NEURL1,PKP2,CDON,SIK1,LMOD1,PPP3CA,TNNI1,PDCD4,TGFB2,PRKAR1A,TCF7L2,ADARB1,DAG1,HLX,KRAS,USP19,MYH7,ANK2,GPER1,USP2,AGT,UNC45A,ACTC1,SLC9A1,COL6A3,NFATC4,FZD7,MYOZ2,CASQ1,ACTN3,TMOD4,HDAC4,LAMA5,ALPK3,DTYMK,BTBD1,EFEMP2,YBX3,CREB1,MYPN,PLEKHM3,TTN,EHD1,WNT4,MYOZ1,GDF15,RAMP2,BHLHA15,TMOD2,OBSL1,LDB3,BMPR1A,CHRNB1,PDLIM7,TCAP,RBPJ,MED1,MYLPF,ZNF689,SOX15,CTF1,KDM6B,FOXO4,FOS,ZNF609,RBPMS2,WFIKKN2,SMAD3,IL4R,ITGA11,RNF165,GSC,TBX2,SETD3,STRA6,YY1,FBXO22,GATA6,UNC45B,ISL1,MYH11,IFT20,RANBP3L,SUPT6H,MRTFB,MBNL3,SKI,MECP2,CACNA1H,SOX8,WFIKKN1,SYPL2,PIEZO1,TSC1,PLPP7,FOXF1,ASS1,LRRC8A,ENG,GLMN,ZFHX3,NFATC3,ACADM,MIR199A1,MIR21,MIR222,MIR23A,MIR125B1,MIR22,MIR24-1,RHOA,DMD,CSRP2,KRT19,PRDM6,CNTF,JPH2,NOG,	grey	VSMC_M10
GO:0033599	0.99	0.04	4	15	regulation of mammary gland epithelial cell proliferation	BP	1	RTN4,ROBO1,RREB1,CCND1	grey	VSMC_M10
GO:0022409	0.99	0.01	79	176	positive regulation of cell-cell adhesion	BP	1	AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,PODXL,NCK2,IL4I1,IL15,BMI1,GLI2,TGFBR2,NCKAP1L,SLC7A1,TRAF6,SOX12,IL1A,DENND6A,IL7,RASGRP1,RIPK2,AP3B1,SOX13,GCNT2,DMTN,NOD2,IGF2,LCK,ICOSLG,GPAM,HLX,SOX2,CD28,RUNX3,ADAM8,DUSP10,BCL6,ITGA4,IL12A,VSIR,PTPN6,STAT5B,FOXP3,RASAL3,ZBTB1,CARD11,ZBTB7B,IL4R,CD74,CCL5,CCL2,YES1,NKAP,VAV1,JAK1,IL7R,SOCS1,DNAJA3,SERPINF2,PRKCZ,PIEZO1,BCL10,MIR21,RHOA,FGA,FSTL3,SOX4,FADD,DPP4,CD46,FUT4,THY1,WNT5A,CD70,TNFSF9,EFNB3,TNFSF13B,HAVCR2	grey	VSMC_M10
GO:0046148	0.99	0.02	20	52	pigment biosynthetic process	BP	1	FECH,SHMT2,TSPO,PPAT,SLC7A11,SLC25A38,RAPGEF2,GMPS,CPOX,COX15,TMEM14C,ALAS1,OCA2,CITED1,COX10,SHMT1,SLC45A2,NFE2L1,WNT5A,FXN	grey	VSMC_M10
GO:0003006	0.99	0.01	336	685	developmental process involved in reproduction	BP	1	HSD17B4,TBPL1,GLI1,YTHDC2,B4GALNT1,CYP27B1,ATAT1,ESR1,FRS2,TSPAN8,STK3,IGF2R,MOV10L1,MAP3K4,PACRG,QKI,BRD2,GDF9,ROS1,HSF2,CCDC134,UBE2B,BAK1,CATSPER3,RSPO3,WASHC5,SMAD5,LRRC6,H3F3C,PTK2,HSD17B3,PTCH1,FANCC,TUT7,MAPK14,DMC1,SPATA31D3,MDFI,TFEB,CFAP69,CNTFR,FANCG,SMARCA2,TDRD6,KIT,ROR2,CCIN,TSGA10,TDRD7,DNAJA1,FOXJ3,SCMH1,EPAS1,MSH2,RAD23B,YTHDC1,CABS1,HOXA13,AREG,HERPUD2,GMCL1,PTN,TNC,NOBOX,GJB5,CCDC155,CREM,TUT4,OSR1,FOXO3,ARMC2,DLD,TXNRD3,APOB,SPATA6,SPATA5,TTC26,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,UTF1,MLH1,GLI2,DACH1,ACOX1,PRDX3,FOXJ1,WDR48,TTC21A,CCNB1IP1,ARRB1,OVOL2,ACVR2A,EOMES,SIRT2,MKKS,SPATA24,ADAM18,SPINT2,GOLGA3,DCN,PANK2,BTG1,SOHLH2,SEMA3A,TEX15,PRKDC,KATNAL1,NCOA4,AMHR2,DHX37,PLAG1,NPHP1,IL1A,CYP7B1,ACVR1B,CEBPA,FOXL2,CASP3,ING2,SPATA9,ROBO2,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,PTK2B,MME,KMT2D,PRKAG1,SFMBT1,VDR,STC1,NKX3-1,AP3B1,TESC,SPINT1,CDYL,SPP1,PKD2,STK4,SYCP1,DNAH1,NPM2,SALL1,DPCD,OCA2,ROPN1L,SIAH1,IGF2,BMPR1B,GAS2,ACTR1A,SRD5A1,NECTIN3,AZIN2,RHBDD1,NEURL1,DDX25,CFAP43,HSF2BP,HYAL3,CCND1,TESMIN,TGFB2,LHX9,SPATA2,RNF114,SNAI1,ABHD2,CDC36,YTHDF2,SPATC1L,TFAP2C,SPO11,TSSK4,CIB1,CBL,ARNT,VASH2,CCDC87,DDX6,ASB1,TAF4,HTRA1,GORASP2,DEDD,CELF3,OSBP2,TDRKH,ZSCAN2,SEPT2,LIMK2,PATZ1,SP3,CATSPER2,CDKN1B,DLG1,OVOL1,SETD2,YBX3,CADM1,FZD5,SPATA32,GGT2,TTC12,BCL6,V	grey	VSMC_M10
GO:1903429	0.99	0.04	4	15	regulation of cell maturation	BP	1	SIRT2,RAC3,RET,OPA1	grey	VSMC_M10
GO:1902749	0.99	0.02	36	87	regulation of cell cycle G2/M phase transition	BP	1	VPS4B,MRNIP,TRIM39,BRSK1,PAXIP1,NEK10,MTA3,RAD17,PKIA,CHMP4C,NBN,ABRAXAS1,DONSON,ZFYVE19,TAOK3,CCND1,DYRK3,SYF2,STOX1,DBF4B,RAD51B,UIMC1,FOXO4,CTC1,TAOK2,RAB11A,FOXN3,RAD51C,SIN3A,TAOK1,FZR1,MECP2,VPS4A,NAE1,BRCC3,NABP1	grey	VSMC_M10
GO:0071559	0.99	0.01	92	205	response to transforming growth factor beta	BP	1	ONECUT2,USP15,SNW1,PPARA,GDF9,SMAD5,PTK2,TAB1,FOXH1,TGFBRAP1,CD109,SDCBP,SPRY1,HDAC2,SOX9,FNDC4,SPRY2,EID2,TGFBR2,OVOL2,FERMT1,SPRED3,SNX25,LPXN,DKK3,ING2,HPGD,IL17RD,MEF2C,SOX6,VEPH1,GCNT2,ITGB6,PXN,SLC2A10,TGFB2,MXRA5,ITGB5,HTRA1,RUNX3,DLX1,SNX6,CREB1,PBLD,MEN1,HTRA3,FBN1,WNT4,COL3A1,GDF15,STK16,STAT3,PPM1A,BMPR1A,PARP1,MPP5,RNF111,TGFB1I1,ITGA3,FOS,CILP,CITED1,WFIKKN2,SMAD3,DNM2,MAPK7,YES1,NLK,TWSG1,JUN,CRK,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,ZFHX3,MIR21,MIR27A,LEMD3,ACVRL1,CLDN1,WNT5A,NRROS,DUSP22,ZFP36L2,LDLRAD4,WNT2,PDGFD,PEG10	grey	VSMC_M10
GO:0010743	0.99	0.03	6	20	regulation of macrophage derived foam cell differentiation	BP	1	PPARA,NR1H2,APOB,NR1H3,ABCA5,AGT	grey	VSMC_M10

GO:0010628	0.99	0.01	397	803	positive regulation of gene expression	BP	1	CD226,ZC3H10,LRP1,RMND1,ESR1,OSR2,PRR16,PABPC1,SNW1,ARID1B,ADM2,HSPA1B,RIMS2,EIF3E,PRKN,AGPAT1,QKI,AGER,GPSM3,IL5,HLA-DPB1,MYC,JMJD4,AGO2,HABP4,ATF4,MAPK14,NTRK2,MAPK13,KDM4C,SOX10,SMO,HSF1,IRF5,MYH9,TTBK1,KIT,NCK2,PLGRKT,NFIL3,GAPDH,DLX5,PDCL3,EXOSC3,CLDN19,RIMS1,MSH2,SPTBN1,TRA2A,EPB41L4B,CXCL8,NOD1,AKIRIN2,PELI1,RSAD2,NR1H2,WHRN,TNC,POU3F3,EGFR,TRIM32,TLR4,IL15,SFRP4,VPS35,MYCN,OSR1,APOB,FGF21,BRAF,TRAF3IP2,SPHK2,HDAC2,HMCES,DHX34,C5AR1,PANX1,PRKD2,CNBP,PHB,SOX9,LACC1,MLH1,CDC123,KDM4A,MYD88,PIBF1,PAXIP1,POU4F1,SPRY2,WNT11,TADA3,SLC24A3,OVOL2,RBMS3,C1QTNF1,TMEM173,ACTG1,PAWR,PLCB1,NUP98,MAFG,FERMT1,CNN2,SHLD1,EIF2AK2,LUM,MAVS,NRG1,DDRGK1,GAS6,HPX,FOXP1,MITF,PKP3,UPF3A,PRKDC,IRF7,CALCOCO1,TRAF6,NR1H4,PLAG1,RET,IL1A,IL37,DNMT3B,GPI,ACVR1B,CEBPA,PIK3CB,PIK3R1,HAND2,ROBO1,MRPS27,PTPRJ,MEF2C,SMARCD1,IL7,BCDIN3D,P2RX7,EPHX2,CELF1,CUX2,USP16,PTK2B,RASGRP1,PRKAG1,ACTG2,EIF2AK4,FGF5,OAS3,RIPK2,VDR,NKX3-1,SLC38A2,F2RL1,F2R,TESC,RIPK1,TP53INP1,POLR3D,PKD2,PLA2R1,TFAP2A,ADTRP,NOD2,CNTN1,TENT5C,DTNBP1,TENT4B,RBM24,PRKAB1,CD40,RAB7B,RHBDD1,IFIH1,CD200,RPUSD4,RPL23,HDAC1,SLC2A10,PPP3CA,TERT,TRPV4,ADRA2A,SULF2,AXIN2,POLR3C,PIAS3,RCC1L,DENND1B,TLR5,KRAS,MAPKAPK2,EGF,RPS6KB2,TTC21B,HSPA8,YTHDF2,SORL1,ANK2,GPER1,NRL,AGT,FGR,TRAF5,ARNT,ACTC1,ARID1A,NFATC4,ANGEL2,OSM,RPS4X,YTHDF1,CELF3,PASK,CD28,FCER1G,GR	grey	VSMC_M10
GO:0006695	0.99	0.02	16	43	cholesterol biosynthetic process	BP	1	PLPP6,APOB,EBP,CYP7A1,ERLIN1,MSMO1,SC5D,SCAP,HSD17B7,POR,TM7SF2,LPCAT3,SREBF1,ACAA2,INSIG2,FGF1	grey	VSMC_M10
GO:1902653	0.99	0.02	16	43	secondary alcohol biosynthetic process	BP	1	PLPP6,APOB,EBP,CYP7A1,ERLIN1,MSMO1,SC5D,SCAP,HSD17B7,POR,TM7SF2,LPCAT3,SREBF1,ACAA2,INSIG2,FGF1	grey	VSMC_M10
GO:1903556	0.99	0.02	16	43	negative regulation of tumor necrosis factor superfamily cytokine production	BP	1	TNFAIP3,TSPO,C6orf106,TLR4,C5AR2,GAS6,NR1H4,IL37,NOD2,VSIR,PTPN6,FOXP3,AKAP8,SYT11,MIR125B1,HAVCR2	grey	VSMC_M10
GO:0052547	0.99	0.01	139	294	regulation of peptidase activity	BP	1	SERPINB8,SERPINB2,TNFAIP8,LRP1,MAP3K5,GRAMD4,AGER,FBLN1,PSMB8,BAK1,MYC,PI16,HSF1,TTBK1,SLC1A1,GAPDH,SVBP,CD109,NOD1,AKIRIN2,AQP1,CASP8AP2,EPHA7,TNFSF15,BCL2L12,HSPE1,CST7,SSPO,RAF1,PRDX3,TIMP4,UBE2O,ARRB1,SPINT2,PRNP,DDRGK1,GAS6,ARL6IP5,ST18,PSMF1,ASPH,GPI,NR4A1,FOXL2,HIP1R,ROBO1,PCOLCE2,DIABLO,HTRA2,RIPK2,SENP1,NKX3-1,ACVR1C,SERPINB1,F2R,SPINT1,PIDD1,PAX2,APLP2,HDAC1,LCK,PDCD6,SOX2,SORL1,GPER1,PSME1,IFI6,AGT,COL6A3,CIDEB,SFN,COL7A1,RPS6KA1,CST6,EGLN3,MGMT,POR,MAPT,FIS1,CTSH,DDX3X,FN1,VSIR,SPOCK2,SERPINC1,SERPINI1,PSME3,PINK1,MUL1,BIRC3,STAT3,PSMA3,ARL6IP1,ATP13A2,EPHA4,ANXA8,BCL2L13,ANXA2,SIMC1,PAPLN,NGFR,TMED10,EFNA1,WFIKKN2,SMAD3,MAP2K5,S100A8,NLE1,C3,GPC3,SERPINF2,BCAP31,P2RX1,WFIKKN1,PARK7,LAMTOR5,BCL10,MIR199A1,MIR21,MIR27B,MIR24-1,RHOA,RPS27L,NOL3,SERPINB5,FADD,CASP8,A2M,MIR339,SERPINE3,ACER2,SERPINB9,BCL2L11,PERP,APH1B,CAAP1,PRR7,CRADD,RARRES1	grey	VSMC_M10
GO:1905820	0.99	0.04	4	15	positive regulation of chromosome separation	BP	1	MAPK15,ANAPC5,ANAPC7,ANAPC4	grey	VSMC_M10
GO:0032271	0.99	0.01	90	199	regulation of protein polymerization	BP	1	ARPC3,AVIL,HSPA1B,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,TTBK1,SLAIN2,NCK2,KIAA1211,TMOD1,PRKCE,SPTBN1,MET,ADD2,CDK5RAP2,FAM49A,MAPRE1,WASF1,EML2,SLC39A12,MAPRE3,SLAIN1,PLEKHG2,FCHSD2,MKKS,NAV3,BAG4,ARHGEF7,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,CLIP1,FMN1,PTK2B,IQGAP2,CYFIP1,DMTN,MAGEL2,CARMIL1,LMOD1,ADD3,SSH1,HCLS1,AP1AR,WASF2,SPTBN2,TMOD4,EPS8,INPP5J,WHAMM,CDKN1B,DLG1,CAPZA1,CDC42EP2,MAPT,TOGARAM1,NCKAP1,NIN,PINK1,ARPC1A,WAS,TMOD2,SPTB,PFN3,HAX1,EVL,CAMSAP3,CDK5R1,SSH2,MLST8,MECP2,CAMSAP1,SPIRE2,PSRC1,WDR63,CARMIL2,RHOA,VASP,GMFG,GRB2,PFN4,COTL1,DRG1	grey	VSMC_M10
GO:0010923	0.99	0.02	11	32	negative regulation of phosphatase activity	BP	1	SEMA4D,IKBKB,BAG4,NCKAP1L,CRY2,TGFB2,TIPRL,BOD1L2,PPP4R4,PPP1R15A,TMEM225B	grey	VSMC_M10
GO:0045785	0.99	0.01	143	306	positive regulation of cell adhesion	BP	1	MIP,AGER,HLA-DRA,HLA-DOB,HLA-DMA,HLA-DPB1,TNFRSF13C,PODXL,IFT74,TEK,CDK6,NCK2,PRKCE,EPB41L4B,PTN,ITGB1BP1,IL4I1,EPHA1,IL15,BMI1,NDNF,PRKD2,FBLN2,RSU1,GLI2,UNC13D,RIN2,TGFBR2,FERMT1,RAC3,BAG4,ARHGEF7,RELL2,NCKAP1L,SLC7A1,TRAF6,SOX12,RET,IL1A,DENND6A,FMN1,PTPRJ,IL7,PTK2B,RASGRP1,RIPK2,DOCK5,AP3B1,RREB1,SOX13,STK4,GCNT2,DMTN,NOD2,LDB1,IGF2,CARMIL1,HYAL1,LCK,PPP3CA,ICOSLG,TGFB2,GPAM,COL16A1,DAG1,HLX,SOX2,DISC1,CASS4,CIB1,CHRD,CD28,RUNX3,DOCK1,CSPG5,EFEMP2,ADAM8,FRMD5,DUSP10,BCL6,ITGA4,IL12A,FN1,VSIR,SPOCK2,PTPN6,TNFSF18,WNT4,STAT5B,CYTH3,TFE3,FOXP3,EPHA4,RASAL3,ZBTB1,CARD11,TMEM102,STX4,ITGA3,ZBTB7B,SMAD3,IL4R,DNM2,CD74,CCL5,CCL2,CCL25,YES1,NKAP,VAV1,JAK1,IL7R,SOCS1,CRK,DNAJA3,SERPINF2,PRKCZ,PIEZO1,TSC1,FOXF1,VAV3,ZFHX3,BCL10,MIR21,MIR27B,RHOA,FGA,FSTL3,ADGRG1,SOX4,FADD,DPP4,CD46,FUT4,THY1,WNT5A,DUSP26,CD70,TNFSF9,LIF,EFNB3,TNFSF13B,HAVCR2	grey	VSMC_M10

GO:0048762	0.99	0.01	89	198	mesenchymal cell differentiation	BP	1	SEMA6A,SOX10,SMO,SEMA4D,SEMA4C,SIX2,RTN4,AKNA,FUZ,SDCBP,OSR1,SPRY1,HDAC2,SOX9,CLASP2,SPRY2,WNT11,TGFBR2,OVOL2,EOMES,JAG1,SPRED3,ALX1,SEMA3D,SEMA3A,NRG1,KBTBD8,RET,HAND2,IL17RD,FAM208A,MEF2C,SEMA4F,TIAM1,LOXL2,TBX5,SEMA3G,GCNT2,PAX2,SEMA4G,KLHL12,USF3,SEMA3F,PDCD4,TGFB2,PEF1,TCF7L2,PDCD6,DAG1,AXIN2,SNAI1,AMELX,GBX2,PHLDB1,LAMA5,SEMA6D,FN1,WNT4,MAPK1,BMPR1A,RADIL,RBPJ,ALDH1A2,SEMA4A,TGFB1I1,EFNA1,MAPK3,TMEM100,SMAD3,GSC,TCOF1,ISL1,RANBP3L,RFLNB,SOX8,ENG,DAB2IP,MIR21,MIR222,POFUT2,NOG,WNT5A,DACT3,SDHAF2,RGCC,LDLRAD4,HEY2,OLFM1,WNT2	grey	VSMC_M10
GO:0010742	0.99	0.03	8	25	macrophage derived foam cell differentiation	BP	1	PPARA,NR1H2,APOB,SOAT2,NR1H3,ABCA5,AGT,SOAT1	grey	VSMC_M10
GO:0090077	0.99	0.03	8	25	foam cell differentiation	BP	1	PPARA,NR1H2,APOB,SOAT2,NR1H3,ABCA5,AGT,SOAT1	grey	VSMC_M10
GO:0036294	0.99	0.02	56	129	cellular response to decreased oxygen levels	BP	1	MYC,PICK1,PRKCE,EPAS1,AQP1,PTN,MGARP,FOXO3,DNMT3A,NDNF,SUV39H2,PLK3,EGLN2,SIRT2,PDK1,COX4I2,TMBIM6,BACH1,STC1,NKX3-1,OPA1,HIF1AN,SIRT4,DNM1L,TERT,SCN2A,AJUBA,USP19,OPRD1,CBL,HYOU1,SLC9A1,KCNK2,TBL2,EGLN3,ADAM8,PDK3,NFE2L2,STOX1,PINK1,SLC2A4,RBPJ,NPEPPS,GATA6,ACAA2,GNB1,TSC1,LCN2,MIR21,KCNK3,NOL3,BNIP3L,RWDD3,TIGAR,RGCC,MIEF1	grey	VSMC_M10
GO:0060348	0.99	0.01	76	172	bone development	BP	1	OSR2,MPIG6B,SMAD5,MAPK14,TEK,SRF,KIT,SEMA4D,DLX5,RAB23,COL27A1,SFRP4,PIP4K2A,ABI1,SOX9,MEGF8,IFT172,TSKU,TGFBR2,SLC38A10,RARB,RYR1,FOXP1,ASXL1,FBXW7,MEF2C,MCPH1,STC1,TFAP2A,TRIM45,ITGB6,BMPR1B,SRD5A1,LRRK1,MAP2K6,TRPV4,SBDS,SLC9B2,SULF2,TRIP11,AXIN2,WASF2,ACTN3,THPO,POR,COL13A1,PTPN6,FBN1,ALPL,FGFR3,MMP13,TULP3,DHRS3,MED1,ANXA2,MSX2,FGF18,TMEM107,CTC1,THBS3,CHAD,FOXN3,GPR68,CDX1,GHR,PTGER4,RANBP3L,RFLNB,SKI,ATP6AP1,ENG,RHOA,BGLAP,SNX10,CCDC154,INSIG2	grey	VSMC_M10
GO:0060216	0.99	0.03	5	18	definitive hemopoiesis	BP	1	RBFOX2,TEK,SP3,HOXB3,ZFP36L2	grey	VSMC_M10
GO:0000076	0.99	0.04	4	15	DNA replication checkpoint signaling	BP	1	RAD17,RAD9B,TIPIN,NAE1	grey	VSMC_M10
GO:0006910	0.99	0.04	4	15	phagocytosis, recognition	BP	1	TUB,PEAR1,SPON2,COLEC12	grey	VSMC_M10
GO:0048771	0.99	0.01	56	129	tissue remodeling	BP	1	TNFAIP3,TNFRSF11B,BAK1,RSPO3,RAC2,EPAS1,PTN,EGFR,NCDN,IL15,ATG5,ACVR2B,JAG1,MITF,TRAF6,IL1A,HAND2,MEF2C,IL7,P2RX7,PTK2B,VDR,F2R,SPP1,LRRK1,ELF3,PPP3CA,TCIRG1,GPR137B,UBASH3B,AGT,ADAM8,PTH1R,GPR137,SUCO,CD38,LIPA,P3H4,SYT7,RBPJ,RAB3D,CSF1R,PPARGC1B,LEPR,ATP6AP1,DEF8,MIR199A1,MIR27B,NOL3,CA2,ACVRL1,BGLAP,SNX10,CSPG4,LIF,HOXA3	grey	VSMC_M10
GO:0051146	0.99	0.01	100	220	striated muscle cell differentiation	BP	1	STAC3,MAML1,FRS2,PPARA,OBSCN,MAPK14,CBY1,PI16,SMO,MYH9,LMOD2,SRF,PGM5,FHL2,TMOD1,TRIM32,BVES,KEL,MYLK3,ATG5,MAMSTR,KLF5,KLHL40,DYRK1B,RARB,ACTG1,RYR1,P2RX2,NRG1,LMOD3,SMYD1,NLN,MYOF,CASP3,MEF2C,JAM2,SOX6,HOMER1,TBX5,BIN3,RBM24,ADAMTS15,IGF2,BDNF,SIK1,LMOD1,PPP3CA,PRKAR1A,KRAS,AGT,ACTC1,SLC9A1,FZD7,MYOZ2,CASQ1,ACTN3,TMOD4,HDAC4,ALPK3,MYPN,TTN,EHD1,MYOZ1,GDF15,BHLHA15,TMOD2,OBSL1,LDB3,BMPR1A,TCAP,RBPJ,KDM6B,IL4R,YY1,FBXO22,GATA6,ISL1,MYH11,IFT20,SKI,CACNA1H,PIEZO1,TSC1,PLPP7,ACADM,MIR199A1,MIR222,MIR23A,MIR24-1,CSRP2,KRT19,SMYD3,SIX1,RGS4,YBX1,POPDC2,MYORG,NKX2-5,RBM38,HEY2	grey	VSMC_M10
GO:0045087	0.99	0.01	221	459	innate immune response	BP	1	CD226,SHMT2,MAP3K5,TNFAIP3,CYP27B1,USP15,TRIM39,XRCC6,PTK2,C6orf106,APOBEC3H,IRF5,GAPDH,PRDX1,SDHAF4,FPR2,REL,ANKRD17,NOD1,AKIRIN2,RSAD2,NR1H2,TRIM32,TLR4,ZC3HAV1,PHB,LACC1,NECTIN2,PVR,OPTN,UNC13D,MYD88,SEC14L1,IKBKB,SIRT2,NMI,TMEM173,CLPB,ACTG1,EIF2AK2,MAVS,HPX,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,HCK,FER,FLNB,OTUD4,ERAP1,PTK2B,RASGRP1,CCL17,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTUIN,IFNGR2,WRNIP1,F2RL1,POLR3D,CHID1,IFIT2,HERC5,NOD2,TOLLIP,CD40,MX2,RAB7B,CD96,IFIH1,OASL,LCK,SP100,CRCP,ADARB1,UNC93B1,POLR3C,TLR5,NCF1,TIFA,ALPK1,YTHDF2,GPER1,SLAMF8,PARP9,DTX3L,PARP14,IFI6,FGR,NLRX1,COCH,FCER1G,NCF2,SETD2,ADAM8,CADM1,DUSP10,CDC42EP2,NONO,HK1,IL12A,MAP4K2,DDX3X,XRCC5,PTPN6,SLC11A1,LAG3,GCH1,MUL1,BIRC3,CFP,STAT5B,WAS,POLR3A,CXCL16,ZBTB1,AKAP8,TKFC,USP18,TNK1,F12,MED1,SPON2,STX4,PYDC1,ITGAM,DCST1,CITED1,ECSIT,AKAP1,STX8,S100A8,SFPQ,BTK,STAT2,POLR3E,TYK2,G3BP1,SIN3A,PSTPIP1,TRAF3,CD74,CCL14,CCL5,RIOK3,CSF1R,COLEC12,CCL7,CCL2,CCL25,YES1,PLD4,RNF135,PPP6C,VAV1,C7,JAK1,C3,NOS2,PTPN2,SOCS1,CIITA,TICAM1,TTC4,LRP8,CRK,CREBBP,ATAD3A,IKBKG,POLR3K,ADAMTS13,CYBA,ASS1,LCN2,STXBP1,AP1G1,BCL10,DAB2IP,ZDHHC1,MIR21,FGA,CCL16,S100A12,OAS1,HIST1H2BK,TRIM68,ZDHHC11,CHGA,DEFB124,FADD,TRIM34,CD46,CASP8,ZCCHC3,A2M,IFNLR1,JCHAIN,KLRG1,CFD,IRGM,IL36G,CLDN1,WNT5A,TRDV3,INAVA,SERPINB9,EREG,VAMP3,HIST1H2BF,IFIT3,HIST1H2BJ,HAVCR2,CCL22	grey	VSMC_M10

GO:0000902	0.99	0.01	389	799	cell morphogenesis	BP	1	ITGA7,NEDD4L,LRP1,SEMA6A,KIF5A,RAB21,MAPK8IP2,TIAM2,MPIG6B,RIMS2,CDC42SE2,PRKN,FBLN1,PARVG,SULT4A1,SHROOM1,FSTL4,SYNGAP1,GFRA3,PTK2,PTCH1,ATF4,PLXNA4,MAPK14,NTRK2,CPNE5,CDC42EP1,RAC2,STRIP2,SMO,MYH9,RBFOX2,CHRNA3,TEK,SRF,KIT,SEMA4D,DLX5,FGD3,ETV1,ZNF135,SEMA4C,BRSK1,RIMS1,RTN4,PHIP,RUFY3,SHANK1,HOXA2,HOXA13,LPAR1,MYH14,EPHA7,WHRN,PTN,ITGB1BP1,MET,EGFR,HECW1,EPHA1,ZMYM6,BVES,KEL,NRCAM,NTF4,WASF1,PLXNA1,SLC26A5,RAB10,ABI1,GOLGA4,GLI2,MEGF8,UNC13D,MYO7A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,MYL12A,CPNE9,FARP1,KIF5C,SYT1,TMEM106B,FEZ2,RAC3,SPINT2,SLC23A2,ARHGEF7,SEMA3D,DIAPH1,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,FGD6,NRG1,NCKAP1L,ULK1,PRKDC,RYK,EPHB1,AKIP1,RET,HCK,TTL,ASXL1,FER,RILPL1,RILPL2,ANKRD27,FLNB,PREX2,PIK3R1,LPXN,CASP3,PARVA,PLS1,ROBO1,ROBO2,SH3D19,ARHGEF28,FZD3,MEF2C,SEMA4F,TLX2,CUX2,P2RY1,ARHGEF26,PTK2B,RAPGEF2,DPYSL2,EIF2AK4,RND1,TIAM1,SLIT1,DOCK5,VDR,STC1,OPA1,NKX6-1,TRIO,AP3B1,NR4A2,RHOBTB2,ZFYVE27,BIN3,FITM2,C8orf37,COL4A3BP,SEMA3G,RREB1,ITPKA,SPP1,STK4,PAX2,CYFIP1,ALCAM,DMTN,SEMA4G,ITGB6,ZNF335,DTNBP1,TAOK3,CAP2,SIAH1,BRWD1,LZTS1,BMPR1B,GAS2,BDNF,PXN,DOCK10,KIAA0319,LGR6,DNM1L,CARMIL1,FGD4,PPP3CA,HECW2,CAPRIN2,SEMA3F,TGFB2,GAP43,ADARB1,DAG1,AUTS2,SSH1,LHX9,CFL1,SART3,CDH24,ADNP,AP1AR,EPB41,YTHDF2,DISC1,LAMB3,CASS4,PDZD8,FGR,CIB1,WASF2,GBX2,DVL3,KALRN,STRADB,NFATC4,FZD7,SS18L1,LAMA5,EPS8,COCH,YT	grey	VSMC_M10
GO:0010575	0.99	0.03	7	23	positive regulation of vascular endothelial growth factor production	BP	1	ATF4,C5AR1,IL1A,SULF2,ARNT,ISL1,C3	grey	VSMC_M10
GO:0072006	0.99	0.02	50	118	nephron development	BP	1	MTSS1,MYC,KLHL3,PTCH1,PODXL,SMO,TEK,TFAP2B,SIX2,POU3F3,OSR1,SOX9,AQP11,FOXJ1,GZF1,WNT11,JAG1,RET,ASXL1,PAX8,EYA1,PLCE1,FMN1,MEF2C,PKD2,PAX2,SALL1,IRX2,SULF2,ENPEP,AGT,LAMA5,PTPRO,DLG1,WNT4,MAGED1,ITGA3,CITED1,IL6R,LHX1,GPC3,PKD1,SOX8,MIR125A,NOG,BASP1,SIX1,LIF,FGF1,PDGFD	grey	VSMC_M10
GO:0043549	0.99	0.01	297	612	regulation of kinase activity	BP	1	ERBB3,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,TNXB,MAP3K4,PRKN,AGER,ROS1,XRCC6,TRIB1,PTK2,TAB1,NTRK2,STK38,CCND3,CDKN2A,ZNF16,CHRNA3,TEK,FBXO7,TTBK1,KIT,SLC1A1,NCK2,ROR2,DNAJA1,FPR2,IBTK,ACP4,MOB1B,EPGN,AREG,WDR91,ETAA1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,EGFR,ARHGEF5,TLR4,EPHA1,CCNY,PRKAR2B,SPRY1,SLC8A2,C5AR1,PIP4K2A,PHB,ABI1,MAPRE3,RALB,PRKAG2,PRDX3,PIBF1,GCKR,SPRY2,WNT11,ALK,TGFBR2,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,PRNP,TAF7,NRG1,CCKBR,NCKAP1L,GAS6,ERCC6,FLT1,RYK,ADRA2B,TRAF6,TRIB3,EPHB1,RET,CEBPA,PIK3CB,PIK3R1,ZFP91,CDK7,CASP3,ROBO1,PLCE1,FBXW7,PTPRJ,PKIA,CCNH,VEGFC,CCNJ,SLA2,MCPH1,MADD,PTK2B,RASGRP1,CCNG2,RAPGEF2,PRKAG1,TIAM1,PAQR3,NLRC5,NBN,CCNJL,PKD2,STK4,DBNDD2,HERC5,NOD2,DTNBP1,TAOK3,CD40,DSTYK,LDB1,IGF2,BMPR1B,NHLRC1,IRS1,NEURL1,CCND1,MAP2K6,PDCD4,TGFB2,ADRA2A,FAM20A,PRKAR1A,ADARB1,DAG1,AJUBA,NCF1,MST1,KRAS,FABP4,EGF,PFKFB2,ADNP,UBASH3B,SORL1,RTRAF,SLAMF8,CASS4,SPATC1L,CACUL1,AGT,FGR,CIB1,CBL,DVL3,STRADB,SFN,PPP2R5A,CAMK2N2,SYAP1,RUBCN,PTPRO,STRADA,EPHB3,DUSP12,PIK3IP1,GPRC5D,SNX6,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,CCNYL1,AIDA,FZD5,YWHAG,DUSP10,MAPT,STOX1,HEXIM2,CEMIP,TTN,DBF4B,EPHB4,MEN1,MAP4K2,DDX3X,XRCC5,DUSP19,PTPN6,PDCD10,TRPT1,ADRA2C,DOK7,SLC11A1,HTT,ZFYVE28,PRKAG3,MARK2,FGFR3,SOCS4,PINK1,SLC27A1,EPHA4,DLG4,ACTB,MAGED1,DVL2,BMPR1A,TSPYL2,CDK12,RGS14,FGFR4,RPLP1,SOCS7,DGKQ,PSEN1,PYDC1,FGF18,LCP2,TAOK2,EFNA1,IL6R,MAP2K1,CD19,LAT,COX1	grey	VSMC_M10
GO:1903317	0.99	0.02	21	54	regulation of protein maturation	BP	1	MYH9,PLGRKT,IL1R2,ACP4,BCL2L12,CST7,PRNP,IFT52,SIRT4,RHBDD1,MELTF,ADAM8,LPCAT3,F12,SNX12,AC138894.1,SERPINF2,NOL3,CNTN2,SOX4,BAG2	grey	VSMC_M10
GO:0061572	0.99	0.01	61	141	actin filament bundle organization	BP	1	PRKN,SHROOM1,MTSS1,BAIAP2L2,SRF,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,EPHA1,LCP1,CLASP2,WNT11,ARRB1,MKKS,ACTG1,FSCN2,PAWR,BAG4,DPYSL3,FAM107A,PIK3R1,PLS1,LIMA1,SORBS1,PTK2B,ALMS1,USH1C,RAPGEF3,DMTN,PXN,CARMIL1,PPFIA1,ARHGAP6,WASF2,SLC9A1,ITGB5,EPS8,WNT4,WAS,PFN3,KCTD13,SMAD3,CORO2B,EVL,PTGER4,TNFAIP1,RFLNB,INPP5K,SERPINF2,SPIRE2,TSC1,FHOD1,MIR21,RHOA,ASAP3,RGCC,PDXP	grey	VSMC_M10
GO:0010544	0.99	0.03	4	15	negative regulation of platelet activation	BP	1	THBD,C1QTNF1,UBASH3B,ABAT	grey	VSMC_M10

GO:0006955	0.99	0.01	505	1012	immune response	BP	1	CD226,LRP1,STX7,SHMT2,MAP3K5,TNFAIP3,CYP27B1,USP15,ENPP3,TRIM39,ESR1,HSPA1B,GRAMD4,AGER,HLA-DRA,HLA-DOB,TAP1,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,XRCC6,CXCL14,PTK2,C6orf106,APOBEC3H,GTPBP1,MAPK14,PLA2G6,MFNG,RAC2,EXOSC4,TFEB,IRF5,LRRC14,TEC,CCL27,KIT,TNFRSF21,IL1R2,NFIL3,SEMA4D,GAPDH,NINJ1,PRDX1,EXOSC3,SDHAF4,PRKCE,MSH2,LAIR1,RTN4,IRAK1BP1,FPR2,REL,ANKRD17,CXCL8,SLC46A2,NOD1,AKIRIN2,AQP1,BACH2,PELI1,LYPD8,PXDN,RSAD2,NR1H2,TNFSF15,IL4I1,TRIM32,TLR4,FCGRT,IL15,ATG5,TRPM4,PUM2,TRAF3IP2,SPHK2,ZC3HAV1,HMCES,BMI1,C5AR2,C5AR1,PRKD2,CST7,PHB,CYSLTR2,ERCC1,LCP1,CD300LF,LACC1,NECTIN2,PVR,EIF2B3,OPTN,GAB2,MLH1,UNC13D,MYD88,SLC22A13,FOXJ1,PAXIP1,IRAK2,SEC14L1,ACKR2,EOMES,IKBKB,JAG1,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,TCIM,NPLOC4,PAWR,PLCL2,SHLD1,EIF2AK2,PRNP,MAVS,AIMP1,NCKAP1L,HPX,FOXP1,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,MARCH8,PLK2,GAPT,HCK,IL1A,IL37,GPI,CAMK4,FER,AHCY,FLNB,OTUD4,LPXN,IRF2,ERAP1,ORAI1,PTPRJ,MEF2C,IL7,PAG1,SLA2,PTK2B,RASGRP1,CCL17,EIF2AK4,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTULIN,NBN,DYSF,IFNGR2,CDH17,RAPGEF3,AP3B1,WRNIP1,F2RL1,POLR3D,COL4A3BP,CHID1,IFIT2,MAPKBP1,ALCAM,HERC5,NOD2,ITGB6,ADCY7,TOLLIP,CD40,GBF1,NFKB2,MX2,RAB7B,MAPKAPK3,GPLD1,DOCK10,CD96,IFIH1,CD200,SPPL3,OASL,RGS1,LCK,BANK1,SP100,ICOSLG,CRCP,MAP2K6,TGFB2,BTN2A2,GPAM,TCIRG1,ADARB1,SNAP23,UNC93B1,POLR3C,HLX,DENND1B,TLR5,CMKLR1,NCF1,MAPKAPK2,TIFA,ALPK1,OTUD7B,OPR	grey	VSMC_M10
GO:0036293	0.99	0.01	119	258	response to decreased oxygen levels	BP	1	AGER,PPARA,MYC,PICK1,TXN2,HSF1,TEK,SRF,SLC1A1,CA9,CAT,PRKCE,EPAS1,AQP1,PTN,MGARP,FOXO3,DNMT3A,NDNF,ERCC2,SLC39A12,ERCC3,SUV39H2,PLK3,XRCC1,RAF1,EGLN2,CYGB,PLAT,TGFBR2,SIRT2,RYR1,P2RX2,PDK1,COX4I2,TM9SF4,DNMT3B,AHCY,CASP3,P2RX3,TMBIM6,VEGFC,PTK2B,BACH1,STC1,NKX3-1,OPA1,LOXL2,NR4A2,HIF1AN,RYR2,SIRT4,DNM1L,TERT,TGFB2,SCN2A,AJUBA,USP19,OPRD1,CBL,HYOU1,ARNT,SLC9A1,KCNK2,USF1,TBL2,EGLN3,SCAP,APOLD1,CDKN1B,ADAM8,PDK3,NFE2L2,CREB1,STOX1,FIS1,FUNDC1,RAMP2,PINK1,ATP1B1,CD38,KCNMA1,SLC2A4,RBPJ,SOD3,AGTRAP,NPEPPS,BNIP1,PKLR,PGF,CHRNB2,SMAD3,GATA6,ALKBH5,NOS2,LONP1,ACAA2,ABAT,GNB1,CREBBP,PLEKHN1,MECP2,CIAO3,CYBA,TSC1,LCN2,HSD11B2,MIR21,MT-CYB,RHOA,KCNK3,NOL3,DPP4,BNIP3L,ACVRL1,RWDD3,TIGAR,RGCC,MIEF1	grey	VSMC_M10
GO:0032212	0.99	0.02	11	32	positive regulation of telomere maintenance via telomerase	BP	1	MAP3K4,MAPK15,POT1,ATR,HMBOX1,MAPKAPK5,XRCC5,MAPK1,MAPK3,PARN,MAP2K7	grey	VSMC_M10
GO:2000001	0.99	0.03	4	15	regulation of DNA damage checkpoint	BP	1	PPP1R10,CRY1,ETAA1,CHEK2	grey	VSMC_M10
GO:0043117	0.99	0.03	4	15	positive regulation of vascular permeability	BP	1	PTP4A3,FGFBP3,TRPV4,CXCR2	grey	VSMC_M10
GO:0006099	0.99	0.02	9	27	tricarboxylic acid cycle	BP	1	ACO2,DHTKD1,MDH2,SUCLG2,SDHC,MDH1B,IDH3A,SDHB,SDHAF2	grey	VSMC_M10
GO:0001666	0.99	0.01	112	244	response to hypoxia	BP	1	AGER,PPARA,MYC,TXN2,HSF1,TEK,SRF,CA9,CAT,PRKCE,EPAS1,AQP1,PTN,MGARP,FOXO3,DNMT3A,NDNF,ERCC2,ERCC3,SUV39H2,PLK3,XRCC1,RAF1,EGLN2,CYGB,PLAT,TGFBR2,SIRT2,RYR1,P2RX2,PDK1,COX4I2,TM9SF4,DNMT3B,AHCY,CASP3,P2RX3,TMBIM6,VEGFC,PTK2B,BACH1,STC1,NKX3-1,OPA1,LOXL2,NR4A2,HIF1AN,RYR2,SIRT4,DNM1L,TERT,TGFB2,SCN2A,AJUBA,USP19,OPRD1,HYOU1,ARNT,SLC9A1,KCNK2,USF1,TBL2,EGLN3,SCAP,APOLD1,CDKN1B,ADAM8,PDK3,NFE2L2,CREB1,STOX1,FIS1,FUNDC1,RAMP2,PINK1,ATP1B1,CD38,KCNMA1,SLC2A4,RBPJ,SOD3,AGTRAP,NPEPPS,PKLR,PGF,CHRNB2,SMAD3,GATA6,ALKBH5,NOS2,LONP1,ACAA2,ABAT,GNB1,CREBBP,PLEKHN1,MECP2,CIAO3,CYBA,HSD11B2,MIR21,MT-CYB,RHOA,KCNK3,NOL3,DPP4,BNIP3L,ACVRL1,RWDD3,TIGAR,RGCC,MIEF1	grey	VSMC_M10
GO:0048333	0.99	0.03	7	23	mesodermal cell differentiation	BP	1	SIX2,EYA1,PAX2,BMPR1A,KDM6B,ITGA3,FOXF1	grey	VSMC_M10
GO:0090263	0.99	0.02	38	92	positive regulation of canonical Wnt signaling pathway	BP	1	RPS12,UBE2B,RSPO3,RNF146,CSNK1E,DAAM2,PTK7,ROR2,DLX5,WNK2,RSPO1,EGFR,SFRP4,TRPM4,PPM1N,SCEL,ARNTL,PRDM15,LGR6,LRRK1,CAPRIN2,TMEM9,SULF2,DKK2,EGF,TTC21B,GID8,FZD9,DDX3X,TBL1XR1,PPM1A,RBPJ,CSNK1G1,SMAD3,NLE1,GPC3,MIR222,SOX4	grey	VSMC_M10
GO:0006284	0.99	0.02	14	39	base-excision repair	BP	1	RPA3,XRCC1,MBD4,FAM168A,WRN,ERCC6,POLL,POLG,APEX2,NEIL1,LIG3,NTHL1,MPG,PRMT6	grey	VSMC_M10
GO:0051017	0.99	0.01	60	139	actin filament bundle assembly	BP	1	PRKN,SHROOM1,MTSS1,BAIAP2L2,SRF,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,EPHA1,LCP1,CLASP2,WNT11,ARRB1,MKKS,ACTG1,FSCN2,PAWR,BAG4,DPYSL3,FAM107A,PIK3R1,PLS1,LIMA1,SORBS1,PTK2B,ALMS1,USH1C,RAPGEF3,DMTN,PXN,CARMIL1,PPFIA1,ARHGAP6,WASF2,SLC9A1,ITGB5,EPS8,WNT4,WAS,PFN3,KCTD13,SMAD3,CORO2B,EVL,PTGER4,TNFAIP1,INPP5K,SERPINF2,SPIRE2,TSC1,FHOD1,MIR21,RHOA,ASAP3,RGCC,PDXP	grey	VSMC_M10
GO:0060314	0.99	0.03	6	20	regulation of ryanodine-sensitive calcium-release channel activity	BP	1	PKD2,CASQ2,CALM1,JPH3,DMD,JPH2	grey	VSMC_M10
GO:0014015	0.99	0.02	18	48	positive regulation of gliogenesis	BP	1	TSPO,SOX10,TTBK1,PTN,EGFR,HDAC2,PLAG1,SYNJ1,NKX6-1,SPINT1,HDAC1,DAG1,TNFRSF1B,PRPF19,SOX8,MIR222,MIR125B1,LIF	grey	VSMC_M10
GO:0014020	0.99	0.02	35	86	primary neural tube formation	BP	1	FZD6,BRD2,PTCH1,PTK7,SEMA4C,FUZ,TEAD2,IFT172,OVOL2,SPINT2,TRAF6,CASP3,FZD3,OPA1,SPINT1,PAX2,PRICKLE1,SUFU,TGFB2,DVL3,GRHL3,LUZP1,SETD2,TULP3,LIAS,DVL2,MKS1,SKI,TSC1,GLMN,BCL10,VASP,NOG,WNT5A,RALA	grey	VSMC_M10
GO:0010543	0.99	0.02	10	30	regulation of platelet activation	BP	1	TEC,PLEK,TLR4,THBD,C1QTNF1,DMTN,UBASH3B,FCER1G,PLA2G4A,ABAT	grey	VSMC_M10

GO:0060065	0.99	0.03	5	18	uterus development	BP	1	ESR1,TGFB2,LHX1,STRA6,WNT5A	grey	VSMC_M10
GO:1901136	0.99	0.01	55	126	carbohydrate derivative catabolic process	BP	1	PDE7B,FUCA2,DPYS,PDE10A,APOBEC3H,ALDH1A1,GDA,CEMIP2,GNPDA2,GALT,ENPP4,NT5E,BPGM,CDADC1,NUDT15,GLB1,MBD4,GPD1L,NEU3,FBXO17,NUDT16,AHCY,AMPD3,GPD1,ENTPD4,FITM2,NUDT18,PDE9A,HYAL1,HYAL3,MGAT1,PDE8A,EDEM3,OVGP1,UPB1,CEMIP,FBXO2,IDUA,GALC,GLA,HEXA,PDE4A,GM2A,NEIL1,NT5M,ADAMTS12,IDS,NTHL1,MLYCD,CTBS,ABHD10,NUDT19,NEU2,HINT1,UPP1	grey	VSMC_M10
GO:0035023	0.99	0.02	27	69	regulation of Rho protein signal transduction	BP	1	CDC42SE2,GPR20,EPS8L1,LPAR1,MET,RAF1,ARRB1,ROBO1,ARHGEF28,F2RL1,F2R,EPS8,BCL6,ABL2,COL3A1,MYO9B,STARD8,ITGA3,KCTD13,RIT2,TNFAIP1,RALBP1,EPS8L3,SCAI,GPR35,ADGRG1,EPS8L2	grey	VSMC_M10
GO:0071456	0.99	0.01	51	119	cellular response to hypoxia	BP	1	MYC,PRKCE,EPAS1,AQP1,PTN,MGARP,FOXO3,DNMT3A,NDNF,SUV39H2,PLK3,EGLN2,SIRT2,PDK1,COX4I2,TMBIM6,BACH1,STC1,NKX3-1,OPA1,HIF1AN,SIRT4,TERT,SCN2A,AJUBA,USP19,OPRD1,HYOU1,SLC9A1,KCNK2,TBL2,EGLN3,ADAM8,PDK3,NFE2L2,STOX1,PINK1,SLC2A4,RBPJ,NPEPPS,GATA6,ACAA2,GNB1,MIR21,KCNK3,NOL3,BNIP3L,RWDD3,TIGAR,RGCC,MIEF1	grey	VSMC_M10
GO:1903364	0.99	0.01	60	137	positive regulation of cellular protein catabolic process	BP	1	LRP1,TNFAIP3,HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,VPS35,ZYG11B,FAF1,BBS7,PLK3,SUMO2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,TRIB3,PLK2,CEBPA,FBXW7,PTK2B,RNFT2,KCNE2,PRICKLE1,RNF144B,USP13,AC013489.1,EGF,DISC1,ARIH2,RNF185,NFE2L2,COP1,SOCS4,DNAJB2,PSMC3,OSBPL7,PSEN1,TAF1,LDLR,KEAP1,RNF128,PSMD10,FBXO22,FMR1,FZR1,BCAP31,SGTA,TMEM259,ZER1,DAB2IP,PSMC1,BAG2,RNFT1,PTTG1IP,DDA1	grey	VSMC_M10
GO:0051155	0.99	0.02	13	37	positive regulation of striated muscle cell differentiation	BP	1	MAML1,MAPK14,TRIM32,MYLK3,MAMSTR,NRG1,LMOD3,SMYD1,MEF2C,RBM24,ACTN3,PIEZO1,MIR199A1	grey	VSMC_M10
GO:0070613	0.99	0.02	20	52	regulation of protein processing	BP	1	MYH9,PLGRKT,IL1R2,ACP4,BCL2L12,CST7,PRNP,IFT52,SIRT4,RHBDD1,MELTF,ADAM8,LPCAT3,F12,SNX12,AC138894.1,SERPINF2,NOL3,CNTN2,BAG2	grey	VSMC_M10
GO:0051438	0.99	0.02	16	43	regulation of ubiquitin-protein transferase activity	BP	1	SKP1,BMI1,USP44,TRIB3,FBXW7,RPL23,DNM1L,DTX3L,RPL11,PINK1,PSEN1,DCUN1D3,FZR1,PARK7,BAG2,UBE2N	grey	VSMC_M10
GO:0009617	0.99	0.01	172	362	response to bacterium	BP	1	TNFAIP3,CYP27B1,FUCA2,RNF5,TSPO,FER1L6,TRIB1,MAPK14,PLA2G6,HSF1,IRF5,ADH5,PRKCE,FPR2,ANKRD17,CXCL8,NOD1,AKIRIN2,AQP1,PELI1,LYPD8,TLR4,MGST2,APOB,CDK19,HDAC2,C5AR1,PTGIR,CUBN,OPTN,MLH1,MYD88,PRDX3,TIMP4,IRAK2,THBD,NFKBIB,SIRT2,DCN,MAVS,FOXP1,TRAF6,HCK,IL1A,IL37,NR4A1,FER,CASP3,ERAP1,HPGD,PLSCR4,MEF2C,NUGGC,NR1H3,OAS3,NLRC5,RIPK2,F2RL1,F2R,ABCC2,MAPKBP1,NOD2,CD40,NFKB2,MAPKAPK3,CD96,HDAC1,RGS1,BANK1,PDCD4,FAM20A,TLR5,MAPKAPK2,FABP4,SCN7A,SLAMF8,FGR,COCH,IL10RA,FCER1G,LYZL6,FZD5,DUSP10,HMCN1,GGT2,VGF,CPS1,IL12A,COMT,UPF1,PYGL,SLC11A1,TNIP2,ALPL,GCH1,PLA2G16,CFP,MAPK1,SGMS1,OTUD5,SCGB1A1,FOXP3,LIAS,AKAP8,RBPJ,TNFRSF1B,SPON2,SYT11,FOS,MAPK3,CITED1,IL6R,MPO,S100A14,S100A8,SCNN1B,BDKRB1,TNIP1,CCL5,COLEC12,CCL2,LITAF,PTGER4,C3,NOS2,IL7R,GPC3,CEP192,JUN,DROSHA,TICAM1,ADAMTS13,CYBA,ASS1,LCN2,GFI1,BCL10,DAB2IP,ADGRL2,PTGFR,MIR21,RHOA,FGA,S100A12,OAS1,HIST1H2BK,CHGA,DEFB124,SLC22A5,CXCL6,CASP8,JCHAIN,CA5B,GNG12,CFD,IRGM,CMPK2,IL36G,CLDN1,WNT5A,INAVA,GGT5,PLAC8,SERPINB9,LRAT,PTGES,KCNJ8,CEBPB,HIST1H2BF,TENT5A,HIST1H2BJ,HAVCR2	grey	VSMC_M10
GO:1904591	0.99	0.02	13	37	positive regulation of protein import	BP	1	MAPK14,SMO,ARHGEF5,MAVS,PIK3R1,HCLS1,BAG3,MAPK1,TARDBP,PSEN1,SMAD3,EFCAB7,ZIC1	grey	VSMC_M10
GO:0080135	0.99	0.01	268	553	regulation of cellular response to stress	BP	1	PHLPP1,LRP1,EYA4,MAP3K5,MRNIP,HELB,PPP1R10,ARMT1,IER3,STK3,MAPK8IP2,MAP3K4,PRKN,AGER,BAK1,NCOA7,MYC,ATF4,HSF1,CDKN2A,POT1,GPR37,FBXO7,CRY1,NUAK1,CDK6,NCK2,GADD45G,KLHL31,PRDX1,SEMA4C,DNAJA1,FKTN,PNPT1,EMC10,MTURN,NOD1,CYREN,ETAA1,ZNF277,NR1H2,PTN,MET,EGFR,TRIM32,TLR4,TRAF1,SDCBP,SLC7A11,FOXO3,DHFR,ERCC1,DDIAS,XRCC1,AQP11,MYD88,PAXIP1,WDR48,PTPRF,FBH1,RNF169,FAM168A,ZMYND11,PAWR,PLCB1,SIRT7,SHLD1,EIF2AK2,RELL2,SEMA3A,DDRGK1,SH3RF2,PPP4R2,TEX15,ARL6IP5,PRKDC,ERCC6,MFHAS1,TRAF6,EPHB1,PLK2,ERCC8,C12orf49,PIK3R1,TAF9,HAND2,ATR,ING2,EYA1,SLF1,ARNTL,FBXW7,USP25,HTRA2,TMBIM6,PTK2B,RASGRP1,NR1H3,RIPK2,NKX3-1,ABRAXAS1,OPA1,SPIDR,AMFR,WRNIP1,SLC38A2,F2RL1,RNFT2,RIPK1,MARCH7,SPP1,PLA2R1,SLF2,NOD2,TAOK3,KIAA0319,TERT,TRPV4,PDCD4,TGFB2,SLC30A10,FBLN5,AXIN2,AJUBA,FICD,NCF1,KRAS,DYRK3,MAPKAPK2,USP13,SNAI1,USP19,CHEK2,EYA3,PARP9,DTX3L,KREMEN1,MCL1,TRAF5,HYOU1,CERS2,FZD7,KCNK2,MAP3K3,RNF185,PDE8A,RNF168,RTEL1,MAGI3,MGMT,DLG1,LRIG2,SETD2,YBX3,MAP3K11,NFE2L2,AIDA,DUSP10,MAPT,MBIP,NONO,BCL6,SYVN1,MEN1,MAP4K2,TNR,LPCAT3,DUSP19,ZCWPW1,MICU1,PDCD10,GCH1,PINK1,MMP3,LTBR,MAPK1,WAS,DDX11,MINK1,RAD52,EPHA4,BMPR1A,PARP1,SHLD2,GPS2,RELL1,DNAJB1,UIMC1,FXR2,WRAP53,VPS13C,KAT7,MUC1,TAOK2,NDEL1,YPEL3,MAPK3,ZBTB7B,AC138894.1,VASH1,TAF9B,MAP2K1,NSMCE1,CORO2B,SFPQ,OTUB2,PSMD10,NCOR1,TRAF3,CD74,MAPK7,SMCHD1,SLC25A23,STK26,ERCC4,PTPN2,TAOK1,RMI2,FMR1,PIAS4,N	grey	VSMC_M10

GO:0003015	0.99	0.01	80	180	heart process	BP	1	NEDD4L,SMAD5,SLC1A1,PPCS,TNNI3,EPAS1,ASB3,BVES,ATG5,TRPM4,SLC8A2,CACNB2,ATP1A3,CELF2,SCN5A,SCN1A,GPD1L,HBEGF,ADRA1D,SEMA3A,SGCG,STC1,KCNJ3,TBX5,TNNC1,KCNE2,DSP,CASQ2,KCNIP2,RYR2,PKP2,DNM1L,KCNJ2,MAP2K6,TNNI1,TGFB2,MYH7,GRK2,ANK2,AGT,ACE2,ATP1A2,ACTC1,SLC9A1,HDAC4,SCN4B,NOS1AP,DLG1,TTN,GCH1,ATP1B1,DES,SLC4A3,THRA,TCAP,ATP1B2,CACNA1G,ATP2A1,CALM1,TBX2,DSG2,SREBF1,ISL1,CYP2J2,ATP2B3,TRPV1,RNF207,CACNA1H,DMD,CHGA,TMEM65,KCNH2,SCN2B,RGS4,POPDC2,KCNJ8,HCN4,NKX2-5,HEY2,KCNG2	grey	VSMC_M10
GO:0061028	0.99	0.02	13	38	establishment of endothelial barrier	BP	1	ZDHHC21,S1PR3,MYD88,IKBKB,PLCB1,MARVELD2,RAPGEF2,RAPGEF3,F2RL1,RAP1B,VCL,FOXP3,CLDN1	grey	VSMC_M10
GO:0008064	0.99	0.01	70	159	regulation of actin polymerization or depolymerization	BP	1	ARPC3,AVIL,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,NCK2,KIAA1211,TMOD1,PLEKHH2,PRKCE,SPTBN1,PLEK,ADD2,FAM49A,WASF1,PLEKHG2,FCHSD2,MKKS,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,FMN1,LIMA1,PTK2B,F2RL1,IQGAP2,CYFIP1,DMTN,MAGEL2,CARMIL1,LMOD1,ADD3,SSH1,HCLS1,AP1AR,WASF2,SPTBN2,TMOD4,EPS8,WHAMM,DLG1,CAPZA1,CDC42EP2,NCKAP1,ARPC1A,WAS,TMOD2,SPTB,PFN3,HAX1,EVL,SSH2,MLST8,SPIRE2,WDR63,CARMIL2,RHOA,VASP,GMFG,GRB2,PFN4,PDXP,COTL1	grey	VSMC_M10
GO:2001135	0.99	0.03	5	18	regulation of endocytic recycling	BP	1	BVES,SORL1,EHD1,GRIPAP1,ARHGAP44	grey	VSMC_M10
GO:0051091	0.99	0.01	92	204	positive regulation of DNA-binding transcription factor activity	BP	1	ESR1,STK3,HSPA1B,AGER,IL5,SMO,HSF1,SRF,FZD1,KIT,ADGRF1,CAT,NOD1,ARHGEF5,TRIM32,TLR4,TRAF1,PRKD2,MYD88,PRDX3,IRAK2,ALK,IKBKB,TMEM173,EIF2AK2,MAVS,TFDP1,DDRGK1,TRAF6,FER,RHEBL1,RIPK2,NKX3-1,NKX6-1,RIPK1,PIDD1,NOD2,CD40,RAB7B,CD200,PPP3CA,SLCO3A1,KRAS,HCLS1,OPRD1,AGT,TSSK4,CIB1,TRAF5,HDAC4,TRIM52,RTKN2,ADAM8,PPP2R5B,SAV1,TNFSF18,CRTC1,RNF25,STK36,PINK1,STAT3,DVL2,CARD11,TAF1,SMAD3,CRTC2,RPS6KA5,S100A8,TRIM37,PRKCB,BTK,BEX1,CAMK2A,PPARGC1B,TICAM1,LRP8,PRKCZ,TRAF2,IKBKG,PARK7,LAMTOR5,BCL10,S100A12,TAF12,TRIM68,TRIM34,WNT5A,DDIT3,RGCC,UBE2N,RPS6KA4,WNT2	grey	VSMC_M10
GO:2000112	0.99	0.01	1446	2822	regulation of cellular macromolecule biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,SHMT2,GLI1,HBS1L,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,EIF3E,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,MED30,IL5,BRD2,RXRB,VGLL2,MRPL13,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,HABP4,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,RPAP2,CBX7,MAPK14,CBY1,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,IGF2BP3,FKTN,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,MTIF2,NFE2L3,PNPT1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,ANKRD17,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,ORC3,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,ASCC3,CDK5RAP2,TRAF1,BCL2L12,LPIN1,IL15,SFRP4,UCP1,	grey	VSMC_M10
GO:0046660	0.99	0.01	36	88	female sex differentiation	BP	1	ESR1,GDF9,BAK1,DMC1,FANCG,KIT,FOXO3,DACH1,ARRB1,ACVR1B,FOXL2,CASP3,ROBO2,ADAMTS1,BMPR1B,GAS2,SRD5A1,HYAL3,LHX9,SPO11,TAF4,VGF,WNT4,PTPRN,STAT5B,INHA,LHX1,STRA6,HSPA5,MSH4,LHX8,UBB,WNT5A,CEBPB,EREG,LHFPL2	grey	VSMC_M10
GO:0001701	0.99	0.01	146	314	in utero embryonic development	BP	1	CNOT2,STK3,PNLDC1,RRP7A,UBE2B,RSPO3,PTCH1,LY6E,TAB1,SOX10,MFNG,SMO,MDFI,TFEB,TAF8,MYH9,ZFAND5,SRF,APBA1,ANKS6,EPAS1,MSH2,RTN4,YTHDC1,ADAMTS3,GJB5,APOB,BMI1,ERCC2,GLI2,XRCC2,CCNB1IP1,TGFBR2,OVOL2,EOMES,CHD8,MAFG,CHTOP,SPINT2,TRAF6,GPI,ACVR1B,CEBPA,CCDC62,HAND2,CNOT1,NBN,DHX35,ACVR1C,SPINT1,COL4A3BP,RPGRIP1L,RTF1,ZBED6,PKD2,STK4,NPM2,ZNF335,TENT5C,IGF2,SH3PXD2A,ELF3,SBDS,DAD1,SNAI1,OTUD7B,POLG2,SLC25A20,ARNT,PLPP4,VASH2,RPL7L1,SYF2,MGAT1,TANC2,SP3,SETD2,YBX3,FZD5,PTH1R,TET1,KIF1BP,PLOD3,NMT1,BCOR,DNAAF2,RUNDC1,ELL,SEC24C,TTLL4,AKAP3,ARHGDIG,MAPK1,WDR74,BMPR1A,WDR19,SLC25A34,RBPJ,MED1,MFN2,RAD51B,SOX15,NDEL1,VASH1,CITED1,ALKBH1,MAP2K1,TMEM100,SMAD3,PPP4R4,KEAP1,SIN3A,AMOT,GATA6,MIB1,CAMSAP3,NLE1,XAB2,JAG2,SUPT6H,NSRP1,INPP5K,APBA3,PKD1,SOX8,FOXF1,TMEM231,TERF2,CMTM3,KRT19,CASP8,ACVRL1,PEMT,NOG,C2CD3,GRB2,C6orf141,BCL2L11,YBX1,LIF,CEBPB,MED21,SLC39A3,HEY2,WNT2,ST8SIA6	grey	VSMC_M10

GO:0001775	0.99	0.01	339	692	cell activation	BP	1	CD226,LRP1,TNFAIP3,ENPP3,FZD6,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,BAK1,XRCC6,MAPK14,MFNG,RAC2,SMO,CCND3,MYH9,FBXO7,SRF,TTBK1,TEC,KIT,TNFRSF21,NCK2,TLN1,NFIL3,PRDX1,EXOSC3,NLRP5,IL11,PRKCE,MSH2,FPR2,SKAP2,CXCL8,SLC46A2,PELI1,BMPER,PLEK,RSAD2,DGKI,IL4I1,EGFR,TLR4,IL15,ATG5,SLC7A11,TRAF3IP2,SPHK2,HMCES,BMI1,CSAR1,CST7,PHB,ERCC1,LCP1,CD300LF,CLPTM1,NECTIN2,GAB2,MLH1,GLI2,UNC13D,MYD88,PIBF1,KLF5,FOXJ1,PAXIP1,CYGB,THBD,IL15RA,PLAT,MYL12A,KLF6,CMTM7,TGFBR2,EOMES,C1QTNF1,NMI,ACTG1,PURA,TCIM,PAWR,PLCB1,PLCL2,SHLD1,PRNP,CLIC1,NCKAP1L,GAS6,FOXP1,PRKDC,SLC7A1,MFHAS1,ADRA2B,TRAF6,EPHB1,SOX12,GAPT,TOX,ZC3H8,IL1A,CAMK4,CEBPA,FER,PIK3CB,PIK3R1,CASP3,PTPRJ,MEF2C,TMEM131L,IL7,TPD52,PAG1,SLA2,P2RY1,PTK2B,RASGRP1,LMBR1L,EIF2AK4,NR1H3,RIPK2,NBN,DYSF,IFNGR2,CDH17,AP3B1,F2RL1,F2R,MARCH7,SOX13,DMTN,NOD2,ITGB6,ZNF335,TOLLIP,CD40,IGF2,GBF1,NFKB2,DCAF1,DOCK10,CD200,PKNOX1,LCK,PPP3CA,BANK1,ICOSLG,ADRA2A,BTN2A2,GPAM,TCIRG1,PRKAR1A,GPR137B,SNAP23,RABL3,SELPLG,HLX,TBC1D10C,UBASH3B,GPER1,SLAMF8,DGKD,THEMIS2,LAT2,FGR,CBL,FZD7,RPS6KA1,HDAC4,SNX4,SNX27,CD28,FCER1G,RUNX3,RNF168,PATZ1,FZD9,SP3,APOLD1,DLG1,PPP2R3C,ADAM8,DGKG,FZD5,DUSP10,MAPT,BLOC1S6,PLA2G4A,BCL6,SYVN1,BATF2,ITGA2B,ITGA4,IL12A,FN1,VSIR,RC3H1,PTPN6,TNFSF18,ADRA2C,FERMT3,CXCR2,SLC11A1,WNT4,LAG3,PTGDR,COL3A1,PPP3CB,TNIP2,DDOST,LTBR,STAT3,VCL,CD38,BST1,C12orf4,STAT5B,WAS,INHA,SCGB1A1,FOXP3	grey	VSMC_M10
GO:0001843	0.99	0.01	33	82	neural tube closure	BP	1	FZD6,BRD2,PTCH1,PTK7,SEMA4C,FUZ,TEAD2,IFT172,SPINT2,TRAF6,CASP3,FZD3,OPA1,SPINT1,PAX2,PRICKLE1,SUFU,TGFB2,DVL3,GRHL3,SETD2,TULP3,LIAS,DVL2,MKS1,SKI,TSC1,GLMN,BCL10,VASP,NOG,WNT5A,RALA	grey	VSMC_M10
GO:0006323	0.99	0.01	51	119	DNA packaging	BP	1	BAZ2A,BRD2,ASF1A,H3F3C,UBN2,SOX9,RSF1,SIRT2,M1AP,MCPH1,SPTY2D1,SYCP1,NAP1L5,RBBP4,SART3,ACIN1,GPER1,H2AFY2,TTN,HIRA,AKAP8L,TSPYL2,AKAP8,PHF8,NAP1L2,NAA60,NAA10,DFFB,CHD5,CHMP1A,CTCF,SYCP3,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,BEND3,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,RNF8,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,TSPYL5	grey	VSMC_M10
GO:0032870	0.99	0.01	214	450	cellular response to hormone stimulus	BP	1	FECH,AP3S1,MARS,PIP4K2C,ESR1,CNOT2,PPARA,PNPLA3,RXRB,PTK2,GKAP1,KDM4C,SOX10,HSF1,CCND3,FOXH1,GPT,RBFOX2,CRY1,KIT,PPAT,DNAJA1,PRKCE,PHIP,CRHR2,AQP1,GRB10,TNC,EGFR,LANCL2,GAB1,LPIN1,UCP1,MGARP,FOXO3,PGRMC2,APOB,FGF21,SESN3,BMI1,PIP4K2A,RAB10,PHB,CYSLTR2,ECHDC3,ATP1A3,TBC1D4,EGLN2,TADA3,AKT2,SNX5,MKKS,RARB,NR1D2,SRA1,TAF7,RNF14,KL,DDRGK1,PTPRA,FOXP1,LEPROTL1,ARID5A,PRKDC,CALCOCO1,NCOA4,TRIB3,LMO2,FAM107A,CYP7B1,DNMT3B,PAX8,NR4A1,FER,IDE,UFSP2,PIK3R1,NCOA2,ROBO2,ZNF366,ARNTL,SORBS1,MEF2C,CNOT1,KMT2D,DDX54,STC1,NKX3-1,OPA1,LPIN3,NKX6-1,NR4A2,CRY2,VPS18,ABCC2,CYFIP1,ADTRP,IGF2,PXN,GPLD1,SRD5A1,IRS1,GRB14,HDAC1,ADRA2A,SLC30A10,NR5A2,ABHD2,SORL1,C2CD5,GPER1,AGT,ATP1A2,SLC9A1,ARID1A,UCN2,HDAC4,SYAP1,USF1,NPAS4,RXRG,POR,NFE2L2,CREB1,YWHAG,RAP1B,PLOD3,CPS1,EIF4EBP2,CTSH,MEN1,SIK2,ESRRA,FBN1,PTGER2,GDF15,RAMP2,STAT3,SLC27A1,STAT5B,RAB8A,PADI2,DNAAF4,GPR173,AKAP8,PARP1,SLC2A4,RAB15,THRA,MAX,MED1,AGTRAP,FOXO4,PKLR,PAGR1,RAB8B,PGF,FOS,NDEL1,ZBTB7B,OGT,ESRRB,PIAS2,PRKCB,SCNN1B,BCAS3,ACACA,NCOR1,CAMK2A,INSR,NPC1,GATA6,PPARGC1B,SREBF1,LPIN2,JSL1,RHOXF1,GHR,LEPR,PTGER4,PTPN2,SOCS1,CRK,INPP5K,GNB1,PDPK1,PRKCZ,CACNA1H,PARK7,SLC25A33,RXRA,CYBA,ASS1,PTGFR,RHOA,INSRR,TRIM24,TRIM68,CA2,BGLAP,SMYD3,DUSP1,CRH,GRB2,SERPINB9,BCL2L11,INSIG2,APC,YWHAH,ZFP36L2,SH2B2,LEPROT,SFR1,GNG2	grey	VSMC_M10
GO:0010762	0.99	0.02	12	35	regulation of fibroblast migration	BP	1	PTK2,PRKCE,HAS1,ITGB1BP1,CYGB,BAG4,ARHGEF7,FER,DMTN,AC138894.1,ARHGAP4,C5orf30	grey	VSMC_M10
GO:0033120	0.99	0.02	10	30	positive regulation of RNA splicing	BP	1	SNW1,HABP4,TRA2A,NUP98,PIK3R1,SLC38A2,HSPA8,CELF3,PRPF19,CIRBP	grey	VSMC_M10
GO:0031396	0.99	0.01	81	180	regulation of protein ubiquitination	BP	1	TNFAIP3,HSPA1B,PRKN,TSPO,DERL1,SKP1,CRY1,SVBP,DNAJA1,RNF20,PRKCE,PELI1,ATG5,BMI1,PAXIP1,WDR48,MYCBP2,SPOPL,SPRY2,KLHL40,ARRB1,NMI,SIRT7,USP44,SH3RF2,TRAF6,TRIM44,TRIB3,FAM107A,SPSB4,FBXW7,RIPK2,MARCH7,PRICKLE1,NOD2,PRMT3,NHLRC1,RPL23,PEF1,PDCD6,SPRTN,DTX3L,PER2,RPL11,SENP2,IVNS1ABP,FBXO33,DDX3X,PINK1,BIRC3,DNAJB2,PHF23,GPS2,GNL3L,FBXO2,RNF111,PSEN1,TAF1,OGT,OTUB2,DCUN1D3,PSMD10,TICAM1,FZR1,PARK7,GLMN,HSPA5,BCL10,UBB,SOX4,BAG2,INAVA,CAMLG,RASSF5,UBE2N,PTTG1IP,CENPX,PRR7,UBE2D1,TSPYL5,RASD2	grey	VSMC_M10

GO:0045321	0.99	0.01	285	586	leukocyte activation	BP	1	CD226,TNFAIP3,ENPP3,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,BAK1,XRCC6,MFNG,RAC2,CCND3,MYH9,FBXO7,SRF,TTBK1,KIT,TNFRSF21,NCK2,NFIL3,PRDX1,EXOSC3,IL11,PRKCE,MSH2,FPR2,SKAP2,CXCL8,SLC46A2,PELI1,RSAD2,IL4I1,TLR4,IL15,ATG5,TRAF3IP2,SPHK2,HMCES,BMI1,C5AR1,CST7,PHB,ERCC1,LCP1,CD300LF,CLPTM1,NECTIN2,GAB2,MLH1,GLI2,UNC13D,MYD88,PIBF1,FOXJ1,PAXIP1,IL15RA,KLF6,CMTM7,TGFBR2,EOMES,NMI,PURA,PAWR,PLCL2,SHLD1,PRNP,NCKAP1L,GAS6,FOXP1,PRKDC,SLC7A1,MFHAS1,TRAF6,EPHB1,SOX12,GAPT,TOX,ZC3H8,IL1A,CAMK4,CEBPA,FER,PIK3R1,CASP3,PTPRJ,MEF2C,TMEM131L,IL7,TPD52,PAG1,SLA2,PTK2B,RASGRP1,LMBR1L,EIF2AK4,NR1H3,RIPK2,NBN,DYSF,IFNGR2,CDH17,AP3B1,F2RL1,MARCH7,SOX13,NOD2,ITGB6,ZNF335,TOLLIP,CD40,IGF2,DCAF1,DOCK10,CD200,PKNOX1,LCK,PPP3CA,BANK1,ICOSLG,BTN2A2,GPAM,TCIRG1,PRKAR1A,GPR137B,SNAP23,RABL3,SELPLG,HLX,TBC1D10C,GPER1,SLAMF8,THEMIS2,LAT2,FGR,CBL,FZD7,HDAC4,SNX4,SNX27,CD28,FCER1G,RUNX3,RNF168,PATZ1,FZD9,SP3,DLG1,PPP2R3C,ADAM8,FZD5,DUSP10,MAPT,BLOC1S6,PLA2G4A,BCL6,SYVN1,BATF2,ITGA4,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,CXCR2,SLC11A1,WNT4,LAG3,PTGDR,PPP3CB,TNIP2,DDOST,LTBR,STAT3,CD38,BST1,C12orf4,STAT5B,WAS,INHA,SCGB1A1,FOXP3,RASAL3,ZBTB1,SHLD2,GPS2,CARD11,RBPJ,TNFRSF1B,TBX21,STX4,PSEN1,SEMA4A,ITGAM,SYT11,KAT7,LCP2,DOCK2,BATF,ZBTB7B,CHRNB2,IL6R,CD19,LAT,SMAD3,IL4R,LDLR,S100A13,PRKCB,BTK,SCNN1B,BCL11B,YY1,CD74,CCL5,STXBP2,CCL2,YES1,JAG2,NKAP,ZNF3,CD320,PRAM	grey	VSMC_M10
GO:1901652	0.99	0.01	177	375	response to peptide	BP	1	LRP1,AP3S1,MARS,PIP4K2C,TNFAIP3,AGER,PPARA,PNPLA3,PTK2,AKR1B1,MAPK14,GKAP1,HSF1,IRF5,CCND3,GPT,TEK,CRY1,PPAT,CAT,PHIP,FPR2,PNPT1,NOD1,AREG,CRHR2,KLF11,GRB10,TLR4,GAB1,LPIN1,MGARP,FOXO3,FGF21,SESN3,PIP4K2A,RAB10,HADHA,CYSLTR2,KHK,EIF2B3,EPM2AIP1,ECHDC3,ATP1A3,TIMP4,KLF5,TBC1D4,AANAT,AKT2,SNX5,JAG1,PRNP,BTG1,KL,PTPRA,LEPROTL1,PRKDC,TRIB3,NR4A1,FER,IDE,PIK3R1,SORBS1,RIPK2,OPA1,LPIN3,NKX6-1,NR4A2,ACVR1C,SRSF6,CRY2,ABCC2,CYFIP1,NOD2,CD40,IGF2,PXN,GPLD1,SRD5A1,IRS1,RPL23,GRB14,TRPV4,SLC30A10,DAG1,SRSF4,SORL1,C2CD5,GPER1,AGT,SLC9A1,SYAP1,USF1,BACE1,SCAP,SNX6,CDKN1B,POR,NFE2L2,CREB1,YWHAG,RAP1B,FIS1,VGF,CPS1,EIF4EBP2,ITGA4,MEN1,SIK2,ESRRA,FBN1,GDF15,MMP13,MMP3,STAT3,PTPRN,SLC27A1,STAT5B,DDX11,RAB8A,EPHA4,GPR173,PARP1,SLC2A4,RAB15,MAX,CACNB1,AGTRAP,VPS13C,PSEN1,CACNA1A,FOXO4,NGFR,KAT7,PKLR,RAB8B,NDEL1,ZBTB7B,OGT,CITED1,UPRT,PRKCB,STAT2,CAMK2A,INSR,SREBF1,LPIN2,GHR,PTPN2,SOCS1,CRK,INPP5K,TRPV1,PDPK1,CACNA1B,PRKCZ,BSG,SLC25A33,CYBA,TSC1,ASS1,TLDC1,LCN2,HSD11B2,MT-CYB,INSRR,CA2,BGLAP,INAVA,GRB2,BCL2L11,INSIG2,APC,BCL2L2,SH2B2,EREG,LEPROT	grey	VSMC_M10
GO:0071345	0.99	0.01	279	574	cellular response to cytokine stimulus	BP	1	RNMT,MAP3K5,TNFAIP3,GFPT2,SLC12A2,HSPA1B,PRKN,AGPAT1,IL5,TCF7,TNFRSF13C,PMM1,PTP4A3,SYNGR1,MAPK14,MAPK13,IRF5,FOXH1,CNTFR,KIT,SLC1A1,TNFRSF21,IL1R2,NFIL3,GAPDH,RAD23B,GSDME,PNPT1,VRK2,CXCL8,PXDN,BSPRY,NR1H2,TRIM32,TLR4,TRAF1,IL15,MYLK3,FOXO3,APOB,BCAT2,TRAF3IP2,BMI1,PHB,SOX9,CD300LF,PDIA3,MYD88,OXSR1,ZFAND6,KLF5,NUMBL,IRAK2,POU4F1,IL15RA,IL17RE,SPRY2,ACKR2,PFKP,IKBKB,MKKS,NMI,TMEM173,ACTG1,PLCB1,BAG4,MAVS,GAS6,HPX,IRF7,DPYSL3,ST18,TRAF6,TRIM44,MRPL15,HCK,ASAH1,IL1A,IL37,CEBPA,FER,MRAS,FLNB,OTUD4,ROBO1,PCOLCE2,IL17RD,IL17RB,PTPRJ,GPD1,IL7,HTRA2,VEGFC,PTK2B,MME,KCNJ11,CCL17,NR1H3,OAS3,NLRC5,RIPK2,OTULIN,IFNGR2,NKX3-1,NKX6-1,ST3GAL6,F2RL1,RIPK1,ABCC2,IFIT2,JARID2,TOLLIP,CD40,RAB7B,INA,OASL,HDAC1,HYAL1,HYAL3,SP100,TCIRG1,NR5A2,SELPLG,PIAS3,CMKLR1,KRAS,FABP4,SPATA2,HCLS1,YTHDF2,GPER1,PARP9,PARP14,CIB1,CBL,TRAF5,ABCG4,OSM,HDAC4,PELI3,EPS8,THPO,IL10RA,FCER1G,YBX3,NFE2L2,CREB1,CDC42EP2,DUOX1,ITGA4,XRCC5,SPOCK2,RC3H1,PTPN6,EFHC2,PDCD10,UPF1,TNFSF18,CXCR2,STIP1,TNIP2,SMPD4,MUL1,BIRC3,STAT3,PTPRN,SPPL2A,SLC27A1,MAPK1,STAT5B,WAS,SGMS1,GREM2,PADI2,SLC2A4,GPS2,USP18,TNFRSF1B,MED1,STX4,PYDC1,ABCD4,MAPK3,DCST1,IL6R,HAX1,EPOR,STX8,IL4R,RPS6KA5,BTK,STAT2,KEAP1,TYK2,YY1,TRAF3,CD74,CCL14,CCL5,CSF1R,SHMT1,CCL7,CCL2,CCL25,GHR,LEPR,JAK1,NOS2,OSMR,LIFR,IL7R,ADAMTS12,PTPN2,SOCS1,LRP8,PIAS4,INPP5K,CDIP1,TRPV1,SPPL2B,TRAF2,AGPAT2,TNFRSF25,ADAMTS13,CYBA,F	grey	VSMC_M10

GO:0016192	0.99	0.01	594	1192	vesicle-mediated transport	BP	1	ATP9B,NME1,VPS4B,NEDD4L,LRP1,STX7,AP3S1,KIF5A,AGAP2,REPS1,CANX,RAB21,MARCH3,HSPA1B,SYNJ2,RIMS2,IGF2R,CDC42SE2,PRKN,AGER,SEPT8,GOPC,VPS52,FAM91A1,WASHC5,PTK2,TSNARE1,EXOC4,SYNGR1,MAPK15,NRBP2,CSNK1E,PLA2G6,COPG2,PICK1,MICALL1,BTBD9,RAC2,MYH9,CHRNA5,STEAP2,WASHC4,APBA1,OCIAD1,USP46,VPS50,SCFD2,KIT,SLC1A1,TGFBRAP1,RGP1,BICD2,CHMP2A,NLRP5,STX17,BRSK1,PRKCE,SMAP1,RIMS1,SPTBN1,FPR2,RIMS3,PPT1,CXCL8,SCRN1,EHBP1,WDR91,FKBP15,TRAPPC12,PLEK,RSPO1,AAK1,NR1H2,DDC,MET,FUZ,TLR4,TRAPPC3,VPS41,BVES,AMPH,FCGRT,IL15,STARD3NL,SFRP4,VPS35,ATG5,SDCBP,PPFIA3,LIN7B,WASF1,EPS15,BCAP29,INTU,SPHK2,ANKRD50,ARHGAP12,MTMR2,NAPA,RAB7A,PIP4K2A,AP2S1,RAB10,COPG1,ARL5B,CACNB2,RUBCNL,SYTL2,COG1,CLASP2,CUBN,RBSN,CD300LF,APOC1,OPTN,GAB2,GOLGA4,LLGL2,RALB,CCDC93,GRIK5,UNC13D,MYD88,TBC1D4,MYO7A,UBE2O,NAPB,IL15RA,SEC22C,RIN2,ACKR2,AKT2,LRP1B,HOOK3,ARRB1,ABCC4,TGFBR2,NEU3,SNX5,AP3M2,FCHSD2,RINL,ANK1,DPY30,ACTG1,YIPF4,ARL5A,SYT1,RAB5A,LIN7A,CNN2,HEATR5B,AP5S1,DNAJC13,FAM160A2,NCKAP1L,GAS6,BET1L,LEPROTL1,VPS16,COPZ1,FAM19A4,STX2,SYT9,SNPH,WASHC2A,TUB,ATP6V1H,LYPLA1,HCK,TMEM87B,TM9SF4,KIF3B,FER,ANKRD27,PIK3CB,VAMP5,HIP1R,CHMP2B,TRAPPC11,MTMR9,XKR6,ERC2,FCHO2,PTPRJ,SCARA3,CHMP4C,WDR54,P2RY1,RASGRP1,LMBR1L,DPYSL2,NR1H3,ALMS1,BMP2K,ARFGAP2,RAB11FIP5,EXOC6B,SEC31A,DYSF,SYNJ1,TPCN1,LOXL2,AP3B1,CHMP7,RHOBTB2,ZFYVE27,AP4B1,BIN3,F2RL1,LOXL4,ANO6,VPS18,TXNDC5,PLA2R1,LGI3,DOP1B,SEC31B,CY	grey	VSMC_M10
GO:0006809	0.99	0.02	21	55	nitric oxide biosynthetic process	BP	1	TSPO,TLR4,PTK2B,SPR,PKD2,MARC2,MARC1,AGT,NOS1AP,GCH1,SMAD3,DNM2,GLA,INSR,NOS2,TICAM1,TRPV1,ASS1,NQO1,MIR199A1,MIR99B	grey	VSMC_M10
GO:0007507	0.99	0.01	225	474	heart development	BP	1	NFATC1,ERBB3,GLI1,ADGRG6,MAML1,FRS2,STK3,PPARA,TBC1D32,SMAD5,LEMD2,PTK2,PTCH1,LY6E,TAB1,MAPK14,CBY1,PI16,PIM1,SMO,FOXH1,IFT74,TEK,PTK7,SRF,FHL2,ANKS6,TNNI3,DNAH11,RTN4,HOXA13,PTN,EGFR,BVES,CNTRL,MYLK3,TEAD2,ATG5,OSR1,ARMC4,TRAF3IP2,SPRY1,BBS7,SETDB2,DRC1,SOX9,GLI2,MEGF8,GALNT11,RAF1,IFT172,FOXJ1,SCN5A,POU4F1,WNT11,TGFBR2,OVOL2,JAG1,MKKS,RARB,RYR1,FREM2,DUSP6,NRG1,PRKDC,SGCG,POFUT1,ASXL1,PAX8,SMYD1,NCOA6,TFDP2,CASP3,HAND2,EYA1,PARVA,ROBO1,ROBO2,PLCE1,MEF2C,ADAMTS1,SOX6,NPY1R,NKX3-1,TBX5,IFT52,TNNC1,COL4A3BP,RPGRIP1L,DSP,PKD2,STK4,RIPPLY3,SALL1,PRICKLE1,DNAH5,JARID2,RBM24,RYR2,SUFU,PKP2,SIK1,TNNI1,PDCD4,TGFB2,TRIP11,PRKAR1A,COX17,AXIN2,SNAI1,MYH7,GRK2,ANK2,GPER1,AP1B1,AGT,ACTC1,SLC9A1,BICC1,NFATC4,FZD7,KCNK2,MMP21,ALPK3,CDKN1B,LUZP1,SETD2,CREB1,TTN,BCOR,EPHB4,MOSPD3,FN1,SAV1,FBN1,CALCRL,COL3A1,PPP3CB,ECE1,RAMP2,TBX19,MAPK1,OBSL1,TTC25,DNAAF4,LDB3,DVL2,BMPR1A,PDLIM7,TCAP,DHRS3,RBPJ,TNFRSF1B,MED1,ALDH1A2,MSX2,PSEN1,KDM6B,ITGA3,EFNA1,MAPK3,CACNA1G,MAP2K1,TMEM100,SMAD3,EPOR,MAP2K5,MKS1,DCTN5,TBX2,STRA6,YY1,DSG2,INSR,GATA6,MIB1,AP2B1,ISL1,ADAP2,ZBTB14,MYH11,OXCT1,IFT20,NDUFV2,GPC3,MBD1,HSPB11,SMYD4,PKD1,RNF207,SYPL2,COL5A1,TSC1,FOXL1,FOXF1,ENG,PSKH1,ACADM,MIR199A1,MIR21,MIR222,MIR23A,MIR24-1,MIR25,SOX4,JPH2,CASP8,ACVRL1,TMEM65,NOG,LBX1,WNT5A,BASP1,SIX1,RGS4,C2CD3,POPDC2,KCNJ8,	grey	VSMC_M10
GO:0090559	0.99	0.02	23	59	regulation of membrane permeability	BP	1	HEBP2,BAK1,TMEM14A,HIP1R,SLC9A1,THEM4,STPG1,FZD9,NMT1,MUL1,STAT3,TMEM102,CAMK2A,ACAA2,NAIF1,MIR29A,NOL3,BNIP3L,BCL2L11,SLC35F6,BCL2L2,PPIF,AC140504.1	grey	VSMC_M10
GO:0044030	0.99	0.03	5	18	regulation of DNA methylation	BP	1	MYC,PARP1,MBD1,MECP2,MIR29A	grey	VSMC_M10
GO:0010562	0.99	0.01	325	669	positive regulation of phosphorus metabolic process	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,MAP3K4,AGER,PPARA,IL5,GDF9,ROS1,XRCC6,PRXL2C,PTK2,TAB1,NTRK2,PLA2G6,HSF1,CCND3,GUCA1B,ZNF16,CHRNA3,TEK,TTBK1,TEC,KIT,SLC1A1,ROR2,SEMA4D,CLDN19,IL11,FPR2,MOB1B,SLC4A4,EPGN,AREG,BMP8A,ETAA1,PLEK,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,HDAC2,SLC8A2,MOB3C,PRKD2,PHB,ABI1,SOX9,SYMPK,MAPRE3,RALB,PRKAG2,RAF1,PIBF1,FBH1,SPRY2,WNT11,ALK,AKT2,ARRB1,TGFBR2,ACVR2A,NEK10,RPTOR,TCIM,HBEGF,PRNP,BAG4,MAVS,NRG1,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,ERCC6,FLT1,RYK,ADRA2B,TRAF6,NR1H4,EPHB1,RET,ACVR1B,OSBP,ZFP91,ROBO1,MTMR9,FBXW7,PTPRJ,GPD1,MEF2C,P2RX7,VEGFC,P2RY1,MADD,PTK2B,RASGRP1,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,FGF5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CDK2AP1,PKD2,STK4,ADTRP,NOD2,CNTN1,TAOK3,CD40,DSTYK,IGF2,BMPR1B,BDNF,GPLD1,IRS1,NEURL1,SPPL3,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K6,TGFB2,ZBTB20,ADRA2A,FAM20A,DAG1,AXIN2,SLCO3A1,AJUBA,NCF1,KRAS,EGF,PFKFB2,HCLS1,ADNP,OPRD1,GPER1,CHEK2,CASS4,SPATC1L,PARP9,PARP14,CACUL1,AGT,FGR,CIB1,ARNT,DVL3,STRADB,PPP2R5A,FZD7,OSM,SYAP1,NTSR1,THPO,STRADA,MLXIPL,EPHB3,PDE8A,LIMK2,DUSP12,GPRC5D,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,PTH1R,MAPT,STOX1,CEMIP,DBF4B,EPHB4,IL12A,MAP4K2,DDX3X,XRCC5,DUSP19,PDCD10,TNFSF18,ADRA2C,DOK7,SLC11A1,GDF15,MARK2,FGFR3,PINK1,ARAF,STAT3,SLC27A1,MAPK1,INHA,EPHA4,DLG4,MAGED1,DVL2,B	grey	VSMC_M10

GO:0045937	0.99	0.01	325	669	positive regulation of phosphate metabolic process	BP	1	ERBB3,MAP3K5,AGAP2,MRNIP,STK3,MAP3K4,AGER,PPARA,IL5,GDF9,ROS1,XRCC6,PRXL2C,PTK2,TAB1,NTRK2,PLA2G6,HSF1,CCND3,GUCA1B,ZNF16,CHRNA3,TEK,TTBK1,TEC,KIT,SLC1A1,ROR2,SEMA4D,CLDN19,IL11,FPR2,MOB1B,SLC4A4,EPGN,AREG,BMP8A,ETAA1,PLEK,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,HDAC2,SLC8A2,MOB3C,PRKD2,PHB,ABI1,SOX9,SYMPK,MAPRE3,RALB,PRKAG2,RAF1,PIBF1,FBH1,SPRY2,WNT11,ALK,AKT2,ARRB1,TGFBR2,ACVR2A,NEK10,RPTOR,TCIM,HBEGF,PRNP,BAG4,MAVS,NRG1,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,ERCC6,FLT1,RYK,ADRA2B,TRAF6,NR1H4,EPHB1,RET,ACVR1B,OSBP,ZFP91,ROBO1,MTMR9,FBXW7,PTPRJ,GPD1,MEF2C,P2RX7,VEGFC,P2RY1,MADD,PTK2B,RASGRP1,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,FGF5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CDK2AP1,PKD2,STK4,ADTRP,NOD2,CNTN1,TAOK3,CD40,DSTYK,IGF2,BMPR1B,BDNF,GPLD1,IRS1,NEURL1,SPPL3,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K6,TGFB2,ZBTB20,ADRA2A,FAM20A,DAG1,AXIN2,SLCO3A1,AJUBA,NCF1,KRAS,EGF,PFKFB2,HCLS1,ADNP,OPRD1,GPER1,CHEK2,CASS4,SPATC1L,PARP9,PARP14,CACUL1,AGT,FGR,CIB1,ARNT,DVL3,STRADB,PPP2R5A,FZD7,OSM,SYAP1,NTSR1,THPO,STRADA,MLXIPL,EPHB3,PDE8A,LIMK2,DUSP12,GPRC5D,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,FZD5,PTH1R,MAPT,STOX1,CEMIP,DBF4B,EPHB4,IL12A,MAP4K2,DDX3X,XRCC5,DUSP19,PDCD10,TNFSF18,ADRA2C,DOK7,SLC11A1,GDF15,MARK2,FGFR3,PINK1,ARAF,STAT3,SLC27A1,MAPK1,INHA,EPHA4,DLG4,MAGED1,DVL2,B	grey	VSMC_M10
GO:0045724	0.99	0.02	6	21	positive regulation of cilium assembly	BP	1	FUZ,ZMYND10,HTT,HAP1,MNS1,WRAP73	grey	VSMC_M10
GO:0043603	0.99	0.01	449	897	cellular amide metabolic process	BP	1	ORMDL2,SEC11C,PAN2,HSD17B4,RPS12,SHMT2,LVRN,HBS1L,MARS,B4GALNT1,TSFM,CPM,RMND1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,EIF3E,PNLDC1,PPT2,QKI,ACSL6,MRPL13,RPS18,MRPL55,JMJD4,AGO2,HABP4,RPS10,TNRC6B,ATF4,TUT7,GTPBP1,NTRK2,PLA2G6,EIF3L,CARNMT1,GDA,GNPDA2,GTPBP2,CLIC5,SLC1A1,NCK2,MRPS9,SPTLC1,GAPDH,CNOT11,AASDH,EXOSC3,RPS14,LRPPRC,PPCS,SRBD1,CHAC2,IGF2BP3,RTN4,PPP2R1A,MTIF2,PNPT1,PPT1,AGO1,EGFR,ASCC3,MGST2,QRSL1,C6orf203,TUT4,SLC7A11,FOXO3,SMPD2,DLD,PUM2,AGK,NANP,SPHK2,DHFR,EEFSEC,MKNK1,NAPEPLD,CNBP,MMACHC,GSTK1,EIF2B3,RPS8,MLH1,CDC123,MTRF1,DPH2,AANAT,RPSA,RPL14,MRPL33,ACER3,TNRC6C,ELOVL1,AKT2,METTL17,NEU3,SPTLC3,MRPS12,PURA,DPH3,HARS,HARS2,BTD,SLC25A15,EIF2AK2,PRNP,CARS2,LSM1,MRPL3,PANK2,AIMP1,PDK1,CLIC1,AMDHD1,RPL31,LARS,EIF4E3,SIRT3,UPF3A,ARL6IP5,PRKDC,MRPL17,CPXM1,SUCLG2,KBTBD8,PAN3,NR1H4,PDHX,MRPL15,NSMAF,MIPEP,ELOVL7,ASAH1,CEBPA,IDE,C12orf65,IMMP1L,NLN,MRPL35,ST8SIA4,GSS,ABCB9,CASP3,ERAP1,RPL6,PCSK1,MRPS27,MRPL19,SCG5,ENC1,HTRA2,MRPS28,CNOT1,CELF1,USP16,PTK2B,ACOT12,CNOT6L,MME,MTHFD2,MAPKAPK5,EIF2AK4,EIF4E2,SPCS1,NSUN3,PAIP2B,FITM2,ORMDL1,FTO,COL4A3BP,ABCC2,CPN1,CYFIP1,NOD2,TENT4B,RBM24,SLC2A13,WARS2,MRPS17,MTRR,PM20D1,CDKAL1,EIF2D,GATC,ASL,MCEE,NEURL1,SPPL3,RPUSD4,YARS2,RPL23,DDX25,GLRX2,RPL4,XPNPEP1,RPS17,BANK1,LTO1,CAPRIN2,IGHMBP2,BDH2,RPL27A,GPAM,FAR2,ACSL5,MRPS35,ABHD4,DIS3L2,MRPL52,ST8SIA2,SGMS2,RCC1L,KLHL25,GIGYF2,MRPS11,ENPEP,R	grey	VSMC_M10
GO:0071071	0.99	0.03	4	15	regulation of phospholipid biosynthetic process	BP	1	LPIN1,NR1H4,LPCAT1,SLC27A1	grey	VSMC_M10
GO:0045862	0.99	0.01	139	297	positive regulation of proteolysis	BP	1	MAP3K5,HSPA1B,GRAMD4,PRKN,AGER,FBLN1,BAK1,RNF217,TRIB1,MYC,PTK2,AGTPBP1,CSNK1E,HSF1,MYH9,TTBK1,SLC1A1,PLGRKT,NOD1,AKIRIN2,CASP8AP2,TNFSF15,TRIM32,ZYG11B,HSPE1,HDAC2,BBS7,PLK3,SUMO2,WDR48,KLHL40,ARRB1,SIRT2,RNF14,DDRGK1,SH3RF2,ARL6IP5,ST18,TRIB3,PLK2,ASPH,CEBPA,FOXL2,HIP1R,ROBO1,PCOLCE2,DIABLO,SH3D19,FBXW7,HTRA2,PTK2B,RIPK2,SENP1,NKX3-1,ACVR1C,F2R,RNFT2,PIDD1,KCNE2,PRICKLE1,RNF144B,GPLD1,RHBDD1,LCK,ADRA2A,PDCD6,SART3,USP13,AC013489.1,EGF,DISC1,GPER1,PSME1,ARIH2,CIDEB,RNF185,MELTF,EGLN3,ADAM8,NFE2L2,MAPT,FIS1,CTSH,DDX3X,COP1,FN1,VSIR,LPCAT3,PSME3,SOCS4,PINK1,MUL1,STAT3,DNAJB2,EPHA4,BCL2L13,F12,TNFRSF1B,FGFR4,PSMC3,OSBPL7,PSEN1,NGFR,EFNA1,TAF1,OGT,SMAD3,CLN6,S100A8,KEAP1,TNIP1,PSMD10,FBXO22,FMR1,FZR1,BCAP31,P2RX1,SGTA,TMEM259,ZER1,BCL10,DAB2IP,MIR21,MIR27B,RHOA,RPS27L,CNTN2,FADD,CASP8,PSMC1,BAG2,RNFT1,ACER2,BCL2L11,PERP,APH1B,DDA1,PRR7,CRADD	grey	VSMC_M10
GO:0036303	0.99	0.02	6	21	lymph vessel morphogenesis	BP	1	ACVR2B,VEGFC,PPP3CB,VASH1,PKD1,ACVRL1	grey	VSMC_M10
GO:2001243	0.99	0.01	34	83	negative regulation of intrinsic apoptotic signaling pathway	BP	1	PRKN,DNAJA1,TRIM32,ARMC10,DDIAS,TAF9,ING2,HTRA2,TMBIM6,NDUFS3,OPA1,MARCH7,HDAC1,SNAI1,MCL1,HYOU1,RTKN2,YBX3,NFE2L2,IVNS1ABP,NONO,SYVN1,DDX3X,PINK1,MUC1,TAF9B,CD74,MAPK7,PARK7,MIR21,NOL3,PTTG1IP,BCL2L2,PPIF	grey	VSMC_M10

GO:0032446	0.99	0.01	344	703	protein modification by small protein conjugation	BP	1	NEDD4L,FEM1C,TRIM36,RMND5B,TNFAIP3,FBXO30,TRIM39,FBXO43,MARCH3,HSPA1B,TULP4,PRKN,RNF5,MED30,TSPO,DERL1,SKP1,UBE2B,RNF217,RNF146,KLHL3,UHRF2,ZC3HC1,FBXL6,FBXO7,KLHDC3,ASB15,CRY1,NFX1,DCAF12,LNX1,FBXO10,DCAF10,SVBP,DNAJA1,RNF20,PRKCE,EPAS1,ASB3,UBE3D,FANCL,PELI1,CNOT4,BSPRY,HECW1,TRIM32,FBXW2,TRAF1,HACE1,NOSIP,ATG5,TRPM4,TRAF3IP2,BMI1,LRRC41,FBXL2,SUMO2,KBTBD6,KCTD21,TRIM54,CAND2,UBE2E2,PAXIP1,WDR48,UBE2O,MYCBP2,UBE3C,SPOPL,FBH1,ASB13,MED8,SPRY2,UBE2E1,KLHL40,CCNB1IP1,ARRB1,RNF169,CBX4,FBXO17,NMI,SIRT7,TPP2,NHLRC3,RNF24,RNF14,RNF122,USP44,DDRGK1,SH3RF2,UBOX5,RYBP,TRIM3,KBTBD8,LNX2,TRAF6,TRIM44,MARCH8,TRIB3,ERCC8,FAM107A,HECTD2,KCTD6,DTX4,SPSB4,ZFP91,RNF181,RNF7,UBE2L6,EYA1,TRPC4AP,FBXW7,TRIM2,HLTF,ENC1,ANAPC5,ANAPC7,ATG10,KLHL2,DDB2,RIPK2,OTULIN,ASB8,HDAC7,AMFR,RNFT2,FBXO21,WDSUB1,VPS18,MARCH7,TTC3,NEURL2,HERC6,PRICKLE1,HERC5,NOD2,PRMT3,TRIM45,HERC2,WSB2,MYLIP,TOLLIP,SIAH1,MAGEL2,NHLRC1,FBXL15,DCAF1,RNF144B,FBXO25,DZIP3,MED10,RNF10,PCGF6,KLHL12,IFIH1,NEURL1,RPL23,HECW2,PEF1,KLHL42,PDCD6,RNF115,RNF123,PIAS3,KLHL25,RNF114,AC013489.1,SPRTN,KLHL24,ASB11,DTX3L,ZNRF3,ABCB11,ARIH2,RNF26,NEDD8,CBL,TRAF5,ARNT,PER2,ASB1,HDAC4,STX1A,PELI3,RNF215,TRIM52,UFC1,DCAF7,RNF185,RNF168,RNF214,BTBD1,RPL11,SENP2,NFE2L2,IVNS1ABP,PHC1,SYVN1,FBXO33,BCOR,KLHDC1,DDX3X,COP1,FBXO24,ATXN7L3,ASB16,RC3H1,SPSB2,KLHL20,TRIM9,UBA52,RNF4,RNF25,ZSWIM8,SOCS4,TMEM129,PINK1,MUL1,	grey	VSMC_M10
GO:0010975	0.99	0.01	176	376	regulation of neuron projection development	BP	1	NME1,NEDD4L,LRP1,SEMA6A,AVIL,RAB21,TIAM2,FSTL4,SYNGAP1,WASHC5,PLXNA4,NTRK2,CHRNA3,FBXO7,PTK7,SRF,FZD1,ROR2,SEMA4D,SEMA4C,BRSK1,TMEM30A,RTN4,RUFY3,ACP4,LPAR1,EPHA7,PTN,HECW1,KEL,RTN4IP1,FIG4,PLXNA1,HDAC2,NDNF,SLC39A12,GOLGA4,MEGF8,PTPRF,TSKU,SS18L2,ALK,TMEM106B,SEMA3D,SPART,PLXNC1,SEMA3A,ULK1,DPYSL3,RYK,RET,TOX,CBFA2T2,ANKRD27,ROBO1,ROBO2,TENM3,ENC1,SEMA4F,TLX2,CUX2,KATNB1,PTK2B,RAPGEF2,DGUOK,TIAM1,PAQR3,OPA1,ZFYVE27,SEMA3G,ITPKA,SPP1,CYFIP1,SEMA4G,CNTN1,MYLIP,LZTS1,BDNF,KIAA0319,DNM1L,PPP3CA,HECW2,CAPRIN2,TRPV4,SEMA3F,MARK1,CFL1,ADNP,DISC1,KREMEN1,AGT,CIB1,RAB17,CERS2,NFATC4,SS18L1,PTPRO,CDKL5,INPP5J,EPHB3,TANC2,LRIG2,WNT3,DGKG,NFE2L2,MAPT,ABL2,SEMA6D,PPP2R5B,EHD1,TNR,FN1,EFHC2,NIN,SERPINI1,CRTC1,DNM3,RETREG3,MARK2,CAMK2G,CD38,OBSL1,CRMP1,EPHA4,ATP1B2,GAK,STX1B,PSEN1,SEMA4A,ITGA3,TRIM46,EFNA1,NDEL1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,NTN1,SNAPIN,PARP6,RIT2,GPRASP2,BHLHB9,ARHGAP44,TRPV2,FBXO38,CDK5R1,THOC2,RRN3,SEZ6,DAB1,LRP8,CRK,L1CAM,ARHGAP4,PLXNA3,AMIGO1,TSC1,NTNG2,FBXO31,GFI1,HSPA5,DAB2IP,MIR222,RHOA,PLK5,CNTN2,GRID2,CNTF,RTN4RL1,THY1,WNT5A,POU3F2,CHN1,YWHAH,EFNB3	grey	VSMC_M10
GO:0030182	0.99	0.01	526	1067	neuron differentiation	BP	1	ADNP2,NME1,NEDD4L,ATP8B1,ONECUT2,TCF4,LRP1,SEMA6A,KIF5A,AVIL,ATAT1,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,AGER,SULT4A1,TSPO,UQCRQ,FSTL4,SYNGAP1,WASHC5,ASAP1,GFRA3,PTK2,PTCH1,ANKS1A,AGTPBP1,PLXNA4,NTRK2,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,MICALL1,RAC2,SMO,RBFOX2,CHRNA3,PRPH2,FBXO7,RORB,PTK7,SRF,FZD1,ADGRF1,TNFRSF21,NCK2,ROR2,SEMA4D,DLX5,ETV1,SEMA4C,BEND6,SVBP,BRSK1,RDH13,RIMS1,TMEM30A,RTN4,GSDME,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,PPT1,MYCL,AREG,EPHA7,WHRN,PTN,MET,TNC,YWHAZ,EGFR,HECW1,TRIM32,NCDN,CDK5RAP2,EPHA1,KEL,MYCN,RTN4IP1,NRCAM,FOXO3,NTF4,FIG4,WASF1,MFSD8,DHFR,PLXNA1,HDAC2,MTMR2,NAPA,DNMT3A,NDNF,RAB10,IQSEC1,ABI1,SOX9,ERCC2,SLC39A12,ERCC3,USH1G,CDNF,GOLGA4,GLI2,MEGF8,KDM4A,IFT172,PTPRF,MYO7A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,WNT11,SLITRK5,ALK,DZANK1,CPNE9,FARP1,KIF5C,SLC4A7,JAG1,FSCN2,SYT1,TMEM106B,LRTOMT,AP000812.5,FEZ2,RAC3,CEP290,SLC23A2,LSM1,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NRG1,NCKAP1L,ULK1,DPYSL3,ERCC6,RYK,ADRA2B,SNPH,EPHB1,PLK2,RET,LGI4,TOX,ZSWIM6,TTL,DNMT3B,CBFA2T2,ANKRD27,ZNF536,PREX2,CASP3,HAND2,DCLK2,EYA1,PLS1,ROBO1,ROBO2,TENM3,ADGRV1,ENC1,FZD3,MEF2C,SEMA4F,FAIM2,HTRA2,NCAM2,TLX2,CUX2,KATNB1,PTK2B,RAPGEF2,DGUOK,DPYSL2,EIF2AK4,NNAT,RND1,TIAM1,PAQR3,SLIT1,USH1C,TENT2,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,CRTAC1,C8orf37,SEMA3G,RPGRIP1L,ITPKA,SPP1,PIGT,PAX2,CYFIP1,ALCAM,TSPAN2,SEMA4G,SALL1,NKD1,CNTN1,ZNF335,DTNBP1,MYL	grey	VSMC_M10
GO:0060977	0.99	0.03	4	16	coronary vasculature morphogenesis	BP	1	HAND2,TBX5,SETD2,HEY2	grey	VSMC_M10
GO:0042307	0.99	0.02	12	35	positive regulation of protein import into nucleus	BP	1	MAPK14,SMO,MAVS,PIK3R1,HCLS1,BAG3,MAPK1,TARDBP,PSEN1,SMAD3,EFCAB7,ZIC1	grey	VSMC_M10
GO:0014910	0.99	0.01	23	60	regulation of smooth muscle cell migration	BP	1	LRP1,TRIB1,TLR4,PLXNA1,MEF2C,ADAMTS1,DOCK5,TERT,GNA13,SSH1,SORL1,AGT,HDAC4,NFE2L2,SEMA6D,BMPR1A,FOXO4,CCL5,DOCK7,CRK,MIR21,RHOA,PDGFD	grey	VSMC_M10
GO:0051496	0.99	0.02	17	47	positive regulation of stress fiber assembly	BP	1	LPAR1,ITGB1BP1,ARHGEF5,EPHA1,WNT11,BAG4,RAPGEF3,PXN,CARMIL1,WNT4,SMAD3,EVL,SERPINF2,TSC1,FHOD1,RHOA,RGCC	grey	VSMC_M10

GO:0007623	0.99	0.01	70	160	circadian rhythm	BP	1	PHLPP1,TPH2,PPARA,ATF4,NTRK2,CSNK1E,BTBD9,FBXL6,RORB,CRY1,NFIL3,DDC,EGFR,HDAC2,SUV39H2,AANAT,MYCBP2,PPP1CB,BHLHE40,NR1D2,PRKDC,HTR7,NUDT12,AHCY,SPSB4,NCOA2,ARNTL,FBXW7,NR1H3,TOP1,CRY2,MAGEL2,SRD5A1,SIK1,HDAC1,ARNTL2,CIART,USP2,PER2,C3orf70,CREB1,NONO,CRTC1,NDUFA9,KDM5A,MAGED1,DDB1,TARDBP,NGFR,FBXL22,OGT,CIPC,CHRNB2,KDM8,SFPQ,SIN3A,NCOR1,SREBF1,RAI1,NOS2,JUN,PER3,GPR157,ASS1,ZFHX3,FBXL8,FBXL12,CRH,PASD1,HS3ST2	grey	VSMC_M10
GO:0045807	0.99	0.01	33	82	positive regulation of endocytosis	BP	1	NEDD4L,LRP1,RAB21,PICK1,PPT1,SFRP4,ARRB1,NCKAP1L,SYNJ1,F2RL1,ANO6,DNM1L,PPP3CA,EGF,DGKD,CBL,AP2M1,CALY,ANKFY1,ANXA2,AC138894.1,DNM2,INSR,MIB1,AP2B1,SGIP1,C3,GPC3,FMR1,ABCA7,WNT5A,LDLRAP1,CBLL1	grey	VSMC_M10
GO:0032515	0.99	0.02	7	23	negative regulation of phosphoprotein phosphatase activity	BP	1	IKBKB,NCKAP1L,CRY2,TIPRL,BOD1L2,PPP4R4,PPP1R15A	grey	VSMC_M10
GO:0003300	0.99	0.01	30	75	cardiac muscle hypertrophy	BP	1	PPARA,PI16,HDAC2,TRPC3,KDM4A,HAND2,TIAM1,JARID2,RYR2,PDE9A,PPP3CA,MYH7,AGT,SLC9A1,HDAC4,TTN,CAMTA2,PARP1,TCAP,TNFRSF1B,SMAD3,YY1,GATA6,MIR199A1,MIR21,MIR23A,MIR24-1,MIR25,RGS4,HEY2	grey	VSMC_M10
GO:0072594	0.99	0.01	168	355	establishment of protein localization to organelle	BP	1	TIMM21,PEX7,TNFAIP3,PEX3,PPP1R10,PRKN,TSPO,HSPA4,FAM53C,MAPK14,TOMM22,RAC2,SMO,PEX6,POT1,FBXO7,PEX1,TRAM2,RAB23,SEC61B,SIX2,DNAJA1,SEC61G,VPS41,MGARP,AGK,TRAF3IP2,RAB7A,RAB10,KPNA3,DNAJC15,IPO13,ZFAND6,GCKR,SEC62,KPNA2,PITRM1,TIMM50,USP36,TMCO6,NUP98,FERMT1,HACL1,ING1,BAG4,MAVS,SRP14,NCOA4,NUP58,MIPEP,IPO11,IMMP1L,PIK3R1,TNPO1,FBXW7,PEX2,PKIA,HTRA2,CSNK2A2,NUP54,SSR3,SPCS1,SPIDR,AP3B1,PEX16,CRY2,TOMM34,PRICKLE1,LONP2,RYR2,SUFU,SIRT4,CABP1,SRPRA,RPL23,PPP3CA,IPO9,TERT,MON1A,OXA1L,HCLS1,HSPA8,HPS4,SORL1,ARIH2,AGT,BAG3,PEX19,RNF215,IL10RA,TOMM40L,VPS37D,EIF4ENIF1,POM121,APOD,FZD5,MAPT,FIS1,NMT1,HK1,H2AFY2,GRPEL1,C11orf65,AP4M1,BCS1L,FAM53A,PINK1,ZFAND2B,STAT3,AP3M1,MAPK1,TIMM17B,PEX26,VPS13D,MED1,MFN2,TSPAN17,NPEPPS,KPNB1,WRAP53,TARDBP,VPS13C,PEX14,PSEN1,NEURL1B,RANBP17,RAB8B,HAX1,ZDHHC15,TNPO2,RAB11A,SMAD3,CALM1,TIMM29,SREBF1,LAMP2,MAIP1,EFCAB7,PAM16,BCAP31,SGTA,PEX10,NUP214,HSPA5,SH3GLB1,VPS4A,MICALL2,BNIP3L,NXT2,TIMM10B,TIMM23B,CACNG7,HIKESHI,DDIT3,TRAM1L1,RALA,PTTG1IP,SNX16,TIMM8B,RHOU,LEPROT,GRPEL2,CACNG5,ZIC1,PEX12,SPCS2,DNAJC19,SEC61A2	grey	VSMC_M10
GO:1901566	0.99	0.01	667	1317	organonitrogen compound biosynthetic process	BP	1	NME1,KDSR,ORMDL2,PAN2,FECH,GLS2,RPS12,SHMT2,ATG12,TBPL1,HBS1L,MARS,B4GALT7,B4GALNT1,TSFM,RXYLT1,ATP5MGL,RMND1,GFPT2,CNOT2,TPH2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,ALDH7A1,ZDHHC14,EIF3E,ALG12,PNLDC1,PPT2,QKI,PPARA,ACSL6,TSPO,MRPL13,A4GALT,RPS18,PMM1,MRPL55,JMJD4,AGO2,HABP4,RPS10,TNRC6B,ATF4,PYCR3,TUT7,GTPBP1,PLA2G6,EIF3L,CKB,GPAA1,ZDHHC21,MOCS1,PSAT1,GUCA1B,IMPDH1,HACD4,MTAP,NMRK1,LARGE1,GPR37,ALDH1A1,GTPBP2,SLC35B2,CWH43,SLC1A1,ST6GAL2,SRD5A3,NCK2,MRPS9,SPTLC1,SLC25A13,GAPDH,CNOT11,AASDH,PPAT,C1GALT1,CHST10,EXOSC3,RPS14,LRPPRC,ALG2,PPCS,SRBD1,TMEM246,PIGF,CHAC2,IGF2BP3,FKTN,HAS1,MTIF2,PNPT1,NT5E,PPT1,DDC,AGO1,EGFR,ASCC3,IL15,ATG5,MGST2,QRSL1,C6orf203,TUT4,SLC7A11,FOXO3,SMPD2,DLD,PUM2,APOB,AGK,BCAT2,NANP,SPHK2,DHFR,CMPK1,HS3ST5,ADCY3,EEFSEC,MKNK1,ALG11,PRKD2,PRTFDC1,POMGNT1,CNBP,AKR1A1,EIF2B3,RPS8,MLH1,CDC123,MTRF1,B4GALT2,CHPF2,DPH2,AQP11,PRKAG2,GALNT11,SLC22A13,ATP5F1C,AANAT,SLC25A38,RPSA,ST6GALNAC2,RPL14,MGAT5B,MRPL33,ACER3,TNRC6C,ELOVL1,CSGALNACT1,AKT2,METTL17,UGGT2,SPTLC3,MRPS12,PURA,IDO2,HBEGF,IDO1,PAWR,PLCB1,TMTC4,DPH3,PGAP2,GALNT15,HARS,HARS2,SLC25A15,EIF2AK2,CARS2,LSM1,MRPL3,PANK2,AIMP1,PDK1,FUT10,RPL31,GXYLT2,LARS,EIF4E3,SIRT3,UPF3A,PRKDC,EOGT,MRPL17,KBTBD8,PAN3,PDHX,APIP,SLC5A8,MRPL15,CSAD,ELOVL7,ASAH1,PANK1,ZDHHC20,POFUT1,CEBPA,NUDT12,C12orf65,MRPL35,AMPD3,PIGU,ST8SIA4,GSS,RPL6,HAND2,ATP5F1A,PCSK1,B3GNT4,MRPS27,MRPL19,ENC1	grey	VSMC_M10
GO:0060537	0.99	0.01	150	323	muscle tissue development	BP	1	STAC3,GLI1,MAML1,FRS2,PPARA,VGLL2,PITX1,SMAD5,LEMD2,PTCH1,LY6E,MAPK14,CBY1,PI16,PIM1,SMO,FOXH1,ZFAND5,SRF,PGM5,FHL2,MEOX2,HIVEP3,TNNI3,MYH14,AKIRIN1,BVES,KEL,MYLK3,ATG5,OSR1,SOX9,KLF5,SCN5A,POU4F1,KLHL40,TGFBR2,SIRT2,RARB,NR1D2,RYR1,DCN,P2RX2,NRG1,LMOD3,EPHB1,SGCG,NR4A1,SMYD1,NLN,FOXL2,FLNB,VAMP5,SAP30,EYA1,ARNTL,MEF2C,SOX6,TLL2,HOMER1,TBX5,BIN3,TNNC1,DSP,PKD2,JARID2,RBM24,RYR2,IGF2,MYH15,NEURL1,PKP2,SIK1,PPP3CA,TNNI1,TGFB2,POGLUT1,PRKAR1A,HLX,USP19,MYH7,AGT,ACTC1,SLC9A1,FZD7,MYOZ2,CASQ1,ACTN3,HDAC4,KCNK2,ALPK3,EFEMP2,DLG1,YBX3,CREB1,TTN,SAV1,MYOZ1,MAPK1,OBSL1,BMPR1A,TCAP,RBPJ,MED1,ALDH1A2,MYLPF,ZNF689,SOX15,MSX2,KDM6B,FOS,CACNA1G,SMAD3,TBX2,STRA6,YY1,DSG2,FBXO22,GATA6,ISL1,MYH11,IFT20,NDUFV2,MRTFB,SKI,SOX8,TSC1,ENG,ACADM,MIR199A1,MIR222,MIR23A,MIR24-1,MIR25,RHOA,DMD,CSRP2,JPH2,NOG,WNT5A,SIX1,RGS4,POPDC2,MYORG,UQCC2,HCN4,C3orf58,NKX2-5,HEY2,WNT2	grey	VSMC_M10

GO:0034644	0.99	0.01	31	77	cellular response to UV	BP	1	BAK1,MYC,ATF4,MAPK13,OPN1SW,AQP1,PTN,ERCC1,XPC,PIK3R1,ATR,MME,EIF2AK4,DDB2,TP53INP1,RHBDD1,HYAL1,HYAL3,NFATC4,MMP3,RHNO1,ZBTB1,PARP1,DDB1,TAF1,YY1,CUL4B,ERCC4,FMR1,CREBBP,IMPACT	grey	VSMC_M10
GO:0034248	0.99	0.01	188	395	regulation of cellular amide metabolic process	BP	1	ORMDL2,PAN2,SHMT2,HBS1L,TSFM,RMND1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,EIF3E,PNLDC1,QKI,MRPL13,JMJD4,AGO2,HABP4,TNRC6B,ATF4,TUT7,NTRK2,PLA2G6,NCK2,GAPDH,CNOT11,EXOSC3,RPS14,LRPPRC,IGF2BP3,RTN4,MTIF2,PNPT1,AGO1,ASCC3,C6orf203,TUT4,SLC7A11,FOXO3,PUM2,SPHK2,DHFR,EEFSEC,MKNK1,CNBP,MLH1,CDC123,MTRF1,DPH2,TNRC6C,AKT2,PURA,DPH3,EIF2AK2,PRNP,LSM1,PDK1,EIF4E3,SIRT3,UPF3A,PRKDC,KBTBD8,PAN3,NR1H4,C12orf65,CASP3,MRPS27,ENC1,CNOT1,CELF1,USP16,PTK2B,CNOT6L,MAPKAPK5,EIF2AK4,EIF4E2,NSUN3,PAIP2B,ORMDL1,FTO,CYFIP1,NOD2,TENT4B,RBM24,SLC2A13,NEURL1,RPUSD4,DDX25,BANK1,CAPRIN2,DIS3L2,RCC1L,KLHL25,GIGYF2,RPS6KB2,YTHDF2,TRNAU1AP,SORL1,RPS6KA1,PER2,DDX6,RPS4X,MTG2,YTHDF1,PASK,CD28,UHMK1,NCBP2,EIF4ENIF1,NSUN5,IGF2BP2,YBX3,PDK3,NFE2L2,EIF4EBP2,DDX3X,RC3H1,UPF1,COA3,SAMD4A,PINK1,STAT3,MAPK1,POLR2G,RTN1,NT5C3B,HAP1,EPHA4,DCP1B,YBX2,CASC3,ZCCHC4,FXR2,TARDBP,TMED10,EFNA1,MAPK3,TOB1,EIF3C,ALKBH1,TNRC6A,LARP6,CNOT8,LARP1,TCOF1,CCL5,SHMT1,UPF3B,PARN,FMR1,DPH1,METTL16,PLEKHN1,CIRBP,ABCA7,TSC1,AARS,BARHL2,MIR29A,MIR21,MIR222,MIR125B1,MIR27B,MIR24-1,MIR27A,RHOA,METTL18,SARNP,AGO4,RPS27L,SOX4,METTL14,NANOS1,MIR339,IMPACT,EIF1B,TIGAR,EIF1,RPUSD3,PPP1R15A,YBX1,ZFP36L2,UQCC2,TRMT10C,DIO2,RC3H2,EXOSC5	grey	VSMC_M10
GO:0071214	0.99	0.01	123	267	cellular response to abiotic stimulus	BP	1	TSPO,BAK1,XRCC6,MYC,HABP4,AKR1B1,ATF4,MAPK14,MAPK13,HSF1,OPN1SW,CRY1,CAMKMT,AQP1,CASP8AP2,PTN,EGFR,TLR4,MKX,SOX9,ERCC1,XPC,MYD88,OXSR1,WNT11,AKT2,CNN2,WRN,PIK3R1,CASP3,ATR,ASIC1,RAD9B,HVCN1,MME,EIF2AK4,DDB2,RAB11FIP5,TMEM150C,TENT2,SPIDR,SLC38A2,CRY2,TP53INP1,PKD2,ITGB6,CD40,GPLD1,TRPM1,RHBDD1,HYAL1,HYAL3,KCNJ2,SLC38A3,TRPV4,SCN2A,DAG1,TLR5,RRH,SAG,CHEK2,AGT,ATP1A2,BAG3,SLC9A1,NFATC4,HDAC4,MGMT,YBX3,NMT1,DDX3X,XRCC5,KCNK4,MICU1,GRK4,MMP3,LTBR,RHNO1,GNB5,ZBTB1,PARP1,SLC2A4,DDB1,WNK3,TNFRSF8,GUCY2D,TAF1,MAPK3,AC138894.1,GPR68,DNM2,YY1,LRRC8E,ADSSL1,CUL4B,PTGER4,SLC25A23,ERCC4,FMR1,CREBBP,TRPV1,PALM,PIEZO1,CYBA,ENG,HSPA5,PKD1L3,BCL10,MIR21,SWI5,INSRR,LRRC8D,FADD,CASP8,IMPACT,GADD45A,GRB2,GPR88,HRAS,TMEM109,CRADD,TSPYL5,GTF2H5	grey	VSMC_M10
GO:0104004	0.99	0.01	123	267	cellular response to environmental stimulus	BP	1	TSPO,BAK1,XRCC6,MYC,HABP4,AKR1B1,ATF4,MAPK14,MAPK13,HSF1,OPN1SW,CRY1,CAMKMT,AQP1,CASP8AP2,PTN,EGFR,TLR4,MKX,SOX9,ERCC1,XPC,MYD88,OXSR1,WNT11,AKT2,CNN2,WRN,PIK3R1,CASP3,ATR,ASIC1,RAD9B,HVCN1,MME,EIF2AK4,DDB2,RAB11FIP5,TMEM150C,TENT2,SPIDR,SLC38A2,CRY2,TP53INP1,PKD2,ITGB6,CD40,GPLD1,TRPM1,RHBDD1,HYAL1,HYAL3,KCNJ2,SLC38A3,TRPV4,SCN2A,DAG1,TLR5,RRH,SAG,CHEK2,AGT,ATP1A2,BAG3,SLC9A1,NFATC4,HDAC4,MGMT,YBX3,NMT1,DDX3X,XRCC5,KCNK4,MICU1,GRK4,MMP3,LTBR,RHNO1,GNB5,ZBTB1,PARP1,SLC2A4,DDB1,WNK3,TNFRSF8,GUCY2D,TAF1,MAPK3,AC138894.1,GPR68,DNM2,YY1,LRRC8E,ADSSL1,CUL4B,PTGER4,SLC25A23,ERCC4,FMR1,CREBBP,TRPV1,PALM,PIEZO1,CYBA,ENG,HSPA5,PKD1L3,BCL10,MIR21,SWI5,INSRR,LRRC8D,FADD,CASP8,IMPACT,GADD45A,GRB2,GPR88,HRAS,TMEM109,CRADD,TSPYL5,GTF2H5	grey	VSMC_M10
GO:0051050	0.99	0.01	321	660	positive regulation of transport	BP	1	VPS4B,NEDD4L,LRP1,STAC3,CPSF6,RAB21,SLC12A2,PRKN,TSPO,BAK1,MCHR1,PTCH1,MAPK14,PLA2G6,PICK1,RAC2,SMO,ABCB1,WNK2,CHMP2A,PRKCE,TMEM30A,FPR2,RUFY3,PPT1,AQP1,NR1H2,ITGB1BP1,EGFR,ARHGEF5,TLR4,TCAF2,IL15,SFRP4,ATG5,SDCBP,TRPM4,FGF21,BRAF,SPHK2,MTMR2,TRPC3,RAB7A,GIPR,CACNB2,CLASP2,CD300LF,PLK3,FRMD4A,STAC,GAB2,UNC13D,SCN5A,IL15RA,AKT2,GPD1L,ARRB1,SNX5,USP36,C1QTNF1,SYT1,RAB5A,APBB3,CEP290,PRNP,MAVS,P2RX2,AIMP1,NCKAP1L,GAS6,SIRT3,SYT9,TUB,TM9SF4,IL1A,OSBP,PIK3R1,HIP1R,GLRX,P2RX3,FBXW7,ORAI1,SORBS1,PTPRJ,HTRA2,P2RX7,VEGFC,ZFAND1,CSNK2A2,P2RY1,KCNJ11,NNAT,NR1H3,PFKM,SYNJ1,HOMER1,IFNGR2,STC1,NKX3-1,NKX6-1,RAPGEF3,F2RL1,F2R,TESC,ANO6,KCNE2,SPP1,PKD2,PLA2R1,NOD2,PLTP,CNTN1,DTNBP1,KCNIP2,RYR2,FAM173B,GPLD1,AZIN2,IRS1,PKP2,DNM1L,PPP3CA,HYAL3,KCNJ2,TERT,PGAP1,SLC38A3,MAP2K6,ABCA5,TGFB2,ADRA2A,ACSL5,TCF7L2,COX17,KCNB1,EGF,PFKFB2,HCLS1,HPS4,GRK2,SORL1,ANK2,C2CD5,GPER1,DGKD,ABCB11,ARIH2,AGT,FGR,CIB1,CBL,ACE2,BAG3,SLC9A1,AP2M1,SFN,CASQ1,STX1A,SNX4,NTSR1,SCN4B,FCER1G,NOS1AP,NCBP2,GLUL,DLG1,CALY,ADAM8,NFE2L2,CREB1,CTDSPL2,FZD5,PLA2G4A,FIS1,CEMIP,NMT1,TTN,SEC16B,EHD1,ZDHHC8,ABCA12,CASK,LPCAT3,MCU,PDCD10,SLC11A1,HTT,CLTCL1,DNM3,PPP3CB,RAB3A,PINK1,ANKFY1,ATP1B1,KCNA1,CD38,MPC2,MAPK1,ARL6IP1,CHRM1,INHA,TMEM30B,STX18,ATP13A2,CNST,HAP1,ACTB,SYT7,GPS2,RAB15,NLGN2,WNK3,STAC2,NPEPPS,ANXA2,ATP1B2,TARDBP,STX1B,STX4,PSEN1,ITGAM,DOCK2,RAB8B,NLGN3,TMED10,TRIM46,	grey	VSMC_M10

GO:0046631	0.99	0.01	40	97	alpha-beta T cell activation	BP	1	AGER,HLA-DRA,RSAD2,IL15,TGFBR2,EOMES,NCKAP1L,FOXP1,TOX,RIPK2,AP3B1,TCIRG1,HLX,CD28,RUNX3,BCL6,IL12A,VSIR,RC3H1,TNFSF18,STAT3,FOXP3,RASAL3,TBX21,SEMA4A,DOCK2,BATF,ZBTB7B,IL6R,IL4R,BCL11B,NKAP,PTGER4,TWSG1,SOCS1,PRKCZ,MIR21,RHOA,PRR7,RC3H2	grey	VSMC_M10
GO:0034097	0.99	0.01	322	659	response to cytokine	BP	1	RNMT,SHMT2,PGGT1B,YTHDC2,MAP3K5,TNFAIP3,CYP27B1,GFPT2,SLC12A2,HSPA1B,PRKN,AGPAT1,IL5,TCF7,TNFRSF13C,PMM1,PTP4A3,SYNGR1,MAPK14,MAPK13,IRF5,FOXH1,SRF,CNTFR,KIT,SLC1A1,TNFRSF21,IL1R2,NFIL3,GAPDH,RAD23B,GSDME,PNPT1,VRK2,REL,CXCL8,PXDN,BSPRY,NR1H2,TRIM32,TLR4,TRAF1,IL15,MYLK3,FOXO3,APOB,BCAT2,TRAF3IP2,BMI1,PHB,SOX9,CD300LF,PDIA3,MYD88,OXSR1,ZFAND6,TIMP4,KLF5,AANAT,NUMBL,IRAK2,HNMT,POU4F1,IL15RA,IL17RE,SPRY2,ACKR2,PFKP,IKBKB,MKKS,NMI,TMEM173,ACTG1,PLCB1,EIF2AK2,BAG4,MAVS,GAS6,HPX,IRF7,DPYSL3,ST18,TRAF6,TRIM44,MRPL15,HCK,ASAH1,IL1A,IL37,CEBPA,FER,MRAS,FLNB,OTUD4,GSS,CASP3,TAF9,ROBO1,PCOLCE2,IL17RD,IL17RB,PTPRJ,GPD1,IL7,HTRA2,VEGFC,PTK2B,MME,KCNJ11,CCL17,NR1H3,OAS3,NLRC5,RIPK2,OTULIN,SYNJ1,IFNGR2,NKX3-1,NKX6-1,ST3GAL6,F2RL1,RIPK1,ABCC2,IFIT2,JARID2,TOLLIP,CD40,NFKB2,MX2,RAB7B,MAPKAPK3,INA,IFIH1,OASL,HDAC1,HYAL1,HYAL3,SP100,TCIRG1,NR5A2,SELPLG,PIAS3,CMKLR1,KRAS,MAPKAPK2,FABP4,SPATA2,HCLS1,YTHDF2,GPER1,PARP9,PARP14,MCL1,CIB1,CBL,TRAF5,ABCG4,OSM,HDAC4,PELI3,EPS8,THPO,IL10RA,FCER1G,SETD2,YBX3,NFE2L2,CREB1,CDC42EP2,DUOX1,GGT2,ITGA4,XRCC5,SPOCK2,RC3H1,PTPN6,EFHC2,KLHL20,PDCD10,UPF1,TNFSF18,CXCR2,SLC11A1,STIP1,COL3A1,PPP3CB,TNIP2,GCH1,SMPD4,DDOST,MUL1,BIRC3,STAT3,PTPRN,CD38,SPPL2A,SLC27A1,MAPK1,STAT5B,WAS,SGMS1,GREM2,PADI2,SCGB1A1,CXCL16,SLC2A4,GPS2,USP18,TMEM102,TNFRSF1B,MED1,ALDH1A2,STX4,PYDC1,ABCD4,FOS,MAPK3,DCST1,CITED1,IL6R,HAX1,EPOR,STX8,IL4R,MAP2K5,RPS6KA5,BTK,S	grey	VSMC_M10
GO:0099024	0.99	0.02	17	47	plasma membrane invagination	BP	1	RAC2,MYH9,ARHGAP12,NCKAP1L,XKR6,RHOBTB2,F2RL1,ANO6,RHOBTB1,DOCK1,ITGAM,C3,ABCA7,SPIRE2,RHOA,HAVCR1,XKR8	grey	VSMC_M10
GO:1904358	0.99	0.02	12	35	positive regulation of telomere maintenance via telomere lengthening	BP	1	MAP3K4,MAPK15,POT1,ATR,HMBOX1,MAPKAPK5,RTEL1,XRCC5,MAPK1,MAPK3,PARN,MAP2K7	grey	VSMC_M10
GO:0031175	0.99	0.01	381	784	neuron projection development	BP	1	NME1,NEDD4L,LRP1,SEMA6A,KIF5A,AVIL,RAB21,MAPK8IP2,TIAM2,RIMS2,PRKN,AGER,SULT4A1,TSPO,FSTL4,SYNGAP1,WASHC5,ASAP1,GFRA3,PTK2,PTCH1,PLXNA4,NTRK2,CPNE5,MICALL1,RAC2,SMO,RBFOX2,CHRNA3,FBXO7,PTK7,SRF,FZD1,ADGRF1,TNFRSF21,NCK2,ROR2,SEMA4D,DLX5,ETV1,SEMA4C,SVBP,BRSK1,RIMS1,TMEM30A,RTN4,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,AREG,EPHA7,WHRN,PTN,TNC,EGFR,HECW1,TRIM32,NCDN,EPHA1,KEL,RTN4IP1,NRCAM,NTF4,FIG4,WASF1,DHFR,PLXNA1,HDAC2,NDNF,RAB10,IQSEC1,ABI1,SLC39A12,USH1G,CDNF,GOLGA4,GLI2,MEGF8,PTPRF,MYO7A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,ALK,CPNE9,FARP1,KIF5C,SYT1,TMEM106B,FEZ2,RAC3,SLC23A2,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NCKAP1L,ULK1,DPYSL3,ERCC6,RYK,EPHB1,PLK2,RET,TOX,TTL,CBFA2T2,ANKRD27,PREX2,CASP3,PLS1,ROBO1,ROBO2,TENM3,ADGRV1,ENC1,FZD3,MEF2C,SEMA4F,NCAM2,TLX2,CUX2,KATNB1,PTK2B,RAPGEF2,DGUOK,DPYSL2,EIF2AK4,TIAM1,PAQR3,SLIT1,USH1C,OPA1,NKX6-1,TRIO,NR4A2,ZFYVE27,CRTAC1,SEMA3G,ITPKA,SPP1,PAX2,CYFIP1,ALCAM,TSPAN2,SEMA4G,CNTN1,ZNF335,DTNBP1,MYLIP,TAOK3,SLC12A5,STMND1,SIAH1,LZTS1,BMPR1B,BICDL1,PSD,BDNF,SRGAP2C,DOCK10,KIAA0319,NEURL1,MTR,LGR6,DNM1L,PPP3CA,HECW2,CAPRIN2,TRPV4,SEMA3F,GAP43,TRIP11,ADARB1,DAG1,AUTS2,MARK1,LHX9,CFL1,ADNP,DISC1,KREMEN1,AGT,CIB1,GBX2,DVL3,RAB17,KALRN,CERS2,NFATC4,VASH2,TRAPPC4,SS18L1,LAMA5,YTHDF1,USP21,PTPRO,CDKL5,SEPT2,INPP5J,EPHB3,TANC2,UHMK1,STRC,LRIG2,APOD,WNT3,KLF7,DGKG,NFE2L2,CREB1,MYPN,	grey	VSMC_M10
GO:0031440	0.99	0.02	8	26	regulation of mRNA 3'-end processing	BP	1	CPSF6,ZC3H3,HSF1,RNF20,YTHDC1,NCBP2,LEO1,PAPOLA	grey	VSMC_M10
GO:0018105	0.99	0.01	113	249	peptidyl-serine phosphorylation	BP	1	BAK1,MAPK14,NTRK2,MAPK13,STK38,CSNK1E,TTBK1,SLC1A1,NCK2,IL11,BRSK1,PRKCE,VRK2,VRK3,EGFR,NTF4,BRAF,MKNK1,PRKD2,RAF1,SPRY2,AKT2,GPD1L,DYRK1B,TGFBR2,IKBKB,RPTOR,PLCL2,MAP4K1,BAG4,GAS6,ULK1,PRKDC,PLK2,RET,CAMK4,MAST4,ATR,DCLK2,CSNK2A2,FNIP2,MAPKAPK5,PAQR3,RIPK2,TOP1,RAPGEF3,RIPK1,STK4,MORC3,DMTN,BDNF,MAPKAPK3,CAPRIN2,CAMKV,PRKX,TTBK2,MARK1,MST1,DYRK3,MAPKAPK2,HCLS1,RPS6KB2,OPRD1,GRK2,CHEK2,TSSK4,RPS6KA1,OSM,INPP5J,MLXIPL,UHMK1,PDK3,PIKFYVE,STOX1,PDCD10,MARK2,MAST3,PINK1,ARAF,MAPK1,STK32B,NSD1,DGKQ,CSNK1G1,TAF1,MAPK3,HAX1,SBK1,RPS6KA5,PRKCB,CAMK2A,MAPK7,MARK3,CDK5R1,SH2D3A,NLK,DOCK7,INPP5K,PDPK1,PRKCZ,PKD1,MTCP1,PARK7,MAPKAP1,AURKC,DMD,IRGM,SMYD3,WNT5A,GADD45A,TXN,LIF,RPS6KA4	grey	VSMC_M10
GO:0055013	0.99	0.01	25	65	cardiac muscle cell development	BP	1	MAML1,PPARA,PI16,SRF,FHL2,BVES,MYLK3,ATG5,TBX5,AGT,ACTC1,ALPK3,TTN,OBSL1,BMPR1A,TCAP,YY1,ISL1,MYH11,MIR199A1,MIR23A,MIR24-1,RGS4,NKX2-5,HEY2	grey	VSMC_M10
GO:0006595	0.99	0.03	4	15	polyamine metabolic process	BP	1	AZIN2,SMS,OAZ1,NNMT	grey	VSMC_M10
GO:0034405	0.99	0.02	10	31	response to fluid shear stress	BP	1	MTSS1,MEF2C,PTK2B,PKD2,NFE2L2,MAP2K5,MAPK7,PKD1,ASS1,CA2	grey	VSMC_M10
GO:1901522	0.99	0.02	6	21	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	BP	1	SMAD5,ATF4,DLX5,CARF,NFE2L2,RBPJ	grey	VSMC_M10
GO:0031663	0.99	0.02	16	44	lipopolysaccharide-mediated signaling pathway	BP	1	TNFAIP3,TRIB1,MAPK14,PRKCE,TLR4,MYD88,IRAK2,TRAF6,HCK,RIPK2,MAPK1,MAPK3,CCL5,CCL2,TICAM1,BCL10	grey	VSMC_M10

GO:0035305	0.99	0.02	14	40	negative regulation of dephosphorylation	BP	1	SEMA4D,IKBKB,BAG4,NCKAP1L,MFHAS1,CRY2,TGFB2,TIPRL,BOD1L2,PPP4R4,INPP5K,PPP1R15A,TMEM225B,ARPP19	grey	VSMC_M10
GO:0030832	0.99	0.01	70	160	regulation of actin filament length	BP	1	ARPC3,AVIL,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,NCK2,KIAA1211,TMOD1,PLEKHH2,PRKCE,SPTBN1,PLEK,ADD2,FAM49A,WASF1,PLEKHG2,FCHSD2,MKKS,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,HIP1R,FMN1,LIMA1,PTK2B,F2RL1,IQGAP2,CYFIP1,DMTN,MAGEL2,CARMIL1,LMOD1,ADD3,SSH1,HCLS1,AP1AR,WASF2,SPTBN2,TMOD4,EPS8,WHAMM,DLG1,CAPZA1,CDC42EP2,NCKAP1,ARPC1A,WAS,TMOD2,SPTB,PFN3,HAX1,EVL,SSH2,MLST8,SPIRE2,WDR63,CARMIL2,RHOA,VASP,GMFG,GRB2,PFN4,PDXP,COTL1	grey	VSMC_M10
GO:0014909	0.99	0.01	26	67	smooth muscle cell migration	BP	1	LRP1,TRIB1,GRB10,TLR4,PLXNA1,PLAT,PARVA,MEF2C,ADAMTS1,DOCK5,TERT,GNA13,SSH1,SORL1,AGT,HDAC4,NFE2L2,SEMA6D,BMPR1A,FOXO4,CCL5,DOCK7,CRK,MIR21,RHOA,PDGFD	grey	VSMC_M10
GO:1902993	0.99	0.02	5	18	positive regulation of amyloid precursor protein catabolic process	BP	1	AGER,CASP3,SLC2A13,EPHA4,EFNA1	grey	VSMC_M10
GO:0010638	0.99	0.01	203	428	positive regulation of organelle organization	BP	1	VPS4B,PAN2,ARPC3,PIP4K2C,PPP1R10,CNOT2,CNOT6,HSPA1B,MAP3K4,PRKN,IL5,UBE2B,BAK1,MTSS1,WASHC5,ASAP1,MAPK15,PLA2G6,BAIAP2L2,PICK1,CDC42EP1,TEK,POT1,FBXO7,LMOD2,CCL27,SLAIN2,NCK2,KIAA1211,PRKCE,PHIP,HOXA13,LPAR1,EPGN,PLEK,TGFA,ITGB1BP1,MET,FUZ,ARHGEF5,CDK5RAP2,EPHA1,MYLK3,VPS35,SDCBP,MGARP,MAPRE1,WASF1,SSBP1,PIP4K2A,SETDB2,ERCC1,LCP1,RALB,SLAIN1,WNT11,AKT2,FCHSD2,SIRT2,ANK1,NAV3,SYT1,PLCB1,DDHD2,BAG4,DCN,FCHSD1,NCKAP1L,ULK1,ARFIP2,LMOD3,SYT9,PAN3,HCK,IL1A,FER,OSBP,HIP1R,ATR,CLIP1,KATNBL1,SLF1,FAM208A,FMN1,HMBOX1,ANAPC5,HTRA2,P2RX7,CNOT1,ANAPC7,KATNB1,PTK2B,CNOT6L,MAPKAPK5,NBN,SYNJ1,OPA1,RAPGEF3,F2RL1,IQGAP2,CYFIP1,SLF2,NPM2,PPHLN1,IGF2,MAGEL2,PXN,DNM1L,CARMIL1,ZMYND10,LMOD1,TRPV4,ZDHHC6,EGF,HCLS1,AP1AR,C2CD5,GPER1,WASF2,CIDEB,CD28,RTEL1,WHAMM,CDKN1B,DLG1,CDC42EP2,MAPT,FIS1,NMT1,TOGARAM1,NCKAP1,XRCC5,MCU,NIN,WNT4,HTT,DDHD1,PINK1,MUL1,ARPC1A,MAPK1,WAS,STX18,DDX11,HAP1,MNS1,VPS13D,PFN3,ANAPC4,ANXA2,MAPK3,HAX1,ADCK1,SMAD3,SFPQ,BCAS3,G3BP1,EVL,INSR,SMCR8,MIEF2,CDK5R1,RALBP1,PARN,SERPINF2,SLX4,MLST8,MECP2,WRAP73,PLXNA3,PARK7,SURF4,SPIRE2,PSRC1,KIAA1324,GPSM2,TSC1,SH3GLB1,TERF2,WDR63,CARMIL2,FHOD1,RHOA,SETDB1,MLLT11,VASP,OOEP,GMFG,IRGM,WNT5A,ZNF304,GRB2,BCL2L11,RGCC,DOC2B,RALA,HRAS,MIEF1,EREG,MAP2K7,PDXP,PPIF,DRG1	grey	VSMC_M10
GO:0006270	0.99	0.02	11	33	DNA replication initiation	BP	1	ORC3,ORC5,PURA,NOC3L,GINS3,NBN,WRNIP1,ORC2,KAT7,WDR18,RPA4	grey	VSMC_M10
GO:0006405	0.99	0.01	27	69	RNA export from nucleus	BP	1	CPSF6,PHAX,NOL6,XPO5,YTHDC1,IWS1,CHTOP,THOC7,DDX25,NCBP2,POM121,SETD2,ENY2,UPF1,NXF1,AKAP8L,FYTTD1,SMG5,NRDE2,ALKBH5,THOC2,SUPT6H,TSC1,NUP214,DDX19A,SARNP,DDX19B	grey	VSMC_M10
GO:0010389	0.99	0.01	33	82	regulation of G2/M transition of mitotic cell cycle	BP	1	VPS4B,MRNIP,TRIM39,BRSK1,MTA3,RAD17,PKIA,CHMP4C,NBN,ABRAXAS1,DONSON,ZFYVE19,TAOK3,CCND1,SYF2,STOX1,DBF4B,RAD51B,UIMC1,FOXO4,CTC1,TAOK2,RAB11A,FOXN3,RAD51C,SIN3A,TAOK1,FZR1,MECP2,VPS4A,NAE1,BRCC3,NABP1	grey	VSMC_M10
GO:0016055	0.99	0.01	175	373	Wnt signaling pathway	BP	1	NFATC1,LRP1,RPS12,GLI1,TNFAIP3,STK3,FZD6,PRKN,TCF7,UBE2B,RSPO3,RNF146,MAPK14,CBY1,CSNK1E,SOX10,DAAM2,MDFI,PTK7,CDK14,FZD1,ROR2,DLX5,WNK2,SOSTDC1,PPP2R1A,RSPO1,GRB10,ATP6V1C2,EGFR,HECW1,FUZ,SFRP4,CCNY,DKKL1,VPS35,TRPM4,FOXO3,SOX9,PPM1N,LRRFIP2,SCEL,TSKU,WNT11,RBMS3,CHD8,UBAC2,RAB5A,FERMT1,RAC3,SPEF1,MITF,CALCOCO1,RYK,PFDN5,CTNND1,DKK3,TRABD2A,ARNTL,FZD3,TMEM131L,CSNK2A2,LMBR1L,TIAM1,OTULIN,AMFR,NR4A2,RTF1,PKD2,SOX13,STK4,SALL1,VANGL1,PRICKLE1,NKD1,FBXW4,LDB1,PRDM15,KLHL12,LGR6,LRRK1,HDAC1,CCND1,CAPRIN2,TERT,TMEM9,SULF2,TCF7L2,DKK2,AXIN2,MARK1,EGF,TTC21B,SOX2,DISC1,ZNRF3,KREMEN1,DVL3,TMEM237,BICC1,NFATC4,FZD7,GID8,PTPRO,GRHL3,FZD9,SENP2,WNT3,CCNYL1,FZD5,DIXDC1,WDR61,DDX3X,CPZ,WNT4,MARK2,DAAM1,TBL1XR1,PPM1A,LEO1,OTUD5,ARHGEF19,DVL2,IGFBP4,DDB1,RBPJ,GRK6,PSEN1,TMEM88,TGFB1I1,ITGA3,CSNK1G1,CITED1,SOX30,SMAD3,MKS1,AC006487.2,CCDC88C,GSC,G3BP1,NLE1,ISL1,NLK,IFT20,GPC3,PIAS4,TLE6,TAX1BP3,ATP6V0C,SKI,PKD1,APC2,CELSR2,FOXL1,DAB2IP,MIR199A1,MIR222,MIR32,RHOA,ZBTB33,BCL7B,TRABD2B,SOX4,NOG,WNT5A,LBX2,CELSR3,DDIT3,DACT3,SDHAF2,SHISA2,APC,NKX2-5,MESD,WNT2	grey	VSMC_M10

GO:0031344	0.99	0.01	257	538	regulation of cell projection organization	BP	1	NME1,NEDD4L,ATP8B1,LRP1,SEMA6A,AVIL,TBC1D30,RAB21,TIAM2,FSTL4,SYNGAP1,WASHC5,MAPK15,PLXNA4,NTRK2,PODXL,CDC42EP1,RAC2,CHRNA3,FBXO7,PTK7,ABHD17B,SRF,FZD1,KIT,ROR2,SEMA4D,SEMA4C,DYNC2LI1,BRSK1,EPS8L1,TMEM30A,RTN4,RUFY3,ACP4,LPAR1,AKIRIN1,EPHA7,PTN,HECW1,FUZ,KEL,VPS35,ATG5,RTN4IP1,FIG4,PLXNA1,HDAC2,NDNF,SLC39A12,GOLGA4,MEGF8,KLF5,PTPRF,TSKU,SPRY2,SS18L2,ALK,TMEM106B,RAB5A,PRNP,ARHGEF7,SEMA3D,SPART,PLXNC1,SEMA3A,ULK1,DPYSL3,RYK,RET,TOX,CBFA2T2,FER,ANKRD27,PIK3R1,PLS1,ROBO1,ROBO2,PLCE1,TENM3,ENC1,SEMA4F,P2RX7,TLX2,CUX2,KATNB1,PTK2B,RAPGEF2,DGUOK,TIAM1,PAQR3,USH1C,HOMER1,OPA1,ZFYVE27,BIN3,F2RL1,ARHGAP24,SEMA3G,RREB1,ITPKA,SPP1,CYFIP1,DMTN,SEMA4G,CNTN1,MYLIP,LZTS1,BDNF,SRGAP2C,KIAA0319,NEURL1,DNM1L,CARMIL1,ZMYND10,PPP3CA,HECW2,CAPRIN2,TRPV4,SEMA3F,GAP43,AUTS2,MARK1,CFL1,ADNP,DISC1,KREMEN1,AGT,CIB1,WASF2,DVL3,RAB17,CERS2,NFATC4,HDAC4,SS18L1,EPS8,PTPRO,CDKL5,INPP5J,EPHB3,LIMK2,TANC2,LRIG2,WNT3,DGKG,NFE2L2,CDC42EP2,MAPT,ABL2,SEMA6D,PPP2R5B,EHD1,TNR,FN1,NCKAP1,EFHC2,NIN,SERPINI1,CRTC1,HTT,DNM3,RAP1GAP,RETREG3,MARK2,CAMK2G,CD38,WAS,OBSL1,CRMP1,SDCCAG8,HAP1,EPHA4,DLG4,MNS1,DVL2,MIEN1,PLEK2,FXR2,ATP1B2,GAK,STX1B,PSEN1,SEMA4A,CNTROB,RAB8B,ITGA3,TRIM46,EFNA1,NDEL1,TENM2,AC138894.1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,CCDC151,NTN1,SNAPIN,MYO9A,DNM2,PARP6,RIT2,BCAS3,GPRASP2,BHLHB9,ARHGAP44,EVL,TRPV2,FBXO38,CDK5R1,THOC2,IFT20,RRN3,SEZ6,DAB1,FMR1,LRP8,CRK,L1C	grey	VSMC_M10
GO:2001242	0.99	0.01	59	135	regulation of intrinsic apoptotic signaling pathway	BP	1	PRKN,NCK2,DNAJA1,GSDME,TRIM32,ARMC10,DDIAS,FBH1,TAF9,ING2,FBXW7,HTRA2,TMBIM6,NDUFS3,NKX3-1,OPA1,MARCH7,SIAH1,DNM1L,HDAC1,LCK,SNAI1,MCL1,HYOU1,RTKN2,RPL11,YBX3,NFE2L2,IVNS1ABP,NONO,FIS1,PRKRA,SYVN1,DDX3X,PINK1,SGMS1,PARP1,DAPK2,MUC1,TAF9B,S100A8,SFPQ,CD74,MAPK7,PTPN2,PIAS4,BCAP31,PARK7,MIR21,MIR27B,UBB,NOL3,DDIT3,BCL2L11,PTTG1IP,PLAGL2,BCL2L2,PPIF,PTPMT1	grey	VSMC_M10
GO:0043903	0.99	0.01	18	49	regulation of biological process involved in symbiotic interaction	BP	1	FUCA2,LY6E,CHMP2A,CXCL8,TRIM32,HS3ST5,NECTIN2,CHMP2B,F2RL1,PC,DDB1,CD74,CIITA,VPS4A,TRIM68,CXCL6,TRIM34,ZNF502	grey	VSMC_M10
GO:0034655	0.99	0.01	157	335	nucleobase-containing compound catabolic process	BP	1	PAN2,PDE7B,ENPP3,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,DPYS,SKIV2L,DXO,EIF3E,PNLDC1,PDE10A,SMPDL3A,CSDC2,AGO2,TNRC6B,TUT7,APOBEC3H,GTPBP1,MAPK14,EXOSC4,HSF1,GDA,GALT,ENPP4,CNOT11,EXOSC3,LRPPRC,PNPT1,NT5E,RNASEH1,AGO1,TUT4,PUM2,TRAF3IP2,MTPAP,ZC3HAV1,DHX34,ENTPD6,CDADC1,NUDT15,FASTK,MLH1,NUDT5,MBD4,DEDD2,MYD88,FBH1,TNRC6C,LSM1,NUDT16,PKP3,UPF3A,PAN3,NUDT12,AHCY,AMPD3,FOXL2,ZCCHC8,TTC37,CNOT1,CELF1,CNOT6L,TENT2,ENTPD4,FITM2,FTO,NUDT18,TENT5C,TENT4B,RBM24,PDE9A,DIS3L2,AXIN2,NUDT17,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,MGAT1,PDE8A,NCBP2,EIF4ENIF1,SIDT2,YBX3,RBM7,SUPV3L1,UPB1,RC3H1,DDX49,UPF1,SLC11A1,RBM10,SAMD4A,ZSWIM8,POLR2G,SCGB1A1,NT5C3B,DCP1B,CASC3,MRPL44,TNFRSF1B,FXR2,TARDBP,SMG5,DNASE2,TOB1,RNASEH2A,TENT5D,NRDE2,TNRC6A,CNOT8,LARP1,PDE4A,NEIL1,SLFN14,ALKBH5,UPF3B,NT5M,PARN,DROSHA,FMR1,TREX2,PAM16,DNASE1,METTL16,PLEKHN1,LSM7,NTHL1,DFFB,CIRBP,TRAF2,DNASE1L1,MLYCD,EDC4,AGO4,ENTPD5,METTL14,NANOS1,DNASE1L2,NUDT19,CACNG7,YBX1,ZFP36L2,TENT5A,MAGOHB,HINT1,UPP1,NMNAT1,RC3H2,EXOSC5	grey	VSMC_M10
GO:0009755	0.99	0.01	61	142	hormone-mediated signaling pathway	BP	1	ESR1,CNOT2,PPARA,RXRB,KDM4C,FOXH1,RBFOX2,CRY1,DNAJA1,CRHR2,LANCL2,PGRMC2,PHB,EGLN2,TADA3,RARB,NR1D2,TAF7,RNF14,DDRGK1,FOXP1,CALCOCO1,NCOA4,CYP7B1,UFSP2,ZNF366,ARNTL,CNOT1,KMT2D,DDX54,NKX3-1,CRY2,VPS18,HDAC1,NR5A2,ABHD2,GPER1,ARID1A,UCN2,RXRG,ESRRA,SLC27A1,PADI2,DNAAF4,PARP1,THRA,MED1,PAGR1,ESRRB,PIAS2,NCOR1,PPARGC1B,ISL1,RHOXF1,GHR,PARK7,RXRA,RHOA,TRIM68,CRH,YWHAH	grey	VSMC_M10
GO:0003073	0.99	0.01	23	60	regulation of systemic arterial blood pressure	BP	1	TNNI3,ADRA1D,P2RX2,GAS6,MME,F2RL1,F2R,ENPEP,AGT,ACE2,NTSR1,PTPRO,ECE1,CORO2B,ASIC2,SERPINF2,TRPV1,MECP2,CYBA,HSD11B2,RHOA,GPR37L1,CRH	grey	VSMC_M10
GO:0035330	0.99	0.02	4	16	regulation of hippo signaling	BP	1	MAPK14,AJUBA,WWC1,MARK3	grey	VSMC_M10

GO:0044087	0.99	0.01	391	801	regulation of cellular component biogenesis	BP	1	VPS4B,ORMDL2,PAN2,ATP8B1,ARPC3,LRP1,PIP4K2C,AVIL,TBC1D30,MDM1,ATAT1,ESR1,CNOT2,CNOT6,SNCAIP,HSPA1B,PRKN,RNF5,IL5,SEPT8,BAK1,MTSS1,WASHC5,ASAP1,H3F3C,PTK2,MAPK15,NTRK2,PODXL,PLA2G6,BAIAP2L2,PICK1,CDC42EP1,RAC2,HSF1,TEK,LINGO2,LMOD2,SRF,TTBK1,SLAIN2,KIT,NCK2,SEMA4D,KIAA1211,CHMP2A,TMOD1,DYNC2LI1,CLDN19,PRKCE,EPS8L1,SPTBN1,SHANK1,LPAR1,AKIRIN1,TRAPPC12,PLEK,LRRN3,EPHA7,NR1H2,ITGB1BP1,MED25,MET,ADD2,FUZ,ARHGEF5,TLR4,CDK5RAP2,EPHA1,VPS35,ATG5,SDCBP,FAM49A,MAPRE1,WASF1,FAF1,SPHK2,NAPA,RAB7A,PIP4K2A,VSTM5,SETDB2,SOX9,EML2,ERCC1,SLC39A12,LCP1,CLASP2,MAPRE3,DNAJC15,RALB,RAF1,MYD88,KLF5,NAPB,SLAIN1,WNT11,SLITRK5,PLEKHG2,IKBKB,CEP295NL,LRFN1,FARP1,FCHSD2,MKKS,ACTG1,NAV3,RAB5A,FEZ2,FERMT1,EIF2AK2,BAG4,ARHGEF7,NUDT16,FCHSD1,NRG1,NCKAP1L,ULK1,SIRT3,ARFIP2,PTPRA,LMOD3,DPYSL3,LRFN3,PAN3,EPHB1,PLK2,NPHP1,HCK,FAM107A,FER,ANKRD27,PIK3R1,CLSTN2,HIP1R,CHMP2B,ATR,TRABD2A,CLIP1,ROBO2,PLCE1,SLF1,TBC1D12,FAM208A,FMN1,ANKRA2,PTPRJ,MEF2C,P2RX7,CNOT1,CHMP4C,CUX2,PTK2B,CNOT6L,FNIP2,RAPGEF2,ALMS1,SLIT1,SPIDR,CDH17,RAPGEF3,TBX5,AMIGO2,BIN3,F2RL1,IQGAP2,ARHGAP24,SPTY2D1,ORMDL1,CYFIP1,SLF2,DMTN,PPHLN1,LDB1,MAGEL2,BDNF,SRGAP2C,PXN,NEURL1,SLK,CARMIL1,PPFIA1,HYAL1,ZMYND10,AC112128.1,LMOD1,ADD3,SEC22B,GAP43,TMEM39A,COL16A1,ADPRH,DAG1,AUTS2,AMIGO3,SSH1,AJUBA,SNAI1,HCLS1,ADNP,ARHGAP6,AP1AR,HSPA8,OPRD1,SORL1,AGT,WASF2,ACE2,SLC9A1,RAB17,SPTBN2,MTMR3,TRAF3IP1,TMOD4,PHLDB1,HD	grey	VSMC_M10
GO:0071560	0.99	0.01	88	199	cellular response to transforming growth factor beta stimulus	BP	1	ONECUT2,USP15,SNW1,PPARA,GDF9,SMAD5,PTK2,TAB1,FOXH1,TGFBRAP1,CD109,SDCBP,SPRY1,HDAC2,SOX9,SPRY2,EID2,TGFBR2,OVOL2,FERMT1,SPRED3,SNX25,LPXN,DKK3,ING2,HPGD,IL17RD,MEF2C,SOX6,VEPH1,GCNT2,ITGB6,PXN,SLC2A10,TGFB2,ITGB5,HTRA1,DLX1,SNX6,CREB1,PBLD,MEN1,HTRA3,FBN1,WNT4,COL3A1,GDF15,STK16,STAT3,PPM1A,BMPR1A,PARP1,MPP5,RNF111,TGFB1I1,ITGA3,FOS,CILP,CITED1,WFIKKN2,SMAD3,DNM2,MAPK7,YES1,NLK,TWSG1,JUN,CRK,CREBBP,PDPK1,SKI,PRDM16,WFIKKN1,ENG,HSPA5,MIR21,MIR27A,LEMD3,ACVRL1,CLDN1,WNT5A,NRROS,DUSP22,ZFP36L2,LDLRAD4,WNT2,PDGFD,PEG10	grey	VSMC_M10
GO:0044248	0.99	0.01	889	1755	cellular catabolic process	BP	1	VPS4B,NEDD4L,PAN2,GLS2,HSD17B4,LRP1,SHMT2,LVRN,ATG12,FEM1C,ALDH8A1,RMND5B,PDE7B,PIP4K2C,TNFAIP3,CYP27B1,AIG1,USP15,EPM2A,CANX,ENPP3,TRIM39,CNOT2,CNOT6,RIDA,MIOX,PABPC1,CPT1B,PHAX,ABHD16A,HSPA1B,DPYS,SKIV2L,DXO,EIF3E,TMEM74,PNLDC1,PRKN,RNF5,PPARA,PDE10A,PSMB8,PNPLA3,PNPLA5,TSPO,MCAT,DERL1,SKP1,SMPDL3A,UBE2B,RNF217,CSDC2,RNF146,ECHDC1,AL096711.2,TRIB1,KLHL3,AGO2,PRXL2C,PTK2,C6orf106,TNRC6B,EXOC4,TUT7,MAPK15,AGTPBP1,APOBEC3H,GTPBP1,MAPK14,NRBP2,CSNK1E,PLA2G6,EXOSC4,FOXRED2,HSF1,FBXL6,TFEB,USP49,GPT,CARNMT1,FBXO7,KLHDC3,GDA,CROT,GNPDA2,DCAF12,GALT,USP46,ENPP4,LNX1,SRD5A3,TGFBRAP1,SPTLC1,GAPDH,CNOT11,PPAT,RGP1,PDCL3,PRDX1,HMGCLL1,ADH5,CHMP2A,FBXO10,EXOSC3,RAB23,CAT,LRPPRC,SEC61B,STX17,RNF20,ATP6V1E2,CHAC2,RAD23B,ETFB,UBE3D,PNPT1,SLC4A4,ECPAS,NT5E,PPT1,SNX14,XPO1,NOD1,RRAGD,PELI1,WDR91,CNOT4,PXDN,RNASEH1,FBXO48,MET,IL4I1,AGO1,ATP6V1C2,HECW1,USP45,TRIM32,ASCC3,VPS41,HACE1,LPIN1,USP38,VPS35,SCOC,ATG5,MGST2,ZYG11B,SDCBP,TUT4,FOXO3,SMPD2,PUM2,MGAM,MFSD8,DDO,APOB,BCAT2,FAF1,FGF21,TRAF3IP2,MTPAP,MTMR2,ZC3HAV1,SESN3,BBS7,RAB7A,DHX34,PIP4K2A,NAPEPLD,FAAH,FBXL13,HADHA,GAD2,ENTPD6,PYGB,CDADC1,NUDT15,ABHD5,ESD,RUBCNL,ATP6V0E2,AKR1A1,APOC1,FBXL2,GLB1,KCTD2,PLK3,SUMO2,FASTK,OPTN,MLH1,NUDT5,USP35,KBTBD6,KCTD21,LIPE,RALB,ATP6V0B,MBD4,DEDD2,KDM4A,AQP11,MYD88,ACOX1,DMAC2,PRDX3,TIMP4,XYLB,UBXN4,UBE3C,HNMT,SPOPL,ACER3,FBH1,TNRC6C,PPP1CB,UBE2E1,KL	grey	VSMC_M10
GO:0046700	0.99	0.01	168	357	heterocycle catabolic process	BP	1	PAN2,PDE7B,ENPP3,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,DPYS,SKIV2L,DXO,EIF3E,PNLDC1,PDE10A,SMPDL3A,CSDC2,AGO2,TNRC6B,TUT7,APOBEC3H,GTPBP1,MAPK14,EXOSC4,HSF1,GDA,GALT,ENPP4,CNOT11,EXOSC3,LRPPRC,PNPT1,NT5E,RNASEH1,IL4I1,AGO1,TUT4,PUM2,TRAF3IP2,MTPAP,ZC3HAV1,DHX34,ENTPD6,CDADC1,NUDT15,FASTK,MLH1,NUDT5,MBD4,DEDD2,MYD88,HNMT,FBH1,TNRC6C,IDO2,IDO1,LSM1,NUDT16,PKP3,UPF3A,PAN3,NUDT12,AHCY,AMPD3,FOXL2,ZCCHC8,TTC37,CNOT1,CELF1,CNOT6L,TENT2,ENTPD4,FITM2,FTO,ABCC2,NUDT18,TENT5C,TENT4B,RBM24,PDE9A,DIS3L2,AXIN2,NUDT17,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,MGAT1,PDE8A,NCBP2,EIF4ENIF1,SIDT2,YBX3,NFE2L2,RBM7,TET1,SUPV3L1,UPB1,MTHFS,RC3H1,DDX49,UPF1,SLC11A1,RBM10,SAMD4A,ZSWIM8,POLR2G,SCGB1A1,NT5C3B,DCP1B,CASC3,MRPL44,TNFRSF1B,FXR2,TARDBP,SMG5,ALDH6A1,DNASE2,TOB1,RNASEH2A,TENT5D,NRDE2,TNRC6A,CNOT8,LARP1,PDE4A,NEIL1,SLFN14,ALKBH5,UPF3B,NT5M,PARN,DROSHA,FMR1,TREX2,PAM16,DNASE1,METTL16,PLEKHN1,LSM7,NTHL1,DFFB,CIRBP,TRAF2,DNASE1L1,MLYCD,EDC4,AGO4,ENTPD5,METTL14,NANOS1,DNASE1L2,NUDT19,CACNG7,ALDH1L1,YBX1,ZFP36L2,TENT5A,PDXP,MAGOHB,HINT1,UPP1,NMNAT1,RC3H2,EXOSC5	grey	VSMC_M10
GO:0046209	0.99	0.01	23	60	nitric oxide metabolic process	BP	1	TSPO,TLR4,PTK2B,SPR,PKD2,MARC2,MARC1,AGT,NOS1AP,POR,CPS1,GCH1,SMAD3,DNM2,GLA,INSR,NOS2,TICAM1,TRPV1,ASS1,NQO1,MIR199A1,MIR99B	grey	VSMC_M10

GO:0071417	0.99	0.01	221	466	cellular response to organonitrogen compound	BP	1	LRP1,AP3S1,MARS,PIP4K2C,PRKN,AGER,PNPLA3,PTK2,AKR1B1,ATF4,NTRK2,MAPK13,GKAP1,HSF1,CCND3,GPT,GABRA1,SLC1A1,PPAT,PHIP,FPR2,NOD1,CRHR2,AQP1,RRAGD,DDC,KLF11,GRB10,TLR4,GAB1,LPIN1,VPS35,MGARP,TRPM4,FOXO3,FGF21,HDAC2,SESN3,DNMT3A,PIP4K2A,RAB10,SOX9,CYSLTR2,ECHDC3,ATP1A3,KLF5,TBC1D4,AANAT,ALK,AKT2,SNX5,SIRT2,RPTOR,RYR1,PRNP,DIAPH1,KL,LARS,PTPRA,LEPROTL1,PRKDC,NR1H4,SLC38A9,TRIB3,HTR7,NR4A1,FER,IDE,PIK3R1,CASP3,P2RX3,CHRM5,RYR3,SORBS1,GPD1,MEF2C,P2RX7,P2RY1,RAPGEF2,RIPK2,STC1,OPA1,SPIDR,LPIN3,NKX6-1,RAPGEF3,CHRM4,NR4A2,PKD2,CYFIP1,DMTN,CASQ2,NOD2,DTNBP1,CHRM3,RYR2,IGF2,PXN,GPLD1,SRD5A1,IRS1,NEURL1,RPL23,GRB14,SLC30A10,COL16A1,SSH1,SORL1,C2CD5,GPER1,SH3BP4,AGT,SLC9A1,SYAP1,USF1,BACE1,SNX6,CALY,POR,NFE2L2,CREB1,YWHAG,HTR3B,RAP1B,FIS1,CPS1,EIF4EBP2,ITGA4,MEN1,SIK2,FDX1,ESRRA,FBN1,COL5A2,GDF15,STAT3,SLC27A1,MAPK1,CHRM1,STAT5B,GNB5,NSG1,DDX11,RAB8A,EPHA4,ACTB,GPR173,PARP1,SLC2A4,RAB15,MAX,RRAGB,CACNB1,AGTRAP,HRH2,PSEN1,CACNA1A,FOXO4,NGFR,PKLR,HCN3,RAB8B,NDEL1,TAF1,MAPK3,ZBTB7B,OGT,PRKCB,LARP1,DNM2,SIN3A,HRH4,CAMK2A,INSR,SHMT1,SREBF1,LPIN2,GHR,GNAL,PTPN2,SOCS1,CRK,INPP5K,GNB1,GNA15,TRPV1,PDPK1,PRKCZ,PALM,SLC25A33,GNAI3,AMIGO1,CYBA,LAMTOR5,ASS1,LCN2,HSPA5,HTR1D,INSRR,DEFB124,CA2,BGLAP,IMPACT,LAMTOR2,SIX1,RGS4,CRH,GRB2,BCL2L11,INSIG2,APC,BCL2L2,SH2B2,CEBPB,GNA14,LEPROT,GNG2,HCN4,PDXP,PDGFD,ARPP19	grey	VSMC_M10
GO:0044270	0.99	0.01	170	361	cellular nitrogen compound catabolic process	BP	1	PAN2,PDE7B,ENPP3,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,DPYS,SKIV2L,DXO,EIF3E,PNLDC1,PDE10A,SMPDL3A,CSDC2,AGO2,TNRC6B,TUT7,APOBEC3H,GTPBP1,MAPK14,EXOSC4,HSF1,GDA,GALT,ENPP4,CNOT11,EXOSC3,LRPPRC,PNPT1,NT5E,RNASEH1,IL4I1,AGO1,TUT4,PUM2,TRAF3IP2,MTPAP,ZC3HAV1,DHX34,ENTPD6,CDADC1,NUDT15,FASTK,MLH1,NUDT5,MBD4,DEDD2,MYD88,HNMT,FBH1,TNRC6C,IDO2,IDO1,LSM1,NUDT16,PKP3,UPF3A,PAN3,NUDT12,AHCY,AMPD3,FOXL2,ZCCHC8,TTC37,CNOT1,CELF1,CNOT6L,TENT2,ENTPD4,FITM2,FTO,ABCC2,NUDT18,TENT5C,TENT4B,RBM24,PM20D1,PDE9A,DIS3L2,AXIN2,NUDT17,MAPKAPK2,GIGYF2,YTHDF2,TRAF5,FASTKD1,ANGEL2,YTHDF1,MGAT1,PDE8A,NCBP2,EIF4ENIF1,SIDT2,YBX3,POR,RBM7,TET1,SUPV3L1,UPB1,ACADL,MTHFS,RC3H1,DDX49,UPF1,SLC11A1,RBM10,SAMD4A,ZSWIM8,POLR2G,SCGB1A1,NT5C3B,DCP1B,CASC3,MRPL44,TNFRSF1B,FXR2,TARDBP,SMG5,ALDH6A1,DNASE2,TOB1,RNASEH2A,TENT5D,NRDE2,TNRC6A,CNOT8,LARP1,PDE4A,NEIL1,SLFN14,ALKBH5,UPF3B,NT5M,PARN,DROSHA,FMR1,TREX2,PAM16,DNASE1,METTL16,PLEKHN1,LSM7,NTHL1,DFFB,CIRBP,TRAF2,DNASE1L1,MLYCD,EDC4,AGO4,ENTPD5,METTL14,NANOS1,DNASE1L2,NUDT19,CACNG7,ALDH1L1,YBX1,ZFP36L2,TENT5A,PDXP,MAGOHB,HINT1,UPP1,NMNAT1,RC3H2,EXOSC5	grey	VSMC_M10
GO:0010467	0.99	0.01	2321	4455	gene expression	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CD226,NME1,SEC11C,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,RNMT,LRP1,RPS12,SHMT2,TBPL1,GLI1,HBS1L,MARS,CLK4,MAP3K5,TNFAIP3,TSFM,HIVEP2,ADAT2,ATP23,PLAGL1,MAML1,HELB,TRIM39,RPP21,CPM,ZBTB2,RMND1,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,TSPAN8,ZFC3H1,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,TFB1M,ZNF706,PHAX,ARID1B,ADM2,HSPA1B,FZD6,RIMS2,ZBTB12,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,MAP3K4,PRKN,AGPAT1,QKI,AGER,TRMU,PPARA,GPSM3,PDE10A,HLA-DRA,HLA-DOB,UTP23,MED30,HLA-DMA,IL5,BRD2,TAF2,HLA-DPB1,ZUP1,RXRB,TSPO,VGLL2,MRPL13,RPS18,RRP7A,HSF2,TCF7,PHF1,BAK1,XRCC6,NCOA7,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,XPNPEP3,MRPL55,JMJD4,AGO2,HABP4,H3F3C,RPS10,C6orf106,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,ATF4,TUT7,ISCA1,RPAP2,CBX7,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,PUF60,C9orf64,CSNK1E,KDM4C,SOX10,EIF3L,PIM1,CMTR1,NRF1,TMPRSS6,EXOSC4,SMO,TSPAN33,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,MYH9,FOXH1,LRRC14,RBM28,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,TTBK1,ZNF318,NFX1,NOL6,XPO5,APBA1,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,NFKBIE,CDK6,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TSR1,TGFBRAP1,PLGRKT,MRPS9,IL1R2,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,S1PR3,PDCL3,PHF14,IPPK,LIPT1,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,TDRD7,MEOX2,ZNF550,KANSL3,BEND6,ZNF26	grey	VSMC_M10

GO:0030855	0.99	0.01	203	430	epithelial cell differentiation	BP	1	ONECUT2,HSD17B4,GLI1,CYP27B1,ESR1,FRS2,ROS1,MTSS1,PTCH1,AKR1B1,ATF4,PODXL,SMO,ZDHHC21,IFT74,PTK7,CDK6,RFX3,DLX5,S1PR3,TDRD7,TMOD1,SIX2,CD109,HOXA7,HOXA13,MYCL,ANXA4,WHRN,PTN,GRHL1,MET,SFRP4,MYCN,SLC7A11,OSR1,INTU,SPRY1,FOXE3,HDAC2,RAB10,SOX9,ERCC2,ERCC3,PTER,GSTK1,PTCH2,MYD88,EVPL,ACVR2B,KLF5,FOXJ1,MYO7A,SCEL,SPRY2,WNT11,AKT2,OVOL2,BFSP1,IKBKB,SLC4A7,JAG1,RARB,LRTOMT,AP000812.5,PLCB1,MAFG,SPRED3,SPINT2,BTG1,NRG1,TAF10,SYNE4,CEP63,TCF15,ASAH1,ASXL1,PAX8,CBFA2T2,RILPL1,RILPL2,FLNB,CASP3,MARVELD2,PLS1,ARNTL,MEF2C,ARHGEF26,RAPGEF2,USH1C,VDR,STC1,NKX6-1,RAPGEF3,F2RL1,SRSF6,DSP,ZBED6,STK4,PAX2,SALL1,PPHLN1,TOLLIP,HDAC1,ELF3,CCND1,CPT1A,BDH2,NR5A2,FAM20C,PRKX,RHCG,DHRS9,ADAMTSL4,TGM1,KDF1,SFN,FZD7,PTPRO,CLIC4,STRC,SIDT2,APOLD1,CDKN1B,MGMT,OVOL1,KLF7,CREB1,RAP1B,PLOD3,CPS1,H2AFY2,MEN1,ABCA12,PYY,SAV1,WNT4,ANXA7,CEP152,CTSV,PLA2G16,VCL,NKX3-2,STAT5B,FOXP3,ACADVL,THRA,RBPJ,MED1,KDM6B,HOXB5,RAB25,TGFB1I1,DLX3,CITED1,MAP2K1,TMEM100,SMAD3,VEZF1,TNMD,CCDC88C,MYO9A,KEAP1,BCL11B,LHX1,GATA6,CAMSAP3,TMEM132E,JAG2,LAMA1,IFT20,ALDOC,FZR1,PDPK1,SOX8,WDR77,FOXF1,TMEM231,HYDIN,MCOLN3,HSF4,MIR21,MIR125B1,RHOA,ARID4A,SOX4,ACVRL1,FOXJ2,MIR99B,CLDN1,WNT5A,TIGAR,BASP1,DNASE1L2,SIX1,ZBED2,TBC1D20,LIF,CEBPB,EREG,PITX3,SGPP1,HEY2	grey	VSMC_M10
GO:0010556	0.99	0.01	1456	2846	regulation of macromolecule biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,ORMDL2,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,SHMT2,PGGT1B,GLI1,HBS1L,MARS,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ZBTB2,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,EIF3E,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,MED30,IL5,BRD2,RXRB,VGLL2,MRPL13,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,HABP4,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,RPAP2,CBX7,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,IGF2BP3,FKTN,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,MTIF2,NFE2L3,PNPT1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,ANKRD17,JAZF1,CREB5,MYCL,XPO1,MTURN,NOD1,ORC3,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,ARHGEF5,TRIM32,TLR4,CCNC,ASCC3,CDK5RAP2,TRAF1,BCL2L12,	grey	VSMC_M10
GO:0007076	0.99	0.02	4	16	mitotic chromosome condensation	BP	1	TTN,AKAP8L,AKAP8,CHMP1A	grey	VSMC_M10
GO:0043161	0.99	0.01	173	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	NEDD4L,FEM1C,RMND5B,CANX,TRIM39,HSPA1B,PRKN,RNF5,DERL1,SKP1,UBE2B,RNF217,TRIB1,CSNK1E,FOXRED2,FBXL6,KLHDC3,DCAF12,SEC61B,RAD23B,UBE3D,ECPAS,XPO1,PELI1,FBXO48,HECW1,ASCC3,HACE1,ZYG11B,SDCBP,FAF1,BBS7,FBXL13,FBXL2,KCTD2,PLK3,SUMO2,KBTBD6,DMAC2,UBXN4,SPOPL,KLHL40,ARRB1,FBXO17,SIRT2,DNAJC18,NPLOC4,NHLRC3,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,CEBPA,ARMC8,SPSB4,TAF9,TRPC4AP,ARNTL,FBXW7,TRIM2,ANAPC5,AUP1,ANAPC7,TMEM67,AMFR,ERLIN1,PRICKLE1,FBXW4,SIAH1,NHLRC1,FBXL15,RNF144B,AMN1,HECW2,PSMD1,KLHL42,PSMB5,AC013489.1,YOD1,USP19,ARIH2,UBXN11,PSMD2,GID8,RNF185,RPL11,RHBDD2,EDEM3,NFE2L2,SYVN1,FBXO33,DERL3,KLHDC1,COP1,TMUB2,DNAJC10,DNAJB12,SPSB2,KLHL20,TRIM9,RNF4,ZSWIM8,SOCS4,TMEM129,ZFAND2B,ARAF,ANKZF1,DNAJB2,TBL1XR1,CALR3,FBXL14,RNF216,FBXL18,DDB1,ANAPC4,FBXO2,PSMC3,TBX21,PSEN1,AREL1,FBXL22,KCTD13,TAF1,OGT,SEL1L,KEAP1,PPP2R5C,PSMD10,FBXO22,FBXO38,CUL4B,TNFAIP1,FZR1,BCAP31,KCTD5,SGTA,FBXL16,PARK7,RNF126,SPSB1,FBXO31,ZER1,GLMN,HSPA5,WWP2,FBXL8,FBXL12,PSMC1,FAM8A1,CAMLG,CRBN,UBE2G1,DDIT3,UBE2U,CDC26,GID4,DDA1,STYX,UBE2G2,MAP1A,DERL2	grey	VSMC_M10
GO:0043966	0.99	0.01	20	54	histone H3 acetylation	BP	1	BRD1,SUPT3H,PHF14,SPHK2,TADA3,TAF10,TAF9,LDB1,ING5,MBIP,ING4,TADA1,KAT7,NAP1L2,CRTC2,SIN3A,NAA60,TAF12,SUPT7L,LIF	grey	VSMC_M10
GO:0060606	0.99	0.01	33	83	tube closure	BP	1	FZD6,BRD2,PTCH1,PTK7,SEMA4C,FUZ,TEAD2,IFT172,SPINT2,TRAF6,CASP3,FZD3,OPA1,SPINT1,PAX2,PRICKLE1,SUFU,TGFB2,DVL3,GRHL3,SETD2,TULP3,LIAS,DVL2,MKS1,SKI,TSC1,GLMN,BCL10,VASP,NOG,WNT5A,RALA	grey	VSMC_M10

GO:0043043	0.99	0.01	277	566	peptide biosynthetic process	BP	1	PAN2,RPS12,SHMT2,HBS1L,MARS,TSFM,RMND1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,EIF3E,PNLDC1,QKI,MRPL13,RPS18,MRPL55,JMJD4,AGO2,HABP4,RPS10,TNRC6B,ATF4,TUT7,GTPBP1,EIF3L,GTPBP2,SLC1A1,NCK2,MRPS9,GAPDH,CNOT11,AASDH,EXOSC3,RPS14,LRPPRC,SRBD1,CHAC2,IGF2BP3,MTIF2,PNPT1,AGO1,EGFR,ASCC3,MGST2,QRSL1,C6orf203,TUT4,SLC7A11,FOXO3,PUM2,DHFR,EEFSEC,MKNK1,CNBP,EIF2B3,RPS8,MLH1,CDC123,MTRF1,DPH2,RPSA,RPL14,MRPL33,TNRC6C,AKT2,METTL17,MRPS12,PURA,DPH3,HARS,HARS2,EIF2AK2,CARS2,LSM1,MRPL3,AIMP1,RPL31,LARS,EIF4E3,UPF3A,PRKDC,MRPL17,KBTBD8,PAN3,MRPL15,C12orf65,MRPL35,GSS,RPL6,PCSK1,MRPS27,MRPL19,ENC1,MRPS28,CNOT1,CELF1,USP16,PTK2B,CNOT6L,MAPKAPK5,EIF2AK4,EIF4E2,NSUN3,PAIP2B,FTO,CYFIP1,NOD2,TENT4B,RBM24,WARS2,MRPS17,CDKAL1,EIF2D,GATC,NEURL1,RPUSD4,YARS2,RPL23,DDX25,RPL4,RPS17,BANK1,LTO1,CAPRIN2,IGHMBP2,BDH2,RPL27A,MRPS35,DIS3L2,MRPL52,RCC1L,KLHL25,GIGYF2,MRPS11,RPS6KB2,YTHDF2,TRNAU1AP,MRPS21,TARS2,DALRD3,RPS27,RPS6KA1,PER2,DDX6,RPS4X,MTG2,YTHDF1,PASK,CD28,UHMK1,NCBP2,EIF4ENIF1,NSUN5,RPL11,IGF2BP2,YBX3,NFE2L2,EFL1,GGT2,LARS2,EIF4EBP2,RPL10L,DDX3X,RC3H1,DARS2,UPF1,RPL27,UBA52,MRPS36,COA3,SAMD4A,PINK1,STAT3,GGT6,MAPK1,POLR2G,NT5C3B,RSL24D1,DCP1B,FARSB,YBX2,CASC3,MRPL44,ZCCHC4,RPL19,RPLP1,FXR2,TARDBP,MRPL10,MRPL27,MAPK3,MTFMT,TOB1,EIF3C,ALKBH1,TNRC6A,MRPL22,LARP6,CNOT8,LARP1,EARS2,TNIP1,TCOF1,CCL5,SHMT1,UPF3B,NDUFA7,MRPS30,MCTS1,RPL23A,PARN,FMR1,DPH1,METTL16,PLEKHN	grey	VSMC_M10
GO:0071222	0.99	0.01	54	126	cellular response to lipopolysaccharide	BP	1	TNFAIP3,TSPO,TRIB1,MAPK14,HSF1,PRKCE,CXCL8,TLR4,CDK19,MYD88,IRAK2,NFKBIB,TRAF6,HCK,IL1A,IL37,PLSCR4,MEF2C,NUGGC,NR1H3,RIPK2,ABCC2,NOD2,CD40,PDCD4,UPF1,TNIP2,MAPK1,SGMS1,AKAP8,TNFRSF1B,SPON2,MAPK3,TNIP1,CCL5,CCL2,LITAF,NOS2,TICAM1,ADAMTS13,ASS1,LCN2,GFI1,BCL10,DAB2IP,MIR21,RHOA,CXCL6,IRGM,CMPK2,IL36G,WNT5A,CEBPB,HAVCR2	grey	VSMC_M10
GO:1903829	0.99	0.01	109	241	positive regulation of cellular protein localization	BP	1	LRP1,STAC3,PRKN,EPB41L2,MAPK14,RAC2,SMO,ABHD17B,PRKCE,SPTBN1,RTN4,TRAPPC12,PTN,ITGB1BP1,EGFR,TCAF2,STAC,AKT2,GPD1L,USP36,PRNP,MAVS,DDRGK1,TM9SF4,PIK3R1,PLS1,CEP250,FBXW7,SORBS1,HTRA2,CSNK2A2,KCNJ11,TERT,GPR137B,SSH1,KCNB1,EGF,HCLS1,EPB41,HPS4,SORL1,C2CD5,GPER1,PARP9,DTX3L,RAB11FIP2,ARIH2,CIB1,BAG3,LIMK2,DLG1,LRIG2,FZD5,MAPT,FIS1,CEMIP,NMT1,ZDHHC8,ABCA12,MEPCE,CNPY4,PINK1,MAPK1,CNST,PARP1,WNK3,GNL3L,STAC2,NPEPPS,WRAP53,TARDBP,STX4,PSEN1,ITGAM,SYT11,NGFR,KAT7,ITGA3,AC138894.1,RAB11A,SMAD3,AP2B1,MIEF2,CDK5R1,EFCAB7,PDPK1,RER1,ABHD17A,ARHGEF16,ABCA7,PARK7,GPSM2,LAMTOR5,TLDC1,SH3GLB1,MICALL2,ABHD17C,CD247,TMEM35A,APC,LIF,HRAS,MIEF1,RHOU,LEPROT,PARD6A,MESD,MAP1A,ZIC1	grey	VSMC_M10
GO:0016072	0.99	0.01	94	206	rRNA metabolic process	BP	1	HELB,TFB1M,UTP23,RRP7A,EXOSC4,NOL6,TSR1,EXOSC3,RPS14,UTP3,MDN1,FCF1,ERCC2,RPS8,DEDD2,RPL14,USP36,ESF1,KRR1,SIRT7,NUDT16,PRKDC,DHX37,BMS1,DIMT1,POP4,URB1,DDX54,NSUN3,RRP12,HELQ,RPUSD2,RPP40,RIOK1,TENT4B,POP5,PDCD11,RPUSD4,RPS17,SBDS,HEATR1,FAM207A,MRPS11,GAR1,YTHDF2,YBEY,NOP9,RPS27,WDR12,RPL7L1,WBP11,NSUN5,DDX47,RPL11,MAPT,POP7,DDX10,DDX49,RPL27,WDR74,MRPL44,NVL,MRM2,TSR2,ZCCHC4,LAS1L,UTP18,KRI1,ZNHIT3,ERI2,RIOK3,SLFN14,UTP6,SNU13,UTP14A,DROSHA,MRM3,METTL16,NOL9,RPUSD1,WDR18,RPL35,ZNHIT6,METTL18,RPP38,MPHOSPH6,RPUSD3,NSA2,C1D,PIH1D2,RPP30,TRMT61B,EXOSC5,GTF2H5	grey	VSMC_M10
GO:0001503	0.99	0.01	152	328	ossification	BP	1	HSD17B4,GLI1,CYP27B1,OSR2,ASF1A,TOB2,SMAD5,H3F3C,PTK2,PTCH1,ATF4,MAPK14,SMO,OSTF1,TEK,RORB,FZD1,CDK6,FHL2,ROR2,SEMA4D,DLX5,OMD,CAT,SIX2,HOXA2,AREG,BMP8A,PTN,TNC,EGFR,TRPM4,OSR1,MKX,BCAP29,INTU,HSPE1,PHB,SOX9,ERCC2,GLI2,ACVR2B,WNT11,SLC24A3,CHRDL2,ACVR2A,JAG1,SIRT7,RYR1,GFRA4,DNAJC13,KL,CLIC1,TRAF6,CEBPA,HAND2,ADGRV1,MEF2C,P2RX7,VEGFC,IGSF10,PTK2B,BMP2K,STC1,HDAC7,ANO6,SPP1,TFAP2A,IGF2,BMPR1B,FBXL15,SUFU,GPLD1,MAP2K6,SBDS,TGFB2,PTHLH,SATB2,TCIRG1,SGMS2,AXIN2,SNAI1,AMELX,SOX2,KREMEN1,FGR,ACTN3,HDAC4,TXLNG,CHRD,RUNX3,FZD9,SP3,WNT3,PTH1R,SRGN,COL13A1,BCOR,MEN1,ANKH,ESRRA,ZBTB40,WNT4,SUCO,COL5A2,ALPL,FGFR3,MMP13,MAPK1,TPM4,BMPR1A,THRA,PDLIM7,DHRS3,RBPJ,MSX2,RIOX1,FGF18,THBS3,MAPK3,TOB1,CITED1,IL6R,SMAD3,ITGA11,CHRDL1,SLC26A2,PPARGC1B,PTGER4,TWSG1,RANBP3L,GPC3,RFLNB,PAM16,SKI,ATP6AP1,SOX8,WDR63,MIR21,MIR27A,RHOA,FSTL3,SP7,BGLAP,MINPP1,SNX10,NOG,WNT5A,CCDC154,RDH14,CEBPB,MESD	grey	VSMC_M10

GO:0198738	0.99	0.01	175	374	cell-cell signaling by wnt	BP	1	NFATC1,LRP1,RPS12,GLI1,TNFAIP3,STK3,FZD6,PRKN,TCF7,UBE2B,RSPO3,RNF146,MAPK14,CBY1,CSNK1E,SOX10,DAAM2,MDFI,PTK7,CDK14,FZD1,ROR2,DLX5,WNK2,SOSTDC1,PPP2R1A,RSPO1,GRB10,ATP6V1C2,EGFR,HECW1,FUZ,SFRP4,CCNY,DKKL1,VPS35,TRPM4,FOXO3,SOX9,PPM1N,LRRFIP2,SCEL,TSKU,WNT11,RBMS3,CHD8,UBAC2,RAB5A,FERMT1,RAC3,SPEF1,MITF,CALCOCO1,RYK,PFDN5,CTNND1,DKK3,TRABD2A,ARNTL,FZD3,TMEM131L,CSNK2A2,LMBR1L,TIAM1,OTULIN,AMFR,NR4A2,RTF1,PKD2,SOX13,STK4,SALL1,VANGL1,PRICKLE1,NKD1,FBXW4,LDB1,PRDM15,KLHL12,LGR6,LRRK1,HDAC1,CCND1,CAPRIN2,TERT,TMEM9,SULF2,TCF7L2,DKK2,AXIN2,MARK1,EGF,TTC21B,SOX2,DISC1,ZNRF3,KREMEN1,DVL3,TMEM237,BICC1,NFATC4,FZD7,GID8,PTPRO,GRHL3,FZD9,SENP2,WNT3,CCNYL1,FZD5,DIXDC1,WDR61,DDX3X,CPZ,WNT4,MARK2,DAAM1,TBL1XR1,PPM1A,LEO1,OTUD5,ARHGEF19,DVL2,IGFBP4,DDB1,RBPJ,GRK6,PSEN1,TMEM88,TGFB1I1,ITGA3,CSNK1G1,CITED1,SOX30,SMAD3,MKS1,AC004687.2,CCDC88C,GSC,G3BP1,NLE1,ISL1,NLK,IFT20,GPC3,PIAS4,TLE6,TAX1BP3,ATP6V0C,SKI,PKD1,APC2,CELSR2,FOXL1,DAB2IP,MIR199A1,MIR222,MIR32,RHOA,ZBTB33,BCL7B,TRABD2B,SOX4,NOG,WNT5A,LBX2,CELSR3,DDIT3,DACT3,SDHAF2,SHISA2,APC,NKX2-5,MESD,WNT2	grey	VSMC_M10
GO:1901699	0.99	0.01	242	508	cellular response to nitrogen compound	BP	1	LRP1,AP3S1,MARS,PIP4K2C,PRKN,AGER,PNPLA3,PTK2,LY6E,AKR1B1,ATF4,NTRK2,MAPK13,GKAP1,HSF1,CCND3,GPT,CHRNA3,GABRA1,SLC1A1,PPAT,PHIP,FPR2,NOD1,CRHR2,AQP1,RRAGD,DDC,KLF11,GRB10,TLR4,GAB1,LPIN1,VPS35,MGARP,TRPM4,FOXO3,FGF21,HDAC2,SESN3,DNMT3A,PIP4K2A,RAB10,SOX9,CYSLTR2,RALB,ECHDC3,ATP1A3,KLF5,TBC1D4,AANAT,ALK,AKT2,SNX5,SIRT2,RPTOR,TMEM173,PLCB1,RYR1,PRNP,DIAPH1,MAVS,KL,LARS,PTPRA,LEPROTL1,PRKDC,NR1H4,SLC38A9,TRIB3,HTR7,NR4A1,FER,IDE,PIK3R1,CASP3,P2RX3,CHRM5,RYR3,SORBS1,GPD1,MEF2C,P2RX7,GUCY1B1,P2RY1,RAPGEF2,RIPK2,STC1,OPA1,SPIDR,LPIN3,NKX6-1,RAPGEF3,CHRM4,NR4A2,PKD2,CYFIP1,DMTN,CASQ2,NOD2,DTNBP1,CHRM3,RYR2,IGF2,PXN,GPLD1,SRD5A1,IRS1,IFIH1,NEURL1,MTR,RPL23,GRB14,SLC30A10,COL16A1,SSH1,GRK2,SORL1,C2CD5,GPER1,RTF2,SH3BP4,AGT,SLC9A1,SYAP1,USF1,BACE1,SNX6,CALY,POR,NFE2L2,CREB1,YWHAG,HTR3B,RAP1B,FIS1,CPS1,EIF4EBP2,ITGA4,MEN1,SIK2,FDX1,ESRRA,FBN1,COL5A2,GDF15,MUL1,MMP3,STAT3,SLC27A1,MAPK1,CHRM1,STAT5B,GNB5,NSG1,DDX11,RAB8A,EPHA4,ACTB,GPR173,PARP1,SLC2A4,RAB15,MAX,DDI2,RRAGB,CACNB1,AGTRAP,HRH2,PSEN1,CACNA1A,FOXO4,NGFR,PKLR,HCN3,RAB8B,NDEL1,TAF1,MAPK3,ZBTB7B,OGT,CHRNB2,PRKCB,LARP1,DNM2,SIN3A,HRH4,CAMK2A,INSR,RIOK3,SHMT1,COLEC12,CDK5R1,SREBF1,LPIN2,GHR,GNAL,PTPN2,SOCS1,FMR1,CRK,INPP5K,GNB1,GNA15,TRPV1,PDPK1,PRKCZ,TRAF2,PALM,SLC25A33,GNAI3,AMIGO1,CYBA,LAMTOR5,ASS1,LCN2,HSPA5,HTR1D,INSRR,DEFB124,CA2,ZCCHC3,BGLAP,IMPACT,LAMTOR2	grey	VSMC_M10
GO:0044321	0.99	0.02	4	16	response to leptin	BP	1	MKKS,CCND1,STAT3,LEPR	grey	VSMC_M10
GO:0046824	0.99	0.01	20	54	positive regulation of nucleocytoplasmic transport	BP	1	CPSF6,MAPK14,SMO,MAVS,GAS6,PIK3R1,RAPGEF3,TCF7L2,HCLS1,BAG3,SFN,NCBP2,CTDSPL2,MAPK1,TARDBP,PSEN1,SMAD3,NRDE2,EFCAB7,ZIC1	grey	VSMC_M10
GO:0033260	0.99	0.01	12	36	nuclear DNA replication	BP	1	DACH1,WRN,NUGGC,GINS3,DONSON,RTF2,RTEL1,BCL6,DBF4B,UPF1,TIPIN,TERF2	grey	VSMC_M10
GO:0033002	0.99	0.01	77	174	muscle cell proliferation	BP	1	GLI1,MAP3K5,TNFAIP3,XRCC6,TRIB1,AKR1B1,MAPK14,PIM1,OGN,AKIRIN1,EGFR,TLR4,IL15,PTGIR,PHB,MYD88,ABCC4,TGFBR2,HBEGF,FOXP1,PRKDC,TRAF6,EPHB1,HPGD,MEF2C,ADAMTS1,TBX5,NQO2,JARID2,TERT,PDCD4,TGFB2,PRKAR1A,TCF7L2,GNA13,GPER1,AGT,HDAC4,KCNK2,EFEMP2,CDKN1B,APOD,IL12A,COMT,XRCC5,SAV1,CALCRL,STAT3,MAPK1,BMPR1A,RBPJ,MFN2,RBPMS2,IL6R,TBX2,CCL5,GATA6,JUN,SERPINF2,GNAI3,CYBA,MIR199A1,MIR21,MIR222,MIR27B,MIR27A,RHOA,FOXJ2,MIR339,NOG,LDLRAP1,SIX1,EREG,C3orf58,HEY2,WNT2,PDGFD	grey	VSMC_M10
GO:0060627	0.99	0.01	190	403	regulation of vesicle-mediated transport	BP	1	VPS4B,NEDD4L,LRP1,RAB21,RIMS2,PRKN,GOPC,MAPK15,PLA2G6,PICK1,BTBD9,RAC2,CHRNA5,APBA1,USP46,CHMP2A,SMAP1,FPR2,RIMS3,PPT1,RSPO1,AAK1,NR1H2,BVES,IL15,SFRP4,ATG5,SDCBP,SPHK2,MTMR2,RAB7A,AP2S1,RAB10,CACNB2,CLASP2,CD300LF,APOC1,GAB2,GRIK5,UNC13D,TBC1D4,IL15RA,AKT2,ARRB1,NEU3,SYT1,RAB5A,CNN2,DNAJC13,NCKAP1L,GAS6,BET1L,SYT9,TUB,LYPLA1,HCK,FER,ANKRD27,PIK3CB,HIP1R,PTPRJ,WDR54,P2RY1,NR1H3,BMP2K,DYSF,SYNJ1,F2RL1,ANO6,VPS18,LGI3,NOD2,DTNBP1,SYT8,DNM1L,ANKRD13A,PPP3CA,HYAL3,PGAP1,ADRA2A,KCNB1,BSN,EGF,ANKRD13D,SORL1,C2CD5,DGKD,FGR,CBL,RAB4A,RAB17,AP2M1,STX1A,SNX4,RUBCN,FCER1G,SEPT2,BACE1,DNAJC5,CSPG5,SH3GL3,CALY,NSF,RUFY2,RAP1B,ABL2,EHD1,CASK,LRPAP1,SLC11A1,PPP3CB,RAB3A,SYN1,ANKFY1,C12orf4,MAPK1,RAB5C,STX18,GRIPAP1,RAB8A,ATP13A2,CNST,HAP1,CPLANE2,DLG4,SYT7,RAB15,RSC1A1,SEPT1,ANXA2,DGKQ,CPLX1,STX1B,STX4,RAB25,ITGAM,SYT11,SNX12,DOCK2,RAB8B,MAPK3,CACNA1G,AC138894.1,RAB11A,MAP2K1,RAB3D,IL4R,CALM1,SYTL4,SNAPIN,PRKCB,DNM2,RIT2,ARHGAP44,SCAMP5,INSR,MIB1,AP2B1,STXBP2,CCL2,CDK5R1,PRAM1,SGIP1,C3,UNC119,GPC3,FMR1,RPH3AL,PDPK1,P2RX1,RAB26,ATP6AP1,CACNA1H,ABCA7,CYBA,FOXF1,STXBP1,AP1G1,VPS4A,MIR199A1,MIR27B,MIR27A,FGA,WNT5A,LDLRAP1,DOC2B,TBC1D20,RALA,CBLL1,LRRTM2	grey	VSMC_M10

GO:0061138	0.99	0.01	63	147	morphogenesis of a branching epithelium	BP	1	ESR1,FRS2,RSPO3,MYC,PTCH1,SOX10,SMO,SRF,SIX2,HOXA13,AREG,MET,TNC,MYCN,SPRY1,PLXNA1,SOX9,GLI2,GZF1,SPRY2,TGFBR2,SPINT2,SEMA3A,PAX8,EYA1,VDR,NKX3-1,SPINT1,PKD2,STK4,PAX2,SALL1,DAG1,KRAS,EGF,AGT,GBX2,NFATC4,LAMA5,CLIC4,DLG1,FZD5,CTSH,WNT4,MAGED1,MED1,CITED1,MKS1,BTBD7,LHX1,LAMA1,GPC3,PKD1,SOX8,FOXF1,ENG,ESRP2,NOG,WNT5A,SIX1,GRB2,FGF1,WNT2	grey	VSMC_M10
GO:0003180	0.99	0.02	9	29	aortic valve morphogenesis	BP	1	NFATC1,SOX9,JAG1,ROBO1,ROBO2,SNAI1,EFNA1,NKX2-5,HEY2	grey	VSMC_M10
GO:0014896	0.99	0.01	31	78	muscle hypertrophy	BP	1	PPARA,PI16,HDAC2,TRPC3,KDM4A,HAND2,TIAM1,JARID2,RYR2,PDE9A,PPP3CA,MYH7,AGT,SLC9A1,HDAC4,TTN,CAMTA2,PARP1,TCAP,TNFRSF1B,SMAD3,YY1,GATA6,CYBA,MIR199A1,MIR21,MIR23A,MIR24-1,MIR25,RGS4,HEY2	grey	VSMC_M10
GO:1903050	0.99	0.01	86	192	regulation of proteolysis involved in cellular protein catabolic process	BP	1	TRIM39,HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,PDCL3,RAD23B,XPO1,ZYG11B,SDCBP,BBS7,NUDT15,PLK3,SUMO2,AQP11,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,RYBP,PSMF1,TRIB3,PLK2,CEBPA,TAF9,FBXW7,USP25,CSNK2A2,PTK2B,FAM192A,RNFT2,MARCH7,KCNE2,PRICKLE1,RNF144B,SUFU,RPL23,USP13,AC013489.1,EGF,USP19,DISC1,PSME1,ARIH2,RNF185,RPL11,NFE2L2,COP1,PSME3,SOCS4,PINK1,ARAF,DNAJB2,DNAAF4,EPHA4,PSMC3,OSBPL7,PSEN1,EFNA1,TAF1,OGT,KEAP1,PSMD10,FBXO22,FMR1,FZR1,BCAP31,SGTA,PKD1,TMEM259,PARK7,ZER1,GLMN,DAB2IP,UBB,PSMC1,BAG2,RNFT1,CAMLG,DDA1,STYX,MAP1A	grey	VSMC_M10
GO:0045687	0.99	0.01	10	31	positive regulation of glial cell differentiation	BP	1	TTBK1,PTN,HDAC2,NKX6-1,SPINT1,HDAC1,DAG1,TNFRSF1B,PRPF19,LIF	grey	VSMC_M10
GO:1904951	0.99	0.01	117	257	positive regulation of establishment of protein localization	BP	1	LRP1,PTP4A3,MAPK14,PLA2G6,RAC2,SMO,PRKCE,TMEM30A,RUFY3,NR1H2,ITGB1BP1,EGFR,ARHGEF5,TLR4,TCAF2,TRPM4,GIPR,PLK3,FRMD4A,AKT2,USP36,APBB3,CEP290,PRNP,MAVS,GAS6,SIRT3,TM9SF4,IL1A,OSBP,PIK3R1,FBXW7,HTRA2,VEGFC,ZFAND1,CSNK2A2,NNAT,PFKM,NKX6-1,RAPGEF3,F2RL1,GPLD1,DNM1L,TGFB2,TCF7L2,KCNB1,PFKFB2,HCLS1,HPS4,SORL1,C2CD5,GPER1,ARIH2,CIB1,BAG3,SFN,GLUL,ADAM8,CTDSPL2,FZD5,FIS1,CEMIP,NMT1,TTN,SEC16B,MCU,PDCD10,PPP3CB,PINK1,CD38,MPC2,MAPK1,CHRM1,TMEM30B,ATP13A2,CNST,NLGN2,NPEPPS,WRAP53,TARDBP,STX4,PSEN1,ITGAM,TMED10,AC138894.1,MYH10,SMAD3,CORO2B,SYTL4,GPR68,BCAS3,MIEF2,CDK5R1,ISL1,OXCT1,EFCAB7,ABAT,RPH3AL,NADK,BCAP31,PRKCZ,OAZ1,BAIAP3,LRRC8A,SH3GLB1,RIPOR1,MICALL2,FGA,SOX4,CRH,DOC2B,HRAS,MIEF1,RHOU,LEPROT,PARD6A,ZIC1	grey	VSMC_M10
GO:0051254	0.99	0.01	677	1357	positive regulation of RNA metabolic process	BP	1	NFATC1,ZNF407,SMARCC2,PAN2,ONECUT2,TCF4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ARID1B,DXO,ZBED4,PNLDC1,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,HABP4,PTCH1,TNRC6B,ATF4,TUT7,GTPBP1,MAPK14,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,IFT74,BICRAL,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,EXOSC3,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,EPCAM,ZNF462,TRA2A,PHIP,HMGN3,NFYC,PNPT1,HOXA2,HOXA7,HOXA13,REL,CREB5,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,TEAD2,SETD7,MYCN,ELF2,TUT4,OSR1,FOXO3,ZXDC,MAMSTR,ATAD2B,KDM7A,ZNF438,HDAC2,PHF10,MAML2,ZC3HAV1,MLLT10,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,MAPRE3,UTF1,SUMO2,MLH1,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,TNRC6C,SS18L2,WNT11,TADA3,SERTAD3,KLF6,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,CEP290,NSD3,ING1,LSM1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,RYBP,MITF,RBPMS,MTA3,PRKDC,IRF7,ERCC6,HOXC13,CALCOCO1,PAN3,ST18,RASL11A,NCOA4,TRAF6,NR1H4,TRIM44,TCF15,SOX12,PLAG1,USF2,RET,LMO2,ZC3H8,DIMT1,ASXL1,IL1A,PAX8,NR4	grey	VSMC_M10
GO:0006415	0.99	0.02	4	16	translational termination	BP	1	JMJD4,MTRF1,C12orf65,UPF1	grey	VSMC_M10
GO:0110020	0.99	0.01	34	86	regulation of actomyosin structure organization	BP	1	LPAR1,ITGB1BP1,MET,ARHGEF5,EPHA1,MYLK3,CLASP2,WNT11,MKKS,ACTG1,BAG4,PIK3R1,ALMS1,RAPGEF3,PXN,CARMIL1,PPFIA1,ARHGAP6,WASF2,SLC9A1,WNT4,WAS,SMAD3,CORO2B,EVL,PTGER4,INPP5K,SERPINF2,TSC1,FHOD1,MIR21,RHOA,ASAP3,RGCC	grey	VSMC_M10
GO:0048659	0.99	0.01	55	128	smooth muscle cell proliferation	BP	1	MAP3K5,TNFAIP3,XRCC6,TRIB1,AKR1B1,OGN,EGFR,TLR4,IL15,PTGIR,PHB,MYD88,ABCC4,TGFBR2,HBEGF,FOXP1,PRKDC,TRAF6,HPGD,MEF2C,ADAMTS1,NQO2,TERT,PDCD4,TCF7L2,GNA13,GPER1,AGT,HDAC4,EFEMP2,CDKN1B,APOD,IL12A,COMT,XRCC5,CALCRL,BMPR1A,MFN2,RBPMS2,IL6R,CCL5,JUN,SERPINF2,GNAI3,CYBA,MIR21,MIR222,MIR27B,MIR27A,RHOA,FOXJ2,MIR339,LDLRAP1,EREG,PDGFD	grey	VSMC_M10
GO:0008585	0.99	0.01	28	72	female gonad development	BP	1	ESR1,GDF9,DMC1,FANCG,KIT,FOXO3,ARRB1,FOXL2,CASP3,ROBO2,ADAMTS1,BMPR1B,GAS2,HYAL3,LHX9,SPO11,TAF4,VGF,WNT4,PTPRN,STAT5B,INHA,HSPA5,MSH4,LHX8,UBB,CEBPB,EREG	grey	VSMC_M10

GO:0030010	0.99	0.01	51	123	establishment of cell polarity	BP	1	PTK2,MYH9,PTK7,BRSK1,RUFY3,CDK5RAP2,TRAF3IP2,SPRY1,RAB10,FRMD4A,LLGL2,FBF1,FOXJ1,SPRY2,FERMT1,FRMD4B,SYNE4,NSFL1C,TCF15,EPHB1,MOS,MCPH1,PTK2B,GBF1,TCIRG1,RAB11FIP2,SNX27,RAP1B,HTT,MARK2,CYTH3,SDCCAG8,ARHGEF11,DOCK2,NDEL1,WWC1,MYO9A,BCAS3,AMOT,CAMSAP3,LAMA1,IFT20,DOCK7,CRK,PRKCZ,PKD1,SAPCD2,GPSM2,FOXF1,RHOA,WNT5A	grey	VSMC_M10
GO:0030330	0.99	0.01	24	63	DNA damage response, signal transduction by p53 class mediator	BP	1	FOXO3,PLK3,PAXIP1,PLK2,ATR,NBN,MARCH7,PIDD1,PLA2R1,SP100,DYRK3,SNAI1,CHEK2,CDKN1B,ING4,MUC1,BATF,PSMD10,CD74,RPS27L,SOX4,ACER2,PTTG1IP,CRADD	grey	VSMC_M10
GO:0042440	0.99	0.01	25	65	pigment metabolic process	BP	1	FECH,SHMT2,TSPO,PPAT,SLC7A11,SLC25A38,HPX,RAPGEF2,GMPS,CPOX,COX15,ABCC2,TMEM14C,ALAS1,OCA2,BDH2,ABCB6,CITED1,COX10,SHMT1,SLC46A1,SLC45A2,NFE2L1,WNT5A,FXN	grey	VSMC_M10
GO:0003176	0.99	0.01	11	34	aortic valve development	BP	1	NFATC1,SOX9,JAG1,ROBO1,ROBO2,SNAI1,RBPJ,TNFRSF1B,EFNA1,NKX2-5,HEY2	grey	VSMC_M10
GO:0008285	0.99	0.01	264	548	negative regulation of cell population proliferation	BP	1	NME1,C18orf54,B4GALT7,TNFAIP3,CYP27B1,ENPP3,RIDA,STK3,HSPA1B,FBLN1,TSPO,BAK1,MTSS1,TRIB1,MYC,TOB2,PTCH1,AGTPBP1,SOX10,CDKN2A,IFT74,SRF,CDK6,SMARCA2,TNFRSF21,NCK2,TFAP2B,ROR2,WNK2,OGN,ZNF268,CLDN19,CD109,FKTN,GSDME,SKAP2,CXCL8,PELI1,AKIRIN1,PTN,ITGB1BP1,MED25,KLF11,IL4I1,FUZ,TRIM32,IL15,SFRP4,INTU,SPRY1,WISP3,PTGIR,PHB,ABI1,SOX9,AQP11,RAF1,DACH1,IFT172,FOXJ1,SPRY2,THAP12,WNT11,TGFBR2,OVOL2,SIRT2,NMI,RARB,PAWR,FERMT1,SPINT2,EIF2AK2,PRNP,ING1,BTG1,AIMP1,TFDP1,FLT1,ST18,TMEM127,EPHB1,IL1A,CEBPA,CASP3,ATP5F1A,ING2,ROBO1,FBXW7,PTPRJ,BTG3,MEF2C,TMEM131L,PEX2,CELF1,ADAMTS1,PTK2B,RAPGEF2,PBRM1,VDR,NKX3-1,TBX5,ACVR1C,F2R,TESC,IFT52,SPINT1,TP53I11,TP53INP1,MARCH7,PKD2,STK4,TFAP2A,MORC3,RIPPLY3,JARID2,ADAMTS8,BMPR1B,NUPR2,GPLD1,RNF10,FAP,NEURL1,CD200,RBBP4,HDAC1,PDCD4,TGFB2,BTN2A2,RBM5,PTHLH,PRKAR1A,ADARB1,GNA13,DIS3L2,TBRG1,AXIN2,SOX2,GPER1,SH3BP4,CIB1,KDF1,CERS2,SFN,BNIPL,PER2,OSM,HDAC4,KCNK2,RUNX3,ING5,EFEMP2,CDKN1B,DLG1,OVOL1,APOD,FZD5,PTH1R,DUSP10,PRKRA,BCL6,P3H2,MEN1,IL12A,COMT,VSIR,CASK,RC3H1,PTPN6,BCHE,SAV1,PDCD10,ING4,RAP1GAP,RBM10,STAT3,DNAJB2,WDR13,PIM2,SCGB1A1,FTH1,FOXP3,MAGED1,RBPJ,TNFRSF8,MED1,ALDH1A2,MFN2,FBXO2,SYNJ2BP,TGFB1I1,FOXO4,NGFR,ZBTB7B,TOB1,VASH1,MAP2K1,SMAD3,TNMD,BTK,CLMN,BCL11B,PPP2R5C,UMOD,GATA6,CCL2,ISL1,SUZ12,TWSG1,PTPN2,GPC3,ZBTB7C,DNAJA3,TAX1BP3,SKI,CHD5,WDR77,CDK10,TSC1,GLMN,MARVELD3,DAB2IP,CTCF,MIR29	grey	VSMC_M10
GO:0009266	0.99	0.01	59	137	response to temperature stimulus	BP	1	HSPA1B,HSF1,SLC25A27,PDCL3,DNAJA1,GRIK2,UCP1,HDAC2,EIF2B3,ASIC3,STAC,CLPB,TCIM,EPHB1,IL1A,ATR,P2RX3,HTRA2,EIF2AK4,TP53INP1,ABCC2,GMPR,SLC12A5,GLRX2,TRPV4,PDCD6,MAPKAPK2,TRPM8,BAG3,SLC9A1,CASQ1,NTSR1,MAPT,VGF,KCNK4,SLC27A1,ACADVL,THRA,DNAJB1,TGFB1I1,NGFR,PKLR,FOS,SLU7,TRPV2,ACOT11,DNAJA3,CREBBP,TRPV3,TRPV1,CIRBP,ACADM,MT-CYB,CASP8,HIKESHI,PLAC8,HSBP1L1,MAP2K7,FGF1	grey	VSMC_M10
GO:0061035	0.99	0.01	23	61	regulation of cartilage development	BP	1	SIX2,MBOAT2,MKX,SOX9,GLI2,WNT11,ZNF219,RARB,SOX6,LOXL2,BMPR1B,PTHLH,AXIN2,POR,NKX3-2,FGF18,SMAD3,ADAMTS12,RFLNB,MIR21,ACVRL1,NOG,WNT5A	grey	VSMC_M10
GO:0046649	0.99	0.01	224	470	lymphocyte activation	BP	1	TNFAIP3,AGER,HLA-DRA,HLA-DOB,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,BAK1,XRCC6,MFNG,RAC2,CCND3,MYH9,FBXO7,SRF,KIT,TNFRSF21,NCK2,NFIL3,PRDX1,EXOSC3,IL11,MSH2,SKAP2,SLC46A2,PELI1,RSAD2,IL4I1,TLR4,IL15,ATG5,TRAF3IP2,HMCES,BMI1,PHB,ERCC1,LCP1,CLPTM1,MLH1,GLI2,UNC13D,MYD88,PIBF1,FOXJ1,PAXIP1,IL15RA,KLF6,CMTM7,TGFBR2,EOMES,PURA,PAWR,PLCL2,SHLD1,PRNP,NCKAP1L,GAS6,FOXP1,PRKDC,SLC7A1,TRAF6,EPHB1,SOX12,GAPT,TOX,ZC3H8,IL1A,CAMK4,PIK3R1,CASP3,PTPRJ,MEF2C,TMEM131L,IL7,TPD52,PAG1,SLA2,PTK2B,RASGRP1,LMBR1L,EIF2AK4,RIPK2,NBN,CDH17,AP3B1,F2RL1,MARCH7,SOX13,NOD2,ZNF335,CD40,IGF2,DCAF1,DOCK10,PKNOX1,LCK,PPP3CA,BANK1,ICOSLG,BTN2A2,GPAM,TCIRG1,PRKAR1A,RABL3,HLX,TBC1D10C,SLAMF8,THEMIS2,LAT2,FGR,FZD7,HDAC4,SNX27,CD28,FCER1G,RUNX3,RNF168,PATZ1,FZD9,SP3,DLG1,PPP2R3C,ADAM8,FZD5,DUSP10,BLOC1S6,BCL6,SYVN1,ITGA4,IL12A,VSIR,RC3H1,PTPN6,TNFSF18,SLC11A1,WNT4,LAG3,PPP3CB,TNIP2,DDOST,STAT3,CD38,BST1,STAT5B,WAS,INHA,SCGB1A1,FOXP3,RASAL3,ZBTB1,SHLD2,GPS2,CARD11,RBPJ,TNFRSF1B,TBX21,PSEN1,SEMA4A,KAT7,DOCK2,BATF,ZBTB7B,CHRNB2,IL6R,CD19,LAT,SMAD3,IL4R,PRKCB,BTK,BCL11B,YY1,CD74,CCL5,CCL2,YES1,JAG2,NKAP,CD320,VAV1,LEPR,PTGER4,TWSG1,IL7R,SUPT6H,PTPN2,SOCS1,DROSHA,TICAM1,DNAJA3,PRKCZ,TSC1,VAV3,LRRC8A,GLMN,AP1G1,BCL10,MIR21,MIR27A,RHOA,LST1,BLOC1S3,SOX4,MAFB,FADD,DPP4,CD46,CASP8,THY1,FGL2,RNF8,CD70,TNFSF9,NHEJ1,ZFP36L2,LAX1,EFNB3,CEBPB,PRR7,TNFSF13B,HAVCR2,RC3H2	grey	VSMC_M10
GO:0051382	0.99	0.02	4	16	kinetochore assembly	BP	1	TRAPPC12,POGZ,RNF4,CENPX	grey	VSMC_M10

GO:0045893	0.99	0.01	618	1244	positive regulation of transcription, DNA-templated	BP	1	NFATC1,ZNF407,SMARCC2,ONECUT2,TCF4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,YEATS4,ESR1,MYRFL,CNOT6,OSR2,SNW1,ARID1B,ZBED4,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,PTCH1,ATF4,MAPK14,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,IFT74,BICRAL,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,EPCAM,ZNF462,PHIP,HMGN3,NFYC,HOXA2,HOXA7,HOXA13,REL,CREB5,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,TEAD2,SETD7,MYCN,ELF2,OSR1,FOXO3,ZXDC,MAMSTR,ATAD2B,KDM7A,ZNF438,HDAC2,PHF10,MAML2,MLLT10,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,MAPRE3,UTF1,SUMO2,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,SS18L2,WNT11,TADA3,SERTAD3,KLF6,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,CEP290,NSD3,ING1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,RYBP,MITF,RBPMS,MTA3,PRKDC,IRF7,ERCC6,HOXC13,CALCOCO1,ST18,RASL11A,NCOA4,TRAF6,NR1H4,TRIM44,TCF15,SOX12,PLAG1,USF2,RET,LMO2,ZC3H8,ASXL1,IL1A,PAX8,NR4A1,ACVR1B,ZNF143,CAMK4,CEBPA,FOXL2,NCOA6,PIK3R1,TFDP2,CDK7,IRF2,TAF9,NCOA2,MED19,CCDC62,TFCP2,HAND2,CSRNP2,ING2,EYA1,ML	grey	VSMC_M10
GO:1903508	0.99	0.01	618	1244	positive regulation of nucleic acid-templated transcription	BP	1	NFATC1,ZNF407,SMARCC2,ONECUT2,TCF4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,YEATS4,ESR1,MYRFL,CNOT6,OSR2,SNW1,ARID1B,ZBED4,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,PTCH1,ATF4,MAPK14,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,IFT74,BICRAL,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,EPCAM,ZNF462,PHIP,HMGN3,NFYC,HOXA2,HOXA7,HOXA13,REL,CREB5,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,TEAD2,SETD7,MYCN,ELF2,OSR1,FOXO3,ZXDC,MAMSTR,ATAD2B,KDM7A,ZNF438,HDAC2,PHF10,MAML2,MLLT10,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,MAPRE3,UTF1,SUMO2,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,SS18L2,WNT11,TADA3,SERTAD3,KLF6,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,CEP290,NSD3,ING1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,RYBP,MITF,RBPMS,MTA3,PRKDC,IRF7,ERCC6,HOXC13,CALCOCO1,ST18,RASL11A,NCOA4,TRAF6,NR1H4,TRIM44,TCF15,SOX12,PLAG1,USF2,RET,LMO2,ZC3H8,ASXL1,IL1A,PAX8,NR4A1,ACVR1B,ZNF143,CAMK4,CEBPA,FOXL2,NCOA6,PIK3R1,TFDP2,CDK7,IRF2,TAF9,NCOA2,MED19,CCDC62,TFCP2,HAND2,CSRNP2,ING2,EYA1,ML	grey	VSMC_M10
GO:1901976	0.99	0.01	10	31	regulation of cell cycle checkpoint	BP	1	PPP1R10,CRY1,ETAA1,CDK5RAP2,DYNC1LI1,ANAPC15,USP44,CHEK2,LCMT1,DUSP1	grey	VSMC_M10
GO:0006333	0.99	0.01	44	106	chromatin assembly or disassembly	BP	1	SMARCC2,BAZ2A,BRD2,ASF1A,H3F3C,UBN2,SOX9,SUV39H2,RSF1,SIRT2,SMARCD1,M1AP,SPTY2D1,NAP1L5,RBBP4,SART3,ARID1A,BAZ1B,H2AFY2,HIRA,PADI2,TSPYL2,PHF8,NAP1L2,NAA60,CTCF,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,BEND3,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,TSPYL5	grey	VSMC_M10
GO:0050878	0.99	0.01	125	273	regulation of body fluid levels	BP	1	NME1,SERPINB2,TSPAN8,MPIG6B,FZD6,FBLN1,SLC22A4,AKR1B1,MAPK14,MYH9,GUCA1B,SRF,TEC,ENPP4,TLN1,TFAP2B,PPAT,PRKCE,AQP1,PLEK,NR1H2,DGKI,GRHL1,MET,EGFR,TLR4,ATG5,SLC7A11,TRAF3IP2,THBD,ELOVL1,PLAT,MYL12A,C1QTNF1,ACTG1,CLIC1,GAS6,ADRA2B,USF2,LSR,GPI,PIK3CB,P2RY1,NR1H3,VDR,HPS5,AP3B1,F2RL1,F2R,ANO6,DMTN,ADTRP,DTNBP1,CHRM3,CD40,FAP,NEURL1,SLC6A3,LCK,CCND1,TRPV4,ADRA2A,ITPK1,PRSS56,UBASH3B,HPS4,DGKD,KDF1,SFN,COPA,USF1,PAFAH2,PTPRO,FCER1G,GRHL3,DGKG,NFE2L2,CREB1,BLOC1S6,PLA2G4A,ITGA2B,ABCA12,FN1,PTPN6,SERPINC1,ADRA2C,FERMT3,HGFAC,COL3A1,VCL,CHRM1,STAT5B,WAS,ACTB,ANXA8,F12,MED1,PEAR1,ANXA2,DGKQ,ALOXE3,ZBTB7B,UPRT,DGKE,CORO2B,SCNN1B,VAV1,MYO5B,ABAT,INPP5K,SERPINF2,P2RX1,ADAMTS13,CELSR2,CEL,CYBA,VAV3,STXBP1,DHODH,HSD11B2,FGA,BLOC1S3,CLDN1,PDSS2,RAP2B	grey	VSMC_M10
GO:0051298	0.99	0.01	24	64	centrosome duplication	BP	1	VPS4B,MDM1,CHMP2A,BRSK1,XPO1,CDK5RAP2,CEP295NL,CEP63,PLK2,CHMP2B,CEP44,CHMP4C,ALMS1,TMEM67,PKD2,AC112128.1,CCDC84,CEP152,CNTROB,TRIM37,CEP192,NUBP1,CHMP1A,C2CD3	grey	VSMC_M10

GO:0048699	0.99	0.01	580	1177	generation of neurons	BP	1	ADNP2,NME1,NEDD4L,ATP8B1,ONECUT2,TCF4,LRP1,SEMA6A,KIF5A,AVIL,ATAT1,FRS2,RAB21,MAPK8IP2,SNW1,TIAM2,RIMS2,PRKN,AGER,SULT4A1,TSPO,UQCRQ,CEP85L,FSTL4,SYNGAP1,WASHC5,ASAP1,GFRA3,PTK2,PTCH1,ANKS1A,AGTPBP1,PLXNA4,NTRK2,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,MICALL1,RAC2,SMO,DAAM2,RBFOX2,CHRNA3,PRPH2,FBXO7,RORB,PTK7,SRF,TTBK1,FZD1,CDK6,KIT,ADGRF1,TNFRSF21,NCK2,ROR2,SEMA4D,DLX5,ETV1,ADGRL3,SEMA4C,BEND6,SVBP,BRSK1,RDH13,RIMS1,TMEM30A,RTN4,GSDME,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,PPT1,MYCL,AREG,EPHA7,AKNA,WHRN,PTN,MET,TNC,YWHAZ,EGFR,HECW1,TRIM32,NCDN,CDK5RAP2,EPHA1,KEL,MYCN,RTN4IP1,NRCAM,FOXO3,NTF4,FIG4,WASF1,MFSD8,DHFR,PLXNA1,HDAC2,MTMR2,NAPA,DNMT3A,NDNF,RAB10,IQSEC1,ABI1,SOX9,ERCC2,SLC39A12,ERCC3,USH1G,CDNF,GOLGA4,GLI2,MEGF8,KDM4A,XRCC2,IFT172,PTPRF,MYO7A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,WNT11,SLITRK5,ALK,HOOK3,DZANK1,CPNE9,FARP1,KIF5C,SLC4A7,BHLHE40,JAG1,SIRT2,FSCN2,SYT1,TMEM106B,LRTOMT,AP000812.5,FEZ2,RAC3,CEP290,SLC23A2,LSM1,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NRG1,NCKAP1L,GAS6,ULK1,DPYSL3,ERCC6,RYK,ADRA2B,SNPH,EPHB1,PLK2,PLAG1,RET,LGI4,TOX,ZSWIM6,TTL,DNMT3B,CBFA2T2,ANKRD27,FAIM,ZNF536,PREX2,CASP3,HAND2,DCLK2,EYA1,PLS1,ROBO1,ROBO2,ARNTL,TENM3,ADGRV1,ENC1,FZD3,MEF2C,ELP3,SEMA4F,FAIM2,HTRA2,VEGFC,NCAM2,TLX2,IGSF10,CUX2,KATNB1,PTK2B,MME,RAPGEF2,DGUOK,DPYSL2,EIF2AK4,NNAT,RND1,TIAM1,PAQR3,SLIT1,USH1C,SYNJ1,TENT2,OPA1,NKX6-	grey	VSMC_M10
GO:0009792	0.99	0.01	256	537	embryo development ending in birth or egg hatching	BP	1	CNOT2,STK3,OSR2,FZD6,PNLDC1,BRD2,TBC1D32,RRP7A,UBE2B,RSPO3,PTCH1,LY6E,TAB1,SOX10,MFNG,SMO,MDFI,TFEB,TAF8,MYH9,ZFAND5,PTK7,SRF,APBA1,ROR2,SEMA4C,MEOX2,ANKS6,SIX2,EPAS1,MSH2,RTN4,YTHDC1,HOXA2,HOXA4,HOXA6,ADAMTS3,HOXA7,AKIRIN2,FUZ,GJB5,TEAD2,MYCN,OSR1,APOB,INTU,BMI1,KIAA1217,ABI1,SOX9,ERCC2,GLI2,MEGF8,PCDH8,XRCC2,IFT172,SCEL,WDR60,WNT11,CCNB1IP1,TGFBR2,OVOL2,ACVR2A,EOMES,CHD8,MAFG,CHTOP,SPINT2,ALX1,PRKDC,KBTBD8,TRAF6,TCF15,POFUT1,GPI,ACVR1B,CEBPA,CASP3,CCDC62,HAND2,EYA1,FZD3,CNOT1,CELF1,NBN,DHX35,NKX3-1,OPA1,ACVR1C,IFT52,SPINT1,COL4A3BP,RPGRIP1L,RTF1,ZBED6,PKD2,STK4,TFAP2A,RIPPLY3,PAX2,NPM2,PRICKLE1,NKD1,ZNF335,TENT5C,IGF2,SUFU,KLHL12,SH3PXD2A,HYAL1,ELF3,SLC2A10,SBDS,TGFB2,SULF2,POGLUT1,PEF1,SATB2,PDCD6,ITPK1,DAD1,NR5A2,AXIN2,SNAI1,OTUD7B,POLG2,SLC25A20,GBX2,ARNT,DVL3,PLPP4,VASH2,RAI2,RPL7L1,CHRD,SYF2,DLX1,MGAT1,GRHL3,TANC2,SP3,DLG1,LUZP1,SETD2,YBX3,HOXD4,HOXD3,FZD5,PTH1R,TET1,KIF1BP,PLOD3,NMT1,TRIP6,BCOR,DNAAF2,MEOX1,RUNDC1,FKBP8,ELL,SEC24C,ECE1,TTLL4,GORAB,GPR161,AKAP3,ARHGDIG,NKX3-2,MAPK1,WDR74,TULP3,LIAS,DVL2,BMPR1A,WDR19,SLC25A34,TCAP,RBPJ,MED1,ALDH1A2,MFN2,RAD51B,SOX15,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,TMEM107,NDEL1,VASH1,CITED1,ALKBH1,MAP2K1,TMEM100,SMAD3,MKS1,PPP4R4,GSC,KEAP1,LHX1,SIN3A,TCOF1,CDX1,AMOT,GATA6,MIB1,CAMSAP3,NLE1,XAB2,CDK5R1,JAG2,ISL1,SUPT6H,NSRP1,INPP5K,APBA3,TLE6,SKI,PKD1,SOX8,ALX3,TSC1,FOXF1,TMEM231,GLMN,	grey	VSMC_M10
GO:0033194	0.99	0.02	4	16	response to hydroperoxide	BP	1	XRCC1,TP53INP1,CD38,MT-ND1	grey	VSMC_M10
GO:0031346	0.99	0.01	138	302	positive regulation of cell projection organization	BP	1	NME1,LRP1,AVIL,RAB21,TIAM2,WASHC5,PLXNA4,NTRK2,CDC42EP1,RAC2,PTK7,SRF,FZD1,KIT,ROR2,SEMA4D,EPS8L1,TMEM30A,RUFY3,AKIRIN1,PTN,FUZ,FIG4,PLXNA1,NDNF,GOLGA4,MEGF8,SS18L2,ALK,TMEM106B,ARHGEF7,PLXNC1,DPYSL3,RET,TOX,CBFA2T2,ANKRD27,PIK3R1,ROBO1,ROBO2,PLCE1,TENM3,ENC1,P2RX7,CUX2,KATNB1,PTK2B,RAPGEF2,TIAM1,OPA1,ZFYVE27,F2RL1,RREB1,ITPKA,CYFIP1,CNTN1,BDNF,NEURL1,DNM1L,CARMIL1,ZMYND10,CAPRIN2,AUTS2,ADNP,DISC1,AGT,WASF2,DVL3,HDAC4,SS18L1,EPS8,CDKL5,WNT3,NFE2L2,CDC42EP2,MAPT,ABL2,PPP2R5B,EHD1,FN1,NCKAP1,NIN,SERPINI1,CRTC1,HTT,DNM3,RETREG3,MARK2,OBSL1,HAP1,EPHA4,DLG4,MNS1,DVL2,MIEN1,PLEK2,ATP1B2,RAB8B,ITGA3,NDEL1,TENM2,ZDHHC15,RAB11A,MAP2K1,NTN1,DNM2,PARP6,RIT2,BCAS3,GPRASP2,BHLHB9,TRPV2,FBXO38,RRN3,FMR1,LRP8,L1CAM,WRAP73,PLXNA3,PALM,EPS8L3,DEF8,AMIGO1,FBXO31,LCN2,FNBP1L,HSPA5,DAB2IP,CARMIL2,MIR21,MIR222,PLK5,CNTF,EPS8L2,WNT5A,APC,RALA,HRAS	grey	VSMC_M10
GO:0071404	1.00	0.02	4	16	cellular response to low-density lipoprotein particle stimulus	BP	1	FGF21,FCER1G,LDLR,NPC1	grey	VSMC_M10
GO:0072332	1.00	0.01	24	63	intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	SNW1,PRKN,MSH2,ARMC10,POU4F1,TAF9,ING2,MARCH7,AEN,CHEK2,RPL11,E2F2,MUC1,TAF9B,CD74,PPP1R13B,CDIP1,MIR21,UBB,RPS27L,PERP,PTTG1IP,TMEM109,HINT1	grey	VSMC_M10
GO:0014812	1.00	0.01	31	79	muscle cell migration	BP	1	LRP1,TRIB1,SMO,AKIRIN1,ITGB1BP1,GRB10,TLR4,PLXNA1,PLAT,PARVA,MEF2C,ADAMTS1,DOCK5,BIN3,TERT,GNA13,SSH1,SORL1,AGT,HDAC4,NFE2L2,SEMA6D,BMPR1A,FOXO4,CCL5,DOCK7,CRK,MIR21,RHOA,SIX1,PDGFD	grey	VSMC_M10
GO:0038061	1.00	0.01	41	99	NIK/NF-kappaB signaling	BP	1	AGER,PTP4A3,PRDX1,REL,NOD1,TNFSF15,EGFR,TLR4,PHB,ALK,NMI,TCIM,EIF2AK2,TRAF6,TRIM44,AKIP1,ZFP91,HDAC7,NOD2,NFKB2,PDCD4,EDARADD,RTKN2,TRIP6,DDX3X,RC3H1,BIRC3,PPM1A,TSPAN6,LITAF,TRAF2,MIR21,MIR125B1,MIR27B,MIR27A,RHOA,NOL3,COPS8,C1QTNF4,HAVCR2,RC3H2	grey	VSMC_M10

GO:0003012	1.00	0.01	154	332	muscle system process	BP	1	NEDD4L,STAC3,PPARA,SNTB1,SMAD5,PLA2G6,PI16,ZDHHC21,CHRNA3,LMOD2,SRF,KIT,TMOD1,TNNI3,ASB3,MYBPC2,MYH14,CLCN1,IL15,TRPM4,FOXO3,HDAC2,TRPC3,CACNB2,STAC,KDM4A,SCN5A,SCN1A,GPD1L,MKKS,RYR1,P2RX2,LMOD3,ADRA2B,ASPH,HTR7,NR4A1,SLMAP,MYOF,HAND2,P2RX3,PLCE1,GUCY1A1,P2RY1,CKMT2,TIAM1,DOCK5,HOMER1,STC1,KCNJ3,F2R,TNNC1,COL4A3BP,KCNE2,DSP,CASQ2,JARID2,KCNIP2,CHRM3,RYR2,RAP1GDS1,PKP2,PDE9A,LMOD1,PPP3CA,KCNJ2,MAP2K6,TNNI1,TRPV4,ADRA2A,SYNM,SULF2,DAG1,MYH7,SCN7A,GRK2,GTF2IRD1,ANK2,GPER1,AGT,ACE2,ATP1A2,ACTC1,SLC9A1,MYOZ2,CASQ1,ACTN3,TMOD4,HDAC4,SCN4B,MYOM3,NOS1AP,DLG1,TTN,ADRA2C,CALCRL,MYOZ1,PRKAG3,CAMK2G,ATP1B1,KCNA1,CD38,KCNMA1,DES,TMOD2,CAMTA2,TPM4,PARP1,CHRNB1,TCAP,TNFRSF1B,STAC2,ARHGEF11,MYL5,CACNA1G,CHRNB2,ATP2A1,SMAD3,CALM1,SCNN1B,TBX2,NMUR2,SETD3,YY1,DTNA,DSG2,GATA6,MYH11,ABAT,TRPV1,P2RX1,GAMT,RNF207,CACNA1H,CYBA,MIR199A1,MIR21,MIR23A,MIR24-1,MIR25,RHOA,HTR1D,DMD,NOL3,CHRNG,CHGA,KCNH2,TNNC2,SCN2B,RGS4,KCNJ8,HCN4,NKX2-5,HEY2	grey	VSMC_M10
GO:0071478	1.00	0.01	65	150	cellular response to radiation	BP	1	BAK1,XRCC6,MYC,ATF4,MAPK14,MAPK13,HSF1,OPN1SW,CRY1,CAMKMT,AQP1,PTN,ERCC1,XPC,AKT2,WRN,PIK3R1,ATR,RAD9B,MME,EIF2AK4,DDB2,TENT2,SPIDR,CRY2,TP53INP1,ITGB6,TRPM1,RHBDD1,HYAL1,HYAL3,RRH,SAG,CHEK2,NFATC4,MGMT,NMT1,XRCC5,GRK4,MMP3,RHNO1,GNB5,ZBTB1,PARP1,DDB1,GUCY2D,TAF1,DNM2,YY1,CUL4B,ERCC4,FMR1,CREBBP,CYBA,HSPA5,MIR21,SWI5,IMPACT,GADD45A,GRB2,GPR88,HRAS,TMEM109,TSPYL5,GTF2H5	grey	VSMC_M10
GO:0046661	1.00	0.01	54	128	male sex differentiation	BP	1	HSD17B4,ESR1,SMAD5,LRRC6,H3F3C,HSD17B3,KIT,ROR2,MSH2,HOXA13,SOX9,ERCC1,UTF1,WDR48,ACVR2A,SEMA3A,NCOA4,AMHR2,DHX37,ING2,NKX3-1,TESC,SRD5A1,CCND1,TGFB2,LHX9,SPATA2,TFAP2C,CBL,ASB1,PATZ1,YBX3,WNT4,CTSV,STAT5B,INHA,KDM5A,BMPR1A,SOX15,ADAM21,ADAM20,GATA6,MAMLD1,SOX8,FSTL3,UBB,ARID4A,AGO4,ADGRG1,WNT5A,BCL2L11,TBC1D20,BCL2L2,LHFPL2	grey	VSMC_M10
GO:0007266	1.00	0.01	48	116	Rho protein signal transduction	BP	1	CDC42SE2,GPR20,CDC42EP1,EPS8L1,CTNNAL1,LPAR1,MET,RAF1,ARRB1,ROBO1,ARHGEF28,RTKN,F2RL1,F2R,ADRA2A,GNA13,CFL1,ARHGAP6,CNKSR1,EPS8,CDC42EP2,BCL6,ABL2,COL3A1,ARHGDIG,WAS,MYO9B,RHOJ,ARHGEF11,STARD8,NGFR,ITGA3,KCTD13,HACD3,NTN1,RIT2,TNFAIP1,RALBP1,TAX1BP3,ARHGAP4,EPS8L3,SCAI,RIPOR1,RHOA,GPR35,ADGRG1,EPS8L2,RHOU	grey	VSMC_M10
GO:0035265	1.00	0.01	57	134	organ growth	BP	1	GLI1,ESR1,STK3,PPARA,LY6E,MAPK14,PI16,PIM1,SMO,BNC2,COL27A1,SOX9,TSKU,SPRY2,TGFBR2,RARB,DUSP6,PLAG1,MEF2C,IL7,STC1,TBX5,STK4,JARID2,IGF2,TGFB2,PRKAR1A,HLX,AGT,KCNK2,YBX3,POR,SAV1,FGFR3,MMP13,MAPK1,BMPR1A,RBPJ,THBS3,WWC1,TBX2,YY1,GATA6,LEPR,MIR199A1,MIR222,MIR23A,MIR24-1,MIR25,NOG,BASP1,FXN,RGS4,BCL2L11,C3orf58,HEY2,WNT2	grey	VSMC_M10
GO:0061042	1.00	0.02	4	16	vascular wound healing	BP	1	TNFAIP3,SLC12A2,NDNF,MCAM	grey	VSMC_M10
GO:0046040	1.00	0.02	4	16	IMP metabolic process	BP	1	PPAT,AMPD3,AMPD1,ADSSL1	grey	VSMC_M10
GO:0010880	1.00	0.02	7	24	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	1	CASQ2,RYR2,ANK2,ATP1A2,CASQ1,CALM1,DMD	grey	VSMC_M10
GO:0043933	1.00	0.01	688	1370	protein-containing complex subunit organization	BP	1	TIMM21,VPS4B,SMARCC2,MIP,ARPC3,BAZ2A,TCF4,SHMT2,AVIL,ATP23,ATAT1,CPSF6,ESR1,STK3,ZNF207,MAPK8IP2,APOM,HSPA1B,SF3A3,TUBGCP6,EIF3E,LYRM7,KCNV1,PRKN,HLA-DRA,HLA-DOB,HLA-DMA,IL5,BRD2,HLA-DPB1,SEPT8,HSD17B8,ASF1A,HSPA4,RRP7A,NDUFA6,BAK1,WASHC5,MYC,ASAP1,LRRC6,JMJD4,AGO2,H3F3C,PTK2,FANCC,MAPK15,CBY1,DMC1,PUF60,PSMD5,BAIAP2L2,PICK1,EIF3L,CDC42EP1,GPAA1,TSPAN33,HSF1,TAF8,CHRNA3,PRPH2,GNMT,TRPM6,LMOD2,TTBK1,APBA1,C12orf45,SLAIN2,NCK2,TLN1,KIAA1211,NINJ1,COA5,CHMP2A,RPS14,TMOD1,PLEKHH2,STX17,SDHAF4,PRKCE,RIMS1,PRPF31,SPTBN1,RTN4,PPP2R1A,MPP6,YTHDC1,PNPT1,SKAP2,SHANK1,ECPAS,SNX14,SRSF10,MDN1,WDR92,TRAPPC12,PLEK,NR1H2,ITGB1BP1,MED25,MET,ADD2,AGO1,TLR4,CDK5RAP2,TRAF1,TEAD2,FAM49A,TRPM4,MAPRE1,WASF1,MFSD8,ARMC4,EPS15,SSBP1,APOB,FAF1,NDUFB2,HIGD1A,UBN2,NAPA,AP2S1,VSTM5,MSRB2,ATPAF1,KCNRG,KPNA3,DRC1,SOX9,EML2,NDUFB6,RUBCNL,SLC39A12,LCP1,TMEM126B,CLASP2,APOC1,MAPRE3,DNAJC15,KCTD2,CDC123,MTRF1,KCTD21,TRIM54,NDUFC2,RALB,RSF1,CLNS1A,CAND2,AQP11,RAF1,MYD88,CELF2,DMAC2,NCKAP5,RPSA,NAPB,SLAIN1,CRNKL1,HGSNAT,PIP4P1,EID2,PLEKHG2,FCHSD2,MKKS,TMEM173,NAV3,SYT1,LIN7A,NUP98,RYR1,FERMT1,NDUFS8,EIF2AK2,PRNP,NDUFAF7,BAG4,TAF7,ARHGEF7,DIAPH1,ATL2,BRF2,SPEF1,FCHSD1,NDUFA12,NRG1,NCKAP1L,ULK1,ARFIP2,MITF,TAF10,LMOD3,VPS16,PRKDC,COX7A1,ACTR6,TTC17,NR1H4,ATXN7,APIP,TGS1,SOAT2,HCK,TM9SF4,NDUFAF2,FAM107A,KCTD6,KCTD15,FER,C12orf65,GPR4,ANKRD37,HERC1,LRWD1,IK4,HIRIP3,TAF9,CHM	grey	VSMC_M10
GO:0071219	1.00	0.01	57	133	cellular response to molecule of bacterial origin	BP	1	TNFAIP3,TSPO,TRIB1,MAPK14,HSF1,PRKCE,CXCL8,TLR4,CDK19,MYD88,IRAK2,NFKBIB,SIRT2,TRAF6,HCK,IL1A,IL37,PLSCR4,MEF2C,NUGGC,NR1H3,RIPK2,ABCC2,NOD2,CD40,PDCD4,FZD5,UPF1,TNIP2,MAPK1,SGMS1,AKAP8,TNFRSF1B,SPON2,MAPK3,TNIP1,CCL5,CCL2,LITAF,NOS2,TICAM1,ADAMTS13,ASS1,LCN2,GFI1,BCL10,DAB2IP,MIR21,RHOA,DEFB124,CXCL6,IRGM,CMPK2,IL36G,WNT5A,CEBPB,HAVCR2	grey	VSMC_M10

GO:0048008	1.00	0.01	17	48	platelet-derived growth factor receptor signaling pathway	BP	1	LRP1,ZFAND5,PTGIR,CSRNP1,PLAT,PDGFRL,FER,HIP1R,PTPRJ,CBL,LRIG2,APOD,RGS14,IFT20,PTPN2,CSPG4,PDGFD	grey	VSMC_M10
GO:0006325	1.00	0.01	138	301	chromatin organization	BP	1	SMARCC2,BAZ2A,ESR1,ARID1B,BRD2,ASF1A,PHF1,MYC,L3MBTL3,L3MBTL2,H3F3C,CBX7,KDM4C,SMARCA2,SCMH1,STPG4,ZNF462,HMGN3,UTP3,SETD7,HDAC2,UBN2,DNMT3A,SETDB2,RCBTB1,FOXA3,SOX9,HDAC11,SUV39H2,NUDT5,RSF1,KDM4A,CBX4,CHD8,SIRT2,ZMYND11,ERCC6,ACTR6,MOS,TOX,SMYD1,ING2,FAM208A,HLTF,SMARCD1,M1AP,SFMBT1,TTI1,TOP1,PBRM1,ABRAXAS1,BAHD1,LOXL2,RSBN1,PHF21A,SPTY2D1,SYCP1,NPM2,PPHLN1,NAP1L5,JARID2,RBBP4,HDAC1,SATB2,SART3,ZNFX1,ARID4B,SNAI1,SOX2,RCCD1,ARID1A,AEBP2,VPS72,HDAC4,SS18L1,BAZ1B,SETD2,TET1,H2AFY2,TADA2B,HIRA,DDX11,KDM5A,PADI2,FOXP3,ACTB,ZBTB1,TSPYL2,KDM5C,PHF8,SOX15,SETD1A,DPF3,KDM6B,NAP1L2,NRDE2,NCOR1,METTL4,SMCHD1,L3MBTL4,SUPT6H,NAA60,HCFC1,PRDM16,MUM1,CHD5,BANP,MTF2,TDRD3,CTCF,SETDB1,SYCP3,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,BEND3,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,HMGN5,HMGN4,RNF8,ZNF304,CHRAC1,GATAD1,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,ZNF518A,HIST1H2BJ,HIST1H4A,CBX2,HIST1H4F,TSPYL5	grey	VSMC_M10
GO:0044271	1.00	0.01	1770	3436	cellular nitrogen compound biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,ORMDL2,SMARCC2,PAN2,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,POLI,RPS12,SHMT2,TBPL1,GLI1,HBS1L,MARS,MAP3K5,B4GALNT1,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,ATP5MGL,HELB,ZBTB2,RMND1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,TFB1M,ZNF706,ALDH7A1,ARID1B,HSPA1B,FZD6,ZBTB12,EIF3E,ZBED4,PNLDC1,MAP3K4,PPT2,PRKN,QKI,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,RXRB,TSPO,VGLL2,MRPL13,RPS18,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,MRPL55,JMJD4,AGO2,HABP4,RPS10,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,EIF3L,PIM1,NRF1,TMPRSS6,SMO,SNAPC3,BNC2,HSF1,PSAT1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,POT1,GPR37,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,SLC35B2,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,ADGRF1,UXS1,NCK2,FHL2,TGFBRAP1,MRPS9,TFAP2B,SPTLC1,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,AASDH,PPAT,REV1,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,LRPPRC,SIX2,PPCS,SRBD1,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,CHAC2,IGF2BP3,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,MTIF2,NFE2L3,PNPT1,ME1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,NT5E,ZN	grey	VSMC_M10
GO:0060070	1.00	0.01	113	250	canonical Wnt signaling pathway	BP	1	RPS12,GLI1,STK3,FZD6,PRKN,TCF7,UBE2B,RSPO3,RNF146,MAPK14,CSNK1E,SOX10,DAAM2,PTK7,CDK14,FZD1,ROR2,DLX5,WNK2,SOSTDC1,RSPO1,EGFR,HECW1,FUZ,SFRP4,CCNY,DKKL1,TRPM4,FOXO3,SOX9,PPM1N,SCEL,WNT11,RBMS3,CHD8,UBAC2,RAB5A,FERMT1,MITF,RYK,PFDN5,CTNND1,DKK3,ARNTL,FZD3,TMEM131L,LMBR1L,OTULIN,AMFR,NR4A2,SOX13,STK4,PRICKLE1,NKD1,PRDM15,LGR6,LRRK1,HDAC1,CAPRIN2,TMEM9,SULF2,TCF7L2,DKK2,AXIN2,EGF,TTC21B,SOX2,DISC1,ZNRF3,KREMEN1,DVL3,BICC1,FZD7,GID8,PTPRO,FZD9,WNT3,CCNYL1,FZD5,DIXDC1,DDX3X,WNT4,TBL1XR1,PPM1A,OTUD5,DVL2,IGFBP4,RBPJ,PSEN1,TMEM88,CSNK1G1,SMAD3,MKS1,CCDC88C,G3BP1,NLE1,ISL1,JFT20,GPC3,TLE6,APC2,DAB2IP,MIR199A1,MIR222,SOX4,NOG,WNT5A,DDIT3,DACT3,SDHAF2,APC,NKX2-5,WNT2	grey	VSMC_M10
GO:0008406	1.00	0.01	72	166	gonad development	BP	1	HSD17B4,ESR1,GDF9,LRRC6,H3F3C,DMC1,FANCG,KIT,MSH2,OSR1,FOXO3,SOX9,ERCC1,UTF1,WDR48,ARRB1,ACVR2A,MKKS,SEMA3A,NCOA4,DHX37,FOXL2,CASP3,ING2,ROBO2,ADAMTS1,NKX3-1,TESC,SALL1,BMPR1B,GAS2,SRD5A1,HYAL3,CCND1,TGFB2,LHX9,SPATA2,TFAP2C,SPO11,CBL,TAF4,PATZ1,YBX3,VGF,WNT4,CTSV,PTPRN,STAT5B,INHA,KDM5A,WDR19,SOX15,ADAM21,ADAM20,GATA6,MAMLD1,SOX8,HSPA5,MSH4,LHX8,FSTL3,UBB,ARID4A,AGO4,ADGRG1,WNT5A,BASP1,BCL2L11,TBC1D20,BCL2L2,CEBPB,EREG	grey	VSMC_M10
GO:0045446	1.00	0.01	36	91	endothelial cell differentiation	BP	1	ZDHHC21,S1PR3,HOXA13,PTN,MET,MYD88,ACVR2B,IKBKB,JAG1,PLCB1,BTG1,NRG1,MARVELD2,ARHGEF26,RAPGEF2,STC1,RAPGEF3,F2RL1,CLIC4,APOLD1,RAP1B,PLOD3,VCL,FOXP3,RBPJ,KDM6B,HOXB5,TMEM100,VEZF1,TNMD,MIR21,ACVRL1,FOXJ2,MIR99B,CLDN1,HEY2	grey	VSMC_M10
GO:0045428	1.00	0.01	15	43	regulation of nitric oxide biosynthetic process	BP	1	TSPO,TLR4,PTK2B,PKD2,AGT,NOS1AP,SMAD3,DNM2,GLA,INSR,TICAM1,TRPV1,ASS1,MIR199A1,MIR99B	grey	VSMC_M10

GO:0043009	1.00	0.01	248	522	chordate embryonic development	BP	1	CNOT2,STK3,OSR2,FZD6,PNLDC1,BRD2,TBC1D32,RRP7A,UBE2B,RSPO3,PTCH1,LY6E,TAB1,SOX10,MFNG,SMO,MDFI,TFEB,TAF8,MYH9,ZFAND5,PTK7,SRF,APBA1,ROR2,SEMA4C,MEOX2,ANKS6,SIX2,EPAS1,MSH2,RTN4,YTHDC1,HOXA2,HOXA4,HOXA6,ADAMTS3,HOXA7,FUZ,GJB5,TEAD2,MYCN,OSR1,APOB,INTU,BMI1,KIAA1217,ABI1,SOX9,ERCC2,GLI2,MEGF8,PCDH8,XRCC2,IFT172,WDR60,WNT11,CCNB1IP1,TGFBR2,OVOL2,ACVR2A,EOMES,CHD8,MAFG,CHTOP,SPINT2,ALX1,PRKDC,KBTBD8,TRAF6,TCF15,POFUT1,GPI,ACVR1B,CEBPA,CASP3,CCDC62,HAND2,EYA1,FZD3,CNOT1,NBN,DHX35,NKX3-1,OPA1,ACVR1C,IFT52,SPINT1,COL4A3BP,RPGRIP1L,RTF1,ZBED6,PKD2,STK4,TFAP2A,RIPPLY3,PAX2,NPM2,PRICKLE1,NKD1,ZNF335,TENT5C,IGF2,SUFU,KLHL12,SH3PXD2A,HYAL1,ELF3,SLC2A10,SBDS,TGFB2,SULF2,POGLUT1,PEF1,SATB2,PDCD6,ITPK1,DAD1,AXIN2,SNAI1,OTUD7B,POLG2,SLC25A20,GBX2,ARNT,DVL3,PLPP4,VASH2,RPL7L1,CHRD,SYF2,DLX1,MGAT1,GRHL3,TANC2,SP3,DLG1,LUZP1,SETD2,YBX3,HOXD4,HOXD3,FZD5,PTH1R,TET1,KIF1BP,PLOD3,NMT1,TRIP6,BCOR,DNAAF2,MEOX1,RUNDC1,FKBP8,ELL,SEC24C,ECE1,TTLL4,GORAB,GPR161,AKAP3,ARHGDIG,NKX3-2,MAPK1,WDR74,TULP3,LIAS,DVL2,BMPR1A,WDR19,SLC25A34,TCAP,RBPJ,MED1,ALDH1A2,MFN2,RAD51B,SOX15,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,TMEM107,NDEL1,VASH1,CITED1,ALKBH1,MAP2K1,TMEM100,SMAD3,MKS1,PPP4R4,GSC,KEAP1,LHX1,SIN3A,TCOF1,CDX1,AMOT,GATA6,MIB1,CAMSAP3,NLE1,XAB2,JAG2,ISL1,SUPT6H,NSRP1,INPP5K,APBA3,SKI,PKD1,SOX8,ALX3,TSC1,FOXF1,TMEM231,GLMN,TERF2,BCL10,	grey	VSMC_M10
GO:0010466	1.00	0.01	63	145	negative regulation of peptidase activity	BP	1	SERPINB8,SERPINB2,TNFAIP8,LRP1,PI16,GAPDH,CD109,AQP1,BCL2L12,CST7,RAF1,PRDX3,TIMP4,UBE2O,SPINT2,PRNP,GAS6,PSMF1,GPI,NR4A1,SERPINB1,SPINT1,PAX2,APLP2,SORL1,IFI6,AGT,COL6A3,SFN,COL7A1,RPS6KA1,CST6,POR,DDX3X,SPOCK2,SERPINC1,SERPINI1,BIRC3,ARL6IP1,ANXA8,ANXA2,SIMC1,PAPLN,TMED10,WFIKKN2,MAP2K5,NLE1,C3,GPC3,SERPINF2,WFIKKN1,PARK7,LAMTOR5,MIR199A1,MIR24-1,NOL3,SERPINB5,A2M,MIR339,SERPINE3,SERPINB9,CAAP1,RARRES1	grey	VSMC_M10
GO:0000075	1.00	0.01	67	155	cell cycle checkpoint signaling	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,MAPK14,CRY1,BRSK1,MSH2,ETAA1,CDK5RAP2,XPC,PLK3,DYNC1LI1,ANAPC15,IK,NEK11,USP44,PRKDC,ERCC6,CEP63,STK33,PLK2,RAD17,ATR,RAD9B,CHMP4C,EIF2AK4,NBN,ABRAXAS1,DONSON,ZFYVE19,PIDD1,TAOK3,CCND1,GIGYF2,CHEK2,ATRIP,SYF2,CDKN1B,TIPRL,RHNO1,PRPF19,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,LCMT1,FOXN3,PSMG2,TAOK1,FZR1,DOT1L,FBXO31,VPS4A,NAE1,RPA4,PLK5,RPS27L,SOX4,DUSP1,APC,BRCC3,CRADD,NABP1	grey	VSMC_M10
GO:2001057	1.00	0.01	23	61	reactive nitrogen species metabolic process	BP	1	TSPO,TLR4,PTK2B,SPR,PKD2,MARC2,MARC1,AGT,NOS1AP,POR,CPS1,GCH1,SMAD3,DNM2,GLA,INSR,NOS2,TICAM1,TRPV1,ASS1,NQO1,MIR199A1,MIR99B	grey	VSMC_M10
GO:0042026	1.00	0.02	4	16	protein refolding	BP	1	HSPA1B,HSPA8,DNAJB2,HSPA5	grey	VSMC_M10
GO:1902680	1.00	0.01	618	1246	positive regulation of RNA biosynthetic process	BP	1	NFATC1,ZNF407,SMARCC2,ONECUT2,TCF4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,YEATS4,ESR1,MYRFL,CNOT6,OSR2,SNW1,ARID1B,ZBED4,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,PTCH1,ATF4,MAPK14,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,IFT74,BICRAL,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,EPCAM,ZNF462,PHIP,HMGN3,NFYC,HOXA2,HOXA7,HOXA13,REL,CREB5,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,TEAD2,SETD7,MYCN,ELF2,OSR1,FOXO3,ZXDC,MAMSTR,ATAD2B,KDM7A,ZNF438,HDAC2,PHF10,MAML2,MLLT10,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,MAPRE3,UTF1,SUMO2,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,SS18L2,WNT11,TADA3,SERTAD3,KLF6,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,CEP290,NSD3,ING1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,RYBP,MITF,RBPMS,MTA3,PRKDC,IRF7,ERCC6,HOXC13,CALCOCO1,ST18,RASL11A,NCOA4,TRAF6,NR1H4,TRIM44,TCF15,SOX12,PLAG1,USF2,RET,LMO2,ZC3H8,ASXL1,IL1A,PAX8,NR4A1,ACVR1B,ZNF143,CAMK4,CEBPA,FOXL2,NCOA6,PIK3R1,TFDP2,CDK7,IRF2,TAF9,NCOA2,MED19,CCDC62,TFCP2,HAND2,CSRNP2,ING2,EYA1,ML	grey	VSMC_M10

GO:0009056	1.00	0.00	1015	2000	catabolic process	BP	1	VPS4B,NEDD4L,PAN2,GLS2,HSD17B4,LRP1,SHMT2,LVRN,ATG12,FEM1C,ALDH8A1,RMND5B,PDE7B,PIP4K2C,TNFAIP3,AGAP2,CYP27B1,AIG1,FUCA2,USP15,EPM2A,CANX,ENPP3,TRIM39,CNOT2,CNOT6,RIDA,MIOX,PABPC1,CPT1B,ALDH7A1,PHAX,ABHD16A,HSPA1B,SYNJ2,DPYS,SKIV2L,DXO,EIF3E,TMEM74,PNLDC1,PRKN,RNF5,PPARA,PDE10A,PSMB8,PNPLA3,PNPLA5,TSPO,MCAT,DERL1,SKP1,SMPDL3A,UBE2B,RNF217,CSDC2,RNF146,ECHDC1,AL096711.2,TRIB1,KLHL3,AGO2,PRXL2C,PTK2,C6orf106,TNRC6B,EXOC4,TUT7,MAPK15,AGTPBP1,APOBEC3H,GTPBP1,MAPK14,NRBP2,CSNK1E,PLA2G6,TMPRSS6,EXOSC4,FOXRED2,HSF1,FBXL6,TFEB,USP49,GPT,CARNMT1,FBXO7,KLHDC3,ALDH1A1,GDA,ABHD17B,CEMIP2,CROT,GNPDA2,DCAF12,GALT,USP46,ENPP4,LNX1,SRD5A3,TGFBRAP1,SPTLC1,GAPDH,CNOT11,PPAT,RGP1,PDCL3,HINT2,PRDX1,HMGCLL1,ADH5,CHMP2A,FBXO10,EXOSC3,RAB23,CAT,LRPPRC,SEC61B,STX17,RNF20,PRKCE,ATP6V1E2,CHAC2,RAD23B,ETFB,UBE3D,PNPT1,SLC4A4,ADAMTS3,ECPAS,NT5E,PPT1,SNX14,XPO1,NOD1,RRAGD,PELI1,BPGM,WDR91,CNOT4,PXDN,RNASEH1,FBXO48,MET,IL4I1,AGO1,ATP6V1C2,EGFR,HECW1,USP45,TRIM32,ASCC3,VPS41,HACE1,LPIN1,USP38,INPP4B,VPS35,SCOC,ATG5,MGST2,ZYG11B,SDCBP,TUT4,FOXO3,SMPD2,PUM2,MGAM,LDAH,MFSD8,DHDH,DDO,APOB,HSD17B14,BCAT2,FAF1,FGF21,TRAF3IP2,MTPAP,MTMR2,ZC3HAV1,SESN3,BBS7,RAB7A,DHX34,PIP4K2A,NAPEPLD,FAAH,FBXL13,HADHA,GAD2,PHB,ENTPD6,SOX9,PYGB,CDADC1,NUDT15,ABHD5,ESD,RUBCNL,ATP6V0E2,AKR1A1,PTER,APOC1,FBXL2,GLB1,KCTD2,PLK3,SUMO2,FASTK,OPTN,MLH1,NUDT5,USP35,KBTBD6,KCTD21,LIPE,DHTK	grey	VSMC_M10
GO:1902895	1.00	0.01	12	37	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SRF,FOXO3,KLF5,TERT,TGFB2,STAT3,BMPR1A,NGFR,FOS,SMAD3,MRTFB,JUN	grey	VSMC_M10
GO:0046596	1.00	0.01	7	24	regulation of viral entry into host cell	BP	1	LY6E,HS3ST5,NECTIN2,CD74,CIITA,TRIM68,TRIM34	grey	VSMC_M10
GO:0009894	1.00	0.01	394	806	regulation of catabolic process	BP	1	NEDD4L,PAN2,LRP1,PIP4K2C,TNFAIP3,AGAP2,EPM2A,TRIM39,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,DXO,PNLDC1,PRKN,RNF5,PPARA,TSPO,RNF217,CSDC2,AL096711.2,TRIB1,AGO2,PRXL2C,PTK2,TNRC6B,EXOC4,TUT7,MAPK15,AGTPBP1,GTPBP1,MAPK14,NRBP2,CSNK1E,HSF1,TFEB,FBXO7,DCAF12,SPTLC1,GAPDH,RGP1,PDCL3,EXOSC3,LRPPRC,PRKCE,ATP6V1E2,RAD23B,PNPT1,SLC4A4,XPO1,NOD1,RRAGD,WDR91,MET,ATP6V1C2,EGFR,HECW1,TRIM32,HACE1,VPS35,SCOC,ZYG11B,SDCBP,TUT4,FOXO3,PUM2,MFSD8,FAF1,FGF21,TRAF3IP2,MTMR2,ZC3HAV1,SESN3,BBS7,RAB7A,DHX34,PIP4K2A,PHB,SOX9,NUDT15,ABHD5,ATP6V0E2,APOC1,FBXL2,PLK3,SUMO2,FASTK,OPTN,MLH1,RALB,ATP6V0B,KDM4A,AQP11,PRKAG2,MYD88,TIMP4,EGLN2,MYCBP2,TNRC6C,PPP1CB,ALK,KLHL40,AKT2,SNX5,USP36,SIRT2,RPTOR,TMEM173,FEZ2,LSM1,DCN,RNF14,NRG1,DDRGK1,SH3RF2,RYBP,ULK1,PKP3,PPP1R3B,PAN3,PSMF1,ATP6V1H,TRIB3,PLK2,DEPP1,DRAM1,CEBPA,IDE,PIK3CB,CASP3,TAF9,HPGD,SH3D19,MTMR9,FBXW7,USP25,GPD1,HTRA2,P2RX7,CNOT1,CELF1,CSNK2A2,PTK2B,CNOT6L,PRKAG1,FAM192A,RIPK2,TPCN1,TENT2,WDR41,RNFT2,TP53INP1,FTO,MARCH7,KCNE2,PRICKLE1,NOD2,NKD1,TENT5C,MYLIP,TENT4B,RBM24,LONP2,LZTS1,ATP6V1B2,RNF144B,SUFU,GPLD1,AZIN2,FAP,IRS1,LPCAT1,RPL23,DNM1L,HECW2,SEC22B,CPT1A,CISD2,ZBTB20,TMEM9,ADRA2A,PSMD1,TMEM39A,DHRSX,GPR137B,USP30,DIS3L2,AXIN2,MAPKAPK2,USP13,GIGYF2,AC013489.1,EGF,USP19,YTHDF2,DISC1,SORL1,ATG16L1,CHEK2,ASB11,PSME1,DTX3L,ABCB11,SH3BP4,ARIH2,MCL1,TRAF5,ARNT,BAG3,CISD1,PPP1R3D,FASTKD1,ANGEL2,CCDC84,MTMR3,ACT	grey	VSMC_M10
GO:0099174	1.00	0.01	6	22	regulation of presynapse organization	BP	1	VPS35,SLITRK5,FARP1,LRFN3,SLITRK2,NTNG2	grey	VSMC_M10
GO:1905606	1.00	0.01	6	22	regulation of presynapse assembly	BP	1	VPS35,SLITRK5,FARP1,LRFN3,SLITRK2,NTNG2	grey	VSMC_M10
GO:0051240	1.00	0.00	518	1050	positive regulation of multicellular organismal process	BP	1	CD226,LRP1,GLI1,CYP27B1,FRS2,RAB21,OSR2,SNW1,TIAM2,ADM2,HSPA1B,RIMS2,AGPAT1,AGER,GPSM3,HLA-DRA,IL5,HLA-DPB1,TSPO,XRCC6,TRIB1,MYC,TOB2,AGO2,ATF4,PLXNA4,MAPK14,NTRK2,MAPK13,SOX10,PIM1,SMO,HSF1,IRF5,TEK,LINGO2,SRF,TTBK1,ENPP4,RFX3,KIT,SLC1A1,ROR2,GADD45G,SEMA4D,GAPDH,PDCL3,NINJ1,EXOSC3,NLRP5,PRKCE,EPAS1,RIMS1,MSH2,SPTBN1,RTN4,RUFY3,EMC10,CXCL8,NOD1,AKIRIN2,AQP1,PELI1,BMPER,RSAD2,LRRN3,NR1H2,PTN,GRB10,IL4I1,EGFR,TRIM32,TLR4,EPHA1,GAB1,LPIN1,IL15,UCP1,ATG5,SDCBP,TRPM4,OSR1,FOXO3,FGF21,SPHK2,SPRY1,PLXNA1,HDAC2,TRPC3,HMCES,C5AR1,PANX1,VSTM5,PRKD2,CST7,PHB,SOX9,SLC39A12,LACC1,SLC4A2,MLH1,GOLGA4,GLI2,MEGF8,XRCC2,MYD88,PIBF1,ACVR2B,FOXJ1,PAXIP1,NUMBL,THBD,POU4F1,TSKU,IL15RA,SS18L2,WNT11,TGFBR2,OVOL2,SNX5,ZNF219,ACVR2A,C1QTNF1,JAG1,MKKS,TMEM173,PLCB1,FERMT1,ALX1,SHLD1,EIF2AK2,ADRA1D,LUM,BTG1,MAVS,PLXNC1,SEMA3A,KL,NCKAP1L,GAS6,FOXP1,LMOD3,PRKDC,IRF7,FLT1,ADRA2B,TRAF6,NR1H4,DHX37,EPHB1,SOX12,PLAG1,RET,TOX,IL1A,PAX8,ACVR1B,ANKRD27,FAIM,PIK3R1,CLSTN2,ERAP1,HAND2,PLS1,ROBO1,P2RX3,ROBO2,ADGRV1,PTPRJ,FZD3,MEF2C,IL7,P2RX7,VEGFC,CELF1,CUX2,SOX6,P2RY1,PTK2B,RASGRP1,MME,ALMS1,TIAM1,EBF2,OAS3,RIPK2,SYNJ1,VDR,NKX3-1,OPA1,NKX6-1,RAPGEF3,LOXL2,TBX5,AP3B1,AMIGO2,ZFYVE27,AGGF1,F2RL1,F2R,TESC,RIPK1,ANO6,SPINT1,POLR3D,RREB1,ITPKA,PLA2R1,SOX13,TFAP2A,GCNT2,PAX2,CYFIP1,DMTN,NOD2,KSR2,ZNF335,CHRM3,PRKAB1,CD40,R	grey	VSMC_M10

GO:0006508	1.00	0.00	648	1295	proteolysis	BP	1	CNDP1,SERPINB8,SERPINB2,VPS4B,SEC11C,NEDD4L,TNFAIP8,LRP1,SHMT2,LVRN,FEM1C,RMND5B,MAP3K5,TNFAIP3,ADGRG6,ATP23,USP15,CANX,TRIM39,CPM,MYRFL,HSPA1B,ADAMTS19,GRAMD4,PRKN,RNF5,AGER,FBLN1,PSMB8,ZUP1,DERL1,SKP1,UBE2B,BAK1,RNF217,RNF146,TRIB1,MYC,KLHL3,XPNPEP3,PTK2,PTCH1,AGTPBP1,IOSD1,CSNK1E,PI16,TMPRSS6,GPAA1,FOXRED2,HSF1,FBXL6,USP49,MYH9,FBXO7,KLHDC3,TTBK1,ADAM22,DCAF12,CAPN11,SUPT3H,USP46,LNX1,SLC1A1,PLGRKT,ERMP1,IL1R2,GAPDH,PDCL3,FBXO10,SVBP,SEC61B,RNF20,CD109,RAD23B,UBE3D,KLK14,KLK13,KLK4,ACP4,ADAMTS3,ECPAS,CPVL,SCRN1,XPO1,NOD1,AKIRIN2,PM20D2,MINDY4,AQP1,CASP8AP2,PELI1,AGBL3,RHBDL2,CNOT4,FBXO48,EPHA7,NR1H2,TNFSF15,HECW1,USP45,TRIM32,ASCC3,FBXW2,HACE1,BCL2L12,USP38,KEL,ZYG11B,SDCBP,DLD,FAF1,HSPE1,HDAC2,BBS7,HMCES,OTUD1,FBXL13,CST7,QPCTL,PRSS23,NUDT15,SSPO,FBXL2,PDIA3,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,AQP11,RAF1,DMAC2,PRDX3,TIMP4,IFT172,WDR48,UBE2O,UBXN4,UBE3C,SPOPL,PLAT,UBE2E1,CAPN14,KLHL40,PITRM1,ARRB1,UGGT2,USP36,TASP1,FBXO17,SIRT2,DNAJC18,NPLOC4,ADAM18,UBAC2,NUP98,GPS1,SPINT2,TPP2,NHLRC3,PRNP,NUDT16,ADAM33,RNF14,RNF122,USP44,DDRGK1,SH3RF2,GAS6,RYBP,TRIM3,PPP2CB,UBXN8,TAF10,ARL6IP5,CPXM1,ST18,NSFL1C,PCBP2,PSMF1,PSMD6,ATXN7,TRIB3,PLK2,NRIP3,RET,MIPEP,ERCC8,ASPH,ASXL1,GPI,KCTD6,NR4A1,CEBPA,IDE,IMMP1L,NLN,ARMC8,UFSP2,FOXL2,OTUD4,SPSB4,USP39,RNF7,CASP3,HIP1R,TAF9,ERAP1,UBE2L6,FBXO8,TRABD2A,PCSK1,ROBO1,TRPC4AP,PCOLCE2,DIABLO,SH3D19,ARNTL,FBXW	grey	VSMC_M10
GO:0032206	1.00	0.01	17	48	positive regulation of telomere maintenance	BP	1	PPP1R10,MAP3K4,MAPK15,POT1,ERCC1,ATR,HMBOX1,MAPKAPK5,NBN,RTEL1,XRCC5,MAPK1,MAPK3,PARN,SLX4,TERF2,MAP2K7	grey	VSMC_M10
GO:1901135	1.00	0.00	388	791	carbohydrate derivative metabolic process	BP	1	NME1,HSD17B4,TBPL1,B4GALT7,PDE7B,B4GALNT1,FUCA2,RXYLT1,ATP5MGL,GFPT2,DPYS,ALG12,PPT2,RNF5,PPARA,PDE10A,ACSL6,A4GALT,PMM1,AGO2,PRXL2C,AKR1B1,APOBEC3H,GTPBP1,PIM1,GPAA1,OARD1,IMPDH1,MTAP,LARGE1,GNMT,ALDH1A1,GDA,CEMIP2,CROT,GNPDA2,GALT,SLC35B2,CWH43,ENPP4,KIT,ST6GAL2,SRD5A3,UXS1,SLC25A13,GAPDH,PPAT,C1GALT1,CHST10,RAB23,ALG2,ERP44,PPCS,TMEM246,PIGF,FKTN,HAS1,SLC4A4,NT5E,PPT1,BPGM,IL15,DLD,NANP,SPHK2,CMPK1,HS3ST5,ADCY3,NDNF,ALG11,PRTFDC1,POMGNT1,CDADC1,NUDT15,DLG2,AKR1A1,GLB1,NUDT5,DHTKD1,B4GALT2,CHPF2,MBD4,AQP11,PRKAG2,GALNT11,ATP5F1C,XYLB,ST6GALNAC2,GCKR,MGAT5B,RBKS,ELOVL1,TGDS,CSGALNACT1,GPD1L,NEU3,PFKP,UGGT2,FBXO17,HBEGF,PAWR,PLCB1,TMTC4,PGAP2,GALNT15,NUDT16,DCN,PANK2,PDK1,FUT10,GXYLT2,EOGT,SUCLG2,PDHX,ELOVL7,PANK1,POFUT1,GPI,ABHD6,AHCY,CBR4,AMPD3,PIGU,ST8SIA4,GK5,ATP5F1A,MCCC2,B3GNT4,GPD1,AGA,P2RX7,MOGS,GUCY1A1,GUCY1B1,ACOT12,RPN2,DGUOK,PRKAG1,GMPS,PFKM,OPA1,ENTPD4,AMFR,ST3GAL6,GALNT5,FITM2,CHST1,AMPD1,NUDT18,GCNT2,PIGT,GLYCTK,ADCY7,FAM173B,GANC,BMPR1B,ADCY2,GPLD1,MCEE,NME4,A3GALT2,ALG10,PDE9A,HYAL1,SLC2A10,HYAL3,PGAP1,TPST1,ZBTB20,TYW1B,GPAM,SULF2,TRIP11,FAR2,ACSL5,POGLUT1,PTHLH,TYW5,TCF7L2,ACP6,DAD1,ST8SIA2,MFN1,EGF,PFKFB2,PRPS2,B3GALT1,B3GNT5,CMAS,PIGM,ENO4,LCMT2,ABCC5,HACD2,GALNT2,ARNT,ADCY4,PIGV,DPAGT1,CTPS2,ALG3,PFKFB4,ACTN3,HDAC4,MAN1C1,RAB1B,THEM5,MGAT1,DNAJC30,MLXIPL,RNF185,PDE8A,PIGX,GAL3ST3,DTYMK,HMGCL,PI	grey	VSMC_M10
GO:0001763	1.00	0.01	67	157	morphogenesis of a branching structure	BP	1	ESR1,FRS2,RSPO3,MYC,PTCH1,SOX10,SMO,SRF,SIX2,RTN4,HOXA13,AREG,EPHA7,MET,TNC,MYCN,SPRY1,PLXNA1,SOX9,GLI2,GZF1,SPRY2,TGFBR2,SPINT2,SEMA3A,PAX8,EYA1,VDR,NKX3-1,SPINT1,PKD2,STK4,PAX2,SALL1,DAG1,KRAS,EGF,AGT,GBX2,NFATC4,LAMA5,CLIC4,DLG1,SETD2,FZD5,COL13A1,CTSH,WNT4,MAGED1,MED1,CITED1,MKS1,BTBD7,LHX1,LAMA1,GPC3,PKD1,SOX8,FOXF1,ENG,ESRP2,NOG,WNT5A,SIX1,GRB2,FGF1,WNT2	grey	VSMC_M10
GO:0014897	1.00	0.01	30	77	striated muscle hypertrophy	BP	1	PPARA,PI16,HDAC2,TRPC3,KDM4A,HAND2,TIAM1,JARID2,RYR2,PDE9A,PPP3CA,MYH7,AGT,SLC9A1,HDAC4,TTN,CAMTA2,PARP1,TCAP,TNFRSF1B,SMAD3,YY1,GATA6,MIR199A1,MIR21,MIR23A,MIR24-1,MIR25,RGS4,HEY2	grey	VSMC_M10
GO:1904029	1.00	0.01	33	83	regulation of cyclin-dependent protein kinase activity	BP	1	TNFAIP3,CCND3,CDKN2A,FBXO7,TTBK1,EGFR,CCNY,MAPRE3,CEBPA,CDK7,CASP3,CCNH,CCNJ,CCNG2,CCNJL,PKD2,HERC5,CCND1,SFN,CDKN1B,STOX1,HEXIM2,MEN1,ACTB,PSMD10,CDK5R1,PKD1,PSRC1,CNPPD1,GADD45A,SPDYA,RGCC,APC	grey	VSMC_M10
GO:0032355	1.00	0.01	43	105	response to estradiol	BP	1	ESR1,PTCH1,HSF1,CAT,AREG,PTN,EGFR,APOB,DNMT3A,MBD4,POU4F1,DNMT3B,GPI,CASP3,CCDC62,HPGD,MMP15,KCNJ11,LCOR,ABCC2,SRD5A1,CCND1,GPER1,AGT,CDKN1B,GGT2,ESRRA,RAMP2,STAT3,CD38,STAT5B,ALDH1A2,MBD1,ASS1,STXBP1,NQO1,PTGFR,CASP8,DUSP1,GGT5,BCL2L11,FAM210B,BCL2L2	grey	VSMC_M10
GO:0046546	1.00	0.01	46	112	development of primary male sexual characteristics	BP	1	HSD17B4,ESR1,LRRC6,H3F3C,KIT,MSH2,SOX9,ERCC1,UTF1,WDR48,ACVR2A,SEMA3A,NCOA4,DHX37,ING2,NKX3-1,TESC,SRD5A1,CCND1,TGFB2,LHX9,SPATA2,TFAP2C,CBL,PATZ1,YBX3,WNT4,CTSV,INHA,KDM5A,SOX15,ADAM21,ADAM20,GATA6,MAMLD1,SOX8,FSTL3,UBB,ARID4A,AGO4,ADGRG1,WNT5A,BCL2L11,TBC1D20,BCL2L2,LHFPL2	grey	VSMC_M10

GO:0120035	1.00	0.01	248	524	regulation of plasma membrane bounded cell projection organization	BP	1	NME1,NEDD4L,ATP8B1,LRP1,SEMA6A,AVIL,TBC1D30,RAB21,TIAM2,FSTL4,SYNGAP1,WASHC5,MAPK15,PLXNA4,NTRK2,PODXL,CDC42EP1,RAC2,CHRNA3,FBXO7,PTK7,ABHD17B,SRF,FZD1,KIT,ROR2,SEMA4D,SEMA4C,DYNC2LI1,BRSK1,EPS8L1,TMEM30A,RTN4,RUFY3,ACP4,LPAR1,AKIRIN1,EPHA7,PTN,HECW1,FUZ,KEL,VPS35,ATG5,RTN4IP1,FIG4,PLXNA1,HDAC2,NDNF,SLC39A12,GOLGA4,MEGF8,KLF5,PTPRF,TSKU,SS18L2,ALK,TMEM106B,RAB5A,PRNP,ARHGEF7,SEMA3D,SPART,PLXNC1,SEMA3A,ULK1,DPYSL3,RYK,RET,TOX,CBFA2T2,FER,ANKRD27,PIK3R1,PLS1,ROBO1,ROBO2,PLCE1,TENM3,ENC1,SEMA4F,P2RX7,TLX2,CUX2,KATNB1,PTK2B,RAPGEF2,DGUOK,TIAM1,PAQR3,USH1C,HOMER1,OPA1,ZFYVE27,BIN3,F2RL1,ARHGAP24,SEMA3G,RREB1,ITPKA,SPP1,CYFIP1,DMTN,SEMA4G,CNTN1,MYLIP,LZTS1,BDNF,SRGAP2C,KIAA0319,NEURL1,DNM1L,CARMIL1,ZMYND10,PPP3CA,HECW2,CAPRIN2,TRPV4,SEMA3F,GAP43,AUTS2,MARK1,CFL1,ADNP,DISC1,KREMEN1,AGT,CIB1,WASF2,RAB17,CERS2,NFATC4,HDAC4,SS18L1,EPS8,PTPRO,CDKL5,INPP5J,EPHB3,LIMK2,TANC2,LRIG2,WNT3,DGKG,NFE2L2,CDC42EP2,MAPT,ABL2,SEMA6D,PPP2R5B,EHD1,TNR,FN1,NCKAP1,EFHC2,NIN,SERPINI1,CRTC1,HTT,DNM3,RAP1GAP,RETREG3,MARK2,CAMK2G,CD38,WAS,OBSL1,CRMP1,SDCCAG8,HAP1,EPHA4,MNS1,MIEN1,PLEK2,FXR2,ATP1B2,GAK,STX1B,PSEN1,SEMA4A,CNTROB,ITGA3,TRIM46,EFNA1,NDEL1,TENM2,AC138894.1,CHRNB2,ZDHHC15,RAB11A,MAP2K1,CCDC151,NTN1,SNAPIN,DNM2,PARP6,RIT2,BCAS3,GPRASP2,BHLHB9,ARHGAP44,EVL,TRPV2,FBXO38,CDK5R1,THOC2,IFT20,RRN3,SEZ6,DAB1,FMR1,LRP8,CRK,L1CAM,ARHGAP4,WRAP73,PLXNA3,PALM,	grey	VSMC_M10
GO:0051056	1.00	0.01	115	259	regulation of small GTPase mediated signal transduction	BP	1	ARHGAP9,TIAM2,CDC42SE2,RGL2,SYNGAP1,FAM13B,OBSCN,GPR20,LRRD1,FGD3,EPS8L1,LPAR1,MET,ARHGEF5,SPRY1,ARHGAP12,ARHGEF4,ARHGAP21,IQSEC1,KBTBD6,RAF1,SPRY2,PSD3,ARRB1,SRGAP3,RASGRP4,MCF2L,ARHGAP26,NRG1,PPP2CB,RASA3,AL359736.1,PIK3CB,PREX2,RASA2,ARHGAP10,FBXO8,ROBO1,PLCE1,ARHGEF28,MADD,RASGRP1,TIAM1,TRIO,F2RL1,F2R,ARHGAP24,GBF1,PSD,ARHGAP32,FGD4,TGFB2,GNA13,AUTS2,RABL3,KRAS,ARHGAP6,CBL,KALRN,ARHGAP30,EPS8,RASA4,BCL6,ABL2,GMIP,COL3A1,RAP1GAP,LZTR1,MYO9B,CYTH3,ARHGEF19,RASAL3,PLEKHG3,IQSEC2,FGD1,MFN2,ARHGEF11,ARHGAP23,STARD8,DOCK2,ITGA3,KCTD13,OGT,DENND4A,MYO9A,DNM2,RIT2,ARHGAP44,AMOT,VAV1,TNFAIP1,RALBP1,ABR,CRK,RAP1GAP2,ARHGAP4,ARHGAP45,EPS8L3,VAV3,RALGPS1,MAPKAP1,SCAI,DENND1A,DAB2IP,GPR35,ADGRG1,EPS8L2,STAMBP,CHN1,STK19,HRAS,CADM4,SH2B2,RHOU,ARPP19	grey	VSMC_M10
GO:0033273	1.00	0.01	29	75	response to vitamin	BP	1	CYP27B1,SNW1,TSPO,PIM1,CAT,PTN,TNC,EGFR,IL15,DNMT3A,GAS6,DNMT3B,VDR,STC1,SPP1,CD40,CCND1,MGMT,BCHE,ALPL,MED1,ALDH1A2,MIR125B1,MT-CYB,SETDB1,TRIM24,BGLAP,PEMT,LRAT	grey	VSMC_M10
GO:0010833	1.00	0.01	28	73	telomere maintenance via telomere lengthening	BP	1	MAP3K4,MAPK15,POT1,ATR,HMBOX1,MAPKAPK5,TENT4B,STN1,TERT,GAR1,RTEL1,XRCC5,MAPK1,PARP1,GNL3L,WRAP53,SMG5,CTC1,PIF1,MAPK3,PARN,ERCC4,SLX4,ZBTB48,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0043276	1.00	0.01	9	30	anoikis	BP	1	PTK2,NTRK2,TFDP1,SIK1,CHEK2,MCL1,DAPK2,IKBKG,ZNF304	grey	VSMC_M10
GO:0016197	1.00	0.01	92	209	endosomal transport	BP	1	VPS4B,AGAP2,REPS1,PRKN,VPS52,WASHC5,MICALL1,WASHC4,VPS50,RGP1,CHMP2A,BVES,VPS35,EPS15,ANKRD50,RAB7A,RAB10,RBSN,CCDC93,UBE2O,SNX5,DPY30,HEATR5B,AP5S1,BET1L,LEPROTL1,VPS16,WASHC2A,TMEM87B,ANKRD27,CHMP2B,CHMP4C,ALMS1,AP3B1,CHMP7,VPS26C,VPS39,GBF1,MAGEL2,RAB7B,DNM1L,VTI1A,DENND1B,TBC1D10C,SORL1,RAB17,SNX4,SNX27,REPS2,STX6,SNX6,SNX32,CALY,PIKFYVE,VPS26A,EHD1,TBC1D14,CLTCL1,ANKFY1,AP5M1,WAS,STX5,NSG1,EPS15L1,GRIPAP1,RAB8A,AP5Z1,ANXA8,SNX12,TBC1D10B,SNX1,RAB11A,ARHGAP44,VPS35L,CLEC16A,MYO5B,VPS53,RILP,SRL,BAIAP3,RNF126,CHMP1A,BTBD8,DENND1A,VPS4A,MICALL2,RASSF9,PHETA1,RAB6B,VAMP3,LEPROT,PLEKHJ1	grey	VSMC_M10
GO:0006338	1.00	0.01	76	175	chromatin remodeling	BP	1	SMARCC2,BAZ2A,ESR1,ARID1B,BRD2,ASF1A,MYC,H3F3C,KDM4C,SMARCA2,SCMH1,HDAC2,UBN2,SOX9,SUV39H2,NUDT5,RSF1,KDM4A,CHD8,ERCC6,ACTR6,SMYD1,SMARCD1,TTI1,TOP1,PBRM1,SPTY2D1,NPM2,NAP1L5,JARID2,RBBP4,HDAC1,SATB2,SART3,ARID1A,VPS72,HDAC4,BAZ1B,SETD2,H2AFY2,TADA2B,HIRA,KDM5A,FOXP3,ACTB,ZBTB1,TSPYL2,KDM5C,KDM6B,NAP1L2,SUPT6H,NAA60,HCFC1,CHD5,CTCF,SYCP3,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,RNF8,CHRAC1,GATAD1,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,TSPYL5	grey	VSMC_M10

GO:0010498	1.00	0.00	205	434	proteasomal protein catabolic process	BP	1	NEDD4L,FEM1C,RMND5B,CANX,TRIM39,HSPA1B,PRKN,RNF5,PSMB8,DERL1,SKP1,UBE2B,RNF217,TRIB1,CSNK1E,FOXRED2,FBXL6,KLHDC3,DCAF12,SEC61B,RAD23B,UBE3D,ECPAS,XPO1,PELI1,FBXO48,HECW1,ASCC3,HACE1,ZYG11B,SDCBP,FAF1,BBS7,FBXL13,NUDT15,FBXL2,KCTD2,PLK3,SUMO2,KBTBD6,AQP11,DMAC2,UBXN4,SPOPL,KLHL40,ARRB1,UGGT2,FBXO17,SIRT2,DNAJC18,NPLOC4,UBAC2,NHLRC3,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,CEBPA,ARMC8,SPSB4,TAF9,TRPC4AP,ARNTL,FBXW7,USP25,TRIM2,ENC1,ANAPC5,AUP1,ANAPC7,FAM192A,TMEM67,AMFR,RNFT2,MARCH7,KCNE2,ERLIN1,PRICKLE1,FBXW4,SIAH1,NHLRC1,FBXL15,RNF144B,RHBDD1,AMN1,HECW2,PSMD1,KLHL42,PSMB5,GET4,USP13,AC013489.1,YOD1,USP19,PSME1,ARIH2,ATE1,UBXN11,PSMD2,GID8,RNF185,RPL11,RHBDD2,EDEM3,NFE2L2,SYVN1,FBXO33,DERL3,KLHDC1,COP1,TMUB2,DNAJC10,DNAJB12,SPSB2,KLHL20,TRIM9,PSME3,RNF4,ZSWIM8,SOCS4,TMEM129,PINK1,ZFAND2B,ARAF,ANKZF1,DNAJB2,PSMA3,SDF2L1,TBL1XR1,CALR3,FBXL14,DNAAF4,RNF216,FBXL18,DDI2,DDB1,PRPF19,ANAPC4,FBXO2,PSMC3,TBX21,OSBPL7,PSEN1,AREL1,FBXL22,KCTD13,TAF1,OGT,SEL1L,KEAP1,PPP2R5C,PSMD10,FBXO22,FBXO38,CUL4B,TNFAIP1,FMR1,FZR1,BCAP31,KCTD5,SGTA,PKD1,FBXL16,TMEM259,PARK7,RNF126,SPSB1,FBXO31,ZER1,GLMN,HSPA5,PSMB7,WWP2,DAB2IP,FBXL8,FBXL12,UBB,PSMC1,BAG2,RNFT1,FAM8A1,CAMLG,CRBN,UBE2G1,DDIT3,UBE2U,CDC26,GID4,DDA1,STYX,UBE2G2,MAP1A,DERL2	grey	VSMC_M10
GO:0006364	1.00	0.01	89	198	rRNA processing	BP	1	HELB,TFB1M,UTP23,RRP7A,EXOSC4,NOL6,TSR1,EXOSC3,RPS14,UTP3,MDN1,FCF1,ERCC2,RPS8,RPL14,USP36,ESF1,KRR1,SIRT7,NUDT16,PRKDC,DHX37,BMS1,DIMT1,POP4,URB1,DDX54,NSUN3,RRP12,HELQ,RPUSD2,RPP40,RIOK1,TENT4B,POP5,PDCD11,RPUSD4,RPS17,SBDS,HEATR1,FAM207A,MRPS11,GAR1,YTHDF2,YBEY,NOP9,RPS27,WDR12,RPL7L1,WBP11,NSUN5,DDX47,RPL11,POP7,DDX10,DDX49,RPL27,WDR74,NVL,MRM2,TSR2,ZCCHC4,LAS1L,UTP18,KRI1,ZNHIT3,ERI2,RIOK3,UTP6,SNU13,UTP14A,MRM3,METTL16,NOL9,RPUSD1,WDR18,RPL35,ZNHIT6,METTL18,RPP38,MPHOSPH6,RPUSD3,NSA2,C1D,PIH1D2,RPP30,TRMT61B,EXOSC5,GTF2H5	grey	VSMC_M10
GO:0008217	1.00	0.01	51	122	regulation of blood pressure	BP	1	TAC3,LVRN,ADM2,PPARA,ADH5,TNNI3,SNX5,MKKS,ADRA1D,P2RX2,GAS6,ADRA2B,ERAP1,VEGFC,GUCY1A1,MME,F2RL1,F2R,ENPEP,AGT,ACE2,ATP1A2,NTSR1,PTPRO,GNB3,ECE1,GCH1,RAMP2,AGTRAP,SMAD3,SCPEP1,CORO2B,BDKRB1,ACSM3,ASIC2,NOS2,ABAT,SERPINF2,TRPV1,P2RX1,MECP2,CYBA,HSD11B2,MIR199A1,MIR27B,RHOA,ERAP2,CHGA,GPR37L1,ACVRL1,CRH	grey	VSMC_M10
GO:0014706	1.00	0.00	140	307	striated muscle tissue development	BP	1	STAC3,GLI1,MAML1,FRS2,PPARA,VGLL2,PITX1,SMAD5,LEMD2,LY6E,MAPK14,CBY1,PI16,PIM1,SMO,FOXH1,SRF,PGM5,FHL2,MEOX2,HIVEP3,TNNI3,MYH14,AKIRIN1,BVES,KEL,MYLK3,ATG5,KLF5,SCN5A,POU4F1,KLHL40,TGFBR2,SIRT2,RARB,NR1D2,RYR1,DCN,P2RX2,NRG1,LMOD3,EPHB1,SGCG,NR4A1,SMYD1,NLN,FOXL2,FLNB,VAMP5,SAP30,EYA1,ARNTL,MEF2C,SOX6,TLL2,HOMER1,TBX5,BIN3,TNNC1,DSP,JARID2,RBM24,RYR2,IGF2,MYH15,NEURL1,PKP2,SIK1,PPP3CA,TNNI1,TGFB2,PRKAR1A,HLX,USP19,MYH7,AGT,ACTC1,SLC9A1,FZD7,MYOZ2,CASQ1,ACTN3,HDAC4,KCNK2,ALPK3,YBX3,CREB1,TTN,SAV1,MYOZ1,MAPK1,OBSL1,BMPR1A,TCAP,RBPJ,MED1,ALDH1A2,MYLPF,ZNF689,SOX15,MSX2,KDM6B,FOS,CACNA1G,SMAD3,TBX2,YY1,DSG2,FBXO22,GATA6,ISL1,MYH11,IFT20,NDUFV2,MRTFB,SKI,SOX8,TSC1,ENG,ACADM,MIR199A1,MIR222,MIR23A,MIR24-1,MIR25,RHOA,DMD,JPH2,NOG,WNT5A,SIX1,RGS4,POPDC2,MYORG,UQCC2,HCN4,C3orf58,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0051168	1.00	0.01	55	131	nuclear export	BP	1	CPSF6,PHAX,NOL6,XPO5,WASHC4,YTHDC1,XPO1,DNAJC27,IWS1,SIRT7,CHTOP,GAS6,THOC7,SDAD1,RAPGEF3,XPO7,ATXN1,DDX25,SP100,TCF7L2,BAG3,NOP9,STRADB,SFN,STRADA,UHMK1,NCBP2,EIF4ENIF1,POM121,DUSP16,SETD2,CTDSPL2,ENY2,UPF1,NXF1,AKAP8L,FYTTD1,SMG5,RANBP17,XPO6,NRDE2,ALKBH5,THOC2,RANBP3L,SUPT6H,PKD1,PARK7,TSC1,NUP214,DDX19A,SARNP,DDX19B,NUPL2,TXN,STYX	grey	VSMC_M10
GO:0090257	1.00	0.01	78	179	regulation of muscle system process	BP	1	PPARA,PI16,ZDHHC21,CHRNA3,SRF,KIT,TNNI3,ASB3,TRPM4,FOXO3,TRPC3,SCN5A,ADRA2B,NR4A1,HAND2,PLCE1,GUCY1A1,DOCK5,STC1,F2R,TNNC1,DSP,CASQ2,JARID2,CHRM3,RYR2,PKP2,PDE9A,PPP3CA,KCNJ2,TNNI1,TRPV4,ADRA2A,DAG1,MYH7,GRK2,GTF2IRD1,ANK2,GPER1,AGT,ACE2,ATP1A2,SLC9A1,CASQ1,ACTN3,HDAC4,DLG1,ADRA2C,CALCRL,PRKAG3,CAMK2G,ATP1B1,KCNA1,KCNMA1,PARP1,TNFRSF1B,MYL5,ATP2A1,SMAD3,CALM1,NMUR2,SETD3,YY1,DSG2,ABAT,P2RX1,RNF207,MIR199A1,MIR21,MIR25,RHOA,DMD,NOL3,CHGA,TNNC2,RGS4,HCN4,NKX2-5	grey	VSMC_M10

GO:0034622	1.00	0.00	409	830	cellular protein-containing complex assembly	BP	1	TIMM21,ARPC3,BAZ2A,TCF4,AVIL,ATP23,ATAT1,CPSF6,ESR1,ZNF207,MAPK8IP2,HSPA1B,SF3A3,TUBGCP6,EIF3E,LYRM7,PRKN,HLA-DRA,HLA-DOB,HLA-DMA,BRD2,HLA-DPB1,SEPT8,ASF1A,HSPA4,RRP7A,NDUFA6,WASHC5,LRRC6,AGO2,H3F3C,PTK2,DMC1,PUF60,PSMD5,BAIAP2L2,PICK1,EIF3L,CDC42EP1,HSF1,CHRNA3,LMOD2,TTBK1,C12orf45,SLAIN2,NCK2,KIAA1211,COA5,CHMP2A,RPS14,TMOD1,SDHAF4,PRKCE,PRPF31,SPTBN1,RTN4,YTHDC1,ECPAS,SRSF10,MDN1,WDR92,TRAPPC12,MED25,MET,ADD2,AGO1,TLR4,CDK5RAP2,FAM49A,MAPRE1,WASF1,ARMC4,EPS15,NDUFB2,HIGD1A,UBN2,NAPA,AP2S1,MSRB2,ATPAF1,DRC1,SOX9,EML2,NDUFB6,SLC39A12,TMEM126B,CLASP2,MAPRE3,NDUFC2,RALB,RSF1,CLNS1A,MYD88,CELF2,DMAC2,RPSA,NAPB,SLAIN1,CRNKL1,PIP4P1,EID2,PLEKHG2,FCHSD2,MKKS,NAV3,NUP98,NDUFS8,EIF2AK2,NDUFAF7,BAG4,TAF7,ARHGEF7,DIAPH1,BRF2,FCHSD1,NDUFA12,NRG1,NCKAP1L,ARFIP2,TAF10,LMOD3,PRKDC,COX7A1,TTC17,TGS1,HCK,TM9SF4,NDUFAF2,FAM107A,FER,ANKRD27,USP39,HIP1R,TAF9,CLP1,RPL6,ATR,CLIP1,UQCC1,ERC2,GCFC2,FCHO2,FMN1,NDUFS3,AAR2,CELF1,PTK2B,CCDC65,TIAM1,USH1C,SYNJ1,SRSF6,IQGAP2,SCAF11,SPTY2D1,NDUFAF6,COX15,TUBGCP5,DNAH1,CYFIP1,DMTN,CASQ2,NAP1L5,DNAH5,MAGEL2,PXN,EIF2D,RAP1GDS1,FOXRED1,RBBP4,DNM1L,CARMIL1,POMP,ZMYND10,LMOD1,ADD3,TRPV4,TMEM9,RBM5,COX17,SNAP23,COPS7B,OXA1L,NDUFB4,SSH1,TBCE,SART3,MRPS11,EGF,COA6,HCLS1,ARHGAP6,AP1AR,TBCEL,TUBGCP4,WASF2,NDUFB3,ZRSR2,RPS27,AP2M1,SPTBN2,TFAM,CASQ1,TMOD4,STX1A,POGZ,EPS8,CELF	grey	VSMC_M10
GO:0032233	1.00	0.01	20	56	positive regulation of actin filament bundle assembly	BP	1	MTSS1,LPAR1,PLEK,ITGB1BP1,ARHGEF5,EPHA1,WNT11,BAG4,RAPGEF3,PXN,CARMIL1,WNT4,PFN3,SMAD3,EVL,SERPINF2,TSC1,FHOD1,RHOA,RGCC	grey	VSMC_M10
GO:0006406	1.00	0.01	19	53	mRNA export from nucleus	BP	1	YTHDC1,IWS1,CHTOP,THOC7,DDX25,SETD2,ENY2,UPF1,NXF1,AKAP8L,FYTTD1,SMG5,ALKBH5,THOC2,SUPT6H,NUP214,DDX19A,SARNP,DDX19B	grey	VSMC_M10
GO:0071427	1.00	0.01	19	53	mRNA-containing ribonucleoprotein complex export from nucleus	BP	1	YTHDC1,IWS1,CHTOP,THOC7,DDX25,SETD2,ENY2,UPF1,NXF1,AKAP8L,FYTTD1,SMG5,ALKBH5,THOC2,SUPT6H,NUP214,DDX19A,SARNP,DDX19B	grey	VSMC_M10
GO:1903523	1.00	0.01	4	17	negative regulation of blood circulation	BP	1	AGER,GRK2,ATP1A2,TRPV1	grey	VSMC_M10
GO:0008630	1.00	0.01	33	84	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	SNW1,BAK1,MSH2,TRIM32,DDIAS,MLH1,FBH1,PRKDC,ERCC6,PIK3R1,TAF9,ING2,HTRA2,FNIP2,MARCH7,SNAI1,AEN,CHEK2,MCL1,CIDEB,SFN,NFATC4,BCL2A1,TNFRSF1B,MUC1,TAF9B,CD74,PIAS4,CDIP1,RPS27L,BCL2L11,BCL2L2,TMEM109	grey	VSMC_M10
GO:0070482	1.00	0.00	127	280	response to oxygen levels	BP	1	AGER,PPARA,MYC,PICK1,TXN2,HSF1,TEK,SRF,SLC1A1,CA9,CAT,PRKCE,EPAS1,CYB5R4,AQP1,PTN,MGARP,FOXO3,HDAC2,DNMT3A,NDNF,ERCC2,SLC39A12,ERCC3,SUV39H2,PLK3,XRCC1,RAF1,EGLN2,CYGB,PLAT,TGFBR2,SIRT2,RYR1,P2RX2,PDK1,COX4I2,TM9SF4,DNMT3B,AHCY,CASP3,P2RX3,TMBIM6,VEGFC,PTK2B,BACH1,STC1,NKX3-1,OPA1,LOXL2,NR4A2,HIF1AN,RYR2,SIRT4,DNM1L,HDAC1,TERT,TGFB2,SCN2A,AJUBA,USP19,OPRD1,POLG,CBL,HYOU1,ARNT,SLC9A1,KCNK2,USF1,NDUFS2,TBL2,EGLN3,SCAP,APOLD1,CDKN1B,ADAM8,PDK3,NFE2L2,CREB1,STOX1,FIS1,FUNDC1,RAMP2,PINK1,ATP1B1,CD38,KCNMA1,SLC2A4,RBPJ,SOD3,AGTRAP,NPEPPS,BNIP1,PKLR,PGF,CHRNB2,SMAD3,GATA6,ALKBH5,NOS2,TMEM199,LONP1,ACAA2,ABAT,GNB1,CREBBP,PLEKHN1,MECP2,ATP6AP1,CIAO3,CYBA,TSC1,LCN2,HSD11B2,MIR21,MT-ATP6,MT-CYB,RHOA,KCNK3,NOL3,DPP4,BNIP3L,ACVRL1,RWDD3,TIGAR,RGCC,MIEF1	grey	VSMC_M10
GO:0060325	1.00	0.01	7	25	face morphogenesis	BP	1	DLX5,CSRNP1,CRISPLD1,STRA6,SKI,ANKRD11,NOG	grey	VSMC_M10
GO:1904888	1.00	0.01	19	54	cranial skeletal system development	BP	1	RAB23,SIX2,HOXA2,MEGF8,TGFBR2,TFAP2A,TGFB2,SETD2,TULP3,WDR19,MSX2,TMEM107,SMAD3,FOXN3,LHX1,ALX3,SIX1,INSIG2,SLC39A3	grey	VSMC_M10
GO:1903900	1.00	0.01	42	104	regulation of viral life cycle	BP	1	PABPC1,PPARA,LY6E,APOBEC3H,CHMP2A,CXCL8,RSAD2,TRIM32,HS3ST5,ZC3HAV1,NECTIN2,KPNA2,EIF2AK2,MAVS,CHMP2B,FAM208A,OAS3,IFIH1,OASL,TMEM39A,ADARB1,NR5A2,STAU1,PC,CD28,DDX3X,DDB1,HACD3,LARP1,TNIP1,CD74,CCL5,CIITA,FMR1,INPP5K,VPS4A,SETDB1,OAS1,TRIM68,TRIM34,ZNF502,FAM111A	grey	VSMC_M10
GO:0048286	1.00	0.01	11	35	lung alveolus development	BP	1	SLC7A11,ASXL1,ITGB6,CREB1,ABCA12,STRA6,GATA6,FOXF1,ATXN1L,LIF,RC3H2	grey	VSMC_M10
GO:0071453	1.00	0.01	60	142	cellular response to oxygen levels	BP	1	MYC,PICK1,PRKCE,EPAS1,AQP1,PTN,MGARP,FOXO3,DNMT3A,NDNF,SUV39H2,PLK3,EGLN2,SIRT2,PDK1,COX4I2,DNMT3B,TMBIM6,BACH1,STC1,NKX3-1,OPA1,HIF1AN,SIRT4,DNM1L,TERT,SCN2A,AJUBA,USP19,OPRD1,CBL,HYOU1,SLC9A1,KCNK2,NDUFS2,TBL2,EGLN3,ADAM8,PDK3,NFE2L2,STOX1,PINK1,SLC2A4,RBPJ,NPEPPS,GATA6,TMEM199,ACAA2,GNB1,ATP6AP1,TSC1,LCN2,MIR21,KCNK3,NOL3,BNIP3L,RWDD3,TIGAR,RGCC,MIEF1	grey	VSMC_M10
GO:0035306	1.00	0.01	16	47	positive regulation of dephosphorylation	BP	1	PLEK,VRK3,SYMPK,MTMR9,MEF2C,GPLD1,SPPL3,PPP2R5A,PINK1,SMAD3,CALM1,PPARGC1B,CAMTA1,CNEP1R1,DUSP26,PPP1R15A	grey	VSMC_M10
GO:0051302	1.00	0.01	58	138	regulation of cell division	BP	1	MYC,PTCH1,ZNF16,EFHC1,NLRP5,CAT,MACC1,PRKCE,TGFA,PTN,ITGB1BP1,INTU,PLK3,SIRT2,PLK2,KIF3B,IL1A,CSPP1,DCDC1,VEGFC,CHMP4C,FGF5,NKX3-1,ZFYVE19,IGF2,KIF13A,PRDM15,TGFB2,CIB1,KDF1,SFN,OSM,SETD2,SUSD2,AHCTF1,PGF,ESRRB,NAP1L2,RAB11A,CALM1,GAREM1,KLHL13,EVI2B,FSD1,TLE6,KLHL21,CDC14A,SH3GLB1,VPS4A,RHOA,AURKC,PLK5,OOEP,YBX1,EREG,PDXP,FGF1,PDGFD	grey	VSMC_M10

GO:0032386	1.00	0.00	132	290	regulation of intracellular transport	BP	1	CPSF6,RAB21,PRKN,MAPK15,MAPK14,RAC2,SMO,SLC1A1,RAB23,TMEM30A,RUFY3,XPO1,ITGB1BP1,TCAF2,BVES,MTMR2,DNAJC27,IWS1,LCP1,PLK3,AKT2,USP36,UBAC2,SIRT7,FERMT1,CEP290,PRNP,BAG4,MAVS,DNAJC13,GAS6,NUP58,TM9SF4,PIK3R1,FBXW7,PKIA,HTRA2,ZFAND1,CSNK2A2,NUP54,RAPGEF3,TNNC1,DMTN,FAM173B,MX2,SUFU,CABP1,SP100,PGAP1,TCF7L2,KCNB1,YOD1,HCLS1,TTC21B,HPS4,SORL1,C2CD5,ARIH2,CIB1,BAG3,SFN,CNIH2,DNAJC30,UHMK1,NCBP2,APOD,SETD2,CALY,CTDSPL2,FZD5,FIS1,CEMIP,NMT1,DERL3,SEC16B,EHD1,ABCA12,C11orf65,PDCD10,PINK1,MAPK1,CHRM1,TMEM30B,STX18,GRIPAP1,ATP13A2,HAP1,AKAP8L,NPEPPS,ANXA2,TARDBP,PSEN1,ITGAM,SNX12,TRIM46,NDEL1,WWC1,MAPK3,HAX1,ATP2A1,MAP2K1,SMAD3,NRDE2,BCAS3,ARHGAP44,MIEF2,CDK5R1,SREBF1,EFCAB7,SUPT6H,INPP5K,BCAP31,OAZ1,PARK7,NUP214,SH3GLB1,RIPOR1,MIR27B,MICALL2,REEP6,BNIP3L,LDLRAP1,BORCS5,TXN,TBC1D20,HRAS,MIEF1,RHOU,LEPROT,UBE2G2,DERL2,ZIC1	grey	VSMC_M10
GO:0032886	1.00	0.00	88	202	regulation of microtubule-based process	BP	1	VPS4B,TRIM36,MDM1,ATAT1,HSPA1B,MAPK15,MPDZ,CFAP69,SLAIN2,BICD2,CHMP2A,DNAH11,XPO1,MET,CDK5RAP2,MAPRE1,ARMC4,DRC1,EML2,SLC39A12,CLASP2,MAPRE3,TRIM54,SLAIN1,CEP295NL,MKKS,NAV3,ARHGEF7,DIAPH1,SPEF1,RASSF7,ATXN7,PLK2,FAM107A,CEP70,CHMP2B,CLIP1,CHMP4C,CFAP20,MCPH1,KATNB1,CCDC65,ALMS1,TMEM67,STMND1,CFAP43,AC112128.1,TRPV4,KLHL42,TTBK2,TTC21B,CFAP45,CIB1,CCDC84,TRAF3IP1,PHLDB1,CNIH2,INPP5J,CDKN1B,CALY,MAPT,TOGARAM1,DIXDC1,NIN,RNF4,MARK2,HAP1,TRIM46,TRIM37,CAMSAP3,CDK5R1,TAOK1,NUBP1,FSD1,PKD1,MECP2,APC2,CAMSAP1,CHMP1A,PSRC1,GPSM2,RHOA,BORCS5,CCSAP,APC,MAP1A,DRG1,MAP6D1	grey	VSMC_M10
GO:0048545	1.00	0.00	116	258	response to steroid hormone	BP	1	FECH,ESR1,CNOT2,TPH2,PPARA,RXRB,TSPO,KDM4C,SOX10,FOXH1,RBFOX2,CRY1,DNAJA1,AREG,AQP1,PTN,EGFR,MGARP,FOXO3,PGRMC2,BMI1,PHB,GLB1,ATP1A3,EGLN2,AANAT,HNMT,TADA3,TGFBR2,TAF7,RNF14,DDRGK1,FOXP1,CALCOCO1,NCOA4,FAM107A,CYP7B1,DNMT3B,GPI,UFSP2,CASP3,NCOA2,ZNF366,ARNTL,CNOT1,KMT2D,NR1H3,DDX54,STC1,NKX3-1,CRY2,VPS18,ABCC2,SPP1,CPN1,ADTRP,SRD5A1,HDAC1,CCND1,TGFB2,KRAS,ABHD2,GPER1,ATP1A2,ARID1A,NPAS4,RXRG,CPS1,ACSBG1,ESRRA,BCHE,RPL27,ALPL,RAMP2,CTSV,CD38,PADI2,SCGB1A1,DNAAF4,PARP1,MED1,PAGR1,FOS,ESRRB,SOX30,CALM1,PIAS2,SCN1B,NCOR1,NPC1,PPARGC1B,SREBF1,ISL1,RHOXF1,GHR,ABCA3,PARK7,RXRA,CYBA,ASS1,AGL,ENG,HSD11B2,RHOA,TRIM68,CA2,BGLAP,SMYD3,CLDN1,DUSP1,CRH,BCL2L11,YWHAH,ZFP36L2,GPR83,PDCD7	grey	VSMC_M10
GO:0001818	1.00	0.00	86	195	negative regulation of cytokine production	BP	1	TNFAIP3,AGER,PPARA,TSPO,C6orf106,TNFRSF21,IL1R2,REL,ANXA4,TLR4,C5AR2,PIBF1,FOXJ1,TSKU,WNT11,ARRB1,NMI,NAV3,NPLOC4,PRNP,NCKAP1L,GAS6,NR1H4,IL37,OAS3,HDAC7,SERPINB1,F2RL1,CHID1,MAPKBP1,NOD2,ADCY7,CD96,CD200,SLC2A10,BANK1,PDCD4,TGFB2,BTN2A2,CMKLR1,OTUD7B,NLRX1,TRAF3IP1,ASB1,HOMER2,APOD,SRGN,BCL6,IL12A,FN1,VSIR,PTPN6,SLC11A1,LAG3,MUL1,INHA,OTUD5,SCGB1A1,FOXP3,RNF216,AKAP8,TBX21,SYT11,MAP2K5,RPS6KA5,BTK,YY1,RNF128,GATA6,SUZ12,PTGER4,TWSG1,MIR199A1,MIR21,MIR222,MIR125B1,MIR27B,MIR24-1,C5orf30,OAS1,MIR125A,DDIT3,CPTP,RGCC,RPS6KA4,HAVCR2	grey	VSMC_M10
GO:0006956	1.00	0.01	8	27	complement activation	BP	1	PHB,CFP,C7,C3,CD46,A2M,CFD,RGCC	grey	VSMC_M10
GO:0035308	1.00	0.01	9	30	negative regulation of protein dephosphorylation	BP	1	IKBKB,NCKAP1L,MFHAS1,CRY2,TIPRL,BOD1L2,PPP4R4,PPP1R15A,ARPP19	grey	VSMC_M10
GO:0098542	1.00	0.00	275	574	defense response to other organism	BP	1	CD226,SHMT2,MAP3K5,TNFAIP3,CYP27B1,USP15,TRIM39,XRCC6,PTK2,C6orf106,APOBEC3H,PLA2G6,EXOSC4,IRF5,GAPDH,PRDX1,SDHAF4,FPR2,REL,ANKRD17,NOD1,AKIRIN2,AQP1,LYPD8,RSAD2,NR1H2,TRIM32,TLR4,IL15,PUM2,TRAF3IP2,ZC3HAV1,C5AR1,PHB,LACC1,NECTIN2,PVR,OPTN,UNC13D,MYD88,SEC14L1,IKBKB,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,NPLOC4,EIF2AK2,MAVS,AIMP1,HPX,FOXP1,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,HCK,FER,FLNB,OTUD4,IRF2,ERAP1,PTK2B,RASGRP1,CCL17,EIF2AK4,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTULIN,IFNGR2,WRNIP1,F2RL1,POLR3D,CHID1,IFIT2,MAPKBP1,HERC5,NOD2,TOLLIP,CD40,MX2,RAB7B,CD96,IFIH1,OASL,LCK,SP100,CRCP,GPAM,ADARB1,UNC93B1,POLR3C,TLR5,NCF1,TIFA,ALPK1,YTHDF2,ATG16L1,GPER1,SLAMF8,PARP9,DTX3L,PARP14,IRF9,IFI6,RNF26,FGR,NLRX1,ABCF3,TRAF3IP1,HTRA1,TRIM52,COCH,FCER1G,NCF2,SETD2,LYZL6,ADAM8,CADM1,DUSP10,CDC42EP2,NONO,RTP4,VGF,HK1,BATF2,IL12A,MAP4K2,DDX3X,XRCC5,PTPN6,SLC11A1,LAG3,GCH1,MUL1,BIRC3,CFP,STAT5B,WAS,POLR3A,CXCL16,FOXP3,RNF216,ZBTB1,WIPI2,AKAP8,TKFC,USP18,TNK1,F12,RBPJ,MED1,SPON2,STX4,PYDC1,ITGAM,SYT11,BATF,MAPK3,DCST1,CITED1,IL6R,ECSIT,AKAP1,STX8,IL4R,MPO,TSPAN6,S100A14,S100A8,SFPQ,BTK,SCNN1B,STAT2,POLR3E,TYK2,G3BP1,SIN3A,PSTPIP1,TRAF3,CD74,CCL14,CCL5,RIOK3,CSF1R,COLEC12,CCL7,CCL2,CCL25,YES1,PLD4,RNF135,PPP6C,VAV1,C7,JAK1,C3,NOS2,IL7R,PTPN2,SOCS1,CIITA,DROSHA,TICAM1,TTC4,LRP8,CRK,CREBBP,ATAD3A,NCBP3,IKBKG,POLR3K,ADAMTS13,CYBA,ASS1,LCN2,STXBP1,AP1G1,BCL10,DAB2IP,IFI44L,Z	grey	VSMC_M10

GO:1903362	1.00	0.00	99	222	regulation of cellular protein catabolic process	BP	1	LRP1,TNFAIP3,TRIM39,HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,RGP1,PDCL3,RAD23B,XPO1,WDR91,VPS35,ZYG11B,SDCBP,MFSD8,FAF1,BBS7,NUDT15,PLK3,SUMO2,AQP11,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,RYBP,PSMF1,TRIB3,PLK2,CEBPA,TAF9,FBXW7,USP25,CSNK2A2,PTK2B,FAM192A,RNFT2,MARCH7,KCNE2,PRICKLE1,MYLIP,RNF144B,SUFU,RPL23,USP13,AC013489.1,EGF,USP19,DISC1,PSME1,ARIH2,RNF185,RPL11,NFE2L2,COP1,PSME3,SOCS4,PINK1,ARAF,DNAJB2,ATP13A2,DNAAF4,EPHA4,PSMC3,ANXA2,OSBPL7,PSEN1,EFNA1,TAF1,OGT,LDLR,KEAP1,RNF128,PSMD10,FBXO22,FMR1,FZR1,BCAP31,SGTA,PKD1,TMEM259,PARK7,ZER1,GLMN,DAB2IP,UBB,PSMC1,BAG2,RNFT1,CAMLG,PTTG1IP,DDA1,STYX,MAP1A	grey	VSMC_M10
GO:0032786	1.00	0.01	7	25	positive regulation of DNA-templated transcription, elongation	BP	1	ERCC6,EAPP,ELL,LEO1,CDK12,KAT7,SUPT6H	grey	VSMC_M10
GO:0043484	1.00	0.00	52	126	regulation of RNA splicing	BP	1	ZC3H10,CLK4,SNW1,QKI,HABP4,PUF60,RBFOX2,SMU1,TRA2A,YTHDC1,PTBP3,SRSF10,FASTK,CELF2,PRX,NUP98,WTAP,PIK3R1,RBM39,TMBIM6,CELF1,RBM12B,SLC38A2,SRSF6,RBM24,RBM5,HSPA8,SRSF4,CELF3,RBM7,RBM10,CDK12,PRPF19,FXR2,RBM25,CLK3,METTL4,RAVER2,MBNL3,NSRP1,FMR1,AFF2,CELF5,METTL16,CIRBP,ESRP2,SRRM4,NOVA1,RBM11,SRSF12,SAP18,RBM38	grey	VSMC_M10
GO:0008584	1.00	0.01	45	111	male gonad development	BP	1	HSD17B4,ESR1,LRRC6,H3F3C,KIT,MSH2,SOX9,ERCC1,UTF1,WDR48,ACVR2A,SEMA3A,NCOA4,DHX37,ING2,NKX3-1,TESC,SRD5A1,CCND1,TGFB2,LHX9,SPATA2,TFAP2C,CBL,PATZ1,YBX3,WNT4,CTSV,INHA,KDM5A,SOX15,ADAM21,ADAM20,GATA6,MAMLD1,SOX8,FSTL3,UBB,ARID4A,AGO4,ADGRG1,WNT5A,BCL2L11,TBC1D20,BCL2L2	grey	VSMC_M10
GO:0042770	1.00	0.00	66	155	signal transduction in response to DNA damage	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,MAPK14,CRY1,BRSK1,MSH2,ETAA1,FOXO3,XPC,PLK3,PAXIP1,NEK11,PRKDC,ERCC6,CEP63,STK33,PLK2,RAD17,ATR,RAD9B,EIF2AK4,NBN,ABRAXAS1,DONSON,MARCH7,PIDD1,PLA2R1,TAOK3,CCND1,SP100,DYRK3,GIGYF2,SNAI1,CHEK2,ATRIP,SYF2,CDKN1B,ING4,TIPRL,RHNO1,PRPF19,UIMC1,FOXO4,EME1,MUC1,TAOK2,BATF,TIPIN,FOXN3,PSMD10,CD74,TAOK1,FZR1,DOT1L,FBXO31,RPA4,RPS27L,SOX4,GADD45A,ACER2,GRB2,PTTG1IP,BRCC3,CRADD	grey	VSMC_M10
GO:0007399	1.00	0.00	933	1867	nervous system development	BP	1	ADNP2,NME1,ERBB3,SMARCC2,NEDD4L,ATP8B1,ONECUT2,TCF4,LRP1,SEMA6A,GLI1,N4BP3,KIF5A,ADGRG6,AVIL,ATAT1,FRS2,RAB21,RIDA,STK3,MAPK8IP2,SNW1,TIAM2,ARID1B,SYNJ2,FZD6,RIMS2,PRKN,QKI,AGER,BRD2,SULT4A1,TSPO,UQCRQ,CEP85L,TBC1D32,FSTL4,SYNGAP1,CCDC134,BAK1,XRCC6,PITX1,WASHC5,ASAP1,LEMD2,GFRA3,PTK2,PTCH1,ANKS1A,FANCC,AGTPBP1,PLXNA4,SUN2,NTRK2,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,MICALL1,CKB,RAC2,SMO,DAAM2,RBFOX2,CHRNA3,LRRC4,PRPH2,LINGO2,FBXO7,ROBB,PTK7,GDA,SRF,TTBK1,ADAM22,GABRA1,APBA1,FZD1,CNTFR,CDK6,SMARCA2,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,TFAP2B,ROR2,SEMA4D,DLX5,EFHC1,NINJ1,CCIN,ETV1,ADGRL3,SEMA4C,BEND6,SVBP,PLPPR1,BRSK1,RDH13,RIMS1,MBOAT7,TMEM30A,DNAH11,RAPGEF5,IGF2BP3,FKTN,RTN4,FPR2,GSDME,UTP3,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,PPT1,MYCL,AREG,AQP1,GJA10,MTF1,LRRN3,EPHA7,AKNA,WHRN,PTN,FOXP2,MET,ADD2,TNC,CTTNBP2,YWHAZ,POU3F3,EGFR,HECW1,FUZ,TRIM32,TLR4,NCDN,CDK5RAP2,EPHA1,LPIN1,KEL,VPS35,TEAD2,SDCBP,MYCN,RTN4IP1,NRCAM,SLC7A11,FOXO3,NTF4,FIG4,WASF1,MFSD8,ARMC4,APOB,INTU,SPHK2,FAT4,DHFR,SPATA5,PLXNA1,KDM7A,GRIN2D,HDAC2,PHF10,MTMR2,NAPA,BBS7,DNMT3A,BMI1,NDNF,C5AR1,VSTM5,RAB10,CST7,IQSEC1,ABI1,SOX9,HDAC11,EED,ERCC2,SLC39A12,ERCC3,SSPO,USH1G,EIF2B3,CDNF,XRCC1,GOLGA4,GLI2,MEGF8,B4GALT2,KDM4A,XRCC2,TIMP4,IFT172,FOXJ1,SCN5A,PTPRF,MYO7A,MYCBP2,NUMBL,MNX1,HNMT,ACER3,POU4F1,TSKU,SZT2,SS18L2,WNT11,SLITRK5,ALK,PRX,AKT2,GDPD5,CMTM8,HOOK3,DZANK1,CPNE9,TGFBR	grey	VSMC_M10
GO:0006412	1.00	0.00	265	548	translation	BP	1	PAN2,RPS12,SHMT2,HBS1L,MARS,TSFM,RMND1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,EIF3E,PNLDC1,QKI,MRPL13,RPS18,MRPL55,JMJD4,AGO2,HABP4,RPS10,TNRC6B,ATF4,TUT7,GTPBP1,EIF3L,GTPBP2,NCK2,MRPS9,GAPDH,CNOT11,EXOSC3,RPS14,LRPPRC,SRBD1,IGF2BP3,MTIF2,PNPT1,AGO1,EGFR,ASCC3,QRSL1,C6orf203,TUT4,FOXO3,PUM2,DHFR,EEFSEC,MKNK1,CNBP,EIF2B3,RPS8,MLH1,CDC123,MTRF1,DPH2,RPSA,RPL14,MRPL33,TNRC6C,AKT2,METTL17,MRPS12,PURA,DPH3,HARS,HARS2,EIF2AK2,CARS2,LSM1,MRPL3,AIMP1,RPL31,LARS,EIF4E3,UPF3A,PRKDC,MRPL17,KBTBD8,PAN3,MRPL15,C12orf65,MRPL35,RPL6,MRPS27,MRPL19,ENC1,MRPS28,CNOT1,CELF1,USP16,PTK2B,CNOT6L,MAPKAPK5,EIF2AK4,EIF4E2,NSUN3,PAIP2B,FTO,CYFIP1,TENT4B,RBM24,WARS2,MRPS17,CDKAL1,EIF2D,GATC,NEURL1,RPUSD4,YARS2,RPL23,DDX25,RPL4,RPS17,BANK1,LTO1,CAPRIN2,IGHMBP2,RPL27A,MRPS35,DIS3L2,MRPL52,RCC1L,KLHL25,GIGYF2,MRPS11,RPS6KB2,YTHDF2,TRNAU1AP,MRPS21,TARS2,DALRD3,RPS27,RPS6KA1,PER2,DDX6,RPS4X,MTG2,YTHDF1,PASK,CD28,UHMK1,NCBP2,EIF4ENIF1,NSUN5,RPL11,IGF2BP2,YBX3,EFL1,GGT2,LARS2,EIF4EBP2,RPL10L,DDX3X,RC3H1,DARS2,UPF1,RPL27,UBA52,MRPS36,COA3,SAMD4A,PINK1,STAT3,MAPK1,POLR2G,NT5C3B,RSL24D1,DCP1B,FARSB,YBX2,CASC3,MRPL44,ZCCHC4,RPL19,RPLP1,FXR2,TARDBP,MRPL10,MRPL27,MAPK3,MTFMT,TOB1,EIF3C,ALKBH1,TNRC6A,MRPL22,LARP6,CNOT8,LARP1,EARS2,TNIP1,TCOF1,CCL5,SHMT1,UPF3B,NDUFA7,MRPS30,MCTS1,RPL23A,PARN,FMR1,DPH1,METTL16,PLEKHN1,MRPL41,LRRC47,MRPS34,CIRBP,MRPS2,TSC1,KARS,AARS,BARHL2,RPL35,MIR	grey	VSMC_M10

GO:0042254	1.00	0.00	117	256	ribosome biogenesis	BP	1	HELB,TFB1M,UTP23,RRP7A,EXOSC4,NOL6,GTPBP10,TSR1,EXOSC3,RPS14,UTP3,XPO1,MDN1,FCF1,ERCC2,RPS8,RPSA,RPL14,METTL17,USP36,ESF1,KRR1,SIRT7,NUDT16,PRKDC,DHX37,BMS1,DIMT1,POP4,RPL6,SDAD1,URB1,DDX54,NSUN3,RRP12,HELQ,RPUSD2,RPP40,RIOK1,TENT4B,POP5,PDCD11,RPUSD4,RPS17,LTO1,SBDS,HEATR1,FAM207A,MRPS11,GAR1,YTHDF2,YBEY,URB2,NOP9,RPS27,WDR12,MTG2,RPL7L1,WBP11,DHX30,GLUL,NSUN5,DDX47,RPL11,EFL1,RPL10L,POP7,DDX3X,DDX10,XRCC5,DDX49,RPL27,WDR74,RSL24D1,NVL,MRM2,TSR2,ZCCHC4,GNL3L,LAS1L,ISG20L2,UTP18,MRPL22,KRI1,ZNHIT3,ERI2,RIOK3,NLE1,UTP6,CUL4B,SNU13,UTP14A,RPL23A,ERAL1,DROSHA,MRM3,METTL16,NOL9,RPUSD1,WDR18,MRPS2,TSC1,RPL35,ZNHIT6,METTL18,ZNF622,RPS27L,RPP38,MPHOSPH6,RPUSD3,NSA2,C1D,PIH1D2,RPP30,TRMT61B,EXOSC5,GTF2H5	grey	VSMC_M10
GO:0051345	1.00	0.00	206	440	positive regulation of hydrolase activity	BP	1	MAP3K5,TBC1D30,TBC1D9B,ESR1,TIAM2,GRAMD4,AGER,FBLN1,BAK1,MYC,ASAP1,C6orf89,TBC1D22B,HSF1,TTBK1,KIT,SLC1A1,SEMA4D,TBC1D8,RGP1,LPAR1,NOD1,AKIRIN2,CASP8AP2,PLEK,NR1H2,TNFSF15,ASAP2,VRK3,EGFR,ARHGEF5,EPHA1,TBC1D9,HSPE1,NAPA,C5AR1,PRKD2,PHB,IQSEC1,ABHD5,RSU1,TBC1D4,FOXJ1,WNT11,AKT2,ARRB1,TBC1D16,TMEM106B,RASGRP4,CHTOP,ARHGEF7,DDRGK1,WRN,LARS,ARL6IP5,FLT1,ST18,ASPH,FOXL2,HIP1R,ROBO1,PCOLCE2,DIABLO,MTMR9,TBC1D12,MEF2C,HTRA2,ARHGEF26,PTK2B,RASGRP1,RAPGEF2,CCL17,NR1H3,TIAM1,RIPK2,SENP1,NKX3-1,RAPGEF3,ACVR1C,F2RL1,F2R,ARHGAP24,PIDD1,CD40,RAP1GDS1,GPLD1,DOCK10,CD200,RGS1,LCK,TBCK,ADPRH,PDCD6,GNA13,ADAP1,DENND1B,ARHGAP6,TBC1D10C,GPER1,PSME1,RAB11FIP2,AGT,DVL3,CIDEB,TOR1AIP1,CDKL5,GRHL3,EGLN3,MAPT,FIS1,ABL2,CTSH,TBC1D2B,GMIP,DDX3X,DNAJC10,RASGRP2,FN1,TBC1D14,VSIR,RABGAP1L,RUNDC1,WNT4,ELMOD1,PSME3,RAP1GAP,FGFR3,PINK1,MUL1,STAT3,DNAJB2,ATP1B1,TBC1D25,GNB5,DDX11,EPHA4,ARHGEF19,DVL2,SYDE1,BCL2L13,TBC1D1,DNAJB1,ARAP2,RGS14,ATP1B2,NGFR,TBC1D10B,EFNA1,NDEL1,SMAD3,CALM1,S100A8,MYO9A,BCAS3,NMUR2,GM2A,TBC1D8B,CCL14,CCL5,PPARGC1B,CCL7,CCL2,CCL25,ADAP2,VAV1,RALBP1,DOCK7,ABR,CRK,BCAP31,GNA15,RAP1GAP2,TAX1BP3,PDPK1,P2RX1,PRKCZ,ARHGEF16,APC2,ARHGAP45,TSC1,MTSS1L,DENND1A,RABGAP1,BCL10,MIR21,MIR27B,RHOA,CCL16,RPS27L,FADD,CASP8,ASAP3,THY1,WNT5A,ACER2,CHN1,RGS4,BCL2L11,PPP1R15A,TBC1D20,PERP,HRAS,APH1B,PRR7,CRADD,CCL22	grey	VSMC_M10
GO:0050686	1.00	0.01	7	25	negative regulation of mRNA processing	BP	1	RNF20,SRSF10,SRSF6,SRSF4,RBM10,SRSF12,SAP18	grey	VSMC_M10
GO:0009954	1.00	0.01	7	25	proximal/distal pattern formation	BP	1	GLI1,OSR1,GLI2,IRX2,DLX1,ALDH1A2,HOXB9	grey	VSMC_M10
GO:0003179	1.00	0.01	17	50	heart valve morphogenesis	BP	1	NFATC1,SOX9,TGFBR2,JAG1,ROBO1,ROBO2,MEF2C,TBX5,TGFB2,SNAI1,BMPR1A,EFNA1,STRA6,SOX4,NKX2-5,HEY2,OLFM1	grey	VSMC_M10
GO:0007004	1.00	0.01	23	63	telomere maintenance via telomerase	BP	1	MAP3K4,MAPK15,POT1,ATR,HMBOX1,MAPKAPK5,TENT4B,STN1,TERT,GAR1,XRCC5,MAPK1,GNL3L,WRAP53,SMG5,CTC1,PIF1,MAPK3,PARN,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0048738	1.00	0.00	80	186	cardiac muscle tissue development	BP	1	GLI1,MAML1,FRS2,PPARA,SMAD5,LY6E,MAPK14,CBY1,PI16,PIM1,FOXH1,SRF,FHL2,TNNI3,BVES,MYLK3,ATG5,SCN5A,POU4F1,TGFBR2,RARB,NRG1,SGCG,MEF2C,SOX6,TBX5,TNNC1,DSP,JARID2,RYR2,PKP2,SIK1,TNNI1,TGFB2,PRKAR1A,MYH7,AGT,ACTC1,SLC9A1,FZD7,KCNK2,ALPK3,CREB1,TTN,SAV1,MAPK1,OBSL1,BMPR1A,TCAP,RBPJ,MED1,ALDH1A2,MSX2,KDM6B,CACNA1G,TBX2,YY1,DSG2,GATA6,ISL1,MYH11,IFT20,NDUFV2,TSC1,ENG,ACADM,MIR199A1,MIR222,MIR23A,MIR24-1,MIR25,JPH2,NOG,WNT5A,RGS4,HCN4,C3orf58,NKX2-5,HEY2,WNT2	grey	VSMC_M10
GO:0043434	1.00	0.00	140	308	response to peptide hormone	BP	1	AP3S1,MARS,PIP4K2C,PPARA,PNPLA3,PTK2,GKAP1,HSF1,CCND3,GPT,TEK,CRY1,PPAT,CAT,PHIP,PNPT1,AREG,CRHR2,GRB10,GAB1,LPIN1,MGARP,FGF21,SESN3,PIP4K2A,RAB10,HADHA,CYSLTR2,KHK,EIF2B3,EPM2AIP1,ECHDC3,TIMP4,TBC1D4,AANAT,AKT2,SNX5,BTG1,KL,PTPRA,LEPROTL1,PRKDC,TRIB3,NR4A1,FER,IDE,PIK3R1,SORBS1,OPA1,LPIN3,NKX6-1,NR4A2,ACVR1C,SRSF6,CRY2,ABCC2,CYFIP1,IGF2,PXN,GPLD1,SRD5A1,IRS1,GRB14,TRPV4,SLC30A10,DAG1,SRSF4,SORL1,C2CD5,GPER1,AGT,SLC9A1,SYAP1,USF1,SCAP,CDKN1B,POR,NFE2L2,CREB1,YWHAG,RAP1B,VGF,CPS1,EIF4EBP2,MEN1,SIK2,ESRRA,FBN1,GDF15,STAT3,PTPRN,SLC27A1,STAT5B,RAB8A,GPR173,PARP1,SLC2A4,RAB15,MAX,AGTRAP,VPS13C,FOXO4,PKLR,RAB8B,NDEL1,ZBTB7B,OGT,CITED1,UPRT,PRKCB,STAT2,CAMK2A,INSR,SREBF1,LPIN2,GHR,PTPN2,SOCS1,CRK,INPP5K,TRPV1,PDPK1,PRKCZ,BSG,SLC25A33,CYBA,TSC1,ASS1,TLDC1,HSD11B2,MT-CYB,INSRR,CA2,BGLAP,GRB2,INSIG2,APC,SH2B2,EREG,LEPROT	grey	VSMC_M10
GO:0000079	1.00	0.01	31	80	regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	TNFAIP3,CCND3,CDKN2A,FBXO7,EGFR,CCNY,MAPRE3,CEBPA,CDK7,CASP3,CCNH,CCNJ,CCNG2,CCNJL,PKD2,HERC5,CCND1,SFN,CDKN1B,HEXIM2,MEN1,ACTB,PSMD10,CDK5R1,PKD1,PSRC1,CNPPD1,GADD45A,SPDYA,RGCC,APC	grey	VSMC_M10
GO:0071166	1.00	0.01	25	67	ribonucleoprotein complex localization	BP	1	NOL6,PRPF31,YTHDC1,XPO1,IWS1,CHTOP,THOC7,SDAD1,DDX25,NOP9,SETD2,ENY2,UPF1,NXF1,AKAP8L,FYTTD1,SMG5,ALKBH5,THOC2,SUPT6H,TSC1,NUP214,DDX19A,SARNP,DDX19B	grey	VSMC_M10

GO:2001252	1.00	0.01	27	72	positive regulation of chromosome organization	BP	1	PPP1R10,MAP3K4,MAPK15,POT1,SSBP1,SETDB2,ERCC1,ATR,SLF1,FAM208A,HMBOX1,MAPKAPK5,NBN,SLF2,PPHLN1,RTEL1,XRCC5,MAPK1,DDX11,MAPK3,SFPQ,PARN,SLX4,TERF2,SETDB1,ZNF304,MAP2K7	grey	VSMC_M10
GO:0052372	1.00	0.01	9	30	modulation by symbiont of entry into host	BP	1	FUCA2,LY6E,CXCL8,HS3ST5,NECTIN2,CD74,CIITA,TRIM68,TRIM34	grey	VSMC_M10
GO:0032200	1.00	0.00	54	130	telomere organization	BP	1	RPA3,PPP1R10,MAP3K4,XRCC6,MYC,H3F3C,MAPK15,POT1,ERCC1,XRCC1,WRN,PRKDC,ATR,HMBOX1,MAPKAPK5,TPRKB,NBN,TENT4B,STN1,LTO1,SP100,TERT,GAR1,RTEL1,XRCC5,UPF1,MAPK1,PARP1,GNL3L,WRAP53,SMG5,YLPM1,CTC1,PIF1,MAPK3,RAD51C,RAD51D,PARN,ERCC4,SLX4,DOT1L,ZBTB48,TERF2,TINF2,HIST1H4B,HIST2H4A,HIST1H4H,HIST1H3F,TEN1,HIST1H3H,HIST1H4D,MAP2K7,HIST1H4A,HIST1H4F	grey	VSMC_M10
GO:0010951	1.00	0.00	58	137	negative regulation of endopeptidase activity	BP	1	SERPINB8,SERPINB2,TNFAIP8,GAPDH,CD109,AQP1,BCL2L12,CST7,RAF1,PRDX3,TIMP4,UBE2O,SPINT2,PRNP,GAS6,PSMF1,GPI,NR4A1,SERPINB1,SPINT1,PAX2,APLP2,SORL1,IFI6,AGT,COL6A3,SFN,COL7A1,RPS6KA1,CST6,POR,DDX3X,SPOCK2,SERPINC1,SERPINI1,BIRC3,ARL6IP1,ANXA8,ANXA2,PAPLN,TMED10,WFIKKN2,MAP2K5,NLE1,C3,SERPINF2,WFIKKN1,PARK7,LAMTOR5,MIR24-1,NOL3,SERPINB5,A2M,MIR339,SERPINE3,SERPINB9,CAAP1,RARRES1	grey	VSMC_M10
GO:0060429	1.00	0.00	391	810	epithelium development	BP	1	ONECUT2,HSD17B4,GLI1,CYP27B1,ESR1,FRS2,STK3,FZD6,BRD2,ROS1,TBC1D32,MTSS1,RSPO3,MYC,SMAD5,KLHL3,PTCH1,AKR1B1,ATF4,PODXL,SOX10,SMO,ZDHHC21,FOXH1,IFT74,PTK7,SRF,CDK6,RFX3,CA9,TFAP2B,ROR2,DLX5,S1PR3,SEMA4C,TDRD7,MEOX2,SOSTDC1,TMOD1,CAT,SIX2,BRSK1,EPCAM,CD109,RTN4,KLK14,HOXA7,HOXA13,MYCL,AREG,BMPER,ANXA4,EPHA7,WHRN,PTN,GRHL1,MET,TNC,POU3F3,EGFR,FUZ,SFRP4,TEAD2,MYCN,SLC7A11,OSR1,INTU,SPRY1,PLXNA1,FOXE3,ARHGAP12,HDAC2,BBS7,BMI1,RAB10,PRKD2,SETDB2,ABI1,SOX9,ERCC2,ERCC3,CLASP2,PTER,GSTK1,PTCH2,GLI2,MEGF8,PCDH8,AQP11,XRCC2,MYD88,EVPL,ACVR2B,KLF5,IFT172,FOXJ1,MYO7A,GZF1,SCEL,SPRY2,WNT11,AKT2,TGFBR2,OVOL2,BFSP1,IKBKB,SLC4A7,JAG1,MKKS,RARB,ACTG1,HBEGF,LRTOMT,AP000812.5,PLCB1,MAFG,FERMT1,SPRED3,SPINT2,FREM2,CEP290,BTG1,SPEF1,SEMA3A,NRG1,FOXP1,TAF10,PRKDC,SYNE4,RYK,CEP63,TRAF6,TCF15,NPHP1,RET,ASAH1,POFUT1,ASXL1,CYP7B1,PAX8,ACVR1B,CBFA2T2,RILPL1,RILPL2,FLNB,CASP3,MARVELD2,HAND2,EYA1,PLS1,ROBO1,TRPC4AP,ROBO2,ARNTL,FMN1,ORAI1,FZD3,MEF2C,VEGFC,ARHGEF26,RAPGEF2,FRAS1,TIAM1,USH1C,VDR,STC1,NKX3-1,OPA1,NKX6-1,RAPGEF3,TBX5,AP3B1,F2RL1,SRSF6,IFT52,ARHGAP24,SPINT1,RPGRIP1L,RREB1,DSP,ZBED6,PKD2,STK4,TFAP2A,PAX2,SALL1,VANGL1,PPHLN1,PRICKLE1,NKD1,TOLLIP,LDB1,RYR2,SUFU,IRX2,HDAC1,ELF3,ALDH1A3,CCND1,CPT1A,BDH2,TGFB2,POGLUT1,ITPK1,NR5A2,FAM20C,PRKX,DAG1,AXIN2,AJUBA,KRAS,SNAI1,EGF,JHY,RHCG,ZNRF3,DHRS9,ADAMTSL4,AGT,GBX2,DVL3,TGM1,KDF1,SFN,NFATC4,FZD7,TRAF3IP1,LAMA5,PTPR	grey	VSMC_M10
GO:0031326	1.00	0.00	1507	2955	regulation of cellular biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,ORMDL2,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,SHMT2,GLI1,HBS1L,MARS,MAP3K5,TNFAIP3,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,MAML1,ZBTB2,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,EIF3E,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,MED30,IL5,BRD2,RXRB,TSPO,VGLL2,MRPL13,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,HABP4,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,RPAP2,CBX7,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,GUCA1B,GPT,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,IGF2BP3,FKTN,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,MTIF2,PPP4R3B,NFE2L3,PNPT1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,ANKRD17,JAZF1,CREB5,MYCL,CXCL8,XPO1,MTURN,NOD1,ORC3,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,PLEK,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOBOX,FAM3C,ARHGEF5,	grey	VSMC_M10
GO:0060323	1.00	0.01	8	28	head morphogenesis	BP	1	DLX5,CSRNP1,CRISPLD1,WNT3,STRA6,SKI,ANKRD11,NOG	grey	VSMC_M10

GO:0006518	1.00	0.00	336	688	peptide metabolic process	BP	1	SEC11C,PAN2,RPS12,SHMT2,LVRN,HBS1L,MARS,TSFM,CPM,RMND1,CNOT2,CNOT6,RIDA,PRR16,PABPC1,ZNF706,EIF3E,PNLDC1,QKI,MRPL13,RPS18,MRPL55,JMJD4,AGO2,HABP4,RPS10,TNRC6B,ATF4,TUT7,GTPBP1,NTRK2,EIF3L,CARNMT1,GTPBP2,CLIC5,SLC1A1,NCK2,MRPS9,GAPDH,CNOT11,AASDH,EXOSC3,RPS14,LRPPRC,SRBD1,CHAC2,IGF2BP3,RTN4,MTIF2,PNPT1,AGO1,EGFR,ASCC3,MGST2,QRSL1,C6orf203,TUT4,SLC7A11,FOXO3,PUM2,DHFR,EEFSEC,MKNK1,CNBP,MMACHC,GSTK1,EIF2B3,RPS8,MLH1,CDC123,MTRF1,DPH2,RPSA,RPL14,MRPL33,TNRC6C,AKT2,METTL17,MRPS12,PURA,DPH3,HARS,HARS2,EIF2AK2,PRNP,CARS2,LSM1,MRPL3,AIMP1,CLIC1,RPL31,LARS,EIF4E3,UPF3A,ARL6IP5,PRKDC,MRPL17,CPXM1,KBTBD8,PAN3,MRPL15,MIPEP,IDE,C12orf65,IMMP1L,NLN,MRPL35,GSS,ABCB9,CASP3,ERAP1,RPL6,PCSK1,MRPS27,MRPL19,SCG5,ENC1,MRPS28,CNOT1,CELF1,USP16,PTK2B,CNOT6L,MME,MAPKAPK5,EIF2AK4,EIF4E2,SPCS1,NSUN3,PAIP2B,FTO,CPN1,CYFIP1,NOD2,TENT4B,RBM24,SLC2A13,WARS2,MRPS17,CDKAL1,EIF2D,GATC,NEURL1,SPPL3,RPUSD4,YARS2,RPL23,DDX25,GLRX2,RPL4,XPNPEP1,RPS17,BANK1,LTO1,CAPRIN2,IGHMBP2,BDH2,RPL27A,MRPS35,DIS3L2,MRPL52,RCC1L,KLHL25,GIGYF2,MRPS11,ENPEP,RPS6KB2,YTHDF2,TRNAU1AP,SORL1,MRPS21,TARS2,DALRD3,ACE2,RPS27,RPS6KA1,PER2,DDX6,RPS4X,ECE2,MTG2,CPXM2,YTHDF1,PASK,CD28,BACE1,UHMK1,NCBP2,PCSK7,EIF4ENIF1,NSUN5,RPL11,IGF2BP2,YBX3,NFE2L2,EFL1,GGT2,LARS2,EIF4EBP2,CTSH,RPL10L,DDX3X,RC3H1,DARS2,UPF1,CPZ,RPL27,UBA52,MRPS36,COA3,ECE1,SAMD4A,PINK1,STAT3,GGT6,DNPEP,MAPK1,POLR2G,RTN1,NT5C3B,RSL24D1,H	grey	VSMC_M10
GO:0071216	1.00	0.00	67	157	cellular response to biotic stimulus	BP	1	TNFAIP3,TSPO,TRIB1,MAPK14,HSF1,PRKCE,CXCL8,TLR4,CDK19,MYD88,IRAK2,FBH1,NFKBIB,SIRT2,TRAF6,HCK,IL1A,IL37,PLSCR4,MEF2C,NUGGC,ATG10,NR1H3,RIPK2,ABCC2,NOD2,CD40,PDCD4,TMCO1,FZD5,UPF1,TNIP2,MAPK1,SGMS1,AKAP8,TNFRSF1B,SPON2,EME1,MAPK3,BTK,TNIP1,CCL5,CCL2,LITAF,NOS2,TICAM1,SLX4,ADAMTS13,ASS1,LCN2,GFI1,HSPA5,BCL10,DAB2IP,MIR21,RHOA,DEFB124,CXCL6,IRGM,CMPK2,IL36G,WNT5A,TIGAR,DDIT3,BCL2L11,CEBPB,HAVCR2	grey	VSMC_M10
GO:0050918	1.00	0.01	16	47	positive chemotaxis	BP	1	LRP1,AGER,FPR2,CXCL8,MET,PTPRJ,VEGFC,F2RL1,IL16,PGF,ALKBH1,SMAD3,CCL5,CCL16,WNT5A,ARTN	grey	VSMC_M10
GO:0001558	1.00	0.00	155	339	regulation of cell growth	BP	1	ADNP2,NEDD4L,LRP1,SEMA6A,CYP27B1,RAB21,HSPA1B,RIMS2,EBAG9,PRKN,PPARA,GDF9,ROS1,FSTL4,H3F3C,PLXNA4,CPNE5,PI16,EXOSC4,CDKN2A,SRF,SMARCA2,SEMA4D,SEMA4C,RIMS1,RTN4,PPP2R1A,RUFY3,PPT1,EPHA7,EGFR,TRIM32,SDCBP,NRCAM,SPHK2,PHB,PTCH2,GOLGA4,MEGF8,EGLN2,WNT11,SERTAD3,CPNE9,RPTOR,HBEGF,SYT1,SLC23A2,ING1,SEMA3D,BTG1,SPART,SEMA3A,ULK1,RYK,TTL,FAM107A,ACVR1B,CDKN2AIP,PLCE1,IL17RB,PTPRJ,SEMA4F,NDUFS3,PTK2B,DPYSL2,NKX6-1,ZFYVE27,PRDM11,SEMA3G,SPP1,CYFIP1,SEMA4G,BDNF,KIAA0319,HYAL1,CAPRIN2,SEMA3F,TGFB2,FBLN5,EI24,ZNF639,ADNP,DISC1,SH3BP4,AGT,CIB1,IP6K2,SLC9A1,SFN,RPS6KA1,CDKL5,CDKN1B,WNT3,MAPT,SUPV3L1,BCL6,SEMA6D,DDX3X,TNR,RASGRP2,FN1,DDX49,MUL1,DNAJB2,CD38,CXCL16,IGFBP4,TSPYL2,ARHGEF11,SEMA4A,TAOK2,TRIM46,NDEL1,RAB11A,TAF9B,SMAD3,NTN1,MAP2K5,S100A8,DNM2,BDKRB1,DCUN1D3,YY1,PSMD10,SIN3A,TRPV2,CDK5R1,EPB41L3,TMEM97,NUBP1,ATAD3A,L1CAM,ARHGAP4,PLXNA3,SLC25A33,PSRC1,CYBA,NAIF1,BARHL2,MIR199A1,RHOA,SERTAD2,ACVRL1,NANOS1,WNT5A,LAMTOR2,FXN,CACNG7,RGS4,DACT3,NME6,N6AMT1,CGRRF1,OLFM1,DERL2	grey	VSMC_M10
GO:0001501	1.00	0.00	191	413	skeletal system development	BP	1	OSR2,MPIG6B,TNFRSF11B,COL11A2,PITX1,SMAD5,MAPK14,MDFI,TEK,ZFAND5,SRF,KIT,ROR2,SEMA4D,DLX5,PRDX1,RAB23,SIX2,HOXA2,HOXA4,HOXA6,HOXA7,HOXA13,BMP8A,COL27A1,MBOAT2,FUZ,SFRP4,MYCN,OSR1,MATN3,MKX,BMI1,PIP4K2A,KIAA1217,EBP,ABI1,SOX9,GLI2,MEGF8,IFT172,WDR48,CSRNP1,TSKU,WDR60,WNT11,TGFBR2,CHRDL2,ZNF219,ACVR2A,MKKS,SLC38A10,RARB,RYR1,ALX1,LUM,DDRGK1,FOXP1,RYK,TCF15,ASXL1,HAND2,EYA1,FBXW7,FMN1,MEF2C,MCPH1,SOX6,VDR,STC1,LOXL2,PRELP,TFAP2A,TRIM45,ITGB6,IGF2,BMPR1B,SUFU,GPLD1,SRD5A1,LRRK1,HYAL1,SLC2A10,HYAL3,MAP2K6,TRPV4,SBDS,SLC9B2,TGFB2,SULF2,TRIP11,PTHLH,SATB2,AXIN2,CMKLR1,SNAI1,HAPLN3,AMELX,TRAPPC2,FGR,WASF2,ACTN3,HDAC4,THPO,CHRD,RUNX3,DLX1,SP3,DLG1,SETD2,HOXD8,HOXD4,HOXD3,POR,PTH1R,PRKRA,COL13A1,ANKH,ESRRA,PTPN6,FBN1,COL3A1,COL5A2,ALPL,FGFR3,MMP13,NKX3-2,TULP3,INHA,BMPR1A,WDR19,THRA,DHRS3,MED1,ANXA2,MSX2,PSEN1,HOXB5,HOXB6,HOXB8,HOXB9,FGF18,TMEM107,CTC1,THBS3,CHAD,MAPK3,WFIKKN2,SMAD3,MKS1,FOXN3,GPR68,GSC,TBX4,LHX1,TCOF1,CDX1,PPARGC1B,NLE1,JAG2,RAI1,GHR,PTGER4,RANBP3L,SPEF2,ADAMTS12,HSPB11,RFLNB,SKI,PKD1,ATP6AP1,WFIKKN1,ALX3,ANKRD11,ENG,MIR21,RHOA,HAPLN4,SOX4,ACVRL1,HOXB3,BGLAP,SNX10,NOG,WNT5A,SIX1,CCDC154,OTOR,INSIG2,SLC39A3,HOXA3	grey	VSMC_M10

GO:0044403	1.00	0.00	90	206	biological process involved in symbiotic interaction	BP	1	VPS4B,YTHDC2,FUCA2,SNW1,HSPA1B,IGF2R,PRKN,LY6E,GAPDH,CHMP2A,CXCL8,EGFR,TRIM32,ATG5,EPS15,HS3ST5,RAB7A,NAPEPLD,KPNA3,PHB,NECTIN2,FBXL2,PVR,MYD88,RPSA,SLC20A2,GAS6,ULK1,THOC7,IDE,CHMP2B,SAP30,CHMP4C,EIF2AK4,TPCN1,F2RL1,ANO6,VPS18,ITGB6,HDAC1,DAG1,ZNF639,SELPLG,CFL1,HSPA8,GRK2,POU2F3,PC,CBL,ACE2,ITGB5,NECTIN4,XPR1,LRRC15,PIKFYVE,FN1,SLC3A2,DDB1,PSMC3,TARDBP,LDLR,SCNN1B,TNIP1,CD74,INSR,CCL5,NPC1,THOC2,JUN,CIITA,FMR1,INPP5K,BSG,RXRA,WWP2,VPS4A,MIR222,HAVCR1,TRIM68,DPP4,CXCL6,TRIM34,CD46,IRGM,SAP30BP,CLDN1,SERPINB9,TBC1D20,ZNF502,EFNB3	grey	VSMC_M10
GO:1901575	1.00	0.00	817	1628	organic substance catabolic process	BP	1	VPS4B,NEDD4L,PAN2,GLS2,HSD17B4,LRP1,SHMT2,LVRN,FEM1C,ALDH8A1,RMND5B,PDE7B,TNFAIP3,AGAP2,CYP27B1,AIG1,FUCA2,USP15,CANX,ENPP3,TRIM39,CNOT2,CNOT6,RIDA,MIOX,PABPC1,CPT1B,ALDH7A1,PHAX,ABHD16A,HSPA1B,SYNJ2,DPYS,SKIV2L,DXO,EIF3E,PNLDC1,PRKN,RNF5,PPARA,PDE10A,PSMB8,PNPLA3,PNPLA5,MCAT,DERL1,SKP1,SMPDL3A,UBE2B,RNF217,CSDC2,RNF146,ECHDC1,TRIB1,KLHL3,AGO2,PRXL2C,PTK2,TNRC6B,TUT7,AGTPBP1,APOBEC3H,GTPBP1,MAPK14,CSNK1E,PLA2G6,EXOSC4,FOXRED2,HSF1,FBXL6,USP49,GPT,CARNMT1,FBXO7,KLHDC3,ALDH1A1,GDA,ABHD17B,CEMIP2,CROT,GNPDA2,DCAF12,GALT,USP46,ENPP4,LNX1,SRD5A3,GAPDH,CNOT11,PPAT,RGP1,PDCL3,HINT2,HMGCLL1,ADH5,FBXO10,EXOSC3,LRPPRC,SEC61B,RNF20,PRKCE,CHAC2,RAD23B,ETFB,UBE3D,PNPT1,SLC4A4,ECPAS,NT5E,PPT1,XPO1,PELI1,BPGM,WDR91,CNOT4,RNASEH1,FBXO48,IL4I1,AGO1,EGFR,HECW1,USP45,TRIM32,ASCC3,HACE1,LPIN1,USP38,INPP4B,VPS35,MGST2,ZYG11B,SDCBP,TUT4,SMPD2,PUM2,MGAM,LDAH,MFSD8,DHDH,DDO,APOB,HSD17B14,BCAT2,FAF1,FGF21,TRAF3IP2,MTPAP,MTMR2,ZC3HAV1,BBS7,RAB7A,DHX34,NAPEPLD,FAAH,FBXL13,HADHA,GAD2,PHB,ENTPD6,SOX9,PYGB,CDADC1,NUDT15,ABHD5,ESD,AKR1A1,APOC1,FBXL2,GLB1,KCTD2,PLK3,SUMO2,FASTK,MLH1,NUDT5,USP35,KBTBD6,KCTD21,LIPE,DHTKD1,MBD4,DEDD2,AQP11,PRKAG2,MYD88,ACOX1,DMAC2,TIMP4,XYLB,EGLN2,MYCBP2,UBXN4,UBE3C,HNMT,SPOPL,RBKS,ACER3,FBH1,TNRC6C,PPP1CB,ALK,UBE2E1,KLHL40,AKT2,GPD1L,ARRB1,NEU3,SNX5,PFKP,UGGT2,USP36,FBXO17,SIRT2,DNAJC18,IDO2,IDO1,NPLOC4,TMEM106B,LRTOMT,AP000	grey	VSMC_M10
GO:0052126	1.00	0.00	52	127	movement in host environment	BP	1	VPS4B,FUCA2,HSPA1B,LY6E,CHMP2A,CXCL8,EGFR,TRIM32,EPS15,HS3ST5,RAB7A,KPNA3,PHB,NECTIN2,PVR,RPSA,SLC20A2,GAS6,IDE,CHMP2B,CHMP4C,TPCN1,VPS18,ITGB6,DAG1,ZNF639,SELPLG,GRK2,PC,CBL,ACE2,ITGB5,NECTIN4,XPR1,PIKFYVE,SLC3A2,DDB1,LDLR,CD74,NPC1,CIITA,BSG,WWP2,VPS4A,HAVCR1,TRIM68,DPP4,TRIM34,CD46,CLDN1,ZNF502,EFNB3	grey	VSMC_M10
GO:0061448	1.00	0.00	88	203	connective tissue development	BP	1	OSR2,COL11A2,PITX1,SMAD5,MAPK14,SRF,ROR2,SIX2,BMP8A,COL27A1,MBOAT2,MYCN,TRPM4,OSR1,PGRMC2,MATN3,MKX,SOX9,GLI2,PAXIP1,TSKU,WNT11,DYRK1B,TGFBR2,CHRDL2,ZNF219,MKKS,RARB,LUM,SPART,DDRGK1,HAND2,MEF2C,SOX6,SLC39A13,EBF2,STC1,LOXL2,FTO,BMPR1B,GPLD1,HYAL1,HYAL3,TRPV4,SULF2,TRIP11,PTHLH,SATB2,AXIN2,SNAI1,AMELX,SORL1,RUNX3,HOXD3,POR,KLF7,PTH1R,ESRRA,FGFR3,MMP13,PLA2G16,NKX3-2,BMPR1A,THRA,FGF18,THBS3,MAPK3,IL6R,SMAD3,TNMD,GHR,OXCT1,ADAMTS12,RFLNB,PKD1,SOX8,COL5A1,SLC25A25,MIR21,UBB,ACVRL1,MIR125A,HOXB3,NOG,WNT5A,OTOR,HOXA3,PDGFD	grey	VSMC_M10
GO:0048646	1.00	0.00	424	877	anatomical structure formation involved in morphogenesis	BP	1	ITGA7,ATP8B1,SEMA6A,TBPL1,TNFAIP3,ADGRG6,FRS2,CNOT2,STK3,ADM2,MPIG6B,SLC12A2,FZD6,PNLDC1,PPARA,BRD2,RRP7A,CCDC134,RSPO3,OBSCN,LEMD2,AGO2,PTK2,PTCH1,EXOC4,AGTPBP1,MAPK14,PODXL,PIM1,MFNG,SMO,MYH9,FOXH1,TEK,LMOD2,PTK7,CEMIP2,SRF,PGM5,TXNRD1,SLC1A1,FHL2,TFAP2B,ROR2,DLX5,PDCL3,C1GALT1,NINJ1,SEMA4C,SHB,CNNM4,MEOX2,TMOD1,SIX2,EPAS1,RDH13,CD109,MBOAT7,RTN4,KLK4,HOXA7,EMC10,CXCL8,EPGN,AQP1,BMPER,WHRN,TGFA,PTN,ITGB1BP1,AGO1,YWHAZ,TSPAN12,FUZ,EPHA1,GAB1,MYLK3,TEAD2,NRCAM,OSR1,NTF4,FIG4,MKX,SPRY1,WISP3,HDAC2,MTMR2,NDNF,C5AR1,PRKD2,ABI1,SOX9,ERCC1,ERCC2,SLC39A12,CLASP2,SLC4A2,NECTIN2,GLI2,PCDH8,UNC13D,XRCC2,ACVR2B,KLF5,IFT172,FOXJ1,SPRY2,WNT11,CCNB1IP1,DYRK1B,TGFBR2,OVOL2,ZNF219,EOMES,ISM1,RELT,JAG1,ACTG1,SPINT2,CEP290,DCN,PANK2,BTG1,AIMP1,LMOD3,PRKDC,KBTBD8,FLT1,TRAF6,TCF15,EPHB1,PLK2,RET,POFUT1,IL1A,GPI,PAX8,NR4A1,PIK3CB,MYOF,CASP3,ERAP1,HAND2,EYA1,PARVA,ROBO1,ROBO2,FBXW7,FMN1,FZD3,MEF2C,FAIM2,VEGFC,CNOT1,TLX2,JAM2,MMP15,ADAMTS1,PTK2B,OTULIN,NKX3-1,OPA1,HDAC7,RAPGEF3,LOXL2,TBX5,AGGF1,IFT52,ARHGAP24,SPINT1,RTF1,STK4,TFAP2A,PAX2,SALL1,PRICKLE1,ADTRP,NKD1,ITGB6,ADAMTS15,CD40,LDB1,NFKB2,SUFU,GPLD1,KLHL12,FAP,IRX2,SH3PXD2A,PKNOX1,HDAC1,HYAL1,ALDH1A3,LMOD1,SP100,TERT,TGFB2,POGLUT1,PEF1,TCIRG1,FAM20A,PRKAR1A,PDCD6,FAM20C,PRKX,DAG1,AXIN2,TCTA,SNAI1,EGF,ENPEP,TTC21B,AMELX,SOX2,ANK2,GNPAT,LAMB3,AGT,MCAM,CIB1,WASF2,GBX2,DVL3,ACTC1,NFATC4,VASH2,C	grey	VSMC_M10
GO:0001570	1.00	0.00	26	71	vasculogenesis	BP	1	QKI,NTRK2,SMO,TNNI3,HOXA13,TEAD2,PAXIP1,RIN2,TGFBR2,FBXW7,RAPGEF2,HDAC7,TBX5,AGGF1,HIF1AN,WARS2,SETD2,RAMP2,CITED1,TMEM100,AMOT,FOXF1,ENG,GLMN,NKX2-5,HEY2	grey	VSMC_M10
GO:0051057	1.00	0.00	19	55	positive regulation of small GTPase mediated signal transduction	BP	1	GPR20,LRRD1,LPAR1,ARRB1,RASGRP4,NRG1,PIK3CB,ROBO1,RASGRP1,F2RL1,F2R,AUTS2,KRAS,COL3A1,GPR35,ADGRG1,STK19,HRAS,ARPP19	grey	VSMC_M10

GO:0006310	1.00	0.00	109	245	DNA recombination	BP	1	RPA3,MRNIP,HELB,MCM9,TCF7,UBE2B,XRCC6,DMC1,KLHDC3,EXOSC3,MSH2,TFPT,CYREN,CCDC155,REV3L,HMCES,ERCC1,ERCC2,XRCC1,MLH1,XRCC2,KIN,ZRANB3,PAXIP1,WDR48,FBH1,KPNA2,CCNB1IP1,MCM8,SHLD1,AP5S1,WRN,PPP4R2,TEX15,PRKDC,ERCC6,XRCC4,TPRKB,NBN,THAP9,HELQ,SPIDR,RAD54B,SYCP1,POLL,CD40,DCAF1,FAN1,HSF2BP,IGHMBP2,CCDC36,SPO11,PGBD5,RECQL,C11orf80,CD28,RNF168,RTEL1,SETD2,NONO,SUPV3L1,BCL6,APEX2,XRCC5,ZCWPW1,POLN,WAS,RHNO1,RAD52,FOXP3,PARP1,SHLD2,AP5Z1,RAD51B,EXD2,TBX21,WRAP53,PAGR1,EME1,BATF,PIF1,SWSAP1,NSMCE1,RAD51C,SFPQ,BCL11B,YY1,RAD51D,LIG3,SMCHD1,IL7R,SUPT6H,ERCC4,RMI2,SLX4,MEIOB,GINS2,TERF2,MSH4,RPA4,SWI5,RNF212B,OOEP,RNF8,NHEJ1,UBE2N,CENPX,SFR1,NABP1	grey	VSMC_M10
GO:0006302	1.00	0.00	99	225	double-strand break repair	BP	1	RPA3,ATP23,MRNIP,HELB,MCM9,XRCC6,DMC1,HSF1,POT1,MSH2,CYREN,CCDC155,REV3L,HMCES,ERCC1,XRCC1,MLH1,XRCC2,WDR48,FBH1,RNF169,SIRT7,MCM8,SHLD1,AP5S1,WRN,PPP4R2,TEX15,PRKDC,ERCC6,ERCC8,HPF1,EYA1,SLF1,XRCC4,NBN,HELQ,ABRAXAS1,SPIDR,RAD54B,SLF2,POLL,FAN1,HSF2BP,CHEK2,EYA3,PARP9,DTX3L,SPO11,CIB1,RECQL,RNF168,RTEL1,MGMT,SETD2,XRCC5,ZCWPW1,POLN,IFFO1,WAS,DDX11,RAD52,PARP1,SHLD2,AP5Z1,PRPF19,RAD51B,UIMC1,EXD2,WRAP53,EME1,SWSAP1,NSMCE1,TDP1,RAD51C,SFPQ,OTUB2,YY1,RAD51D,LIG3,SMCHD1,ERCC4,RMI2,PIAS4,NUDT16L1,SLX4,MEIOB,PAXX,SPIRE2,GINS2,RPA4,SWI5,OOEP,RNF8,NHEJ1,UBE2N,BRCC3,SFR1,NABP1	grey	VSMC_M10
GO:0035264	1.00	0.00	43	108	multicellular organism growth	BP	1	H3F3C,PTCH1,SMO,APBA1,ERCC1,ERCC2,XRCC2,WDR48,MKKS,RARB,TAF10,ERCC6,PLAG1,PLS1,HTRA2,CELF1,FTO,SLC12A5,IGF2,SLC4A10,SLC6A3,GPAM,ADARB1,GIGYF2,SPTBN2,CLIC4,CREB1,FKBP8,GDF15,STAT3,STAT5B,CTC1,SCNN1B,RAI1,GHR,GAMT,SLC25A25,DIO3,POU3F2,FXN,PLAC8,TAL2,RC3H2	grey	VSMC_M10
GO:0001649	1.00	0.00	82	190	osteoblast differentiation	BP	1	HSD17B4,GLI1,ASF1A,SMAD5,H3F3C,PTK2,PTCH1,ATF4,MAPK14,SMO,RORB,FZD1,CDK6,FHL2,SEMA4D,DLX5,CAT,HOXA2,AREG,TNC,TRPM4,BCAP29,HSPE1,PHB,SOX9,GLI2,ACVR2B,WNT11,ACVR2A,JAG1,SIRT7,DNAJC13,CLIC1,CEBPA,HAND2,MEF2C,VEGFC,HDAC7,SPP1,IGF2,BMPR1B,SUFU,MAP2K6,PTHLH,SATB2,TCIRG1,AXIN2,SNAI1,AMELX,SOX2,HDAC4,CHRD,WNT3,PTH1R,MEN1,ESRRA,WNT4,SUCO,ALPL,TPM4,BMPR1A,PDLIM7,MSX2,RIOX1,TOB1,CITED1,IL6R,SMAD3,ITGA11,TWSG1,RANBP3L,SKI,ATP6AP1,SOX8,WDR63,MIR21,MIR27A,SP7,BGLAP,NOG,RDH14,CEBPB	grey	VSMC_M10
GO:0006470	1.00	0.00	100	228	protein dephosphorylation	BP	1	PHLPP1,EYA4,PTP4A3,RPAP2,PPP1R16A,NUAK1,PTPDC1,PPP2R1A,PPP4R3B,ACP4,RNGTT,VRK3,MTMR2,SYMPK,PPM1N,PTPRF,PPP1CB,TIMM50,MTMR14,IKBKB,PTPRQ,DUSP6,NCKAP1L,PPP4R2,PPP2CB,PTPRA,PPP1R3B,MFHAS1,MTMR7,EYA1,PTPRJ,RPRD1B,CRY2,PTPN5,PPM1K,SPPL3,LRRK1,LCK,PPP3CA,PPP2R2D,PPA2,SSH1,PPP1R3E,UBASH3B,EYA3,PPP2R5A,PPP1R3D,ILKAP,MTMR3,PTPRO,DUSP18,DUSP12,DLG1,PPM1J,CTDSPL2,DUSP10,CTTNBP2NL,PPP2R5B,PPM1L,DUSP19,PPP1R2C,PTPN6,HTT,PPP3CB,PINK1,CAMK2G,TIPRL,PPM1A,PPP2R5E,BOD1L2,UBLCP1,PTPN21,CALM1,PPP4R4,RPRD1A,PPP2R5C,DUSP14,PPP6C,PTPN2,SSH2,MTM1,MTMR1,CAMTA1,TSC1,CDC14A,LRRC39,PHLPP2,LRRC40,MINPP1,NCEH1,CNEP1R1,DUSP26,DUSP1,SDHAF2,PPP1R15A,DUSP22,STYX,PDXP,PTPMT1,ARPP19	grey	VSMC_M10
GO:2001237	1.00	0.00	30	79	negative regulation of extrinsic apoptotic signaling pathway	BP	1	EYA4,TNFAIP3,HSPA1B,ZC3HC1,PHIP,RAF1,ZMYND11,IL1A,FAIM,EYA1,IL7,FAIM2,RIPK1,TERT,TCF7L2,EYA3,IFI6,MCL1,STRADB,PEA15,PELI3,DDX3X,HTT,PSME3,MAP2K5,MAPK7,PARK7,MIR222,FGA,NOL3	grey	VSMC_M10
GO:1901701	1.00	0.00	431	887	cellular response to oxygen-containing compound	BP	1	ADNP2,ZNF236,NME1,FECH,LRP1,AP3S1,MARS,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,ESR1,SNW1,PRKN,AGER,PNPLA3,TSPO,TRIB1,PTK2,ERCC6L2,PTCH1,FANCC,LY6E,AKR1B1,ATF4,MAPK14,NTRK2,MAPK13,PLA2G6,GKAP1,SOX10,PIM1,SMO,HSF1,CCND3,GPT,CHRNA3,GPR37,RORB,ALDH1A1,PTK7,SRF,SLC1A1,PPAT,PRDX1,ADH5,PRKCE,PHIP,FPR2,HMGN3,HOXA2,CXCL8,NOD1,CRHR2,AQP1,RRAGD,ZNF277,PTN,KLF11,MET,GRB10,TNC,EGFR,LANCL2,TLR4,GAB1,LPIN1,IL15,UCP1,VPS35,TEAD2,MGARP,TRPM4,OSR1,FOXO3,CDK19,FGF21,SPHK2,DHFR,HDAC2,ADCY3,SESN3,DNMT3A,BMI1,PIP4K2A,RAB10,SOX9,CYSLTR2,ESD,AKR1A1,ECHDC3,GRIK5,RAF1,ATP1A3,MYD88,PRDX3,KLF5,TBC1D4,AANAT,IRAK2,POU4F1,WNT11,ALK,AKT2,SNX5,NFKBIB,SIRT2,RPTOR,PAWR,PLCB1,MAP4K1,SLC23A2,PRNP,KL,GAS6,LARS,PTPRA,LEPROTL1,PRKDC,NCOA4,TRAF6,NR1H4,SLC38A9,TRIB3,RET,CYP7A1,HCK,NDUFAF2,HTR7,IL1A,IL37,DNMT3B,NR4A1,FER,IDE,OSBP,PIK3R1,CCDC62,P2RX3,CHRM5,RYR3,PLSCR4,SORBS1,GPD1,MEF2C,SMARCD1,NUGGC,HTRA2,P2RX7,ZFAND1,GUCY1B1,P2RY1,PTK2B,RAPGEF2,KCNJ11,NR1H3,TIAM1,LCOR,RAB11FIP5,RIPK2,VDR,STC1,OPA1,SPIDR,LPIN3,NKX6-1,RAPGEF3,CHRM4,NR4A2,SLC38A2,TESC,RIPK1,TP53INP1,ABCC2,SPP1,ZBED6,PKD2,PAX2,CYFIP1,DMTN,TWNK,NOD2,DTNBP1,ADCY7,CHRM3,CD40,RYR2,IGF2,ADCY2,PXN,GPLD1,SRD5A1,IRS1,NEURL1,MTR,RPL23,DNM1L,GLRX2,GRB14,PPP3CA,CPT1A,MAP2K6,SLC9B2,PDCD4,ZBTB20,ADRA2A,SLC30A10,FBLN5,COL16A1,DAG1,SSH1,KCNB1,NCF1,GRAMD1B,GRK2,SORL1,POLG,C2CD5,GPER1,CHEK2,RAB11FIP2,SH3BP4,AGT,I	grey	VSMC_M10
GO:0080164	1.00	0.00	15	45	regulation of nitric oxide metabolic process	BP	1	TSPO,TLR4,PTK2B,PKD2,AGT,NOS1AP,SMAD3,DNM2,GLA,INSR,TICAM1,TRPV1,ASS1,MIR199A1,MIR99B	grey	VSMC_M10

GO:0006278	1.00	0.00	23	64	RNA-dependent DNA biosynthetic process	BP	1	MAP3K4,MAPK15,POT1,ATR,HMBOX1,MAPKAPK5,TENT4B,STN1,TERT,GAR1,XRCC5,MAPK1,GNL3L,WRAP53,SMG5,CTC1,PIF1,MAPK3,PARN,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0048511	1.00	0.00	97	223	rhythmic process	BP	1	PHLPP1,ESR1,TPH2,PPARA,GDF9,ATF4,NTRK2,CSNK1E,BTBD9,FBXL6,NFYA,RORB,CRY1,NFIL3,PTN,DDC,EGFR,CREM,FOXO3,HDAC2,ENOX1,SUV39H2,TIMP4,AANAT,MYCBP2,PPP1CB,ARRB1,BHLHE40,NR1D2,PRKDC,HTR7,NUDT12,AHCY,SPSB4,CASP3,NCOA2,ROBO2,ARNTL,FBXW7,ADAMTS1,NR1H3,TOP1,CRY2,BMPR1B,GAS2,MAGEL2,NFKB2,SRD5A1,DNM1L,SIK1,HDAC1,MAP2K6,TGFB2,ARNTL2,ADNP,CIART,USP2,PER2,C3orf70,CREB1,NONO,CRTC1,PTPRN,NDUFA9,STAT5B,KDM5A,MAGED1,KDM5C,DDB1,TARDBP,NGFR,FBXL22,OGT,CIPC,CHRNB2,KDM8,SFPQ,SIN3A,NCOR1,CDK5R1,SREBF1,RAI1,NOS2,ENOX2,JUN,CREBBP,PER3,GPR157,ASS1,HSPA5,ZFHX3,FBXL8,FBXL12,CRH,PASD1,HS3ST2,EREG	grey	VSMC_M10
GO:0001822	1.00	0.00	109	248	kidney development	BP	1	RIDA,OSR2,TBC1D32,MTSS1,MYC,SMAD5,KLHL3,PTCH1,AKR1B1,PODXL,SMO,TEK,PTK7,TFAP2B,PPAT,C1GALT1,ANKS6,CAT,SIX2,EPCAM,BMPER,EPHA7,POU3F3,CNTRL,OSR1,TRAF3IP2,SPRY1,SOX9,GLI2,AQP11,FOXJ1,GZF1,WNT11,JAG1,RARB,FREM2,CEP290,DCN,RET,ASXL1,PAX8,HPGD,EYA1,ROBO2,PLCE1,FMN1,MEF2C,ADAMTS1,MME,FRAS1,NKX3-1,RPGRIP1L,PKD2,TFAP2A,PAX2,SALL1,IRX2,TGFB2,SULF2,PRKX,ENPEP,AP1B1,AGT,BICC1,TRAF3IP1,LAMA5,PTPRO,DLG1,OVOL1,CTSH,FBN1,CXCR2,WNT4,EPHA4,MAGED1,ALDH1A2,ITGA3,TMED10,CITED1,IL6R,SMAD3,LHX1,STRA6,AP2B1,NLE1,ZBTB14,IFT20,GPC3,HSPB11,PKD1,SOX8,TSC1,ASS1,PKD1L3,RHOA,FSTL3,SOX4,FADD,CA2,MIR125A,NOG,WNT5A,BASP1,SIX1,BCL2L11,LIF,KCNJ8,FGF1,PDGFD	grey	VSMC_M10
GO:0044409	1.00	0.00	42	106	entry into host	BP	1	FUCA2,HSPA1B,LY6E,CXCL8,EGFR,EPS15,HS3ST5,KPNA3,PHB,NECTIN2,PVR,RPSA,SLC20A2,GAS6,IDE,TPCN1,VPS18,ITGB6,DAG1,ZNF639,SELPLG,GRK2,CBL,ACE2,ITGB5,NECTIN4,XPR1,PIKFYVE,SLC3A2,LDLR,CD74,NPC1,CIITA,BSG,WWP2,HAVCR1,TRIM68,DPP4,TRIM34,CD46,CLDN1,EFNB3	grey	VSMC_M10
GO:0045930	1.00	0.00	80	186	negative regulation of mitotic cell cycle	BP	1	YTHDC2,HECA,MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,FBXO7,BRSK1,MSH2,EGFR,CDK5RAP2,TPRA1,XPC,PLK3,DYNC1LI1,ANAPC15,IK,NEK11,BTG1,USP44,PRKDC,STK33,PLK2,FAM107A,RAD17,FZD3,BTG3,RAD9B,CHMP4C,NBN,NKX3-1,ABRAXAS1,DONSON,ZFYVE19,PIDD1,PKD2,TAOK3,CCND1,GIGYF2,CHEK2,ANGEL2,SYF2,CDKN1B,DLG1,OVOL1,BCL6,BRINP2,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,SMAD3,LCMT1,FOXN3,DCUN1D3,NLE1,CCL2,TOM1L2,PSMG2,TAOK1,FZR1,FBXO31,VPS4A,NAE1,MIR29A,MIR21,PLK5,RPS27L,SOX4,DUSP1,RGCC,NME6,APC,ZFP36L2,BRCC3,CRADD,NABP1	grey	VSMC_M10
GO:0003170	1.00	0.00	20	58	heart valve development	BP	1	NFATC1,SOX9,TGFBR2,JAG1,ROBO1,ROBO2,MEF2C,TBX5,TGFB2,SNAI1,BMPR1A,RBPJ,TNFRSF1B,EFNA1,STRA6,ZBTB14,SOX4,NKX2-5,HEY2,OLFM1	grey	VSMC_M10
GO:0090330	1.00	0.01	4	18	regulation of platelet aggregation	BP	1	C1QTNF1,DMTN,UBASH3B,ABAT	grey	VSMC_M10
GO:0030261	1.00	0.01	9	31	chromosome condensation	BP	1	H3F3C,MCPH1,ACIN1,GPER1,TTN,AKAP8L,AKAP8,DFFB,CHMP1A	grey	VSMC_M10
GO:0048589	1.00	0.00	234	501	developmental growth	BP	1	NEDD4L,LRP1,SEMA6A,GLI1,ESR1,RAB21,STK3,RIMS2,PRKN,PPARA,GDF9,FSTL4,H3F3C,PTCH1,LY6E,PLXNA4,MAPK14,CPNE5,SOX10,PI16,PIM1,SMO,BNC2,TAF8,LARGE1,PTK7,SRF,APBA1,TEC,SEMA4D,NINJ1,SEMA4C,RIMS1,RTN4,RUFY3,AREG,AKIRIN1,COL27A1,EPHA7,PTN,TNC,NRCAM,FOXO3,WASF1,SPRY1,PLXNA1,SOX9,ERCC1,ERCC2,GOLGA4,GLI2,MEGF8,XRCC2,KLF5,WDR48,TSKU,SPRY2,WNT11,CPNE9,TGFBR2,MKKS,RARB,SYT1,PLCB1,SLC23A2,DUSP6,SEMA3D,SPART,SEMA3A,ULK1,TAF10,PRKDC,ERCC6,RYK,PLAG1,TTL,PLS1,FMN1,MEF2C,SEMA4F,IL7,HTRA2,CELF1,TLL2,KMT2D,DPYSL2,EIF2AK4,TIAM1,SLIT1,NBN,STC1,NKX6-1,TBX5,ZFYVE27,ACVR1C,BIN3,FTO,SEMA3G,RTF1,SPP1,STK4,CYFIP1,ALCAM,SEMA4G,SALL1,NKD1,JARID2,SLC12A5,IGF2,BMPR1B,GAS2,BDNF,SLC4A10,KIAA0319,LGR6,SLC6A3,PPP3CA,SBDS,SEMA3F,TGFB2,GAP43,GPAM,PRKAR1A,ADARB1,DAG1,AUTS2,HLX,GIGYF2,ADNP,SOX2,DISC1,ARIH2,AGT,KDF1,SPTBN2,FZD7,ACTN3,KCNK2,CDKL5,CLIC4,FZD9,CDKN1B,APOD,YBX3,WNT3,POR,CREB1,SPG11,DUSP10,MAPT,SEMA6D,ITGA4,TNR,FN1,SAV1,NIN,FLRT1,FKBP8,PPP3CB,MYOZ1,GDF15,FGFR3,MMP13,MUL1,STAT3,VCL,MAPK1,STAT5B,NINJ2,ENO3,BMPR1A,RBPJ,MED1,RAD51B,SOX15,SEMA4A,NLGN3,CTC1,THBS3,TRIM46,NDEL1,WWC1,ALKBH1,RAB11A,SMAD3,NTN1,DNM2,SCNN1B,TBX2,LHX1,STRA6,YY1,SIN3A,TRPV2,INSR,GATA6,CDK5R1,RAI1,GHR,LEPR,SLC9A6,L1CAM,PRKCZ,ARHGAP4,GAMT,PLXNA3,SLC25A25,BARHL2,MIR199A1,MIR222,MIR23A,MIR24-1,MIR25,IMPACT,NOG,WNT5A,BASP1,DIO3,POU3F2,FXN,CACNG7,SIX1,RGS4,PLAC8,BCL2L11,LLPH,EREG,C	grey	VSMC_M10
GO:0003158	1.00	0.00	42	107	endothelium development	BP	1	ZDHHC21,S1PR3,HOXA13,PTN,MET,PRKD2,MYD88,ACVR2B,IKBKB,JAG1,PLCB1,BTG1,NRG1,FOXP1,MARVELD2,ARHGEF26,RAPGEF2,STC1,RAPGEF3,F2RL1,CLIC4,APOLD1,RAP1B,PLOD3,VCL,FOXP3,RBPJ,KDM6B,HOXB5,TMEM100,VEZF1,TNMD,ADAMTS12,LCN2,MIR21,RHOA,ACVRL1,FOXJ2,MIR99B,CLDN1,FGF1,HEY2	grey	VSMC_M10

GO:0034641	1.00	0.00	2536	4878	cellular nitrogen compound metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,ORMDL2,SEC11C,ZC3H10,SMARCC2,PAN2,ATP8B1,FECH,ONECUT2,BAZ2A,TCF4,POLI,HSD17B4,RNMT,RPS12,SHMT2,EYA4,LVRN,TBPL1,GLI1,HBS1L,MARS,PDE7B,CLK4,MAP3K5,B4GALNT1,RPA3,TNFAIP3,TSFM,HIVEP2,ADAT2,ATP23,PLAGL1,MAML1,MRNIP,ENPP3,ATP5MGL,HELB,RPP21,PPP1R10,CPM,ZBTB2,RMND1,CPSF6,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,SNCAIP,PABPC1,SNW1,TFB1M,ZNF706,CPT1B,ALDH7A1,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,MAP3K4,PPT2,PRKN,QKI,AGER,TRMU,PPARA,PDE10A,ACSL6,UTP23,MED30,SLC22A4,IL5,BRD2,TAF2,RXRB,TSPO,VGLL2,MCM9,ASF1A,MRPL13,RPS18,RRP7A,HSF2,TCF7,PHF1,SMPDL3A,UBE2B,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,MRPL55,JMJD4,AGO2,PRXL2C,HABP4,RPS10,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,LY6E,AKR1B1,ZC3H3,ATF4,TUT7,MAPK15,RPAP2,CBX7,APOBEC3H,GTPBP1,MAPK14,NTRK2,UHRF2,CBY1,DMC1,PUF60,C9orf64,CSNK1E,PLA2G6,PICK1,KDM4C,SOX10,EIF3L,PIM1,CMTR1,BTBD9,NRF1,TMPRSS6,EXOSC4,SMO,SNAPC3,BNC2,HSF1,PSAT1,OARD1,NFYA,FOXP4,MDFI,TFEB,CPSF1,USP49,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,IMPDH1,LRRC14,RBM28,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,CARNMT1,IFT74,BICRAL,GNMT,POT1,GPR37,KLHDC3,RORB,ZNF300,PRDM4,CRY1,GDA,DMTF1,CROT,SRF,SMU1,ZNF318,NFX1,NOL6,GNPDA2,XPO5,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,GALT,SLC35B2,NFKBIE,FANCG,SUPT3H,SMARCA2,CLIC5,ENPP4,RFX3,KIT,SLC	grey	VSMC_M10
GO:0001935	1.00	0.00	50	123	endothelial cell proliferation	BP	1	TEK,PDCL3,EMC10,BMPER,ITGB1BP1,PRKD2,THAP1,RPTOR,AIMP1,FLT1,NR4A1,ATP5F1A,MEF2C,VEGFC,LOXL2,AGGF1,IGF2,PDCD6,PRKX,EGF,ARNT,VASH2,DLG1,ITGA4,IL12A,PDCD10,STAT3,ALDH1A2,SYNJ2BP,NGFR,PGF,VASH1,NOX5,TNMD,CCL2,PDPK1,CYBA,MIR29A,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,ACVRL1,ZNF580,WNT5A,RGCC,WNT2	grey	VSMC_M10
GO:0009303	1.00	0.01	10	33	rRNA transcription	BP	1	MARS,IPPK,GTF3C6,SIRT7,GTF3C3,DEDD,H2AFY2,DDX11,TCOF1,GTF3C4	grey	VSMC_M10
GO:0006473	1.00	0.00	71	168	protein acetylation	BP	1	ATAT1,YEATS4,BRD1,SUPT3H,HINT2,PHF14,KANSL3,ING3,ATG5,SPHK2,HDAC2,BMI1,IWS1,PAXIP1,AANAT,TADA3,ARRB1,TAF7,EP400,TAF10,SDR16C5,TAF9,ARNTL,PHF20,KANSL2,RAPGEF3,LDB1,HDAC1,AUTS2,MRGBP,ING5,POR,MAPT,MBIP,DDX3X,TADA2B,NAA40,ING4,NAA30,TADA1,FOXP3,MSL1,MED24,KAT7,MUC1,TAF1,MAPK3,OGT,NAP1L2,CRTC2,RPS6KA5,SIN3A,ISL1,TAOK1,GLYR1,CREBBP,NAA60,NAA10,HCFC1,MECP2,CHD5,PARK7,GTF3C4,CTCF,TAF12,SOX4,CPA4,BEND3,SUPT7L,LIF,RPS6KA4	grey	VSMC_M10
GO:0009889	1.00	0.00	1533	3010	regulation of biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,ORMDL2,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,SHMT2,PGGT1B,GLI1,HBS1L,MARS,MAP3K5,TNFAIP3,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,MAML1,ZBTB2,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,ARID1B,HSPA1B,FZD6,ZBTB12,EIF3E,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,MED30,IL5,BRD2,RXRB,TSPO,VGLL2,MRPL13,HSF2,TCF7,PHF1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,HABP4,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,RPAP2,CBX7,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,FOXH1,GUCA1B,GPT,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,GNMT,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,NCK2,FHL2,TGFBRAP1,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,LRPPRC,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,EPCAM,SP4,IGF2BP3,FKTN,PPP2R1A,ZNF462,PHIP,HMGN3,NFYC,MTIF2,PPP4R3B,NFE2L3,PNPT1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,ANKRD17,JAZF1,CREB5,MYCL,CXCL8,XPO1,MTURN,NOD1,ORC3,AKIRIN2,SRSF10,CASP8AP2,BACH2,ZNF692,PELI1,AKIRIN1,MTF1,PLEK,ZNF618,SNIP1,ANXA4,PCBP1,NR1H2,AKNA,ZNF350,ITGB1BP1,FOXP2,GRHL1,MED25,KLF11,MET,IL4I1,AGO1,POU3F3,EGFR,LANCL2,ING3,NOB	grey	VSMC_M10
GO:0071426	1.00	0.00	24	66	ribonucleoprotein complex export from nucleus	BP	1	NOL6,YTHDC1,XPO1,IWS1,CHTOP,THOC7,SDAD1,DDX25,NOP9,SETD2,ENY2,UPF1,NXF1,AKAP8L,FYTTD1,SMG5,ALKBH5,THOC2,SUPT6H,TSC1,NUP214,DDX19A,SARNP,DDX19B	grey	VSMC_M10
GO:0030100	1.00	0.00	74	174	regulation of endocytosis	BP	1	NEDD4L,LRP1,RAB21,PICK1,BTBD9,USP46,SMAP1,PPT1,RSPO1,AAK1,NR1H2,SFRP4,SDCBP,MTMR2,AP2S1,APOC1,ARRB1,NEU3,RAB5A,NCKAP1L,PIK3CB,HIP1R,WDR54,NR1H3,BMP2K,SYNJ1,F2RL1,ANO6,DNM1L,ANKRD13A,PPP3CA,EGF,ANKRD13D,DGKD,CBL,RAB4A,RAB17,AP2M1,RUBCN,SH3GL3,CALY,RUFY2,ABL2,LRPAP1,PPP3CB,ANKFY1,RAB5C,DLG4,ANXA2,DGKQ,STX1B,SYT11,SNX12,AC138894.1,CALM1,DNM2,RIT2,SCAMP5,INSR,MIB1,AP2B1,SGIP1,C3,UNC119,GPC3,FMR1,ABCA7,MIR199A1,MIR27B,MIR27A,WNT5A,LDLRAP1,CBLL1,LRRTM2	grey	VSMC_M10
GO:0030177	1.00	0.00	50	124	positive regulation of Wnt signaling pathway	BP	1	RPS12,TNFAIP3,UBE2B,RSPO3,RNF146,CSNK1E,DAAM2,PTK7,ROR2,DLX5,WNK2,RSPO1,ATP6V1C2,EGFR,SFRP4,TRPM4,PPM1N,SCEL,ARNTL,SALL1,NKD1,PRDM15,LGR6,LRRK1,CAPRIN2,TERT,TMEM9,SULF2,DKK2,EGF,TTC21B,DISC1,GID8,FZD9,WNT3,DIXDC1,DDX3X,TBL1XR1,PPM1A,RBPJ,CSNK1G1,SMAD3,NLE1,GPC3,ATP6V0C,SKI,MIR222,SOX4,WNT5A,LBX2	grey	VSMC_M10

GO:0007548	1.00	0.00	89	206	sex differentiation	BP	1	HSD17B4,ESR1,GDF9,BAK1,SMAD5,LRRC6,H3F3C,HSD17B3,DMC1,CNTFR,FANCG,KIT,ROR2,MSH2,HOXA13,OSR1,FOXO3,SOX9,ERCC1,UTF1,DACH1,WDR48,ARRB1,ACVR2A,MKKS,SEMA3A,NCOA4,AMHR2,DHX37,ACVR1B,FOXL2,CASP3,ING2,ROBO2,ADAMTS1,NKX3-1,TESC,SALL1,BMPR1B,GAS2,SRD5A1,HYAL3,CCND1,TGFB2,LHX9,SPATA2,TFAP2C,SPO11,CBL,ASB1,TAF4,PATZ1,YBX3,VGF,WNT4,CTSV,PTPRN,STAT5B,INHA,KDM5A,BMPR1A,WDR19,SOX15,ADAM21,ADAM20,LHX1,STRA6,GATA6,MAMLD1,PKD1,SOX8,HSPA5,MSH4,LHX8,FSTL3,UBB,ARID4A,AGO4,ADGRG1,WNT5A,BASP1,BCL2L11,TBC1D20,BCL2L2,CEBPB,EREG,CBX2,LHFPL2,DNAJC19	grey	VSMC_M10
GO:0001817	1.00	0.00	231	492	regulation of cytokine production	BP	1	CD226,LRP1,TNFAIP3,HSPA1B,AGPAT1,AGER,PPARA,GPSM3,HLA-DPB1,TSPO,C6orf106,ATF4,MAPK14,MAPK13,IRF5,KIT,TNFRSF21,IL1R2,GAPDH,S1PR3,SPTBN1,IGF2BP3,REL,NOD1,AKIRIN2,PELI1,RSAD2,ANXA4,TRIM32,TLR4,IL15,ATG5,TRPM4,SPHK2,HDAC2,C5AR2,C5AR1,PANX1,PRKD2,PHB,LACC1,MYD88,PIBF1,FOXJ1,TSKU,WNT11,ARRB1,NMI,TMEM173,NAV3,NPLOC4,PLCB1,FERMT1,EIF2AK2,PRNP,LUM,MAVS,NCKAP1L,GAS6,FOXP1,IRF7,TRAF6,NR1H4,IL1A,IL37,PIK3R1,DTX4,PTPRJ,IL7,P2RX7,RASGRP1,OAS3,RIPK2,HDAC7,SERPINB1,F2RL1,F2R,RIPK1,POLR3D,CHID1,PLA2R1,MAPKBP1,NOD2,ITGB6,ADCY7,CD40,RAB7B,CD96,IFIH1,CD200,HDAC1,SLC2A10,BANK1,ICOSLG,TRPV4,PDCD4,TGFB2,ADRA2A,BTN2A2,GPAM,SULF2,POLR3C,DENND1B,TLR5,CMKLR1,MAPKAPK2,OTUD7B,SORL1,RNF26,AGT,FGR,ACE2,ARNT,NLRX1,NFATC4,TRAF3IP1,ASB1,OSM,CD28,FCER1G,HOMER2,IGF2BP2,APOD,SETD2,ADAM8,CADM1,CREB1,FZD5,SRGN,IL16,BCL6,HK1,IL12A,DDX3X,FN1,VSIR,PTPN6,SLC11A1,LAG3,MUL1,STAT3,STAT5B,POLR3A,INHA,OTUD5,SCGB1A1,FOXP3,RNF216,BMPR1A,AKAP8,CARD11,TNFRSF1B,TNFRSF8,SPON2,TBX21,PSEN1,PYDC1,SYT11,TMED10,BATF,ZBTB7B,IL6R,SMAD3,IL4R,MAP2K5,NOX5,S100A13,RPS6KA5,BTK,G3BP1,YY1,RNF128,SCAMP5,TRAF3,CD74,RIOK3,CSF1R,GATA6,PLD4,LITAF,ISL1,RNF135,SUZ12,PTGER4,C3,NOS2,TWSG1,SOCS1,TICAM1,SERPINF2,PRKCZ,TRAF2,AGPAT2,PARK7,CYBA,SLC7A5,LAMTOR5,GLMN,BCL10,MIR199A1,MIR21,MIR222,MIR125B1,MIR27B,MIR24-1,C5orf30,OAS1,DEFB124,FADD,CXCL6,BTN1A1,CD46	grey	VSMC_M10
GO:0046718	1.00	0.00	39	100	viral entry into host cell	BP	1	HSPA1B,LY6E,EGFR,EPS15,HS3ST5,KPNA3,PHB,NECTIN2,PVR,RPSA,SLC20A2,GAS6,IDE,TPCN1,VPS18,ITGB6,DAG1,ZNF639,SELPLG,GRK2,ACE2,ITGB5,NECTIN4,XPR1,PIKFYVE,SLC3A2,LDLR,CD74,NPC1,CIITA,BSG,WWP2,HAVCR1,TRIM68,DPP4,TRIM34,CD46,CLDN1,EFNB3	grey	VSMC_M10
GO:0071479	1.00	0.00	23	64	cellular response to ionizing radiation	BP	1	XRCC6,MAPK14,HSF1,WRN,ATR,RAD9B,SPIDR,ITGB6,CHEK2,MGMT,XRCC5,RHNO1,DNM2,CYBA,HSPA5,MIR21,SWI5,GADD45A,GRB2,HRAS,TMEM109,TSPYL5,GTF2H5	grey	VSMC_M10
GO:0032878	1.00	0.01	6	24	regulation of establishment or maintenance of cell polarity	BP	1	TEK,RUFY3,LLGL2,PTK2B,RAP1B,BCAS3	grey	VSMC_M10
GO:0071824	1.00	0.00	69	163	protein-DNA complex subunit organization	BP	1	SMARCC2,BAZ2A,TCF4,ESR1,BRD2,ASF1A,MYC,H3F3C,DMC1,TAF8,TRAPPC12,UBN2,SOX9,RSF1,TAF7,BRF2,ACTR6,TAF9,SMARCD1,SPTY2D1,NAP1L5,RPL23,RBBP4,GTF2E1,SART3,ARID1A,VPS72,POGZ,SETD2,CREB1,H2AFY2,TAF6,HIRA,RNF4,RAD52,TSPYL2,THRA,TAF1,NAP1L2,RAD51C,SUPT6H,RRN3,NAA60,CHD5,TAF1C,CTCF,SYCP3,TSPYL4,TAF12,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,RNF8,HIST1H4D,HIST2H2BF,CENPX,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,HEY2,TSPYL5,GTF2H5	grey	VSMC_M10
GO:0002313	1.00	0.01	4	18	mature B cell differentiation involved in immune response	BP	1	MFNG,PTK2B,CDH17,DOCK10	grey	VSMC_M10
GO:0048468	1.00	0.00	785	1587	cell development	BP	1	NME1,NEDD4L,ATP8B1,ONECUT2,HSD17B4,LRP1,SEMA6A,STAC3,TBPL1,YTHDC2,KIF5A,ADGRG6,AVIL,MAML1,ATAT1,ESR1,FRS2,RAB21,MAPK8IP2,SNW1,TIAM2,MPIG6B,RIMS2,MOV10L1,BRD1,PRKN,PACRG,QKI,AGER,PPARA,FBLN1,IL5,PARVG,SULT4A1,TSPO,GDF9,UQCRQ,ROS1,FSTL4,SYNGAP1,UBE2B,CATSPER3,WASHC5,TRIB1,SMAD5,ASAP1,L3MBTL3,OBSCN,H3F3C,GFRA3,PTK2,PTCH1,ANKS1A,FANCC,AKR1B1,ATF4,TUT7,AGTPBP1,PLXNA4,NTRK2,DMC1,PODXL,CPNE5,PICK1,SOX10,PI16,MICALL1,RAC2,SMO,ZDHHC21,DAAM2,FLNC,MYH9,RBFOX2,IFT74,CHRNA3,TEK,PRPH2,FBXO7,RORB,LMOD2,PTK7,SRF,TTBK1,ADAM22,CFAP69,FZD1,PGM5,FANCG,CDK6,SMARCA2,RFX3,KIT,ADGRF1,TNFRSF21,NCK2,FHL2,ROR2,SEMA4D,DLX5,S1PR3,ETV1,SEMA4C,TMOD1,SVBP,BRSK1,EPAS1,RDH13,RIMS1,MSH2,TMEM30A,RTN4,FPR2,YTHDC1,RUFY3,ACP4,SHANK1,HOXA2,CYB5R4,HOXA13,LPAR1,PPT1,PTBP3,AREG,BPGM,GMCL1,COL27A1,EPHA7,WHRN,PTN,ITGB1BP1,MET,TNC,YWHAZ,EGFR,HECW1,NOBOX,TRIM32,TLR4,NCDN,EPHA1,BVES,IL15,KEL,CCDC155,MYLK3,ATG5,MYCN,RTN4IP1,NRCAM,TUT4,OSR1,FOXO3,ARMC2,DLD,NTF4,FIG4,WASF1,MKX,MFSD8,DHFR,SPRY1,PLXNA1,FOXE3,HDAC2,MTMR2,TTC26,NDNF,C5AR1,PANX1,PIP4K2A,RAB10,IQSEC1,ABI1,SOX9,RSPH6A,HDAC11,TOPAZ1,ERCC1,ERCC2,SLC39A12,NECTIN2,USH1G,EIF2B3,CDNF,MLH1,GOLGA4,GLI2,MEGF8,KDM4A,UNC13D,XRCC2,MYD88,KLF5,FOXJ1,PTPRF,MYO7A,TTC21A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,SLITRK5,ALK,KLHL40,PRX,CCNB1IP1,AKT2,HOOK3,DZANK1,CPNE9,TGFBR2,OVOL2,BFSP1,IKBKB,FARP1,KIF5C,SLC4A7,BHLHE40,JAG1,SIRT2,M	grey	VSMC_M10

GO:0002376	1.00	0.00	828	1656	immune system process	BP	1	CD226,NME1,PHLPP1,LRP1,STX7,SHMT2,MAP3K5,TNFAIP3,CYP27B1,USP15,ENPP3,TRIM39,ESR1,STK3,MPIG6B,SLC12A2,HSPA1B,BRD1,NUDCD1,GRAMD4,AGER,GPSM3,HLA-DRA,HLA-DOB,PSMB8,TAP1,HLA-DMA,IL5,HLA-DPB1,TCF7,TNFRSF13C,CCDC134,BAK1,XRCC6,TRIB1,CXCL14,MYC,TOB2,SMAD5,L3MBTL3,PTK2,C6orf106,FANCC,ATF4,APOBEC3H,GTPBP1,MAPK14,PLA2G6,PIM1,MFNG,RAC2,EXOSC4,HSF1,TFEB,IRF5,KCP,CCND3,MYH9,LRRC14,ZNF16,RBFOX2,TEK,FBXO7,SRF,TTBK1,TEC,CCL27,CDK6,KIT,TNFRSF21,NCK2,IL1R2,ROR2,NFIL3,SEMA4D,GAPDH,NINJ1,PRDX1,EXOSC3,RPS14,TMEM190,IL11,SDHAF4,PRKCE,SMAP1,EPAS1,MSH2,LAIR1,CD109,RTN4,IRAK1BP1,FPR2,SKAP2,HOXA7,REL,ANKRD17,PTBP3,CXCL8,SLC46A2,MTURN,NOD1,AKIRIN2,AQP1,BACH2,PELI1,LYPD8,BPGM,CYREN,AKIRIN1,CNOT4,PXDN,PLEK,RSAD2,NR1H2,TNFSF15,PTN,ADD2,IL4I1,TRIM32,TLR4,BVES,FCGRT,IL15,ATG5,TRPM4,SLC7A11,OSTM1,FOXO3,ZBTB24,PUM2,TRAF3IP2,SPHK2,PODXL2,ZC3HAV1,HMCES,BMI1,C5AR2,C5AR1,PIP4K2A,RAB10,PRKD2,CST7,PHB,ABI1,SOX9,CYSLTR2,ERCC1,ERCC2,LCP1,CD300LF,LACC1,CLPTM1,NECTIN2,PVR,EIF2B3,OPTN,GAB2,MLH1,GLI2,DHTKD1,UNC13D,RAF1,MYD88,OXSR1,PRDX3,SLC22A13,PIBF1,FOXJ1,PAXIP1,SLC25A38,IRAK2,SEC14L1,POU4F1,IL15RA,KLF6,ACKR2,CMTM7,TGFBR2,ACVR2A,EOMES,IKBKB,JAG1,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,PURA,TCIM,IDO2,IDO1,NPLOC4,PAWR,PLCB1,PLCL2,RASGRP4,CNN2,SHLD1,C12orf29,EIF2AK2,PRNP,ASH2L,MAVS,AIMP1,FUT10,NCKAP1L,GAS6,HPX,FOXP1,MITF,ARID5A,PRKDC,IRF7,FAM19A4,SLC7A1,MFHAS1,FLT	grey	VSMC_M10
GO:0071396	1.00	0.00	195	422	cellular response to lipid	BP	1	ADNP2,NME1,FECH,TNFAIP3,CYP27B1,ESR1,CNOT2,SNW1,PPARA,RXRB,TSPO,TRIB1,PTCH1,MAPK14,KDM4C,SOX10,PIM1,SMO,HSF1,FOXH1,RBFOX2,RORB,CRY1,PTK7,DNAJA1,PRKCE,HOXA2,CXCL8,AQP1,PTN,TNC,EGFR,LANCL2,TLR4,IL15,UCP1,TEAD2,MGARP,OSR1,FOXO3,PGRMC2,CDK19,SPHK2,HDAC2,ADCY3,BMI1,PHB,SOX9,ATP1A3,MYD88,EGLN2,IRAK2,POU4F1,WNT11,TADA3,NFKBIB,MAP4K1,TAF7,RNF14,DDRGK1,FOXP1,CALCOCO1,NCOA4,TRAF6,NR1H4,RET,CYP7A1,HCK,FAM107A,IL1A,CYP7B1,IL37,DNMT3B,UFSP2,CCDC62,ZNF366,ARNTL,PLSCR4,MEF2C,SMARCD1,NUGGC,HTRA2,CNOT1,PTK2B,KMT2D,NR1H3,LCOR,RIPK2,DDX54,VDR,STC1,NKX3-1,TESC,CRY2,VPS18,ABCC2,SPP1,PAX2,ADTRP,NOD2,CD40,ADCY2,GPLD1,SRD5A1,IRS1,DNM1L,HDAC1,CPT1A,PDCD4,DAG1,ABHD2,GRAMD1B,GPER1,ATP1A2,ARID1A,FZD7,NPAS4,RXRG,WNT3,PDK3,CREB1,FIS1,ABL2,CPS1,BRINP2,FDX1,XRCC5,ESRRA,KCNK4,UPF1,GPBAR1,TNIP2,MAPK1,SGMS1,PADI2,DNAAF4,AKAP8,PARP1,TNFRSF1B,MED1,ALDH1A2,SPON2,OSBPL7,PAGR1,MAPK3,ESRRB,LDLR,PIAS2,SCNN1B,TNIP1,NCOR1,CCL5,NPC1,PPARGC1B,CCL2,YES1,LITAF,SREBF1,ISL1,RHOXF1,NOS2,TICAM1,LRP8,PARK7,ADAMTS13,RXRA,ASS1,LCN2,GFI1,BCL10,DAB2IP,MIR21,MIR125B1,RHOA,TRIM24,TRIM68,CXCL6,BGLAP,IRGM,CMPK2,IL36G,SMYD3,CLDN1,WNT5A,CRH,BCL2L11,FAM210B,INSIG2,ZNF35,YWHAH,ZFP36L2,BCL2L2,CEBPB,HAVCR2,WNT2	grey	VSMC_M10
GO:0043122	1.00	0.00	85	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	TNFAIP3,TRIM39,ESR1,PRKN,SLC35B2,GAPDH,PRKCE,LPAR1,REL,ANKRD17,NOD1,PELI1,TRIM32,TLR4,TRAF1,TRAF3IP2,SPHK2,PPM1N,OPTN,MYD88,ZFAND6,IKBKB,ZMYND11,MAVS,TRAF6,NR1H4,TMEM9B,PLK2,RIPK2,F2RL1,F2R,RIPK1,ZDHHC13,PIDD1,MAPKBP1,NOD2,CD40,OTUD7A,HDAC1,AJUBA,TIFA,ALPK1,OTUD7B,TRAF5,NLRX1,GOLT1B,TRIM52,MAP3K3,TAB3,TNIP2,PINK1,MUL1,BIRC3,LTBR,PPM1A,PIM2,CARD11,CC2D1A,TSPAN6,S100A13,PRKCB,TNIP1,TRAF3,CD74,RIOK3,LITAF,TICAM1,MIB2,PDPK1,TRAF2,IKBKG,LAMTOR5,BCL10,DAB2IP,RHOA,S100A12,TRIM68,FADD,TRIM34,CASP8,C18orf32,WNT5A,INAVA,UBE2N,LURAP1L	grey	VSMC_M10
GO:0034613	1.00	0.00	720	1451	cellular protein localization	BP	1	TIMM21,MTCH2,NEDD4L,LRP1,STX7,STAC3,AP3S1,KIF5A,MAP7,PEX7,TNFAIP3,PEX3,TBC1D30,MRNIP,TBC1D9B,PPP1R10,ESR1,RAB21,SNX31,ZDHHC14,RIMS2,EMC2,PRRT1,PRKN,PACRG,AGER,SEPT8,TSPO,GOPC,MCM9,HSPA4,TBC1D32,DERL1,SKP1,SEPT3,SYNGAP1,FAM91A1,WASHC5,LRRC6,EPB41L2,OBSCN,LEMD2,FAM53C,C6orf106,PTCH1,TSNARE1,SIL1,SYNGR1,MAPK15,SUN2,MAPK14,TOMM22,CSNK1E,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,GPAA1,SMO,ZDHHC21,TSPAN33,CNTLN,TAF8,LRRC4,PEX6,POT1,FBXO7,ABHD17B,ADAM22,XPO5,APBA1,SEPT10,PEX1,SCFD2,SLC1A1,TGFBRAP1,TBC1D8,TRAM2,BICD2,RAB23,SEC61B,STX17,SIX2,DNAJA1,PRKCE,RIMS1,MSH2,TMEM30A,DNAH11,ASB3,SPTBN1,RTN4,RUFY3,EMC10,XPO1,RRAGD,CEP68,TRAPPC12,PTN,ITGB1BP1,YWHAZ,SEC61G,EGFR,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,SLC7A11,MAPRE1,LIN7B,TULP2,AGK,BRAF,BCAP29,TRAF3IP2,TTC26,DNAJC27,NAPA,KPTN,RAB7A,AP2S1,RAB10,COPG1,KPNA3,SOX9,ARL5B,CACNB2,LCP1,SYTL2,CLASP2,DLG2,MAPRE3,DNAJC15,PLK3,STAC,OPTN,GOLGA4,RALB,IPO13,AQP11,GRIK5,ZFAND6,TAF3,PIBF1,KLF5,TBC1D4,FOXJ1,MYO7A,TTC21A,NAPB,GCKR,EMC3,SZT2,SEC62,WNT11,KPNA2,MYL12A,AKT2,PITRM1,GPD1L,HOOK3,TIMM50,SNX5,USP36,IKBKB,TBC1D16,AP3M2,KIF5C,ANK1,NPLOC4,ARL5A,UBAC2,RAB5A,LIN7A,ASPSCR1,TMCO6,IK,NUP98,SIRT7,FERMT1,HACL1,MCM8,CEP290,PRNP,ING1,BAG4,DIAPH1,MAVS,FUT10,DDRGK1,WRN,GAS6,ARFIP2,PKP3,CHAMP1,VPS16,COPZ1,ARL6IP5,MFHAS1,STX2,SRP14,NSFL1C,NCOA4,WASHC2A,TUB,KCNIP3,LYPLA1,NPHP1,NUP58,MIPEP,TM9SF4,ZDHHC20,IPO11,RILPL1,RILPL2,IMMP1L,	grey	VSMC_M10

GO:2001236	1.00	0.00	49	121	regulation of extrinsic apoptotic signaling pathway	BP	1	EYA4,TNFAIP3,STK3,HSPA1B,ZC3HC1,PHIP,TRAF1,BCL2L12,FAF1,PDIA3,DEDD2,RAF1,ZMYND11,RET,IL1A,FAIM,EYA1,IL7,FAIM2,HTRA2,MADD,RIPK1,STK4,BMPR1B,SP100,TERT,TCF7L2,GPER1,EYA3,IFI6,MCL1,AGT,STRADB,PEA15,PELI3,DDX3X,HTT,PSME3,LTBR,STX4,MAP2K5,MAPK7,TRAF2,PARK7,BCL10,MIR222,FGA,NOL3,FADD	grey	VSMC_M10
GO:0051603	1.00	0.00	305	639	proteolysis involved in cellular protein catabolic process	BP	1	VPS4B,NEDD4L,FEM1C,RMND5B,TNFAIP3,USP15,CANX,TRIM39,HSPA1B,PRKN,RNF5,PSMB8,DERL1,SKP1,UBE2B,RNF217,RNF146,TRIB1,KLHL3,PTK2,AGTPBP1,CSNK1E,FOXRED2,FBXL6,USP49,FBXO7,KLHDC3,DCAF12,USP46,LNX1,PDCL3,FBXO10,SEC61B,RNF20,RAD23B,UBE3D,ECPAS,XPO1,PELI1,CNOT4,FBXO48,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,ZYG11B,SDCBP,FAF1,BBS7,FBXL13,NUDT15,FBXL2,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,AQP11,DMAC2,UBXN4,UBE3C,SPOPL,UBE2E1,KLHL40,ARRB1,UGGT2,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,UBAC2,NHLRC3,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,KCTD6,CEBPA,IDE,ARMC8,SPSB4,RNF7,TAF9,UBE2L6,FBXO8,TRPC4AP,ARNTL,FBXW7,USP25,TRIM2,ENC1,ANAPC5,AUP1,ANAPC7,CHMP4C,CSNK2A2,CTSO,USP16,PTK2B,FAM192A,TMEM67,AMFR,RNFT2,FBXO21,MARCH7,KCNE2,ERLIN1,TTC3,PRICKLE1,MYLIP,FBXW4,TOLLIP,SIAH1,LONP2,NHLRC1,FBXL15,RNF144B,SUFU,OTUD7A,FAP,RHBDD1,RPL23,AMN1,HECW2,PSMD1,KLHL42,USP30,RNF115,RNF123,PSMB5,GET4,KLHL25,USP13,RNF114,AC013489.1,YOD1,EGF,USP19,OTUD7B,DISC1,PSME1,DTX3L,ZNRF3,CACUL1,ARIH2,USP2,RNF26,NEDD8,CBL,ATE1,UBXN11,PSMD2,RNF215,GID8,USP21,VPS37D,RNF185,RNF168,RPL11,RHBDD2,EDEM3,NFE2L2,SYVN1,FBXO33,CTSH,DERL3,KLHDC1,COP1,TMUB2,DNAJC10,RC3H1,DNAJB12,SPSB2,KLHL20,TRIM9,PSME3,UBA52,USP37,USP48,RNF4,ZSWIM8,SOCS4,TMEM129,CTSV,PINK1,ZFAND2B,ARAF,ANKZF1,DNAJB2,PSMA3,SDF2L1,TBL1XR1,CALR3,RNF167,FBXL14,DNAAF4,EPHA4,RNF216,FBXL18,DDI	grey	VSMC_M10
GO:2001026	1.00	0.01	4	18	regulation of endothelial cell chemotaxis	BP	1	MET,PRKD2,FGF18,FGF1	grey	VSMC_M10
GO:0048709	1.00	0.00	24	67	oligodendrocyte differentiation	BP	1	NTRK2,SOX10,DAAM2,TNFRSF21,PTN,HDAC2,SOX9,HDAC11,ERCC2,EIF2B3,NRG1,SOX6,NKX6-1,SOX13,TSPAN2,HDAC1,DAG1,DLX1,NSUN5,DUSP10,CNTNAP1,TNFRSF1B,SOX8,CNTN2	grey	VSMC_M10
GO:0006413	1.00	0.00	39	99	translational initiation	BP	1	EIF3E,AGO2,HABP4,ATF4,EIF3L,NCK2,MTIF2,EIF2B3,CDC123,EIF2AK2,EIF4E3,EIF2AK4,EIF4E2,PAIP2B,EIF2D,RPS17,BANK1,LTO1,KLHL25,RPS6KB2,YTHDF2,YTHDF1,UHMK1,NCBP2,EIF4EBP2,DDX3X,POLR2G,MTFMT,EIF3C,ALKBH1,LARP1,CCL5,MCTS1,FMR1,IMPACT,EIF1B,EIF1,PPP1R15A,EIF1AD	grey	VSMC_M10
GO:0051054	1.00	0.00	75	176	positive regulation of DNA metabolic process	BP	1	EYA4,MRNIP,PPP1R10,MAP3K4,UBE2B,MYC,MAPK15,HSF1,POT1,EXOSC3,STPG4,MSH2,EGFR,HMCES,PRKD2,ERCC1,ERCC2,XRCC1,MLH1,PAXIP1,WDR48,FAM168A,SHLD1,WRN,PRKDC,ERCC6,TOX,OTUD4,ATR,EYA1,SLF1,HMBOX1,PTK2B,MAPKAPK5,NBN,ABRAXAS1,SPIDR,SLF2,NPM2,CD40,POLG2,EYA3,PARP9,DTX3L,CD28,RNF168,RTEL1,MGMT,XRCC5,ZCWPW1,MAPK1,WAS,DDX11,PARP1,SHLD2,NVL,FGFR4,UIMC1,TBX21,WRAP53,MAPK3,SMCHD1,PARN,SLX4,MECP2,SPIRE2,TERF2,OOEP,TIGAR,RNF8,RGCC,UBE2N,BRCC3,MAP2K7,CBX8	grey	VSMC_M10
GO:0044257	1.00	0.00	328	685	cellular protein catabolic process	BP	1	VPS4B,NEDD4L,LRP1,FEM1C,RMND5B,TNFAIP3,USP15,CANX,TRIM39,HSPA1B,PRKN,RNF5,PSMB8,DERL1,SKP1,UBE2B,RNF217,RNF146,TRIB1,KLHL3,PTK2,AGTPBP1,CSNK1E,FOXRED2,FBXL6,USP49,FBXO7,KLHDC3,DCAF12,USP46,LNX1,RGP1,PDCL3,FBXO10,SEC61B,RNF20,RAD23B,UBE3D,ECPAS,PPT1,XPO1,PELI1,WDR91,CNOT4,FBXO48,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,VPS35,ZYG11B,SDCBP,MFSD8,FAF1,BBS7,RAB7A,FBXL13,NUDT15,FBXL2,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,AQP11,DMAC2,UBXN4,UBE3C,SPOPL,UBE2E1,KLHL40,ARRB1,SNX5,UGGT2,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,TMEM106B,UBAC2,NHLRC3,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,KCTD6,CEBPA,IDE,ARMC8,SPSB4,RNF7,TAF9,UBE2L6,FBXO8,TRPC4AP,ARNTL,FBXW7,USP25,TRIM2,ENC1,ANAPC5,HTRA2,AUP1,ANAPC7,CHMP4C,CSNK2A2,CTSO,USP16,PTK2B,FAM192A,TMEM67,AMFR,RNFT2,FBXO21,RIPK1,MARCH7,KCNE2,ERLIN1,TTC3,PRICKLE1,MYLIP,FBXW4,TOLLIP,SIAH1,LONP2,NHLRC1,FBXL15,RNF144B,SUFU,OTUD7A,FAP,RHBDD1,RPL23,AMN1,HECW2,PSMD1,KLHL42,TCIRG1,USP30,RNF115,RNF123,PSMB5,GET4,KLHL25,USP13,RNF114,AC013489.1,YOD1,EGF,USP19,OTUD7B,DISC1,CHEK2,PSME1,DTX3L,ZNRF3,CACUL1,ARIH2,USP2,RNF26,NEDD8,CBL,ATE1,UBXN11,PSMD2,RNF215,GID8,USP21,VPS37D,RNF185,RNF168,RPL11,PISD,RHBDD2,EDEM3,NFE2L2,SYVN1,FBXO33,CTSH,DERL3,KLHDC1,COP1,TMUB2,DNAJC10,RC3H1,DNAJB12,SPSB2,KLHL20,TRIM9,PSME3,UBA52,USP37,USP48,RNF4,ZSWIM8,SOCS4,TMEM129,CTSV,PINK1,ZFAND2B,ARAF,AN	grey	VSMC_M10

GO:0007169	1.00	0.00	232	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	ERBB3,LRP1,SEMA6A,AP3S1,PIP4K2C,FRS2,IGF2R,ROS1,FSTL4,MTSS1,GFRA3,PTK2,PTP4A3,ANKS1A,MAPK14,NTRK2,GKAP1,CCND3,CHRNA3,TEK,ZFAND5,KIT,NCK2,ROR2,RTN4,PHIP,ACP4,ADAMTS3,EPGN,AREG,EPHA7,TGFA,MET,GRB10,EGFR,TSPAN12,FUZ,EPHA1,GAB1,NTF4,WASF1,FGF21,BRAF,SPRY1,SESN3,RAB7A,PIP4K2A,PRKD2,PTGIR,ABI1,SOX9,GAB2,RAF1,CSRNP1,SPRY2,PLAT,ALK,AKT2,NEU3,SNX5,SIRT2,HBEGF,PDE6G,PLCB1,RASGRP4,ARHGEF7,DCN,GFRA4,KL,NRG1,PTPRA,LEPROTL1,ANKS1B,FLT1,RYK,PDGFRL,EPHB1,RET,HCK,FGFBP3,FER,IDE,PIK3CB,PIK3R1,CASP3,HIP1R,ROBO1,PLCE1,FBXW7,SORBS1,ARHGEF28,PTPRJ,VEGFC,WDR54,PTK2B,RAPGEF2,TIAM1,FGF5,NKX3-1,OPA1,ZFYVE27,CYFIP1,DSTYK,DOK2,IGF2,BDNF,PXN,MAPKAPK3,GPLD1,IRS1,NEURL1,GRB14,LCK,ADRA2A,SLC30A10,SULF2,PDCD6,RNF115,NCF1,MAPKAPK2,GIGYF2,LRIT3,EGF,UBASH3B,SORL1,C2CD5,GPER1,GFRA1,DGKD,DOK5,CASS4,IFI6,AGT,FGR,CBL,ARNT,KALRN,NFATC4,CNKSR1,REPS2,PDE6H,EPHB3,SNX6,LRIG2,APOD,ANGPTL1,PPP2R5B,EIF4EBP2,EPHB4,IL12A,SIK2,GIGYF1,WNT4,FLRT1,SHC4,ZFYVE28,GDF15,FGFR3,SOCS4,ZFAND2B,STAT3,MAPK1,STAT5B,HAP1,EPHA4,IGFBP4,SLC2A4,CHURC1,TNK1,DOK3,RBPJ,RGS14,FGFR4,DGKQ,PSEN1,FGF18,FOXO4,NGFR,LCP2,PGF,EFNA1,NDEL1,ZBTB7B,OGT,CILP,SH2B1,TNMD,RPS6KA5,PRKCB,GAREM1,INSR,CSF1R,YES1,CDK5R1,ESM1,SREBF1,GHR,VAV1,IFT20,ADAMTS12,PTPN2,SOCS1,CRK,INPP5K,PDPK1,PRKCZ,RNF126,FGF22,MVB12B,DAB2IP,MIR29A,MIR199A1,MIR21,INSRR,EFNA4,DOK4,NOG,WNT5A,CHN1,CSPG4,GRB2,SHISA2,APC,MYORG,CADM4,EFNB3,SH2B2,EREG,LEPROT,FGF1,PDGFD,FRS	grey	VSMC_M10
GO:0022008	1.00	0.00	622	1272	neurogenesis	BP	1	ADNP2,NME1,ERBB3,NEDD4L,ATP8B1,ONECUT2,TCF4,LRP1,SEMA6A,KIF5A,ADGRG6,AVIL,ATAT1,FRS2,RAB21,MAPK8IP2,SNW1,TIAM2,RIMS2,PRKN,AGER,SULT4A1,TSPO,UQCRQ,CEP85L,FSTL4,SYNGAP1,WASHC5,ASAP1,LEMD2,GFRA3,PTK2,PTCH1,ANKS1A,AGTPBP1,PLXNA4,SUN2,NTRK2,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,MICALL1,RAC2,SMO,DAAM2,RBFOX2,CHRNA3,PRPH2,FBXO7,RORB,PTK7,SRF,TTBK1,ADAM22,FZD1,CDK6,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,ROR2,SEMA4D,DLX5,ETV1,ADGRL3,SEMA4C,BEND6,SVBP,BRSK1,RDH13,RIMS1,MBOAT7,TMEM30A,RTN4,FPR2,GSDME,RUFY3,ACP4,SHANK1,HOXA2,LPAR1,PPT1,MYCL,AREG,EPHA7,AKNA,WHRN,PTN,MET,TNC,YWHAZ,EGFR,HECW1,TRIM32,TLR4,NCDN,CDK5RAP2,EPHA1,KEL,MYCN,RTN4IP1,NRCAM,FOXO3,NTF4,FIG4,WASF1,MFSD8,FAT4,DHFR,PLXNA1,HDAC2,MTMR2,NAPA,DNMT3A,NDNF,C5AR1,RAB10,IQSEC1,ABI1,SOX9,HDAC11,ERCC2,SLC39A12,ERCC3,USH1G,EIF2B3,CDNF,GOLGA4,GLI2,MEGF8,KDM4A,XRCC2,IFT172,PTPRF,MYO7A,MYCBP2,NUMBL,MNX1,POU4F1,TSKU,SZT2,SS18L2,WNT11,SLITRK5,ALK,PRX,AKT2,HOOK3,DZANK1,CPNE9,FARP1,KIF5C,SLC4A7,BHLHE40,JAG1,SIRT2,RARB,FSCN2,NAV3,SYT1,TMEM106B,LRTOMT,AP000812.5,FEZ2,RAC3,CEP290,SLC23A2,LSM1,SEMA3D,SPART,PLXNC1,SEMA3A,CHL1,UNC5D,NRG1,NCKAP1L,GAS6,ULK1,DPYSL3,ERCC6,RYK,ADRA2B,SNPH,EPHB1,PLK2,PLAG1,RET,LGI4,TOX,ZSWIM6,TTL,DNMT3B,CBFA2T2,ANKRD27,FAIM,ZNF536,PREX2,CASP3,HAND2,DCLK2,EYA1,PLS1,ROBO1,ROBO2,ARNTL,TENM3,ADGRV1,ENC1,FZD3,MEF2C,ELP3,SEMA4F,FAIM2,HTRA2,VEGFC,NCAM2,TLX2,IGSF10,CUX2,SOX6,P2RY1,KA	grey	VSMC_M10
GO:0000302	1.00	0.00	76	177	response to reactive oxygen species	BP	1	MAP3K5,TNFAIP3,BAK1,ERCC6L2,FANCC,MAPK13,HSF1,GPR37,PRDX1,CAT,AREG,AQP1,ZNF277,MET,EGFR,UCP1,FOXO3,DHFR,HDAC2,SESN3,NUDT15,PLK3,PRDX3,PAWR,PPP2CB,ERCC6,FER,CASP3,PTK2B,RIPK1,PKD2,PAX2,PXN,GLRX2,HYAL1,FBLN5,NCF1,PDE8A,APOD,NFE2L2,MAPT,PDCD10,GCH1,PINK1,ANKZF1,PTPRN,MAPK1,SCGB1A1,SOD3,KDM6B,FOS,MAPK3,MPO,BTK,MAPK7,PPARGC1B,STK26,JUN,CRK,PARK7,LCN2,NQO1,MIR21,MT-ND6,PJVK,GPR37L1,ZNF580,IMPACT,FXN,DUSP1,HBA2,TXN,APOPT1,CBX8,PPIF,PDGFD	grey	VSMC_M10
GO:0032434	1.00	0.00	49	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	TRIM39,HSPA1B,PRKN,RNF217,TRIB1,CSNK1E,RAD23B,XPO1,ZYG11B,SDCBP,BBS7,PLK3,SUMO2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,RYBP,TRIB3,PLK2,CEBPA,TAF9,PRICKLE1,RNF144B,AC013489.1,ARIH2,RPL11,NFE2L2,COP1,SOCS4,ARAF,DNAJB2,PSEN1,TAF1,OGT,KEAP1,PSMD10,FBXO22,FZR1,BCAP31,SGTA,PARK7,ZER1,GLMN,CAMLG,DDA1,STYX,MAP1A	grey	VSMC_M10

GO:0016071	1.00	0.00	278	586	mRNA metabolic process	BP	1	ZC3H10,PAN2,RNMT,CPSF6,CNOT2,CNOT6,RIDA,PABPC1,SNW1,HSPA1B,SKIV2L,SF3A3,DXO,EIF3E,PNLDC1,QKI,CSDC2,AGO2,HABP4,TNRC6B,ZC3H3,ATF4,TUT7,GTPBP1,MAPK14,PUF60,CMTR1,EXOSC4,HSF1,CPSF1,USP49,RBM28,RBFOX2,SMU1,CNOT11,EXOSC3,RNF20,TSEN34,PRPF31,TRA2A,YTHDC1,PNPT1,PTBP3,RNGTT,SRSF10,PRPF4,SNIP1,SNRNP27,LSM10,AGO1,SCAF1,TUT4,PRPF38A,PUM2,TRAF3IP2,MTPAP,FOXE3,ZC3HAV1,DHX34,C5AR1,SYMPK,IWS1,CLASRP,PCF11,FASTK,MLH1,WBP4,CLNS1A,MYD88,CELF2,KIN,TNRC6C,RBM26,CRNKL1,IK,NUP98,ZMAT2,CWC15,TRMT6,BAG4,LSM1,NUDT16,WTAP,PPP4R2,PKP3,UPF3A,PHRF1,POLR2I,PAN3,PCBP2,THOC7,TGS1,CSTF3,SREK1IP1,GPATCH1,NUDT12,SREK1,USP39,PRMT9,CLP1,TFCP2,ZCCHC8,TTC37,GCFC2,RBM39,CNOT1,AAR2,CELF1,CNOT6L,RPRD1B,SCAF4,DHX35,TENT2,RPUSD2,AP3B1,SRSF6,SCAF11,PRPF4B,FTO,BCAS2,TENT5C,TENT4B,RBM24,PDCD11,SMNDC1,RBM5,CPSF2,ADARB1,DIS3L2,AXIN2,SART3,ACIN1,MAPKAPK2,GIGYF2,HSPA8,SRSF4,TRUB1,YTHDF2,RPRD2,PCBP3,CSTF1,TRAF5,ZRSR2,ZMAT5,FASTKD1,ANGEL2,METTL8,YTHDF1,CELF3,SYF2,WBP11,NCBP2,EIF4ENIF1,DDX47,BUD13,YBX3,MFAP1,RBM7,NONO,SUPV3L1,GEMIN2,SNRPD3,PRPF39,SUGP1,SUGP2,RC3H1,DHX8,UPF1,ECD,SLC11A1,CWF19L2,ESS2,RBM10,SAMD4A,CPSF4,STAT3,POLR2G,LEO1,AP002990.1,SCGB1A1,NT5C3B,DCP1B,ZBTB1,AKAP8L,CASC3,CDK12,PRPF19,MED1,LSM8,FXR2,TARDBP,RBM25,SMG5,KHDC4,TOB1,LUC7L3,SLU7,TENT5D,COIL,NRDE2,TNRC6A,CSTF2,SFPQ,CNOT8,LARP1,PAPOLA,RPRD1A,RBM41,SLFN14,XAB2,ALKBH5,UPF3B,SREBF1,THOC2,RAVER2,SNU13,SUPT6H,RBMX2,PARN,M	grey	VSMC_M10
GO:0030879	1.00	0.00	45	114	mammary gland development	BP	1	NME1,ESR1,PTCH1,SMO,PPAT,SOSTDC1,RTN4,AREG,TGFA,SOX9,GLI2,AKT2,TGFBR2,NRG1,USF2,ROBO1,ORAI1,VDR,RREB1,NEURL1,SLC6A3,ELF3,CCND1,EGF,MGMT,WNT3,CREB1,SERPINC1,WNT4,MAPK1,STAT5B,MED1,HOXB9,ZBTB7B,UPRT,NTN1,TBX2,CSF1R,FOXF1,ATP2C2,DHODH,WNT5A,BCL2L11,CEBPB,WNT2	grey	VSMC_M10
GO:0010035	1.00	0.00	202	435	response to inorganic substance	BP	1	NEDD4L,FECH,MAP3K5,TNFAIP3,TPH2,SLC12A2,PRKN,TNFRSF11B,TSPO,BAK1,PTCH1,FANCC,AKR1B1,MAPK13,CPNE5,HSF1,GPR37,KIT,SLC1A1,SLC25A13,PRDX1,CAT,ALG2,AREG,AQP1,MTF1,ZNF277,MET,EGFR,FOXO3,APOB,BRAF,DHFR,HDAC2,TRPC3,DNMT3A,SLC26A5,ATP7B,ENTPD6,GIPR,ERCC1,DLG2,KHK,PRDX3,SCN5A,AANAT,CPNE9,SYT1,PAWR,RYR1,PRNP,PPP2CB,ERCC6,SYT9,CYB5A,IL1A,GPI,CEBPA,GSS,CASP3,RYR3,ADGRV1,MEF2C,CYP2R1,ZFAND1,HVCN1,GUCY1B1,XRCC4,PTK2B,SLC39A13,CPNE2,SEC31A,HOMER1,SPIDR,LOXL2,SLC38A2,RIPK1,TNNC1,ABCC2,PKD2,TFAP2A,PAX2,DMTN,CASQ2,ADCY7,KCNIP2,RYR2,SYT8,SLC41A1,GPLD1,A3GALT2,MTR,GLRX2,SLC6A3,PPP3CA,CCND1,TERT,TESMIN,SLC30A10,FBLN5,PEF1,TCIRG1,PDCD6,NCF1,FABP4,ADNP,AMELX,RTF2,NFATC4,CARF,CLIC4,PDE8A,BACE1,DTYMK,D2HGDH,CDKN1B,NFE2L2,CREB1,RASA4,MAPT,SORD,SLC30A4,FIS1,CPS1,TTN,RASGRP2,PDCD10,ANXA7,GCH1,PINK1,MMP3,ABCB6,ANKZF1,KCNA1,ADCY10,MAPK1,KCNMA1,DDX11,ATP13A2,SCGB1A1,DLG4,PARP1,SYT7,DDI2,GPHN,MIEN1,SOD3,KDM6B,SYT11,PKLR,FOS,MAPK3,CACNA1G,MPO,CALM1,S100A8,DNM2,NPC1,MAPK7,SLFN14,SLC25A23,LONP1,STK26,JUN,ABAT,FMR1,CRK,TRAF2,CACNA1H,PARK7,BSG,ADAMTS13,CPNE7,ASS1,LCN2,HSPA5,NQO1,MIR21,MT-ND6,MT-CYB,FGA,FSTL3,KCNK3,MT1X,GPR37L1,CASP8,CA2,BGLAP,ZNF580,IMPACT,CLDN1,WNT5A,TIGAR,FXN,DUSP1,HBA2,TXN,PTGES,CBX8,PPIF,KCNMB4,PDGFD	grey	VSMC_M10
GO:0070198	1.00	0.00	8	29	protein localization to chromosome, telomeric region	BP	1	POT1,ATR,TERT,XRCC5,GNL3L,WRAP53,TERF2,TINF2	grey	VSMC_M10
GO:0006516	1.00	0.01	5	21	glycoprotein catabolic process	BP	1	FBXO17,EDEM3,FBXO2,ADAMTS12,NEU2	grey	VSMC_M10
GO:0009100	1.00	0.00	134	299	glycoprotein metabolic process	BP	1	B4GALT7,RXYLT1,GFPT2,ALG12,RNF5,PMM1,AGO2,LARGE1,ST6GAL2,SRD5A3,C1GALT1,CHST10,ALG2,ERP44,FKTN,IL15,HS3ST5,NDNF,ALG11,POMGNT1,B4GALT2,CHPF2,AQP11,GALNT11,ST6GALNAC2,MGAT5B,CSGALNACT1,UGGT2,FBXO17,HBEGF,PAWR,PLCB1,TMTC4,GALNT15,DCN,FUT10,GXYLT2,EOGT,POFUT1,ST8SIA4,B3GNT4,AGA,MOGS,RPN2,AMFR,ST3GAL6,GALNT5,GCNT2,GANC,BMPR1B,ALG10,HYAL1,SLC2A10,SULF2,TRIP11,POGLUT1,TCF7L2,DAD1,ST8SIA2,B3GALT1,B3GNT5,GALNT2,DPAGT1,ALG3,MAN1C1,RAB1B,MGAT1,RNF185,GAL3ST3,XXYLT1,EDEM3,TET1,PLOD3,SOAT1,SYVN1,DERL3,ALG9,MGAT2,B3GALNT1,KDELC2,CHST3,SPOCK2,GAL3ST4,CHST7,DDOST,AC022400.6,GALNT8,CHST12,GALNT16,FBXO2,IDUA,PSEN1,KRTCAP2,OGT,POMT2,GLCE,ST8SIA5,COG7,GALNT1,TNIP1,MPI,NPC1,ALG6,ADAMTS12,HS6ST2,PMM2,ALG1,B3GALT6,ABCA7,PARK7,ABO,ADAMTS13,GBGT1,FOXL1,ST6GALNAC4,ST3GAL2,ST6GALNAC5,FUT4,ENTPD5,DHDDS,TMEM258,POFUT2,ACER2,HS6ST3,IL33,POMK,CHSY3,POMGNT2,NEU2,B4GALT3,ISPD,SLC35C1,HS2ST1,ST8SIA6	grey	VSMC_M10
GO:0051701	1.00	0.00	62	150	biological process involved in interaction with host	BP	1	VPS4B,FUCA2,HSPA1B,LY6E,CHMP2A,CXCL8,EGFR,TRIM32,ATG5,EPS15,HS3ST5,RAB7A,KPNA3,PHB,NECTIN2,PVR,RPSA,SLC20A2,GAS6,ULK1,THOC7,IDE,CHMP2B,CHMP4C,TPCN1,ANO6,VPS18,ITGB6,DAG1,ZNF639,SELPLG,GRK2,PC,CBL,ACE2,ITGB5,NECTIN4,XPR1,PIKFYVE,SLC3A2,DDB1,LDLR,TNIP1,CD74,INSR,NPC1,THOC2,CIITA,BSG,RXRA,WWP2,VPS4A,HAVCR1,TRIM68,DPP4,TRIM34,CD46,IRGM,CLDN1,SERPINB9,ZNF502,EFNB3	grey	VSMC_M10

GO:1903320	1.00	0.00	92	211	regulation of protein modification by small protein conjugation or removal	BP	1	TNFAIP3,HSPA1B,PRKN,TSPO,DERL1,SKP1,CRY1,SVBP,DNAJA1,RNF20,PRKCE,EPAS1,PELI1,ATG5,BMI1,PAXIP1,WDR48,MYCBP2,SPOPL,SPRY2,KLHL40,ARRB1,NMI,SIRT7,USP44,SH3RF2,TRAF6,TRIM44,TRIB3,FAM107A,OTUD4,SPSB4,FBXW7,RIPK2,MARCH7,PRICKLE1,NOD2,PRMT3,TOLLIP,NHLRC1,RPL23,PEF1,PDCD6,PIAS3,SART3,SPRTN,DTX3L,ARNT,PER2,HDAC4,RPL11,SENP2,IVNS1ABP,FBXO33,DDX3X,PINK1,MUL1,BIRC3,DNAJB2,PHF23,GPS2,GNL3L,FBXO2,RNF111,PSEN1,TAF1,OGT,OTUB2,DCUN1D3,TNIP1,PSMD10,TICAM1,PIAS4,FZR1,PARK7,GLMN,HSPA5,BCL10,UBB,SOX4,BAG2,RWDD3,INAVA,CAMLG,RASSF5,UBE2N,PTTG1IP,CENPX,PRR7,UBE2D1,TSPYL5,RASD2	grey	VSMC_M10
GO:0007584	1.00	0.00	56	137	response to nutrient	BP	1	CYP27B1,SNW1,TNFRSF11B,TSPO,PIM1,HSF1,SRF,ABCG5,CAT,ABCG8,PTN,TNC,EGFR,IL15,DNMT3A,GIPR,ERCC1,TGFBR2,GAS6,NR1H4,USF2,DNMT3B,AHCY,VDR,STC1,SPP1,NOD2,CD40,CCND1,DAD1,AMELX,GNPAT,USF1,HMGCL,MGMT,SLC16A1,POR,SERPINC1,BCHE,ALPL,MED1,ALDH1A2,PKLR,OGT,OXCT1,ASS1,AGL,NQO1,MIR125B1,MT-CYB,SETDB1,TRIM24,SLC6A19,BGLAP,PEMT,LRAT	grey	VSMC_M10
GO:0043516	1.00	0.00	8	29	regulation of DNA damage response, signal transduction by p53 class mediator	BP	1	ATR,MARCH7,PLA2R1,DYRK3,SNAI1,PSMD10,CD74,PTTG1IP	grey	VSMC_M10
GO:0001816	1.00	0.00	236	504	cytokine production	BP	1	NFATC1,CD226,LRP1,TNFAIP3,HSPA1B,AGPAT1,AGER,PPARA,GPSM3,HLA-DPB1,TSPO,C6orf106,ATF4,MAPK14,MAPK13,IRF5,KIT,TNFRSF21,IL1R2,GAPDH,S1PR3,SPTBN1,IGF2BP3,ADAMTS3,REL,NOD1,AKIRIN2,PELI1,RSAD2,ANXA4,TRIM32,TLR4,IL15,ATG5,TRPM4,SPHK2,HDAC2,C5AR2,C5AR1,PANX1,PRKD2,PHB,LACC1,MYD88,PIBF1,FOXJ1,TSKU,WNT11,ARRB1,NMI,TMEM173,NAV3,NPLOC4,PLCB1,FERMT1,EIF2AK2,PRNP,LUM,MAVS,NCKAP1L,GAS6,FOXP1,IRF7,TRAF6,NR1H4,IL1A,IL37,PIK3R1,DTX4,PTPRJ,IL7,P2RX7,RASGRP1,OAS3,RIPK2,HDAC7,SERPINB1,F2RL1,F2R,RIPK1,POLR3D,CHID1,PLA2R1,MAPKBP1,NOD2,ITGB6,ADCY7,CD40,RAB7B,CD96,IFIH1,CD200,HDAC1,SLC2A10,BANK1,ICOSLG,TRPV4,PDCD4,TGFB2,ADRA2A,BTN2A2,GPAM,SULF2,POLR3C,DENND1B,TLR5,CMKLR1,MAPKAPK2,OTUD7B,SORL1,RNF26,AGT,FGR,ACE2,ARNT,NLRX1,NFATC4,TRAF3IP1,ASB1,OSM,CD28,FCER1G,HOMER2,IGF2BP2,APOD,SETD2,ADAM8,CADM1,CREB1,FZD5,SRGN,IL16,BCL6,HK1,IL12A,DDX3X,FN1,VSIR,PTPN6,SLC11A1,LAG3,MUL1,STAT3,STAT5B,POLR3A,INHA,OTUD5,SCGB1A1,FOXP3,RNF216,BMPR1A,AKAP8,CARD11,TNFRSF1B,TNFRSF8,SPON2,TBX21,PSEN1,PYDC1,SYT11,TMED10,BATF,ZBTB7B,IL6R,SMAD3,IL4R,MAP2K5,NOX5,S100A13,RPS6KA5,BTK,G3BP1,YY1,RNF128,SCAMP5,TRAF3,CD74,RIOK3,CSF1R,GATA6,PLD4,LITAF,ISL1,RNF135,SUZ12,PTGER4,C3,NOS2,TWSG1,SOCS1,TICAM1,SERPINF2,PRKCZ,TRAF2,AGPAT2,PARK7,CYBA,SLC7A5,LAMTOR5,GLMN,BCL10,NFATC3,MIR199A1,MIR21,MIR222,MIR125B1,MIR27B,MIR24-1,C5orf30,OAS1,ADGRG1,DEFB124,FADD,CXCL6,BTN	grey	VSMC_M10
GO:0010611	1.00	0.00	17	51	regulation of cardiac muscle hypertrophy	BP	1	PPARA,PI16,TRPC3,HAND2,JARID2,PDE9A,PPP3CA,AGT,SLC9A1,PARP1,TNFRSF1B,SMAD3,YY1,MIR199A1,MIR21,MIR25,RGS4	grey	VSMC_M10
GO:0065004	1.00	0.00	54	132	protein-DNA complex assembly	BP	1	BAZ2A,TCF4,ESR1,BRD2,ASF1A,H3F3C,DMC1,TRAPPC12,UBN2,SOX9,RSF1,TAF7,BRF2,TAF9,SPTY2D1,NAP1L5,RBBP4,SART3,POGZ,CREB1,H2AFY2,TAF6,HIRA,RNF4,RAD52,TSPYL2,THRA,TAF1,NAP1L2,RAD51C,RRN3,NAA60,TAF1C,TSPYL4,TAF12,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,HIST1H4D,HIST2H2BF,CENPX,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,HEY2,TSPYL5,GTF2H5	grey	VSMC_M10
GO:2000058	1.00	0.00	59	143	regulation of ubiquitin-dependent protein catabolic process	BP	1	TRIM39,HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,PDCL3,RAD23B,XPO1,ZYG11B,SDCBP,BBS7,PLK3,SUMO2,KLHL40,SIRT2,RNF14,DDRGK1,SH3RF2,RYBP,TRIB3,PLK2,CEBPA,TAF9,FBXW7,CSNK2A2,PTK2B,PRICKLE1,RNF144B,SUFU,RPL23,AC013489.1,EGF,DISC1,ARIH2,RPL11,NFE2L2,COP1,SOCS4,ARAF,DNAJB2,PSEN1,TAF1,OGT,KEAP1,PSMD10,FBXO22,FZR1,BCAP31,SGTA,PARK7,ZER1,GLMN,CAMLG,DDA1,STYX,MAP1A	grey	VSMC_M10
GO:0051321	1.00	0.00	82	192	meiotic cell cycle	BP	1	YTHDC2,FBXO43,TUBGCP6,MOV10L1,UBE2B,WASHC5,MAPK15,SUN2,DMC1,MYH9,KLHDC3,ZNF318,FOXJ3,CCDC155,TOPAZ1,ERCC1,MLH1,XRCC2,CCNB1IP1,SIRT2,PLCB1,SIRT7,TEX15,MOS,ING2,M1AP,NBN,RAD54B,EXD1,TUBGCP5,SYCP1,SYCP2L,NPM2,HSF2BP,PRKAR1A,CCDC36,YTHDF2,SPO11,TUBGCP4,GPR3,C11orf80,HORMAD2,PDIK1L,TDRKH,OVOL1,RBM7,TEX12,MAJIN,ZCWPW1,STAG3,WNT4,TUBG1,P3H4,MNS1,RAD51B,SEPT1,EME1,SYCE2,RAD51C,RAD51D,ERCC4,FZR1,SLX4,MEIOB,SPIRE2,MSH4,AURKC,UBB,SYCP3,RNF212B,AGO4,OOEP,FOXJ2,ZSCAN21,SYCE1L,WNT5A,DUSP1,SPDYA,BCL2L11,LIF,CENPX,EREG	grey	VSMC_M10

GO:0051241	1.00	0.00	356	743	negative regulation of multicellular organismal process	BP	1	NME1,SERPINB2,SEMA6A,TNFAIP3,FRS2,TSPAN8,STK3,ZNF706,APOM,SLC12A2,AGER,PPARA,TNFRSF11B,TSPO,FSTL4,SYNGAP1,TRIB1,MYC,TOB2,C6orf106,PTCH1,ATF4,SOX10,PI16,SMO,DAAM2,TEK,FBXO7,ALDH1A1,CRY1,SRF,CDK6,TNFRSF21,IL1R2,SEMA4D,SEMA4C,MEOX2,SOSTDC1,ABCG5,SVBP,ABCG8,RTN4,RUFY3,HOXA7,REL,ANXA4,EPHA7,NR1H2,PTN,ITGB1BP1,AGO1,EGFR,FUZ,TLR4,LPIN1,IL15,MYCN,TRPM4,OSR1,FIG4,MKX,SPRY1,WISP3,FOXE3,LAMA4,HS3ST5,MTMR2,C5AR2,SOX9,APOC1,GLI2,KDM4A,PIBF1,ACVR2B,FOXJ1,THBD,TSKU,SPRY2,PLAT,WNT11,HOOK3,ARRB1,TGFBR2,OVOL2,C1QTNF1,ISM1,SIRT2,NMI,RARB,NAV3,NPLOC4,PLCL2,FERMT1,SPRED3,PRNP,SEMA3D,DCN,SPART,SEMA3A,GFRA4,NCKAP1L,GAS6,ULK1,RYK,NR1H4,PLK2,ZC3H8,IL37,PAX8,ABHD6,PIK3CB,PIK3R1,ROBO1,ROBO2,IL17RD,ARNTL,FBXW7,MEF2C,TMEM131L,SEMA4F,P2RX7,TLX2,JAM2,GUCY1A1,ADAMTS1,SOX6,PTK2B,RAPGEF2,SFMBT1,NR1H3,OAS3,RAB11FIP5,SLIT1,DOCK5,STC1,NKX3-1,HDAC7,NKX6-1,LOXL2,TBX5,ACVR1C,SERPINB1,F2RL1,F2R,SRSF6,CRY2,SEMA3G,SPP1,CHID1,STK4,MAPKBP1,PAX2,SEMA4G,PRICKLE1,ADTRP,NOD2,JARID2,MYLIP,ADCY7,ZNF423,CD96,RNF10,FAP,KIAA0319,CD200,SLC2A10,PPP3CA,BANK1,USF3,SP100,MAP2K6,SEMA3F,PDCD4,TGFB2,BTN2A2,PTHLH,GPR137B,PIAS3,HLX,CMKLR1,TCTA,USP19,OTUD7B,UBASH3B,GRK2,SORL1,SLAMF8,KREMEN1,AGT,ATP1A2,NLRX1,CERS2,NFATC4,FZD7,TRAF3IP1,ASB1,ACTN3,KCNK2,USF1,PTPRO,RUNX3,DLX1,ZBTB46,PATZ1,HOMER2,CDKN1B,E2F2,APOD,YBX3,WNT3,KLF7,DUSP10,SRGN,BCL6,SEMA6D,BCOR,IL12A,COMT,TNR,FN1,VSIR,RC3H1,PTPN6,GPR137,SAV1	grey	VSMC_M10
GO:0035303	1.00	0.00	41	106	regulation of dephosphorylation	BP	1	PPP1R16A,NUAK1,SEMA4D,PLEK,VRK3,LPIN1,MTMR2,SYMPK,IKBKB,BAG4,NCKAP1L,MFHAS1,CHRM5,MTMR9,MEF2C,CRY2,GPLD1,SPPL3,TGFB2,PPP2R5A,MTMR3,PPP2R3C,PPP1R2C,HTT,PINK1,TIPRL,BOD1L2,SMG5,SMAD3,CALM1,PPP4R4,PPARGC1B,MTMR1,INPP5K,CAMTA1,TSC1,CNEP1R1,DUSP26,PPP1R15A,TMEM225B,ARPP19	grey	VSMC_M10
GO:0040008	1.00	0.00	242	518	regulation of growth	BP	1	ADNP2,NEDD4L,LRP1,SEMA6A,GLI1,CYP27B1,YEATS4,RAB21,STK3,HSPA1B,RIMS2,EBAG9,PRKN,PPARA,GDF9,ROS1,FSTL4,H3F3C,PTCH1,PLXNA4,MAPK14,CPNE5,PI16,PIM1,EXOSC4,SMO,CDKN2A,SRF,SMARCA2,SEMA4D,SEMA4C,RIMS1,RTN4,PPP2R1A,PNPT1,RUFY3,PPT1,EPHA7,EGFR,ING3,TRIM32,SDCBP,NRCAM,SPHK2,ARMC10,PHB,PTCH2,GOLGA4,KCTD21,MEGF8,EGLN2,WNT11,SERTAD3,CPNE9,TGFBR2,MKKS,RPTOR,HBEGF,SYT1,PLCB1,SLC23A2,ING1,DUSP6,SEMA3D,BTG1,SPART,SEMA3A,WRN,GAS6,ULK1,PRKDC,RYK,TTL,FAM107A,KCTD6,ACVR1B,ING2,CDKN2AIP,PLS1,PLCE1,IL17RB,PTPRJ,MEF2C,SEMA4F,IL7,HTRA2,NDUFS3,CELF1,TLL2,PTK2B,DPYSL2,NKX6-1,TBX5,ZFYVE27,PRDM11,FTO,SEMA3G,SPP1,STK4,CYFIP1,SEMA4G,NKD1,JARID2,IGF2,DCAF1,BDNF,KIAA0319,SLC6A3,HYAL1,CAPRIN2,SEMA3F,TGFB2,GAP43,FBLN5,GPAM,IGSF11,EI24,HEPACAM,ZNF639,HLX,ADNP,DISC1,SH3BP4,AGT,CIB1,IP6K2,SLC9A1,SFN,BNIPL,RPS6KA1,OSM,ACTN3,KCNK2,MRGBP,CDKL5,ING5,CSPG5,CDKN1B,YBX3,WNT3,CREB1,DUSP10,MAPT,SUPV3L1,BCL6,SEMA6D,DDX3X,TNR,RASGRP2,FN1,SAV1,DDX49,ING4,MYOZ1,GDF15,FGFR3,SOCS4,MUL1,STAT3,DNAJB2,CD38,MAPK1,STAT5B,CXCL16,IGFBP4,BMPR1A,TSPYL2,RBPJ,ARHGEF11,SOCS7,SOX15,SEMA4A,TAOK2,TRIM46,NDEL1,WWC1,RAB11A,TAF9B,SMAD3,NTN1,MAP2K5,S100A8,DNM2,BDKRB1,TBX2,DCUN1D3,YY1,PSMD10,SIN3A,TRPV2,INSR,GATA6,CDK5R1,RAI1,MCTS1,EPB41L3,GHR,TMEM97,ENOX2,GPC3,SOCS1,NUBP1,ATAD3A,L1CAM,ARHGAP4,GAMT,PLXNA3,SLC25A33,PSRC1,CYBA,NAIF1,BARHL2,DAB2IP,MIR199A1,MIR222,MIR25,RHOA,SERTAD2,MT1X,AC	grey	VSMC_M10
GO:0048701	1.00	0.00	12	40	embryonic cranial skeleton morphogenesis	BP	1	SIX2,HOXA2,TGFBR2,TFAP2A,SETD2,TULP3,WDR19,SMAD3,LHX1,ALX3,SIX1,SLC39A3	grey	VSMC_M10
GO:1901565	1.00	0.00	524	1069	organonitrogen compound catabolic process	BP	1	VPS4B,NEDD4L,GLS2,LRP1,SHMT2,LVRN,FEM1C,ALDH8A1,RMND5B,PDE7B,TNFAIP3,AGAP2,USP15,CANX,TRIM39,RIDA,ALDH7A1,ABHD16A,HSPA1B,DPYS,PRKN,RNF5,PDE10A,PSMB8,DERL1,SKP1,UBE2B,RNF217,RNF146,TRIB1,KLHL3,PTK2,AGTPBP1,APOBEC3H,CSNK1E,PLA2G6,FOXRED2,FBXL6,USP49,GPT,CARNMT1,FBXO7,KLHDC3,GDA,ABHD17B,CEMIP2,GNPDA2,DCAF12,USP46,ENPP4,LNX1,PPAT,RGP1,PDCL3,HMGCLL1,FBXO10,SEC61B,RNF20,CHAC2,RAD23B,UBE3D,ECPAS,NT5E,PPT1,XPO1,PELI1,WDR91,CNOT4,FBXO48,IL4I1,EGFR,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,VPS35,ZYG11B,SDCBP,SMPD2,MFSD8,DDO,APOB,BCAT2,FAF1,BBS7,RAB7A,FBXL13,GAD2,PHB,SOX9,CDADC1,NUDT15,APOC1,FBXL2,GLB1,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,MBD4,AQP11,DMAC2,TIMP4,EGLN2,MYCBP2,UBXN4,UBE3C,HNMT,SPOPL,ACER3,UBE2E1,KLHL40,ARRB1,NEU3,SNX5,UGGT2,USP36,FBXO17,SIRT2,DNAJC18,IDO2,IDO1,NPLOC4,TMEM106B,LRTOMT,AP000812.5,UBAC2,GGACT,NHLRC3,NUDT16,RNF14,RNF122,NRG1,USP44,AMDHD1,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,LYPLA1,CSAD,ASAH1,ERCC8,KCTD6,CEBPA,THNSL2,IDE,NUDT12,AHCY,ARMC8,AMPD3,SPSB4,RNF7,TAF9,ERAP1,UBE2L6,FBXO8,MCCC2,TRPC4AP,SH3D19,ARNTL,FBXW7,USP25,TRIM2,ENC1,CHDH,ANAPC5,HTRA2,AUP1,ANAPC7,CHMP4C,CSNK2A2,CTSO,USP16,PTK2B,FAM192A,SDSL,IVD,TMEM67,ENTPD4,AMFR,HOGA1,RNFT2,FBXO21,RIPK1,FITM2,MARCH7,HIBCH,GLS,ABCC2,KCNE2,CPN1,ERLIN1,NUDT18,ACAD8,TTC3,PRICKLE1,NKD1,MYLIP,FBXW4,TOLLIP,SIAH1,LONP2,MTRR,NHLRC1,FBXL15,RNF14	grey	VSMC_M10
GO:0060055	1.00	0.00	6	24	angiogenesis involved in wound healing	BP	1	TNFAIP3,SLC12A2,SRF,NDNF,DAG1,MCAM	grey	VSMC_M10
GO:0010921	1.00	0.00	24	68	regulation of phosphatase activity	BP	1	NUAK1,SEMA4D,PLEK,VRK3,LPIN1,IKBKB,BAG4,NCKAP1L,MTMR9,MEF2C,CRY2,GPLD1,TGFB2,PPP1R2C,HTT,TIPRL,BOD1L2,SMAD3,CALM1,PPP4R4,PPARGC1B,TSC1,PPP1R15A,TMEM225B	grey	VSMC_M10
GO:0014003	1.00	0.00	7	27	oligodendrocyte development	BP	1	SOX10,HDAC11,ERCC2,EIF2B3,NSUN5,CNTNAP1,CNTN2	grey	VSMC_M10

GO:0032784	1.00	0.00	16	49	regulation of DNA-templated transcription, elongation	BP	1	TSFM,POU4F1,ZMYND11,ERCC6,EAPP,LDB1,RNF168,ELL,NELFA,LEO1,CDK12,KAT7,SUPT6H,RF00100,HTATSF1,RNF8	grey	VSMC_M10
GO:0045935	1.00	0.00	736	1489	positive regulation of nucleobase-containing compound metabolic process	BP	1	NFATC1,ZNF407,SMARCC2,PAN2,ONECUT2,TCF4,EYA4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,MRNIP,PPP1R10,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ARID1B,DXO,ZBED4,PNLDC1,MAP3K4,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,UBE2B,XRCC6,NCOA7,PITX1,MYC,SMAD5,AGO2,PRXL2C,HABP4,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,GTPBP1,MAPK14,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,GUCA1B,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,EXOSC3,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,STPG4,EPCAM,MSH2,ZNF462,TRA2A,PHIP,HMGN3,NFYC,PNPT1,SLC4A4,HOXA2,HOXA7,HOXA13,REL,CREB5,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,TEAD2,SETD7,MYCN,ELF2,TUT4,OSR1,FOXO3,ZXDC,MAMSTR,ATAD2B,KDM7A,ZNF438,HDAC2,PHF10,MAML2,ZC3HAV1,MLLT10,HMCES,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,ERCC2,MAPRE3,UTF1,SUMO2,XRCC1,MLH1,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,WDR48,CSRNP1,METTL23,POU4F1,TNRC6C,SS18L2,WNT11,TADA3,SERTAD3,KLF6,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,FAM168A,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,SHLD1,CEP290,NSD3,ING1,LSM1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,WRN,RYBP,MITF,RBPMS,MTA3,PRKDC,IRF7,ERCC6,H	grey	VSMC_M10
GO:2001251	1.00	0.00	28	77	negative regulation of chromosome organization	BP	1	ZNF207,H3F3C,POT1,CDK5RAP2,ERCC1,XRCC1,DYNC1LI1,ANAPC15,IK,USP44,NBN,TENT4B,STN1,RTEL1,PARP1,GNL3L,CTC1,PIF1,LCMT1,ERCC4,PSMG2,SLX4,NAA10,TERF2,TINF2,TEN1,DUSP1,APC	grey	VSMC_M10
GO:0044786	1.00	0.00	12	40	cell cycle DNA replication	BP	1	DACH1,WRN,NUGGC,GINS3,DONSON,RTF2,RTEL1,BCL6,DBF4B,UPF1,TIPIN,TERF2	grey	VSMC_M10
GO:0007064	1.00	0.00	5	22	mitotic sister chromatid cohesion	BP	1	SLF1,SLF2,POGZ,MAU2,NAA10	grey	VSMC_M10
GO:0048608	1.00	0.00	148	330	reproductive structure development	BP	1	HSD17B4,GLI1,CYP27B1,ESR1,FRS2,STK3,MAP3K4,GDF9,CCDC134,BAK1,RSPO3,LRRC6,H3F3C,PTK2,HSD17B3,PTCH1,MAPK14,DMC1,MDFI,TFEB,FANCG,KIT,ROR2,EPAS1,MSH2,HOXA13,PTN,TNC,GJB5,OSR1,FOXO3,SOX9,ERCC1,UTF1,GLI2,PRDX3,WDR48,ARRB1,OVOL2,ACVR2A,EOMES,MKKS,SPINT2,DCN,SEMA3A,NCOA4,DHX37,PLAG1,CYP7B1,CEBPA,FOXL2,CASP3,ING2,ROBO2,ADAMTS1,MME,VDR,STC1,NKX3-1,TESC,SPINT1,SPP1,PKD2,STK4,SALL1,IGF2,BMPR1B,GAS2,SRD5A1,HYAL3,CCND1,TGFB2,LHX9,SPATA2,SNAI1,TFAP2C,SPO11,CBL,ARNT,VASH2,ASB1,TAF4,HTRA1,DEDD,PATZ1,SP3,CDKN1B,DLG1,SETD2,YBX3,FZD5,VGF,MEN1,PTPN6,WNT4,CTSV,PTPRN,MAPK1,STAT5B,INHA,KDM5A,WDR19,RBPJ,MED1,SOX15,ADAM21,ADAM20,DLX3,MAPK3,VASH1,CITED1,ALKBH1,MAP2K1,EPOR,LHX1,STRA6,GATA6,C3,MAMLD1,PKD1,SOX8,BSG,WDR77,HSPA5,MSH4,LHX8,FSTL3,UBB,KRT19,ARID4A,AGO4,ADGRG1,SERPINB5,CASP8,NOG,WNT5A,BASP1,TCF23,GRB2,BCL2L11,TBC1D20,LIF,BCL2L2,CEBPB,EREG,HEY2,WNT2,DNAJC19	grey	VSMC_M10
GO:1901796	1.00	0.00	31	83	regulation of signal transduction by p53 class mediator	BP	1	PRKN,NUAK1,ARMC10,PLK3,PIP4P1,SETD9,TAF9,ATRING2,MAPKAPK5,MARCH7,PLA2R1,RPL23,MAP2K6,DYRK3,SNAI1,CHEK2,USP2,RPL11,MUC1,TAF1,TAF9B,PSMD10,CD74,CHD5,MIR21,PRMT6,UBB,TRIM24,TP53RK,PTTG1IP	grey	VSMC_M10
GO:0001945	1.00	0.00	6	25	lymph vessel development	BP	1	ACVR2B,VEGFC,PPP3CB,VASH1,PKD1,ACVRL1	grey	VSMC_M10
GO:0035307	1.00	0.00	10	35	positive regulation of protein dephosphorylation	BP	1	VRK3,SYMPK,SPPL3,PPP2R5A,PINK1,CALM1,CAMTA1,CNEP1R1,DUSP26,PPP1R15A	grey	VSMC_M10
GO:0002062	1.00	0.00	34	91	chondrocyte differentiation	BP	1	OSR2,MAPK14,SIX2,COL27A1,MBOAT2,OSR1,MKX,SOX9,GLI2,TSKU,TGFBR2,ZNF219,RARB,MEF2C,SOX6,LOXL2,BMPR1B,GPLD1,SULF2,TRIP11,PTHLH,AXIN2,AMELX,RUNX3,POR,PTH1R,FGFR3,NKX3-2,BMPR1A,FGF18,SMAD3,ADAMTS12,RFLNB,ACVRL1	grey	VSMC_M10
GO:0050000	1.00	0.00	25	70	chromosome localization	BP	1	VPS4B,UBE2B,CHMP2A,TRAPPC12,CCDC155,MLH1,PIBF1,CHAMP1,TTL,CHMP2B,CHMP4C,KATNB1,CHMP7,AC112128.1,SPO11,MAJIN,IFFO1,SEPT1,KPNB1,NDEL1,RAB11A,CHMP1A,PSRC1,VPS4A,GEM	grey	VSMC_M10
GO:0071901	1.00	0.00	35	93	negative regulation of protein serine/threonine kinase activity	BP	1	TNFAIP3,STK38,CDKN2A,FBXO7,DNAJA1,PRKAR2B,SPRY1,PRKAG2,SPRY2,CEBPA,PIK3CB,CASP3,PTPRJ,PKIA,PAQR3,DTNBP1,PDCD4,PRKAR1A,SORL1,AGT,CDKN1B,AIDA,DUSP10,HEXIM2,MEN1,DUSP19,PTPN6,RGS14,INPP5K,DAB2IP,MIR24-1,GADD45A,DUSP1,APC,LAX1	grey	VSMC_M10
GO:0051170	1.00	0.00	53	132	import into nucleus	BP	1	PPP1R10,FAM53C,MAPK14,SMO,RAB23,SIX2,BACH2,TRAF3IP2,KPNA3,IPO13,GCKR,KPNA2,TMCO6,NUP98,FERMT1,ING1,MAVS,NUP58,IPO11,PIK3R1,TNPO1,PKIA,NUP54,PRKAG1,CRY2,PRICKLE1,SUFU,CABP1,RPL23,PPP3CA,IPO9,HCLS1,AGT,BAG3,EIF4ENIF1,POM121,APOD,FAM53A,STAT3,MAPK1,MED1,KPNB1,TARDBP,PSEN1,RANBP17,TNPO2,SMAD3,EFCAB7,NUP214,NXT2,HIKESHI,PTTG1IP,ZIC1	grey	VSMC_M10

GO:0043123	1.00	0.00	63	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	PRKN,SLC35B2,GAPDH,PRKCE,LPAR1,REL,ANKRD17,NOD1,PELI1,TRIM32,TLR4,TRAF3IP2,MYD88,IKBKB,MAVS,TRAF6,TMEM9B,PLK2,RIPK2,F2RL1,F2R,RIPK1,ZDHHC13,NOD2,CD40,AJUBA,TIFA,ALPK1,TRAF5,GOLT1B,TRIM52,MAP3K3,TAB3,TNIP2,PINK1,MUL1,BIRC3,LTBR,PPM1A,PIM2,CARD11,CC2D1A,TSPAN6,S100A13,PRKCB,CD74,LITAF,TICAM1,MIB2,TRAF2,IKBKG,LAMTOR5,BCL10,RHOA,S100A12,TRIM68,FADD,TRIM34,CASP8,C18orf32,INAVA,UBE2N,LURAP1L	grey	VSMC_M10
GO:0051094	1.00	0.00	475	982	positive regulation of developmental process	BP	1	NEDD4L,TCF4,LRP1,GLI1,CYP27B1,MAML1,FRS2,RAB21,STK3,OSR2,SNW1,TIAM2,ADM2,HSPA1B,RIMS2,BRD1,PRKN,AGER,HLA-DRA,IL5,TSPO,XRCC6,TRIB1,MYC,SMAD5,AGO2,PTCH1,PLXNA4,MAPK14,NTRK2,CSNK1E,CPNE5,KDM4C,SOX10,PIM1,SMO,HSF1,CDKN2A,ZNF16,TEK,LINGO2,SRF,TTBK1,RFX3,KIT,ROR2,SEMA4D,PDCL3,NINJ1,EXOSC3,BEND6,ZNF268,NLRP5,SMAP1,RIMS1,MSH2,RTN4,RUFY3,SHANK1,EMC10,CXCL8,MTURN,AQP1,BMPER,AKIRIN1,LRRN3,PTN,IL4I1,EGFR,TRIM32,EPHA1,GAB1,IL15,SFRP4,MYLK3,DKKL1,VPS35,SDCBP,NRCAM,TRPM4,OSR1,FOXO3,APOB,MAMSTR,SPRY1,PLXNA1,HDAC2,HMCES,C5AR1,VSTM5,NAPEPLD,PRKD2,SOX9,SLC39A12,CLASP2,SLC4A2,PTCH2,MLH1,GOLGA4,GLI2,MEGF8,AAMDC,KDM4A,UNC13D,XRCC2,ACVR2B,KLF5,FOXJ1,PAXIP1,NUMBL,POU4F1,IL15RA,SS18L2,WNT11,ALK,RIN2,CPNE9,TGFBR2,OVOL2,ZNF219,ACVR2A,JAG1,SIRT2,MKKS,SYT1,PAWR,TMEM106B,PLCB1,RAC3,ALX1,SHLD1,SLC23A2,DDHD2,ARHGEF7,DCN,BTG1,PLXNC1,SEMA3A,KL,CLIC1,NRG1,NCKAP1L,GAS6,LMOD3,PRKDC,FLT1,ADRA2B,TRAF6,TCF15,DHX37,EPHB1,SOX12,PLAG1,RET,TOX,IL1A,DNMT3B,PAX8,ACVR1B,CEBPA,SMYD1,ANKRD27,FAIM,CLSTN2,ERAP1,PLS1,ROBO1,ROBO2,ARNTL,ADGRV1,FZD3,MEF2C,IL7,P2RX7,VEGFC,CELF1,CUX2,SOX6,PTK2B,RASGRP1,MME,RAPGEF2,TIAM1,RIPK2,DOCK5,SYNJ1,VDR,OPA1,NKX6-1,CDS1,RAPGEF3,LOXL2,TBX5,AP3B1,AMIGO2,ZFYVE27,AGGF1,TESC,RIPK1,ANO6,SPINT1,RREB1,ITPKA,SOX13,STK4,TFAP2A,GCNT2,HIF1AN,PAX2,CYFIP1,DMTN,ADAMTS20,ZNF335,RBM24,CD40,IGF2,BMPR1B,R	grey	VSMC_M10
GO:0009790	1.00	0.00	402	841	embryo development	BP	1	ITGA7,GLI1,FRS2,CNOT2,STK3,OSR2,FZD6,PNLDC1,BRD2,VPS52,TBC1D32,RRP7A,CCDC134,UBE2B,PITX1,RSPO3,SMAD5,PTCH1,LY6E,EXOC4,ATF4,TAB1,PICK1,SOX10,MFNG,SMO,MDFI,TFEB,TAF8,MYH9,FOXH1,ZFAND5,PTK7,SRF,APBA1,TXNRD1,KIT,C2orf49,ROR2,DLX5,SEMA4C,MEOX2,ANKS6,NLRP5,SIX2,EPAS1,STPG4,MSH2,RTN4,RAD23B,KCNQ4,YTHDC1,HOXA2,HOXA4,HOXA6,ADAMTS3,HOXA7,HOXA13,CXCL8,AKIRIN2,WHRN,FUZ,GJB5,TEAD2,MYCN,SOBP,OSR1,DLD,APOB,INTU,TPRA1,LAMA4,HDAC2,BBS7,DNMT3A,BMI1,KIAA1217,MYO3A,SETDB2,ABI1,SOX9,ERCC1,ERCC2,ERCC3,CLASP2,DLG2,USH1G,GLI2,MEGF8,PCDH8,XRCC2,IFT172,WDR48,MYO7A,LMBR1,SCEL,WDR60,SPRY2,WNT11,CCNB1IP1,TGFBR2,OVOL2,ACVR2A,EOMES,CHD8,MKKS,RARB,PLCB1,MAFG,CHTOP,SPINT2,ALX1,FREM2,CEP290,SEMA3A,PRKDC,KBTBD8,FLT1,TRAF6,TCF15,RET,POFUT1,GPI,PAX8,ACVR1B,CEBPA,CASP3,CCDC62,HAND2,EYA1,PLS1,MAB21L2,FAM208A,FZD3,MEF2C,VEGFC,CNOT1,TLX2,CELF1,MMP15,FRAS1,NBN,USH1C,DHX35,TOP1,NKX3-1,OPA1,TBX5,ACVR1C,IFT52,SPINT1,COL4A3BP,RPGRIP1L,RTF1,ZBED6,PKD2,STK4,TFAP2A,RIPPLY3,PAX2,NPM2,SALL1,PRICKLE1,NKD1,ZNF335,TENT5C,FBXW4,LDB1,RYR2,IGF2,SUFU,KLHL12,IRX2,SH3PXD2A,CDON,HDAC1,HYAL1,ELF3,ALDH1A3,SLC2A10,PGAP1,SBDS,SEMA3F,TGFB2,SULF2,POGLUT1,PEF1,SATB2,PRKAR1A,PDCD6,ITPK1,DAD1,NR5A2,DAG1,AXIN2,HLX,CFL1,SNAI1,SOX2,OTUD7B,YTHDF2,POLG2,LAMB3,SLC25A20,GBX2,ARNT,DVL3,KDF1,PLPP4,VASH2,COL7A1,FZD7,ITGB5,MYO3B,PHLDB1,LAMA5,RAI2,RPL7L1,CHRD,SYF2,DLX1,MGAT1,GRHL3,TANC2,SP3,STRC,SP9,DLG	grey	VSMC_M10
GO:0051303	1.00	0.00	24	68	establishment of chromosome localization	BP	1	VPS4B,UBE2B,CHMP2A,TRAPPC12,CCDC155,MLH1,PIBF1,CHAMP1,TTL,CHMP2B,CHMP4C,KATNB1,CHMP7,AC112128.1,SPO11,MAJIN,SEPT1,KPNB1,NDEL1,RAB11A,CHMP1A,PSRC1,VPS4A,GEM	grey	VSMC_M10
GO:0097193	1.00	0.00	106	242	intrinsic apoptotic signaling pathway	BP	1	MAP3K5,SNW1,PRKN,BAK1,ATF4,NCK2,DNAJA1,MSH2,GSDME,TRIM32,ARMC10,DDIAS,MLH1,POU4F1,FBH1,PDK1,ARL6IP5,PRKDC,ERCC6,TRIB3,PIK3R1,CASP3,TAF9,ING2,DIABLO,FBXW7,HTRA2,TMBIM6,NDUFS3,FNIP2,NBN,NKX3-1,OPA1,MARCH7,SIAH1,DNM1L,HDAC1,LCK,SCN2A,SNAI1,AEN,QRICH1,CHEK2,IFI6,MCL1,HYOU1,CIDEB,SFN,NFATC4,RTKN2,RPL11,E2F2,YBX3,NFE2L2,IVNS1ABP,NONO,FIS1,PRKRA,SYVN1,BCL2A1,PRODH,DDX3X,DNAJC10,PDCD10,PINK1,SGMS1,PARP1,TNFRSF1B,DAPK2,MUC1,ATP2A1,TAF9B,S100A8,SFPQ,CD74,MAPK7,PPP1R13B,PTPN2,PIAS4,CDIP1,BCAP31,TRAF2,PARK7,DAB2IP,MIR21,MIR27B,UBB,ZNF622,MLLT11,RPS27L,NOL3,DDIT3,BCL2L11,PPP1R15A,APOPT1,PERP,PTTG1IP,HRAS,PLAGL2,BCL2L2,TMEM109,CEBPB,PPIF,HINT1,SGPP1,PTPMT1	grey	VSMC_M10

GO:0061458	1.00	0.00	149	333	reproductive system development	BP	1	HSD17B4,GLI1,CYP27B1,ESR1,FRS2,STK3,MAP3K4,GDF9,CCDC134,BAK1,RSPO3,LRRC6,H3F3C,PTK2,HSD17B3,PTCH1,MAPK14,DMC1,MDFI,TFEB,FANCG,KIT,RORR2,EPAS1,MSH2,HOXA13,PTN,TNC,GJB5,OSR1,FOXO3,SOX9,ERCC1,UTF1,GLI2,PRDX3,WDR48,ARRB1,OVOL2,ACVR2A,EOMES,MKKS,SPINT2,DCN,SEMA3A,NCOA4,DHX37,PLAG1,CYP7B1,CEBPA,FOXL2,CASP3,ING2,ROBO2,ADAMTS1,MME,VDR,STC1,NKX3-1,TESC,SPINT1,SPP1,PKD2,STK4,SALL1,IGF2,BMPR1B,GAS2,SRD5A1,HYAL3,CCND1,TGFB2,LHX9,SPATA2,SNAI1,TFAP2C,SPO11,CBL,ARNT,VASH2,ASB1,TAF4,HTRA1,DEDD,PATZ1,SP3,CDKN1B,DLG1,SETD2,YBX3,FZD5,VGF,MEN1,PTPN6,WNT4,CTSV,PTPRN,MAPK1,STAT5B,INHA,KDM5A,WDR19,RBPJ,MED1,SOX15,ADAM21,ADAM20,DLX3,MAPK3,VASH1,CITED1,UBE2Q1,ALKBH1,MAP2K1,EPOR,LHX1,STRA6,GATA6,C3,MAMLD1,PKD1,SOX8,BSG,WDR77,HSPA5,MSH4,LHX8,FSTL3,UBB,KRT19,ARID4A,AGO4,ADGRG1,SERPINB5,CASP8,NOG,WNT5A,BASP1,TCF23,GRB2,BCL2L11,TBC1D20,LIF,BCL2L2,CEBPB,EREG,HEY2,WNT2,DNAJC19	grey	VSMC_M10
GO:0042060	1.00	0.00	147	329	wound healing	BP	1	SERPINB2,ERBB3,MAP3K5,TNFAIP3,TSPAN8,MPIG6B,SLC12A2,FZD6,PPARA,FBLN1,PTK2,MAPK14,C6orf89,MYH9,PTK7,SRF,TEC,ENPP4,TLN1,CLDN19,PRKCE,CD109,EPB41L4B,PLEK,TGFA,DGKI,TNC,EGFR,TLR4,SLC7A11,NDNF,CLASP2,RAF1,EVPL,THBD,TSKU,PLAT,MYL12A,TGFBR2,C1QTNF1,ACTG1,HBEGF,FERMT1,CNN2,DCN,FUT10,CLIC1,NRG1,GAS6,ADRA2B,IL1A,PIK3CB,MYOF,CASP3,P2RY1,DYSF,HPS5,AP3B1,F2RL1,F2R,SRSF6,ARHGAP24,ANO6,RREB1,DSP,DMTN,ADTRP,ITGB6,DTNBP1,CD40,FAP,LCK,PPP3CA,TGFB2,ADRA2A,ITPK1,DAG1,FGFR1OP2,PRSS56,AJUBA,UBASH3B,HPS4,DGKD,MCAM,FZD7,USF1,PAFAH2,FCER1G,GRHL3,DGKG,NFE2L2,MIA3,DUOX1,BLOC1S6,PLA2G4A,ITGA2B,FN1,CASK,PTPN6,SERPINC1,PDCD10,ADRA2C,FERMT3,HGFAC,SLC11A1,WNT4,COL3A1,MYOZ1,RAB3A,VCL,WAS,ARHGEF19,ACTB,SYT7,ANXA8,F12,PEAR1,ANXA2,DGKQ,SYT11,DGKE,SMAD3,SYTL4,S100A8,VAV1,ABAT,CRK,SERPINF2,P2RX1,ADAMTS13,COL5A1,VAV3,STXBP1,CARMIL2,MIR29A,RHOA,FGA,BLOC1S3,ACVRL1,NOG,CLDN1,WNT5A,HRAS,CADM4,EREG,RAP2B,FGF1	grey	VSMC_M10
GO:1901798	1.00	0.00	6	24	positive regulation of signal transduction by p53 class mediator	BP	1	ATR,PLA2R1,RPL23,RPL11,CHD5,UBB	grey	VSMC_M10
GO:0002064	1.00	0.00	71	173	epithelial cell development	BP	1	ONECUT2,HSD17B4,ESR1,FRS2,ROS1,AKR1B1,ATF4,PODXL,SMO,ZDHHC21,IFT74,CDK6,RFX3,S1PR3,TMOD1,HOXA13,WHRN,MET,SOX9,MYD88,KLF5,FOXJ1,MYO7A,BFSP1,IKBKB,SLC4A7,JAG1,RARB,LRTOMT,AP000812.5,PLCB1,SPINT2,ASXL1,RILPL1,RILPL2,FLNB,MARVELD2,PLS1,ARNTL,ARHGEF26,RAPGEF2,STC1,NKX6-1,RAPGEF3,F2RL1,ADAMTSL4,KDF1,SFN,CLIC4,STRC,SIDT2,RAP1B,PLOD3,ABCA12,VCL,NKX3-2,FOXP3,RAB25,VEZF1,TNMD,CCDC88C,BCL11B,PDPK1,SOX8,HYDIN,ARID4A,CLDN1,WNT5A,TIGAR,DNASE1L2,TBC1D20	grey	VSMC_M10
GO:0014743	1.00	0.00	17	52	regulation of muscle hypertrophy	BP	1	PPARA,PI16,TRPC3,HAND2,JARID2,PDE9A,PPP3CA,AGT,SLC9A1,PARP1,TNFRSF1B,SMAD3,YY1,MIR199A1,MIR21,MIR25,RGS4	grey	VSMC_M10
GO:0043085	1.00	0.00	421	875	positive regulation of catalytic activity	BP	1	ERBB3,MAP3K5,AGAP2,CYP27B1,TBC1D30,MRNIP,TBC1D9B,ESR1,STK3,TIAM2,GRAMD4,MAP3K4,AGER,FBLN1,ROS1,SKP1,BAK1,XRCC6,MYC,ASAP1,PTK2,TAB1,MAPK15,MAPK14,NTRK2,C6orf89,TBC1D22B,HSF1,CCND3,GUCA1B,ZNF16,CHRNA3,TEK,POT1,TTBK1,KIT,SLC1A1,ROR2,SEMA4D,TBC1D8,RGP1,SDHAF4,MSH2,FPR2,MOB1B,LPAR1,EPGN,NOD1,AREG,AKIRIN2,CASP8AP2,ETAA1,PLEK,EPHA7,NR1H2,TNFSF15,TGFA,ASAP2,ITGB1BP1,MET,VRK3,EGFR,ARHGEF5,TLR4,EPHA1,TBC1D9,CCNY,SSBP1,HSPE1,DHFR,NAPA,SLC8A2,BMI1,C5AR1,PRKD2,PHB,IQSEC1,ABI1,ABHD5,RSU1,MAPRE3,XRCC1,EPM2AIP1,RALB,PRKAG2,PIBF1,TBC1D4,FOXJ1,SPRY2,WNT11,ALK,AKT2,ARRB1,TGFBR2,TBC1D16,NEK10,RPTOR,TCIM,HBEGF,TMEM106B,RASGRP4,CHTOP,PRNP,ARHGEF7,NRG1,DDRGK1,WRN,NCKAP1L,GAS6,LARS,SIRT3,ARL6IP5,ERCC6,FLT1,RYK,ST8,ADRA2B,TRAF6,TRIB3,EPHB1,RET,ASPH,PIK3CB,FOXL2,ZFP91,HIP1R,ROBO1,PCOLCE2,DIABLO,MTMR9,TBC1D12,FBXW7,ORAI1,HMBOX1,MEF2C,HTRA2,VEGFC,XRCC4,ARHGEF26,MADD,PTK2B,RASGRP1,RAPGEF2,MAPKAPK5,PRKAG1,CCL17,NR1H3,TIAM1,SERINC5,RIPK2,NBN,SENP1,VDR,NKX3-1,RAPGEF3,NR4A2,ACVR1C,F2RL1,F2R,ARHGAP24,PIDD1,PKD2,STK4,NPM2,NOD2,TAOK3,CD40,DSTYK,FAM173B,IGF2,BMPR1B,RAP1GDS1,GPLD1,DOCK10,AZIN2,IRS1,NEURL1,CD200,RGS1,LCK,CCND1,TERT,MAP2K6,TGFB2,ADRA2A,TBCK,FAM20A,ADPRH,COX17,PDCD6,GNA13,DAG1,AJUBA,ISCU,ADAP1,DENND1B,NCF1,KRAS,EGF,PFKFB2,ADNP,ARHGAP6,TBC1D10C,POLG2,SORL1,GPER1,CASS4,PSME1,SPATC1L,DTX3L,RAB11FIP2,CACUL1,AGT,FGR,CIB1,DVL3,CIDEB,STRADB,SYAP1,TOP1MT1,CDKL5,ETFDA,CDH3,EPHB3,PHSP1	grey	VSMC_M10
GO:0001569	1.00	0.00	6	25	branching involved in blood vessel morphogenesis	BP	1	SRF,TGFBR2,STK4,GBX2,NFATC4,ENG	grey	VSMC_M10

GO:0010468	1.00	0.00	1747	3428	regulation of gene expression	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CD226,NME1,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,LRP1,SHMT2,GLI1,HBS1L,MARS,CLK4,MAP3K5,TNFAIP3,TSFM,HIVEP2,PLAGL1,MAML1,TRIM39,ZBTB2,RMND1,YEATS4,ESR1,MYRFL,CNOT2,TSPAN8,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,PHAX,ARID1B,ADM2,HSPA1B,FZD6,RIMS2,ZBTB12,SKIV2L,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,MAP3K4,PRKN,AGPAT1,QKI,AGER,PPARA,GPSM3,MED30,IL5,BRD2,HLA-DPB1,ZUP1,RXRB,TSPO,VGLL2,MRPL13,HSF2,TCF7,PHF1,BAK1,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,HABP4,H3F3C,C6orf106,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,RPAP2,CBX7,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,PUF60,CSNK1E,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,EXOSC4,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,TTBK1,ZNF318,NFX1,XPO5,APBA1,CDK14,FZD1,MTERF1,NFXL1,NFKBIE,CDK6,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,TNFRSF21,NCK2,FHL2,TGFBRAP1,PLGRKT,IL1R2,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,S1PR3,PDCL3,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,TDRD7,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,MACC1,LRPPRC,CLDN19,SIX2,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,EPAS1,RIMS1,EPCAM,MSH2,SP4,SPTBN1,IGF2BP3,PPP2R1A,ZNF462,TRA2A,PHIP,HMGN3,YTHDC1,NFYC,MTIF2,EPB41L4B,NFE2L3,PNPT1,ACP4,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,PUS10,ZNF483,JAZF1,CR	grey	VSMC_M10
GO:1903827	1.00	0.00	209	454	regulation of cellular protein localization	BP	1	NEDD4L,LRP1,STX7,STAC3,PRKN,GOPC,EPB41L2,C6orf106,MAPK14,CSNK1E,RAC2,SMO,ABHD17B,SLC1A1,RAB23,DNAJA1,PRKCE,TMEM30A,SPTBN1,RTN4,RUFY3,XPO1,TRAPPC12,PTN,ITGB1BP1,EGFR,TCAF2,SLC7A11,DNAJC27,LCP1,PLK3,STAC,RALB,AKT2,GPD1L,USP36,UBAC2,SIRT7,FERMT1,CEP290,PRNP,BAG4,MAVS,DDRGK1,GAS6,MFHAS1,NSFL1C,LYPLA1,NUP58,TM9SF4,POLR1A,PIK3R1,DCLK2,PLS1,CEP250,CCDC66,FBXW7,SORBS1,PKIA,HTRA2,ZFAND1,CSNK2A2,NUP54,KCNJ11,RAB11FIP5,SPIDR,RAPGEF3,DMTN,GBF1,NHLRC1,BDNF,SUFU,CABP1,PPFIA1,ANKRD13A,SP100,TERT,TCF7L2,GPR137B,DAG1,TTBK2,SSH1,KCNB1,YOD1,EGF,HCLS1,OTUD7B,EPB41,HPS4,SORL1,C2CD5,GPER1,PARP9,DTX3L,RAB11FIP2,ARIH2,CIB1,DVL3,BAG3,AP2M1,SFN,PPP2R5A,STX6,LIMK2,UHMK1,GLUL,FZD9,DLG1,LRIG2,APOD,SETD2,LRRC15,CTDSPL2,FZD5,MAPT,FIS1,CEMIP,NMT1,LZTFL1,DERL3,SEC16B,ZDHHC8,ABCA12,C11orf65,MEPCE,PDCD10,CNPY4,PINK1,MAPK1,CHRM1,TMEM30B,GRIPAP1,ATP13A2,CNST,ACTB,MAGED1,PARP1,IQSEC2,RSC1A1,NVL,WNK3,GNL3L,STAC2,NPEPPS,WRAP53,TARDBP,STX4,PSEN1,ITGAM,SYT11,NGFR,KAT7,ITGA3,TRIM46,NDEL1,AC138894.1,HAX1,RAB11A,SMAD3,STX8,BCAS3,ARHGAP44,SIN3A,AP2B1,MIEF2,CDK5R1,SREBF1,EFCAB7,GPC3,INPP5K,BCAP31,TAX1BP3,PDPK1,PRKCZ,RER1,OAZ1,ABHD17A,ARHGEF16,SAPCD2,ABCA7,PARK7,GPSM2,LAMTOR5,TLDC1,SH3GLB1,VPS4A,RIPOR1,MICALL2,BNIP3L,ABHD17C,CD247,WNT5A,LDLRAP1,TMEM35A,RASSF5,TXN,APC,LIF,HRAS,MIEF1,RHOU,LEPROT,PARD6A,UBE2G2,MRAP2,MESD,MAP1A,DERL2,ZIC1	grey	VSMC_M10
GO:0070727	1.00	0.00	722	1462	cellular macromolecule localization	BP	1	TIMM21,MTCH2,NEDD4L,LRP1,STX7,STAC3,AP3S1,KIF5A,MAP7,PEX7,TNFAIP3,PEX3,TBC1D30,MRNIP,TBC1D9B,PPP1R10,ESR1,RAB21,SNX31,ZDHHC14,RIMS2,EMC2,PRRT1,PRKN,PACRG,AGER,SEPT8,TSPO,GOPC,MCM9,HSPA4,TBC1D32,DERL1,SKP1,SEPT3,SYNGAP1,FAM91A1,WASHC5,LRRC6,EPB41L2,OBSCN,LEMD2,FAM53C,C6orf106,PTCH1,TSNARE1,SIL1,SYNGR1,MAPK15,SUN2,MAPK14,TOMM22,CSNK1E,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,GPAA1,SMO,ZDHHC21,TSPAN33,CNTLN,TAF8,LRRC4,PEX6,POT1,FBXO7,ABHD17B,ADAM22,XPO5,APBA1,SEPT10,PEX1,SCFD2,SLC1A1,TGFBRAP1,TBC1D8,TRAM2,BICD2,EXOSC3,RAB23,SEC61B,STX17,SIX2,DNAJA1,PRKCE,RIMS1,MSH2,TMEM30A,DNAH11,ASB3,SPTBN1,RTN4,RUFY3,EMC10,XPO1,RRAGD,CEP68,TRAPPC12,PTN,ITGB1BP1,YWHAZ,SEC61G,EGFR,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,SLC7A11,MAPRE1,LIN7B,TULP2,AGK,BRAF,BCAP29,TRAF3IP2,TTC26,DNAJC27,NAPA,KPTN,RAB7A,AP2S1,RAB10,COPG1,KPNA3,SOX9,ARL5B,CACNB2,LCP1,SYTL2,CLASP2,DLG2,MAPRE3,DNAJC15,PLK3,STAC,OPTN,GOLGA4,RALB,IPO13,AQP11,GRIK5,ZFAND6,TAF3,PIBF1,KLF5,TBC1D4,FOXJ1,MYO7A,TTC21A,NAPB,GCKR,EMC3,SZT2,SEC62,WNT11,KPNA2,MYL12A,AKT2,PITRM1,GPD1L,HOOK3,TIMM50,SNX5,USP36,IKBKB,TBC1D16,AP3M2,KIF5C,ANK1,NPLOC4,ARL5A,UBAC2,RAB5A,LIN7A,ASPSCR1,TMCO6,IK,NUP98,SIRT7,FERMT1,HACL1,MCM8,CEP290,PRNP,ING1,BAG4,DIAPH1,MAVS,FUT10,DDRGK1,WRN,GAS6,ARFIP2,PKP3,CHAMP1,VPS16,COPZ1,ARL6IP5,MFHAS1,STX2,SRP14,NSFL1C,NCOA4,WASHC2A,TUB,KCNIP3,LYPLA1,NPHP1,NUP58,MIPEP,TM9SF4,ZDHHC20,IPO11,RILPL1,RIL	grey	VSMC_M10
GO:0001101	1.00	0.00	41	107	response to acid chemical	BP	1	PNPLA3,AKR1B1,NTRK2,HSF1,RRAGD,PTN,FGF21,SESN3,DNMT3A,RPTOR,CRLS1,LARS,SLC38A9,GSS,CASP3,TMBIM6,OPA1,PKD2,NEURL1,COL16A1,SH3BP4,CDKN1B,CREB1,CPS1,COL5A2,RRAGB,SOCS1,AMIGO1,CYBA,LAMTOR5,ASS1,TLDC1,DHODH,NQO1,RHOA,PEMT,LAMTOR2,SIX1,BCL2L2,CEBPB,PDGFD	grey	VSMC_M10

GO:2001020	1.00	0.00	85	200	regulation of response to DNA damage stimulus	BP	1	EYA4,MRNIP,HELB,PPP1R10,ARMT1,IER3,MYC,HSF1,POT1,CRY1,CYREN,ETAA1,EGFR,TRIM32,ERCC1,DDIAS,XRCC1,PAXIP1,WDR48,FBH1,RNF169,FAM168A,SIRT7,SHLD1,PPP4R2,TEX15,PRKDC,ERCC6,ERCC8,TAF9,ATR,ING2,EYA1,SLF1,NKX3-1,ABRAXAS1,SPIDR,WRNIP1,MARCH7,PLA2R1,SLF2,AXIN2,DYRK3,SNAI1,CHEK2,EYA3,PARP9,DTX3L,MCL1,RNF168,RTEL1,MGMT,SETD2,MAPT,ZCWPW1,WAS,DDX11,RAD52,PARP1,SHLD2,UIMC1,FXR2,WRAP53,KAT7,MUC1,TAF9B,NSMCE1,OTUB2,PSMD10,CD74,SMCHD1,ERCC4,RMI2,FMR1,PIAS4,NUDT16L1,SPIRE2,TERF2,OOEP,TIGAR,RNF8,UBE2N,PTTG1IP,BRCC3,CBX8	grey	VSMC_M10
GO:0034110	1.00	0.00	6	25	regulation of homotypic cell-cell adhesion	BP	1	C1QTNF1,DMTN,UBASH3B,CCL5,JAK1,ABAT	grey	VSMC_M10
GO:0051346	1.00	0.00	106	242	negative regulation of hydrolase activity	BP	1	SERPINB8,SERPINB2,TNFAIP8,LRP1,PI16,SEMA4D,GAPDH,TNNI3,CD109,AQP1,BCL2L12,SPHK2,SPRY1,CST7,APOC1,RAF1,PRDX3,TIMP4,UBE2O,SPRY2,ARRB1,IKBKB,MKKS,SPINT2,PRNP,BAG4,NCKAP1L,GAS6,PSMF1,GPI,NR4A1,PXK,TMBIM6,SERPINB1,SPINT1,CRY2,PLA2R1,PAX2,APLP2,TGFB2,OXA1L,FICD,SORL1,SH3BP4,IFI6,AGT,COL6A3,SFN,COL7A1,RPS6KA1,CST6,POR,RASA4,GMIP,VCPKMT,DDX3X,SPOCK2,SERPINC1,SERPINI1,BIRC3,TIPRL,ARL6IP1,KDM5A,ANXA8,ANXA2,SIMC1,BOD1L2,PAPLN,TMED10,WFIKKN2,MAP2K5,PPP4R4,BCAS3,NEIL1,CAMK2A,MAPK7,AMOT,NLE1,LEPR,C3,GPC3,PAM16,SERPINF2,PRKCZ,WFIKKN1,PARK7,GPSM1,TSC1,LAMTOR5,TERF2,DAB2IP,MIR199A1,MIR21,MIR24-1,NOL3,SERPINB5,A2M,MIR339,SERPINE3,SERPINB9,PPP1R15A,HRAS,CAAP1,PPIF,TMEM225B,RARRES1	grey	VSMC_M10
GO:0061437	1.00	0.00	6	25	renal system vasculature development	BP	1	TEK,OSR1,PKD2,IL6R,MIR125A,PDGFD	grey	VSMC_M10
GO:0061440	1.00	0.00	6	25	kidney vasculature development	BP	1	TEK,OSR1,PKD2,IL6R,MIR125A,PDGFD	grey	VSMC_M10
GO:0050684	1.00	0.00	46	118	regulation of mRNA processing	BP	1	ZC3H10,CPSF6,SNW1,QKI,ZC3H3,PUF60,HSF1,RBFOX2,SMU1,RNF20,TRA2A,YTHDC1,SRSF10,IWS1,CELF2,NUP98,WTAP,RBM39,CELF1,SRSF6,RBM24,RBM5,HSPA8,SRSF4,CELF3,NCBP2,RBM7,RBM10,LEO1,PRPF19,FXR2,RBM25,PAPOLA,RAVER2,SUPT6H,MBNL3,NSRP1,FMR1,CELF5,METTL16,CIRBP,SRRM4,NOVA1,RBM11,SRSF12,SAP18	grey	VSMC_M10
GO:0001936	1.00	0.00	43	111	regulation of endothelial cell proliferation	BP	1	TEK,PDCL3,EMC10,PRKD2,RPTOR,AIMP1,FLT1,NR4A1,ATP5F1A,MEF2C,VEGFC,AGGF1,IGF2,PDCD6,EGF,ARNT,VASH2,ITGA4,IL12A,PDCD10,STAT3,ALDH1A2,SYNJ2BP,NGFR,PGF,VASH1,TNMD,CCL2,PDPK1,CYBA,MIR29A,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,ACVRL1,ZNF580,WNT5A,RGCC,WNT2	grey	VSMC_M10
GO:0008380	1.00	0.00	162	356	RNA splicing	BP	1	ZC3H10,CLK4,PABPC1,SNW1,SF3A3,QKI,HABP4,PUF60,USP49,RBM28,RBFOX2,SMU1,TSEN34,PRPF31,PPP2R1A,TRA2A,YTHDC1,PTBP3,SRSF10,PRPF4,SNIP1,SNRNP27,LSM10,SCAF1,PRPF38A,IWS1,CLASRP,FASTK,WBP4,CLNS1A,CELF2,CRNKL1,PRX,IK,NUP98,ZMAT2,CWC15,LSM1,WTAP,PPP4R2,THOC7,TGS1,SREK1IP1,GPATCH1,SREK1,PIK3R1,USP39,CLP1,ZCCHC8,GCFC2,RBM39,TMBIM6,AAR2,CELF1,USB1,DHX35,RBM12B,SLC38A2,SRSF6,SCAF11,PRPF4B,BCAS2,RBM24,ZBTB8OS,SMNDC1,RBM5,SART3,ACIN1,HSPA8,SRSF4,RTRAF,ZRSR2,ZMAT5,PPIG,CELF3,SYF2,WBP11,NCBP2,DDX47,BUD13,MFAP1,RBM7,IVNS1ABP,NONO,GEMIN2,SNRPD3,PRPF39,SUGP1,SUGP2,DHX8,TRPT1,ECD,CWF19L2,ESS2,RBM10,AKAP8L,CASC3,CDK12,PRPF19,LSM8,CCDC130,FXR2,TARDBP,RBM25,KHDC4,LUC7L3,SLU7,COIL,NRDE2,SFPQ,CLK3,RBM41,XAB2,METTL4,RNF113B,THOC2,RAVER2,SNU13,SUPT6H,RBMX2,MBNL3,NSRP1,FMR1,AFF2,CELF5,METTL16,SRRM2,LSM7,CIRBP,LUC7L,C9orf78,TXNL4B,PRMT7,ESRP2,ZRANB2,SRSF11,RNVU1-6,RNU5E-1,RNU5B-1,SRRM4,HTATSF1,NOL3,RP9,METTL14,RNU4ATAC,RF00003,SNRPC,NOVA1,RNU2-1,RNU4-2,RBM11,SRSF12,ZCRB1,YBX1,RNU4-1,MAGOHB,SAP18,SRRM1,PDCD7,RBM38,SNRNP25,PRKRIP1	grey	VSMC_M10
GO:0007166	1.00	0.00	964	1935	cell surface receptor signaling pathway	BP	1	NFATC1,CD226,ITGA7,ERBB3,SLC39A5,ONECUT2,LRP1,RPS12,SEMA6A,EYA4,AP3S1,GLI1,PIP4K2C,TNFAIP3,ADGRG6,USP15,MAML1,FRS2,STK3,MAPK8IP2,SNW1,MPIG6B,HSPA1B,FZD6,RIMS2,IGF2R,PRKN,AGPAT1,AGER,PPARA,IL5,HLA-DPB1,GDF9,ROS1,TBC1D32,FSTL4,TCF7,TNFRSF13C,UBE2B,BAK1,MTSS1,RSPO3,RNF146,TRIB1,SMAD5,MCHR1,LEMD2,GRM4,GFRA3,PTK2,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,ZC3H3,TAB1,PLXNA4,MAPK14,NTRK2,CBY1,CSNK1E,PLA2G6,GKAP1,SOX10,ZC3HC1,MFNG,SMO,HSF1,DAAM2,MDFI,IRF5,KCP,CCND3,MYH9,FOXH1,GUCA1B,IFT74,CHRNA3,TEK,GRM8,CHRNA5,ZFAND5,PTK7,BAG1,DLK2,CDK14,FZD1,CNTFR,TEC,OCIAD1,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,TGFBRAP1,IL1R2,TLN1,TFAP2B,ROR2,SEMA4D,DLX5,S1PR3,WNK2,ADGRL3,SEMA4C,SOSTDC1,BEND6,PRKCE,RIMS1,CD109,SPTBN1,RTN4,PPP2R1A,PHIP,FPR2,ACP4,SHANK1,VRK2,ADAMTS3,HOXA13,CXCL8,EPGN,AREG,BMP8A,CRHR2,TMEM17,CASP8AP2,PELI1,BMPER,PXDN,PLEK,RSPO1,AAK1,ANXA4,EPHA7,NR1H2,TGFA,PTN,ITGB1BP1,MET,GRB10,ATP6V1C2,EGFR,TSPAN12,HECW1,FUZ,TRIM32,TLR4,EPHA1,GRIK2,IQUB,TRAF1,BCL2L12,GAB1,IL15,SFRP4,CCNY,DKKL1,VPS35,SDCBP,TRPM4,FOXO3,NTF4,WASF1,FAF1,FGF21,BRAF,INTU,TRAF3IP2,SPRY1,PLXNA1,GRIN2D,HDAC2,MAML2,MTMR2,TTC26,SESN3,BBS7,SLC8A2,RAB7A,C5AR2,C5AR1,PIP4K2A,PRKD2,PTGIR,PHB,ABI1,SOX9,GIPR,PPM1N,CD300LF,NECTIN2,PDIA3,EIF2B3,PTCH2,GAB2,LRRFIP2,KCTD21,LLGL2,GLI2,MEGF8,DEDD2,GRIK5,GALNT11,RAF1,MYD88,OXSR1,TIMP4,PIBF1,ACVR2B,IFT172,PTPRF,UBE2O,CSRNP1,NUMBL,IRAK2,SCEL,TSKU,IL15RA,IL17RE,SPRY2,PLAT,WNT11,ALK,AGKP2,AKT3,APP	grey	VSMC_M10

GO:0030162	1.00	0.00	253	538	regulation of proteolysis	BP	1	SERPINB8,SERPINB2,TNFAIP8,LRP1,MAP3K5,TRIM39,HSPA1B,GRAMD4,PRKN,AGER,FBLN1,PSMB8,BAK1,RNF217,TRIB1,MYC,PTK2,AGTPBP1,CSNK1E,PI16,HSF1,MYH9,TTBK1,SLC1A1,PLGRKT,IL1R2,GAPDH,PDCL3,SVBP,CD109,RAD23B,ACP4,XPO1,NOD1,AKIRIN2,AQP1,CASP8AP2,EPHA7,NR1H2,TNFSF15,TRIM32,BCL2L12,ZYG11B,SDCBP,HSPE1,HDAC2,BBS7,CST7,NUDT15,SSPO,PLK3,SUMO2,AQP11,RAF1,PRDX3,TIMP4,WDR48,UBE2O,SPOPL,PLAT,KLHL40,ARRB1,SIRT2,SPINT2,PRNP,RNF14,DDRGK1,SH3RF2,GAS6,RYBP,ARL6IP5,ST18,PSMF1,TRIB3,PLK2,ASPH,GPI,NR4A1,CEBPA,IDE,FOXL2,OTUD4,HIP1R,TAF9,ROBO1,PCOLCE2,DIABLO,SH3D19,FBXW7,USP25,HTRA2,CSNK2A2,PTK2B,FAM192A,NR1H3,RIPK2,SENP1,NKX3-1,ACVR1C,SERPINB1,F2R,RNFT2,IFT52,SPINT1,MARCH7,PIDD1,KCNE2,PAX2,PRICKLE1,APLP2,RNF144B,SUFU,SIRT4,GPLD1,RHBDD1,TM4SF20,RPL23,HDAC1,LCK,ADRA2A,PDCD6,SART3,USP13,AC013489.1,EGF,USP19,SOX2,DISC1,SORL1,GPER1,PSME1,ARIH2,IFI6,AGT,NEDD8,COL6A3,CIDEB,SFN,COL7A1,RPS6KA1,RNF185,CST6,MELTF,EGLN3,RPL11,MGMT,LRIG2,ADAM8,POR,NFE2L2,MAPT,FIS1,CTSH,DDX3X,COP1,FN1,VSIR,LPCAT3,SPOCK2,SERPINC1,SERPINI1,PSME3,SOCS4,PINK1,MUL1,BIRC3,ARAF,STAT3,DNAJB2,PSMA3,ARL6IP1,ATP13A2,DNAAF4,EPHA4,ANXA8,BCL2L13,F12,CLN8,TNFRSF1B,FGFR4,PSMC3,ANXA2,SIMC1,OSBPL7,PSEN1,PAPLN,SNX12,NGFR,TMED10,EFNA1,TAF1,OGT,AC138894.1,WFIKKN2,SMAD3,MAP2K5,CLN6,S100A8,KEAP1,TNIP1,PSMD10,TRAF3,FBXO22,NLE1,C3,GPC3,FMR1,FZR1,SERPINF2,BCAP31,P2RX1,SGTA,PKD1,TMEM259,WFIKKN1,PARK7,LAMTOR5,ZER1,GLMN,BC	grey	VSMC_M10
GO:0033365	1.00	0.00	351	737	protein localization to organelle	BP	1	TIMM21,MTCH2,PEX7,TNFAIP3,PEX3,MRNIP,PPP1R10,ESR1,EMC2,PRKN,TSPO,MCM9,HSPA4,TBC1D32,SKP1,LRRC6,OBSCN,LEMD2,FAM53C,C6orf106,MAPK15,SUN2,MAPK14,TOMM22,MICALL1,RAC2,GPAA1,SMO,CNTLN,TAF8,PEX6,POT1,FBXO7,ABHD17B,ADAM22,PEX1,TRAM2,BICD2,RAB23,SEC61B,SIX2,DNAJA1,MSH2,TMEM30A,DNAH11,RTN4,EMC10,XPO1,CEP68,TRAPPC12,SEC61G,VPS41,VPS35,MGARP,MAPRE1,TULP2,AGK,BCAP29,TRAF3IP2,TTC26,KPTN,RAB7A,RAB10,KPNA3,SOX9,ARL5B,MAPRE3,DNAJC15,OPTN,IPO13,GRIK5,ZFAND6,TAF3,PIBF1,TTC21A,GCKR,EMC3,SZT2,SEC62,KPNA2,PITRM1,HOOK3,TIMM50,USP36,ARL5A,UBAC2,TMCO6,IK,NUP98,FERMT1,HACL1,MCM8,ING1,BAG4,DIAPH1,MAVS,DDRGK1,WRN,CHAMP1,MFHAS1,SRP14,NSFL1C,NCOA4,WASHC2A,TUB,NUP58,MIPEP,IPO11,IMMP1L,POLR1A,PIK3R1,ATR,DCLK2,EMC4,SLF1,CEP250,TNPO1,FAM208A,CCDC66,FBXW7,PEX2,PKIA,HTRA2,AUP1,CSNK2A2,MCPH1,NUP54,XRCC4,ARL2BP,PAQR3,SSR3,SPCS1,SPIDR,AP3B1,CHMP7,PEX16,CRY2,TOMM34,MORC3,SLF2,PPHLN1,PRICKLE1,TOLLIP,ZNF423,LONP2,RYR2,GBF1,SUFU,SIRT4,CABP1,SRPRA,RPL23,DNM1L,ZMYND10,ANKRD13A,PPP3CA,IPO9,SP100,TERT,MON1A,TCIRG1,GPR137B,OXA1L,DAG1,TBRG1,TTBK2,INTS13,GET4,EGF,HCLS1,TTC21B,HSPA8,OTUD7B,HPS4,DISC1,SORL1,ANK2,PARP9,DTX3L,SH3BP4,SPO11,ARIH2,AGT,BAG3,PEX19,BBS1,TOR1AIP1,RNF215,IL10RA,TOMM40L,VPS37D,PACS1,LIMK2,GLUL,EIF4ENIF1,RPL11,POM121,DLG1,APOD,SETD2,FZD5,MIA3,MAPT,PIKFYVE,FIS1,SRGN,NMT1,LZTFL1,HK1,H2AFY2,SEC16B,EHD1,MFSD1,DDX3X,MAU2,GRPEL1,XRCC5,C11orf65,MEPCE,FAM149B1,AP4	grey	VSMC_M10
GO:0051310	1.00	0.00	18	55	metaphase plate congression	BP	1	VPS4B,CHMP2A,TRAPPC12,MLH1,PIBF1,CHAMP1,TTL,CHMP2B,CHMP4C,CHMP7,AC112128.1,SEPT1,KPNB1,RAB11A,CHMP1A,PSRC1,VPS4A,GEM	grey	VSMC_M10
GO:0051641	1.00	0.00	1152	2295	cellular localization	BP	1	TIMM21,MTCH2,VPS4B,NEDD4L,MYO1A,LRP1,STX7,STAC3,AP3S1,KIF5A,MAP7,PEX7,TNFAIP3,AGAP2,REPS1,PEX3,CANX,TBC1D30,MRNIP,TBC1D9B,PPP1R10,CPSF6,ESR1,RAB21,SNCAIP,SNX31,CPT1B,PHAX,ZDHHC14,SYNJ2,SERAC1,RIMS2,EMC2,PRRT1,PRKN,PACRG,AGER,TAP1,KIF3A,SEPT8,TSPO,GOPC,MCM9,VPS52,HSPA4,TBC1D32,DERL1,SKP1,SEPT3,SYNGAP1,UBE2B,BAK1,FAM91A1,WASHC5,LRRC6,EPB41L2,OBSCN,LEMD2,GRM4,FAM53C,C6orf106,PTCH1,TSNARE1,EXOC4,SIL1,SYNGR1,MAPK15,AGTPBP1,SUN2,MAPK14,TOMM22,NRBP2,CSNK1E,PLA2G6,COPG2,PICK1,MICALL1,TBC1D22B,BTBD9,RAC2,GPAA1,SMO,ZDHHC21,TSPAN33,CNTLN,TFEB,TAF8,MYH9,IFT74,CHRNA3,LRRC4,CHRNA5,PEX6,POT1,FBXO7,ABHD17B,ADAM22,NOL6,STEAP2,XPO5,WASHC4,APBA1,SEPT10,PEX1,USP46,VPS50,SCFD2,KIT,SLC1A1,TGFBRAP1,TBC1D8,TRAM2,RGP1,BICD2,CHMP2A,EXOSC3,RAB23,DYNC2LI1,NLRP5,LRPPRC,SEC61B,STX17,SIX2,DNAJA1,BRSK1,PRKCE,RIMS1,MSH2,PRPF31,TMEM30A,DNAH11,ASB3,SPTBN1,RTN4,HMGN3,YTHDC1,RIMS3,IBTK,RUFY3,EMC10,PPT1,ALB,XPO1,SRSF10,RRAGD,BACH2,AFTPH,CEP68,WDR91,TRAPPC12,PLEK,PTN,ITGB1BP1,DDC,YWHAZ,SEC61G,EGFR,TRAPPC3,TCAF2,CDK5RAP2,VPS41,BVES,AMPH,STARD3NL,TBC1D9,CCDC155,VPS35,ATG5,SDCBP,MGARP,TRPM4,SLC7A11,MAPRE1,PPFIA3,LIN7B,WASF1,EPS15,TULP2,AGK,BRAF,BCAP29,TRAF3IP2,SPHK2,ANKRD50,SPRY1,GRIN2D,MTMR2,TTC26,DNAJC27,TRPC3,NAPA,KPTN,BBS7,SLC8A2,RAB7A,PIP4K2A,AP2S1,KIF3C,ARHGAP21,RAB10,COPG1,ATP7B,KPNA3,SOX9,MYO7B,ARL5B,CACNB2,IWS1,LCP1,SYTL2,KLC3,CLASP2,DLG2,RBSN,NECTIN2,MAPRE3,DNAJC15,P	grey	VSMC_M10
GO:0006606	1.00	0.00	51	129	protein import into nucleus	BP	1	PPP1R10,FAM53C,MAPK14,SMO,RAB23,SIX2,TRAF3IP2,KPNA3,IPO13,GCKR,KPNA2,TMCO6,NUP98,FERMT1,ING1,MAVS,NUP58,IPO11,PIK3R1,TNPO1,PKIA,NUP54,CRY2,PRICKLE1,SUFU,CABP1,RPL23,PPP3CA,IPO9,HCLS1,AGT,BAG3,EIF4ENIF1,POM121,APOD,FAM53A,STAT3,MAPK1,MED1,KPNB1,TARDBP,PSEN1,RANBP17,TNPO2,SMAD3,EFCAB7,NUP214,NXT2,HIKESHI,PTTG1IP,ZIC1	grey	VSMC_M10

GO:0044843	1.00	0.00	75	180	cell cycle G1/S phase transition	BP	1	GLI1,TRIM39,CCND3,CDKN2A,FBXO7,CDK14,CDK6,PPAT,ANKRD17,LSM10,KLF11,EGFR,PLK3,UBE2E2,RPTOR,TCIM,PLCB1,TFDP1,DDRGK1,TAF10,PRKDC,PLK2,FAM107A,ACVR1B,FBXW7,ADAMTS1,BACH1,PIDD1,PKD2,CDK18,HYAL1,PPP3CA,CCND1,TERT,GIGYF2,CHEK2,PSME1,CACUL1,CDK15,CDKN1B,DLG1,MAP3K11,SUSD2,MEN1,DDX3X,MEPCE,PTPN6,ECD,PSME3,USP37,PIM2,PHF8,PAGR1,MUC1,TAF1,ESRRB,DCUN1D3,CAMK2A,CCL2,PPP6C,CUL4B,PKD1,CDK10,FBXO31,GFI1,MIR29A,MIR222,PLK5,E2F6,RPS27L,SOX4,SPDYA,RGCC,APC,CRADD	grey	VSMC_M10
GO:0007167	1.00	0.00	355	752	enzyme linked receptor protein signaling pathway	BP	1	ERBB3,SLC39A5,ONECUT2,LRP1,SEMA6A,AP3S1,PIP4K2C,USP15,FRS2,SNW1,IGF2R,PPARA,GDF9,ROS1,FSTL4,MTSS1,SMAD5,LEMD2,GFRA3,PTK2,PTP4A3,ANKS1A,ZC3H3,TAB1,MAPK14,NTRK2,GKAP1,KCP,CCND3,FOXH1,GUCA1B,CHRNA3,TEK,ZFAND5,KIT,NCK2,TGFBRAP1,TFAP2B,ROR2,DLX5,SOSTDC1,CD109,SPTBN1,RTN4,PHIP,ACP4,ADAMTS3,HOXA13,EPGN,AREG,BMP8A,BMPER,EPHA7,TGFA,PTN,MET,GRB10,EGFR,TSPAN12,FUZ,EPHA1,GAB1,SFRP4,SDCBP,NTF4,WASF1,FGF21,BRAF,SPRY1,SESN3,RAB7A,PIP4K2A,PRKD2,PTGIR,ABI1,SOX9,GAB2,MEGF8,RAF1,ACVR2B,PTPRF,UBE2O,CSRNP1,SPRY2,PLAT,ALK,AKT2,EID2,TGFBR2,OVOL2,NEU3,SNX5,ACVR2A,SIRT2,HBEGF,PDE6G,PLCB1,RASGRP4,FERMT1,SPRED3,ARHGEF7,DCN,SPART,GFRA4,KL,NRG1,GAS6,PTPRA,RBPMS,LEPROTL1,ANKS1B,FLT1,RYK,AMHR2,PDGFRL,EPHB1,RET,HCK,FGFBP3,ACVR1B,FER,IDE,PIK3CB,SNX25,PIK3R1,LPXN,CASP3,HIP1R,DKK3,ING2,HPGD,ROBO1,PLCE1,IL17RD,FBXW7,SORBS1,ARHGEF28,PTPRJ,VEGFC,WDR54,PTK2B,RAPGEF2,SLC33A1,TIAM1,FGF5,VEPH1,NKX3-1,OPA1,TRIO,ZFYVE27,ACVR1C,GCNT2,CYFIP1,HIVEP1,ITGB6,ZNF423,DSTYK,DOK2,IGF2,BMPR1B,FBXL15,BDNF,PXN,MAPKAPK3,GPLD1,IRS1,KIAA0319,NEURL1,GRB14,LCK,SLC2A10,PDCD4,TGFB2,ADRA2A,SLC30A10,SULF2,PDCD6,RNF115,NCF1,HJV,MAPKAPK2,GIGYF2,LRIT3,EGF,UBASH3B,SORL1,C2CD5,GPER1,GFRA1,DGKD,DOK5,CASS4,IFI6,AGT,FGR,CBL,ARNT,KALRN,NFATC4,ITGB5,HTRA1,CNKSR1,REPS2,CHRD,PDE6H,DLX1,EPHB3,SNX6,LRIG2,APOD,CREB1,CTDSPL2,PBLD,ANGPTL1,PPP2R5B,EIF4EBP2,EPHB4,MEN1,IL12A,SIK2,GIGYF1,PPM1L,HTRA3,FBN1,WNT4,FLRT1,FKBP8,SHC	grey	VSMC_M10
GO:0051225	1.00	0.00	38	101	spindle assembly	BP	1	VPS4B,ZNF207,HSPA1B,TUBGCP6,WASHC5,MAPK15,CHMP2A,CCDC155,MAPRE1,CCDC61,CLASP2,MAPRE3,MLH1,PIBF1,CEP63,KIF3B,CHMP2B,CHMP4C,ABRAXAS1,TUBGCP5,AC112128.1,CHEK2,TUBGCP4,ABRAXAS2,TOGARAM1,RNF4,SEPT1,KPNB1,RAB11A,NCOR1,CEP192,WRAP73,CHMP1A,GPSM2,RHOA,AURKC,CCSAP,DRG1	grey	VSMC_M10
GO:0010243	1.00	0.00	378	793	response to organonitrogen compound	BP	1	NME1,LRP1,AP3S1,MARS,PIP4K2C,TNFAIP3,CANX,PRKN,RNF5,AGER,PPARA,PNPLA3,TSPO,DERL1,PTK2,AKR1B1,ATF4,MAPK14,NTRK2,MAPK13,GKAP1,FOXRED2,HSF1,IRF5,CCND3,GPT,TEK,CRY1,GABRA1,SLC1A1,PPAT,CAT,SEC61B,PRKCE,PHIP,FPR2,PNPT1,ECPAS,NOD1,AREG,CRHR2,AQP1,RRAGD,PTN,DDC,KLF11,GRB10,EGFR,TLR4,GAB1,LPIN1,VPS35,MGST2,MGARP,TRPM4,FOXO3,FGF21,PRKAR2B,DHFR,HDAC2,TRPC3,SESN3,DNMT3A,C5AR1,PANX1,PIP4K2A,RAB10,HADHA,SOX9,CYSLTR2,KHK,EIF2B3,EPM2AIP1,ECHDC3,AQP11,ATP1A3,MYD88,TIMP4,KLF5,TBC1D4,AANAT,UBXN4,THBD,HNMT,ALK,AKT2,ABCC4,SNX5,UGGT2,FBXO17,JAG1,SIRT2,RPTOR,DNAJC18,NPLOC4,UBAC2,RYR1,CRLS1,PRNP,DIAPH1,BTG1,P2RX2,KL,LARS,PTPRA,UBXN8,LEPROTL1,PRKDC,NR1H4,SLC38A9,TRIB3,HTR7,DNMT3B,GPI,NR4A1,FER,IDE,PIK3R1,GSS,CASP3,P2RX3,CHRM5,RYR3,USP25,SORBS1,GPD1,MEF2C,ASIC1,TMBIM6,P2RX7,AUP1,P2RY1,PTK2B,RAPGEF2,KCNJ11,TIAM1,RIPK2,HOMER1,STC1,TMEM67,OPA1,SPIDR,LPIN3,NKX6-1,AMFR,RAPGEF3,CHRM4,NR4A2,ACVR1C,SRSF6,RNFT2,CRY2,ABCC2,ERLIN1,PKD2,CYFIP1,DMTN,CASQ2,ADTRP,NOD2,DTNBP1,CHRM3,CD40,RYR2,IGF2,GRM2,PXN,GPLD1,SRD5A1,IRS1,RHBDD1,NEURL1,RPL23,GRB14,SLC6A3,HDAC1,PPP3CA,CCND1,CPT1A,TRPV4,SLC30A10,COL16A1,DAG1,SSH1,GET4,USP13,YOD1,USP19,SRSF4,SORL1,C2CD5,GPER1,SH3BP4,AGT,SLC9A1,PEA15,SYAP1,USF1,FCER1G,RNF185,BACE1,HOMER2,SCAP,SNX6,CDKN1B,MGMT,RHBDD2,CALY,POR,EDEM3,NFE2L2,CREB1,YWHAG,HTR3B,MIA3,RAP1B,DUOX1,FIS1,VGF,SYVN1,CPS1,EIF4EBP2,DERL3,ITGA4,ME	grey	VSMC_M10

GO:0051179	1.00	0.00	2354	4586	localization	BP	1	ATP9B,TIMM21,MTCH2,NME1,VPS4B,ERBB3,SLC39A5,NEDD4L,APOF,ATP8B1,ONECUT2,MIP,ARPC3,CCDC68,STARD6,MYO1A,LRP1,STX7,SLC18B1,SEMA6A,STAC3,AP3S1,SLC2A12,KIF5A,MAP7,SLC26A10,PEX7,B4GALNT1,TNFAIP3,AGAP2,HEBP2,REPS1,CYP27B1,PEX3,SLC16A7,SRGAP1,CANX,TBC1D30,MRNIP,ATP5MGL,TBC1D9B,PPP1R10,CPSF6,ESR1,RAB21,NIPAL2,SNCAIP,SNX24,SNX31,MAPK8IP2,CPT1B,PHAX,MARCH3,APOM,ZDHHC14,SLC12A2,HSPA1B,SYNJ2,SERAC1,RIMS2,IGF2R,SLC27A6,EMC2,CDC42SE2,KCNV1,PRRT1,PRKN,PACRG,QKI,RNF5,AGER,PPARA,GPSM3,FBLN1,TAP1,SLC22A4,CALHM4,KIF3A,SEPT8,TSPO,GDF9,GOPC,SLC35F1,CEP85L,MCM9,VPS52,HSPA4,TBC1D32,DERL1,SMDT1,SKP1,SEPT3,SYNGAP1,UBE2B,BAK1,FAM91A1,CATSPER3,WASHC5,TRIB1,CXCL14,MYC,LRRC6,KLHL3,EPB41L2,MCHR1,PKD2L2,OBSCN,KCNK9,LEMD2,AGO2,GRM4,GFRA3,PTK2,FAM53C,C6orf106,SLC45A4,PTP4A3,PTCH1,TSNARE1,ANKS1A,LY6E,ZC3H3,EXOC4,SIL1,SYNGR1,MAPK15,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,TOMM22,CBY1,PODXL,NRBP2,KCNJ4,CSNK1E,TMEM184B,PLA2G6,COPG2,PICK1,SOX10,MICALL1,PIM1,MEST,TBC1D22B,BTBD9,RAC2,STRIP2,GPAA1,SMO,ZDHHC21,TSPAN33,TTC39B,HSF1,CNTLN,MDFI,TFEB,PLIN2,TOMM6,SLC39A4,ATP6V1F,TAF8,MYH9,GUCA1B,MFSD3,APOL4,RBFOX2,APOL6,IFT74,CHRNA3,TEK,LRRC4,CHRNA5,PEX6,TRPM6,POT1,FBXO7,CRY1,ZFAND5,PTK7,ABHD17B,CROT,SRF,ABCB1,SLC25A40,ADAM22,ABCC10,NOL6,STEAP2,CFAP69,GABRA1,XPO5,WASHC4,APBA1,CNGA1,SLC41A2,TMEM63B,SEPT10,CCL27,PEX1,SLC35B2,NFKBIE,OCIAD1,CDK6,USP46,CLIC5,VPS50,SLC25A27,SCFD2,RFX3,KIT,SLC1A1,C	grey	VSMC_M10
GO:0022616	1.00	0.00	4	20	DNA strand elongation	BP	1	POT1,NBN,TERT,LIG3	grey	VSMC_M10
GO:0071103	1.00	0.00	84	200	DNA conformation change	BP	1	BAZ2A,HELB,BRD2,MCM9,ASF1A,XRCC6,H3F3C,POT1,MTERF1,ASCC3,SSBP1,UBN2,SOX9,ERCC2,ERCC3,GTF2F2,RSF1,ZRANB3,FBH1,CHD8,SIRT2,PURA,MCM8,WRN,M1AP,DQX1,MCPH1,NBN,TOP1,HELQ,RAD54B,WRNIP1,SPTY2D1,SYCP1,TWNK,NAP1L5,RAD54L2,RBBP4,IGHMBP2,SART3,ACIN1,GPER1,RECQL,RTEL1,SUPV3L1,H2AFY2,TTN,DDX3X,XRCC5,HIRA,DDX11,AKAP8L,TSPYL2,AKAP8,PHF8,PIF1,NAP1L2,G3BP1,NAA60,NAA10,DFFB,CHD5,CHMP1A,CTCF,SYCP3,TSPYL4,HIST1H2BK,HIST1H4B,HIST2H4A,HIST1H4H,BEND3,SMYD3,HIST1H3F,ITGB3BP,HIST1H3H,RNF8,HIST1H4D,HIST2H2BF,HIST1H2BF,HIST1H2BM,HIST1H2BJ,HIST1H4A,HIST1H4F,TSPYL5	grey	VSMC_M10
GO:0072001	1.00	0.00	110	256	renal system development	BP	1	RIDA,OSR2,TBC1D32,MTSS1,MYC,SMAD5,KLHL3,PTCH1,AKR1B1,PODXL,SMO,TEK,PTK7,TFAP2B,PPAT,C1GALT1,ANKS6,CAT,SIX2,EPCAM,BMPER,EPHA7,POU3F3,CNTRL,OSR1,TRAF3IP2,SPRY1,SOX9,GLI2,AQP11,FOXJ1,GZF1,WNT11,JAG1,RARB,FREM2,CEP290,DCN,RET,ASXL1,PAX8,HPGD,EYA1,ROBO2,PLCE1,FMN1,MEF2C,ADAMTS1,MME,FRAS1,NKX3-1,RPGRIP1L,PKD2,TFAP2A,PAX2,SALL1,IRX2,TGFB2,SULF2,PRKX,ENPEP,AP1B1,AGT,BICC1,TRAF3IP1,LAMA5,PTPRO,DLG1,OVOL1,CTSH,FBN1,CXCR2,WNT4,EPHA4,MAGED1,ALDH1A2,ITGA3,TMED10,CITED1,IL6R,SMAD3,LHX1,STRA6,AP2B1,NLE1,ZBTB14,IFT20,GPC3,HSPB11,PKD1,SOX8,TSC1,FOXF1,ASS1,PKD1L3,RHOA,FSTL3,SOX4,FADD,CA2,MIR125A,NOG,WNT5A,BASP1,SIX1,BCL2L11,LIF,KCNJ8,FGF1,PDGFD	grey	VSMC_M10
GO:0009605	1.00	0.00	880	1770	response to external stimulus	BP	1	CD226,SERPINB2,PHLPP1,LRP1,SEMA6A,SHMT2,MARS,KIF5A,MAP3K5,TNFAIP3,CYP27B1,FUCA2,USP15,ENPP3,TRIM39,ESR1,TSPAN8,TPH2,SNW1,SLC12A2,PRKN,RNF5,AGER,PPARA,GPSM3,TNFRSF11B,TSPO,BAK1,FER1L6,XRCC6,TRIB1,CXCL14,PKD2L2,HABP4,GFRA3,PTK2,C6orf106,PTCH1,ATF4,APOBEC3H,PLXNA4,MAPK14,MAPK13,PLA2G6,PICK1,PIM1,RAC2,EXOSC4,SMO,TXN2,HSF1,FBXL6,TFEB,SLC39A4,IRF5,OPN1SW,GPT,TEK,PRPH2,CRY1,SRF,TTBK1,NUAK1,CCL27,PHF24,CDK6,USP46,ENPP4,KIT,SLC1A1,PLGRKT,SEMA4D,GAPDH,DLX5,NINJ1,PRDX1,ETV1,ADH5,SEMA4C,ABCG5,CAT,ABCG8,CLDN19,CAMKMT,BRSK1,SDHAF4,PRKCE,CD109,FPR2,GSDME,SHANK1,HOXA2,LPAR1,REL,NT5E,ANKRD17,ALB,CXCL8,NOD1,AKIRIN2,BMP8A,AQP1,RRAGD,CASP8AP2,GJA10,PELI1,LYPD8,AKIRIN1,RSAD2,EPHA7,NR1H2,AKNA,WHRN,PTN,MET,TNC,EGFR,TRIM32,TLR4,EPHA1,GRIK2,VPS41,GAB1,IL15,UCP1,VPS35,ATG5,MGST2,NRCAM,TRPM4,FOXO3,SMPD2,PUM2,MKX,APOB,CDK19,FGF21,TRAF3IP2,PLXNA1,GRIN2D,HDAC2,ZC3HAV1,TRPC3,KPTN,SESN3,DNMT3A,C5AR2,C5AR1,SLC26A5,NAPEPLD,PRKD2,PTGIR,CST7,PHB,FOXA3,SOX9,GIPR,ERCC1,NUDT15,XPC,CLASP2,CUBN,LACC1,NECTIN2,DNAJC15,PVR,ASIC3,OPTN,MLH1,GLI2,MEGF8,RALB,KDM4A,PRKAG2,UNC13D,RAF1,MYD88,OXSR1,PRDX3,TIMP4,SCN1A,PTPRF,MYCBP2,IRAK2,FNDC4,THBD,SCEL,SEC14L1,SZT2,PPP1CB,PLAT,WNT11,ALK,ACKR2,CMTM7,CMTM8,TGFBR2,IKBKB,C1QTNF1,PLEKHB1,KIF5C,BHLHE40,CHD8,NFKBIB,SIRT2,MKKS,NMI,ZMYND11,RPTOR,TMEM173,CLPB,ACTG1,HBEGF,NR1D2,NPLOC4,FEZ2,RASGRP4,CNN2,EIF2AK2,SEMA3D,DCN,MAVS,PLXNC1,SEMA3A,CHL1,UNC	grey	VSMC_M10
GO:0010761	1.00	0.00	14	46	fibroblast migration	BP	1	PTK2,ZFAND5,PRKCE,HAS1,ITGB1BP1,CYGB,BAG4,ARHGEF7,FER,DMTN,AC138894.1,ARHGAP4,C5orf30,LAMTOR2	grey	VSMC_M10

GO:0007249	1.00	0.00	95	222	I-kappaB kinase/NF-kappaB signaling	BP	1	TNFAIP3,TRIM39,ESR1,PRKN,SLC35B2,GAPDH,PRKCE,IRAK1BP1,LPAR1,REL,ANKRD17,NOD1,PELI1,SNIP1,TRIM32,TLR4,TRAF1,TRAF3IP2,SPHK2,PPM1N,OPTN,MYD88,ZFAND6,IRAK2,IKBKB,ZMYND11,MAVS,DDRGK1,TRAF6,NR1H4,TMEM9B,PLK2,FAIM,RIPK2,F2RL1,F2R,RIPK1,ZDHHC13,PIDD1,MAPKBP1,NOD2,CD40,OTUD7A,HDAC1,AJUBA,TIFA,ALPK1,OTUD7B,TRAF5,NLRX1,GOLT1B,TRIM52,MAP3K3,TAB3,TNIP2,PINK1,MUL1,BIRC3,LTBR,PPM1A,PIM2,CARD11,CC2D1A,HACD3,TSPAN6,S100A13,PRKCB,BTK,TNIP1,TRAF3,CD74,RIOK3,LITAF,TICAM1,MIB2,PDPK1,TRAF2,IKBKG,LAMTOR5,BCL10,DAB2IP,MIR27B,RHOA,S100A12,TRIM68,DEFB124,FADD,TRIM34,CASP8,C18orf32,WNT5A,INAVA,UBE2N,NKIRAS2,LURAP1L	grey	VSMC_M10
GO:0071407	1.00	0.00	204	448	cellular response to organic cyclic compound	BP	1	FECH,CYP27B1,ESR1,CNOT2,SNW1,PRKN,PPARA,PNPLA3,RXRB,SMAD5,PTCH1,ATF4,KDM4C,SOX10,PIM1,SMO,HSF1,FOXH1,RBFOX2,CRY1,GABRA1,SLC1A1,DNAJA1,AQP1,PTN,TNC,EGFR,IL15,VPS35,MGARP,TRPM4,FOXO3,PGRMC2,HDAC2,ADCY3,BMI1,PHB,GLI2,RALB,ATP1A3,KLF5,EGLN2,AANAT,POU4F1,ALK,TADA3,SIRT2,TMEM173,RYR1,TAF7,DIAPH1,MAVS,RNF14,DDRGK1,FOXP1,ARL6IP5,CALCOCO1,NCOA4,NR1H4,CYP7A1,HTR7,FAM107A,CYP7B1,DNMT3B,CEBPA,UFSP2,CASP3,CCDC62,P2RX3,ZNF366,CHRM5,RYR3,ARNTL,GPD1,MEF2C,P2RX7,CNOT1,P2RY1,KMT2D,RAPGEF2,LCOR,DDX54,VDR,STC1,NKX3-1,SPIDR,RAPGEF3,CHRM4,CRY2,VPS18,ABCC2,SPP1,PKD2,DMTN,CASQ2,ADTRP,NOD2,DTNBP1,CHRM3,RYR2,ADCY2,GPLD1,SRD5A1,IFIH1,DNM1L,HDAC1,DAG1,SSH1,ABHD2,GRAMD1B,GPER1,CHEK2,ATP1A2,SLC9A1,ARID1A,NPAS4,CDKN1B,MGMT,RXRG,SLC16A1,CALY,HTR3B,RAP1B,FIS1,CPS1,FDX1,ESRRA,GPBAR1,ALPL,MUL1,STAT3,MAPK1,CHRM1,GNB5,NSG1,PADI2,DNAAF4,ACTB,PARP1,MED1,HRH2,OSBPL7,PKLR,HCN3,PAGR1,TAF1,MAPK3,ESRRB,PIAS2,LARP1,DNM2,SCN1B,SIN3A,NCOR1,HRH4,CCL5,NPC1,RIOK3,PPARGC1B,COLEC12,CCL2,ISL1,RHOXF1,GNAL,LRP8,INPP5K,GNB1,GNA15,TRPV1,HCFC1,PARK7,PALM,GNAI3,RXRA,CYBA,FOXF1,ASS1,HSPA5,MIR21,MIR125B1,RHOA,HTR1D,TRIM24,TRIM68,CASP8,ZCCHC3,BGLAP,IMPACT,SMYD3,SIX1,RGS4,CRH,BCL2L11,FAM210B,INSIG2,YWHAH,ZFP36L2,BCL2L2,CEBPB,GNA14,GNG2,HCN4,PDXP,ARPP19	grey	VSMC_M10
GO:1901698	1.00	0.00	404	845	response to nitrogen compound	BP	1	NME1,LRP1,AP3S1,MARS,PIP4K2C,TNFAIP3,CANX,PRKN,RNF5,AGER,PPARA,PNPLA3,TSPO,DERL1,PTK2,LY6E,AKR1B1,ATF4,MAPK14,NTRK2,MAPK13,GKAP1,FOXRED2,HSF1,IRF5,CCND3,GPT,CHRNA3,TEK,CRY1,GABRA1,SLC1A1,PPAT,CAT,SEC61B,PRKCE,PHIP,FPR2,PNPT1,ECPAS,NOD1,AREG,CRHR2,AQP1,RRAGD,PELI1,PTN,DDC,KLF11,GRB10,EGFR,TLR4,GAB1,LPIN1,VPS35,MGST2,MGARP,TRPM4,FOXO3,FGF21,PRKAR2B,DHFR,HDAC2,TRPC3,SESN3,DNMT3A,C5AR1,PANX1,PIP4K2A,RAB10,HADHA,SOX9,CYSLTR2,KHK,EIF2B3,EPM2AIP1,RALB,ECHDC3,AQP11,ATP1A3,MYD88,TIMP4,KLF5,TBC1D4,AANAT,UBXN4,THBD,HNMT,ALK,AKT2,ABCC4,SNX5,UGGT2,FBXO17,JAG1,SIRT2,RPTOR,DNAJC18,TMEM173,NPLOC4,UBAC2,PLCB1,RYR1,CRLS1,PRNP,DIAPH1,BTG1,MAVS,P2RX2,KL,LARS,PTPRA,UBXN8,LEPROTL1,PRKDC,NR1H4,SLC38A9,TRIB3,HTR7,DNMT3B,GPI,NR4A1,FER,IDE,PIK3R1,GSS,CASP3,P2RX3,CHRM5,RYR3,USP25,SORBS1,GPD1,MEF2C,ASIC1,TMBIM6,P2RX7,AUP1,GUCY1B1,P2RY1,PTK2B,RAPGEF2,KCNJ11,TIAM1,RIPK2,HOMER1,STC1,TMEM67,OPA1,SPIDR,LPIN3,NKX6-1,AMFR,RAPGEF3,CHRM4,NR4A2,ACVR1C,SRSF6,RNFT2,CRY2,ABCC2,ERLIN1,PKD2,CYFIP1,DMTN,CASQ2,ADTRP,NOD2,DTNBP1,CHRM3,CD40,RYR2,IGF2,GRM2,PXN,GPLD1,SRD5A1,IRS1,RHBDD1,IFIH1,NEURL1,MTR,RPL23,GRB14,SLC6A3,HDAC1,PPP3CA,CCND1,CPT1A,TRPV4,SLC30A10,COL16A1,RFTN2,DAG1,SSH1,GET4,MARC2,MARC1,USP13,YOD1,USP19,SRSF4,GRK2,SORL1,C2CD5,GPER1,RTF2,SH3BP4,AGT,SLC9A1,PEA15,SYAP1,USF1,FCER1G,RNF185,BACE1,HOMER2,SCAP,SNX6,CDKN1B,MGMT,RHBDD2,CALY,POR,EDEM3,NF	grey	VSMC_M10
GO:0000281	1.00	0.00	21	63	mitotic cytokinesis	BP	1	VPS4B,TRIM36,EFHC1,MITD1,CHMP2A,SPTBN1,DCDC1,CHMP2B,CHMP4C,RTKN,CHMP7,KLHDC8B,EFHC2,CNTROB,MYH10,UNC119,CHMP1A,VPS4A,RHOA,STAMBP,APC	grey	VSMC_M10
GO:0007094	1.00	0.00	10	36	mitotic spindle assembly checkpoint signaling	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:0071173	1.00	0.00	10	36	spindle assembly checkpoint signaling	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:0071174	1.00	0.00	10	36	mitotic spindle checkpoint signaling	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10

GO:0016049	1.00	0.00	180	399	cell growth	BP	1	ADNP2,NEDD4L,LRP1,SEMA6A,CYP27B1,RAB21,HSPA1B,RIMS2,EBAG9,PRKN,PPARA,GDF9,ROS1,FSTL4,H3F3C,PLXNA4,CPNE5,PI16,EXOSC4,CDKN2A,SRF,SMARCA2,SEMA4D,SEMA4C,RIMS1,RTN4,PPP2R1A,RUFY3,PPT1,EPHA7,EGFR,TRIM32,SDCBP,NRCAM,WASF1,SPHK2,PLXNA1,PHB,SOX9,PTCH2,GOLGA4,MEGF8,EGLN2,WNT11,SERTAD3,CPNE9,TGFBR2,RPTOR,HBEGF,SYT1,SLC23A2,ING1,SEMA3D,BTG1,SPART,SEMA3A,ULK1,RYK,TTL,FAM107A,ACVR1B,CDKN2AIP,PLCE1,IL17RB,PTPRJ,SEMA4F,NDUFS3,PTK2B,KMT2D,DPYSL2,EIF2AK4,TIAM1,SLIT1,NKX6-1,ZFYVE27,BIN3,PRDM11,SEMA3G,SPP1,CYFIP1,ALCAM,SEMA4G,BDNF,KIAA0319,HYAL1,CAPRIN2,SEMA3F,TGFB2,FBLN5,EI24,AUTS2,ZNF639,ADNP,DISC1,SH3BP4,ARIH2,AGT,CIB1,IP6K2,SLC9A1,SFN,RPS6KA1,CDKL5,CDKN1B,WNT3,SPG11,MAPT,SUPV3L1,BCL6,SEMA6D,ITGA4,DDX3X,TNR,RASGRP2,FN1,DDX49,NIN,FLRT1,PPP3CB,MUL1,DNAJB2,VCL,CD38,CXCL16,IGFBP4,TSPYL2,ARHGEF11,SEMA4A,NLGN3,TAOK2,TRIM46,NDEL1,RAB11A,TAF9B,SMAD3,NTN1,MAP2K5,S100A8,DNM2,BDKRB1,DCUN1D3,YY1,PSMD10,SIN3A,TRPV2,CDK5R1,EPB41L3,TMEM97,SLC9A6,NUBP1,ATAD3A,L1CAM,PRKCZ,ARHGAP4,PLXNA3,SLC25A33,PSRC1,CYBA,NAIF1,BARHL2,MIR199A1,MIR23A,MIR24-1,RHOA,SERTAD2,ACVRL1,NANOS1,IMPACT,WNT5A,LAMTOR2,FXN,CACNG7,RGS4,DACT3,LLPH,NME6,N6AMT1,CGRRF1,OLFM1,DERL2	grey	VSMC_M10
GO:0072012	1.00	0.00	5	23	glomerulus vasculature development	BP	1	TEK,OSR1,IL6R,MIR125A,PDGFD	grey	VSMC_M10
GO:0022613	1.00	0.00	172	376	ribonucleoprotein complex biogenesis	BP	1	HELB,CPSF6,TFB1M,SF3A3,EIF3E,UTP23,RRP7A,AGO2,PUF60,EIF3L,EXOSC4,NOL6,GTPBP10,C12orf45,TSR1,EXOSC3,RPS14,PRPF31,YTHDC1,UTP3,XPO1,SRSF10,MDN1,AGO1,FCF1,ERCC2,RPS8,CLNS1A,CELF2,RPSA,RPL14,CRNKL1,METTL17,USP36,ESF1,KRR1,SIRT7,NUDT16,PRKDC,DHX37,TGS1,BMS1,DIMT1,POP4,USP39,TAF9,CLP1,RPL6,ATR,GCFC2,AAR2,CELF1,SDAD1,URB1,DDX54,NSUN3,RRP12,HELQ,RPUSD2,SRSF6,SCAF11,RPP40,RIOK1,TENT4B,EIF2D,POP5,PDCD11,RPUSD4,RPS17,LTO1,SBDS,RBM5,HEATR1,FAM207A,SART3,MRPS11,GAR1,YTHDF2,YBEY,URB2,ZRSR2,NOP9,RPS27,WDR12,MTG2,CELF3,RPL7L1,WBP11,DHX30,GLUL,NSUN5,DDX47,RPL11,EFL1,GEMIN2,SNRPD3,PRPF39,RPL10L,POP7,DDX3X,DDX10,XRCC5,DDX49,RPL27,WDR74,RSL24D1,NVL,MRM2,PRPF19,TSR2,ZCCHC4,GNL3L,LAS1L,ISG20L2,KHDC4,EIF3C,LUC7L3,SLU7,UTP18,COIL,MRPL22,KRI1,ZNHIT3,ERI2,RIOK3,NLE1,XAB2,UTP6,CUL4B,MCTS1,SNU13,UTP14A,RPL23A,ERAL1,DROSHA,MRM3,CELF5,METTL16,NOL9,RPUSD1,WDR18,LUC7L,MRPS2,TSC1,RPL35,ZNHIT6,PRMT7,RNVU1-6,RNU5E-1,RNU5B-1,METTL18,ZNF622,AGO4,RPS27L,NOL3,RPP38,MPHOSPH6,RNU4ATAC,RF00003,SNRPC,RNU2-1,RPUSD3,NSA2,RNU4-2,C1D,SRSF12,RNU4-1,PIH1D2,RPP30,TRMT61B,EXOSC5,GTF2H5	grey	VSMC_M10
GO:0043534	1.00	0.00	41	108	blood vessel endothelial cell migration	BP	1	MYH9,SRF,MEOX2,ITGB1BP1,PRKD2,PLK2,NR4A1,ATP5F1A,ROBO1,FBXW7,MEF2C,VEGFC,PTK2B,HDAC7,ADTRP,CD40,GPLD1,CIB1,MAP3K3,NFE2L2,MIA3,EPHB4,PDCD10,RHOJ,FGF18,EFNA1,VASH1,MAP2K5,AMOT,PDPK1,MECP2,MIR199A1,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,ACVRL1,GADD45A,RGCC	grey	VSMC_M10
GO:0010629	1.00	0.00	365	766	negative regulation of gene expression	BP	1	NME1,ZC3H10,PAN2,BAZ2A,LRP1,SHMT2,TNFAIP3,ESR1,CNOT2,CNOT6,RIDA,PABPC1,HSPA1B,SKIV2L,DXO,MOV10L1,EIF3E,PNLDC1,PRKN,AGER,PPARA,TSPO,MRPL13,BAK1,CSDC2,AGO2,H3F3C,C6orf106,TNRC6B,ATF4,TUT7,GTPBP1,MAPK14,EXOSC4,SMO,HSF1,TTBK1,XPO5,TNFRSF21,IL1R2,GAPDH,CNOT11,EXOSC3,CLDN19,SCMH1,IGF2BP3,PNPT1,ACP4,REL,PUS10,PTBP3,CXCL8,AKIRIN2,SRSF10,SNIP1,ANXA4,NR1H2,AGO1,EGFR,TLR4,BCL2L12,MYCN,TUT4,PUM2,TRAF3IP2,DHFR,MTPAP,ZC3HAV1,DNMT3A,BMI1,DHX34,C5AR2,CST7,SETDB2,SOX9,FASTK,MLH1,KDM4A,MYD88,PIBF1,FOXJ1,SFMBT2,POU4F1,TSKU,TNRC6C,WNT11,SLC24A3,ARRB1,OVOL2,RBMS3,SIRT2,MKKS,NMI,PURA,NAV3,NPLOC4,PAWR,FERMT1,EIF2AK2,PRNP,LSM1,NUDT16,DDRGK1,NCKAP1L,GAS6,TEX15,FOXP1,PKP3,UPF3A,PRKDC,PAN3,NR1H4,PLAG1,IL37,ACVR1B,NUDT12,CLP1,HAND2,ROBO1,TTC37,FAM208A,FBXW7,ENC1,MEF2C,BCDIN3D,TMBIM6,CNOT1,CELF1,CNOT6L,EIF2AK4,EIF4E2,OAS3,TENT2,PAIP2B,VDR,NKX3-1,BAHD1,HDAC7,SERPINB1,F2RL1,SRSF6,RIPK1,TP53INP1,FTO,EXD1,ABCC2,CHID1,MAPKBP1,PPHLN1,NOD2,TENT5C,ADCY7,TENT4B,RBM24,SIRT4,CD96,CD200,HDAC1,SLC2A10,PPP3CA,BANK1,CAPRIN2,TERT,PDCD4,TGFB2,BTN2A2,DIS3L2,AXIN2,AJUBA,PIAS3,CMKLR1,ZNFX1,MAPKAPK2,GIGYF2,ADNP,SRSF4,OTUD7B,OPRD1,YTHDF2,GPER1,PARP9,PARP15,PARP14,PC,TRAF5,NLRX1,FASTKD1,ANGEL2,DDX6,TRAF3IP1,ASB1,YTHDF1,TDRKH,CD28,NCBP2,EIF4ENIF1,HOMER2,IGF2BP2,APOD,YBX3,CREB1,UPK3B,MAPT,TET1,STOX1,SRGN,SUPV3L1,PRKRA,BCL6,H2AFY2,EIF4EBP2,IL12A,DDX3X,FN1,VSIR,RC3H1,PTPN6,PDCD10,UPF1,SLC11A	grey	VSMC_M10

GO:0051247	1.00	0.00	555	1140	positive regulation of protein metabolic process	BP	1	ERBB3,NEDD4L,LRP1,MAP3K5,TNFAIP3,AGAP2,MRNIP,RMND1,STK3,PRR16,PABPC1,SNW1,HSPA1B,EIF3E,GRAMD4,MAP3K4,PRKN,AGER,FBLN1,IL5,GDF9,DERL1,SKP1,PHF1,BAK1,RNF217,XRCC6,TRIB1,MYC,JMJD4,AGO2,HABP4,PTK2,TAB1,AGTPBP1,NTRK2,CSNK1E,PLA2G6,C6orf89,HSF1,CCND3,MYH9,CHRNA3,TEK,CRY1,TTBK1,TEC,KIT,SLC1A1,NCK2,PLGRKT,ROR2,SEMA4D,CLDN19,IL11,RNF20,FPR2,MOB1B,EPGN,NOD1,AREG,AKIRIN2,BMP8A,CASP8AP2,PELI1,ETAA1,RSPO1,EPHA7,NR1H2,TNFSF15,TGFA,ITGB1BP1,VRK3,EGFR,HECW1,ARHGEF5,TRIM32,TLR4,HACE1,IL15,CCNY,VPS35,ZYG11B,SDCBP,NTF4,FAF1,FGF21,BRAF,HSPE1,SPHK2,HDAC2,BBS7,SLC8A2,RAB7A,BMI1,MOB3C,PRKD2,CNBP,PHB,ABI1,SOX9,SYMPK,MAPRE3,PLK3,SUMO2,CDC123,RALB,PRKAG2,RAF1,PIBF1,PAXIP1,WDR48,EGLN2,MYCBP2,FBH1,SPRY2,WNT11,KLHL40,AKT2,ARRB1,TGFBR2,ACVR2A,SIRT2,NMI,NEK10,RPTOR,TCIM,HBEGF,PAWR,ASPSCR1,PLCB1,CHTOP,NSD3,PRNP,BAG4,MAVS,RNF14,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,HPX,RBPMS,UPF3A,ARL6IP5,PRKDC,ERCC6,FLT1,ST18,ADRA2B,TRAF6,TRIB3,PLK2,SDR16C5,RET,ASPH,FAM107A,DNMT3B,ACVR1B,CEBPA,IDE,FOXL2,OSBP,SPSB4,ZFP91,CASP3,HIP1R,TRABD2A,ING2,ROBO1,PCOLCE2,DIABLO,MRPS27,SH3D19,ARNTL,FBXW7,PTPRJ,HTRA2,VEGFC,P2RY1,USP16,ATG10,MADD,PTK2B,RASGRP1,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,NR1H3,TIAM1,FGF5,RIPK2,NBN,SENP1,NKX3-1,SLC25A37,RAPGEF3,ACVR1C,F2R,RNFT2,RIPK1,MARCH7,CDK2AP1,PIDD1,KCNE2,RTF1,PKD2,STK4,PRICKLE1,ADTRP,NOD2,NKD1,CNTN1,JARID2,MYLIP,TAOK3,TENT4B,TOLLIP,SLC2A13,CD40,LDB1,IGF2,BMPR1B,	grey	VSMC_M10
GO:2000278	1.00	0.00	35	95	regulation of DNA biosynthetic process	BP	1	MAP3K4,MYC,MAPK15,POT1,PRKD2,DACH1,TFDP1,PARP4,ATR,HMBOX1,PTK2B,MAPKAPK5,TENT4B,STN1,POLG2,KCNK2,MEN1,XRCC5,MAPK1,NVL,GNL3L,FGFR4,WRAP53,SMG5,CTC1,PIF1,MAPK3,PARN,TERF2,ACVRL1,TINF2,TEN1,DUSP1,RGCC,MAP2K7	grey	VSMC_M10
GO:0042542	1.00	0.00	46	118	response to hydrogen peroxide	BP	1	MAP3K5,TNFAIP3,BAK1,MAPK13,HSF1,GPR37,CAT,AREG,AQP1,ZNF277,MET,FOXO3,HDAC2,PRDX3,PAWR,PPP2CB,CASP3,PTK2B,RIPK1,PAX2,GLRX2,PDE8A,NFE2L2,PDCD10,PINK1,ANKZF1,KDM6B,MAPK7,STK26,JUN,CRK,PARK7,LCN2,NQO1,MIR21,MT-ND6,GPR37L1,ZNF580,IMPACT,FXN,DUSP1,HBA2,TXN,CBX8,PPIF,PDGFD	grey	VSMC_M10
GO:0000082	1.00	0.00	65	160	G1/S transition of mitotic cell cycle	BP	1	CCND3,CDKN2A,FBXO7,CDK14,CDK6,PPAT,ANKRD17,LSM10,KLF11,EGFR,PLK3,UBE2E2,RPTOR,PLCB1,TFDP1,TAF10,PRKDC,PLK2,FAM107A,ACVR1B,ADAMTS1,BACH1,PIDD1,PKD2,CDK18,HYAL1,PPP3CA,CCND1,TERT,GIGYF2,CHEK2,PSME1,CACUL1,CDK15,CDKN1B,DLG1,DDX3X,MEPCE,PTPN6,ECD,PSME3,USP37,PIM2,PHF8,MUC1,ESRRB,DCUN1D3,CAMK2A,CCL2,PPP6C,CUL4B,PKD1,CDK10,FBXO31,GFI1,MIR29A,MIR222,PLK5,E2F6,RPS27L,SOX4,SPDYA,RGCC,APC,CRADD	grey	VSMC_M10
GO:0080134	1.00	0.00	468	970	regulation of response to stress	BP	1	CD226,SERPINB2,PHLPP1,LRP1,EYA4,MAP3K5,TNFAIP3,USP15,MRNIP,ENPP3,HELB,PPP1R10,ARMT1,ESR1,IER3,TSPAN8,STK3,MAPK8IP2,SLC12A2,MAP3K4,PRKN,AGER,PPARA,GPSM3,BAK1,XRCC6,NCOA7,MYC,PTK2,C6orf106,ATF4,MAPK14,MAPK13,HSF1,CDKN2A,TEK,POT1,GPR37,FBXO7,CRY1,ABCB1,TTBK1,NUAK1,CDK6,ENPP4,NCK2,GADD45G,NINJ1,KLHL31,PRDX1,SEMA4C,CLDN19,DNAJA1,PRKCE,CD109,FKTN,FPR2,PNPT1,EMC10,NT5E,MTURN,NOD1,AKIRIN2,CYREN,ETAA1,ZNF277,NR1H2,AKNA,PTN,MET,EGFR,TRIM32,TLR4,TRAF1,IL15,VPS35,MGST2,SDCBP,SLC7A11,FOXO3,CDK19,TRAF3IP2,DHFR,TRPC3,SESN3,NAPEPLD,CST7,ERCC1,CLASP2,LACC1,DDIAS,NECTIN2,PVR,XRCC1,OPTN,AQP11,MYD88,PAXIP1,WDR48,PTPRF,FNDC4,THBD,SEC14L1,FBH1,PLAT,RNF169,IKBKB,C1QTNF1,FAM168A,SIRT2,NMI,ZMYND11,TMEM173,ACTG1,HBEGF,NR1D2,NPLOC4,PAWR,PLCB1,SIRT7,FERMT1,SHLD1,EIF2AK2,MAVS,RELL2,SEMA3A,DDRGK1,SH3RF2,PPP4R2,HPX,TEX15,FOXP1,ARL6IP5,PRKDC,IRF7,ERCC6,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,EPHB1,PLK2,HCK,ERCC8,ACOX2,IL37,C12orf49,CEBPA,PIK3R1,TAF9,EREAP1,HAND2,ATR,ING2,EYA1,SLF1,ARNTL,FBXW7,USP25,MEF2C,HTRA2,TMBIM6,CELF1,SETD6,MCPH1,PTK2B,RASGRP1,EIF2AK4,NR1H3,TRAFD1,OAS3,NLRC5,RIPK2,OTULIN,NKX3-1,ABRAXAS1,OPA1,SPIDR,AMFR,WRNIP1,SLC38A2,F2RL1,F2R,SRSF6,RNFT2,RIPK1,ANO6,POLR3D,MARCH7,RREB1,SPP1,PLA2R1,MAPKBP1,SLF2,DMTN,ADTRP,HERC5,NOD2,TAOK3,CD96,FAP,KIAA0319,CD200,CD200R1L,PPP3CA,TERT,TRPV4,PDCD4,TGFB2,ADRA2A,SLC30A10,FBLN5,AXIN2,POLR3C,AJUBA,FICD,NCF1,KRA	grey	VSMC_M10

GO:0040017	1.00	0.00	211	462	positive regulation of locomotion	BP	1	ONECUT2,LRP1,SEMA6A,AGER,GPSM3,AGO2,PTK2,SUN2,PODXL,RAC2,SMO,TEK,CFAP69,CCL27,KIT,ROR2,SEMA4D,SEMA4C,ZNF268,PRKCE,EPCAM,RTN4,FPR2,EPB41L4B,RUFY3,EMC10,CXCL8,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,TRIM32,TLR4,TCAF2,EPHA1,BVES,GAB1,SDCBP,C5AR1,SLC26A5,PRKD2,IQSEC1,SOX9,CLASP2,MEGF8,OXSR1,SPRY2,WNT11,RIN2,AKT2,TGFBR2,ACTG1,HBEGF,FERMT1,BAG4,ARHGEF7,SEMA3D,DIAPH1,SEMA3A,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,FLT1,PLK2,RET,FAM107A,GPI,ACVR1B,FER,PIK3CB,PIK3R1,ATP5F1A,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,ADAMTS1,PTK2B,RAPGEF2,TIAM1,DOCK5,HDAC7,F2RL1,F2R,ANO6,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,CD40,SRGAP2C,GPLD1,LGR6,DNM1L,CARMIL1,HYAL1,PPP3CA,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,CD99,PRSS56,SSH1,CMKLR1,SNAI1,EGF,GPER1,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,HDAC4,MAP3K3,DOCK1,ELP6,ADAM8,LRRC15,NFE2L2,MIA3,DUOX1,CCAR1,IL16,CEMIP,SEMA6D,TRIP6,CTSH,ITGA2B,ITGA4,IL12A,FN1,VSIR,SPOCK2,MCU,PDCD10,TNFSF18,FERMT3,CXCR2,STAT3,MAPK1,RHOJ,SYNE2,CXCL16,SYDE1,TMEM102,MIEN1,STX4,SEMA4A,RAB25,FGF18,FOXO4,ITGA3,PGF,DAPK2,ZNF609,MAPK3,IL6R,RAB11A,SMAD3,NTN1,S100A14,BDKRB1,BCAS3,CD74,INSR,CCL5,CSF1R,CCL7,DOCK7,CRK,PDPK1,FBXO31,FOXF1,LCN2,HSPA5,DAB2IP,CARMIL2,RIPOR1,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR27B,MIR27A,RHOA,DEFB124,FADD,LAMB1,ZNF580,THY1,CLDN1,WNT5A,ZNF304,ARTN,APC,HRAS,FGF1,CBLL1,PDGFD	grey	VSMC_M10
GO:0018193	1.00	0.00	481	997	peptidyl-amino acid modification	BP	1	ERBB3,CLK4,ATAT1,YEATS4,SNW1,ZDHHC14,BRD1,P4HA2,IL5,ROS1,PHF1,BAK1,NCOA7,PTK2,AGTPBP1,MAPK14,NTRK2,UHRF2,MAPK13,STK38,CSNK1E,ZDHHC21,HSF1,TEK,PRDM4,TTBK1,TEC,SUPT3H,KIT,SLC1A1,NCK2,ROR2,SEMA4D,GAPDH,PDCL3,HINT2,PHF14,LIPT1,ADH5,KANSL3,CAMKMT,IL11,BRSK1,PRKCE,PPP2R1A,IBTK,VRK2,EPGN,AREG,FKBP9,AGBL3,FKBP15,EPHA7,TGFA,MET,VRK3,EGFR,ING3,EPHA1,IL15,ATG5,SETD7,TRPM4,NTF4,BRAF,SPHK2,HDAC2,BMI1,NDNF,MKNK1,PRKD2,SETDB2,ABI1,QPCTL,EED,IWS1,CRTAP,SUV39H2,SUMO2,DPH2,KDM4A,PRKAG2,GALNT11,RAF1,OXSR1,PRDX3,PIBF1,PAXIP1,EGLN2,MGAT5B,SPRY2,ALK,TTLL3,TADA3,AKT2,GPD1L,ARRB1,DYRK1B,TGFBR2,UGGT2,IKBKB,CBX4,SIRT2,RPTOR,AATK,DPY30,HBEGF,PLCL2,MAP4K1,DPH3,SIRT7,EIF2AK2,NSD3,PRNP,NDUFAF7,BAG4,TAF7,DCN,ASH2L,NRG1,EP400,GAS6,HPX,ULK1,SIRT3,TAF10,PRKDC,EOGT,ERCC6,FLT1,NR1H4,EPHB1,PLK2,SDR16C5,RET,HCK,TTL,ZDHHC20,ASPH,EEF1AKMT1,DNMT3B,ACVR1B,CAMK4,FER,SMYD1,MAST4,OSBP,HPF1,TAF9,PRMT9,ATR,DCLK2,EYA1,FBXW7,PTPRJ,AGBL2,PHF20,IL7,SETD6,CSNK2A2,CFAP20,ART3,PTK2B,FNIP2,KMT2D,RPN2,MAPKAPK5,ARL2BP,NNAT,PAQR3,KANSL2,RIPK2,SENP1,TOP1,HDAC7,RAPGEF3,LOXL2,GOLGA7B,RIPK1,LOXL4,RTF1,STK4,MORC3,HIF1AN,DMTN,NOD2,PRMT3,SIRT5,WDR82,CNTN1,ZNF335,JARID2,TOLLIP,RBBP5,CD40,DSTYK,LDB1,FAM173B,IGF2,DCAF1,BDNF,SIRT4,MAPKAPK3,IFIH1,NEURL1,LRRK1,HDAC1,LCK,BANK1,CAPRIN2,ZDHHC23,MAP2K6,TPST1,ADRA2A,POGLUT1,ZDHHC6,CAMKV,DAD1,PRKX,TTBK2,AUTS2,MARK1,PIAS3,NCF1,MST1,DYRK3,MAPKAPK2,EGF,HCLS1,ADNP,RPS6KB2,	grey	VSMC_M10
GO:0032270	1.00	0.00	517	1066	positive regulation of cellular protein metabolic process	BP	1	ERBB3,LRP1,MAP3K5,TNFAIP3,AGAP2,MRNIP,RMND1,STK3,PRR16,PABPC1,SNW1,HSPA1B,EIF3E,GRAMD4,MAP3K4,PRKN,AGER,FBLN1,IL5,GDF9,DERL1,SKP1,PHF1,BAK1,RNF217,XRCC6,TRIB1,MYC,JMJD4,AGO2,HABP4,PTK2,TAB1,AGTPBP1,NTRK2,CSNK1E,PLA2G6,C6orf89,HSF1,CCND3,MYH9,CHRNA3,TEK,CRY1,TTBK1,TEC,KIT,SLC1A1,NCK2,PLGRKT,ROR2,SEMA4D,CLDN19,IL11,RNF20,FPR2,MOB1B,EPGN,NOD1,AREG,AKIRIN2,BMP8A,CASP8AP2,PELI1,ETAA1,RSPO1,EPHA7,NR1H2,TNFSF15,TGFA,ITGB1BP1,VRK3,EGFR,ARHGEF5,TRIM32,TLR4,IL15,CCNY,VPS35,ZYG11B,SDCBP,NTF4,FAF1,FGF21,BRAF,HSPE1,SPHK2,HDAC2,BBS7,SLC8A2,BMI1,MOB3C,PRKD2,CNBP,PHB,ABI1,SOX9,SYMPK,MAPRE3,PLK3,SUMO2,CDC123,RALB,PRKAG2,RAF1,PIBF1,PAXIP1,WDR48,MYCBP2,FBH1,SPRY2,WNT11,KLHL40,AKT2,ARRB1,TGFBR2,ACVR2A,SIRT2,NMI,NEK10,RPTOR,TCIM,HBEGF,ASPSCR1,CHTOP,NSD3,PRNP,BAG4,MAVS,RNF14,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,HPX,RBPMS,UPF3A,ARL6IP5,PRKDC,ERCC6,FLT1,ST18,ADRA2B,TRAF6,TRIB3,PLK2,SDR16C5,RET,ASPH,FAM107A,DNMT3B,ACVR1B,CEBPA,FOXL2,OSBP,SPSB4,ZFP91,HIP1R,TRABD2A,ING2,ROBO1,PCOLCE2,DIABLO,MRPS27,SH3D19,ARNTL,FBXW7,PTPRJ,HTRA2,VEGFC,P2RY1,USP16,ATG10,MADD,PTK2B,RASGRP1,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,NR1H3,TIAM1,FGF5,RIPK2,NBN,SENP1,NKX3-1,RAPGEF3,ACVR1C,F2R,RNFT2,RIPK1,MARCH7,CDK2AP1,PIDD1,KCNE2,RTF1,PKD2,STK4,PRICKLE1,ADTRP,NOD2,CNTN1,JARID2,TAOK3,TENT4B,TOLLIP,CD40,IGF2,BMPR1B,NHLRC1,RNF144B,BDNF,GPLD1,RHBDD1,NEURL1,SPPL3,RPUSD4,LRRK1,HDAC1,LCK,BANK1,CC	grey	VSMC_M10
GO:0045669	1.00	0.00	18	56	positive regulation of osteoblast differentiation	BP	1	SMAD5,ACVR2B,ACVR2A,JAG1,CLIC1,CEBPA,MEF2C,BMPR1B,WNT4,SUCO,BMPR1A,PDLIM7,IL6R,ATP6AP1,WDR63,MIR21,MIR27A,CEBPB	grey	VSMC_M10
GO:0007062	1.00	0.00	14	47	sister chromatid cohesion	BP	1	MCMBP,SLF1,FBXW7,SLF2,AXIN2,HORMAD2,POGZ,MAU2,STAG3,DDX11,RAD51C,SFPQ,NAA10,CTCF	grey	VSMC_M10
GO:0045931	1.00	0.00	36	97	positive regulation of mitotic cell cycle	BP	1	VPS4B,PPP1R10,HSF1,CCND3,ANKRD17,LSM10,EGFR,UBE2E2,RPTOR,PLCB1,TFDP1,MTA3,TTL,ANAPC5,ANAPC7,ADAMTS1,NKX3-1,HYAL1,CCND1,TERT,USP2,STOX1,DBF4B,DDX3X,MEPCE,STAT5B,ANAPC4,RAD51B,RAB11A,RAD51C,SIN3A,MECP2,CDK10,MIR29A,MIR222,RGCC	grey	VSMC_M10

GO:0042127	1.00	0.00	601	1230	regulation of cell population proliferation	BP	1	NME1,ERBB3,C18orf54,SHMT2,PGGT1B,GLI1,B4GALT7,MAP3K5,RPA3,TNFAIP3,TSPAN31,CYP27B1,ENPP3,ESR1,FRS2,CNOT6,RIDA,STK3,OSR2,HSPA1B,AGER,FBLN1,IL5,HLA-DPB1,TSPO,GDF9,TNFRSF13C,BAK1,XRCC6,MTSS1,TRIB1,MYC,TOB2,PTK2,PTCH1,AKR1B1,MAPK15,AGTPBP1,MAPK14,NTRK2,KDM4C,SOX10,PIM1,RAC2,SMO,HSF1,CCND3,CDKN2A,ZNF16,RBFOX2,IFT74,TEK,SRF,NUAK1,CNTFR,CDK6,SMARCA2,SLC25A27,KIT,TNFRSF21,NCK2,TFAP2B,ROR2,DLX5,S1PR3,TBC1D8,PDCL3,WNK2,OGN,ZNF268,CLDN19,SIX2,IL11,EPCAM,CD109,FKTN,RTN4,PHIP,GSDME,SKAP2,FANCL,EMC10,CXCL8,EPGN,AREG,AKIRIN2,AQP1,PELI1,AKIRIN1,TGFA,PTN,ITGB1BP1,MED25,KLF11,TNC,IL4I1,POU3F3,EGFR,FUZ,TRIM32,TLR4,EPHA1,IL15,SFRP4,SDCBP,MYCN,TRPM4,SLC7A11,OSR1,FOXO3,EPS15,FGF21,INTU,SPHK2,CDCA7,SPRY1,WISP3,FOXE3,HDAC2,BMI1,C5AR2,C5AR1,PRKD2,PTGIR,CNBP,PHB,ABI1,SOX9,BEX4,GAB2,CDC123,GLI2,AQP11,RAF1,MYD88,DACH1,PRDX3,KLF5,IFT172,FOXJ1,SCN5A,WDR48,ACER3,SPRY2,THAP12,WNT11,ALK,AKT2,RBBP9,ARRB1,ABCC4,EID2,TGFBR2,OVOL2,JAG1,SIRT2,NMI,RPTOR,RARB,PURA,HBEGF,PAWR,MAFG,FERMT1,CHTOP,SPINT2,CNN2,EIF2AK2,PRNP,ADRA1D,ING1,ASH2L,BTG1,MAB21L1,AIMP1,NRG1,TFDP1,CCKBR,DDRGK1,NCKAP1L,GAS6,FOXP1,MITF,MTA3,PRKDC,SLC7A1,FLT1,ST18,CIAO1,TMEM127,TRAF6,EPHB1,PLAG1,HCK,TOX,IL1A,CYP7B1,NR4A1,CEBPA,FER,CASP3,HAND2,ATP5F1A,ING2,HPGD,EYA1,ROBO1,MAB21L2,FBXW7,PTPRJ,FZD3,BTG3,MEF2C,TMEM131L,PEX2,IL7,VEGFC,CELF1,ADAMTS1,PTK2B,CNOT6L,KMT2D,RAPGEF2,RPRD1B,EAPP,TIAM1,FG	grey	VSMC_M10
GO:0009628	1.00	0.00	427	891	response to abiotic stimulus	BP	1	FECH,MAP7,MRNIP,CPT1B,SLC12A2,HSPA1B,BRD1,MAP3K4,AGER,PPARA,TSPO,SYNGAP1,UBE2B,BAK1,XRCC6,MYC,PKD2L2,HABP4,PTK2,PTCH1,AKR1B1,ATF4,MAPK14,MAPK13,PICK1,TXN2,HSF1,FBXL6,OPN1SW,TEK,PRPH2,CRY1,SRF,ABCB1,PHF24,FANCG,SLC25A27,KIT,SLC1A1,CA9,PDCL3,REV1,ETV1,ABCG5,CAT,CAMKMT,DNAJA1,BRSK1,PRKCE,EPAS1,RDH13,MSH2,CYB5R4,AQP1,CASP8AP2,GJA10,WHRN,PTN,TNC,EGFR,TRIM32,TLR4,GRIK2,UCP1,MGARP,SLC7A11,FOXO3,SMPD2,MKX,HDAC2,TRPC3,DNMT3A,NDNF,SLC26A5,SOX9,ERCC1,XPC,ERCC2,SLC39A12,ERCC3,EIF2B3,SUV39H2,ASIC3,PLK3,XRCC1,STAC,B4GALT2,RAF1,XRCC2,MYD88,OXSR1,ZRANB3,SCN1A,PAXIP1,EGLN2,AANAT,CYGB,THBD,SCEL,HNMT,PPP1CB,PLAT,WNT11,AKT2,TGFBR2,XRRA1,PLEKHB1,BHLHE40,SIRT2,MKKS,CLPB,TCIM,RYR1,CNN2,DDHD2,DCN,P2RX2,PDK1,WRN,PRKDC,ERCC6,EPHB1,COX4I2,NPHP1,TM9SF4,ERCC8,IL1A,DNMT3B,GPI,NR4A1,AHCY,PIK3R1,PRIMPOL,CASP3,ATR,EYA1,P2RX3,CEP250,CCDC66,ADGRV1,FZD3,ASIC1,HTRA2,SCARA3,TMBIM6,VEGFC,RAD9B,CYP2R1,HVCN1,P2RY1,XRCC4,PTK2B,MME,BACH1,EIF2AK4,DDB2,RAB11FIP5,TMEM150C,TENT2,STC1,NKX3-1,ABRAXAS1,OPA1,SPIDR,CDS1,RAD54B,KCNJ3,LOXL2,NR4A2,SLC38A2,CRY2,TP53INP1,ABCC2,PKD2,HIF1AN,CYFIP1,ITGB6,GMPR,SLC12A5,CD40,RYR2,SLC4A10,SIRT4,GPLD1,TRPM1,KIAA0319,RHBDD1,DNM1L,GLRX2,SIK1,HDAC1,HYAL1,HYAL3,CCND1,ICOSLG,KCNJ2,TERT,SLC38A3,TRPV4,TGFB2,PDCD6,SCN2A,DAG1,AJUBA,TLR5,KRAS,MAPKAPK2,PITPNM1,RRH,AEN,USP19,OPRD1,DISC1,POLG,SPRTN,SAG,CHEK2,EYA3,TRPM8,USP2,AGT,CBL,HYOU1,ARNT,ATP1A2,BAG3,SLC9A1	grey	VSMC_M10
GO:0016310	1.00	0.00	705	1440	phosphorylation	BP	1	NME1,ERBB3,LRP1,CLK4,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,ATP23,USP15,MAML1,MRNIP,STK3,ADM2,TNXB,MAP3K4,PRRT1,PRKN,AGER,PPARA,FBLN1,IL5,BRD2,GDF9,ROS1,UBE2B,BAK1,XRCC6,TRIB1,SMAD5,OBSCN,PRXL2C,PTK2,TAB1,MAPK15,MAPK14,NTRK2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,PIM1,CKB,HSF1,ADCK5,CCND3,CDKN2A,ZNF16,NMRK1,CHRNA3,TEK,TRPM6,FBXO7,CRY1,PTK7,TTBK1,NUAK1,CDK14,TEC,CDK6,KIT,SLC1A1,NCK2,ROR2,SEMA4D,GAPDH,CDK20,PDCL3,WNK2,IPPK,KLHL31,CLDN19,DNAJA1,IL11,BRSK1,PRKCE,CD109,SPTBN1,PPP2R1A,PHIP,FPR2,IBTK,ACP4,MOB1B,VRK2,SLC4A4,EPGN,AREG,BMP8A,BPGM,BMPER,WDR91,ETAA1,RSPO1,AAK1,EPHA7,TNFSF15,TGFA,ITGB1BP1,DGKI,MET,VRK3,GRB10,YWHAZ,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,MYLK3,SDCBP,NTF4,AGK,CDK19,FGF21,BRAF,PRKAR2B,SPHK2,SPRY1,CMPK1,HDAC2,SLC8A2,C5AR1,PIP4K2A,MKNK1,MOB3C,PRKD2,MYO3A,PHB,ABI1,SOX9,MAPRE3,KHK,PLK3,FASTK,LIPE,DHTKD1,RALB,PRKAG2,RAF1,OXSR1,PRDX3,XYLB,PIBF1,ACVR2B,ITPKC,IRAK2,GCKR,RBKS,FBH1,SPRY2,WNT11,ALK,TADA3,AKT2,GPD1L,ARRB1,DYRK1B,TGFBR2,PFKP,PGM2L1,ACVR2A,IKBKB,SIRT2,NEK10,RPTOR,AATK,TCIM,HBEGF,PTPRQ,PLCL2,MAP4K1,EIF2AK2,PRNP,DUSP6,NEK11,BAG4,TAF7,PANK2,MAVS,PDK1,CDKL4,NRG1,CCKBR,DDRGK1,NCKAP1L,GAS6,HPX,ULK1,PTPRA,RBPMS,PRKDC,ERCC6,FLT1,RYK,PAN3,ADRA2B,TRAF6,STK33,AMHR2,TRIB3,EPHB1,PLK2,MOS,RET,HCK,PANK1,GPI,ACVR1B,CAMK4,CEBPA,FER,PIK3CB,SNX25,MAST4,OSBP,PIK3R1,ZFP91,CDK7,CASP3,GK5,RAD17,CLP1,ATR,DCLK2,ROBO1,PLCE1,FBXW7,PTPRJ,GPD1,PKIA,IL7,CCNH,P2RX7,VEG	grey	VSMC_M10
GO:0033673	1.00	0.00	79	191	negative regulation of kinase activity	BP	1	PIP4K2C,TNFAIP3,PRKN,TRIB1,STK38,CDKN2A,FBXO7,DNAJA1,IBTK,ACP4,ITGB1BP1,EPHA1,PRKAR2B,SPRY1,PIP4K2A,PRKAG2,PRDX3,GCKR,SPRY2,PTPRQ,TAF7,TRIB3,CEBPA,PIK3CB,CASP3,PTPRJ,PKIA,PAQR3,DBNDD2,DTNBP1,PDCD4,PRKAR1A,ADARB1,AJUBA,FABP4,UBASH3B,SORL1,RTRAF,AGT,CBL,SFN,PPP2R5A,CAMK2N2,RUBCN,PTPRO,PIK3IP1,SNX6,CDKN1B,AIDA,YWHAG,DUSP10,MAPT,HEXIM2,MEN1,DUSP19,PTPN6,ZFYVE28,SOCS4,RGS14,PSEN1,PYDC1,COX11,SMCR8,PTPN2,INPP5K,PDPK1,PARK7,DBNDD1,DAB2IP,MIR24-1,SMYD3,THY1,GADD45A,DUSP26,DUSP1,APC,DUSP22,LAX1,PRKRIP1	grey	VSMC_M10
GO:0010039	1.00	0.00	6	26	response to iron ion	BP	1	TFAP2A,SLC6A3,CCND1,ABAT,LCN2,FXN	grey	VSMC_M10

GO:0030029	1.00	0.00	308	662	actin filament-based process	BP	1	NEDD4L,ARPC3,MYO1A,LRP1,AGAP2,AVIL,TNXB,PRKN,PARVG,SHROOM1,MTSS1,WASHC5,EPB41L2,OBSCN,SUN2,BAIAP2L2,PICK1,CDC42EP1,RAC2,DAAM2,FLNC,MYH9,TEK,LMOD2,PTK7,SRF,PGM5,CCL27,KIT,NCK2,TLN1,KIAA1211,PDCL3,FGD3,CCIN,TMOD1,PLEKHH2,NLRP5,CLDN19,PRKCE,SPTBN1,EPB41L4B,RUFY3,SHANK1,LPAR1,AQP1,EHBP1,MYH14,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,TRIM32,EPHA1,GAB1,CCDC155,MYLK3,SDCBP,FAM49A,TRPM4,WASF1,ARHGAP12,KPTN,MSRB2,IQSEC1,ABI1,MYO7B,CACNB2,LCP1,CLASP2,LLGL2,FOXJ1,SCN5A,SCN1A,MYO7A,WNT11,GPD1L,ARRB1,PLEKHG2,IKBKB,FARP1,FCHSD2,MKKS,ACTG1,FSCN2,PAWR,RAC3,CNN2,BAG4,DIAPH1,FCHSD1,ARHGAP26,FGD6,NCKAP1L,ARFIP2,LMOD3,DPYSL3,TTC17,NPHP1,HCK,FAM107A,FER,MRAS,FLNB,PIK3R1,HIP1R,PARVA,PLS1,FMN1,LIMA1,SORBS1,EPB41L1,RTKN,SDAD1,PTK2B,RND1,ALMS1,USH1C,STC1,RAPGEF3,KCNJ3,RHOBTB2,BIN3,F2RL1,IQGAP2,TNNC1,KCNE2,ITPKA,DSP,CYFIP1,DMTN,DTNBP1,RYR2,NUAK2,GAS2,MAGEL2,PXN,RAP1GDS1,ELMO2,INA,PKP2,CARMIL1,PPFIA1,FGD4,LMOD1,ADD3,KCNJ2,TRPV4,ADRA2A,TBCK,PRKAR1A,AUTS2,SSH1,CFL1,SHROOM2,KRAS,HCLS1,ARHGAP6,MYH7,AP1AR,EPB41,ANK2,CASS4,SPATC1L,WASF2,ATP1A2,ACTC1,SLC9A1,SPTBN2,MYOZ2,CASQ1,ITGB5,ACTN3,TMOD4,EPS8,SCN4B,RHOBTB1,FARP2,GRHL3,LIMK2,NOS1AP,WHAMM,DLG1,FRMD5,CAPZA1,MYPN,CDC42EP2,BCL6,ABL2,TTN,DIXDC1,NCKAP1,MCU,ABLIM2,WNT4,MYOZ1,ARPC1A,TRPM7,SMTNL2,BST1,DAAM1,WAS,TMOD2,MYO9B,OBSL1,MINK1,RHOJ,TPM4,SYNE2,ARHGEF19,ACTB,SHROOM4,LDB3,SPTB,WIPF2,SYDE1,IQSEC2,PDLIM7,TCAP,P	grey	VSMC_M10
GO:2001234	1.00	0.00	78	187	negative regulation of apoptotic signaling pathway	BP	1	EYA4,TNFAIP3,MAPK8IP2,HSPA1B,PRKN,ZC3HC1,TMEM14A,DNAJA1,PHIP,TRIM32,BMI1,ARMC10,DDIAS,RAF1,ZMYND11,IL1A,FAIM,TAF9,ING2,EYA1,IL7,FAIM2,HTRA2,TMBIM6,NDUFS3,CSNK2A2,OPA1,NR4A2,RIPK1,MARCH7,BDNF,HDAC1,TERT,TCF7L2,SNAI1,EYA3,IFI6,MCL1,HYOU1,STRADB,PEA15,PELI3,RTKN2,FZD9,YBX3,NFE2L2,IVNS1ABP,NONO,SYVN1,DDX3X,WNT4,HTT,PSME3,PINK1,PSEN1,MUC1,TAF9B,MAP2K5,PSMD10,CD74,MAPK7,NLE1,ACAA2,PAM16,PARK7,GNAI3,MIR21,MIR222,FGA,NOL3,NOG,FXN,SLC35F6,PTTG1IP,BCL2L2,CAAP1,PPIF,AC140504.1	grey	VSMC_M10
GO:0019058	1.00	0.00	102	239	viral life cycle	BP	1	VPS4B,YTHDC2,PABPC1,HSPA1B,PRKN,PPARA,LY6E,APOBEC3H,CHMP2A,CXCL8,RSAD2,PCBP1,EGFR,TRIM32,ATG5,EPS15,HS3ST5,ZC3HAV1,RAB7A,KPNA3,PHB,NECTIN2,FBXL2,PVR,RPSA,KPNA2,SLC20A2,ATG16L2,RAB5A,EIF2AK2,MAVS,GAS6,PCBP2,IDE,CHMP2B,FAM208A,CHMP4C,EIF2AK4,SPCS1,OAS3,TPCN1,CHMP7,VPS18,ITGB6,IFIH1,OASL,TMEM39A,ADARB1,NR5A2,DAG1,ZNF639,SELPLG,STAU1,HSPA8,GRK2,ATG16L1,PC,ACE2,DDX6,ITGB5,NECTIN4,XPR1,RAB1B,CD28,VPS37D,LRRC15,PIKFYVE,DDX3X,PI4KA,SLC3A2,DDB1,HACD3,LDLR,LARP1,TNIP1,CD74,CCL5,NPC1,CCL2,CIITA,FMR1,INPP5K,BSG,CHMP1A,LAMTOR5,MVB12B,WWP2,VPS4A,MIR222,HTATSF1,HAVCR1,SETDB1,OAS1,TRIM68,DPP4,TRIM34,CD46,CLDN1,TBC1D20,ZNF502,EFNB3,FAM111A	grey	VSMC_M10
GO:0045766	1.00	0.00	52	133	positive regulation of angiogenesis	BP	1	ADM2,AGO2,TEK,PDCL3,NINJ1,EMC10,CXCL8,AQP1,BMPER,EPHA1,GAB1,C5AR1,PRKD2,SLC39A12,TGFBR2,BTG1,FLT1,IL1A,ERAP1,VEGFC,PTK2B,RAPGEF3,AGGF1,CD40,HYAL1,TERT,PDCD6,VASH2,NFE2L2,CTSH,CXCR2,RAMP2,STAT3,FGF18,PGF,PRKCB,GATA6,ISL1,JAK1,C3,PDPK1,ENG,MIR29A,MIR199A1,MIR21,MIR27B,ACVRL1,MIR125A,MIR99B,WNT5A,ZNF304,FGF1	grey	VSMC_M10
GO:1904018	1.00	0.00	52	133	positive regulation of vasculature development	BP	1	ADM2,AGO2,TEK,PDCL3,NINJ1,EMC10,CXCL8,AQP1,BMPER,EPHA1,GAB1,C5AR1,PRKD2,SLC39A12,TGFBR2,BTG1,FLT1,IL1A,ERAP1,VEGFC,PTK2B,RAPGEF3,AGGF1,CD40,HYAL1,TERT,PDCD6,VASH2,NFE2L2,CTSH,CXCR2,RAMP2,STAT3,FGF18,PGF,PRKCB,GATA6,ISL1,JAK1,C3,PDPK1,ENG,MIR29A,MIR199A1,MIR21,MIR27B,ACVRL1,MIR125A,MIR99B,WNT5A,ZNF304,FGF1	grey	VSMC_M10
GO:0009725	1.00	0.00	305	652	response to hormone	BP	1	FECH,AP3S1,MARS,PIP4K2C,CYP27B1,ESR1,CNOT2,TPH2,PPARA,TNFRSF11B,PNPLA3,RXRB,TSPO,PTK2,AKR1B1,GKAP1,KDM4C,SOX10,TXN2,HSF1,CCND3,FOXH1,GPT,RBFOX2,TEK,CRY1,SRF,STEAP2,KIT,FHL2,PPAT,CAT,DNAJA1,PRKCE,PHIP,PNPT1,ME1,AREG,CRHR2,AQP1,PTN,GRB10,TNC,EGFR,LANCL2,GAB1,LPIN1,SFRP4,UCP1,MGARP,FOXO3,PGRMC2,APOB,FGF21,SESN3,BMI1,SLC26A5,PIP4K2A,RAB10,HADHA,PHB,CYSLTR2,GLB1,KHK,EIF2B3,EPM2AIP1,ECHDC3,ATP1A3,TIMP4,TBC1D4,EGLN2,AANAT,HNMT,TADA3,AKT2,TGFBR2,SNX5,MKKS,RARB,NR1D2,SRA1,CRLS1,TAF7,ASH2L,BTG1,RNF14,KL,DDRGK1,PTPRA,FOXP1,LEPROTL1,ARID5A,PRKDC,CALCOCO1,NCOA4,TUB,TRIB3,LMO2,FAM107A,CYP7B1,DNMT3B,GPI,PAX8,NR4A1,FER,IDE,UFSP2,NCOA6,PIK3R1,CASP3,NCOA2,ROBO2,ZNF366,ARNTL,SORBS1,MEF2C,CNOT1,PTK2B,KMT2D,NR1H3,DDX54,STC1,NKX3-1,OPA1,LPIN3,NKX6-1,NR4A2,ACVR1C,SRSF6,CRY2,VPS18,ABCC2,SPP1,CPN1,CYFIP1,ADTRP,RBBP5,IGF2,PXN,GPLD1,SRD5A1,IRS1,GRB14,HDAC1,CCND1,TRPV4,TGFB2,ADRA2A,SLC30A10,NR5A2,DAG1,PIAS3,KRAS,HCLS1,ABHD2,SRSF4,SORL1,C2CD5,GPER1,AGT,ATP1A2,SLC9A1,ARID1A,UCN2,HDAC4,SYAP1,USF1,NPAS4,DTYMK,SCAP,CDKN1B,RXRG,POR,NFE2L2,CREB1,YWHAG,SORD,RAP1B,PLOD3,VGF,CPS1,EIF4EBP2,CTSH,MEN1,ACSBG1,SIK2,COMT,ESRRA,BCHE,FBN1,RPL27,PTGER2,ALPL,GDF15,RAMP2,CTSV,STAT3,PTPRN,CD38,SLC27A1,MAPK1,STAT5B,RAB8A,PADI2,SCGB1A1,DNAAF4,GPR173,AKAP8,PARP1,SLC2A4,RAB15,THRA,MAX,MED1,AGTRAP,ANXA2,VPS13C,FOXO4,PKLR,PAGR1,RAB8B,ITGA3,PGF,FOS,NDEL1,ZBTB7B,OGT,ESRRB,CITED1,UPRT,SOX3	grey	VSMC_M10

GO:2001233	1.00	0.00	129	292	regulation of apoptotic signaling pathway	BP	1	EYA4,TNFAIP3,TRIM39,STK3,MAPK8IP2,HSPA1B,PRKN,ZC3HC1,NCK2,TMEM14A,DNAJA1,PHIP,GSDME,TRIM32,TRAF1,BCL2L12,FAF1,BMI1,ARMC10,DDIAS,PDIA3,DEDD2,RAF1,FBH1,ZMYND11,RET,IL1A,FAIM,TAF9,ING2,EYA1,FBXW7,IL7,FAIM2,HTRA2,TMBIM6,NDUFS3,CSNK2A2,MADD,NKX3-1,OPA1,NR4A2,RIPK1,MARCH7,STK4,SIAH1,BMPR1B,BDNF,DNM1L,HDAC1,LCK,SP100,TERT,TCF7L2,SNAI1,GPER1,EYA3,IFI6,MCL1,AGT,HYOU1,STRADB,NFATC4,PEA15,PELI3,RTKN2,ING5,FZD9,RPL11,YBX3,NFE2L2,IVNS1ABP,NONO,FIS1,PRKRA,SYVN1,CTSH,DDX3X,WNT4,HTT,PSME3,PINK1,LTBR,SGMS1,MAGED1,PARP1,STX4,PSEN1,NGFR,DAPK2,MUC1,TAF9B,MAP2K5,S100A8,SFPQ,PSMD10,CD74,MAPK7,NLE1,PTPN2,ACAA2,PIAS4,PAM16,BCAP31,TRAF2,PARK7,GNAI3,BCL10,DAB2IP,MIR21,MIR222,MIR27B,FGA,UBB,NOL3,FADD,NOG,FXN,DDIT3,BCL2L11,SLC35F6,PTTG1IP,PLAGL2,BCL2L2,CAAP1,CRADD,PPIF,PTPMT1,AC140504.1	grey	VSMC_M10
GO:0001655	1.00	0.00	122	283	urogenital system development	BP	1	GLI1,ESR1,FRS2,RIDA,OSR2,TBC1D32,MTSS1,MYC,SMAD5,KLHL3,PTCH1,AKR1B1,PODXL,SMO,TEK,PTK7,TFAP2B,PPAT,C1GALT1,ANKS6,CAT,SIX2,EPCAM,HOXA13,BMPER,EPHA7,TNC,POU3F3,CNTRL,OSR1,TRAF3IP2,SPRY1,SOX9,GLI2,AQP11,FOXJ1,GZF1,WNT11,JAG1,RARB,FREM2,CEP290,DCN,PLAG1,RET,ASXL1,CYP7B1,PAX8,HPGD,EYA1,ROBO2,PLCE1,FMN1,MEF2C,ADAMTS1,MME,FRAS1,NKX3-1,RPGRIP1L,PKD2,TFAP2A,PAX2,SALL1,SRD5A1,IRX2,TGFB2,SULF2,PRKX,ENPEP,AP1B1,AGT,BICC1,TRAF3IP1,LAMA5,PTPRO,EPHB3,CDKN1B,DLG1,OVOL1,CTSH,FBN1,CXCR2,WNT4,EPHA4,MAGED1,ALDH1A2,ITGA3,TMED10,CITED1,IL6R,SMAD3,LHX1,STRA6,AP2B1,NLE1,ZBTB14,IFT20,GPC3,HSPB11,PKD1,SOX8,WDR77,TSC1,FOXF1,ASS1,PKD1L3,RHOA,FSTL3,SERPINB5,SOX4,FADD,CA2,MIR125A,NOG,WNT5A,BASP1,SIX1,BCL2L11,LIF,KCNJ8,FGF1,PDGFD	grey	VSMC_M10
GO:2000147	1.00	0.00	207	455	positive regulation of cell motility	BP	1	ONECUT2,LRP1,SEMA6A,AGER,GPSM3,AGO2,PTK2,SUN2,PODXL,RAC2,SMO,TEK,CFAP69,CCL27,KIT,ROR2,SEMA4D,SEMA4C,ZNF268,PRKCE,EPCAM,RTN4,FPR2,EPB41L4B,RUFY3,EMC10,CXCL8,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,TRIM32,TLR4,TCAF2,EPHA1,GAB1,SDCBP,C5AR1,SLC26A5,PRKD2,IQSEC1,SOX9,CLASP2,OXSR1,SPRY2,WNT11,RIN2,AKT2,TGFBR2,ACTG1,HBEGF,FERMT1,BAG4,ARHGEF7,SEMA3D,DIAPH1,SEMA3A,DRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,FLT1,PLK2,RET,FAM107A,GPI,ACVR1B,FER,PIK3CB,PIK3R1,ATP5F1A,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,ADAMTS1,PTK2B,RAPGEF2,TIAM1,DOCK5,HDAC7,F2RL1,F2R,ANO6,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,CD40,SRGAP2C,GPLD1,LGR6,DNM1L,CARMIL1,HYAL1,PPP3CA,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,CD99,PRSS56,SSH1,CMKLR1,SNAI1,EGF,GPER1,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,HDAC4,MAP3K3,DOCK1,ELP6,ADAM8,LRRC15,NFE2L2,MIA3,DUOX1,CCAR1,CEMIP,SEMA6D,TRIP6,CTSH,ITGA2B,ITGA4,IL12A,FN1,VSIR,SPOCK2,MCU,PDCD10,TNFSF18,FERMT3,CXCR2,STAT3,MAPK1,RHOJ,SYNE2,CXCL16,SYDE1,TMEM102,MIEN1,STX4,SEMA4A,RAB25,FGF18,FOXO4,ITGA3,PGF,DAPK2,ZNF609,MAPK3,IL6R,RAB11A,SMAD3,NTN1,S100A14,BDKRB1,BCAS3,CD74,INSR,CCL5,CSF1R,CCL7,DOCK7,CRK,PDPK1,FBXO31,FOXF1,LCN2,HSPA5,DAB2IP,CARMIL2,RIPOR1,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR27B,MIR27A,RHOA,DEFB124,FADD,LAMB1,ZNF580,THY1,CLDN1,WNT5A,ZNF304,APC,HRAS,FGF1,CBLL1,PDGFD	grey	VSMC_M10
GO:1902533	1.00	0.00	346	731	positive regulation of intracellular signal transduction	BP	1	ERBB3,LRP1,MAP3K5,USP15,FRS2,STK3,MAPK8IP2,HSPA1B,MAP3K4,PRKN,AGER,RGL2,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,TAB1,NTRK2,PLA2G6,TEK,GPR37,LRRD1,SLC35B2,KIT,NCK2,ROR2,GADD45G,SEMA4D,GAPDH,SEMA4C,CAT,IL11,PRKCE,RTN4,FPR2,GSDME,EMC10,LPAR1,REL,ANKRD17,SLC46A2,MTURN,EPGN,NOD1,RRAGD,PELI1,BMPER,TGFA,ITGB1BP1,MET,EGFR,ARHGEF5,TRIM32,TLR4,TRAF1,SDCBP,PUM2,FGF21,BRAF,TRAF3IP2,SPHK2,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,SOX9,GIPR,RAF1,MYD88,FBH1,SPRY2,WNT11,ALK,DYNC1LI1,ARRB1,PIP4P1,IKBKB,C1QTNF1,NMI,NEK10,RPTOR,TCIM,HBEGF,PDE6G,PLCB1,RASGRP4,EIF2AK2,ADRA1D,BAG4,DCN,MAVS,RELL2,SEMA3A,P2RX2,KL,NRG1,SH3RF2,NCKAP1L,GAS6,LARS,ARL6IP5,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,TRIM44,SLC38A9,TMEM9B,ST5,PLK2,MOS,RET,PIK3CB,HAND2,ATR,ROBO1,P2RX3,PLCE1,FBXW7,ADGRV1,PTPRJ,GUCY1A1,P2RY1,MADD,PTK2B,RASGRP1,RAPGEF2,CCL17,TIAM1,RIPK2,NKX3-1,F2RL1,F2R,NQO2,RIPK1,ZDHHC13,PLA2R1,GCNT2,NOD2,TAOK3,CD40,DSTYK,SIAH1,IGF2,SPPL3,RPL23,OASL,DNM1L,LRRK1,LCK,BANK1,MAP2K6,TRPV4,PDCD4,TGFB2,ADRA2A,SLC30A10,TCF7L2,EDARADD,GPR137B,AUTS2,AJUBA,NCF1,KRAS,EGF,HCLS1,SOX2,TIFA,ALPK1,GPER1,DOK5,CASS4,SPATC1L,MCL1,AGT,FGR,CIB1,CBL,TRAF5,DVL3,SLC9A1,GOLT1B,FZD7,OSM,TRIM52,THPO,CD28,PDE6H,MAP3K3,PDE8A,RTKN2,NOS1AP,RPL11,SIK3,MAP3K11,ADAM8,FZD5,MBIP,RAP1B,TAB3,STOX1,FIS1,PRKRA,TRIP6,MAP4K2,DDX3X,FN1,DUSP19,RC3H1,PTPN6,GPR137,PDCD10,ADRA2C,GPBAR1,COL3A1,TNIP2,GDF15,FGFR3,PINK1,MUL1,B		
GO:2000114	1.00	0.00	4	21	regulation of establishment of cell polarity	BP	1	RUFY3,PTK2B,RAP1B,BCAS3	grey	VSMC_M10

GO:0006952	1.00	0.00	457	949	defense response	BP	1	CD226,SHMT2,MAP3K5,TNFAIP3,CYP27B1,USP15,ENPP3,TRIM39,ESR1,MAPK8IP2,AGER,PPARA,GPSM3,TAP1,IL5,XRCC6,PTK2,C6orf106,APOBEC3H,MAPK14,MAPK13,PLA2G6,EXOSC4,HSF1,IRF5,TEK,TTBK1,NFX1,USP46,KIT,SLC1A1,PLGRKT,IL1R2,GAPDH,S1PR3,NINJ1,PRDX1,RAB23,SDHAF4,FPR2,REL,NT5E,ANKRD17,CXCL8,NOD1,AKIRIN2,AQP1,LYPD8,RSAD2,NR1H2,AKNA,PTN,EGFR,TRIM32,TLR4,IL15,MYLK3,VPS35,MGST2,PUM2,CDK19,TRAF3IP2,ZC3HAV1,C5AR2,C5AR1,NAPEPLD,PTGIR,CST7,PHB,LACC1,NECTIN2,PVR,OPTN,PSG3,UNC13D,MYD88,IRAK2,FNDC4,SEC14L1,ACER3,IL17RE,ACKR2,RBMS3,IKBKB,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,NR1D2,NPLOC4,EIF2AK2,MAVS,AIMP1,HPX,FOXP1,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,PLK2,HCK,IL1A,IL37,PXK,PARP4,CAMK4,CEBPA,FER,AHCY,FLNB,OTUD4,IRF2,ERAP1,IL17RB,MEF2C,ASIC1,CELF1,SETD6,MCPH1,PTK2B,RASGRP1,CCL17,EIF2AK4,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTULIN,IFNGR2,AP3B1,WRNIP1,F2RL1,F2R,RIPK1,ANO6,CHST1,POLR3D,ABCC2,SPP1,CHID1,IFIT2,MAPKBP1,TSPAN2,PLA2G4B,HERC5,NOD2,ITGB6,ADCY7,TOLLIP,CD40,BMPR1B,MX2,RAB7B,CD96,IFIH1,CD200,OASL,CD200R1L,HYAL1,ELF3,LCK,HYAL3,SP140,SP100,ICOSLG,CRCP,TPST1,TRPV4,PDCD4,GPAM,TCIRG1,ADARB1,SNAP23,UNC93B1,POLR3C,TLR5,CMKLR1,NCF1,MAPKAPK2,FABP4,FCMR,SPATA2,TIFA,ALPK1,YTHDF2,ATG16L1,GPER1,SLAMF8,CERS6,PARP9,DTX3L,PARP14,THEMIS2,IRF9,IFI6,RNF26,AGT,FGR,ACE2,ATP1A2,NLRX1,ABCF3,NFATC4,TRAF3IP1,OSM,HDAC4,HTRA1,SNX4,TRIM52,COCH,CD28,FCER1G,NCF2,APOD,SETD2,LYZL6,ADAM8,CADM1,OLR1,NFE2	grey	VSMC_M10
GO:0110053	1.00	0.00	100	237	regulation of actin filament organization	BP	1	ARPC3,AVIL,PRKN,MTSS1,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,NCK2,KIAA1211,TMOD1,PLEKHH2,PRKCE,SPTBN1,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,EPHA1,FAM49A,WASF1,CLASP2,WNT11,PLEKHG2,FCHSD2,MKKS,ACTG1,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FER,PIK3R1,HIP1R,FMN1,LIMA1,PTK2B,ALMS1,RAPGEF3,F2RL1,IQGAP2,CYFIP1,DMTN,MAGEL2,PXN,CARMIL1,PPFIA1,LMOD1,ADD3,SSH1,HCLS1,ARHGAP6,AP1AR,WASF2,SLC9A1,SPTBN2,TMOD4,EPS8,WHAMM,DLG1,CAPZA1,CDC42EP2,NCKAP1,WNT4,ARPC1A,WAS,TMOD2,SPTB,PFN3,HAX1,SMAD3,CORO2B,EVL,PTGER4,SSH2,INPP5K,SERPINF2,MLST8,SPIRE2,TSC1,WDR63,CARMIL2,FHOD1,MIR21,RHOA,VASP,GMFG,ASAP3,RGS4,GRB2,RGCC,PFN4,PDXP,COTL1	grey	VSMC_M10
GO:0007264	1.00	0.00	196	437	small GTPase mediated signal transduction	BP	1	ARHGAP9,RAB21,TIAM2,CDC42SE2,RGL2,SYNGAP1,FAM13B,OBSCN,GPR20,GRAP2,CDC42EP1,RAC2,CDKN2A,LRRD1,FGD3,EPS8L1,RAPGEF5,CTNNAL1,LPAR1,MET,ARHGEF5,HACE1,SDCBP,WASF1,SPRY1,ARHGAP12,ARHGEF4,ARHGAP21,IQSEC1,KBTBD6,RALB,RAF1,SPRY2,PSD3,RIN2,ARRB1,SRGAP3,RASGRP4,RAC3,MCF2L,ARHGAP26,NRG1,PPP2CB,ARFIP2,RASA3,PLK2,AL359736.1,MRAS,PIK3CB,PREX2,RASA2,ARHGAP10,FBXO8,ROBO1,PLCE1,ARHGEF28,RTKN,MADD,RASGRP1,RHEBL1,RAPGEF2,MAPKAPK5,RND1,TIAM1,RASGEF1B,DOCK5,TRIO,RAPGEF3,RHOBTB2,F2RL1,F2R,ARHGAP24,RREB1,CYFIP1,KSR2,DOK2,GBF1,PSD,ARHGAP32,DOCK10,FGD4,TGFB2,ADRA2A,GNA13,AUTS2,RABL3,CFL1,KRAS,ARHGAP6,RAB42,CBL,WASF2,RAB4A,RASL10A,KALRN,CNKSR1,ARHGAP30,EPS8,RHOBTB1,FARP2,DOCK1,CDC42EP2,RASA4,RAP1B,BCL6,ABL2,GMIP,RASGRP2,RFXANK,NCKAP1,COL3A1,RAP1GAP,LZTR1,ARHGDIG,WAS,MYO9B,CYTH3,RHOJ,ARHGEF19,RASAL3,PLEKHG3,RAB15,IQSEC2,DOK3,FGD1,MFN2,ARHGEF11,ARHGAP23,KPNB1,STARD8,RIT1,NGFR,DOCK2,ITGA3,KCTD13,OGT,HACD3,DENND4A,LAT,NTN1,CCDC88C,MYO9A,DNM2,RIT2,G3BP1,ARHGAP44,AMOT,VAV1,SH2D3A,KSR1,TNFAIP1,RALBP1,RAB33A,DOCK7,JUN,DAB1,ABR,CRK,DNAJA3,GNB1,RAP1GAP2,TAX1BP3,ARHGAP4,ARHGAP45,PARK7,EPS8L3,GPSM2,VAV3,RALGPS1,MAPKAP1,SCAI,DENND1A,DAB2IP,RIPOR1,RRAD,RHOA,SETDB1,GPR35,ADGRG1,EPS8L2,STAMBP,RND3,CHN1,ZNF304,GRB2,RABIF,RALA,STK19,HRAS,CADM4,SH2B2,RHOU,RAP2B,RAB39A,RAPGEFL1,ARPP19	grey	VSMC_M10
GO:0001932	1.00	0.00	402	845	regulation of protein phosphorylation	BP	1	ERBB3,LRP1,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,TNXB,MAP3K4,PRKN,AGER,FBLN1,IL5,GDF9,UBE2B,BAK1,XRCC6,TRIB1,PTK2,TAB1,NTRK2,STK38,PLA2G6,HSF1,CCND3,CDKN2A,CHRNA3,TEK,FBXO7,TTBK1,TEC,KIT,SLC1A1,NCK2,ROR2,SEMA4D,PDCL3,KLHL31,CLDN19,DNAJA1,IL11,PRKCE,CD109,PPP2R1A,PHIP,FPR2,IBTK,ACP4,MOB1B,EPGN,AREG,BMP8A,BMPER,ETAA1,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,PRKAR2B,SPRY1,HDAC2,SLC8A2,C5AR1,MOB3C,PRKD2,PHB,ABI1,SOX9,MAPRE3,RALB,PRKAG2,RAF1,PIBF1,FBH1,SPRY2,WNT11,TADA3,AKT2,GPD1L,ARRB1,TGFBR2,ACVR2A,SIRT2,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,PLCL2,PRNP,DUSP6,BAG4,TAF7,MAVS,NRG1,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,PRKDC,ERCC6,FLT1,ADRA2B,TRAF6,TRIB3,RET,ACVR1B,CEBPA,FER,PIK3CB,SNX25,OSBP,ZFP91,CDK7,CASP3,ROBO1,PLCE1,FBXW7,PTPRJ,PKIA,IL7,CCNH,VEGFC,CCNJ,P2RY1,MADD,PTK2B,RASGRP1,CCNG2,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,PAQR3,FGF5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CCNJL,CDK2AP1,PKD2,STK4,DBNDD2,DMTN,ADTRP,HERC5,NOD2,CNTN1,DTNBP1,TAOK3,CD40,ROPN1L,IGF2,BMPR1B,NHLRC1,BDNF,NEURL1,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K6,PDCD4,TGFB2,ADRA2A,FAM20A,PRKAR1A,ADARB1,DAG1,AXIN2,SLCO3A1,AJUBA,NCF1,MST1,KRAS,FABP4,EGF,HCLS1,ADNP,OPRD1,UBASH3B,SORL1,RTRAF,GPER1,CHEK2,CASS4,SPATC1L,PARP9,PARP14,CACUL1,AGT,FGR,CIB1,CBL,DVL3,STRADB,SFN,TRAF3IP1,OSM,CAMK2N2,SYAP1,PTPRO,THPO,STRADA,INPP5J,MLXIPL	grey	VSMC_M10

GO:0061640	1.00	0.00	31	87	cytoskeleton-dependent cytokinesis	BP	1	VPS4B,TRIM36,SEPT8,SEPT3,WASHC5,SEPT10,EFHC1,MITD1,CHMP2A,SPTBN1,DCDC1,CHMP2B,CHMP4C,RTKN,SEPT11,CHMP7,BIN3,KLHDC8B,SEPT2,EFHC2,SEPT1,CNTROB,MYH10,NOX5,UNC119,SPIRE2,CHMP1A,VPS4A,RHOA,STAMBP,APC	grey	VSMC_M10
GO:0010639	1.00	0.00	129	297	negative regulation of organelle organization	BP	1	AVIL,TBC1D30,MDM1,ZNF207,FBXO43,PRKN,TSPO,H3F3C,PICK1,POT1,LMOD2,KIAA1211,TMEM14A,TMOD1,PLEKHH2,SPTBN1,SHANK1,MET,ADD2,CDK5RAP2,MAPRE1,RAB7A,EML2,ERCC1,CLASP2,XRCC1,TRIM54,TBC1D4,DYNC1LI1,MKKS,NAV3,ANAPC15,IK,FEZ2,ARHGEF7,SPEF1,USP44,LMOD3,ATXN7,ANKRD27,PIK3R1,HIP1R,LIMA1,KATNB1,NBN,TMEM67,OPA1,DMTN,TENT4B,STN1,DNM1L,CARMIL1,PPFIA1,LMOD1,ADD3,SEC22B,TMEM39A,PRKAR1A,USP30,TTBK2,SSH1,ARHGAP6,CIB1,WASF2,SPTBN2,CCDC84,TMOD4,EPS8,INPP5J,RTEL1,LIMK2,FZD9,CAPZA1,MAPT,C11orf65,PINK1,MUL1,WAS,TMOD2,PARP1,PHF23,SPTB,GNL3L,CTC1,PIF1,ADCK1,LCMT1,CORO2B,TRIM37,DNM2,PSMD10,SMCR8,CAMSAP3,TOM1L2,ERCC4,PSMG2,TAOK1,NUBP1,SSH2,ACAA2,MTM1,INPP5K,PAM16,SLX4,NAA10,APC2,CAMSAP1,CDK10,ODF2L,TERF2,WDR63,CARMIL2,MIR21,NOL3,TINF2,GMFG,TEN1,TIGAR,FXN,DUSP1,SLC35F6,NME6,APC,LIF,BCL2L2,PFN4,PPIF,AC140504.1,MAP6D1	grey	VSMC_M10
GO:0001938	1.00	0.00	27	78	positive regulation of endothelial cell proliferation	BP	1	TEK,PDCL3,EMC10,PRKD2,RPTOR,NR4A1,VEGFC,AGGF1,IGF2,PDCD6,EGF,ARNT,VASH2,ITGA4,STAT3,PGF,PDPK1,CYBA,MIR29A,MIR21,MIR23A,MIR27B,MIR27A,ACVRL1,ZNF580,WNT5A,WNT2	grey	VSMC_M10
GO:0070925	1.00	0.00	331	705	organelle assembly	BP	1	VPS4B,PAN2,ONECUT2,STX7,ATG12,TBPL1,PIP4K2C,AVIL,TBC1D30,MDM1,ATAT1,CNOT2,CNOT6,ZNF207,HSPA1B,TUBGCP6,RNF5,IL5,KIF3A,TBC1D32,RRP7A,UBE2B,WASHC5,ASAP1,LRRC6,OBSCN,MAPK15,IFT74,LMOD2,SRF,CFAP69,PGM5,RFX3,PTPDC1,CHMP2A,RPS14,TMOD1,RAB23,DYNC2LI1,STX17,CEP162,MDN1,TMEM17,WDR92,TRAPPC12,FUZ,CDK5RAP2,IQUB,CCDC155,MYLK3,ATG5,SDCBP,ARMC2,MAPRE1,PUM2,ARMC4,INTU,SPATA6,TTC26,BBS7,RAB7A,PIP4K2A,DRC1,CCDC61,RSPH6A,LCP1,CLASP2,NECTIN2,MAPRE3,MLH1,RALB,GALNT11,FBF1,PIBF1,IFT172,FOXJ1,MYO7A,RPSA,WDR60,TTLL3,CCDC13,ABCC4,CEP295NL,LRFN1,MKKS,ATG16L2,TMEM173,ACTG1,RAB5A,FEZ2,CDS2,CEP290,SPEF1,ULK1,LMOD3,PRKDC,TMEM80,PAN3,CEP63,NSFL1C,DHX37,PLK2,HCK,KIF3B,RILPL1,RILPL2,CEP70,CHMP2B,RPL6,CEP44,PARVA,PLS1,CEP250,TBC1D12,CCDC66,AUP1,TCTN3,CNOT1,IFT81,CCDC113,CHMP4C,CFAP20,CNOT6L,CCDC65,ALMS1,ABRAXAS1,TMEM67,CDS1,CHMP7,IFT52,FITM2,TP53INP1,RPGRIP1L,TUBGCP5,DNAH1,DNAH5,ZNF423,GBF1,RAB7B,NEURL1,CFAP43,ZMYND10,AC112128.1,LMOD1,SEC22B,SBDS,GAP43,TMEM39A,TCIRG1,ARMC9,PRKAR1A,ADPRH,CFAP46,TTBK2,MRPS11,CLCN4,ALPK1,JHY,YTHDF2,HPS4,DISC1,ATG16L1,OFD1,FITM1,CHEK2,TUBGCP4,ACTC1,BAG3,RPS27,RAB17,TMEM237,MTMR3,MYOZ2,DDX6,TRAF3IP1,CASQ1,TMOD4,BBS1,GORASP2,LAMA5,POGZ,ABRAXAS2,YTHDF1,CDKL5,RAB1B,VPS37D,SEPT2,FARP2,DHX30,LIMK2,EIF4ENIF1,RPL11,KIF9,MYPN,SPG11,MAPT,EFL1,PIKFYVE,CFAP161,TTC12,TOGARAM1,TTN,ATG2A,EHD1,RPL10L,DNAAF2,DDX3X,SPAG16,NRXN2,TBC1D14,XRCC5,RC3H1,F	grey	VSMC_M10
GO:1902532	1.00	0.00	183	407	negative regulation of intracellular signal transduction	BP	1	PHLPP1,SEMA6A,TNFAIP3,EPM2A,TRIM39,PPP1R10,ESR1,PRKN,PPARA,PDE10A,FBLN1,SYNGAP1,UBE2B,MYC,LEMD2,MAPK14,STK38,FHL2,WNK2,KLHL31,DNAJA1,FKTN,PLEK,ITGB1BP1,MET,VRK3,TRIM32,TLR4,SPRY1,ARHGAP12,KPTN,SESN3,ARMC10,PHB,PPM1N,DDIAS,OPTN,SEC14L1,SZT2,SPRY2,GPD1L,ARRB1,NMI,ZMYND11,NPLOC4,SPRED3,PRNP,DUSP6,SH3RF2,SIRT3,PPP2CB,RASA3,TMEM127,NR1H4,PIK3CB,RASA2,TAF9,ING2,ARNTL,PTPRJ,HTRA2,TMBIM6,P2RX7,NDUFS3,SLA2,MAPKAPK5,PAQR3,OPA1,HDAC7,F2RL1,ARHGAP24,RIPK1,MARCH7,MAPKBP1,TAOK3,DUSP8,PRDM15,OTUD7A,HDAC1,BANK1,PDCD4,TGFB2,PDCD6,DAG1,AJUBA,DYRK3,SNAI1,TBC1D10C,OTUD7B,SORL1,GPER1,DGKD,CHEK2,SH3BP4,MCL1,AGT,CIB1,HYOU1,NLRX1,MYOZ2,ACTN3,RTKN2,PIK3IP1,HOMER2,DUSP16,DLG1,YBX3,DGKG,NFE2L2,AIDA,IVNS1ABP,DUSP10,RASA4,NONO,BCL6,SYVN1,ABL2,MEN1,DDX3X,DUSP19,PTPN6,MYOZ1,PINK1,MUL1,OTUD3,LZTR1,PPM1A,RASAL3,GPS2,TKFC,RGS14,MFN2,SYNJ2BP,ITGA3,KCTD13,MUC1,EFNA1,WWC1,TAF9B,TSPAN6,ARHGAP44,TNIP1,PSMD10,NCOR1,CD74,RIOK3,MAPK7,MARK3,LITAF,TNFAIP1,PTPN2,TNFAIP8L1,INPP5K,MGRN1,ABCA7,PARK7,TSC1,MAPKAP1,MARVELD3,SCAI,DAB2IP,MIR29A,MIR21,MIR27B,RHOA,DUSP2,NOL3,CHRNA10,CASP8,PDZD3,STAMBP,DUSP26,DUSP1,DDIT3,DUSP4,C3orf33,LIF,PTTG1IP,BCL2L2,LAX1,C1QL4,PPIF,RNF152	grey	VSMC_M10
GO:0031577	1.00	0.00	10	37	spindle checkpoint signaling	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10

GO:0051272	1.00	0.00	212	466	positive regulation of cellular component movement	BP	1	ONECUT2,LRP1,SEMA6A,AGER,GPSM3,AGO2,PTK2,SUN2,PODXL,RAC2,SMO,TEK,CFAP69,CCL27,KIT,ROR2,SEMA4D,SEMA4C,ZNF268,PRKCE,EPCAM,RTN4,FPR2,EPB41L4B,RUFY3,EMC10,CXCL8,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,TRIM32,TLR4,TCAF2,EPHA1,GAB1,SDCBP,C5AR1,SLC26A5,PRKD2,IQSEC1,SOX9,CLASP2,OXSR1,SPRY2,WNT11,RIN2,AKT2,TGFBR2,ACTG1,HBEGF,FERMT1,BAG4,ARHGEF7,SEMA3D,DIAPH1,SEMA3A,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,FLT1,PLK2,RET,FAM107A,GPI,ACVR1B,FER,PIK3CB,PIK3R1,ATP5F1A,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,ADAMTS1,PTK2B,RAPGEF2,TIAM1,DOCK5,HDAC7,F2RL1,F2R,ANO6,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,CD40,SRGAP2C,GPLD1,LGR6,DNM1L,CARMIL1,HYAL1,PPP3CA,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,CD99,PRSS56,SSH1,CMKLR1,SNAI1,EGF,GPER1,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,HDAC4,MAP3K3,DOCK1,ELP6,CALY,ADAM8,LRRC15,NFE2L2,MIA3,DUOX1,CCAR1,CEMIP,BCL6,SEMA6D,TRIP6,CTSH,ITGA2B,ITGA4,IL12A,FN1,VSIR,SPOCK2,MCU,PDCD10,TNFSF18,FERMT3,CXCR2,STAT3,MAPK1,RHOJ,SYNE2,CXCL16,SYDE1,TMEM102,MIEN1,STX4,SEMA4A,RAB25,FGF18,FOXO4,ITGA3,PGF,DAPK2,TRIM46,ZNF609,MAPK3,IL6R,ATP2A1,RAB11A,SMAD3,NTN1,S100A14,BDKRB1,BCAS3,CD74,INSR,CCL5,CSF1R,CCL7,DOCK7,CRK,PDPK1,FBXO31,FOXF1,LCN2,HSPA5,DAB2IP,CARMIL2,RIPOR1,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR27B,MIR27A,RHOA,DEFB124,FADD,LAMB1,ZNF580,THY1,CLDN1,WNT5A,BORCS5,ZNF304,APC,HRAS,FGF1,CBLL1,PDGFD	grey	VSMC_M10
GO:1902903	1.00	0.00	143	327	regulation of supramolecular fiber organization	BP	1	ARPC3,AVIL,HSPA1B,PRKN,MTSS1,WASHC5,BAIAP2L2,PICK1,CDC42EP1,LMOD2,SLAIN2,NCK2,KIAA1211,TMOD1,PLEKHH2,PRKCE,SPTBN1,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,CDK5RAP2,EPHA1,MYLK3,FAM49A,MAPRE1,WASF1,EML2,SLC39A12,CLASP2,MAPRE3,TRIM54,SLAIN1,WNT11,PLEKHG2,FCHSD2,MKKS,ACTG1,NAV3,BAG4,ARHGEF7,SPEF1,FCHSD1,NCKAP1L,ARFIP2,LMOD3,ATXN7,PFDN5,HCK,FER,PIK3R1,HIP1R,CLIP1,FMN1,LIMA1,KATNB1,PTK2B,ALMS1,RAPGEF3,F2RL1,IQGAP2,CYFIP1,DMTN,MAGEL2,PXN,CARMIL1,PPFIA1,LMOD1,ADD3,TRPV4,TTBK2,SSH1,HCLS1,ARHGAP6,AP1AR,HSPA8,CIB1,WASF2,SLC9A1,SPTBN2,TMOD4,EPS8,INPP5J,WHAMM,EFEMP2,CDKN1B,DLG1,CAPZA1,CDC42EP2,MAPT,TOGARAM1,NCKAP1,NIN,WNT4,ARPC1A,WAS,TMOD2,SPTB,PFN3,PFDN4,PSEN1,HAX1,SMAD3,CORO2B,LDLR,EVL,CAMSAP3,CDK5R1,PTGER4,TAOK1,SSH2,INPP5K,SERPINF2,MLST8,MECP2,APC2,VBP1,PARK7,CAMSAP1,SPIRE2,PSRC1,TSC1,WDR63,CARMIL2,FHOD1,MIR21,RHOA,VASP,GMFG,ASAP3,RGS4,GRB2,RGCC,APC,PFN4,PDXP,MAP1A,COTL1,DRG1,MAP6D1	grey	VSMC_M10
GO:0019083	1.00	0.00	13	45	viral transcription	BP	1	SNW1,TRIM32,RSF1,USF2,HDAC1,ZNF639,POU2F3,USF1,PSMC3,TARDBP,CCL5,JUN,INPP5K	grey	VSMC_M10
GO:0003013	1.00	0.00	197	437	circulatory system process	BP	1	NEDD4L,TAC3,LRP1,LVRN,SLC16A7,ADM2,SLC12A2,AGER,PPARA,SMAD5,PTP4A3,PLA2G6,ZDHHC21,TEK,ABCB1,SLC1A1,TBC1D8,ADH5,MEOX2,PPCS,TNNI3,EPAS1,ASB3,SLC4A4,SLC1A4,ITGB1BP1,EGFR,BVES,KEL,MYLK3,ATG5,TRPM4,SLC8A2,CACNB2,ATP1A3,CELF2,SCN5A,SCN1A,SLC24A3,GPD1L,ABCC4,SNX5,MKKS,HBEGF,ADRA1D,SEMA3A,P2RX2,GAS6,SLC7A1,ADRA2B,SGCG,HTR7,FGFBP3,MYOF,ERAP1,PTPRJ,VEGFC,GUCY1A1,GUCY1B1,P2RY1,MME,DOCK5,STC1,KCNJ3,TBX5,SLC38A2,F2RL1,F2R,SLC38A1,TNNC1,ABCC2,KCNE2,DSP,ABCG2,CASQ2,KCNIP2,CHRM3,SLC2A13,RYR2,RAP1GDS1,PKP2,DNM1L,SLC2A10,KCNJ2,SLC38A3,MAP2K6,TNNI1,TRPV4,TGFB2,ADRA2A,SLCO3A1,ENPEP,MYH7,GRK2,ANK2,GPER1,AGT,ABCC5,ACE2,ATP1A2,ACTC1,SLC9A1,SLCO1C1,PER2,HDAC4,NTSR1,SLC29A2,PTPRO,SCN4B,NOS1AP,DLG1,SLC16A1,OLR1,PLOD3,CPS1,TTN,ADRA2C,CXCR2,GNB3,PTGER2,ECE1,GCH1,RAMP2,ATP1B1,SMTNL2,CD38,SLC27A1,SLC38A5,KCNMA1,DES,SLC4A3,SLC29A4,SLC2A4,THRA,TCAP,SOD3,AGTRAP,ATP1B2,HRH2,SLC7A3,CACNA1G,ABCC3,ATP2A1,SMAD3,SCPEP1,CORO2B,CALM1,SCNN1B,BDKRB1,TBX2,ACSM3,DSG2,INSR,ASIC2,YES1,SREBF1,ISL1,LEPR,NOS2,CYP2J2,ABAT,ATP2B3,SERPINF2,TRPV1,P2RX1,MECP2,RNF207,CACNA1H,CYBA,SLC7A5,HSD11B2,MIR199A1,MIR21,MIR23A,MIR27B,RHOA,HTR1D,FGA,DMD,FABP5,ERAP2,CHGA,SLC22A5,GPR37L1,ACVRL1,TMEM65,KCNH2,SCN2B,RGS4,CRH,POPDC2,KCNJ8,HCN4,NKX2-5,KCNMB4,HEY2,KCNG2	grey	VSMC_M10

GO:0008015	1.00	0.00	164	369	blood circulation	BP	1	NEDD4L,TAC3,LVRN,ADM2,AGER,PPARA,SMAD5,PTP4A3,PLA2G6,ZDHHC21,TEK,SLC1A1,TBC1D8,ADH5,MEOX2,TNNI3,EPAS1,ASB3,ITGB1BP1,EGFR,BVES,KEL,MYLK3,ATG5,TRPM4,SLC8A2,CACNB2,ATP1A3,CELF2,SCN5A,SCN1A,GPD1L,SNX5,MKKS,HBEGF,ADRA1D,SEMA3A,P2RX2,GAS6,ADRA2B,SGCG,HTR7,FGFBP3,MYOF,ERAP1,PTPRJ,VEGFC,GUCY1A1,GUCY1B1,P2RY1,MME,DOCK5,STC1,KCNJ3,TBX5,F2RL1,F2R,TNNC1,KCNE2,DSP,CASQ2,KCNIP2,CHRM3,RYR2,RAP1GDS1,PKP2,DNM1L,KCNJ2,MAP2K6,TNNI1,TRPV4,TGFB2,ADRA2A,ENPEP,MYH7,GRK2,ANK2,GPER1,AGT,ACE2,ATP1A2,ACTC1,SLC9A1,PER2,HDAC4,NTSR1,PTPRO,SCN4B,NOS1AP,DLG1,OLR1,PLOD3,CPS1,TTN,ADRA2C,CXCR2,GNB3,PTGER2,ECE1,GCH1,RAMP2,ATP1B1,SMTNL2,CD38,KCNMA1,DES,SLC4A3,THRA,TCAP,SOD3,AGTRAP,ATP1B2,HRH2,CACNA1G,ATP2A1,SMAD3,SCPEP1,CORO2B,CALM1,SCNN1B,BDKRB1,TBX2,ACSM3,DSG2,ASIC2,YES1,SREBF1,ISL1,NOS2,CYP2J2,ABAT,ATP2B3,SERPINF2,TRPV1,P2RX1,MECP2,RNF207,CACNA1H,CYBA,HSD11B2,MIR199A1,MIR21,MIR23A,MIR27B,RHOA,HTR1D,FGA,DMD,ERAP2,CHGA,GPR37L1,ACVRL1,TMEM65,KCNH2,SCN2B,RGS4,CRH,POPDC2,KCNJ8,HCN4,NKX2-5,KCNMB4,HEY2,KCNG2	grey	VSMC_M10
GO:0009611	1.00	0.00	190	422	response to wounding	BP	1	SERPINB2,ERBB3,LRP1,GLI1,MAP3K5,TNFAIP3,TSPAN8,MPIG6B,SLC12A2,FZD6,AGER,PPARA,FBLN1,TSPO,PTK2,MAPK14,C6orf89,TXN2,MYH9,PTK7,SRF,TEC,ENPP4,SLC1A1,TLN1,CLDN19,PRKCE,CD109,EPB41L4B,PLEK,TGFA,PTN,DGKI,TNC,EGFR,TLR4,SLC7A11,DHFR,NDNF,GIPR,CLASP2,RAF1,EVPL,PTPRF,THBD,TSKU,PLAT,MYL12A,TGFBR2,C1QTNF1,ACTG1,HBEGF,FERMT1,CNN2,DCN,CHL1,FUT10,CLIC1,NRG1,GAS6,DPYSL3,ADRA2B,IL1A,PIK3CB,MYOF,CASP3,P2RY1,PLLP,DYSF,HPS5,AP3B1,MORN4,F2RL1,F2R,SRSF6,ARHGAP24,ANO6,RREB1,SPP1,DSP,DMTN,ADTRP,ITGB6,DTNBP1,CD40,FAP,KIAA0319,MTR,LCK,PPP3CA,TGFB2,ADRA2A,GAP43,SULF2,ITPK1,DAG1,FGFR1OP2,PRSS56,AJUBA,ABHD2,SOX2,UBASH3B,HPS4,DGKD,KREMEN1,MCAM,CERS2,FZD7,KCNK2,USF1,PAFAH2,FCER1G,GRHL3,LRIG2,APOD,DGKG,NFE2L2,MIA3,DUOX1,BLOC1S6,PLA2G4A,ITGA2B,TNR,FN1,CASK,PTPN6,SERPINC1,PDCD10,ADRA2C,FERMT3,HGFAC,SLC11A1,WNT4,COL3A1,MYOZ1,RAB3A,VCL,WAS,EPHA4,ARHGEF19,ACTB,SYT7,ANXA8,MAX,F12,PEAR1,ANXA2,DGKQ,SYT11,NDEL1,VASH1,MAP2K1,DGKE,SMAD3,SYTL4,S100A8,ISL1,VAV1,ABAT,CRK,SERPINF2,P2RX1,MAPK8IP3,ADAMTS13,COL5A1,FOXF1,VAV3,STXBP1,CARMIL2,RIPOR1,MIR29A,MIR21,MIR222,RHOA,FGA,BLOC1S3,NOL3,CNTF,ACVRL1,RTN4RL1,NOG,CLDN1,WNT5A,HRAS,ZFP36L2,CADM4,EREG,RAP2B,FGF1,NMNAT1	grey	VSMC_M10
GO:0022414	1.00	0.00	496	1029	reproductive process	BP	1	TAC3,HSD17B4,TBPL1,TRIM36,GLI1,YTHDC2,B4GALNT1,CYP27B1,ATAT1,ESR1,FRS2,TSPAN8,STK3,FBXO43,MAPK8IP2,TUBGCP6,IGF2R,MOV10L1,MAP3K4,PACRG,QKI,FBLN1,BRD2,GDF9,ROS1,MCM9,HSF2,CCDC134,UBE2B,BAK1,CATSPER3,RSPO3,WASHC5,TOB2,SMAD5,LRRC6,AGO2,H3F3C,PTK2,HSD17B3,PTCH1,FANCC,AKR1B1,TUT7,MAPK15,SUN2,MAPK14,DMC1,PLA2G6,PICK1,SPATA31D3,MDFI,TFEB,MYH9,KLHDC3,ZNF318,CFAP69,CNTFR,FANCG,SMARCA2,CLIC5,TDRD6,KIT,RLN1,ROR2,PPAT,CCIN,TSGA10,TDRD7,NLRP5,DNAJA1,FOXJ3,SCMH1,EPAS1,RIMS1,MSH2,DNAH11,RAD23B,SPACA6,YTHDC1,KLK14,CABS1,FANCL,HOXA13,AREG,GJA10,HERPUD2,GMCL1,PTN,TNC,EGFR,NOBOX,GJB5,CCDC155,DKKL1,CREM,TUT4,OSR1,FOXO3,ARMC2,DLD,DDO,TXNRD3,APOB,IZUMO1,SPATA6,SPHK2,SPATA5,HDAC2,ADCY3,TTC26,TRPC3,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,UTF1,PSG3,MLH1,GLI2,XRCC2,DACH1,ACOX1,PRDX3,TIMP4,FOXJ1,WDR48,TTC21A,THBD,PLAT,TTLL3,CCNB1IP1,ARRB1,TGFBR2,OVOL2,ACVR2A,EOMES,SIRT2,MKKS,SPATA24,IDO1,ADAM18,PLCB1,SIRT7,SPINT2,MCM8,GOLGA3,DCN,PANK2,BTG1,SOHLH2,SEMA3A,FUT10,TEX15,UBXN8,PRKDC,KATNAL1,STX2,ADRA2B,NCOA4,AMHR2,DHX37,MOS,PLAG1,NPHP1,IL1A,CYP7B1,ACVR1B,CEBPA,FOXL2,CASP3,ING2,HPGD,SPATA9,ROBO2,WDR66,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,P2RY1,PTK2B,MME,KMT2D,PRKAG1,SFMBT1,NBN,VDR,STC1,NKX3-1,RAD54B,AP3B1,SLC38A2,ACVR1C,SLC38A1,TESC,SPINT1,CDYL,EXD1,ABCC2,SPP1,TUBGCP5,PKD2,STK4,SYCP1,DNAH1,PLA2G4B,SYCP2L,NPM2,SALL1,PLTP,DN	grey	VSMC_M10
GO:0051383	1.00	0.00	4	21	kinetochore organization	BP	1	TRAPPC12,POGZ,RNF4,CENPX	grey	VSMC_M10

GO:0000003	1.00	0.00	497	1031	reproduction	BP	1	TAC3,HSD17B4,TBPL1,TRIM36,GLI1,YTHDC2,B4GALNT1,CYP27B1,ATAT1,ESR1,FRS2,TSPAN8,STK3,FBXO43,MAPK8IP2,TUBGCP6,IGF2R,MOV10L1,MAP3K4,PACRG,QKI,FBLN1,BRD2,GDF9,ROS1,MCM9,HSF2,CCDC134,UBE2B,BAK1,CATSPER3,RSPO3,WASHC5,TOB2,SMAD5,LRRC6,AGO2,H3F3C,PTK2,HSD17B3,PTCH1,FANCC,AKR1B1,TUT7,MAPK15,SUN2,MAPK14,DMC1,PLA2G6,PICK1,SPATA31D3,MDFI,TFEB,MYH9,KLHDC3,ZNF318,CFAP69,CNTFR,FANCG,SMARCA2,CLIC5,TDRD6,KIT,RLN1,ROR2,PPAT,CCIN,TSGA10,TDRD7,NLRP5,DNAJA1,FOXJ3,SCMH1,EPAS1,RIMS1,MSH2,DNAH11,RAD23B,SPACA6,YTHDC1,KLK14,CABS1,FANCL,HOXA13,AREG,GJA10,HERPUD2,GMCL1,PTN,TNC,EGFR,NOBOX,GJB5,CCDC155,DKKL1,CREM,TUT4,OSR1,FOXO3,ARMC2,DLD,DDO,TXNRD3,APOB,IZUMO1,SPATA6,SPHK2,SPATA5,HDAC2,ADCY3,TTC26,TRPC3,DNMT3A,PANX1,FOXA3,SOX9,RSPH6A,TOPAZ1,ERCC1,SLC4A2,NECTIN2,CRTAP,UTF1,PSG3,MLH1,GLI2,XRCC2,DACH1,ACOX1,PRDX3,TIMP4,FOXJ1,WDR48,TTC21A,THBD,PLAT,TTLL3,CCNB1IP1,ARRB1,TGFBR2,OVOL2,ACVR2A,EOMES,SIRT2,MKKS,SPATA24,IDO1,ADAM18,PLCB1,SIRT7,SPINT2,MCM8,GOLGA3,DCN,PANK2,BTG1,SOHLH2,SEMA3A,FUT10,TEX15,UBXN8,PRKDC,KATNAL1,STX2,ADRA2B,NCOA4,AMHR2,DHX37,MOS,PLAG1,NPHP1,IL1A,CYP7B1,ACVR1B,CEBPA,FOXL2,CASP3,ING2,HPGD,SPATA9,ROBO2,WDR66,ARNTL,SPAG4,M1AP,IFT81,CELF1,JAM2,CSNK2A2,ADAMTS1,P2RY1,PTK2B,MME,KMT2D,PRKAG1,SFMBT1,NBN,VDR,STC1,NKX3-1,RAD54B,AP3B1,SLC38A2,ACVR1C,SLC38A1,TESC,SPINT1,CDYL,EXD1,ABCC2,SPP1,TUBGCP5,PKD2,STK4,SYCP1,DNAH1,PLA2G4B,SYCP2L,NPM2,SALL1,PLTP,DN	grey	VSMC_M10
GO:0043535	1.00	0.00	31	87	regulation of blood vessel endothelial cell migration	BP	1	MEOX2,ITGB1BP1,PRKD2,PLK2,ATP5F1A,FBXW7,MEF2C,VEGFC,HDAC7,CD40,CIB1,MAP3K3,NFE2L2,PDCD10,RHOJ,FGF18,EFNA1,VASH1,MAP2K5,PDPK1,MECP2,MIR199A1,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,ACVRL1,GADD45A,RGCC	grey	VSMC_M10
GO:1901700	1.00	0.00	600	1234	response to oxygen-containing compound	BP	1	ADNP2,ZNF236,NME1,FECH,LRP1,AP3S1,MARS,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,ESR1,SNW1,APOM,IGF2R,PRKN,AGER,PPARA,PNPLA3,RXRB,TSPO,BAK1,TRIB1,PTK2,ERCC6L2,PTCH1,FANCC,LY6E,AKR1B1,ATF4,MAPK14,NTRK2,MAPK13,PLA2G6,GKAP1,SOX10,PIM1,SMO,TXN2,HSF1,IRF5,CCND3,GPT,MTAP,CHRNA3,TEK,GPR37,RORB,ALDH1A1,CRY1,PTK7,SRF,USP46,SLC1A1,CA9,PPAT,PRDX1,ADH5,CAT,PRKCE,PHIP,FPR2,HMGN3,PNPT1,ME1,HOXA2,CXCL8,NOD1,AREG,AKIRIN2,CRHR2,AQP1,RRAGD,PELI1,ZNF277,PTN,FOXP2,KLF11,MET,GRB10,TNC,EGFR,LANCL2,TLR4,GAB1,LPIN1,IL15,UCP1,VPS35,TEAD2,MGST2,SETD7,MGARP,TRPM4,OSR1,FOXO3,APOB,CDK19,FGF21,SPHK2,DHFR,HDAC2,ADCY3,TRPC3,SESN3,DNMT3A,BMI1,C5AR1,PANX1,SLC26A5,PIP4K2A,RAB10,HADHA,PTGIR,SOX9,GIPR,CYSLTR2,ERCC1,NUDT15,ESD,AKR1A1,GLB1,KHK,EIF2B3,PLK3,XRCC1,EPM2AIP1,ECHDC3,MBD4,GRIK5,RAF1,ATP1A3,MYD88,PRDX3,TIMP4,KLF5,TBC1D4,AANAT,IRAK2,GCKR,THBD,HNMT,POU4F1,WNT11,ALK,AKT2,TGFBR2,SNX5,JAG1,NFKBIB,SIRT2,RPTOR,PAWR,PLCB1,MAP4K1,CRLS1,SLC23A2,PRNP,DCN,BTG1,P2RX2,KL,GAS6,LARS,PPP2CB,PTPRA,FOXP1,LEPROTL1,PRKDC,ERCC6,NCOA4,TRAF6,NR1H4,SLC38A9,TRIB3,RET,CYP7A1,HCK,NDUFAF2,ASXL1,HTR7,IL1A,IL37,DNMT3B,GPI,NR4A1,FER,IDE,OSBP,PIK3R1,GSS,CASP3,NCOA2,CCDC62,HPGD,P2RX3,CHRM5,RYR3,PLSCR4,SORBS1,GPD1,MEF2C,SMARCD1,NUGGC,HTRA2,TMBIM6,P2RX7,ZFAND1,MMP15,GUCY1B1,P2RY1,PTK2B,RAPGEF2,KCNJ11,NR1H3,TIAM1,LCOR,RAB11FIP5,RIPK2,SYNJ1,HOMER1,VDR,STC1,NKX3-1,OPA1,SPIDR,LPIN3,NKX6-	grey	VSMC_M10
GO:0030036	1.00	0.00	276	600	actin cytoskeleton organization	BP	1	ARPC3,MYO1A,LRP1,AGAP2,AVIL,TNXB,PRKN,PARVG,SHROOM1,MTSS1,WASHC5,EPB41L2,OBSCN,BAIAP2L2,PICK1,CDC42EP1,RAC2,DAAM2,FLNC,MYH9,TEK,LMOD2,PTK7,SRF,PGM5,CCL27,KIT,NCK2,TLN1,KIAA1211,PDCL3,FGD3,CCIN,TMOD1,PLEKHH2,NLRP5,CLDN19,PRKCE,SPTBN1,EPB41L4B,RUFY3,SHANK1,LPAR1,AQP1,EHBP1,MYH14,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,TRIM32,EPHA1,GAB1,CCDC155,MYLK3,SDCBP,FAM49A,WASF1,ARHGAP12,KPTN,MSRB2,IQSEC1,ABI1,MYO7B,LCP1,CLASP2,LLGL2,FOXJ1,MYO7A,WNT11,ARRB1,PLEKHG2,IKBKB,FARP1,FCHSD2,MKKS,ACTG1,FSCN2,PAWR,RAC3,CNN2,BAG4,DIAPH1,FCHSD1,ARHGAP26,FGD6,NCKAP1L,ARFIP2,LMOD3,DPYSL3,TTC17,NPHP1,HCK,FAM107A,FER,MRAS,FLNB,PIK3R1,HIP1R,PARVA,PLS1,FMN1,LIMA1,SORBS1,EPB41L1,RTKN,SDAD1,PTK2B,RND1,ALMS1,USH1C,RAPGEF3,RHOBTB2,BIN3,F2RL1,IQGAP2,ITPKA,CYFIP1,DMTN,DTNBP1,NUAK2,GAS2,MAGEL2,PXN,RAP1GDS1,ELMO2,INA,CARMIL1,PPFIA1,FGD4,LMOD1,ADD3,TRPV4,ADRA2A,TBCK,PRKAR1A,AUTS2,SSH1,CFL1,SHROOM2,KRAS,HCLS1,ARHGAP6,AP1AR,EPB41,CASS4,SPATC1L,WASF2,ACTC1,SLC9A1,SPTBN2,MYOZ2,CASQ1,ITGB5,ACTN3,TMOD4,EPS8,RHOBTB1,FARP2,GRHL3,LIMK2,NOS1AP,WHAMM,DLG1,FRMD5,CAPZA1,MYPN,CDC42EP2,BCL6,ABL2,TTN,DIXDC1,NCKAP1,MCU,ABLIM2,WNT4,MYOZ1,ARPC1A,TRPM7,SMTNL2,BST1,DAAM1,WAS,TMOD2,OBSL1,MINK1,RHOJ,TPM4,ARHGEF19,ACTB,SHROOM4,LDB3,SPTB,SYDE1,IQSEC2,PDLIM7,TCAP,PLEK2,PFN3,FGD1,ARHGEF11,WASHC3,STARD8,DOCK2,KCTD13,TAOK2,AC138894.1,HAX1,MYH10,SMAD3,GAS7,CORO2B,BCAS3,SETD3,ARHGAP44,EVL,PSTPIP1	grey	VSMC_M10
GO:0035767	1.00	0.00	5	24	endothelial cell chemotaxis	BP	1	MET,PRKD2,NR4A1,FGF18,FGF1	grey	VSMC_M10
GO:1902100	1.00	0.00	11	40	negative regulation of metaphase/anaphase transition of cell cycle	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,MOS,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:0032467	1.00	0.00	6	27	positive regulation of cytokinesis	BP	1	PRKCE,KIF3B,CSPP1,CDC14A,RHOA,AURKC	grey	VSMC_M10

GO:0050792	1.00	0.00	45	119	regulation of viral process	BP	1	PABPC1,PPARA,LY6E,APOBEC3H,CHMP2A,CXCL8,RSAD2,TRIM32,HS3ST5,ZC3HAV1,RAB7A,NECTIN2,RSF1,KPNA2,EIF2AK2,MAVS,CHMP2B,FAM208A,OAS3,IFIH1,OASL,TMEM39A,ADARB1,NR5A2,STAU1,PC,CD28,DDX3X,DDB1,HACD3,LARP1,TNIP1,CD74,CCL5,CIITA,FMR1,INPP5K,VPS4A,SETDB1,OAS1,TRIM68,TRIM34,TBC1D20,ZNF502,FAM111A	grey	VSMC_M10
GO:0070199	1.00	0.00	5	24	establishment of protein localization to chromosome	BP	1	POT1,SPIDR,TERT,H2AFY2,WRAP53	grey	VSMC_M10
GO:0034502	1.00	0.00	30	86	protein localization to chromosome	BP	1	MRNIP,ESR1,MCM9,LEMD2,POT1,MSH2,TRAPPC12,IK,MCM8,CHAMP1,ATR,SLF1,FAM208A,XRCC4,SPIDR,CHMP7,SLF2,PPHLN1,TERT,SPO11,SETD2,H2AFY2,MAU2,XRCC5,IFFO1,GNL3L,WRAP53,TERF2,CTCF,TINF2	grey	VSMC_M10
GO:0008608	1.00	0.00	7	30	attachment of spindle microtubules to kinetochore	BP	1	ZNF207,SIRT2,CHAMP1,ABRAXAS1,ABRAXAS2,AURKC,APC	grey	VSMC_M10
GO:0050793	1.00	0.00	913	1852	regulation of developmental process	BP	1	NFATC1,NME1,ITGA7,NEDD4L,TCF4,LRP1,SEMA6A,GLI1,TNFAIP3,CYP27B1,MAML1,ATAT1,ESR1,FRS2,CNOT2,RAB21,STK3,OSR2,SNW1,TIAM2,ZNF706,ADM2,SLC12A2,HSPA1B,FZD6,RIMS2,BRD1,CDC42SE2,PRKN,AGER,PPARA,HLA-DRA,FBLN1,TNFRSF11B,IL5,TSPO,GDF9,FSTL4,TCF7,SYNGAP1,XRCC6,RSPO3,TRIB1,MYC,TOB2,SMAD5,ASAP1,AGO2,PTK2,PTCH1,ATF4,PLXNA4,MAPK14,NTRK2,CSNK1E,CPNE5,KDM4C,SOX10,PI16,PIM1,CDC42EP1,RAC2,STRIP2,SMO,ZDHHC21,HSF1,DAAM2,TAF8,MYH9,CDKN2A,ZNF16,RBFOX2,CHRNA3,TEK,LINGO2,FBXO7,RORB,PTK7,CEMIP2,SRF,TTBK1,DLK2,NUAK1,OCIAD1,CDK6,RFX3,KIT,TNFRSF21,TFAP2B,ROR2,SEMA4D,S1PR3,PDCL3,NINJ1,FGD3,OMD,ZNF135,EXOSC3,SEMA4C,SOSTDC1,BEND6,ZNF268,NLRP5,SIX2,BRSK1,SMAP1,RIMS1,MSH2,CD109,RTN4,PPP2R1A,PHIP,PNPT1,RUFY3,SHANK1,HOXA2,HOXA7,EMC10,LPAR1,ANKRD17,PTBP3,MYCL,CXCL8,SLC46A2,MTURN,AREG,AQP1,MYH14,BMPER,AKIRIN1,CNOT4,LRRN3,ZNF277,EPHA7,NR1H2,MBOAT2,PTN,ITGB1BP1,GRHL1,ST7,IL4I1,AGO1,YWHAZ,EGFR,TSPAN12,HECW1,FUZ,TRIM32,TLR4,CDK5RAP2,EPHA1,ZMYM6,BVES,GAB1,LPIN1,IL15,SFRP4,KEL,MYLK3,DKKL1,VPS35,TEAD2,SDCBP,MYCN,RTN4IP1,NRCAM,TRPM4,OSR1,FOXO3,NTF4,FIG4,MKX,APOB,MAMSTR,SPRY1,PLXNA1,WISP3,FOXE3,LAMA4,HDAC2,MTMR2,HMCES,C5AR1,SLC26A5,VSTM5,NAPEPLD,PRKD2,CST7,SOX9,SLC39A12,CLASP2,CLPTM1,SLC4A2,PTCH2,MLH1,GOLGA4,GLI2,MEGF8,AAMDC,KDM4A,UNC13D,RAF1,XRCC2,ACVR2B,KLF5,FOXJ1,PAXIP1,PTPRF,NUMBL,POU4F1,TSKU,IL15RA,SPRY2,SS18L2,WNT11,ALK,MYL12A,RIN2,HOOK3,CPNE	grey	VSMC_M10
GO:0043542	1.00	0.00	80	195	endothelial cell migration	BP	1	PTK2,PTP4A3,MYH9,TEK,SRF,MEOX2,SVBP,EMC10,BMPER,PTN,ITGB1BP1,MET,PRKD2,PAXIP1,RIN2,DCN,FOXP1,PLK2,GPI,NR4A1,PIK3CB,LPXN,ATP5F1A,ROBO1,FBXW7,MEF2C,VEGFC,PTK2B,STC1,HDAC7,LOXL2,ADTRP,CD40,PXN,GPLD1,FAP,SP100,PDCD6,PRKX,EGF,AGT,CIB1,MAP3K3,PATZ1,GLUL,NFE2L2,MIA3,EPHB4,S100P,PDCD10,RHOJ,SYNJ2BP,SEMA4A,FGF18,EFNA1,VASH1,MAP2K5,BCAS3,AMOT,PDPK1,MECP2,LCN2,DAB2IP,MIR29A,MIR199A1,MIR21,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,DPP4,ACVRL1,ZNF580,WNT5A,GADD45A,RGCC,FGF1,S100A2	grey	VSMC_M10
GO:0060548	1.00	0.00	356	754	negative regulation of cell death	BP	1	ADNP2,SERPINB2,VPS4B,ERBB3,TNFAIP8,LRP1,EYA4,TNFAIP3,AGAP2,PPP1R10,IER3,MAPK8IP2,HSPA1B,PRKN,PACRG,PPARA,RGL2,SYNGAP1,UBE2B,NCOA7,MYC,PTK2,AKR1B1,ATF4,NTRK2,NRBP2,SOX10,PIM1,ZC3HC1,SMO,HSF1,ZNF16,TEK,GPR37,FBXO7,BAG1,CNTFR,SLC25A27,KIT,SLC1A1,FHL2,TFAP2B,SEMA4D,TMEM14A,CHMP2A,ZNF268,CAT,DNAJA1,EPCAM,MSH2,PHIP,REL,PPT1,ALB,SLC46A2,AQP1,PELI1,ANXA4,TGFA,MET,YWHAZ,POU3F3,EGFR,TRIM32,BCL2L12,VPS35,TEAD2,ATG5,SLC7A11,OSR1,NTF4,FGF21,BRAF,HIGD1A,WISP3,FOXE3,HDAC2,BMI1,NDNF,C5AR1,ARMC10,SOX9,DDIAS,PLK3,GLI2,KDM4A,RAF1,XRCC2,ZFAND6,PRDX3,UBE2O,POU4F1,SPRY2,WNT11,AKT2,ARRB1,CBX4,CHD8,ZMYND11,TCIM,SLC23A2,EIF2AK2,PRNP,BAG4,SPEF1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,NR1H4,APIP,PLK2,HCK,IL1A,GPI,PAX8,NR4A1,FAIM,PIK3R1,CASP3,HIP1R,TAF9,ARHGAP10,GBE1,HAND2,ING2,EYA1,FZD3,MEF2C,NUGGC,IL7,FAIM2,HTRA2,TMBIM6,NDUFS3,CSNK2A2,PTK2B,CIAPIN1,OPA1,NR4A2,AMIGO2,F2R,SRSF6,RIPK1,MARCH7,PIDD1,WISP2,ZBED6,TXNDC5,TFAP2A,PAX2,ADAMTS20,NOD2,SIRT5,DSTYK,NUAK2,PM20D1,RNF144B,BDNF,SIRT4,RHBDD1,CD200,HDAC1,TERT,PDCD4,SLC30A10,GPAM,TCF7L2,DAD1,INPP5A,CFL1,KRAS,DYRK3,FCMR,SNAI1,HCLS1,ADNP,SORL1,EYA3,IFI6,MCL1,CIB1,CBL,HYOU1,BAG3,SLC9A1,STRADB,SFN,NFATC4,RPS6KA1,PEA15,PELI3,NTSR1,PAFAH2,CD28,WDR73,DLX1,PDE8A,RTKN2,DNAJC5,FZD9,SNX6,CDKN1B,MGMT,YBX3,ADAM8,POR,NFE2L2,CREB1,IVNS1ABP,NONO,SUPV3L1,BCL6,SYVN1,BCL2A1,CTSH,DDX3X,KLHL20,PDCD10,TNFSF18,LRPAP1,CXCR2,WNT4,HTT,PSME3,	grey	VSMC_M10
GO:0090068	1.00	0.00	73	180	positive regulation of cell cycle process	BP	1	VPS4B,GLI1,PPP1R10,UBE2B,MAPK15,CCND3,ZNF16,PRKCE,PHIP,HOXA13,ANKRD17,EPGN,TGFA,LSM10,EGFR,TOPAZ1,UBE2E2,DYNC1LI1,SIRT2,RPTOR,PLCB1,NUDT16,TFDP1,DDRGK1,MTA3,NSFL1C,KIF3B,IL1A,CSPP1,SLF1,ANAPC5,ANAPC7,ADAMTS1,SLF2,NPM2,IGF2,HYAL1,CCND1,TERT,DYRK3,EGF,USP19,CHEK2,CD28,STOX1,DBF4B,DDX3X,MEPCE,WNT4,RHNO1,DDX11,ANAPC4,MED1,RAD51B,SOX15,PAGR1,RAB11A,RAD51C,SFPQ,SIN3A,INSR,MECP2,CDK10,GPSM2,CDC14A,MIR29A,MIR222,RHOA,AURKC,OOEP,WNT5A,RGCC,EREG	grey	VSMC_M10
GO:0007080	1.00	0.00	12	43	mitotic metaphase plate congression	BP	1	VPS4B,CHMP2A,PIBF1,CHAMP1,CHMP2B,CHMP4C,CHMP7,KPNB1,RAB11A,CHMP1A,PSRC1,VPS4A	grey	VSMC_M10

GO:0072331	1.00	0.00	54	139	signal transduction by p53 class mediator	BP	1	SNW1,PRKN,NUAK1,MSH2,FOXO3,ARMC10,PLK3,PAXIP1,POU4F1,PIP4P1,SETD9,PLK2,TAF9,ATR,ING2,MAPKAPK5,NBN,MARCH7,PIDD1,PLA2R1,RPL23,SP100,MAP2K6,DYRK3,SNAI1,AEN,CHEK2,USP2,RPL11,CDKN1B,E2F2,ING4,MUC1,BATF,TAF1,TAF9B,PSMD10,CD74,PPP1R13B,CDIP1,CHD5,MIR21,PRMT6,UBB,RPS27L,TRIM24,SOX4,TP53RK,ACER2,PERP,PTTG1IP,TMEM109,CRADD,HINT1	grey	VSMC_M10
GO:0006397	1.00	0.00	183	407	mRNA processing	BP	1	ZC3H10,PAN2,RNMT,CPSF6,PABPC1,SNW1,SF3A3,QKI,CSDC2,HABP4,ZC3H3,PUF60,CMTR1,HSF1,CPSF1,USP49,RBM28,RBFOX2,SMU1,RNF20,TSEN34,PRPF31,TRA2A,YTHDC1,PNPT1,PTBP3,RNGTT,SRSF10,PRPF4,SNIP1,SNRNP27,LSM10,SCAF1,PRPF38A,MTPAP,SYMPK,IWS1,CLASRP,PCF11,WBP4,CLNS1A,CELF2,KIN,RBM26,CRNKL1,IK,NUP98,ZMAT2,CWC15,LSM1,WTAP,PPP4R2,PHRF1,PAN3,THOC7,TGS1,CSTF3,SREK1IP1,GPATCH1,SREK1,USP39,PRMT9,CLP1,ZCCHC8,GCFC2,RBM39,AAR2,CELF1,CNOT6L,RPRD1B,SCAF4,DHX35,TENT2,SRSF6,SCAF11,PRPF4B,BCAS2,TENT4B,RBM24,PDCD11,SMNDC1,RBM5,CPSF2,ADARB1,SART3,ACIN1,HSPA8,SRSF4,RPRD2,CSTF1,ZRSR2,ZMAT5,CELF3,SYF2,WBP11,NCBP2,DDX47,BUD13,MFAP1,RBM7,NONO,GEMIN2,SNRPD3,PRPF39,SUGP1,SUGP2,DHX8,ECD,CWF19L2,ESS2,RBM10,CPSF4,LEO1,AP002990.1,AKAP8L,CASC3,CDK12,PRPF19,LSM8,FXR2,TARDBP,RBM25,KHDC4,LUC7L3,SLU7,COIL,NRDE2,CSTF2,SFPQ,PAPOLA,RPRD1A,RBM41,XAB2,ALKBH5,THOC2,RAVER2,SNU13,SUPT6H,RBMX2,MBNL3,NSRP1,FMR1,AFF2,CELF5,METTL16,SRRM2,NCBP3,LSM7,CIRBP,LUC7L,C9orf78,CMTR2,TXNL4B,PRMT7,ESRP2,ZRANB2,SRSF11,RNVU1-6,RNU5E-1,RNU5B-1,SRRM4,HTATSF1,NOL3,METTL14,RNU4ATAC,RF00003,SNRPC,NOVA1,RNU2-1,RPUSD3,RNU4-2,RBM11,SRSF12,ZCRB1,YBX1,RNU4-1,MAGOHB,SAP18,SRRM1,RBM38,ZNF473,SNRNP25,PRKRIP1	grey	VSMC_M10
GO:2000573	1.00	0.00	19	60	positive regulation of DNA biosynthetic process	BP	1	MAP3K4,MYC,MAPK15,POT1,PRKD2,ATR,HMBOX1,PTK2B,MAPKAPK5,POLG2,XRCC5,MAPK1,NVL,FGFR4,WRAP53,MAPK3,PARN,RGCC,MAP2K7	grey	VSMC_M10
GO:0042325	1.00	0.00	461	967	regulation of phosphorylation	BP	1	ERBB3,LRP1,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,TNXB,MAP3K4,PRKN,AGER,PPARA,FBLN1,IL5,GDF9,ROS1,UBE2B,BAK1,XRCC6,TRIB1,PRXL2C,PTK2,TAB1,NTRK2,STK38,PLA2G6,HSF1,CCND3,CDKN2A,ZNF16,CHRNA3,TEK,FBXO7,TTBK1,TEC,KIT,SLC1A1,NCK2,ROR2,SEMA4D,PDCL3,KLHL31,CLDN19,DNAJA1,IL11,PRKCE,CD109,PPP2R1A,PHIP,FPR2,IBTK,ACP4,MOB1B,SLC4A4,EPGN,AREG,BMP8A,BMPER,WDR91,ETAA1,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,GRB10,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,PRKAR2B,SPRY1,HDAC2,SLC8A2,C5AR1,PIP4K2A,MOB3C,PRKD2,PHB,ABI1,SOX9,MAPRE3,RALB,PRKAG2,RAF1,PRDX3,PIBF1,GCKR,FBH1,SPRY2,WNT11,ALK,TADA3,AKT2,GPD1L,ARRB1,TGFBR2,ACVR2A,IKBKB,SIRT2,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,PLCL2,PRNP,DUSP6,BAG4,TAF7,MAVS,NRG1,CCKBR,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,PRKDC,ERCC6,FLT1,RYK,ADRA2B,TRAF6,TRIB3,EPHB1,RET,ACVR1B,CEBPA,FER,PIK3CB,SNX25,OSBP,PIK3R1,ZFP91,CDK7,CASP3,RAD17,ROBO1,PLCE1,FBXW7,PTPRJ,GPD1,PKIA,IL7,CCNH,P2RX7,VEGFC,CCNJ,SLA2,MCPH1,P2RY1,MADD,PTK2B,RASGRP1,CCNG2,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,PAQR3,FGF5,NLRC5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CCNJL,CDK2AP1,PKD2,STK4,DBNDD2,DMTN,ADTRP,HERC5,NOD2,CNTN1,DTNBP1,TAOK3,CD40,DSTYK,ROPN1L,LDB1,IGF2,BMPR1B,NHLRC1,BDNF,IRS1,NEURL1,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K6,PDCD4,TGFB2,ZBTB20,ADRA2A,FAM20A,PRKAR1A,ADARB1,DAG1,AXIN2,SLCO3A1,AJUBA,NCF1,MST1,KRAS,FABP4,EGF,PFKFB2,HCLS1,ADNP,O	grey	VSMC_M10
GO:0023057	1.00	0.00	503	1048	negative regulation of signaling	BP	1	NFATC1,PHLPP1,ERBB3,ONECUT2,LRP1,SEMA6A,EYA4,GLI1,PIP4K2C,TNFAIP3,EPM2A,TRIM39,PPP1R10,ESR1,CNOT2,STK3,MAPK8IP2,MPIG6B,HSPA1B,FZD6,GRAMD4,PRRT1,PRKN,AGER,PPARA,PDE10A,FBLN1,FSTL4,SYNGAP1,UBE2B,TRIB1,MYC,LEMD2,PTCH1,MAPK14,CBY1,STK38,PLA2G6,PICK1,SOX10,ZC3HC1,MDFI,FOXH1,LRRC14,CRY1,SRF,DLK2,NCK2,FHL2,IL1R2,ROR2,TMEM14A,WNK2,KLHL31,SOSTDC1,BEND6,DNAJA1,IL11,CD109,FKTN,PPP2R1A,PHIP,KLK14,ACP4,CXCL8,BMP8A,BMPER,PXDN,PLEK,NR1H2,ITGB1BP1,MET,VRK3,GRB10,EGFR,HECW1,FUZ,TRIM32,TLR4,SFRP4,DKKL1,FOXO3,SPRY1,ARHGAP12,MTMR2,KPTN,SESN3,RAB7A,BMI1,PIP4K2A,ARMC10,PTGIR,PHB,SOX9,GIPR,PPM1N,CD300LF,DDIAS,PTCH2,OPTN,KBTBD6,KCTD21,GLI2,MEGF8,RAF1,PIBF1,IFT172,SEC14L1,TSKU,SZT2,SPRY2,WNT11,GPD1L,ARRB1,EID2,SNX5,RBMS3,CHD8,NMI,ZMYND11,TCIM,NPLOC4,PAWR,UBAC2,PLCL2,FERMT1,SPRED3,PRNP,DUSP6,DCN,SPART,DDRGK1,SH3RF2,GAS6,SIRT3,PPP2CB,RASA3,FOXP1,LEPROTL1,MFHAS1,TMEM127,NR1H4,RGS20,PLK2,PFDN5,NDUFAF2,FAM3D,ASXL1,IL1A,CYP7B1,RGS7BP,KCTD6,ABHD6,CBFA2T2,FAIM,PIK3CB,SNX25,ZNF536,OTUD4,RASA2,LPXN,TAF9,CTNND1,DKK3,TRABD2A,ING2,EYA1,ROBO1,ZNF366,IL17RD,ARNTL,FBXW7,PTPRJ,TMEM131L,ASIC1,IL7,FAIM2,HTRA2,TMBIM6,P2RX7,NDUFS3,CNOT1,CSNK2A2,SLA2,PTK2B,LMBR1L,KCNJ11,MAPKAPK5,NR1H3,PAQR3,VEPH1,OAS3,NLRC5,RAB11FIP5,NKX3-1,OPA1,HDAC7,AMFR,NR4A2,ACVR1C,F2RL1,ARHGAP24,RIPK1,CRY2,VPS18,MARCH7,RPGRIP1L,SOX13,STK4,MAPKBP1,HIF1AN,PRICKLE1,NOD2,NKD1,TAOK3,	grey	VSMC_M10
GO:0045841	1.00	0.00	10	38	negative regulation of mitotic metaphase/anaphase transition	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10

GO:0002181	1.00	0.00	43	111	cytoplasmic translation	BP	1	RPS12,EIF3E,RPS18,RPS10,EIF3L,RPS14,CNBP,EIF2B3,RPS8,DPH2,RPSA,RPL14,DPH3,RPL31,RPL6,RBM24,EIF2D,RPL23,RPL4,RPS17,RPL27A,YTHDF2,RPS27,RPS4X,RPL11,YBX3,RPL27,UBA52,RPL19,RPLP1,EIF3C,MCTS1,RPL23A,FMR1,DPH1,AARS,RPL35,RPS15A,TMA7,RPL21,RWDD1,DRG1,RPL37A	grey	VSMC_M10
GO:0000723	1.00	0.00	44	118	telomere maintenance	BP	1	RPA3,PPP1R10,MAP3K4,XRCC6,MYC,MAPK15,POT1,ERCC1,XRCC1,WRN,PRKDC,ATR,HMBOX1,MAPKAPK5,TPRKB,NBN,TENT4B,STN1,LTO1,SP100,TERT,GAR1,RTEL1,XRCC5,UPF1,MAPK1,PARP1,GNL3L,WRAP53,SMG5,YLPM1,CTC1,PIF1,MAPK3,RAD51C,RAD51D,PARN,ERCC4,SLX4,ZBTB48,TERF2,TINF2,TEN1,MAP2K7	grey	VSMC_M10
GO:0002183	1.00	0.00	7	30	cytoplasmic translational initiation	BP	1	EIF3E,EIF3L,EIF2B3,EIF2D,YTHDF2,EIF3C,MCTS1	grey	VSMC_M10
GO:0010594	1.00	0.00	62	157	regulation of endothelial cell migration	BP	1	PTK2,TEK,MEOX2,SVBP,EMC10,BMPER,PTN,ITGB1BP1,MET,PRKD2,RIN2,DCN,FOXP1,PLK2,GPI,PIK3CB,ATP5F1A,FBXW7,MEF2C,VEGFC,PTK2B,STC1,HDAC7,CD40,GPLD1,SP100,PDCD6,EGF,AGT,CIB1,MAP3K3,PATZ1,GLUL,NFE2L2,PDCD10,RHOJ,SYNJ2BP,SEMA4A,FGF18,EFNA1,VASH1,MAP2K5,BCAS3,PDPK1,MECP2,LCN2,DAB2IP,MIR29A,MIR199A1,MIR21,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,ACVRL1,ZNF580,WNT5A,GADD45A,RGCC,FGF1	grey	VSMC_M10
GO:0033688	1.00	0.00	4	22	regulation of osteoblast proliferation	BP	1	EIF2AK2,SMAD3,SOX8,RHOA	grey	VSMC_M10
GO:1901991	1.00	0.00	55	142	negative regulation of mitotic cell cycle phase transition	BP	1	MRNIP,TRIM39,ZNF207,FBXO7,BRSK1,CDK5RAP2,TPRA1,PLK3,DYNC1LI1,ANAPC15,IK,USP44,PRKDC,PLK2,FAM107A,RAD17,CHMP4C,NBN,ABRAXAS1,DONSON,ZFYVE19,PIDD1,PKD2,TAOK3,CCND1,GIGYF2,CHEK2,SYF2,CDKN1B,DLG1,UIMC1,FOXO4,MUC1,TAOK2,LCMT1,FOXN3,DCUN1D3,CCL2,PSMG2,TAOK1,FZR1,FBXO31,VPS4A,NAE1,MIR29A,PLK5,RPS27L,SOX4,DUSP1,RGCC,APC,ZFP36L2,BRCC3,CRADD,NABP1	grey	VSMC_M10
GO:0030335	1.00	0.00	199	443	positive regulation of cell migration	BP	1	ONECUT2,LRP1,SEMA6A,AGER,GPSM3,AGO2,PTK2,SUN2,PODXL,RAC2,SMO,TEK,CCL27,KIT,ROR2,SEMA4D,SEMA4C,ZNF268,PRKCE,RTN4,FPR2,EPB41L4B,RUFY3,EMC10,CXCL8,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,TRIM32,TLR4,TCAF2,EPHA1,GAB1,SDCBP,C5AR1,PRKD2,IQSEC1,SOX9,CLASP2,OXSR1,SPRY2,WNT11,RIN2,AKT2,TGFBR2,ACTG1,HBEGF,FERMT1,BAG4,ARHGEF7,SEMA3D,DIAPH1,SEMA3A,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,FLT1,PLK2,RET,FAM107A,GPI,ACVR1B,FER,PIK3CB,PIK3R1,ATP5F1A,ELP3,SEMA4F,VEGFC,JAM2,ADAMTS1,PTK2B,RAPGEF2,TIAM1,DOCK5,HDAC7,F2RL1,F2R,ANO6,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,CD40,SRGAP2C,GPLD1,LGR6,DNM1L,CARMIL1,HYAL1,PPP3CA,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,CD99,PRSS56,SSH1,CMKLR1,SNAI1,EGF,GPER1,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,HDAC4,MAP3K3,DOCK1,ELP6,ADAM8,LRRC15,NFE2L2,MIA3,CCAR1,CEMIP,SEMA6D,TRIP6,CTSH,ITGA2B,ITGA4,IL12A,FN1,VSIR,MCU,PDCD10,TNFSF18,FERMT3,CXCR2,STAT3,MAPK1,RHOJ,SYNE2,CXCL16,SYDE1,TMEM102,MIEN1,STX4,SEMA4A,RAB25,FGF18,FOXO4,ITGA3,PGF,DAPK2,ZNF609,MAPK3,IL6R,RAB11A,SMAD3,S100A14,BDKRB1,BCAS3,CD74,INSR,CCL5,CSF1R,CCL7,DOCK7,CRK,PDPK1,FBXO31,FOXF1,LCN2,HSPA5,DAB2IP,CARMIL2,RIPOR1,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR27B,MIR27A,RHOA,DEFB124,FADD,LAMB1,ZNF580,THY1,CLDN1,WNT5A,ZNF304,APC,HRAS,FGF1,CBLL1,PDGFD	grey	VSMC_M10
GO:0009059	1.00	0.00	1813	3569	macromolecule biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,ORMDL2,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,POLI,RPS12,SHMT2,ATG12,TBPL1,PGGT1B,GLI1,HBS1L,MARS,B4GALT7,MAP3K5,RPA3,TNFAIP3,TSFM,HIVEP2,PLAGL1,RXYLT1,MAML1,HELB,ZBTB2,RMND1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,TFB1M,ZNF706,ARID1B,ZDHHC14,HSPA1B,FZD6,ZBTB12,EIF3E,ALG12,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,PDE10A,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,MCM9,MRPL13,RPS18,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,MRPL55,JMJD4,AGO2,HABP4,RPS10,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,EIF3L,PIM1,NRF1,TMPRSS6,GPAA1,SMO,ZDHHC21,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,LARGE1,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,NFKBIE,CWH43,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,ST6GAL2,SRD5A3,NCK2,FHL2,TGFBRAP1,MRPS9,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,C1GALT1,CHST10,REV1,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,MCMBP,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,LRPPRC,ALG2,SIX2,SRBD1,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,TMEM246,RNF20,EPAS1,PIGF,EPCAM,SP4,IGF2BP3,FKTN,PPP2R1A,ZNF462,PHIP,HMGN3,HAS1,NFYC,MTIF2,NFE2L3,PNPT1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,ANKRD17,JAZF1,C	grey	VSMC_M10
GO:0000413	1.00	0.00	8	32	protein peptidyl-prolyl isomerization	BP	1	FKBP9,FKBP15,PPIG,FKBP8,PPIL2,FKBP7,PPIC,PPIF	grey	VSMC_M10

GO:0010648	1.00	0.00	502	1047	negative regulation of cell communication	BP	1	NFATC1,PHLPP1,ERBB3,ONECUT2,LRP1,SEMA6A,EYA4,GLI1,PIP4K2C,TNFAIP3,EPM2A,TRIM39,PPP1R10,ESR1,CNOT2,STK3,MAPK8IP2,MPIG6B,HSPA1B,FZD6,GRAMD4,PRRT1,PRKN,AGER,PPARA,PDE10A,FBLN1,FSTL4,SYNGAP1,UBE2B,TRIB1,MYC,LEMD2,PTCH1,MAPK14,CBY1,STK38,PLA2G6,PICK1,SOX10,ZC3HC1,MDFI,FOXH1,LRRC14,CRY1,SRF,DLK2,NCK2,FHL2,IL1R2,ROR2,TMEM14A,WNK2,KLHL31,SOSTDC1,BEND6,DNAJA1,IL11,CD109,FKTN,PPP2R1A,PHIP,KLK14,ACP4,CXCL8,BMP8A,BMPER,PXDN,PLEK,NR1H2,ITGB1BP1,MET,VRK3,GRB10,EGFR,HECW1,FUZ,TRIM32,TLR4,SFRP4,DKKL1,FOXO3,SPRY1,ARHGAP12,MTMR2,KPTN,SESN3,RAB7A,BMI1,PIP4K2A,ARMC10,PTGIR,PHB,SOX9,GIPR,PPM1N,CD300LF,DDIAS,PTCH2,OPTN,KBTBD6,KCTD21,GLI2,MEGF8,RAF1,PIBF1,IFT172,SEC14L1,TSKU,SZT2,SPRY2,WNT11,GPD1L,ARRB1,EID2,SNX5,RBMS3,CHD8,NMI,ZMYND11,TCIM,NPLOC4,PAWR,UBAC2,PLCL2,FERMT1,SPRED3,PRNP,DUSP6,DCN,SPART,DDRGK1,SH3RF2,GAS6,SIRT3,PPP2CB,RASA3,FOXP1,LEPROTL1,MFHAS1,TMEM127,NR1H4,RGS20,PLK2,PFDN5,NDUFAF2,FAM3D,ASXL1,IL1A,CYP7B1,RGS7BP,KCTD6,ABHD6,CBFA2T2,FAIM,PIK3CB,SNX25,ZNF536,OTUD4,RASA2,LPXN,TAF9,CTNND1,DKK3,TRABD2A,ING2,EYA1,ROBO1,ZNF366,IL17RD,ARNTL,FBXW7,PTPRJ,TMEM131L,ASIC1,IL7,FAIM2,HTRA2,TMBIM6,P2RX7,NDUFS3,CNOT1,CSNK2A2,SLA2,PTK2B,LMBR1L,KCNJ11,MAPKAPK5,NR1H3,PAQR3,VEPH1,OAS3,NLRC5,RAB11FIP5,NKX3-1,OPA1,HDAC7,AMFR,NR4A2,ACVR1C,F2RL1,ARHGAP24,RIPK1,CRY2,VPS18,MARCH7,RPGRIP1L,SOX13,STK4,MAPKBP1,HIF1AN,PRICKLE1,NOD2,NKD1,TAOK3,	grey	VSMC_M10
GO:1901987	1.00	0.00	135	311	regulation of cell cycle phase transition	BP	1	VPS4B,GLI1,MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,MAPK15,MAPK14,CCND3,ZNF16,FBXO7,CRY1,BRSK1,MSH2,ANKRD17,ETAA1,LSM10,EGFR,CDK5RAP2,TPRA1,TOPAZ1,XPC,ERCC2,ERCC3,PLK3,UBE2E2,PAXIP1,DYNC1LI1,SIRT2,NEK10,RPTOR,TCIM,ANAPC15,PLCB1,IK,NEK11,USP44,TFDP1,DDRGK1,MTA3,PRKDC,ERCC6,CEP63,STK33,PLK2,MOS,FAM107A,RAD17,ATR,FBXW7,ANAPC5,PKIA,ANAPC7,RAD9B,CHMP4C,ADAMTS1,EIF2AK4,NBN,ABRAXAS1,DONSON,ZFYVE19,PIDD1,PKD2,NPM2,TAOK3,HYAL1,HECW2,CCND1,TERT,DYRK3,GIGYF2,CHEK2,PSME1,ATRIP,SYF2,CDKN1B,DLG1,OVOL1,STOX1,SUSD2,DBF4B,MEN1,DDX3X,MEPCE,PTPN6,ECD,PSME3,TIPRL,RHNO1,DDB1,PRPF19,ANAPC4,RAD51B,UIMC1,FOXO4,PAGR1,CTC1,EME1,MUC1,TAOK2,TAF1,RAB11A,TIPIN,LCMT1,FOXN3,RAD51C,DCUN1D3,SIN3A,CCL2,PSMG2,TAOK1,FZR1,DOT1L,PKD1,MECP2,CDK10,FBXO31,CDC14A,VPS4A,NAE1,MIR29A,MIR222,RPA4,PLK5,RPS27L,SOX4,DUSP1,RGCC,APC,CDC26,ZFP36L2,BRCC3,CRADD,NABP1	grey	VSMC_M10
GO:0006913	1.00	0.00	109	257	nucleocytoplasmic transport	BP	1	PPP1R10,CPSF6,PHAX,FAM53C,MAPK14,SMO,NOL6,XPO5,WASHC4,RAB23,SIX2,YTHDC1,XPO1,BACH2,TRAF3IP2,DNAJC27,KPNA3,IWS1,IPO13,GCKR,KPNA2,TMCO6,NUP98,SIRT7,FERMT1,CHTOP,ING1,MAVS,GAS6,UPF3A,THOC7,NUP58,IPO11,PIK3R1,TNPO1,PKIA,SDAD1,NUP54,PRKAG1,RAPGEF3,CRY2,PRICKLE1,XPO7,ATXN1,MX2,SUFU,CABP1,RPL23,DDX25,PPP3CA,IPO9,SP100,TCF7L2,HCLS1,AGT,BAG3,NOP9,STRADB,SFN,STRADA,UHMK1,NCBP2,EIF4ENIF1,POM121,DUSP16,APOD,SETD2,CTDSPL2,ENY2,UPF1,FAM53A,STAT3,MAPK1,NXF1,AKAP8L,FYTTD1,RGS14,MED1,KPNB1,TARDBP,PSEN1,SMG5,RANBP17,CITED1,TNPO2,XPO6,SMAD3,NRDE2,ALKBH5,UPF3B,THOC2,EFCAB7,RANBP3L,SUPT6H,PKD1,PARK7,TSC1,NUP214,DDX19A,ANKRD54,SARNP,DDX19B,NXT2,NUPL2,HIKESHI,TXN,PTTG1IP,STYX,ZIC1	grey	VSMC_M10
GO:0051169	1.00	0.00	109	257	nuclear transport	BP	1	PPP1R10,CPSF6,PHAX,FAM53C,MAPK14,SMO,NOL6,XPO5,WASHC4,RAB23,SIX2,YTHDC1,XPO1,BACH2,TRAF3IP2,DNAJC27,KPNA3,IWS1,IPO13,GCKR,KPNA2,TMCO6,NUP98,SIRT7,FERMT1,CHTOP,ING1,MAVS,GAS6,UPF3A,THOC7,NUP58,IPO11,PIK3R1,TNPO1,PKIA,SDAD1,NUP54,PRKAG1,RAPGEF3,CRY2,PRICKLE1,XPO7,ATXN1,MX2,SUFU,CABP1,RPL23,DDX25,PPP3CA,IPO9,SP100,TCF7L2,HCLS1,AGT,BAG3,NOP9,STRADB,SFN,STRADA,UHMK1,NCBP2,EIF4ENIF1,POM121,DUSP16,APOD,SETD2,CTDSPL2,ENY2,UPF1,FAM53A,STAT3,MAPK1,NXF1,AKAP8L,FYTTD1,RGS14,MED1,KPNB1,TARDBP,PSEN1,SMG5,RANBP17,CITED1,TNPO2,XPO6,SMAD3,NRDE2,ALKBH5,UPF3B,THOC2,EFCAB7,RANBP3L,SUPT6H,PKD1,PARK7,TSC1,NUP214,DDX19A,ANKRD54,SARNP,DDX19B,NXT2,NUPL2,HIKESHI,TXN,PTTG1IP,STYX,ZIC1	grey	VSMC_M10
GO:0001889	1.00	0.00	43	116	liver development	BP	1	ONECUT2,GLI1,TNFAIP3,IGF2R,ACO2,PTCH1,PNPT1,TGFA,PTN,MET,EGFR,SOX9,TAF10,LSR,CEBPA,FBXW7,CSNK2A2,RPGRIP1L,PKD2,JARID2,SRD5A1,CCND1,CPT1A,SULF2,HLX,KRAS,RPS6KA1,HMGCL,SP3,CPS1,WNT4,MED1,ALDH1A2,RPL19,SMAD3,GATA6,PKD1,ASS1,ACADM,CLDN1,HRAS,CEBPB,FGF1	grey	VSMC_M10
GO:0007098	1.00	0.00	42	115	centrosome cycle	BP	1	VPS4B,MDM1,KIF3A,CNTLN,HEPACAM2,CHMP2A,BRSK1,XPO1,CEP68,CDK5RAP2,XRCC2,CEP295NL,CEP63,NSFL1C,PLK2,KIF3B,CHMP2B,CEP44,CEP250,CETN3,CHMP4C,MCPH1,ALMS1,TMEM67,PKD2,AC112128.1,CCDC84,KIAA1614,SLC16A1,NIN,CEP152,UXT,SDCCAG8,CNTROB,NDEL1,TRIM37,CEP192,NUBP1,CHMP1A,GADD45A,C2CD3,PARD6A	grey	VSMC_M10

GO:0033993	1.00	0.00	305	657	response to lipid	BP	1	ADNP2,NME1,VPS4B,FECH,TNFAIP3,CYP27B1,ESR1,CNOT2,TPH2,RIDA,SNW1,IGF2R,PPARA,RXRB,TSPO,TRIB1,PTCH1,MAPK14,KDM4C,SOX10,PIM1,SMO,HSF1,FOXH1,MTAP,RBFOX2,RORB,CRY1,PTK7,CA9,ADH5,CAT,DNAJA1,PRKCE,HOXA2,CXCL8,AREG,AKIRIN2,AQP1,PELI1,PTN,FOXP2,TNC,EGFR,LANCL2,TLR4,IL15,UCP1,TEAD2,MGST2,MGARP,OSR1,FOXO3,PGRMC2,APOB,CDK19,SPHK2,HDAC2,ADCY3,DNMT3A,BMI1,C5AR1,PTGIR,PHB,SOX9,GIPR,GLB1,MBD4,ATP1A3,MYD88,PRDX3,TIMP4,EGLN2,AANAT,IRAK2,THBD,HNMT,POU4F1,WNT11,TADA3,TGFBR2,NFKBIB,MAP4K1,CRLS1,TAF7,DCN,RNF14,DDRGK1,FOXP1,CALCOCO1,NCOA4,TRAF6,NR1H4,RET,CYP7A1,HCK,ASXL1,FAM107A,IL1A,CYP7B1,IL37,DNMT3B,GPI,NR4A1,FER,UFSP2,CASP3,NCOA2,CCDC62,HPGD,ZNF366,ARNTL,PLSCR4,MEF2C,SMARCD1,NUGGC,HTRA2,CNOT1,MMP15,PTK2B,KMT2D,KCNJ11,NR1H3,LCOR,RIPK2,DDX54,SYNJ1,VDR,STC1,NKX3-1,F2R,TESC,CRY2,VPS18,ABCC2,SPP1,CPN1,PAX2,ADTRP,NOD2,GDAP2,CD40,NFKB2,ADCY2,MAPKAPK3,GPLD1,SRD5A1,CD96,IRS1,DNM1L,HDAC1,CCND1,CPT1A,PDCD4,TGFB2,DAG1,KRAS,MAPKAPK2,ABHD2,GRAMD1B,GPER1,GNPAT,AGT,CBL,ATP1A2,ARID1A,FZD7,NPAS4,NTSR1,IL10RA,HMGCL,CDKN1B,RXRG,WNT3,PDK3,CREB1,DUSP10,FIS1,GGT2,ABL2,CPS1,CTSH,BRINP2,ACSBG1,IL12A,DNAAF2,FDX1,COMT,XRCC5,ESRRA,KCNK4,BCHE,UPF1,GPBAR1,RPL27,SLC11A1,TNIP2,ALPL,GCH1,RAMP2,CTSV,STAT3,CD38,MAPK1,STAT5B,SGMS1,OTUD5,PADI2,SCGB1A1,DNAAF4,FOXP3,LIAS,AKAP8,PARP1,TNFRSF1B,MED1,ALDH1A2,SPON2,OSBPL7,PAGR1,FOS,MAPK3,ESRRB,CITED1,SOX30,MPO,	grey	VSMC_M10
GO:0006468	1.00	0.00	589	1223	protein phosphorylation	BP	1	ERBB3,LRP1,CLK4,MAP3K5,TNFAIP3,AGAP2,ATP23,USP15,MAML1,MRNIP,STK3,ADM2,TNXB,MAP3K4,PRRT1,PRKN,AGER,FBLN1,IL5,BRD2,GDF9,ROS1,UBE2B,BAK1,XRCC6,TRIB1,SMAD5,OBSCN,PTK2,TAB1,MAPK15,MAPK14,NTRK2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,PIM1,HSF1,ADCK5,CCND3,CDKN2A,CHRNA3,TEK,TRPM6,FBXO7,CRY1,PTK7,TTBK1,NUAK1,CDK14,TEC,CDK6,KIT,SLC1A1,NCK2,ROR2,SEMA4D,CDK20,PDCL3,WNK2,KLHL31,CLDN19,DNAJA1,IL11,BRSK1,PRKCE,CD109,SPTBN1,PPP2R1A,PHIP,FPR2,IBTK,ACP4,MOB1B,VRK2,EPGN,AREG,BMP8A,BMPER,ETAA1,RSPO1,AAK1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,YWHAZ,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,MYLK3,SDCBP,NTF4,CDK19,FGF21,BRAF,PRKAR2B,SPRY1,HDAC2,SLC8A2,C5AR1,MKNK1,MOB3C,PRKD2,MYO3A,PHB,ABI1,SOX9,MAPRE3,PLK3,FASTK,LIPE,RALB,PRKAG2,RAF1,OXSR1,PIBF1,ACVR2B,IRAK2,FBH1,SPRY2,WNT11,ALK,TADA3,AKT2,GPD1L,ARRB1,DYRK1B,TGFBR2,ACVR2A,IKBKB,SIRT2,NEK10,RPTOR,AATK,TCIM,HBEGF,PTPRQ,PLCL2,MAP4K1,EIF2AK2,PRNP,DUSP6,NEK11,BAG4,TAF7,MAVS,PDK1,CDKL4,NRG1,DDRGK1,NCKAP1L,GAS6,HPX,ULK1,PTPRA,RBPMS,PRKDC,ERCC6,FLT1,PAN3,ADRA2B,TRAF6,STK33,AMHR2,TRIB3,EPHB1,PLK2,MOS,RET,HCK,ACVR1B,CAMK4,CEBPA,FER,PIK3CB,SNX25,MAST4,OSBP,PIK3R1,ZFP91,CDK7,CASP3,ATR,DCLK2,ROBO1,PLCE1,FBXW7,PTPRJ,PKIA,IL7,CCNH,VEGFC,CCNJ,CSNK2A2,P2RY1,MADD,PTK2B,RASGRP1,CCNG2,FNIP2,RAPGEF2,MOB1A,MAPKAPK5,DGUOK,PRKAG1,EIF2AK4,ARL2BP,TIAM1,BMP2K,PAQR3,FGF5,RIPK2,NBN,TOP1,NKX3-1,TRIO,RAPGEF3,ACVR1C,RIPK1,PRPF4B,CCNJL,CDK2	grey	VSMC_M10
GO:0051784	1.00	0.00	15	51	negative regulation of nuclear division	BP	1	ZNF207,FBXO43,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,PRKAR1A,LCMT1,TOM1L2,PSMG2,DUSP1,NME6,APC,LIF	grey	VSMC_M10
GO:1901576	1.00	0.00	2212	4324	organic substance biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,KDSR,ORMDL2,SMARCC2,PAN2,ATP8B1,FECH,ONECUT2,GLS2,BAZ2A,TCF4,POLI,RPS12,SHMT2,ATG12,TBPL1,PGGT1B,GLI1,HBS1L,MARS,B4GALT7,PIP4K2C,MAP3K5,PEX7,B4GALNT1,RPA3,TNFAIP3,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,RXYLT1,MAML1,LTC4S,ATP5MGL,HELB,ZBTB2,RMND1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,TFB1M,ZNF706,ALDH7A1,ARID1B,ZDHHC14,HSPA1B,SYNJ2,SERAC1,FZD6,ZBTB12,EIF3E,ALG12,CYP21A2,ZBED4,PNLDC1,MAP3K4,AGPAT4,PPT2,PRKN,AGPAT1,QKI,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,PNPLA3,RXRB,TSPO,MCAT,VGLL2,HSD17B8,MCM9,MRPL13,A4GALT,RPS18,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,MRPL55,JMJD4,AGO2,HABP4,RPS10,HSD17B3,KDM3B,PTP4A3,PTCH1,TNRC6B,AKR1B1,ATF4,PYCR3,TUT7,MAPK15,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,EIF3L,PIM1,CKB,NRF1,TMPRSS6,GPAA1,SMO,ZDHHC21,SNAPC3,BNC2,HSF1,MOCS1,PSAT1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,GPT,IMPDH1,HACD4,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,LARGE1,GNMT,POT1,GPR37,RORB,ZNF300,PRDM4,ALDH1A1,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,SLC35B2,NFKBIE,CWH43,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,ADGRF1,PLPP6,ST6GAL2,SRD5A3,UXS1,NCK2,FHL2,TGFBRAP1,MRPS9,TFAP2B,SPTLC1,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,AASDH,PPAT,C1GALT1,CHST10,HINT2,REV1,PHF14,IPPK,HMGCLL1,ETV1,IN	grey	VSMC_M10
GO:0051985	1.00	0.00	11	41	negative regulation of chromosome segregation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,MOS,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:1905819	1.00	0.00	11	41	negative regulation of chromosome separation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,MOS,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10

GO:0042176	1.00	0.00	150	342	regulation of protein catabolic process	BP	1	NEDD4L,LRP1,TNFAIP3,AGAP2,TRIM39,HSPA1B,PRKN,RNF217,TRIB1,PTK2,AGTPBP1,CSNK1E,RGP1,PDCL3,RAD23B,XPO1,WDR91,EGFR,HECW1,TRIM32,HACE1,VPS35,ZYG11B,SDCBP,MFSD8,FAF1,BBS7,RAB7A,PHB,SOX9,NUDT15,PLK3,SUMO2,AQP11,TIMP4,EGLN2,MYCBP2,KLHL40,SIRT2,RNF14,NRG1,DDRGK1,SH3RF2,RYBP,PSMF1,TRIB3,PLK2,CEBPA,IDE,TAF9,SH3D19,FBXW7,USP25,CSNK2A2,PTK2B,FAM192A,RNFT2,MARCH7,KCNE2,PRICKLE1,NKD1,MYLIP,RNF144B,SUFU,GPLD1,AZIN2,LPCAT1,RPL23,HECW2,SEC22B,TMEM9,ADRA2A,PSMD1,USP13,AC013489.1,EGF,USP19,DISC1,SORL1,CHEK2,ASB11,PSME1,ARIH2,CCDC84,PSMD2,DEDD,RNF185,RPL11,CDKN1B,LRIG2,ADAM8,NSF,NFE2L2,COP1,PSME3,SOCS4,PINK1,ARAF,DNAJB2,STX5,ATP13A2,DNAAF4,EPHA4,DDB1,TNFRSF1B,PSMC3,ANXA2,OSBPL7,PSEN1,SNX12,AREL1,SNX1,EFNA1,TAF1,OGT,SMAD3,LDLR,KEAP1,RNF128,PSMD10,FBXO22,NOS2,GPC3,FMR1,RILP,FZR1,BCAP31,SGTA,RAB26,OAZ1,PKD1,APC2,TMEM259,PARK7,BANP,ZER1,GLMN,WWP2,DAB2IP,UBB,PSMC1,BAG2,RNFT1,WNT5A,CAMLG,APC,PTTG1IP,DDA1,STYX,MAP1A	grey	VSMC_M10
GO:0010557	1.00	0.00	697	1433	positive regulation of macromolecule biosynthetic process	BP	1	NFATC1,ZNF407,SMARCC2,ONECUT2,TCF4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,RMND1,YEATS4,ESR1,MYRFL,CNOT6,OSR2,PRR16,PABPC1,SNW1,ARID1B,EIF3E,ZBED4,MAP3K4,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,JMJD4,AGO2,HABP4,PTCH1,ATF4,MAPK15,MAPK14,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,EPCAM,ZNF462,PHIP,HMGN3,NFYC,HOXA2,HOXA7,HOXA13,REL,CREB5,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,IL15,TEAD2,SETD7,MYCN,ELF2,OSR1,FOXO3,ZXDC,SSBP1,FAF1,MAMSTR,ATAD2B,KDM7A,ZNF438,HDAC2,PHF10,MAML2,MLLT10,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,MAPRE3,UTF1,SUMO2,EPM2AIP1,CDC123,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,SS18L2,WNT11,TADA3,SERTAD3,KLF6,AKT2,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,PAWR,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,CEP290,NSD3,ING1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,RYBP,MITF,RBPMS,UPF3A,MTA3,PRKDC,IRF7,ERCC6,HOXC13,CALCOCO1,ST18,RASL11A,NCOA4,TRAF6,NR1H4,TRIM44,TCF15,SOX12,PLAG1,USF2,RET,LMO2,ZC3H8,ASXL1,IL1A,PAX8,NR4A1,ACVR1B,ZNF14	grey	VSMC_M10
GO:0009058	1.00	0.00	2248	4393	biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,KDSR,ORMDL2,SMARCC2,PAN2,ATP8B1,FECH,ONECUT2,GLS2,BAZ2A,TCF4,POLI,RPS12,SHMT2,ATG12,TBPL1,PGGT1B,GLI1,HBS1L,MARS,B4GALT7,PIP4K2C,MAP3K5,PEX7,B4GALNT1,RPA3,TNFAIP3,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,RXYLT1,MAML1,LTC4S,ATP5MGL,HELB,ZBTB2,RMND1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,TFB1M,ZNF706,ALDH7A1,ARID1B,ZDHHC14,HSPA1B,SYNJ2,SERAC1,FZD6,ZBTB12,EIF3E,ALG12,CYP21A2,ZBED4,PNLDC1,MAP3K4,AGPAT4,PPT2,PRKN,AGPAT1,QKI,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,PNPLA3,RXRB,TSPO,MCAT,VGLL2,HSD17B8,MCM9,MRPL13,A4GALT,RPS18,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,MRPL55,JMJD4,AGO2,HABP4,RPS10,HSD17B3,KDM3B,PTP4A3,PTCH1,TNRC6B,AKR1B1,ATF4,PYCR3,TUT7,MAPK15,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,EIF3L,PIM1,CKB,NRF1,TMPRSS6,GPAA1,SMO,ZDHHC21,SNAPC3,BNC2,HSF1,MOCS1,PSAT1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,GPT,IMPDH1,HACD4,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,LARGE1,GNMT,POT1,GPR37,RORB,ZNF300,PRDM4,ALDH1A1,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,SLC35B2,NFKBIE,CWH43,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,ADGRF1,PLPP6,ST6GAL2,SRD5A3,UXS1,NCK2,FHL2,TGFBRAP1,MRPS9,TFAP2B,SPTLC1,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,AASDH,TRAM2,PPAT,C1GALT1,CHST10,HINT2,REV1,PHF14,IPPK,HMGCLL1,	grey	VSMC_M10

GO:0097190	1.00	0.00	214	471	apoptotic signaling pathway	BP	1	ERBB3,EYA4,MAP3K5,TNFAIP3,TRIM39,STK3,MAPK8IP2,SNW1,HSPA1B,PRKN,BAK1,ATF4,PLA2G6,ZC3HC1,NCK2,TMEM14A,DNAJA1,MSH2,TFPT,PHIP,GSDME,GGCT,CASP8AP2,TRIM32,TRAF1,BCL2L12,FOXO3,FAF1,BMI1,ARMC10,DDIAS,PDIA3,FASTK,MLH1,DEDD2,RAF1,POU4F1,FBH1,TIMM50,ZMYND11,PAWR,PDK1,ARL6IP5,PRKDC,ERCC6,TRIB3,RET,IL1A,ACVR1B,FAIM,PIK3R1,CASP3,HIP1R,TAF9,ING2,EYA1,DIABLO,FBXW7,IL7,FAIM2,HTRA2,TMBIM6,P2RX7,NDUFS3,CSNK2A2,MADD,FNIP2,NBN,SENP1,NKX3-1,OPA1,NR4A2,RIPK1,MARCH7,PIDD1,STK4,SIAH1,BMPR1B,BDNF,DNM1L,HDAC1,LCK,SP100,TERT,TGFB2,TCF7L2,PDCD6,SCN2A,SNAI1,AEN,GPER1,QRICH1,CHEK2,EYA3,IFI6,MCL1,AGT,CIB1,HYOU1,BAG3,CIDEB,STRADB,SFN,NFATC4,PEA15,PELI3,DIDO1,DEDD,CD28,RTKN2,ING5,FZD9,DDX47,RPL11,E2F2,YBX3,NFE2L2,IVNS1ABP,NONO,FIS1,PRKRA,NMT1,SYVN1,BCL2A1,CTSH,PRODH,IL12A,DDX3X,DNAJC10,PDCD10,WNT4,HTT,PSME3,CASP12,FGFR3,PINK1,MUL1,LTBR,CD38,SGMS1,MAGED1,PARP1,TMEM102,TNFRSF1B,STX4,PSEN1,ITGAM,NGFR,DAP3,DAPK2,MUC1,IL6R,ATP2A1,TAF9B,SMAD3,MAP2K5,S100A8,SFPQ,BTK,PSMD10,CD74,MAPK7,NLE1,PPP1R13B,PTPN2,JUN,TICAM1,ACAA2,PIAS4,CDIP1,PAM16,BCAP31,PDPK1,TRAF2,TNFRSF25,PARK7,GNAI3,BCL10,DAB2IP,MIR21,MIR222,MIR27B,FGA,UBB,ZNF622,MLLT11,RPS27L,NOL3,FADD,BNIP3L,CASP8,NOG,FXN,DDIT3,CRH,CD70,BCL2L11,PPP1R15A,SLC35F6,APOPT1,PERP,PTTG1IP,HRAS,PLAGL2,BCL2L2,TMEM109,CAAP1,CEBPB,CRADD,PPIF,HINT1,SGPP1,PTPMT1,AC140504.1	grey	VSMC_M10
GO:0010941	1.00	0.00	593	1223	regulation of cell death	BP	1	ADNP2,MTCH2,NME1,SERPINB2,VPS4B,PHLPP1,ERBB3,GLS2,TNFAIP8,LRP1,EYA4,MAP3K5,TNFAIP3,AGAP2,HEBP2,TRIM39,PPP1R10,ESR1,FRS2,IER3,STK3,MAPK8IP2,HSPA1B,IGF2R,PRKN,PACRG,PPARA,TSPO,RGL2,SYNGAP1,UBE2B,BAK1,NCOA7,MYC,GRM4,PTK2,AKR1B1,ATF4,NTRK2,TOMM22,NRBP2,SOX10,PIM1,ZC3HC1,SMO,HSF1,IRF5,CDKN2A,ZNF16,TEK,GPR37,FBXO7,BAG1,CNTFR,SLC25A27,KIT,SLC1A1,NCK2,FHL2,TFAP2B,SPTLC1,GADD45G,SEMA4D,TMEM14A,CHMP2A,FBXO10,ZNF268,CAT,DNAJA1,EPCAM,MSH2,TFPT,RTN4,PHIP,GSDME,HOXA13,REL,PPT1,ALB,SLC46A2,NOD1,AQP1,PELI1,ANXA4,EPHA7,TGFA,PTN,KLF11,MET,YWHAZ,POU3F3,EGFR,ING3,TRIM32,TLR4,TRAF1,BCL2L12,SFRP4,DKKL1,VPS35,TEAD2,ATG5,MYCN,SLC7A11,OSR1,FOXO3,NTF4,CDK19,FAF1,FGF21,BRAF,SPHK2,HIGD1A,SPRY1,WISP3,FOXE3,HDAC2,DNMT3A,BMI1,NDNF,C5AR1,ARMC10,PHB,SOX9,ZNF746,ERCC3,DDIAS,PDIA3,PLK3,GLI2,DEDD2,KDM4A,GRIK5,RAF1,XRCC2,ZFAND6,PRDX3,UBE2O,EGLN2,ACER3,POU4F1,FBH1,SPRY2,CIDEC,WNT11,ALK,AKT2,ARRB1,USP36,CBX4,CHD8,SIRT2,ZMYND11,RARB,TCIM,IDO1,PAWR,SRA1,SLC23A2,EIF2AK2,PRNP,ING1,DUSP6,BAG4,ARHGEF7,BTG1,SPEF1,RNF122,DDRGK1,SH3RF2,WRN,NCKAP1L,GAS6,RYBP,FOXP1,MITF,ARL6IP5,PRKDC,IRF7,TRAF6,NR1H4,APIP,EPHB1,PLK2,RET,HCK,NSMAF,ASAH1,ZC3H8,IL1A,ACOX2,GPI,PAX8,NR4A1,RILPL1,FAIM,PIK3CB,FOXL2,PIK3R1,CASP3,HIP1R,TAF9,ARHGAP10,GBE1,HAND2,ING2,HPGD,EYA1,DIABLO,FBXW7,TRIM2,FZD3,MEF2C,NUGGC,IL7,FAIM2,HTRA2,TMBIM6,TCTN3,NDUFS3,C3orf38,CELF1,CSNK2A2,RTKN,MADD,KATNB1,PTK2B,RAPGEF2,CIAPIN1,PNMA2,RIPK2,V	grey	VSMC_M10
GO:0031023	1.00	0.00	47	127	microtubule organizing center organization	BP	1	VPS4B,MDM1,KIF3A,MPDZ,CNTLN,HEPACAM2,CHMP2A,BRSK1,XPO1,CEP68,CDK5RAP2,CCDC61,CLASP2,XRCC2,FOXJ1,CEP295NL,CEP63,NSFL1C,PLK2,KIF3B,CHMP2B,CEP44,CEP250,CETN3,CHMP4C,MCPH1,ALMS1,TMEM67,PKD2,AC112128.1,CCDC84,KIAA1614,SLC16A1,NIN,CEP152,UXT,SDCCAG8,CNTROB,NDEL1,TRIM37,BCAS3,CEP192,NUBP1,CHMP1A,GADD45A,C2CD3,PARD6A	grey	VSMC_M10
GO:0051239	1.00	0.00	956	1937	regulation of multicellular organismal process	BP	1	CD226,NME1,SERPINB2,LRP1,SEMA6A,GLI1,TNFAIP3,CYP27B1,ESR1,FRS2,CNOT2,TSPAN8,RAB21,STK3,OSR2,SNW1,TIAM2,ZNF706,APOM,ADM2,SLC12A2,HSPA1B,RIMS2,BRD1,AGPAT1,AGER,PPARA,GPSM3,HLA-DRA,TNFRSF11B,IL5,HLA-DPB1,TSPO,GDF9,FSTL4,TCF7,SYNGAP1,XRCC6,TRIB1,MYC,TOB2,AGO2,PTK2,C6orf106,PTCH1,ATF4,PLXNA4,MAPK14,NTRK2,MAPK13,SOX10,PI16,PIM1,SMO,ZDHHC21,HSF1,DAAM2,IRF5,ZNF16,RBFOX2,CHRNA3,TEK,LINGO2,FBXO7,ALDH1A1,CRY1,CEMIP2,SRF,TTBK1,CDK6,ENPP4,RFX3,KIT,SLC1A1,TNFRSF21,IL1R2,RORR2,GADD45G,SEMA4D,GAPDH,S1PR3,PDCL3,NINJ1,OMD,EXOSC3,SEMA4C,MEOX2,SOSTDC1,NLRP5,ABCG5,SVBP,ABCG8,SIX2,PRKCE,SMAP1,TNNI3,EPAS1,RIMS1,MSH2,CD109,ASB3,SPTBN1,IGF2BP3,RTN4,EPB41L4B,RUFY3,SHANK1,HOXA7,EMC10,REL,MYCL,CXCL8,SLC46A2,MTURN,NOD1,AKIRIN2,AQP1,PELI1,BMPER,CNOT4,RSAD2,LRRN3,ANXA4,EPHA7,NR1H2,MBOAT2,PTN,ITGB1BP1,GRHL1,MET,GRB10,IL4I1,AGO1,EGFR,TSPAN12,FUZ,TRIM32,TLR4,EPHA1,BVES,DLGAP3,GAB1,LPIN1,IL15,SFRP4,UCP1,ATG5,SDCBP,MYCN,TRPM4,OSR1,FOXO3,FIG4,MKX,FGF21,INTU,SPHK2,SPRY1,PLXNA1,WISP3,GRIN2D,FOXE3,LAMA4,HDAC2,HS3ST5,MTMR2,TRPC3,SLC8A2,HMCES,BMI1,C5AR2,C5AR1,PANX1,VSTM5,PRKD2,CST7,PHB,IQSEC1,SOX9,CACNB2,SLC39A12,CLASP2,LACC1,CLPTM1,APOC1,SLC4A2,PTCH2,MLH1,GOLGA4,GLI2,MEGF8,KDM4A,ATP1A3,XRCC2,MYD88,CELF2,PIBF1,ACVR2B,FOXJ1,SCN5A,PAXIP1,NUMBL,THBD,POU4F1,TSKU,IL15RA,SPRY2,SS18L2,PLAT,WNT11,RIN2,GPD1L,HOOK3,ARRB1,TGFBR2,OVOL2,SNX5,ZNF219,ACVR2A,IKBKB,C1QTNF1,IS	grey	VSMC_M10
GO:0061008	1.00	0.00	44	119	hepaticobiliary system development	BP	1	ONECUT2,GLI1,TNFAIP3,IGF2R,ACO2,PTCH1,PNPT1,TGFA,PTN,MET,EGFR,SOX9,TAF10,LSR,CEBPA,FBXW7,CSNK2A2,RPGRIP1L,PKD2,JARID2,SRD5A1,CCND1,CPT1A,SULF2,HLX,KRAS,RPS6KA1,HMGCL,SP3,CPS1,WNT4,MED1,ALDH1A2,RPL19,SMAD3,MKS1,GATA6,PKD1,ASS1,ACADM,CLDN1,HRAS,CEBPB,FGF1	grey	VSMC_M10

GO:0034645	1.00	0.00	1792	3533	cellular macromolecule biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,POLI,RPS12,SHMT2,ATG12,TBPL1,GLI1,HBS1L,MARS,B4GALT7,MAP3K5,RPA3,TNFAIP3,TSFM,HIVEP2,PLAGL1,RXYLT1,MAML1,HELB,ZBTB2,RMND1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,TFB1M,ZNF706,ARID1B,ZDHHC14,HSPA1B,FZD6,ZBTB12,EIF3E,ALG12,ZBED4,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,PDE10A,MED30,IL5,BRD2,TAF2,RXRB,VGLL2,MCM9,MRPL13,RPS18,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,MRPL55,JMJD4,AGO2,HABP4,RPS10,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,MAPK15,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,KDM4C,SOX10,EIF3L,PIM1,NRF1,TMPRSS6,GPAA1,SMO,ZDHHC21,SNAPC3,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,BICRAL,LARGE1,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,ZNF318,NFX1,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,NFKBIE,CWH43,SUPT3H,SMARCA2,RFX3,KIT,ADGRF1,ST6GAL2,SRD5A3,NCK2,FHL2,TGFBRAP1,MRPS9,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,C1GALT1,CHST10,REV1,PHF14,IPPK,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,MCMBP,ZNF268,ZNF667,ZNF787,PHF3,ZNF691,CAT,MACC1,LRPPRC,ALG2,SIX2,SRBD1,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,TMEM246,RNF20,EPAS1,PIGF,EPCAM,SP4,IGF2BP3,FKTN,PPP2R1A,ZNF462,PHIP,HMGN3,HAS1,NFYC,MTIF2,NFE2L3,PNPT1,HOXA2,TAF1D,HOXA4,HOXA6,HOXA7,HOXA13,REL,ZNF483,ANKRD17,JAZF1,CREB5,MYCL,XPO1,MTURN,NO	grey	VSMC_M10
GO:0008104	1.00	0.00	1004	2028	protein localization	BP	1	TIMM21,MTCH2,VPS4B,NEDD4L,ATP8B1,CCDC68,LRP1,STX7,STAC3,AP3S1,KIF5A,MAP7,PEX7,TNFAIP3,AGAP2,PEX3,CANX,TBC1D30,MRNIP,TBC1D9B,PPP1R10,ESR1,RAB21,SNX24,SNX31,PHAX,ZDHHC14,SLC12A2,RIMS2,EMC2,PRRT1,PRKN,PACRG,AGER,TAP1,KIF3A,SEPT8,TSPO,GOPC,MCM9,VPS52,HSPA4,TBC1D32,DERL1,SKP1,SEPT3,SYNGAP1,FAM91A1,WASHC5,LRRC6,EPB41L2,OBSCN,LEMD2,FAM53C,C6orf106,PTP4A3,PTCH1,TSNARE1,EXOC4,SIL1,SYNGR1,MAPK15,SUN2,MAPK14,TOMM22,CBY1,CSNK1E,PLA2G6,COPG2,PICK1,MICALL1,TBC1D22B,RAC2,GPAA1,SMO,ZDHHC21,TSPAN33,CNTLN,MDFI,TOMM6,TAF8,MYH9,LRRC4,PEX6,POT1,FBXO7,ABHD17B,ADAM22,XPO5,WASHC4,APBA1,SEPT10,PEX1,NFKBIE,VPS50,SCFD2,RFX3,SLC1A1,TGFBRAP1,TFAP2B,TBC1D8,TRAM2,BICD2,CHMP2A,RAB23,SVBP,SEC61B,STX17,SIX2,DNAJA1,PRKCE,RIMS1,MSH2,TMEM30A,DNAH11,ASB3,SPTBN1,RTN4,HMGN3,RUFY3,SHANK1,CYB5R4,EMC10,PPT1,SNX14,XPO1,SNX30,BMP8A,RRAGD,EHBP1,AFTPH,CEP68,TRAPPC12,PLEK,RSAD2,AAK1,NR1H2,WHRN,PTN,ITGB1BP1,YWHAZ,SEC61G,EGFR,FUZ,ARHGEF5,TLR4,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,TRPM4,SLC7A11,MAPRE1,LIN7B,EPS15,TULP2,APOB,AGK,FAF1,BRAF,BCAP29,TRAF3IP2,ANKRD50,TTC26,DNAJC27,NAPA,KPTN,BBS7,RAB7A,AP2S1,RAB10,COPG1,KPNA3,SOX9,GIPR,ARL5B,CACNB2,LCP1,ERCC3,SYTL2,COG1,CLASP2,DLG2,CUBN,RBSN,MAPRE3,DNAJC15,PLK3,FRMD4A,STAC,OPTN,GOLGA4,LLGL2,RALB,IPO13,STEAP3,AQP11,CCDC93,GRIK5,RAF1,ZFAND6,TAF3,PIBF1,KLF5,TBC1D4,FOXJ1,MYO7A,TTC21A,MYCBP2,NAPB,GCKR,EMC3,SZT2,SEC62,SEC22C,WNT11,KPNA2,MYL12A,AK	grey	VSMC_M10
GO:0023056	1.00	0.00	608	1258	positive regulation of signaling	BP	1	CD226,ERBB3,LRP1,RPS12,GLI1,MAP3K5,TNFAIP3,CYP27B1,USP15,TRIM39,FRS2,STK3,MAPK8IP2,SNW1,HSPA1B,RIMS2,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,IL5,GDF9,RGL2,UBE2B,BAK1,RSPO3,RNF146,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,AKR1B1,ZC3H3,TAB1,NTRK2,CSNK1E,PLA2G6,GKAP1,MFNG,SMO,DAAM2,KCP,TEK,GPR37,PTK7,LRRD1,SLC35B2,OCIAD1,KIT,SLC1A1,NCK2,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,WNK2,NINJ1,SEMA4C,CAT,IL11,PRKCE,RIMS1,RTN4,PHIP,FPR2,GSDME,RIMS3,KLK14,SHANK1,ADAMTS3,EMC10,LPAR1,REL,ANKRD17,SLC46A2,MTURN,EPGN,NOD1,AREG,BMP8A,CRHR2,RRAGD,PELI1,BMPER,RSPO1,RSAD2,AAK1,TGFA,PTN,ITGB1BP1,MET,GRB10,ATP6V1C2,EGFR,LANCL2,ARHGEF5,TRIM32,TLR4,GRIK2,TRAF1,BVES,SFRP4,VPS35,SDCBP,TRPM4,PUM2,WASF1,EPS15,FAF1,FGF21,BRAF,INTU,TRAF3IP2,SPHK2,GRIN2D,DNAJC27,SLC8A2,C5AR2,C5AR1,PRKD2,PHB,SOX9,GIPR,PPM1N,CACNB2,CD300LF,NECTIN2,PDIA3,DEDD2,RAF1,MYD88,PIBF1,ACVR2B,IFT172,UBE2O,SCEL,FBH1,SPRY2,WNT11,ALK,DYNC1LI1,ARRB1,PIP4P1,NEU3,SNX5,ACVR2A,IKBKB,C1QTNF1,JAG1,NMI,NEK10,RPTOR,TCIM,HBEGF,SYT1,PDE6G,PLCB1,RASGRP4,FERMT1,EIF2AK2,PRNP,ADRA1D,BAG4,DCN,MAVS,RELL2,SEMA3A,P2RX2,AIMP1,KL,NRG1,SH3RF2,NCKAP1L,GAS6,HPX,LARS,SIRT3,FOXP1,RBPMS,ARL6IP5,IRF7,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,TRIM44,SLC38A9,TMEM9B,ST5,PLK2,MOS,RET,ASXL1,FAM107A,FGFBP3,C12orf49,ACVR1B,PIK3CB,OSBP,PIK3R1,CLSTN2,HIP1R,HAND2,ATR,ING2,CDKN2AIP,ROBO1,P2RX3,ROBO2,PLCE1,ARNTL,FBXW7,ADGRV1,SORBS1,PTPRJ,IL7,HTRA2,GUCY1A1,CUX2,P2RY1,MADD,PTK2B,RASGRP1,MME,	grey	VSMC_M10

GO:0022603	1.00	0.00	354	761	regulation of anatomical structure morphogenesis	BP	1	ITGA7,NEDD4L,LRP1,SEMA6A,TNFAIP3,ESR1,FRS2,RAB21,TIAM2,ADM2,SLC12A2,FZD6,RIMS2,CDC42SE2,PRKN,FBLN1,TNFRSF11B,FSTL4,SYNGAP1,RSPO3,AGO2,PTK2,PLXNA4,NTRK2,CPNE5,CDC42EP1,RAC2,STRIP2,SMO,MYH9,CHRNA3,TEK,PTK7,CEMIP2,SRF,KIT,ROR2,SEMA4D,PDCL3,NINJ1,FGD3,ZNF135,SEMA4C,SIX2,BRSK1,RIMS1,RTN4,PHIP,RUFY3,EMC10,LPAR1,CXCL8,AQP1,MYH14,BMPER,EPHA7,PTN,ITGB1BP1,AGO1,TSPAN12,HECW1,FUZ,EPHA1,ZMYM6,BVES,GAB1,KEL,VPS35,OSR1,SPRY1,PLXNA1,WISP3,C5AR1,SLC26A5,PRKD2,SOX9,SLC39A12,CLASP2,GOLGA4,MEGF8,UNC13D,FOXJ1,SPRY2,SS18L2,WNT11,MYL12A,CPNE9,TGFBR2,ISM1,SYT1,RAC3,SLC23A2,DDHD2,ARHGEF7,SEMA3D,DCN,DIAPH1,BTG1,SPART,SPEF1,PLXNC1,SEMA3A,FGD6,ULK1,FOXP1,PRKDC,FLT1,RYK,PLK2,RET,HCK,IL1A,PAX8,ANKRD27,PIK3CB,ERAP1,PARVA,ROBO1,ROBO2,SH3D19,FZD3,MEF2C,SEMA4F,VEGFC,TLX2,CUX2,ADAMTS1,P2RY1,PTK2B,RAPGEF2,RND1,TIAM1,DOCK5,OPA1,RAPGEF3,RHOBTB2,ZFYVE27,AGGF1,FITM2,SEMA3G,RREB1,ITPKA,SPP1,PAX2,CYFIP1,DMTN,SEMA4G,VANGL1,PRICKLE1,NKD1,CD40,BRWD1,LZTS1,GAS2,BDNF,KIAA0319,DNM1L,CARMIL1,FGD4,HYAL1,PPP3CA,HECW2,CAPRIN2,SP100,TERT,SEMA3F,TGFB2,POGLUT1,ZDHHC6,PDCD6,DAG1,CFL1,EGF,ADNP,AP1AR,EPB41,JHY,DISC1,CASS4,PDZD8,ZNRF3,AGT,FGR,CIB1,DVL3,NFATC4,VASH2,FZD7,PHLDB1,SS18L1,EPS8,COCH,CDKL5,RHOBTB1,GRHL3,EPHB3,TANC2,DOCK1,GLUL,MELTF,CSPG5,E2F2,DLG1,WNT3,NFE2L2,TBCCD1,CDC42EP2,MAPT,STOX1,FIS1,BCL6,SEMA6D,CTSH,TNR,FN1,C11orf65,RC3H1,MCU,NIN,CXCR2,WNT4,HSPG2,DNM3,DDHD1,MARK2,RAMP2,PINK1,MUL	grey	VSMC_M10
GO:0006469	1.00	0.00	68	172	negative regulation of protein kinase activity	BP	1	TNFAIP3,TRIB1,STK38,CDKN2A,FBXO7,DNAJA1,IBTK,ACP4,ITGB1BP1,EPHA1,PRKAR2B,SPRY1,PRKAG2,SPRY2,PTPRQ,TAF7,TRIB3,CEBPA,PIK3CB,CASP3,PTPRJ,PKIA,PAQR3,DBNDD2,DTNBP1,PDCD4,PRKAR1A,ADARB1,FABP4,UBASH3B,SORL1,RTRAF,AGT,CBL,SFN,CAMK2N2,PTPRO,SNX6,CDKN1B,AIDA,YWHAG,DUSP10,HEXIM2,MEN1,DUSP19,PTPN6,ZFYVE28,SOCS4,RGS14,PSEN1,PYDC1,SMCR8,PTPN2,INPP5K,PDPK1,PARK7,DBNDD1,DAB2IP,MIR24-1,SMYD3,THY1,GADD45A,DUSP26,DUSP1,APC,DUSP22,LAX1,PRKRIP1	grey	VSMC_M10
GO:0048584	1.00	0.00	727	1488	positive regulation of response to stimulus	BP	1	CD226,ERBB3,LRP1,STX7,RPS12,EYA4,GLI1,MAP3K5,TNFAIP3,CYP27B1,USP15,MRNIP,TRIM39,FRS2,STK3,MAPK8IP2,SNW1,HSPA1B,RIMS2,MAP3K4,PRKN,AGPAT1,AGER,GPSM3,HLA-DRA,IL5,HLA-DPB1,GDF9,RGL2,UBE2B,BAK1,XRCC6,RSPO3,RNF146,MYC,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,AKR1B1,ZC3H3,TAB1,NTRK2,MAPK13,CSNK1E,PLA2G6,GKAP1,MFNG,RAC2,SMO,DAAM2,KCP,CDKN2A,TEK,GPR37,PTK7,TTBK1,TEC,LRRD1,CCL27,SLC35B2,OCIAD1,ENPP4,KIT,TNFRSF21,NCK2,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,WNK2,NINJ1,EXOSC3,SEMA4C,CAT,IL11,PRKCE,RIMS1,MSH2,RTN4,PHIP,FPR2,GSDME,KLK14,SHANK1,ADAMTS3,EMC10,LPAR1,REL,ANKRD17,CXCL8,SLC46A2,MTURN,EPGN,NOD1,AREG,AKIRIN2,BMP8A,RRAGD,PELI1,BMPER,AKIRIN1,RSPO1,RSAD2,AAK1,TGFA,PTN,ITGB1BP1,MET,GRB10,ATP6V1C2,EGFR,LANCL2,ARHGEF5,TRIM32,TLR4,TRAF1,IL15,SFRP4,VPS35,MGST2,SDCBP,TRPM4,FOXO3,PUM2,WASF1,CDK19,FAF1,FGF21,BRAF,INTU,TRAF3IP2,SPHK2,DNAJC27,TRPC3,HMCES,C5AR2,C5AR1,NAPEPLD,PRKD2,PHB,SOX9,GIPR,PPM1N,CD300LF,NECTIN2,PDIA3,PVR,EIF2B3,XRCC1,OPTN,GAB2,MLH1,MEGF8,ECHDC3,DEDD2,RAF1,MYD88,OXSR1,SLC22A13,PIBF1,ACVR2B,IFT172,PAXIP1,WDR48,UBE2O,THBD,SCEL,FBH1,SPRY2,WNT11,ALK,DYNC1LI1,ARRB1,PIP4P1,NEU3,SNX5,ACVR2A,IKBKB,C1QTNF1,FAM168A,JAG1,NMI,NEK10,RPTOR,TMEM173,ACTG1,TCIM,HBEGF,PDE6G,PAWR,PLCB1,PLCL2,RASGRP4,FERMT1,SHLD1,EIF2AK2,PRNP,ADRA1D,BAG4,DCN,MAVS,RELL2,SEMA3A,P2RX2,KL,NRG1,SH3RF2,NCKAP1L,GAS6,HPX,LARS,FOXP1,RBPMS,ARL6IP5,PRKDC,IRF7,ERCC6,MFHAS1,FLT1,RYK,ADRA2B,T	grey	VSMC_M10
GO:0018208	1.00	0.00	14	48	peptidyl-proline modification	BP	1	P4HA2,FKBP9,FKBP15,CRTAP,EGLN2,PPIG,EGLN3,P3H2,FKBP8,PPIL2,P3H3,FKBP7,PPIC,PPIF	grey	VSMC_M10
GO:0043666	1.00	0.00	13	47	regulation of phosphoprotein phosphatase activity	BP	1	NUAK1,VRK3,IKBKB,NCKAP1L,CRY2,PPP1R2C,HTT,TIPRL,BOD1L2,CALM1,PPP4R4,TSC1,PPP1R15A	grey	VSMC_M10
GO:0034508	1.00	0.00	6	28	centromere complex assembly	BP	1	H3F3C,TRAPPC12,POGZ,RNF4,ITGB3BP,CENPX	grey	VSMC_M10
GO:1901990	1.00	0.00	99	237	regulation of mitotic cell cycle phase transition	BP	1	VPS4B,MRNIP,TRIM39,ZNF207,CCND3,FBXO7,BRSK1,ANKRD17,LSM10,EGFR,CDK5RAP2,TPRA1,XPC,ERCC2,ERCC3,PLK3,UBE2E2,DYNC1LI1,SIRT2,RPTOR,ANAPC15,PLCB1,IK,NEK11,USP44,TFDP1,MTA3,PRKDC,PLK2,FAM107A,RAD17,ANAPC5,PKIA,ANAPC7,CHMP4C,ADAMTS1,NBN,ABRAXAS1,DONSON,ZFYVE19,PIDD1,PKD2,NPM2,TAOK3,HYAL1,HECW2,CCND1,TERT,GIGYF2,CHEK2,PSME1,SYF2,CDKN1B,DLG1,STOX1,DBF4B,DDX3X,MEPCE,PTPN6,ECD,PSME3,DDB1,ANAPC4,RAD51B,UIMC1,FOXO4,CTC1,MUC1,TAOK2,RAB11A,LCMT1,FOXN3,RAD51C,DCUN1D3,SIN3A,CCL2,PSMG2,TAOK1,FZR1,PKD1,MECP2,CDK10,FBXO31,CDC14A,VPS4A,NAE1,MIR29A,MIR222,PLK5,RPS27L,SOX4,DUSP1,RGCC,APC,CDC26,ZFP36L2,BRCC3,CRADD,NABP1	grey	VSMC_M10
GO:0033044	1.00	0.00	66	168	regulation of chromosome organization	BP	1	PPP1R10,ZNF207,MAP3K4,MYC,H3F3C,MAPK15,POT1,TRAPPC12,CDK5RAP2,SSBP1,SETDB2,ERCC1,XRCC1,DYNC1LI1,ANAPC15,IK,USP44,MOS,ATR,SLF1,FAM208A,HMBOX1,ANAPC5,ANAPC7,MCPH1,MAPKAPK5,NBN,SLF2,PPHLN1,TENT4B,STN1,HECW2,AXIN2,RTEL1,MAPT,XRCC5,UPF1,RNF4,MAPK1,DDX11,PARP1,ANAPC4,GNL3L,SMG5,YLPM1,CTC1,PIF1,MAPK3,LCMT1,SFPQ,PARN,ERCC4,PSMG2,RMI2,SLX4,NAA10,TERF2,CTCF,SETDB1,TINF2,TEN1,DUSP1,ZNF304,APC,CDC26,MAP2K7	grey	VSMC_M10

GO:0009653	1.00	0.00	1008	2050	anatomical structure morphogenesis	BP	1	NFATC1,ITGA7,NEDD4L,ATP8B1,ONECUT2,LRP1,SEMA6A,EYA4,TBPL1,GLI1,KIF5A,TNFAIP3,ADGRG6,CPM,ESR1,FRS2,CNOT2,IER3,RAB21,STK3,OSR2,MAPK8IP2,TIAM2,ADM2,MPIG6B,SLC12A2,FZD6,RIMS2,CDC42SE2,PNLDC1,PRKN,QKI,PPARA,FBLN1,TNFRSF11B,BRD2,PARVG,SULT4A1,SHROOM1,VPS52,TBC1D32,RRP7A,FSTL4,SYNGAP1,CCDC134,BAK1,MTSS1,PITX1,RSPO3,MYC,SMAD5,KLHL3,OBSCN,LEMD2,AGO2,GFRA3,PTK2,PTCH1,FANCC,LY6E,EXOC4,ATF4,TAB1,AGTPBP1,PLXNA4,MAPK14,NTRK2,PODXL,CPNE5,SOX10,PIM1,CDC42EP1,MFNG,RAC2,STRIP2,SMO,MDFI,MYH9,FOXH1,RBFOX2,CHRNA3,TEK,RORB,LMOD2,ZFAND5,PTK7,CEMIP2,SRF,PGM5,TXNRD1,KIT,SLC1A1,CA9,FHL2,C2orf49,TFAP2B,ROR2,SEMA4D,DLX5,S1PR3,PDCL3,C1GALT1,NINJ1,FGD3,ETV1,ZNF135,SEMA4C,SHB,CNNM4,TDRD7,MEOX2,SOSTDC1,TMOD1,RAB23,SIX2,COL9A1,BRSK1,TNNI3,EPAS1,RDH13,RIMS1,CD109,MBOAT7,DNAH11,IGF2BP3,RTN4,PHIP,KCNQ4,KLK14,PNPT1,KLK4,RUFY3,ACP4,SHANK1,HOXA2,HOXA4,HOXA6,HOXA7,HOXA13,EMC10,LPAR1,PTBP3,CXCL8,EPGN,AREG,AQP1,MYH14,BMPER,COL27A1,EPHA7,WHRN,TGFA,PTN,ITGB1BP1,MET,TNC,AGO1,YWHAZ,EGFR,TSPAN12,HECW1,FUZ,EPHA1,ZMYM6,BVES,GJB5,GAB1,SFRP4,KEL,MYLK3,DKKL1,VPS35,TEAD2,MYCN,NRCAM,SOBP,OSR1,FOXO3,DLD,NTF4,FIG4,WASF1,MKX,SSBP1,APOB,FGF21,BRAF,INTU,SPRY1,PLXNA1,WISP3,FOXE3,ARHGAP12,HDAC2,MTMR2,BBS7,BMI1,NDNF,C5AR1,SLC26A5,RAB10,PRKD2,MYO3A,SETDB2,FOXA3,ABI1,SOX9,ERCC1,ERCC2,SLC39A12,CLASP2,SLC4A2,NECTIN2,USH1G,XRCC1,GOLGA4,GLI2,MEGF8,PCDH8,UNC13D,XRCC2,ACVR2B,KLF5,IFT172,FOXJ1,SCN5	grey	VSMC_M10
GO:0033046	1.00	0.00	10	39	negative regulation of sister chromatid segregation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:0033048	1.00	0.00	10	39	negative regulation of mitotic sister chromatid segregation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:2000816	1.00	0.00	10	39	negative regulation of mitotic sister chromatid separation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:1901998	1.00	0.00	7	31	toxin transport	BP	1	DNAJA1,ATP6V0A1,SLC29A4,CRTC2,CCT6B,MTMR12,HSPA5	grey	VSMC_M10
GO:0032465	1.00	0.00	23	72	regulation of cytokinesis	BP	1	PRKCE,PLK3,PLK2,KIF3B,CSPP1,DCDC1,CHMP4C,ZFYVE19,KIF13A,SETD2,AHCTF1,RAB11A,CALM1,KLHL13,FSD1,KLHL21,CDC14A,SH3GLB1,VPS4A,RHOA,AURKC,PLK5,PDXP	grey	VSMC_M10
GO:0048585	1.00	0.00	593	1229	negative regulation of response to stimulus	BP	1	NFATC1,SERPINB2,PHLPP1,ERBB3,ONECUT2,LRP1,SEMA6A,EYA4,GLI1,PIP4K2C,TNFAIP3,USP15,EPM2A,ENPP3,HELB,TRIM39,PPP1R10,ESR1,CNOT2,TSPAN8,STK3,MAPK8IP2,MPIG6B,SLC12A2,HSPA1B,FZD6,GRAMD4,PRKN,PPARA,PDE10A,FBLN1,FSTL4,SYNGAP1,UBE2B,NCOA7,TRIB1,MYC,LEMD2,C6orf106,PTCH1,MAPK14,CBY1,STK38,SOX10,ZC3HC1,HSF1,MDFI,FOXH1,LRRC14,TEK,GPR37,CRY1,DLK2,CDK6,NCK2,FHL2,IL1R2,ROR2,SEMA4D,TMEM14A,WNK2,KLHL31,SEMA4C,SOSTDC1,BEND6,CLDN19,DNAJA1,CD109,FKTN,PPP2R1A,PHIP,FPR2,KLK14,ACP4,NT5E,CXCL8,BMPER,CYREN,PXDN,PLEK,NR1H2,ITGB1BP1,MET,VRK3,GRB10,IL4I1,EGFR,HECW1,FUZ,TRIM32,TLR4,SFRP4,DKKL1,VPS35,FOXO3,SPRY1,ARHGAP12,MTMR2,KPTN,SESN3,RAB7A,BMI1,C5AR2,PIP4K2A,ARMC10,PTGIR,CST7,PHB,SOX9,GIPR,PPM1N,ERCC1,CLASP2,CD300LF,DDIAS,PTCH2,XRCC1,OPTN,KBTBD6,KCTD21,GLI2,MEGF8,AQP11,RAF1,PIBF1,IFT172,FOXJ1,FNDC4,THBD,SEC14L1,TSKU,FBH1,SZT2,SPRY2,PLAT,WNT11,GPD1L,ARRB1,EID2,SNX5,RBMS3,RNF169,C1QTNF1,CHD8,SIRT2,MKKS,NMI,ZMYND11,TCIM,NR1D2,NPLOC4,PAWR,UBAC2,PLCL2,FERMT1,SPRED3,SHLD1,PRNP,DUSP6,SEMA3D,DCN,SPART,SEMA3A,DDRGK1,SH3RF2,NCKAP1L,GAS6,SIRT3,PPP2CB,RASA3,FOXP1,LEPROTL1,PRKDC,ERCC6,MFHAS1,RYK,TMEM127,PCBP2,NR1H4,RGS20,PLK2,PFDN5,HCK,NDUFAF2,ASXL1,IL1A,CYP7B1,RGS7BP,KCTD6,CBFA2T2,FER,FAIM,PIK3CB,SNX25,ZNF536,OTUD4,RASA2,LPXN,TAF9,CTNND1,DKK3,TRABD2A,ING2,EYA1,ROBO1,ROBO2,ZNF366,IL17RD,ARNTL,FBXW7,USP25,PTPRJ,TMEM131L,SEMA4F,IL7,FAIM2,HTRA2,TMBIM6,P2RX7,NDUFS3,CNOT1,CSNK2A2,SLA2,L	grey	VSMC_M10
GO:0009967	1.00	0.00	541	1127	positive regulation of signal transduction	BP	1	CD226,ERBB3,LRP1,RPS12,GLI1,MAP3K5,TNFAIP3,CYP27B1,USP15,TRIM39,FRS2,STK3,MAPK8IP2,SNW1,HSPA1B,RIMS2,MAP3K4,PRKN,AGPAT1,AGER,IL5,GDF9,RGL2,UBE2B,BAK1,RSPO3,RNF146,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,AKR1B1,ZC3H3,TAB1,NTRK2,CSNK1E,PLA2G6,GKAP1,MFNG,SMO,DAAM2,KCP,TEK,GPR37,PTK7,LRRD1,SLC35B2,OCIAD1,KIT,NCK2,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,WNK2,NINJ1,SEMA4C,CAT,IL11,PRKCE,RIMS1,RTN4,PHIP,FPR2,GSDME,KLK14,SHANK1,ADAMTS3,EMC10,LPAR1,REL,ANKRD17,SLC46A2,MTURN,EPGN,NOD1,AREG,BMP8A,RRAGD,PELI1,BMPER,RSPO1,RSAD2,AAK1,TGFA,ITGB1BP1,MET,GRB10,ATP6V1C2,EGFR,LANCL2,ARHGEF5,TRIM32,TLR4,TRAF1,SFRP4,VPS35,SDCBP,TRPM4,PUM2,WASF1,FAF1,FGF21,BRAF,INTU,TRAF3IP2,SPHK2,DNAJC27,C5AR2,C5AR1,PRKD2,PHB,SOX9,GIPR,PPM1N,CD300LF,NECTIN2,PDIA3,DEDD2,RAF1,MYD88,PIBF1,ACVR2B,IFT172,UBE2O,SCEL,FBH1,SPRY2,WNT11,ALK,DYNC1LI1,ARRB1,PIP4P1,NEU3,SNX5,ACVR2A,IKBKB,C1QTNF1,JAG1,NMI,NEK10,RPTOR,TCIM,HBEGF,PDE6G,PLCB1,RASGRP4,FERMT1,EIF2AK2,ADRA1D,BAG4,DCN,MAVS,RELL2,SEMA3A,P2RX2,KL,NRG1,SH3RF2,NCKAP1L,GAS6,HPX,LARS,FOXP1,RBPMS,ARL6IP5,IRF7,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,TRIM44,SLC38A9,TMEM9B,ST5,PLK2,MOS,RET,ASXL1,FGFBP3,C12orf49,ACVR1B,PIK3CB,PIK3R1,HIP1R,HAND2,ATR,ING2,CDKN2AIP,ROBO1,P2RX3,ROBO2,PLCE1,ARNTL,FBXW7,ADGRV1,SORBS1,PTPRJ,IL7,HTRA2,GUCY1A1,CUX2,P2RY1,MADD,PTK2B,RASGRP1,KMT2D,RAPGEF2,CCL17,NR1H3,TIAM1,BMP2K,NLRC5,RIPK2,HOMER1,NKX3-1,OPA1,F2RL1,F2R,NQO2,RIPK1,ZDHHC13,PKD2,PLA2	grey	VSMC_M10
GO:0043114	1.00	0.00	10	40	regulation of vascular permeability	BP	1	PTP4A3,TEK,MYLK3,FGFBP3,PTPRJ,TRPV4,CXCR2,RAMP2,YES1,MIR23A	grey	VSMC_M10

GO:0010948	1.00	0.00	98	237	negative regulation of cell cycle process	BP	1	MRNIP,TRIM39,PPP1R10,MDM1,MDC1,ZNF207,FBXO43,MAPK14,FBXO7,CRY1,CHMP2A,BRSK1,MSH2,ETAA1,CDK5RAP2,TPRA1,XPC,PLK3,DYNC1LI1,ANAPC15,IK,NEK11,USP44,PRKDC,ERCC6,CEP63,STK33,PLK2,MOS,FAM107A,RAD17,ATR,RAD9B,CHMP4C,EIF2AK4,NBN,ABRAXAS1,TMEM67,DONSON,ZFYVE19,PIDD1,PKD2,TAOK3,CCND1,PRKAR1A,GIGYF2,GPER1,CHEK2,CCDC84,ATRIP,SYF2,CDKN1B,DLG1,OVOL1,BCL6,SUSD2,PPP2R5B,MEN1,TIPRL,RHNO1,PRPF19,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,LCMT1,FOXN3,TRIM37,DCUN1D3,CCL2,TOM1L2,PSMG2,TAOK1,NUBP1,FZR1,NAA10,DOT1L,FBXO31,TERF2,VPS4A,DAB2IP,NAE1,MIR29A,RPA4,PLK5,RPS27L,SOX4,DUSP1,RGCC,NME6,APC,LIF,ZFP36L2,BRCC3,CRADD,NABP1	grey	VSMC_M10
GO:0051336	1.00	0.00	352	754	regulation of hydrolase activity	BP	1	SERPINB8,SERPINB2,TNFAIP8,LRP1,ARHGAP9,MAP3K5,TBC1D30,TBC1D9B,ESR1,TIAM2,GRAMD4,AGER,FBLN1,PSMB8,SYNGAP1,BAK1,MYC,ASAP1,PTK2,PLXNA4,NTRK2,C6orf89,PI16,TBC1D22B,HSF1,TTBK1,NUAK1,KIT,SLC1A1,SEMA4D,GAPDH,TBC1D8,RGP1,FGD3,SVBP,TNNI3,CD109,LPAR1,PPT1,NOD1,AKIRIN2,AQP1,CASP8AP2,PLEK,EPHA7,NR1H2,TNFSF15,ASAP2,ITGB1BP1,MET,VRK3,EGFR,ARHGEF5,EPHA1,BCL2L12,BVES,LPIN1,TBC1D9,HSPE1,SPHK2,SPRY1,PLXNA1,ARHGAP12,NAPA,C5AR1,PRKD2,CST7,PHB,IQSEC1,ABHD5,SSPO,RSU1,APOC1,RAF1,PRDX3,TIMP4,TBC1D4,FOXJ1,UBE2O,SPRY2,WNT11,AKT2,ARRB1,IKBKB,TBC1D16,MKKS,TMEM106B,RASGRP4,CHTOP,SPINT2,PRNP,BAG4,ARHGEF7,PLXNC1,FGD6,DDRGK1,WRN,NCKAP1L,GAS6,LARS,RASA3,ARL6IP5,FLT1,ST18,PSMF1,ASPH,GPI,NR4A1,PXK,SBF2,FOXL2,RASA2,HIP1R,ROBO1,PCOLCE2,DIABLO,MTMR9,TBC1D12,MEF2C,HTRA2,TMBIM6,ARHGEF26,PTK2B,RASGRP1,RAPGEF2,CCL17,NR1H3,TIAM1,OAS3,RIPK2,SENP1,NKX3-1,RAPGEF3,ACVR1C,SERPINB1,F2RL1,F2R,IQGAP2,ARHGAP24,SPINT1,CRY2,TNNC1,PIDD1,PLA2R1,PAX2,CD40,APLP2,RAP1GDS1,GPLD1,DOCK10,CD200,OASL,FGD4,HDAC1,RGS1,LCK,TGFB2,TBCK,ADPRH,PDCD6,GPR137B,GNA13,OXA1L,AJUBA,ADAP1,DENND1B,FICD,ARHGAP6,TBC1D10C,SOX2,SORL1,GPER1,PSME1,RAB11FIP2,SH3BP4,IFI6,AGT,DVL3,COL6A3,CIDEB,SFN,COL7A1,RPS6KA1,TOR1AIP1,CDKL5,GRHL3,EPHB3,CST6,EGLN3,MGMT,POR,RASA4,MAPT,FIS1,TRAPPC6B,BCL6,ABL2,RASAL2,CTSH,TBC1D2B,GMIP,VCPKMT,DDX3X,DNAJC10,RASGRP2,FN1,TBC1D14,VSIR,RABGAP1L,SPOCK2,PPP1R2C,SERPINC1,SERPINI1,RUNDC1,WN	grey	VSMC_M10
GO:0071459	1.00	0.00	4	23	protein localization to chromosome, centromeric region	BP	1	TRAPPC12,IK,CHAMP1,CTCF	grey	VSMC_M10
GO:0140694	1.00	0.00	130	305	non-membrane-bounded organelle assembly	BP	1	VPS4B,PAN2,MDM1,CNOT2,CNOT6,ZNF207,HSPA1B,TUBGCP6,IL5,RRP7A,WASHC5,ASAP1,OBSCN,MAPK15,LMOD2,SRF,PGM5,CHMP2A,RPS14,TMOD1,MDN1,TRAPPC12,CDK5RAP2,CCDC155,MYLK3,MAPRE1,PUM2,CCDC61,LCP1,CLASP2,MAPRE3,MLH1,PIBF1,RPSA,CEP295NL,ACTG1,CDS2,LMOD3,PRKDC,PAN3,CEP63,DHX37,PLK2,HCK,KIF3B,CHMP2B,RPL6,CEP44,PLS1,AUP1,CNOT1,CHMP4C,CNOT6L,ALMS1,ABRAXAS1,CDS1,FITM2,TUBGCP5,AC112128.1,LMOD1,SBDS,PRKAR1A,MRPS11,YTHDF2,FITM1,CHEK2,TUBGCP4,ACTC1,RPS27,MYOZ2,DDX6,CASQ1,TMOD4,POGZ,ABRAXAS2,YTHDF1,FARP2,DHX30,EIF4ENIF1,RPL11,KIF9,MYPN,MAPT,EFL1,TOGARAM1,TTN,RPL10L,DDX3X,XRCC5,RC3H1,CEP152,MYOZ1,RNF4,PRRC2C,TMOD2,OBSL1,LDB3,TCAP,SEPT1,KPNB1,ZFYVE1,CNTROB,ATXN2L,UBAP2L,RAB11A,TRIM37,MRPL22,TMEM159,G3BP1,NCOR1,NLE1,MYH11,RPL23A,ERAL1,CEP192,WRAP73,CIRBP,CHMP1A,MRPS2,GPSM2,RHOA,AURKC,CSRP2,BSCL2,KRT19,RPS27L,CCSAP,C2CD3,CENPX,DRG1	grey	VSMC_M10
GO:1901988	1.00	0.00	81	201	negative regulation of cell cycle phase transition	BP	1	MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,MAPK14,FBXO7,CRY1,BRSK1,MSH2,ETAA1,CDK5RAP2,TPRA1,XPC,PLK3,DYNC1LI1,ANAPC15,IK,NEK11,USP44,PRKDC,ERCC6,CEP63,STK33,PLK2,MOS,FAM107A,RAD17,ATR,RAD9B,CHMP4C,EIF2AK4,NBN,ABRAXAS1,DONSON,ZFYVE19,PIDD1,PKD2,TAOK3,CCND1,GIGYF2,CHEK2,ATRIP,SYF2,CDKN1B,DLG1,OVOL1,SUSD2,MEN1,TIPRL,RHNO1,PRPF19,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,LCMT1,FOXN3,DCUN1D3,CCL2,PSMG2,TAOK1,FZR1,DOT1L,FBXO31,VPS4A,NAE1,MIR29A,RPA4,PLK5,RPS27L,SOX4,DUSP1,RGCC,APC,ZFP36L2,BRCC3,CRADD,NABP1	grey	VSMC_M10

GO:0009888	1.00	0.00	670	1389	tissue development	BP	1	ITGA7,ONECUT2,HSD17B4,SEMA6A,STAC3,GLI1,CYP27B1,MAML1,ESR1,FRS2,STK3,OSR2,FZD6,PPARA,BRD2,COL11A2,VGLL2,ROS1,VPS52,TBC1D32,MTSS1,PITX1,RSPO3,MYC,SMAD5,KLHL3,LEMD2,PTCH1,LY6E,AKR1B1,EXOC4,ATF4,MAPK14,CBY1,PODXL,SOX10,PI16,PIM1,MEST,SMO,ZDHHC21,BNC2,FOXH1,IFT74,ZFAND5,PTK7,SRF,PGM5,TXNRD1,CDK6,RFX3,CA9,FHL2,TFAP2B,ROR2,SEMA4D,DLX5,S1PR3,OMD,SEMA4C,CNNM4,TDRD7,MEOX2,SOSTDC1,TMOD1,CAT,SIX2,HIVEP3,BRSK1,TNNI3,EPCAM,CD109,RTN4,KLK14,KLK4,HOXA7,HOXA13,MYCL,AREG,BMP8A,MYH14,BMPER,AKIRIN1,ANXA4,COL27A1,EPHA7,AKNA,WHRN,MBOAT2,PTN,ITGB1BP1,GRHL1,MET,TNC,POU3F3,EGFR,FUZ,BVES,GJB5,SFRP4,KEL,MYLK3,TEAD2,ATG5,SDCBP,MYCN,TRPM4,SLC7A11,OSR1,PGRMC2,MATN3,NTF4,MKX,INTU,SPRY1,PLXNA1,FOXE3,ARHGAP12,HDAC2,BBS7,BMI1,RAB10,PRKD2,SETDB2,ABI1,SOX9,ERCC2,ERCC3,CLASP2,PTER,SLC4A2,GSTK1,PTCH2,GLI2,MEGF8,PCDH8,AQP11,XRCC2,MYD88,EVPL,ACVR2B,KLF5,IFT172,FOXJ1,SCN5A,PAXIP1,MYO7A,GZF1,SCEL,POU4F1,TSKU,SPRY2,WNT11,KLHL40,SLC24A3,AKT2,DYRK1B,TGFBR2,OVOL2,CHRDL2,BFSP1,ZNF219,ACVR2A,EOMES,IKBKB,SLC4A7,JAG1,SIRT2,MKKS,RARB,ACTG1,HBEGF,NR1D2,LRTOMT,AP000812.5,PLCB1,MAFG,RYR1,FERMT1,SPRED3,SPINT2,ALX1,FREM2,CEP290,SEMA3D,LUM,DCN,BTG1,SPART,SPEF1,SEMA3A,P2RX2,KL,NRG1,TFDP1,DDRGK1,GAS6,FOXP1,TAF10,LMOD3,PRKDC,KBTBD8,SYNE4,STX2,RYK,CEP63,TRAF6,TCF15,EPHB1,NPHP1,RET,HCK,TOX,ASAH1,SGCG,POFUT1,ASXL1,CYP7B1,GPI,PAX8,NR4A1,ACVR1B,CBFA2T2,SMYD1,RILPL1,RILPL2,NLN,FOXL2,FLNB,VAMP5,CASP3,MAR	grey	VSMC_M10
GO:0007017	1.00	0.00	331	715	microtubule-based process	BP	1	VPS4B,CCDC68,AP3S1,TRIM36,KIF5A,MAP7,KATNA1,MDM1,ATAT1,CCDC170,RAB21,ZNF207,HSPA1B,TUBGCP6,KIF3A,UBE2B,CATSPER3,WASHC5,LRRC6,MAPK15,AGTPBP1,SUN2,COPG2,MPDZ,CNTLN,MYH9,IFT74,CFAP69,APBA1,SLAIN2,PEX1,HEPACAM2,RFX3,GAPDH,EFHC1,BICD2,CHMP2A,DYNC2LI1,NLRP5,LRPPRC,DNAJA1,BRSK1,DNAH11,CABS1,XPO1,CEP68,WDR92,MET,CDK5RAP2,CCDC155,MGARP,ARMC2,MAPRE1,WASF1,ARMC4,APOB,SPRY1,TCTE3,ADCY3,TTC26,KIF3C,ARHGAP21,COPG1,DRC1,CCDC61,RSPH6A,NINL,EML2,SLC39A12,KLC3,CLASP2,DLG2,MAPRE3,TCTEX1D4,PLK3,MLH1,LLGL2,TRIM54,XRCC2,NCKAP5,PIBF1,IFT172,FOXJ1,TTC21A,SLAIN1,KIZ,WDR60,SPRY2,CFAP61,CLIP4,TTLL3,CCDC13,DYNC1LI1,HOOK3,CEP295NL,AP3M2,KIF5C,MKKS,NEK10,PURA,NAV3,ARHGEF7,DIAPH1,SPEF1,RASSF7,KATNAL1,CEP63,NSFL1C,ATXN7,TUB,PLK2,DNAH10,MOS,TTL,KIF3B,FAM107A,FER,CEP70,CHMP2B,DCLK2,ING2,CEP44,CLIP1,DNAH6,WDR66,CEP250,CCDC66,CETN3,NCKAP5L,IFT81,CHMP4C,CFAP20,MCPH1,KIFC3,KATNB1,RASGRP1,CCDC65,ALMS1,ABRAXAS1,TMEM67,OPA1,AP3B1,IFT52,TUBB2A,TUBGCP5,PKD2,DNAH1,PLTP,DNAH5,DTNBP1,DPCD,TUBA1A,STMND1,ROPN1L,KIF13A,BICDL1,SRGAP2C,KIF21A,NEURL1,SLK,FIGN,CFAP43,ZMYND10,AC112128.1,SLC9B1,TRPV4,SBDS,SLC9B2,KLHL42,CFAP46,DAG1,TTBK2,INTS13,MARK1,TBCE,CFL1,TTC21B,HSPA8,JHY,DISC1,OFD1,CFAP45,TBCEL,ENO4,CHEK2,TTLL13P,TSSK4,TUBGCP4,CIB1,BAG3,CCDC84,TRAF3IP1,PHLDB1,ABRAXAS2,CELF3,KIAA1614,CNIH2,WDR73,INPP5J,LIMK2,CATSPER2,CDKN1B,SIK3,DLG1,SAXO2,SLC16A1,KIF9,PPP2R3C,SETD2,MAP3K11,CALY,TTC30A,SP	grey	VSMC_M10
GO:0070848	1.00	0.00	258	570	response to growth factor	BP	1	SLC39A5,ONECUT2,ARPC3,SEMA6A,MARS,USP15,FRS2,SNW1,PPARA,GDF9,MYC,SMAD5,LEMD2,PTK2,PTP4A3,TAB1,MAPK14,NTRK2,MICALL1,KCP,FOXH1,TGFBRAP1,TFAP2B,ROR2,DLX5,SOSTDC1,CAT,CD109,HAS1,ADAMTS3,HOXA13,CXCL8,BMP8A,BMPER,PTN,ITGB1BP1,DDC,GRB10,TNC,EGFR,TSPAN12,FUZ,TLR4,GAB1,SFRP4,SDCBP,FOXO3,NTF4,WASF1,FGF21,SPRY1,HDAC2,NDNF,PRKD2,SOX9,MEGF8,RAF1,ACVR2B,UBE2O,FNDC4,SPRY2,EID2,TGFBR2,OVOL2,ACVR2A,SIRT2,FERMT1,SPRED3,SPINT2,DUSP6,BAG4,LUM,DCN,SPART,KL,GAS6,FLT1,AMHR2,FGFBP3,NR4A1,ACVR1B,FER,PIK3CB,SNX25,LPXN,CASP3,DKK3,ING2,HPGD,ROBO1,IL17RD,MEF2C,HTRA2,VEGFC,SOX6,P2RY1,RAPGEF2,SLC33A1,FGF5,VEPH1,ZFYVE27,ACVR1C,SPINT1,GCNT2,PAX2,CYFIP1,HIVEP1,ITGB6,ZNF423,DSTYK,BMPR1B,FBXL15,BDNF,PXN,SRD5A1,HYAL1,SLC2A10,PDCD4,TGFB2,SULF2,PDCD6,MXRA5,HJV,MAPKAPK2,LRIT3,SOX2,OPRD1,SORL1,DOK5,AGT,CIB1,CBL,ARNT,ITGB5,HTRA1,SYAP1,CHRD,RUNX3,DLX1,PDE8A,DTYMK,SNX6,CREB1,CTDSPL2,PBLD,MAPT,CPS1,PPP2R5B,EHD1,MEN1,IL12A,CASK,HTRA3,FBN1,WNT4,FLRT1,FKBP8,COL3A1,RAP1GAP,GDF15,RAMP2,FGFR3,STK16,STAT3,MAPK1,STAT5B,PPM1A,GREM2,SCGB1A1,HAP1,BMPR1A,PARP1,CHURC1,MPP5,RBPJ,TNFRSF1B,MED1,FGFR4,RNF111,TGFB1I1,FGF18,NGFR,ITGA3,PGF,FOS,RBPMS2,MAPK3,CILP,TOB1,CITED1,WFIKKN2,TMEM100,SMAD3,MAP2K5,TNMD,CSTF2,PRKCB,RNF165,DNM2,LHX1,GAREM1,CHRDL1,CCL5,MAPK7,GATA6,FAM83G,CCL2,YES1,NLK,TWSG1,ADAMTS12,GPC3,JUN,LRP8,CRK,INPP5K,CREBBP,TRPV1,PDPK1,SKI,PRDM16,WFIKKN1,FGF22,LCN2,ENG,MTSS1L,HSPA5,ZFH	grey	VSMC_M10
GO:1900180	1.00	0.00	42	116	regulation of protein localization to nucleus	BP	1	C6orf106,MAPK14,SMO,RAB23,FERMT1,MAVS,MFHAS1,NUP58,POLR1A,PIK3R1,DCLK2,PKIA,NUP54,SUFU,CABP1,TERT,HCLS1,OTUD7B,PARP9,DTX3L,BAG3,LIMK2,GLUL,APOD,MEPCE,MAPK1,ATP13A2,MAGED1,PARP1,NVL,TARDBP,PSEN1,NGFR,KAT7,SMAD3,SIN3A,EFCAB7,PARK7,LAMTOR5,RASSF5,LIF,ZIC1	grey	VSMC_M10

GO:0006457	1.00	0.00	66	166	protein folding	BP	1	CANX,HSPA1B,ALG12,SIL1,BAG1,CDC37L1,PDCL3,ERP44,DNAJA1,NFYC,FKBP9,HSPE1,CRTAP,PDIA3,CCT8L2,MKKS,DNAJC18,BAG4,FUT10,PFDN5,PDRG1,MOGS,ZMYND10,TBCE,HSPA8,TBCEL,PDIA5,UNC45A,BAG3,PPIG,PEX19,DNAJC5,DNAJC10,GRPEL1,DNAJB12,DNAJC4,FKBP8,DNAJB2,SDF2L1,PPIL2,CALR3,DNAJB1,PFDN4,GAK,AHSP,NUDCD2,CD74,UNC45B,CCT6B,DNAJA3,SGTA,VBP1,TOR1B,TOR2A,HSPA5,ENTPD5,TBCA,BAG2,WDR83OS,POFUT2,SDF2,GRPEL2,PPIC,PPIF,MESD,DNAJC19	grey	VSMC_M10
GO:0010632	1.00	0.00	84	208	regulation of epithelial cell migration	BP	1	PTK2,TEK,MEOX2,SVBP,PRKCE,RTN4,EPB41L4B,EMC10,BMPER,PTN,ITGB1BP1,MET,PRKD2,IQSEC1,SOX9,CLASP2,RIN2,TGFBR2,HBEGF,DCN,SEMA3A,FOXP1,PLK2,GPI,PIK3CB,ATP5F1A,FBXW7,MEF2C,VEGFC,PTK2B,DOCK5,STC1,HDAC7,RREB1,CD40,GPLD1,HYAL1,SP100,TGFB2,PDCD6,EGF,AGT,CIB1,MAP3K3,DOCK1,PATZ1,GLUL,NFE2L2,DUSP10,CTSH,PDCD10,RHOJ,SYNJ2BP,SEMA4A,RAB25,FGF18,ITGA3,EFNA1,VASH1,RAB11A,MAP2K5,BCAS3,EVL,PDPK1,MECP2,LCN2,MARVELD3,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,ACVRL1,ZNF580,WNT5A,GADD45A,RGCC,FGF1	grey	VSMC_M10
GO:0009968	1.00	0.00	461	973	negative regulation of signal transduction	BP	1	NFATC1,PHLPP1,ERBB3,ONECUT2,LRP1,SEMA6A,EYA4,GLI1,PIP4K2C,TNFAIP3,EPM2A,TRIM39,PPP1R10,ESR1,CNOT2,STK3,MAPK8IP2,MPIG6B,HSPA1B,FZD6,GRAMD4,PRKN,PPARA,PDE10A,FBLN1,FSTL4,SYNGAP1,UBE2B,TRIB1,MYC,LEMD2,PTCH1,MAPK14,CBY1,STK38,SOX10,ZC3HC1,MDFI,FOXH1,LRRC14,CRY1,DLK2,NCK2,FHL2,IL1R2,ROR2,TMEM14A,WNK2,KLHL31,SOSTDC1,BEND6,DNAJA1,CD109,FKTN,PPP2R1A,PHIP,KLK14,ACP4,CXCL8,BMPER,PXDN,PLEK,NR1H2,ITGB1BP1,MET,VRK3,GRB10,EGFR,HECW1,FUZ,TRIM32,TLR4,SFRP4,DKKL1,FOXO3,SPRY1,ARHGAP12,MTMR2,KPTN,SESN3,RAB7A,BMI1,PIP4K2A,ARMC10,PTGIR,PHB,SOX9,GIPR,PPM1N,CD300LF,DDIAS,PTCH2,OPTN,KBTBD6,KCTD21,GLI2,MEGF8,RAF1,PIBF1,IFT172,SEC14L1,TSKU,SZT2,SPRY2,WNT11,GPD1L,ARRB1,EID2,SNX5,RBMS3,CHD8,NMI,ZMYND11,TCIM,NPLOC4,PAWR,UBAC2,PLCL2,FERMT1,SPRED3,PRNP,DUSP6,DCN,SPART,DDRGK1,SH3RF2,GAS6,SIRT3,PPP2CB,RASA3,FOXP1,LEPROTL1,MFHAS1,TMEM127,NR1H4,RGS20,PFDN5,ASXL1,IL1A,CYP7B1,RGS7BP,KCTD6,CBFA2T2,FAIM,PIK3CB,SNX25,ZNF536,OTUD4,RASA2,LPXN,TAF9,CTNND1,DKK3,TRABD2A,ING2,EYA1,ROBO1,ZNF366,IL17RD,ARNTL,FBXW7,PTPRJ,TMEM131L,IL7,FAIM2,HTRA2,TMBIM6,P2RX7,NDUFS3,CNOT1,CSNK2A2,SLA2,LMBR1L,MAPKAPK5,NR1H3,PAQR3,VEPH1,OAS3,NLRC5,NKX3-1,OPA1,HDAC7,AMFR,NR4A2,F2RL1,ARHGAP24,RIPK1,CRY2,VPS18,MARCH7,RPGRIP1L,SOX13,STK4,MAPKBP1,HIF1AN,PRICKLE1,NOD2,NKD1,TAOK3,DUSP8,RAB7B,BDNF,SUFU,PRDM15,OTUD7A,IRS1,NEURL1,GRB14,HDAC1,RGS1,DDIT4L,SLC2A10,BANK1,TERT,PDCD	grey	VSMC_M10
GO:0010647	1.00	0.00	602	1251	positive regulation of cell communication	BP	1	CD226,ERBB3,LRP1,RPS12,GLI1,MAP3K5,TNFAIP3,CYP27B1,USP15,TRIM39,FRS2,STK3,MAPK8IP2,SNW1,HSPA1B,RIMS2,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,IL5,GDF9,RGL2,UBE2B,BAK1,RSPO3,RNF146,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,AKR1B1,ZC3H3,TAB1,NTRK2,CSNK1E,PLA2G6,GKAP1,MFNG,SMO,DAAM2,KCP,TEK,GPR37,PTK7,LRRD1,SLC35B2,OCIAD1,KIT,SLC1A1,NCK2,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,WNK2,NINJ1,SEMA4C,CAT,IL11,PRKCE,RIMS1,RTN4,PHIP,FPR2,GSDME,RIMS3,KLK14,SHANK1,ADAMTS3,EMC10,LPAR1,REL,ANKRD17,SLC46A2,MTURN,EPGN,NOD1,AREG,BMP8A,CRHR2,RRAGD,PELI1,BMPER,RSPO1,RSAD2,AAK1,TGFA,PTN,ITGB1BP1,MET,GRB10,ATP6V1C2,EGFR,LANCL2,ARHGEF5,TRIM32,TLR4,GRIK2,TRAF1,SFRP4,VPS35,SDCBP,TRPM4,PUM2,WASF1,FAF1,FGF21,BRAF,INTU,TRAF3IP2,SPHK2,GRIN2D,DNAJC27,SLC8A2,C5AR2,C5AR1,PRKD2,PHB,SOX9,GIPR,PPM1N,CACNB2,CD300LF,NECTIN2,PDIA3,DEDD2,RAF1,MYD88,PIBF1,ACVR2B,IFT172,UBE2O,SCEL,FBH1,SPRY2,WNT11,ALK,DYNC1LI1,ARRB1,PIP4P1,NEU3,SNX5,ACVR2A,IKBKB,C1QTNF1,JAG1,NMI,NEK10,RPTOR,TCIM,HBEGF,SYT1,PDE6G,PLCB1,RASGRP4,FERMT1,EIF2AK2,PRNP,ADRA1D,BAG4,DCN,MAVS,RELL2,SEMA3A,P2RX2,AIMP1,KL,NRG1,SH3RF2,NCKAP1L,GAS6,HPX,LARS,SIRT3,FOXP1,RBPMS,ARL6IP5,IRF7,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,TRIM44,SLC38A9,TMEM9B,ST5,PLK2,MOS,RET,ASXL1,FAM107A,FGFBP3,C12orf49,ACVR1B,PIK3CB,OSBP,PIK3R1,CLSTN2,HIP1R,HAND2,ATR,ING2,CDKN2AIP,ROBO1,P2RX3,ROBO2,PLCE1,ARNTL,FBXW7,ADGRV1,SORBS1,PTPRJ,IL7,HTRA2,GUCY1A1,CUX2,P2RY1,MADD,PTK2B,RASGRP1,MME,KMT2D,RAPG	grey	VSMC_M10
GO:0006403	1.00	0.00	67	171	RNA localization	BP	1	CPSF6,PHAX,QKI,ZC3H3,HSF1,NOL6,XPO5,BICD2,EXOSC3,LRPPRC,IGF2BP3,YTHDC1,PNPT1,XPO1,IWS1,TGFBR2,KIF5C,NUP98,CHTOP,UPF3A,THOC7,NUP58,ATR,CETN3,NUP54,MX2,DDX25,RFTN2,RTRAF,NCBP2,SIDT2,POM121,SENP2,IGF2BP2,SETD2,ENY2,UPF1,PARP11,NXF1,AHCTF1,AKAP8L,CASC3,FYTTD1,WRAP53,SMG5,RANBP17,NRDE2,ZNHIT3,YY1,ALKBH5,UPF3B,THOC2,SUPT6H,PARN,FMR1,NCBP3,TSC1,NUP214,DDX19A,ZNHIT6,SARNP,DDX19B,NXT2,NUPL2,YBX1,MRPL18,MAGOHB	grey	VSMC_M10

GO:0071495	1.00	0.00	481	1018	cellular response to endogenous stimulus	BP	1	SLC39A5,FECH,ONECUT2,ARPC3,LRP1,AP3S1,MARS,PIP4K2C,USP15,ESR1,FRS2,CNOT2,SNW1,PRKN,AGER,PPARA,PNPLA3,RXRB,GDF9,SMAD5,LEMD2,PTK2,AKR1B1,ATF4,TAB1,NTRK2,MAPK13,GKAP1,KDM4C,SOX10,MICALL1,HSF1,KCP,CCND3,FOXH1,GPT,RBFOX2,CRY1,GABRA1,KIT,SLC1A1,TGFBRAP1,TFAP2B,ROR2,DLX5,PPAT,SOSTDC1,DNAJA1,PRKCE,CD109,PHIP,FPR2,HAS1,HOXA13,CXCL8,NOD1,BMP8A,CRHR2,AQP1,RRAGD,BMPER,PTN,ITGB1BP1,DDC,KLF11,GRB10,TNC,EGFR,LANCL2,FUZ,TLR4,GAB1,LPIN1,SFRP4,UCP1,VPS35,SDCBP,MGARP,TRPM4,FOXO3,PGRMC2,NTF4,WASF1,APOB,FGF21,SPRY1,HDAC2,SESN3,DNMT3A,BMI1,NDNF,PIP4K2A,RAB10,PRKD2,PHB,SOX9,CYSLTR2,MEGF8,ECHDC3,ATP1A3,ACVR2B,KLF5,TBC1D4,UBE2O,EGLN2,AANAT,FBH1,SPRY2,ALK,TADA3,AKT2,EID2,TGFBR2,OVOL2,SNX5,ACVR2A,SIRT2,MKKS,RPTOR,RARB,NR1D2,SRA1,RYR1,FERMT1,SPRED3,SPINT2,PRNP,BAG4,TAF7,DIAPH1,SPART,RNF14,KL,DDRGK1,LARS,PTPRA,FOXP1,LEPROTL1,ARID5A,PRKDC,CALCOCO1,NCOA4,NR1H4,SLC38A9,TRIB3,LMO2,HTR7,FAM107A,CYP7B1,DNMT3B,PAX8,FGFBP3,NR4A1,FER,IDE,UFSP2,SNX25,PIK3R1,LPXN,CASP3,NCOA2,DKK3,ING2,HPGD,P2RX3,ROBO2,ZNF366,CHRM5,IL17RD,RYR3,ARNTL,SORBS1,GPD1,MEF2C,P2RX7,CNOT1,SOX6,P2RY1,KMT2D,RAPGEF2,SLC33A1,FGF5,VEPH1,RIPK2,DDX54,STC1,NKX3-1,OPA1,SPIDR,LPIN3,NKX6-1,RAPGEF3,CHRM4,NR4A2,SPINT1,CRY2,VPS18,ABCC2,PKD2,GCNT2,PAX2,CYFIP1,DMTN,CASQ2,ADTRP,HIVEP1,NOD2,ITGB6,DTNBP1,CHRM3,ZNF423,DSTYK,RYR2,IGF2,BMPR1B,FBXL15,BDNF,PXN,GPLD1,SRD5A1,IRS1,NEURL1,RPL23,GRB14,HDAC1,HYAL1,SLC2A10,P	grey	VSMC_M10
GO:0010634	1.00	0.00	54	143	positive regulation of epithelial cell migration	BP	1	TEK,PRKCE,RTN4,EPB41L4B,EMC10,ITGB1BP1,MET,PRKD2,IQSEC1,SOX9,CLASP2,RIN2,TGFBR2,HBEGF,FOXP1,PLK2,GPI,PIK3CB,ATP5F1A,VEGFC,PTK2B,DOCK5,HDAC7,RREB1,CD40,GPLD1,HYAL1,TGFB2,PDCD6,EGF,AGT,CIB1,MAP3K3,DOCK1,NFE2L2,CTSH,RHOJ,RAB25,FGF18,ITGA3,RAB11A,BCAS3,PDPK1,LCN2,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR27B,MIR27A,ZNF580,WNT5A,FGF1	grey	VSMC_M10
GO:1902099	1.00	0.00	17	58	regulation of metaphase/anaphase transition of cell cycle	BP	1	ZNF207,MAPK15,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,MOS,ANAPC5,ANAPC7,HECW2,ANAPC4,LCMT1,PSMG2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0071363	1.00	0.00	245	545	cellular response to growth factor stimulus	BP	1	SLC39A5,ONECUT2,ARPC3,SEMA6A,MARS,USP15,FRS2,SNW1,PPARA,GDF9,SMAD5,LEMD2,PTK2,PTP4A3,TAB1,MAPK14,NTRK2,MICALL1,KCP,FOXH1,TGFBRAP1,TFAP2B,ROR2,DLX5,SOSTDC1,CAT,CD109,HAS1,ADAMTS3,HOXA13,CXCL8,BMP8A,BMPER,PTN,ITGB1BP1,DDC,GRB10,EGFR,TSPAN12,FUZ,TLR4,GAB1,SFRP4,SDCBP,FOXO3,NTF4,WASF1,FGF21,SPRY1,HDAC2,NDNF,PRKD2,SOX9,MEGF8,RAF1,ACVR2B,UBE2O,SPRY2,EID2,TGFBR2,OVOL2,ACVR2A,SIRT2,FERMT1,SPRED3,SPINT2,BAG4,DCN,SPART,KL,GAS6,FLT1,AMHR2,FGFBP3,NR4A1,ACVR1B,PIK3CB,SNX25,LPXN,CASP3,DKK3,ING2,HPGD,ROBO1,IL17RD,MEF2C,HTRA2,VEGFC,SOX6,RAPGEF2,SLC33A1,FGF5,VEPH1,ZFYVE27,ACVR1C,SPINT1,GCNT2,PAX2,CYFIP1,HIVEP1,ITGB6,ZNF423,DSTYK,BMPR1B,FBXL15,BDNF,PXN,SRD5A1,HYAL1,SLC2A10,PDCD4,TGFB2,SULF2,PDCD6,HJV,MAPKAPK2,LRIT3,OPRD1,SORL1,DOK5,AGT,CIB1,CBL,ARNT,ITGB5,HTRA1,SYAP1,CHRD,DLX1,PDE8A,DTYMK,SNX6,CREB1,CTDSPL2,PBLD,MAPT,CPS1,PPP2R5B,EHD1,MEN1,IL12A,CASK,HTRA3,FBN1,WNT4,FLRT1,FKBP8,COL3A1,RAP1GAP,GDF15,RAMP2,FGFR3,STK16,STAT3,STAT5B,PPM1A,GREM2,HAP1,BMPR1A,PARP1,CHURC1,MPP5,RBPJ,TNFRSF1B,MED1,FGFR4,RNF111,TGFB1I1,FGF18,NGFR,ITGA3,PGF,FOS,RBPMS2,MAPK3,CILP,TOB1,CITED1,WFIKKN2,TMEM100,SMAD3,MAP2K5,TNMD,CSTF2,PRKCB,RNF165,DNM2,LHX1,GAREM1,CHRDL1,CCL5,MAPK7,GATA6,FAM83G,CCL2,YES1,NLK,TWSG1,ADAMTS12,GPC3,JUN,LRP8,CRK,INPP5K,CREBBP,TRPV1,PDPK1,SKI,PRDM16,WFIKKN1,FGF22,LCN2,ENG,MTSS1L,HSPA5,DAB2IP,DYNC1LI2,MIR199A1,MIR21,MIR23A,MIR27B,MIR27A,FSTL3,LEMD3,PLK5,ACVR	grey	VSMC_M10
GO:0045229	1.00	0.00	103	251	external encapsulating structure organization	BP	1	LRP1,C6orf15,SERAC1,ADAMTS19,TNXB,FBLN1,TNFRSF11B,COL11A2,COL14A1,TMPRSS6,COL9A1,HAS1,KLK4,ADAMTS3,PXDN,COL27A1,ST7,NDNF,SOX9,FBLN2,ERCC2,LCP1,CLASP2,CRTAP,FERMT1,SPINT2,COL6A6,COL6A5,LUM,GAS6,TCF15,MMP15,ADAMTS1,TLL2,LOXL2,LOXL4,SPINT1,ADAMTS20,ADTRP,ADAMTS15,ADAMTS8,GAS2,NFKB2,FAP,COL17A1,ELF3,SLC2A10,TGFB2,FBLN5,SULF2,COL16A1,DAG1,LAMB3,ADAMTSL4,AGT,TGM1,PHLDB1,MMP21,MELTF,EFEMP2,LAMC1,ADAMTSL3,KIF9,ADAM8,PLOD3,COL13A1,MMP11,TNR,SPOCK2,NID2,COL3A1,COL5A2,RAMP2,CTSV,MMP13,MMP3,P3H4,TNFRSF1B,FGFR4,ANXA2,PAPLN,VIPAS39,SMAD3,ADAMTS10,MYH11,ADAMTS12,MMP23B,SERPINF2,VWA1,MMP25,ADAMTS13,COL5A1,NTNG2,FOXF1,ENG,HAS3,CARMIL2,ATXN1L,SERPINB5,DPP4,LAMB1,RGCC,COL8A2	grey	VSMC_M10
GO:0051783	1.00	0.00	41	114	regulation of nuclear division	BP	1	ZNF207,FBXO43,UBE2B,PHIP,HOXA13,EPGN,TGFA,CDK5RAP2,DYNC1LI1,SIRT2,ANAPC15,PLCB1,IK,USP44,MOS,IL1A,ANAPC5,ANAPC7,NPM2,IGF2,PRKAR1A,EGF,GPR3,CD28,WNT4,OBSL1,ANAPC4,LCMT1,INSR,TOM1L2,PSMG2,FZR1,OOEP,WNT5A,DUSP1,RGCC,NME6,APC,LIF,EREG,PDXP	grey	VSMC_M10

GO:0000375	1.00	0.00	109	259	RNA splicing, via transesterification reactions	BP	1	ZC3H10,PABPC1,SNW1,SF3A3,QKI,PUF60,USP49,RBFOX2,SMU1,PRPF31,TRA2A,YTHDC1,SRSF10,PRPF4,SNIP1,PRPF38A,WBP4,CLNS1A,CELF2,CRNKL1,IK,NUP98,ZMAT2,CWC15,LSM1,WTAP,TGS1,GPATCH1,USP39,ZCCHC8,GCFC2,RBM39,AAR2,CELF1,DHX35,SRSF6,SCAF11,PRPF4B,BCAS2,RBM24,SMNDC1,RBM5,SART3,HSPA8,SRSF4,ZRSR2,CELF3,SYF2,WBP11,NCBP2,BUD13,MFAP1,RBM7,GEMIN2,SNRPD3,PRPF39,DHX8,CWF19L2,ESS2,RBM10,CASC3,PRPF19,LSM8,FXR2,RBM25,KHDC4,LUC7L3,SLU7,COIL,SFPQ,RBM41,XAB2,RAVER2,SNU13,RBMX2,MBNL3,NSRP1,FMR1,CELF5,METTL16,SRRM2,LSM7,CIRBP,LUC7L,C9orf78,TXNL4B,PRMT7,ESRP2,RNVU1-6,RNU5E-1,RNU5B-1,SRRM4,HTATSF1,NOL3,METTL14,RNU4ATAC,RF00003,SNRPC,NOVA1,RNU2-1,RNU4-2,RBM11,SRSF12,ZCRB1,RNU4-1,MAGOHB,SAP18,SRRM1,SNRNP25	grey	VSMC_M10
GO:0000377	1.00	0.00	107	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1	ZC3H10,PABPC1,SNW1,SF3A3,QKI,PUF60,USP49,RBFOX2,SMU1,PRPF31,TRA2A,YTHDC1,SRSF10,PRPF4,SNIP1,PRPF38A,WBP4,CLNS1A,CELF2,CRNKL1,IK,NUP98,ZMAT2,CWC15,WTAP,TGS1,GPATCH1,USP39,ZCCHC8,GCFC2,RBM39,AAR2,CELF1,DHX35,SRSF6,SCAF11,PRPF4B,BCAS2,RBM24,RBM5,SART3,HSPA8,SRSF4,ZRSR2,CELF3,SYF2,WBP11,NCBP2,BUD13,MFAP1,RBM7,GEMIN2,SNRPD3,PRPF39,DHX8,CWF19L2,ESS2,RBM10,CASC3,PRPF19,LSM8,FXR2,RBM25,KHDC4,LUC7L3,SLU7,COIL,SFPQ,RBM41,XAB2,RAVER2,SNU13,RBMX2,MBNL3,NSRP1,FMR1,CELF5,METTL16,SRRM2,LSM7,CIRBP,LUC7L,C9orf78,TXNL4B,PRMT7,ESRP2,RNVU1-6,RNU5E-1,RNU5B-1,SRRM4,HTATSF1,NOL3,METTL14,RNU4ATAC,RF00003,SNRPC,NOVA1,RNU2-1,RNU4-2,RBM11,SRSF12,ZCRB1,RNU4-1,MAGOHB,SAP18,SRRM1,SNRNP25	grey	VSMC_M10
GO:0000398	1.00	0.00	107	255	mRNA splicing, via spliceosome	BP	1	ZC3H10,PABPC1,SNW1,SF3A3,QKI,PUF60,USP49,RBFOX2,SMU1,PRPF31,TRA2A,YTHDC1,SRSF10,PRPF4,SNIP1,PRPF38A,WBP4,CLNS1A,CELF2,CRNKL1,IK,NUP98,ZMAT2,CWC15,WTAP,TGS1,GPATCH1,USP39,ZCCHC8,GCFC2,RBM39,AAR2,CELF1,DHX35,SRSF6,SCAF11,PRPF4B,BCAS2,RBM24,RBM5,SART3,HSPA8,SRSF4,ZRSR2,CELF3,SYF2,WBP11,NCBP2,BUD13,MFAP1,RBM7,GEMIN2,SNRPD3,PRPF39,DHX8,CWF19L2,ESS2,RBM10,CASC3,PRPF19,LSM8,FXR2,RBM25,KHDC4,LUC7L3,SLU7,COIL,SFPQ,RBM41,XAB2,RAVER2,SNU13,RBMX2,MBNL3,NSRP1,FMR1,CELF5,METTL16,SRRM2,LSM7,CIRBP,LUC7L,C9orf78,TXNL4B,PRMT7,ESRP2,RNVU1-6,RNU5E-1,RNU5B-1,SRRM4,HTATSF1,NOL3,METTL14,RNU4ATAC,RF00003,SNRPC,NOVA1,RNU2-1,RNU4-2,RBM11,SRSF12,ZCRB1,RNU4-1,MAGOHB,SAP18,SRRM1,SNRNP25	grey	VSMC_M10
GO:0007015	1.00	0.00	161	373	actin filament organization	BP	1	ARPC3,MYO1A,AVIL,PRKN,SHROOM1,MTSS1,WASHC5,BAIAP2L2,PICK1,CDC42EP1,RAC2,LMOD2,SRF,NCK2,KIAA1211,TMOD1,PLEKHH2,NLRP5,PRKCE,SPTBN1,RUFY3,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,EPHA1,CCDC155,FAM49A,WASF1,ARHGAP12,KPTN,MSRB2,ABI1,MYO7B,LCP1,CLASP2,MYO7A,WNT11,ARRB1,PLEKHG2,FCHSD2,MKKS,ACTG1,FSCN2,PAWR,RAC3,BAG4,DIAPH1,FCHSD1,NCKAP1L,ARFIP2,LMOD3,DPYSL3,TTC17,HCK,FAM107A,FER,PIK3R1,HIP1R,PLS1,FMN1,LIMA1,SORBS1,PTK2B,RND1,ALMS1,USH1C,RAPGEF3,RHOBTB2,BIN3,F2RL1,IQGAP2,CYFIP1,DMTN,GAS2,MAGEL2,PXN,ELMO2,CARMIL1,PPFIA1,LMOD1,ADD3,TRPV4,SSH1,CFL1,SHROOM2,HCLS1,ARHGAP6,AP1AR,CASS4,SPATC1L,WASF2,ACTC1,SLC9A1,SPTBN2,ITGB5,TMOD4,EPS8,RHOBTB1,WHAMM,DLG1,CAPZA1,CDC42EP2,TTN,NCKAP1,MCU,WNT4,ARPC1A,WAS,TMOD2,TPM4,SHROOM4,SPTB,TCAP,PFN3,WASHC3,KCTD13,HAX1,SMAD3,GAS7,CORO2B,EVL,PSTPIP1,PPARGC1B,MYO1D,MPRIP,MYO1F,PTGER4,TNFAIP1,CORO6,SSH2,MYO5B,RFLNB,INPP5K,CORO7,SERPINF2,TLE6,MLST8,SPIRE2,TSC1,WDR63,CARMIL2,FHOD1,MIR21,MICALL2,RHOA,VASP,OOEP,GMFG,ASAP3,RND3,SAMD14,RGS4,GRB2,RGCC,PFN4,PDXP,COTL1	grey	VSMC_M10
GO:0045786	1.00	0.00	130	306	negative regulation of cell cycle	BP	1	YTHDC2,TNFAIP3,HECA,MRNIP,TRIM39,PPP1R10,MDM1,MDC1,ZNF207,FBXO43,MAPK14,CDKN2A,FBXO7,CRY1,CDK6,CHMP2A,BRSK1,MSH2,ETAA1,EGFR,CDK5RAP2,TPRA1,XPC,PLK3,DYNC1LI1,ANAPC15,IK,NEK11,BTG1,USP44,PRKDC,ERCC6,CEP63,STK33,PLK2,MOS,FAM107A,NR4A1,CEBPA,CASP3,RAD17,ATR,HPGD,FZD3,BTG3,HTRA2,RAD9B,CHMP4C,EIF2AK4,NBN,NKX3-1,ABRAXAS1,TMEM67,DONSON,ZFYVE19,PIDD1,PKD2,TAOK3,NUPR2,CCND1,PDCD4,PRKAR1A,GIGYF2,GPER1,CHEK2,ANGEL2,CCDC84,ATRIP,SYF2,RUNX3,CDKN1B,DLG1,OVOL1,HEXIM2,BCL6,SUSD2,PPP2R5B,BRINP2,MEN1,TAF6,PLA2G16,TIPRL,RHNO1,INHA,RNF167,TSPYL2,PRPF19,UIMC1,FOXO4,EME1,MUC1,TAOK2,TIPIN,SMAD3,LCMT1,FOXN3,TRIM37,DCUN1D3,NLE1,PPP1R13B,CCL2,TOM1L2,PSMG2,TAOK1,TP53I13,NUBP1,FZR1,NAA10,DOT1L,CHMP1A,FBXO31,TERF2,VPS4A,DAB2IP,NAE1,MIR29A,MIR21,RPA4,PLK5,RPS27L,SOX4,DUSP1,RGCC,NME6,APC,LIF,ZFP36L2,BRCC3,CRADD,NABP1	grey	VSMC_M10

GO:0044265	1.00	0.00	448	947	cellular macromolecule catabolic process	BP	1	VPS4B,NEDD4L,PAN2,LRP1,FEM1C,RMND5B,TNFAIP3,USP15,CANX,TRIM39,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,SKIV2L,DXO,EIF3E,PNLDC1,PRKN,RNF5,PSMB8,DERL1,SKP1,UBE2B,RNF217,CSDC2,RNF146,TRIB1,KLHL3,AGO2,PTK2,TNRC6B,TUT7,AGTPBP1,GTPBP1,MAPK14,CSNK1E,EXOSC4,FOXRED2,HSF1,FBXL6,USP49,FBXO7,KLHDC3,DCAF12,USP46,LNX1,CNOT11,RGP1,PDCL3,FBXO10,EXOSC3,LRPPRC,SEC61B,RNF20,RAD23B,UBE3D,PNPT1,ECPAS,PPT1,XPO1,PELI1,WDR91,CNOT4,RNASEH1,FBXO48,AGO1,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,VPS35,ZYG11B,SDCBP,TUT4,PUM2,MFSD8,FAF1,TRAF3IP2,MTPAP,ZC3HAV1,BBS7,RAB7A,DHX34,FBXL13,NUDT15,FBXL2,KCTD2,PLK3,SUMO2,FASTK,MLH1,USP35,KBTBD6,KCTD21,DEDD2,AQP11,MYD88,DMAC2,UBXN4,UBE3C,SPOPL,FBH1,TNRC6C,UBE2E1,KLHL40,ARRB1,SNX5,UGGT2,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,TMEM106B,UBAC2,NHLRC3,LSM1,NUDT16,RNF14,RNF122,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,PKP3,UPF3A,PAN3,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,ERCC8,KCTD6,CEBPA,IDE,NUDT12,ARMC8,FOXL2,SPSB4,RNF7,TAF9,UBE2L6,ZCCHC8,FBXO8,TRPC4AP,TTC37,ARNTL,FBXW7,USP25,TRIM2,ENC1,ANAPC5,HTRA2,AUP1,CNOT1,ANAPC7,CELF1,CHMP4C,CSNK2A2,CTSO,USP16,PTK2B,CNOT6L,FAM192A,TENT2,TMEM67,AMFR,RNFT2,FBXO21,RIPK1,FTO,MARCH7,KCNE2,ERLIN1,TTC3,PRICKLE1,TENT5C,MYLIP,FBXW4,TENT4B,RBM24,TOLLIP,SIAH1,LONP2,NHLRC1,FBXL15,RNF144B,SUFU,OTUD7A,FAP,RHBDD1,RPL23,AMN1,HECW2,PSMD1,KLHL42,TCIRG1,USP30,DIS3L2,RNF115,AXIN2,RNF123,PSMB5,GET4,KLHL25,MAPKAPK2,USP13,GI	grey	VSMC_M10
GO:0051338	1.00	0.00	326	706	regulation of transferase activity	BP	1	ERBB3,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,TNXB,MAP3K4,PRKN,AGER,ROS1,SKP1,XRCC6,TRIB1,MYC,PTK2,TAB1,MAPK15,NTRK2,STK38,CCND3,CDKN2A,ZNF16,CHRNA3,TEK,POT1,FBXO7,TTBK1,KIT,SLC1A1,NCK2,ROR2,DNAJA1,FPR2,IBTK,ACP4,MOB1B,EPGN,AREG,WDR91,ETAA1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,EGFR,ARHGEF5,TLR4,EPHA1,CCNY,PRKAR2B,SPRY1,SLC8A2,BMI1,C5AR1,PIP4K2A,PHB,ABI1,MAPRE3,EPM2AIP1,RALB,PRKAG2,PRDX3,PIBF1,GCKR,SPRY2,WNT11,ALK,TGFBR2,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,PRNP,TAF7,NRG1,USP44,CCKBR,NCKAP1L,GAS6,ERCC6,FLT1,RYK,ADRA2B,TRAF6,TRIB3,EPHB1,RET,PARP4,CEBPA,PIK3CB,PIK3R1,ZFP91,CDK7,CASP3,ROBO1,PLCE1,FBXW7,HMBOX1,PTPRJ,PKIA,CCNH,VEGFC,CCNJ,SLA2,MCPH1,MADD,PTK2B,RASGRP1,CCNG2,RAPGEF2,MAPKAPK5,PRKAG1,TIAM1,PAQR3,SERINC5,NLRC5,NBN,CCNJL,PKD2,STK4,DBNDD2,HERC5,NOD2,DTNBP1,TAOK3,CD40,DSTYK,LDB1,IGF2,BMPR1B,NHLRC1,IRS1,NEURL1,CD200,RPL23,DNM1L,CCND1,MAP2K6,PDCD4,TGFB2,ADRA2A,FAM20A,PRKAR1A,ADARB1,DAG1,AJUBA,NCF1,MST1,KRAS,FABP4,EGF,PFKFB2,ADNP,UBASH3B,POLG2,SORL1,RTRAF,SLAMF8,CASS4,SPATC1L,DTX3L,CACUL1,AGT,FGR,CIB1,CBL,DVL3,STRADB,SFN,PPP2R5A,CAMK2N2,SYAP1,RUBCN,PTPRO,STRADA,EPHB3,DUSP12,PIK3IP1,GPRC5D,RPL11,SNX6,CDKN1B,DLG1,PPP2R3C,MAP3K11,ADAM8,CCNYL1,AIDA,FZD5,YWHAG,DUSP10,MAPT,STOX1,HEXIM2,CEMIP,TTN,DBF4B,EPHB4,MEN1,MAP4K2,DDX3X,XRCC5,DUSP19,PTPN6,PDCD10,TRPT1,ADRA2C,DOK7,SLC11A1,HTT,ZFYVE28,PRKAG3,MARK2,FGFR3,SOCS4,PINK1,SLC27A1,MAPK1,EPHA4,PPP1R3F,DLG4,	grey	VSMC_M10
GO:0043536	1.00	0.00	15	53	positive regulation of blood vessel endothelial cell migration	BP	1	PRKD2,PLK2,ATP5F1A,VEGFC,HDAC7,CD40,CIB1,MAP3K3,NFE2L2,RHOJ,FGF18,PDPK1,MIR23A,MIR27B,MIR27A	grey	VSMC_M10
GO:0048525	1.00	0.00	18	61	negative regulation of viral process	BP	1	LY6E,APOBEC3H,RSAD2,TRIM32,ZC3HAV1,EIF2AK2,MAVS,FAM208A,OAS3,IFIH1,OASL,TNIP1,CCL5,CIITA,INPP5K,SETDB1,OAS1,FAM111A	grey	VSMC_M10
GO:0033687	1.00	0.00	5	27	osteoblast proliferation	BP	1	OSR2,EIF2AK2,SMAD3,SOX8,RHOA	grey	VSMC_M10
GO:0030154	1.00	0.00	1481	2966	cell differentiation	BP	1	ADNP2,NFATC1,NME1,ITGA7,ERBB3,SLC39A5,NEDD4L,ATP8B1,ONECUT2,TCF4,HSD17B4,LRP1,SEMA6A,EYA4,STAC3,TBPL1,GLI1,YTHDC2,KIF5A,NHSL1,CYP27B1,ADGRG6,AVIL,MAML1,ATAT1,ESR1,FRS2,CNOT2,RAB21,STK3,OSR2,PRRC2A,MAPK8IP2,SNW1,TIAM2,MPIG6B,HSPA1B,RIMS2,MOV10L1,BRD1,MAP3K4,PRKN,PACRG,QKI,AGER,PPARA,HLA-DRA,FBLN1,PSMB8,IL5,PARVG,PNPLA3,SULT4A1,RXRB,TSPO,GDF9,UQCRQ,ROS1,CEP85L,ASF1A,VPS52,FSTL4,TCF7,SYNGAP1,ANXA13,UBE2B,BAK1,XRCC6,MTSS1,CATSPER3,PITX1,WASHC5,TRIB1,MYC,TOB2,SMAD5,ASAP1,L3MBTL3,OBSCN,LEMD2,H3F3C,GFRA3,PTK2,PTCH1,ANKS1A,FANCC,AKR1B1,ATF4,TUT7,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,UHRF2,CBY1,DMC1,PODXL,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,PI16,MICALL1,PIM1,SPATA31D3,MFNG,RAC2,SMO,ZDHHC21,HSF1,DAAM2,FLNC,MDFI,KCP,TAF8,MYH9,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,PRPH2,FBXO7,RORB,LMOD2,PTK7,SRF,TTBK1,ADAM22,DLK2,YIPF3,CFAP69,FZD1,PGM5,OCIAD1,FANCG,CDK6,SMARCA2,TDRD6,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TFAP2B,ROR2,NFIL3,GADD45G,SEMA4D,DLX5,S1PR3,C1GALT1,NINJ1,CCIN,ETV1,ADGRL3,SEMA4C,SHB,RPS14,TDRD7,SOSTDC1,TMOD1,BEND6,ZNF268,CAT,SVBP,SIX2,FOXJ3,HIVEP3,TMEM190,IL11,BRSK1,SMAP1,TNNI3,EPAS1,RDH13,RIMS1,EPCAM,ABCB5,MSH2,CD109,MBOAT7,TMEM30A,RTN4,PPP2R1A,FPR2,YTHDC1,GSDME,RUFY3,ACP4,SHANK1,HOXA2,HOXA7,CYB5R4,HOXA13,LPAR1,ANKRD17,PPT1,PTBP3,MYCL,SLC46A2,MTURN,AREG,BMP8A,BPGM,AKIRIN1,CNOT4,PLEK,RSAD2,ANXA4,GMCL1,COL27A1,EPHA7,NR1H2,AKNA,	grey	VSMC_M10

GO:0043066	1.00	0.00	305	662	negative regulation of apoptotic process	BP	1	SERPINB2,ERBB3,TNFAIP8,LRP1,EYA4,TNFAIP3,AGAP2,PPP1R10,IER3,MAPK8IP2,HSPA1B,PRKN,PPARA,RGL2,SYNGAP1,UBE2B,MYC,PTK2,AKR1B1,NTRK2,NRBP2,SOX10,PIM1,ZC3HC1,SMO,HSF1,ZNF16,TEK,BAG1,CNTFR,SLC25A27,SLC1A1,FHL2,TFAP2B,SEMA4D,TMEM14A,ZNF268,CAT,DNAJA1,EPCAM,MSH2,PHIP,PPT1,ALB,SLC46A2,AQP1,ANXA4,TGFA,YWHAZ,POU3F3,EGFR,TRIM32,BCL2L12,ATG5,OSR1,NTF4,FGF21,BRAF,HIGD1A,FOXE3,HDAC2,BMI1,NDNF,C5AR1,ARMC10,SOX9,DDIAS,PLK3,GLI2,RAF1,XRCC2,ZFAND6,PRDX3,UBE2O,POU4F1,SPRY2,WNT11,AKT2,ARRB1,CBX4,CHD8,ZMYND11,TCIM,EIF2AK2,PRNP,BAG4,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,NR1H4,APIP,PLK2,HCK,IL1A,GPI,PAX8,NR4A1,FAIM,PIK3R1,CASP3,HIP1R,TAF9,ARHGAP10,GBE1,HAND2,ING2,EYA1,FZD3,MEF2C,NUGGC,IL7,FAIM2,HTRA2,TMBIM6,NDUFS3,CSNK2A2,PTK2B,CIAPIN1,OPA1,NR4A2,AMIGO2,F2R,SRSF6,RIPK1,MARCH7,PIDD1,TXNDC5,TFAP2A,PAX2,ADAMTS20,NOD2,SIRT5,DSTYK,NUAK2,RNF144B,BDNF,SIRT4,RHBDD1,HDAC1,TERT,PDCD4,SLC30A10,GPAM,TCF7L2,DAD1,CFL1,KRAS,DYRK3,FCMR,SNAI1,HCLS1,ADNP,EYA3,IFI6,MCL1,CIB1,CBL,HYOU1,BAG3,SLC9A1,STRADB,SFN,NFATC4,RPS6KA1,PEA15,PELI3,NTSR1,PAFAH2,CD28,WDR73,DLX1,RTKN2,DNAJC5,FZD9,SNX6,CDKN1B,MGMT,YBX3,ADAM8,POR,NFE2L2,IVNS1ABP,NONO,SUPV3L1,BCL6,SYVN1,BCL2A1,CTSH,DDX3X,KLHL20,PDCD10,TNFSF18,CXCR2,WNT4,HTT,PSME3,FKBP8,TNIP2,RAMP2,PINK1,BIRC3,ARAF,CD38,NKX3-2,ARL6IP1,STAT5B,PIM2,PSEN2,DDB1,CLN8,MIEN1,WNK3,MED1,BNIP1,PSEN1,AREL1,MUC1,EFNA1,AC138	grey	VSMC_M10
GO:0006260	1.00	0.00	93	230	DNA replication	BP	1	POLI,GLI1,RPA3,HELB,MCM9,REV1,MCMBP,PPP2R1A,ANKRD17,ORC3,ETAA1,EGFR,LPIN1,SSBP1,FAF1,REV3L,ORC5,GLI2,DACH1,KIN,ZRANB3,FBH1,MGME1,PURA,SIRT7,WRN,PRIMPOL,RAD17,ATR,NOC3L,NUGGC,GINS3,NBN,TOP1,WRNIP1,DONSON,CDK2AP1,NPM2,TWNK,POLL,STN1,RBBP4,IGHMBP2,TBRG1,EGF,ZGRF1,POLG2,POLG,RTF2,ORC2,RECQL,RTEL1,ING5,BCL6,DBF4B,UPF1,ING4,USP37,POLN,DDX11,TSPYL2,EXD2,KAT7,KCTD13,CTC1,EME1,PIF1,RNASEH2A,TIPIN,SIN3A,LIG3,METTL4,NT5M,TNFAIP1,JUN,RMI2,DNAJA3,NFIC,SLX4,WDR18,TTF1,GINS2,TERF2,RPA4,OOEP,ACVRL1,DTD1,REPIN1,HRAS,FAM111A,CENPX,EREG,CINP	grey	VSMC_M10
GO:0030163	1.00	0.00	381	815	protein catabolic process	BP	1	VPS4B,NEDD4L,LRP1,FEM1C,RMND5B,TNFAIP3,AGAP2,USP15,CANX,TRIM39,HSPA1B,PRKN,RNF5,PSMB8,DERL1,SKP1,UBE2B,RNF217,RNF146,TRIB1,KLHL3,PTK2,AGTPBP1,CSNK1E,FOXRED2,FBXL6,USP49,FBXO7,KLHDC3,ABHD17B,DCAF12,USP46,LNX1,RGP1,PDCL3,FBXO10,SEC61B,RNF20,RAD23B,UBE3D,ECPAS,PPT1,XPO1,PELI1,WDR91,CNOT4,FBXO48,EGFR,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,VPS35,ZYG11B,SDCBP,MFSD8,APOB,FAF1,BBS7,RAB7A,FBXL13,PHB,SOX9,NUDT15,FBXL2,KCTD2,PLK3,SUMO2,USP35,KBTBD6,KCTD21,AQP11,DMAC2,TIMP4,EGLN2,MYCBP2,UBXN4,UBE3C,SPOPL,UBE2E1,KLHL40,ARRB1,SNX5,UGGT2,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,TMEM106B,UBAC2,NHLRC3,RNF14,RNF122,NRG1,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,LYPLA1,ERCC8,KCTD6,CEBPA,IDE,ARMC8,SPSB4,RNF7,TAF9,UBE2L6,FBXO8,TRPC4AP,SH3D19,ARNTL,FBXW7,USP25,TRIM2,ENC1,ANAPC5,HTRA2,AUP1,ANAPC7,CHMP4C,CSNK2A2,CTSO,USP16,PTK2B,FAM192A,TMEM67,AMFR,RNFT2,FBXO21,RIPK1,MARCH7,KCNE2,ERLIN1,TTC3,PRICKLE1,NKD1,MYLIP,FBXW4,TOLLIP,SIAH1,LONP2,NHLRC1,FBXL15,RNF144B,SUFU,GPLD1,OTUD7A,AZIN2,FAP,RHBDD1,LPCAT1,RPL23,AMN1,HECW2,SEC22B,TMEM9,LYPLAL1,ADRA2A,PSMD1,KLHL42,TCIRG1,USP30,RNF115,RNF123,PSMB5,GET4,KLHL25,USP13,RNF114,AC013489.1,YOD1,EGF,USP19,HSPA8,OTUD7B,DISC1,SORL1,CHEK2,ASB11,PSME1,DTX3L,ZNRF3,CACUL1,ARIH2,USP2,RNF26,NEDD8,CBL,BAG3,ATE1,CCDC84,UBXN11,PSMD2,RNF215,DEDD,GID8,USP21,VPS37D,RNF185,RNF168,RPL11,PISD,CDKN1B,LRIG2,RHBD	grey	VSMC_M10
GO:0030198	1.00	0.00	102	250	extracellular matrix organization	BP	1	LRP1,C6orf15,SERAC1,ADAMTS19,TNXB,FBLN1,TNFRSF11B,COL11A2,COL14A1,TMPRSS6,COL9A1,HAS1,KLK4,ADAMTS3,PXDN,COL27A1,ST7,NDNF,SOX9,FBLN2,ERCC2,LCP1,CLASP2,CRTAP,FERMT1,SPINT2,COL6A6,COL6A5,LUM,GAS6,TCF15,MMP15,ADAMTS1,TLL2,LOXL2,LOXL4,SPINT1,ADAMTS20,ADTRP,ADAMTS15,ADAMTS8,GAS2,NFKB2,FAP,COL17A1,ELF3,SLC2A10,TGFB2,FBLN5,SULF2,COL16A1,DAG1,LAMB3,ADAMTSL4,AGT,PHLDB1,MMP21,MELTF,EFEMP2,LAMC1,ADAMTSL3,KIF9,ADAM8,PLOD3,COL13A1,MMP11,TNR,SPOCK2,NID2,COL3A1,COL5A2,RAMP2,CTSV,MMP13,MMP3,P3H4,TNFRSF1B,FGFR4,ANXA2,PAPLN,VIPAS39,SMAD3,ADAMTS10,MYH11,ADAMTS12,MMP23B,SERPINF2,VWA1,MMP25,ADAMTS13,COL5A1,NTNG2,FOXF1,ENG,HAS3,CARMIL2,ATXN1L,SERPINB5,DPP4,LAMB1,RGCC,COL8A2	grey	VSMC_M10

GO:0042981	1.00	0.00	522	1092	regulation of apoptotic process	BP	1	MTCH2,NME1,SERPINB2,PHLPP1,ERBB3,GLS2,TNFAIP8,LRP1,EYA4,MAP3K5,TNFAIP3,AGAP2,TRIM39,PPP1R10,ESR1,FRS2,IER3,STK3,MAPK8IP2,HSPA1B,IGF2R,PRKN,PPARA,TSPO,RGL2,SYNGAP1,UBE2B,BAK1,MYC,GRM4,PTK2,AKR1B1,ATF4,NTRK2,TOMM22,NRBP2,SOX10,PIM1,ZC3HC1,SMO,HSF1,IRF5,CDKN2A,ZNF16,TEK,BAG1,CNTFR,SLC25A27,SLC1A1,NCK2,FHL2,TFAP2B,SPTLC1,GADD45G,SEMA4D,TMEM14A,FBXO10,ZNF268,CAT,DNAJA1,EPCAM,MSH2,TFPT,RTN4,PHIP,GSDME,HOXA13,PPT1,ALB,SLC46A2,NOD1,AQP1,ANXA4,EPHA7,TGFA,PTN,KLF11,YWHAZ,POU3F3,EGFR,ING3,TRIM32,TRAF1,BCL2L12,SFRP4,DKKL1,ATG5,SLC7A11,OSR1,FOXO3,NTF4,CDK19,FAF1,FGF21,BRAF,SPHK2,HIGD1A,SPRY1,FOXE3,HDAC2,BMI1,NDNF,C5AR1,ARMC10,PHB,SOX9,ERCC3,DDIAS,PDIA3,PLK3,GLI2,DEDD2,GRIK5,RAF1,XRCC2,ZFAND6,PRDX3,UBE2O,EGLN2,POU4F1,FBH1,SPRY2,CIDEC,WNT11,ALK,AKT2,ARRB1,USP36,CBX4,CHD8,SIRT2,ZMYND11,RARB,TCIM,IDO1,PAWR,SRA1,EIF2AK2,PRNP,DUSP6,BAG4,ARHGEF7,BTG1,RNF122,DDRGK1,SH3RF2,WRN,NCKAP1L,GAS6,RYBP,FOXP1,MITF,ARL6IP5,PRKDC,IRF7,TRAF6,NR1H4,APIP,PLK2,RET,HCK,NSMAF,ZC3H8,IL1A,GPI,PAX8,NR4A1,FAIM,PIK3CB,FOXL2,PIK3R1,CASP3,HIP1R,TAF9,ARHGAP10,GBE1,HAND2,ING2,HPGD,EYA1,DIABLO,FBXW7,TRIM2,FZD3,MEF2C,NUGGC,IL7,FAIM2,HTRA2,TMBIM6,TCTN3,NDUFS3,C3orf38,CSNK2A2,RTKN,MADD,PTK2B,RAPGEF2,CIAPIN1,PNMA2,RIPK2,VDR,NKX3-1,OPA1,NR4A2,AMIGO2,ACVR1C,F2R,SRSF6,NQO2,RIPK1,ANO6,PRDM11,TP53INP1,MARCH7,PIDD1,TXNDC5,PLA2R1,IFIT2,STK4,TFAP2A,PAX2,ADAMTS20,NOD	grey	VSMC_M10
GO:0044249	1.00	0.00	2176	4271	cellular biosynthetic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,NME1,KDSR,ORMDL2,SMARCC2,PAN2,ATP8B1,FECH,ONECUT2,GLS2,BAZ2A,TCF4,POLI,RPS12,SHMT2,ATG12,TBPL1,GLI1,HBS1L,MARS,B4GALT7,PIP4K2C,MAP3K5,PEX7,B4GALNT1,RPA3,TNFAIP3,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,RXYLT1,MAML1,LTC4S,ATP5MGL,HELB,ZBTB2,RMND1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,TFB1M,ZNF706,ALDH7A1,ARID1B,ZDHHC14,HSPA1B,SYNJ2,SERAC1,FZD6,ZBTB12,EIF3E,ALG12,ZBED4,PNLDC1,MAP3K4,AGPAT4,PPT2,PRKN,AGPAT1,QKI,AGER,PPARA,PDE10A,ACSL6,MED30,IL5,BRD2,TAF2,PNPLA3,RXRB,TSPO,MCAT,VGLL2,HSD17B8,MCM9,MRPL13,A4GALT,RPS18,HSF2,TCF7,PHF1,XRCC6,NCOA7,PMM1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,MRPL55,JMJD4,AGO2,HABP4,RPS10,HSD17B3,KDM3B,PTP4A3,PTCH1,TNRC6B,AKR1B1,ATF4,PYCR3,TUT7,MAPK15,RPAP2,CBX7,GTPBP1,MAPK14,CBY1,PLA2G6,KDM4C,SOX10,EIF3L,PIM1,NRF1,TMPRSS6,GPAA1,SMO,ZDHHC21,SNAPC3,BNC2,HSF1,MOCS1,PSAT1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,TAF8,FOXH1,GUCA1B,GPT,IMPDH1,HACD4,LRRC14,MTAP,CDKN2A,ZNF16,RBFOX2,NMRK1,IFT74,BICRAL,LARGE1,POT1,GPR37,RORB,ZNF300,PRDM4,ALDH1A1,CRY1,DMTF1,SRF,ZNF318,NFX1,GNPDA2,CDK14,FZD1,MTERF1,NFXL1,GTPBP2,SLC35B2,NFKBIE,CWH43,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,ADGRF1,ST6GAL2,SRD5A3,UXS1,NCK2,FHL2,TGFBRAP1,MRPS9,TFAP2B,SPTLC1,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,AASDH,PPAT,C1GALT1,CHST10,REV1,PHF14,IPPK,HMGCLL1,ETV1,INPP4A,ZNF135,EXOSC3,RPS14,ZNF154,ME	grey	VSMC_M10
GO:0045839	1.00	0.00	12	46	negative regulation of mitotic nuclear division	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,TOM1L2,PSMG2,DUSP1,NME6,APC	grey	VSMC_M10
GO:0035304	1.00	0.00	23	74	regulation of protein dephosphorylation	BP	1	PPP1R16A,NUAK1,VRK3,SYMPK,IKBKB,NCKAP1L,MFHAS1,CRY2,SPPL3,PPP2R5A,PPP1R2C,HTT,PINK1,TIPRL,BOD1L2,CALM1,PPP4R4,CAMTA1,TSC1,CNEP1R1,DUSP26,PPP1R15A,ARPP19	grey	VSMC_M10
GO:0006796	1.00	0.00	1062	2150	phosphate-containing compound metabolic process	BP	1	NME1,PHLPP1,ERBB3,HSD17B4,LRP1,EYA4,TBPL1,PDE7B,CLK4,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,ATP23,USP15,MAML1,MRNIP,ENPP3,ATP5MGL,ARMT1,GFPT2,STK3,ABHD16A,ADM2,SYNJ2,SERAC1,DPYS,TNXB,MAP3K4,PRRT1,AGPAT4,PPT2,PRKN,AGPAT1,AGER,PPARA,PDE10A,ACSL6,FBLN1,IL5,BRD2,PNPLA3,GDF9,ROS1,SMPDL3A,UBE2B,BAK1,XRCC6,TRIB1,SMAD5,OBSCN,PRXL2C,PTK2,PTP4A3,TAB1,MAPK15,RPAP2,GTPBP1,MAPK14,NTRK2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,PIM1,CKB,GPAA1,HSF1,MOCS1,ADCK5,CCND3,GUCA1B,PPP1R16A,IMPDH1,CDKN2A,ZNF16,NMRK1,CHRNA3,TEK,TRPM6,FBXO7,CRY1,PTK7,GDA,CROT,TTBK1,NUAK1,CDK14,TEC,SLC35B2,CWH43,CDK6,KIT,SLC1A1,PLPP6,SRD5A3,NCK2,SLC25A13,ROR2,SEMA4D,GAPDH,CDK20,PPAT,PDCL3,PTPDC1,WNK2,IPPK,KLHL31,INPP4A,RAB23,CLDN19,PPCS,DNAJA1,PLPPR1,IL11,BRSK1,TMEM246,TMEM86B,PRKCE,PIGF,CD109,MBOAT7,SPTBN1,PPP2R1A,PHIP,FPR2,PPP4R3B,IBTK,ACP4,MOB1B,VRK2,SLC4A4,ME1,NT5E,PPT1,EPGN,AREG,BMP8A,RNGTT,BPGM,BMPER,WDR91,ETAA1,PLEK,RSPO1,AAK1,EPHA7,NR1H2,MBOAT2,TNFSF15,TGFA,ITGB1BP1,DGKI,MET,VRK3,GRB10,YWHAZ,EGFR,ARHGEF5,TLR4,EPHA1,LPIN1,INPP4B,IL15,CCNY,MYLK3,SDCBP,SMPD2,DLD,NTF4,FIG4,AGK,CDK19,FGF21,BRAF,NANP,PRKAR2B,SPHK2,SPRY1,CMPK1,HDAC2,ADCY3,MTMR2,SLC8A2,C5AR1,PIP4K2A,MKNK1,MOB3C,NAPEPLD,PRKD2,HADHA,MYO3A,SELENOI,PHB,ABI1,ENTPD6,SOX9,SYMPK,PPM1N,NUDT15,ABHD5,DLG2,AKR1A1,LACC1,APOC1,MAPRE3,KHK,PLK3,FASTK,NUDT5,LIPE,DHTKD1,RALB,MBD4,PRKAG2,RAF1,OXSR1,PRDX3,TAMM41,SLC22A13,ATP5F1C,XYLB,P	grey	VSMC_M10
GO:0033047	1.00	0.00	10	41	regulation of mitotic sister chromatid segregation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,LCMT1,PSMG2,DUSP1,APC	grey	VSMC_M10
GO:0007052	1.00	0.00	38	109	mitotic spindle organization	BP	1	VPS4B,ZNF207,HSPA1B,SUN2,EFHC1,CHMP2A,CCDC61,CLASP2,PIBF1,PLK2,KIF3B,CHMP2B,CHMP4C,ABRAXAS1,AC112128.1,SBDS,INTS13,TBCE,CHEK2,ABRAXAS2,TOGARAM1,EFHC2,TUBG1,CEP126,KPNB1,RAB11A,CEP192,FSD1,PKD1,MECP2,WRAP73,CHMP1A,PSRC1,GPSM2,RHOA,AURKC,CCSAP,DRG1	grey	VSMC_M10

GO:0009607	1.00	0.00	402	856	response to biotic stimulus	BP	1	CD226,SHMT2,MAP3K5,TNFAIP3,CYP27B1,FUCA2,USP15,TRIM39,RNF5,TSPO,BAK1,FER1L6,XRCC6,TRIB1,CXCL14,PTK2,C6orf106,APOBEC3H,MAPK14,PLA2G6,EXOSC4,SMO,HSF1,IRF5,CDK6,GAPDH,PRDX1,ADH5,SDHAF4,PRKCE,FPR2,GSDME,REL,ANKRD17,CXCL8,NOD1,AKIRIN2,AQP1,PELI1,LYPD8,RSAD2,NR1H2,IL4I1,TRIM32,TLR4,IL15,ATG5,MGST2,PUM2,APOB,CDK19,TRAF3IP2,HDAC2,ZC3HAV1,CSAR1,PTGIR,PHB,CUBN,LACC1,NECTIN2,PVR,OPTN,MLH1,UNC13D,MYD88,DACH1,PRDX3,TIMP4,SLC22A13,IRAK2,THBD,SEC14L1,HNMT,FBH1,RBMS3,IKBKB,NFKBIB,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,NPLOC4,EIF2AK2,DCN,MAVS,AIMP1,HPX,FOXP1,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,HCK,IL1A,IL37,NR4A1,FER,FLNB,OTUD4,CASP3,IRF2,ERAP1,HPGD,PLSCR4,PTPRJ,MEF2C,NUGGC,AUP1,ATG10,PTK2B,RASGRP1,CCL17,EIF2AK4,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTULIN,IFNGR2,WRNIP1,F2RL1,F2R,POLR3D,ABCC2,CHID1,IFIT2,MAPKBP1,HERC5,NOD2,ITGB6,TOLLIP,CD40,GBF1,NFKB2,MX2,RAB7B,MAPKAPK3,CD96,FAP,IFIH1,OASL,HDAC1,HYAL1,RGS1,LCK,HYAL3,BANK1,SP100,CRCP,PDCD4,GPAM,FAM20A,ADARB1,UNC93B1,POLR3C,CFL1,TLR5,NCF1,MAPKAPK2,FABP4,SCN7A,TIFA,ALPK1,YTHDF2,ATG16L1,GPER1,SLAMF8,PARP9,DTX3L,PARP14,IRF9,IFI6,RNF26,FGR,NLRX1,ABCF3,TRAF3IP1,HTRA1,TRIM52,COCH,XPR1,IL10RA,FCER1G,NCF2,PPP2R3C,SETD2,LYZL6,ADAM8,TMCO1,CADM1,FZD5,IVNS1ABP,DUSP10,HMCN1,CDC42EP2,NONO,PRKRA,RTP4,GGT2,VGF,HK1,CPS1,BATF2,IL12A,MAP4K2,DDX3X,COMT,XRCC5,PTPN6,UPF1,PYGL,SLC11A1,LAG3,TNIP2,ALPL,GCH1,MUL1,PLA2G16,BIRC3,CFP,	grey	VSMC_M10
GO:0019080	1.00	0.00	28	86	viral gene expression	BP	1	CANX,SNW1,EIF3L,TRIM32,RSF1,ST6GALNAC2,PCBP2,USF2,MOGS,EIF2AK4,SPCS1,EIF2D,HDAC1,ZNF639,PARP9,POU2F3,USF1,MGAT1,MGAT2,PSMC3,TARDBP,GALNT1,CCL5,MCTS1,JUN,INPP5K,ST6GALNAC4,ST3GAL2	grey	VSMC_M10
GO:0043062	1.00	0.00	102	251	extracellular structure organization	BP	1	LRP1,C6orf15,SERAC1,ADAMTS19,TNXB,FBLN1,TNFRSF11B,COL11A2,COL14A1,TMPRSS6,COL9A1,HAS1,KLK4,ADAMTS3,PXDN,COL27A1,ST7,NDNF,SOX9,FBLN2,ERCC2,LCP1,CLASP2,CRTAP,FERMT1,SPINT2,COL6A6,COL6A5,LUM,GAS6,TCF15,MMP15,ADAMTS1,TLL2,LOXL2,LOXL4,SPINT1,ADAMTS20,ADTRP,ADAMTS15,ADAMTS8,GAS2,NFKB2,FAP,COL17A1,ELF3,SLC2A10,TGFB2,FBLN5,SULF2,COL16A1,DAG1,LAMB3,ADAMTSL4,AGT,PHLDB1,MMP21,MELTF,EFEMP2,LAMC1,ADAMTSL3,KIF9,ADAM8,PLOD3,COL13A1,MMP11,TNR,SPOCK2,NID2,COL3A1,COL5A2,RAMP2,CTSV,MMP13,MMP3,P3H4,TNFRSF1B,FGFR4,ANXA2,PAPLN,VIPAS39,SMAD3,ADAMTS10,MYH11,ADAMTS12,MMP23B,SERPINF2,VWA1,MMP25,ADAMTS13,COL5A1,NTNG2,FOXF1,ENG,HAS3,CARMIL2,ATXN1L,SERPINB5,DPP4,LAMB1,RGCC,COL8A2	grey	VSMC_M10
GO:0032880	1.00	0.00	318	693	regulation of protein localization	BP	1	NEDD4L,LRP1,STX7,STAC3,SLC12A2,PRKN,GOPC,EPB41L2,C6orf106,PTP4A3,PTCH1,MAPK14,CSNK1E,PLA2G6,PICK1,RAC2,SMO,ABHD17B,RFX3,SLC1A1,TFAP2B,RAB23,DNAJA1,PRKCE,TMEM30A,SPTBN1,RTN4,HMGN3,RUFY3,XPO1,BMP8A,TRAPPC12,RSAD2,AAK1,NR1H2,PTN,ITGB1BP1,EGFR,ARHGEF5,TLR4,TCAF2,TRPM4,SLC7A11,DNAJC27,GIPR,LCP1,PLK3,FRMD4A,STAC,LLGL2,RALB,MYCBP2,AKT2,GPD1L,USP36,UBAC2,APBB3,DPH3,SIRT7,FERMT1,CEP290,PRNP,BAG4,MAVS,DDRGK1,GAS6,SIRT3,MFHAS1,SYT9,NSFL1C,NR1H4,LYPLA1,NUP58,TM9SF4,NDUFAF2,FAM3D,IL1A,OSBP,POLR1A,PIK3R1,DCLK2,PLS1,CEP250,ARNTL,CCDC66,FBXW7,SORBS1,PKIA,HTRA2,VEGFC,ZFAND1,CSNK2A2,NUP54,KCNJ11,NNAT,NR1H3,TIAM1,RAB11FIP5,PFKM,SLC8B1,NKX3-1,SPIDR,NKX6-1,RAPGEF3,ACVR1C,F2RL1,F2R,ZBED6,SYCP1,DMTN,ADTRP,GBF1,NHLRC1,BDNF,SUFU,SIRT4,GPLD1,IRS1,CABP1,CD200,DNM1L,PPFIA1,HDAC1,ANKRD13A,PPP3CA,SP100,TERT,CPT1A,SLC9B2,TGFB2,ADRA2A,TCIRG1,TCF7L2,GPR137B,DAG1,TTBK2,SSH1,KCNB1,YOD1,EGF,PFKFB2,HCLS1,HSPA8,OTUD7B,EPB41,HPS4,SORL1,C2CD5,GPER1,PARP9,DTX3L,RAB11FIP2,ARIH2,CIB1,DVL3,BAG3,AP2M1,SFN,PPP2R5A,PER2,STX1A,STX6,LIMK2,UHMK1,GLUL,FZD9,SIDT2,DLG1,LRIG2,SLC16A1,APOD,SETD2,ADAM8,LRRC15,KLF7,CTDSPL2,FZD5,MAPT,FIS1,CEMIP,NMT1,LZTFL1,TTN,DERL3,SEC16B,ZDHHC8,IL12A,ENY2,ABCA12,RABGAP1L,C11orf65,MEPCE,MCU,PDCD10,CNPY4,PPP3CB,PINK1,VCL,CD38,MPC2,ARHGDIG,MAPK1,CHRM1,TMEM30B,GRIPAP1,RAB8A,ATP13A2,CNST,ACTB,MAGED1,PARP1,SYT7,IQSEC2,TBC1D1,RSC1A1,NLGN2,NVL,WNK3,GNL3L,STA	grey	VSMC_M10
GO:0006261	1.00	0.00	50	137	DNA-dependent DNA replication	BP	1	HELB,MCM9,MCMBP,ORC3,ETAA1,SSBP1,REV3L,ORC5,DACH1,ZRANB3,FBH1,MGME1,PURA,SIRT7,WRN,PRIMPOL,ATR,NOC3L,NUGGC,GINS3,NBN,WRNIP1,DONSON,CDK2AP1,TWNK,ZGRF1,POLG2,POLG,RTF2,ORC2,RECQL,RTEL1,BCL6,DBF4B,UPF1,POLN,DDX11,EXD2,KAT7,EME1,TIPIN,LIG3,METTL4,DNAJA3,WDR18,TERF2,RPA4,OOEP,FAM111A,CENPX	grey	VSMC_M10

GO:0044093	1.00	0.00	548	1151	positive regulation of molecular function	BP	1	NME1,ERBB3,LRP1,STAC3,MAP3K5,AGAP2,CYP27B1,TBC1D30,MRNIP,TBC1D9B,ESR1,STK3,TIAM2,HSPA1B,EIF3E,GRAMD4,MAP3K4,PRKN,AGER,FBLN1,IL5,ROS1,DERL1,SKP1,BAK1,XRCC6,MYC,ASAP1,PTK2,TAB1,MAPK15,MAPK14,NTRK2,C6orf89,TBC1D22B,MFNG,SMO,HSF1,CCND3,GUCA1B,ZNF16,CHRNA3,TEK,POT1,SRF,ABCB1,TTBK1,FZD1,KIT,SLC1A1,ADGRF1,ROR2,SEMA4D,TBC1D8,RGP1,WNK2,CAT,SDHAF4,MSH2,FPR2,MOB1B,LPAR1,EPGN,NOD1,AREG,AKIRIN2,CASP8AP2,ETAA1,PLEK,ZNF618,EPHA7,NR1H2,TNFSF15,TGFA,ASAP2,ITGB1BP1,MED25,MET,ADD2,VRK3,EGFR,ARHGEF5,TRIM32,TLR4,EPHA1,TRAF1,TBC1D9,CCNY,MAPRE1,SSBP1,FGF21,HSPE1,DHFR,HDAC2,NAPA,SLC8A2,BMI1,C5AR1,PRKD2,PHB,IQSEC1,ABI1,ABHD5,CACNB2,ERCC2,RSU1,MAPRE3,XRCC1,STAC,EPM2AIP1,RALB,PRKAG2,MYD88,PRDX3,PIBF1,TBC1D4,FOXJ1,IRAK2,POU4F1,SPRY2,WNT11,ALK,AKT2,ARRB1,TGFBR2,IKBKB,TBC1D16,SIRT2,NEK10,RPTOR,TMEM173,TCIM,HBEGF,TMEM106B,PLCL2,DPH3,RASGRP4,CHTOP,EIF2AK2,PRNP,ARHGEF7,MAVS,NRG1,TFDP1,DDRGK1,WRN,NCKAP1L,GAS6,LARS,SIRT3,PPP2CB,ARL6IP5,ERCC6,FLT1,RYK,ST18,ADRA2B,TRAF6,TRIB3,EPHB1,PLK2,RET,ASPH,FER,IDE,PIK3CB,FOXL2,ZFP91,HIP1R,HAND2,ROBO1,GLRX,PCOLCE2,DIABLO,MTMR9,TBC1D12,FBXW7,ORAI1,HMBOX1,MEF2C,HTRA2,VEGFC,XRCC4,ARHGEF26,MADD,PTK2B,RASGRP1,RHEBL1,RAPGEF2,KCNJ11,MAPKAPK5,PRKAG1,CCL17,NR1H3,TIAM1,SERINC5,EBF2,RIPK2,NBN,SENP1,IFNGR2,VDR,NKX3-1,NKX6-1,AMFR,RAPGEF3,NR4A2,ACVR1C,F2RL1,F2R,TESC,ARHGAP24,RIPK1,PIDD1,KCNE2,PKD2,STK4,NPM2,NO	grey	VSMC_M10
GO:0006915	1.00	0.00	696	1436	apoptotic process	BP	1	MTCH2,NME1,SERPINB2,PHLPP1,ERBB3,GLS2,TNFAIP8,LRP1,SEMA6A,EYA4,MAP3K5,TNFAIP3,AGAP2,PLAGL1,TRIM39,PPP1R10,ESR1,FRS2,IER3,STK3,MAPK8IP2,SNW1,HSPA1B,IGF2R,EBAG9,GRAMD4,PRKN,PPARA,TNFRSF11B,TSPO,RGL2,SYNGAP1,UBE2B,BAK1,MYC,GRM4,PTK2,AKR1B1,ATF4,MAPK14,NTRK2,TOMM22,PUF60,NRBP2,PLA2G6,SOX10,PIM1,ZC3HC1,SMO,HSF1,IRF5,CDKN2A,ZNF16,TEK,BAG1,CNTFR,SLC25A27,SLC1A1,FAM32A,TNFRSF21,NCK2,FHL2,TFAP2B,SPTLC1,GADD45G,SEMA4D,GAPDH,TMEM14A,PDCL3,HINT2,FBXO10,SHB,ZNF268,CAT,DNAJA1,PRKCE,EPCAM,MSH2,TFPT,RTN4,PPP2R1A,PHIP,GSDME,HOXA13,PPT1,ALB,SLC46A2,NOD1,GGCT,AQP1,CASP8AP2,WDR92,ANXA4,EPHA7,TNFSF15,TGFA,PTN,KLF11,YWHAZ,POU3F3,EGFR,ING3,TRIM32,TRAF1,BCL2L12,SFRP4,DKKL1,VPS35,ATG5,SLC7A11,OSR1,FOXO3,NTF4,CDK19,FAF1,FGF21,BRAF,BCAP29,TRAF3IP2,SPHK2,CDCA7,HIGD1A,SPRY1,FOXE3,HDAC2,DNMT3A,BMI1,NDNF,C5AR1,ARMC10,PHB,SOX9,TOPAZ1,ERCC2,ERCC3,DDIAS,PDIA3,PLK3,FASTK,MLH1,GLI2,RALB,DEDD2,STEAP3,GRIK5,RAF1,XRCC2,MYD88,ZFAND6,PRDX3,UBE2O,EGLN2,CSRNP1,POU4F1,FBH1,SPRY2,CIDEC,WNT11,ALK,AKT2,ARRB1,TIMM50,TGFBR2,USP36,CBX4,RELT,CHD8,SIRT2,ZMYND11,RARB,TCIM,IDO1,PAWR,SRA1,TMTC4,DPF1,EIF2AK2,PRNP,DUSP6,BAG4,ARHGEF7,BTG1,SEMA3A,UNC5D,RNF122,AIMP1,PDK1,TFDP1,DDRGK1,SH3RF2,WRN,NCKAP1L,GAS6,RYBP,PPP2CB,FOXP1,MITF,TAF10,RASSF7,ARL6IP5,PRKDC,IRF7,ERCC6,TRAF6,NR1H4,APIP,KCNIP3,SLC5A8,TRIB3,PLK2,MAL,RET,HCK,NSMAF,ZC3H8,IL1A,DRAM1,GPI,PAX8,NR4A1,ACVR1B,FAIM,PIK3CB,FOXL2,C19orf12,PIK3R1,CAS	grey	VSMC_M10
GO:0060341	1.00	0.00	309	675	regulation of cellular localization	BP	1	NEDD4L,LRP1,STX7,STAC3,CPSF6,RAB21,PRKN,GOPC,BAK1,EPB41L2,C6orf106,MAPK15,MAPK14,CSNK1E,PLA2G6,RAC2,SMO,ABHD17B,SLC1A1,RAB23,DNAJA1,BRSK1,PRKCE,TMEM30A,SPTBN1,RTN4,HMGN3,RUFY3,XPO1,TRAPPC12,PTN,ITGB1BP1,EGFR,TCAF2,BVES,ATG5,TRPM4,SLC7A11,SPHK2,MTMR2,DNAJC27,TRPC3,IWS1,LCP1,PLK3,STAC,GAB2,RALB,UNC13D,AKT2,GPD1L,USP36,UBAC2,SIRT7,FERMT1,CEP290,PRNP,BAG4,DIAPH1,MAVS,DNAJC13,P2RX2,DDRGK1,GAS6,MFHAS1,NSFL1C,NR1H4,LYPLA1,NUP58,TM9SF4,NDUFAF2,TTL,FER,OSBP,POLR1A,PIK3R1,DCLK2,PLS1,P2RX3,CEP250,CCDC66,FBXW7,SORBS1,PKIA,HTRA2,TMBIM6,P2RX7,ZFAND1,CSNK2A2,NUP54,PTK2B,KCNJ11,TIAM1,RAB11FIP5,SPIDR,RAPGEF3,F2R,TNNC1,ZBED6,PKD2,DMTN,CASQ2,RYR2,FAM173B,GBF1,NHLRC1,MX2,BDNF,SUFU,GPLD1,CABP1,PPFIA1,ANKRD13A,SP100,TERT,PGAP1,SLC9B2,ADRA2A,TCF7L2,GPR137B,DAG1,TTBK2,SSH1,ISCU,KCNB1,YOD1,EGF,HCLS1,TTC21B,OTUD7B,EPB41,UBASH3B,HPS4,SORL1,ANK2,C2CD5,GPER1,PARP9,DTX3L,RAB11FIP2,ARIH2,FGR,CIB1,ATP1A2,DVL3,BAG3,AP2M1,SFN,PPP2R5A,CASQ1,SNX4,NTSR1,KIAA1614,CNIH2,STX6,DNAJC30,LIMK2,UHMK1,NCBP2,GLUL,FZD9,SIDT2,DLG1,LRIG2,APOD,SETD2,CALY,LRRC15,KLF7,CTDSPL2,FZD5,MAPT,FIS1,CEMIP,NMT1,LZTFL1,DERL3,SEC16B,EHD1,ZDHHC8,ENY2,ABCA12,C11orf65,MEPCE,PTPN6,PDCD10,CNPY4,HTT,PPP3CB,PINK1,C12orf4,MPC2,MAPK1,CHRM1,TMEM30B,STX18,GRIPAP1,ATP13A2,CNST,HAP1,ACTB,AKAP8L,MAGED1,PARP1,IQSEC2,RSC1A1,NLGN2,NVL,WNK3,GNL3L,STAC2,NPEPPS,ANXA2,WRAP53,TARDBP,STX4,PSEN1,ITGAM,SYT11,SNX12,NGFR,KAT7,IT	grey	VSMC_M10

GO:0008219	1.00	0.00	773	1587	cell death	BP	1	ADNP2,MTCH2,NME1,SERPINB2,VPS4B,PHLPP1,ERBB3,GLS2,TNFAIP8,LRP1,SEMA6A,EYA4,MAP3K5,TNFAIP3,AGAP2,HEBP2,PLAGL1,TRIM39,PPP1R10,ESR1,FRS2,IER3,STK3,SNCAIP,MAPK8IP2,SNW1,HSPA1B,IGF2R,EBAG9,GRAMD4,PRKN,PACRG,PPARA,TNFRSF11B,TSPO,RGL2,SYNGAP1,UBE2B,BAK1,NCOA7,MYC,GRM4,PTK2,AKR1B1,ATF4,MAPK14,NTRK2,TOMM22,PUF60,NRBP2,PLA2G6,SOX10,PIM1,ZC3HC1,SMO,HSF1,IRF5,CDKN2A,ZNF16,TEK,GPR37,FBXO7,BAG1,CNTFR,SLC25A27,KIT,SLC1A1,FAM32A,TNFRSF21,NCK2,FHL2,TFAP2B,SPTLC1,GADD45G,SEMA4D,GAPDH,TMEM14A,PDCL3,HINT2,NINJ1,CHMP2A,FBXO10,SHB,ZNF268,CAT,DNAJA1,PRKCE,EPCAM,MSH2,TFPT,RTN4,PPP2R1A,PHIP,GSDME,HOXA13,REL,PPT1,ALB,SLC46A2,NOD1,GGCT,AQP1,CASP8AP2,PELI1,WDR92,ANXA4,EPHA7,TNFSF15,TGFA,PTN,KLF11,MET,YWHAZ,POU3F3,EGFR,ING3,TRIM32,TLR4,TRAF1,BCL2L12,SFRP4,DKKL1,VPS35,TEAD2,ATG5,MYCN,SLC7A11,OSR1,FOXO3,NTF4,CDK19,FAF1,FGF21,BRAF,BCAP29,TRAF3IP2,SPHK2,CDCA7,HIGD1A,SPRY1,WISP3,FOXE3,HDAC2,DNMT3A,BMI1,NDNF,C5AR1,ARMC10,PRKD2,PHB,SOX9,TOPAZ1,ZNF746,ERCC2,ERCC3,DDIAS,PDIA3,PLK3,FASTK,OPTN,MLH1,GLI2,RALB,DEDD2,STEAP3,KDM4A,GRIK5,RAF1,XRCC2,MYD88,ZFAND6,PRDX3,UBE2O,EGLN2,CSRNP1,ACER3,POU4F1,FBH1,SPRY2,CIDEC,WNT11,ALK,AKT2,ARRB1,TIMM50,TGFBR2,USP36,CBX4,RELT,CHD8,SIRT2,ZMYND11,RARB,TCIM,IDO1,PAWR,SRA1,TMTC4,DPF1,SLC23A2,EIF2AK2,PRNP,ING1,DUSP6,BAG4,ARHGEF7,BTG1,SPEF1,SEMA3A,UNC5D,RNF122,AIMP1,PDK1,TFDP1,DDRGK1,SH3RF2,WRN,NCKAP1L,GAS6,RYBP,PPP2CB,FOXP1,MITF,TAF10,RASSF7,ARL6	grey	VSMC_M10
GO:0045787	1.00	0.00	99	243	positive regulation of cell cycle	BP	1	VPS4B,PGGT1B,GLI1,YTHDC2,PPP1R10,UBE2B,MAPK15,C6orf89,HSF1,CCND3,ZNF16,PRKCE,PHIP,HOXA13,ANKRD17,EPGN,TGFA,LSM10,EGFR,TRIM32,CCNY,TOPAZ1,MAPRE3,UBE2E2,DYNC1LI1,SIRT2,RPTOR,PLCB1,NUDT16,TFDP1,DDRGK1,MTA3,NSFL1C,TTL,KIF3B,IL1A,CSPP1,SLF1,ANAPC5,ANAPC7,ADAMTS1,NKX3-1,ZBED6,PKD2,SLF2,NPM2,IGF2,HYAL1,CCND1,TERT,TGFB2,DYRK3,EGF,USP19,CHEK2,USP2,TGM1,CD28,CDKN1B,OVOL1,STOX1,DBF4B,DDX3X,MEPCE,WNT4,STAT5B,RHNO1,DDX11,ANAPC4,MED1,RAD51B,SOX15,PAGR1,RAB11A,RAD51C,SFPQ,PSMD10,SIN3A,INSR,CDK5R1,PKD1,HCFC1,MECP2,CDK10,PSRC1,GPSM2,CDC14A,MIR29A,MIR222,RHOA,AURKC,RPS15A,OOEP,FOXG1,WNT5A,SPDYA,BCL2L11,RGCC,EREG	grey	VSMC_M10
GO:0048732	1.00	0.00	142	335	gland development	BP	1	NME1,ONECUT2,GLI1,TNFAIP3,ESR1,FRS2,IGF2R,TSPO,PITX1,ACO2,PTCH1,LY6E,SOX10,SMO,ZDHHC21,SRF,PPAT,SOSTDC1,RTN4,PNPT1,HOXA13,SLC46A2,AREG,TGFA,PTN,MET,TNC,EGFR,PLXNA1,SOX9,GLI2,RAF1,WNT11,AKT2,TGFBR2,SEMA3A,NRG1,CCKBR,TAF10,PRKDC,PLAG1,USF2,LSR,ASXL1,CYP7B1,PAX8,CEBPA,DKK3,HAND2,ROBO1,FBXW7,ORAI1,CSNK2A2,VDR,NKX3-1,RPGRIP1L,RREB1,PKD2,SALL1,JARID2,IGF2,SRD5A1,NEURL1,SLC6A3,ELF3,ALDH1A3,CCND1,CPT1A,TGFB2,SULF2,DAG1,HLX,KRAS,EGF,SOX2,RPS6KA1,LAMA5,EPHB3,HMGCL,SP3,CDKN1B,MGMT,WNT3,HOXD3,CREB1,CPS1,SERPINC1,WNT4,RAP1GAP,TBX19,MAPK1,STAT5B,ZBTB1,BMPR1A,THRA,RBPJ,MED1,ALDH1A2,RPL19,PSEN1,HOXB9,CTC1,MAPK3,ZBTB7B,UPRT,MAP2K1,SMAD3,NTN1,BTBD7,TBX2,BCL11B,STRA6,CSF1R,GATA6,ISL1,LAMA1,TWSG1,PKD1,WDR77,FOXF1,ASS1,ATP2C2,DHODH,ESRP2,ACADM,FSTL3,SERPINB5,MAFB,FADD,HOXB3,NOG,CLDN1,WNT5A,POU3F2,SIX1,BCL2L11,HRAS,CEBPB,NKX2-5,FGF1,WNT2,HOXA3	grey	VSMC_M10
GO:0043207	1.00	0.00	383	820	response to external biotic stimulus	BP	1	CD226,SHMT2,MAP3K5,TNFAIP3,CYP27B1,FUCA2,USP15,TRIM39,RNF5,TSPO,BAK1,FER1L6,XRCC6,TRIB1,CXCL14,PTK2,C6orf106,APOBEC3H,MAPK14,PLA2G6,EXOSC4,HSF1,IRF5,CDK6,GAPDH,PRDX1,ADH5,SDHAF4,PRKCE,FPR2,GSDME,REL,ANKRD17,CXCL8,NOD1,AKIRIN2,AQP1,PELI1,LYPD8,RSAD2,NR1H2,TRIM32,TLR4,IL15,ATG5,MGST2,PUM2,APOB,CDK19,TRAF3IP2,HDAC2,ZC3HAV1,C5AR1,PTGIR,PHB,CUBN,LACC1,NECTIN2,PVR,OPTN,MLH1,UNC13D,MYD88,PRDX3,TIMP4,IRAK2,THBD,SEC14L1,IKBKB,NFKBIB,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,NPLOC4,EIF2AK2,DCN,MAVS,AIMP1,HPX,FOXP1,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,HCK,IL1A,IL37,NR4A1,FER,FLNB,OTUD4,CASP3,IRF2,ERAP1,HPGD,PLSCR4,MEF2C,NUGGC,AUP1,PTK2B,RASGRP1,CCL17,EIF2AK4,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTULIN,IFNGR2,WRNIP1,F2RL1,F2R,POLR3D,ABCC2,CHID1,IFIT2,MAPKBP1,HERC5,NOD2,ITGB6,TOLLIP,CD40,GBF1,NFKB2,MX2,RAB7B,MAPKAPK3,CD96,IFIH1,OASL,HDAC1,HYAL1,RGS1,LCK,HYAL3,BANK1,SP100,CRCP,PDCD4,GPAM,FAM20A,ADARB1,UNC93B1,POLR3C,CFL1,TLR5,NCF1,MAPKAPK2,FABP4,SCN7A,TIFA,ALPK1,YTHDF2,ATG16L1,GPER1,SLAMF8,PARP9,DTX3L,PARP14,IRF9,IFI6,RNF26,FGR,NLRX1,ABCF3,TRAF3IP1,HTRA1,TRIM52,COCH,XPR1,IL10RA,FCER1G,NCF2,PPP2R3C,SETD2,LYZL6,ADAM8,CADM1,FZD5,IVNS1ABP,DUSP10,HMCN1,CDC42EP2,NONO,PRKRA,RTP4,GGT2,VGF,HK1,CPS1,BATF2,IL12A,MAP4K2,DDX3X,COMT,XRCC5,PTPN6,UPF1,PYGL,SLC11A1,LAG3,TNIP2,ALPL,GCH1,MUL1,PLA2G16,BIRC3,CFP,MAPK1,STAT5B,WAS,POLR3A,SGMS1,PIM2,OTUD5,SCGB1A1,CXCL16,FOXP3,R	grey	VSMC_M10

GO:0051707	1.00	0.00	383	820	response to other organism	BP	1	CD226,SHMT2,MAP3K5,TNFAIP3,CYP27B1,FUCA2,USP15,TRIM39,RNF5,TSPO,BAK1,FER1L6,XRCC6,TRIB1,CXCL14,PTK2,C6orf106,APOBEC3H,MAPK14,PLA2G6,EXOSC4,HSF1,IRF5,CDK6,GAPDH,PRDX1,ADH5,SDHAF4,PRKCE,FPR2,GSDME,REL,ANKRD17,CXCL8,NOD1,AKIRIN2,AQP1,PELI1,LYPD8,RSAD2,NR1H2,TRIM32,TLR4,IL15,ATG5,MGST2,PUM2,APOB,CDK19,TRAF3IP2,HDAC2,ZC3HAV1,C5AR1,PTGIR,PHB,CUBN,LACC1,NECTIN2,PVR,OPTN,MLH1,UNC13D,MYD88,PRDX3,TIMP4,IRAK2,THBD,SEC14L1,IKBKB,NFKBIB,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,NPLOC4,EIF2AK2,DCN,MAVS,AIMP1,HPX,FOXP1,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,HCK,IL1A,IL37,NR4A1,FER,FLNB,OTUD4,CASP3,IRF2,ERAP1,HPGD,PLSCR4,MEF2C,NUGGC,AUP1,PTK2B,RASGRP1,CCL17,EIF2AK4,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTULIN,IFNGR2,WRNIP1,F2RL1,F2R,POLR3D,ABCC2,CHID1,IFIT2,MAPKBP1,HERC5,NOD2,ITGB6,TOLLIP,CD40,GBF1,NFKB2,MX2,RAB7B,MAPKAPK3,CD96,IFIH1,OASL,HDAC1,HYAL1,RGS1,LCK,HYAL3,BANK1,SP100,CRCP,PDCD4,GPAM,FAM20A,ADARB1,UNC93B1,POLR3C,CFL1,TLR5,NCF1,MAPKAPK2,FABP4,SCN7A,TIFA,ALPK1,YTHDF2,ATG16L1,GPER1,SLAMF8,PARP9,DTX3L,PARP14,IRF9,IFI6,RNF26,FGR,NLRX1,ABCF3,TRAF3IP1,HTRA1,TRIM52,COCH,XPR1,IL10RA,FCER1G,NCF2,PPP2R3C,SETD2,LYZL6,ADAM8,CADM1,FZD5,IVNS1ABP,DUSP10,HMCN1,CDC42EP2,NONO,PRKRA,RTP4,GGT2,VGF,HK1,CPS1,BATF2,IL12A,MAP4K2,DDX3X,COMT,XRCC5,PTPN6,UPF1,PYGL,SLC11A1,LAG3,TNIP2,ALPL,GCH1,MUL1,PLA2G16,BIRC3,CFP,MAPK1,STAT5B,WAS,POLR3A,SGMS1,PIM2,OTUD5,SCGB1A1,CXCL16,FOXP3,R	grey	VSMC_M10
GO:0048869	1.00	0.00	1513	3033	cellular developmental process	BP	1	ADNP2,NFATC1,NME1,ITGA7,ERBB3,SLC39A5,NEDD4L,ATP8B1,ONECUT2,TCF4,HSD17B4,LRP1,SEMA6A,EYA4,STAC3,TBPL1,GLI1,YTHDC2,KIF5A,MAP3K5,NHSL1,CYP27B1,ADGRG6,AVIL,MAML1,ATAT1,ESR1,FRS2,CNOT2,RAB21,STK3,OSR2,PRRC2A,MAPK8IP2,SNW1,TIAM2,MPIG6B,HSPA1B,RIMS2,MOV10L1,BRD1,MAP3K4,PRKN,PACRG,QKI,AGER,PPARA,HLA-DRA,FBLN1,PSMB8,IL5,PARVG,PNPLA3,SULT4A1,RXRB,TSPO,GDF9,UQCRQ,ROS1,CEP85L,ASF1A,VPS52,FSTL4,TCF7,SYNGAP1,ANXA13,UBE2B,BAK1,XRCC6,MTSS1,CATSPER3,PITX1,WASHC5,TRIB1,MYC,TOB2,SMAD5,ASAP1,L3MBTL3,OBSCN,LEMD2,H3F3C,GFRA3,PTK2,PTCH1,ANKS1A,FANCC,AKR1B1,ATF4,TUT7,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,UHRF2,CBY1,DMC1,PODXL,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,PI16,MICALL1,PIM1,SPATA31D3,MFNG,RAC2,SMO,ZDHHC21,HSF1,DAAM2,FLNC,MDFI,KCP,TAF8,MYH9,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,PRPH2,FBXO7,RORB,LMOD2,PTK7,SRF,TTBK1,ADAM22,DLK2,YIPF3,CFAP69,NUAK1,FZD1,PGM5,OCIAD1,FANCG,CDK6,SMARCA2,TDRD6,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TFAP2B,ROR2,NFIL3,GADD45G,SEMA4D,DLX5,S1PR3,C1GALT1,NINJ1,CCIN,ETV1,ADGRL3,SEMA4C,SHB,RPS14,TDRD7,SOSTDC1,TMOD1,BEND6,ZNF268,CAT,SVBP,SIX2,FOXJ3,HIVEP3,TMEM190,IL11,BRSK1,SMAP1,TNNI3,EPAS1,RDH13,RIMS1,EPCAM,ABCB5,MSH2,CD109,MBOAT7,TMEM30A,RTN4,PPP2R1A,FPR2,YTHDC1,GSDME,PNPT1,RUFY3,ACP4,SHANK1,HOXA2,HOXA7,CYB5R4,HOXA13,LPAR1,ANKRD17,PPT1,PTBP3,MYCL,SLC46A2,MTURN,AREG,BMP8A,MYH14,BPGM,AKIRIN1,CNOT4,PLEK,RSAD2,ANXA4,GMC	grey	VSMC_M10
GO:0033036	1.00	0.00	1166	2356	macromolecule localization	BP	1	ATP9B,TIMM21,MTCH2,VPS4B,NEDD4L,APOF,ATP8B1,CCDC68,STARD6,LRP1,STX7,STAC3,AP3S1,KIF5A,MAP7,PEX7,B4GALNT1,TNFAIP3,AGAP2,PEX3,CANX,TBC1D30,MRNIP,TBC1D9B,PPP1R10,CPSF6,ESR1,RAB21,SNX24,SNX31,CPT1B,PHAX,APOM,ZDHHC14,SLC12A2,SERAC1,RIMS2,SLC27A6,EMC2,PRRT1,PRKN,PACRG,QKI,AGER,PPARA,TAP1,KIF3A,SEPT8,TSPO,GDF9,GOPC,MCM9,VPS52,HSPA4,TBC1D32,DERL1,SKP1,SEPT3,SYNGAP1,FAM91A1,WASHC5,LRRC6,EPB41L2,OBSCN,LEMD2,FAM53C,C6orf106,PTP4A3,PTCH1,TSNARE1,ZC3H3,EXOC4,SIL1,SYNGR1,MAPK15,SUN2,MAPK14,TOMM22,CBY1,CSNK1E,PLA2G6,COPG2,PICK1,MICALL1,MEST,TBC1D22B,RAC2,GPAA1,SMO,ZDHHC21,TSPAN33,TTC39B,HSF1,CNTLN,MDFI,PLIN2,TOMM6,TAF8,MYH9,APOL4,APOL6,LRRC4,PEX6,POT1,FBXO7,CRY1,ABHD17B,CROT,ABCB1,ADAM22,NOL6,XPO5,WASHC4,APBA1,SEPT10,PEX1,NFKBIE,VPS50,SCFD2,RFX3,SLC1A1,TGFBRAP1,TFAP2B,TBC1D8,TRAM2,BICD2,CHMP2A,EXOSC3,RAB23,ABCG5,SVBP,ABCG8,LRPPRC,SEC61B,STX17,SIX2,DNAJA1,PRKCE,RIMS1,MSH2,TMEM30A,DNAH11,ASB3,SPTBN1,IGF2BP3,RTN4,HMGN3,YTHDC1,PNPT1,RUFY3,SHANK1,CYB5R4,EMC10,PPT1,SNX14,XPO1,SNX30,BMP8A,RRAGD,EHBP1,AFTPH,CEP68,TRAPPC12,PLEK,RSAD2,AAK1,NR1H2,WHRN,PTN,ITGB1BP1,YWHAZ,SEC61G,EGFR,FUZ,ARHGEF5,TLR4,TCAF2,VPS41,TBC1D9,VPS35,SDCBP,MGARP,TRPM4,SLC7A11,MAPRE1,LIN7B,LDAH,EPS15,TULP2,APOB,AGK,FAF1,BRAF,BCAP29,MFSD2B,TRAF3IP2,ANKRD50,TTC26,DNAJC27,NAPA,KPTN,BBS7,RAB7A,PIP4K2A,AP2S1,RAB10,COPG1,KPNA3,SOX9,GIPR,ARL5B,ABHD5,CACNB2,IWS1,LCP1,ERCC3,SYTL2,COG1,CLASP2,	grey	VSMC_M10
GO:0030071	1.00	0.00	15	55	regulation of mitotic metaphase/anaphase transition	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,ANAPC5,ANAPC7,HECW2,ANAPC4,LCMT1,PSMG2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0044784	1.00	0.00	17	60	metaphase/anaphase transition of cell cycle	BP	1	ZNF207,MAPK15,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,ANAPC5,ANAPC7,HECW2,ANAPC4,LCMT1,PSMG2,DUSP1,APC,CDC26	grey	VSMC_M10

GO:0014070	1.00	0.00	322	703	response to organic cyclic compound	BP	1	NME1,FECH,CYP27B1,ESR1,CNOT2,TPH2,SNW1,PRKN,PPARA,TAF2,PNPLA3,RXRB,TSPO,BAK1,SMAD5,PTCH1,ATF4,KDM4C,SOX10,PIM1,SMO,TXN2,HSF1,PLIN2,FOXH1,MTAP,RBFOX2,TEK,CRY1,GABRA1,SLC1A1,CA9,CAT,DNAJA1,PRKCE,PNPT1,AREG,AQP1,PELI1,PTN,FOXP2,TNC,EGFR,IL15,VPS35,MGARP,TRPM4,SLC7A11,FOXO3,PGRMC2,APOB,PRKAR2B,DHFR,HDAC2,ADCY3,TRPC3,DNMT3A,BMI1,PANX1,SLC26A5,PHB,GLB1,GLI2,RALB,MBD4,ATP1A3,KLF5,EGLN2,AANAT,THBD,HNMT,POU4F1,ALK,TADA3,ABCC4,TGFBR2,SIRT2,TMEM173,RYR1,CRLS1,DUSP6,TAF7,LUM,DIAPH1,MAVS,RNF14,P2RX2,DDRGK1,FOXP1,ARL6IP5,CALCOCO1,NCOA4,NR1H4,CYP7A1,HTR7,FAM107A,CYP7B1,DNMT3B,GPI,CEBPA,UFSP2,CASP3,NCOA2,CCDC62,HPGD,P2RX3,ZNF366,CHRM5,RYR3,ARNTL,GPD1,MEF2C,P2RX7,CNOT1,MMP15,P2RY1,PTK2B,KMT2D,RAPGEF2,KCNJ11,NR1H3,TIAM1,LCOR,RIPK2,DDX54,HOMER1,VDR,STC1,NKX3-1,OPA1,SPIDR,RAPGEF3,CHRM4,CRY2,VPS18,ABCC2,SPP1,CPN1,PKD2,DMTN,CASQ2,ADTRP,NOD2,DTNBP1,CHRM3,CD40,LONP2,RYR2,GRM2,ADCY2,GPLD1,SRD5A1,IFIH1,DNM1L,SLC6A3,HDAC1,CCND1,CPT1A,TGFB2,RFTN2,CHKA,DAG1,SSH1,KRAS,ABHD2,GRAMD1B,GPER1,CHEK2,AGT,NEDD8,CBL,ATP1A2,SLC9A1,ARID1A,PEA15,NPAS4,HOMER2,CDKN1B,MGMT,RXRG,SLC16A1,CALY,HTR3B,RAP1B,DUOX1,FIS1,GGT2,VGF,CPS1,ACSBG1,FDX1,COMT,ESRRA,BCHE,GPBAR1,RPL27,ANXA7,ALPL,RAMP2,CTSV,MUL1,STAT3,PTPRN,CD38,MAPK1,CHRM1,SLC3A2,STAT5B,GNB5,NSG1,PADI2,SCGB1A1,DNAAF4,FOXP3,ACTB,PARP1,EPHX1,SDK1,MED1,ALDH1A2,DGKQ,HRH2,OSBPL7,PKLR,HCN3,PA	grey	VSMC_M10
GO:0042221	1.00	0.00	1460	2921	response to chemical	BP	1	ADNP2,ZNF236,NME1,VPS4B,SLC39A5,NEDD4L,FECH,ONECUT2,ARPC3,RNMT,LRP1,SEMA6A,SHMT2,AP3S1,PGGT1B,YTHDC2,MARS,KIF5A,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,CANX,LTC4S,ESR1,FRS2,GFPT2,CNOT2,TPH2,RIDA,SNW1,APOM,SLC12A2,HSPA1B,IGF2R,PRKN,PACRG,AGPAT1,RNF5,AGER,PPARA,GPSM3,TNFRSF11B,IL5,TAF2,PNPLA3,RXRB,TSPO,GDF9,HSPA4,DERL1,TCF7,TNFRSF13C,UBE2B,BAK1,XRCC6,NCOA7,PMM1,TRIB1,CXCL14,MYC,SMAD5,LEMD2,PRXL2C,GFRA3,PTK2,ERCC6L2,KDM3B,PTP4A3,PTCH1,FANCC,LY6E,AKR1B1,ATF4,TAB1,SYNGR1,PLXNA4,MAPK14,NTRK2,MAPK13,CPNE5,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,MICALL1,PIM1,RAC2,SMO,FOXRED2,TXN2,HSF1,PLIN2,IRF5,KCP,CCND3,FOXH1,GPT,MTAP,ZNF16,RBFOX2,CHRNA3,TEK,CHRNA5,TRPM6,GPR37,FBXO7,RORB,ALDH1A1,CRY1,PTK7,SRF,ABCB1,STEAP2,CFAP69,GABRA1,FZD1,CNTFR,TXNRD1,CCL27,USP46,KIT,SLC1A1,CA9,TNFRSF21,NCK2,FHL2,TGFBRAP1,PLGRKT,ERMP1,IL1R2,TFAP2B,SLC25A13,ROR2,NFIL3,SEMA4D,GAPDH,DLX5,PPAT,NINJ1,PRDX1,ETV1,ADH5,SEMA4C,SOSTDC1,ABCG5,CAT,ABCG8,ALG2,SEC61B,ERP44,DNAJA1,PRKCE,EPAS1,CD109,PPP2R1A,RAD23B,PHIP,FPR2,HMGN3,HAS1,GSDME,PNPT1,SHANK1,VRK2,ME1,HOXA2,ADAMTS3,CYB5R4,HOXA13,LPAR1,REL,ECPAS,ALB,CXCL8,XPO1,NOD1,AREG,AKIRIN2,BMP8A,CRHR2,AQP1,RRAGD,PELI1,BMPER,AKIRIN1,HERPUD2,PXDN,BSPRY,MTF1,ZNF277,EPHA7,NR1H2,TGFA,PTN,ITGB1BP1,FOXP2,DDC,KLF11,MET,GRB10,TNC,EGFR,LANCL2,TSPAN12,FUZ,TRIM32,TLR4,EPHA1,TRAF1,GAB1,LPIN1,IL15,SFRP4,MYLK3,UCP1,VPS35,TEAD2,ATG5,MGST2,SETD7,SDCBP,NRCAM,MGARP,TRPM4,SL	grey	VSMC_M10
GO:0010595	1.00	0.00	36	105	positive regulation of endothelial cell migration	BP	1	TEK,EMC10,ITGB1BP1,MET,PRKD2,RIN2,FOXP1,PLK2,GPI,PIK3CB,ATP5F1A,VEGFC,PTK2B,HDAC7,CD40,GPLD1,PDCD6,EGF,AGT,CIB1,MAP3K3,NFE2L2,RHOJ,FGF18,BCAS3,PDPK1,LCN2,MIR29A,MIR199A1,MIR21,MIR23A,MIR27B,MIR27A,ZNF580,WNT5A,FGF1	grey	VSMC_M10
GO:0043067	1.00	0.00	533	1119	regulation of programmed cell death	BP	1	MTCH2,NME1,SERPINB2,PHLPP1,ERBB3,GLS2,TNFAIP8,LRP1,EYA4,MAP3K5,TNFAIP3,AGAP2,TRIM39,PPP1R10,ESR1,FRS2,IER3,STK3,MAPK8IP2,HSPA1B,IGF2R,PRKN,PPARA,TSPO,RGL2,SYNGAP1,UBE2B,BAK1,MYC,GRM4,PTK2,AKR1B1,ATF4,NTRK2,TOMM22,NRBP2,SOX10,PIM1,ZC3HC1,SMO,HSF1,IRF5,CDKN2A,ZNF16,TEK,BAG1,CNTFR,SLC25A27,KIT,SLC1A1,NCK2,FHL2,TFAP2B,SPTLC1,GADD45G,SEMA4D,TMEM14A,FBXO10,ZNF268,CAT,DNAJA1,EPCAM,MSH2,TFPT,RTN4,PHIP,GSDME,HOXA13,PPT1,ALB,SLC46A2,NOD1,AQP1,PELI1,ANXA4,EPHA7,TGFA,PTN,KLF11,MET,YWHAZ,POU3F3,EGFR,ING3,TRIM32,TRAF1,BCL2L12,SFRP4,DKKL1,ATG5,SLC7A11,OSR1,FOXO3,NTF4,CDK19,FAF1,FGF21,BRAF,SPHK2,HIGD1A,SPRY1,FOXE3,HDAC2,BMI1,NDNF,C5AR1,ARMC10,PHB,SOX9,ERCC3,DDIAS,PDIA3,PLK3,GLI2,DEDD2,GRIK5,RAF1,XRCC2,ZFAND6,PRDX3,UBE2O,EGLN2,ACER3,POU4F1,FBH1,SPRY2,CIDEC,WNT11,ALK,AKT2,ARRB1,USP36,CBX4,CHD8,SIRT2,ZMYND11,RARB,TCIM,IDO1,PAWR,SRA1,EIF2AK2,PRNP,DUSP6,BAG4,ARHGEF7,BTG1,RNF122,DDRGK1,SH3RF2,WRN,NCKAP1L,GAS6,RYBP,FOXP1,MITF,ARL6IP5,PRKDC,IRF7,TRAF6,NR1H4,APIP,PLK2,RET,HCK,NSMAF,ASAH1,ZC3H8,IL1A,GPI,PAX8,NR4A1,FAIM,PIK3CB,FOXL2,PIK3R1,CASP3,HIP1R,TAF9,ARHGAP10,GBE1,HAND2,ING2,HPGD,EYA1,DIABLO,FBXW7,TRIM2,FZD3,MEF2C,NUGGC,IL7,FAIM2,HTRA2,TMBIM6,TCTN3,NDUFS3,C3orf38,CSNK2A2,RTKN,MADD,PTK2B,RAPGEF2,CIAPIN1,PNMA2,RIPK2,VDR,NKX3-1,OPA1,NR4A2,AMIGO2,ACVR1C,F2RL1,F2R,SRSF6,NQO2,RIPK1,ANO6,PRDM11,TP53INP1,MARCH7,PIDD1,TXNDC5,PLA2R1,IFIT2,STK4,TFAP2A,PAX2,ADAMTS	grey	VSMC_M10

GO:0019220	1.00	0.00	507	1074	regulation of phosphate metabolic process	BP	1	ERBB3,LRP1,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,TNXB,MAP3K4,PRKN,AGER,PPARA,FBLN1,IL5,GDF9,ROS1,UBE2B,BAK1,XRCC6,TRIB1,PRXL2C,PTK2,TAB1,NTRK2,STK38,PLA2G6,HSF1,CCND3,GUCA1B,PPP1R16A,CDKN2A,ZNF16,CHRNA3,TEK,FBXO7,TTBK1,NUAK1,TEC,KIT,SLC1A1,NCK2,ROR2,SEMA4D,PDCL3,KLHL31,CLDN19,DNAJA1,IL11,PRKCE,CD109,PPP2R1A,PHIP,FPR2,IBTK,ACP4,MOB1B,SLC4A4,EPGN,AREG,BMP8A,BMPER,WDR91,ETAA1,PLEK,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,GRB10,EGFR,ARHGEF5,TLR4,EPHA1,LPIN1,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,PRKAR2B,SPHK2,SPRY1,HDAC2,MTMR2,SLC8A2,C5AR1,PIP4K2A,MOB3C,PRKD2,PHB,ABI1,SOX9,SYMPK,LACC1,APOC1,MAPRE3,RALB,PRKAG2,RAF1,PRDX3,PIBF1,GCKR,FBH1,SPRY2,WNT11,ALK,TADA3,AKT2,GPD1L,ARRB1,TGFBR2,ACVR2A,IKBKB,SIRT2,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,PLCL2,PRNP,DUSP6,BAG4,TAF7,MAVS,PDK1,NRG1,CCKBR,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,PRKDC,ERCC6,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,NR1H4,TRIB3,EPHB1,RET,ACVR1B,CEBPA,FER,PIK3CB,SNX25,OSBP,PIK3R1,ZFP91,CDK7,CASP3,RAD17,ROBO1,PLCE1,CHRM5,MTMR9,FBXW7,PTPRJ,GPD1,MEF2C,PKIA,IL7,CCNH,P2RX7,VEGFC,CCNJ,SLA2,MCPH1,P2RY1,MADD,PTK2B,RASGRP1,CCNG2,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,PAQR3,FGF5,NLRC5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CRY2,CCNJL,CDK2AP1,PKD2,STK4,DBNDD2,DMTN,ADTRP,HERC5,NOD2,CNTN1,DTNBP1,TAOK3,CD40,DSTYK,ROPN1L,LDB1,FAM173B,IGF2,BMPR1B,NHLRC1,BDNF,GPLD1,IRS1,NEURL1,SPPL3,LPCAT1,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K	grey	VSMC_M10
GO:0051174	1.00	0.00	507	1074	regulation of phosphorus metabolic process	BP	1	ERBB3,LRP1,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,TNXB,MAP3K4,PRKN,AGER,PPARA,FBLN1,IL5,GDF9,ROS1,UBE2B,BAK1,XRCC6,TRIB1,PRXL2C,PTK2,TAB1,NTRK2,STK38,PLA2G6,HSF1,CCND3,GUCA1B,PPP1R16A,CDKN2A,ZNF16,CHRNA3,TEK,FBXO7,TTBK1,NUAK1,TEC,KIT,SLC1A1,NCK2,ROR2,SEMA4D,PDCL3,KLHL31,CLDN19,DNAJA1,IL11,PRKCE,CD109,PPP2R1A,PHIP,FPR2,IBTK,ACP4,MOB1B,SLC4A4,EPGN,AREG,BMP8A,BMPER,WDR91,ETAA1,PLEK,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,GRB10,EGFR,ARHGEF5,TLR4,EPHA1,LPIN1,IL15,CCNY,SDCBP,NTF4,FGF21,BRAF,PRKAR2B,SPHK2,SPRY1,HDAC2,MTMR2,SLC8A2,C5AR1,PIP4K2A,MOB3C,PRKD2,PHB,ABI1,SOX9,SYMPK,LACC1,APOC1,MAPRE3,RALB,PRKAG2,RAF1,PRDX3,PIBF1,GCKR,FBH1,SPRY2,WNT11,ALK,TADA3,AKT2,GPD1L,ARRB1,TGFBR2,ACVR2A,IKBKB,SIRT2,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,PLCL2,PRNP,DUSP6,BAG4,TAF7,MAVS,PDK1,NRG1,CCKBR,DDRGK1,NCKAP1L,GAS6,HPX,RBPMS,PRKDC,ERCC6,MFHAS1,FLT1,RYK,ADRA2B,TRAF6,NR1H4,TRIB3,EPHB1,RET,ACVR1B,CEBPA,FER,PIK3CB,SNX25,OSBP,PIK3R1,ZFP91,CDK7,CASP3,RAD17,ROBO1,PLCE1,CHRM5,MTMR9,FBXW7,PTPRJ,GPD1,MEF2C,PKIA,IL7,CCNH,P2RX7,VEGFC,CCNJ,SLA2,MCPH1,P2RY1,MADD,PTK2B,RASGRP1,CCNG2,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,PAQR3,FGF5,NLRC5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CRY2,CCNJL,CDK2AP1,PKD2,STK4,DBNDD2,DMTN,ADTRP,HERC5,NOD2,CNTN1,DTNBP1,TAOK3,CD40,DSTYK,ROPN1L,LDB1,FAM173B,IGF2,BMPR1B,NHLRC1,BDNF,GPLD1,IRS1,NEURL1,SPPL3,LPCAT1,LRRK1,HDAC1,BANK1,CCND1,CAPRIN2,MAP2K	grey	VSMC_M10
GO:0043069	1.00	0.00	312	681	negative regulation of programmed cell death	BP	1	SERPINB2,ERBB3,TNFAIP8,LRP1,EYA4,TNFAIP3,AGAP2,PPP1R10,IER3,MAPK8IP2,HSPA1B,PRKN,PPARA,RGL2,SYNGAP1,UBE2B,MYC,PTK2,AKR1B1,NTRK2,NRBP2,SOX10,PIM1,ZC3HC1,SMO,HSF1,ZNF16,TEK,BAG1,CNTFR,SLC25A27,KIT,SLC1A1,FHL2,TFAP2B,SEMA4D,TMEM14A,ZNF268,CAT,DNAJA1,EPCAM,MSH2,PHIP,PPT1,ALB,SLC46A2,AQP1,PELI1,ANXA4,TGFA,MET,YWHAZ,POU3F3,EGFR,TRIM32,BCL2L12,ATG5,OSR1,NTF4,FGF21,BRAF,HIGD1A,FOXE3,HDAC2,BMI1,NDNF,C5AR1,ARMC10,SOX9,DDIAS,PLK3,GLI2,RAF1,XRCC2,ZFAND6,PRDX3,UBE2O,POU4F1,SPRY2,WNT11,AKT2,ARRB1,CBX4,CHD8,ZMYND11,TCIM,EIF2AK2,PRNP,BAG4,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,PRKDC,IRF7,NR1H4,APIP,PLK2,HCK,IL1A,GPI,PAX8,NR4A1,FAIM,PIK3R1,CASP3,HIP1R,TAF9,ARHGAP10,GBE1,HAND2,ING2,EYA1,FZD3,MEF2C,NUGGC,IL7,FAIM2,HTRA2,TMBIM6,NDUFS3,CSNK2A2,PTK2B,CIAPIN1,OPA1,NR4A2,AMIGO2,F2R,SRSF6,RIPK1,MARCH7,PIDD1,TXNDC5,TFAP2A,PAX2,ADAMTS20,NOD2,SIRT5,DSTYK,NUAK2,RNF144B,BDNF,SIRT4,RHBDD1,HDAC1,TERT,PDCD4,SLC30A10,GPAM,TCF7L2,DAD1,CFL1,KRAS,DYRK3,FCMR,SNAI1,HCLS1,ADNP,EYA3,IFI6,MCL1,CIB1,CBL,HYOU1,BAG3,SLC9A1,STRADB,SFN,NFATC4,RPS6KA1,PEA15,PELI3,NTSR1,PAFAH2,CD28,WDR73,DLX1,RTKN2,DNAJC5,FZD9,SNX6,CDKN1B,MGMT,YBX3,ADAM8,POR,NFE2L2,IVNS1ABP,NONO,SUPV3L1,BCL6,SYVN1,BCL2A1,CTSH,DDX3X,KLHL20,PDCD10,TNFSF18,CXCR2,WNT4,HTT,PSME3,FKBP8,TNIP2,RAMP2,PINK1,BIRC3,ARAF,CD38,NKX3-2,ARL6IP1,STAT5B,PIM2,PSEN2,DDB1,CLN8,MIEN1,WNK3,MED1,BNIP1,PSEN1,AREL1,MUC1,EFNA1,AC138	grey	VSMC_M10

GO:0042326	1.00	0.00	130	311	negative regulation of phosphorylation	BP	1	LRP1,PIP4K2C,TNFAIP3,PRKN,PPARA,FBLN1,UBE2B,BAK1,TRIB1,STK38,CDKN2A,FBXO7,NCK2,SEMA4D,KLHL31,DNAJA1,CD109,PPP2R1A,IBTK,ACP4,ITGB1BP1,GRB10,EPHA1,PRKAR2B,SPRY1,PIP4K2A,PRKAG2,PRDX3,PIBF1,GCKR,SPRY2,GPD1L,ARRB1,SIRT2,PTPRQ,PRNP,DUSP6,TAF7,PRKDC,TRIB3,CEBPA,PIK3CB,SNX25,CASP3,PTPRJ,PKIA,PAQR3,DBNDD2,DMTN,DTNBP1,LRRK1,PDCD4,PRKAR1A,ADARB1,AJUBA,FABP4,UBASH3B,SORL1,RTRAF,PARP14,AGT,CIB1,CBL,SFN,PPP2R5A,TRAF3IP1,ACTN3,HDAC4,CAMK2N2,RUBCN,PTPRO,INPP5J,MLXIPL,PIK3IP1,SNX6,CDKN1B,AIDA,YWHAG,DUSP10,MAPT,HEXIM2,MEN1,DNAJC10,DUSP19,PTPN6,FKBP8,ZFYVE28,SOCS4,STAT3,INHA,RGS14,DGKQ,TARDBP,PSEN1,PYDC1,COX11,CALM1,BDKRB1,NCOR1,SMCR8,SUZ12,PTPN2,SOCS1,INPP5K,PDPK1,PRKCZ,PARK7,DBNDD1,PIP5KL1,ENG,DAB2IP,MIR27B,MIR24-1,DMD,MIR125A,IMPACT,NOG,SMYD3,THY1,TIGAR,GADD45A,DUSP26,DUSP1,APC,DUSP22,LAX1,CADM4,LDLRAD4,PARD6A,PRKRIP1	grey	VSMC_M10
GO:0051348	1.00	0.00	87	219	negative regulation of transferase activity	BP	1	PIP4K2C,TNFAIP3,PRKN,TRIB1,STK38,CDKN2A,POT1,FBXO7,DNAJA1,IBTK,ACP4,ITGB1BP1,EPHA1,PRKAR2B,SPRY1,PIP4K2A,PRKAG2,PRDX3,GCKR,SPRY2,PTPRQ,TAF7,USP44,TRIB3,CEBPA,PIK3CB,CASP3,PTPRJ,PKIA,PAQR3,DBNDD2,DTNBP1,RPL23,PDCD4,PRKAR1A,ADARB1,AJUBA,FABP4,UBASH3B,SORL1,RTRAF,DTX3L,AGT,CBL,SFN,PPP2R5A,CAMK2N2,RUBCN,PTPRO,PIK3IP1,RPL11,SNX6,CDKN1B,AIDA,YWHAG,DUSP10,MAPT,HEXIM2,MEN1,DUSP19,PTPN6,ZFYVE28,SOCS4,RGS14,PSEN1,PYDC1,PIF1,COX11,SMCR8,PTPN2,INPP5K,PDPK1,PARK7,DBNDD1,DAB2IP,MIR24-1,BAG2,SMYD3,THY1,TEN1,GADD45A,DUSP26,DUSP1,APC,DUSP22,LAX1,PRKRIP1	grey	VSMC_M10
GO:0006793	1.00	0.00	1068	2169	phosphorus metabolic process	BP	1	NME1,PHLPP1,ERBB3,HSD17B4,LRP1,EYA4,TBPL1,PDE7B,CLK4,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,ATP23,USP15,MAML1,MRNIP,ENPP3,ATP5MGL,ARMT1,GFPT2,STK3,ABHD16A,ADM2,SYNJ2,SERAC1,DPYS,TNXB,MAP3K4,PRRT1,AGPAT4,PPT2,PRKN,AGPAT1,AGER,PPARA,PDE10A,ACSL6,FBLN1,IL5,BRD2,PNPLA3,GDF9,ROS1,SMPDL3A,UBE2B,BAK1,XRCC6,TRIB1,SMAD5,OBSCN,PRXL2C,PTK2,PTP4A3,TAB1,MAPK15,RPAP2,GTPBP1,MAPK14,NTRK2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,PIM1,CKB,GPAA1,HSF1,MOCS1,ADCK5,CCND3,GUCA1B,PPP1R16A,IMPDH1,CDKN2A,ZNF16,NMRK1,CHRNA3,TEK,TRPM6,FBXO7,CRY1,PTK7,GDA,CROT,TTBK1,GNPDA2,NUAK1,CDK14,TEC,GALT,SLC35B2,CWH43,CDK6,KIT,SLC1A1,PLPP6,SRD5A3,UXS1,NCK2,SLC25A13,ROR2,SEMA4D,GAPDH,CDK20,PPAT,PDCL3,PTPDC1,WNK2,IPPK,KLHL31,INPP4A,RAB23,CLDN19,PPCS,DNAJA1,PLPPR1,IL11,BRSK1,TMEM246,TMEM86B,PRKCE,PIGF,CD109,MBOAT7,SPTBN1,PPP2R1A,PHIP,FPR2,PPP4R3B,IBTK,ACP4,MOB1B,VRK2,SLC4A4,ME1,NT5E,PPT1,EPGN,AREG,BMP8A,RNGTT,BPGM,BMPER,WDR91,ETAA1,PLEK,RSPO1,AAK1,EPHA7,NR1H2,MBOAT2,TNFSF15,TGFA,ITGB1BP1,DGKI,MET,VRK3,GRB10,YWHAZ,EGFR,ARHGEF5,TLR4,EPHA1,LPIN1,INPP4B,IL15,CCNY,MYLK3,SDCBP,SMPD2,DLD,NTF4,FIG4,AGK,CDK19,FGF21,BRAF,NANP,PRKAR2B,SPHK2,SPRY1,CMPK1,HDAC2,ADCY3,MTMR2,SLC8A2,C5AR1,PIP4K2A,MKNK1,MOB3C,NAPEPLD,PRKD2,HADHA,MYO3A,SELENOI,PHB,ABI1,ENTPD6,SOX9,SYMPK,PPM1N,NUDT15,ABHD5,DLG2,AKR1A1,LACC1,APOC1,MAPRE3,KHK,PLK3,FASTK,NUDT5,LIPE,DHTKD1,RALB,MBD4,PRKAG2,RAF1,OXSR1,PRDX3,TAMM41,SLC22A	grey	VSMC_M10
GO:0051304	1.00	0.00	27	85	chromosome separation	BP	1	ZNF207,MAPK15,CDK5RAP2,MLH1,DYNC1LI1,ANAPC15,IK,USP44,MOS,ANAPC5,M1AP,ANAPC7,CSNK2A2,HECW2,DIS3L2,ANAPC4,EME1,LCMT1,ERCC4,PSMG2,SLX4,MEIOB,MSH4,DUSP1,APC,CDC26,CENPX	grey	VSMC_M10
GO:0012501	1.00	0.00	713	1474	programmed cell death	BP	1	MTCH2,NME1,SERPINB2,PHLPP1,ERBB3,GLS2,TNFAIP8,LRP1,SEMA6A,EYA4,MAP3K5,TNFAIP3,AGAP2,PLAGL1,TRIM39,PPP1R10,ESR1,FRS2,IER3,STK3,MAPK8IP2,SNW1,HSPA1B,IGF2R,EBAG9,GRAMD4,PRKN,PPARA,TNFRSF11B,TSPO,RGL2,SYNGAP1,UBE2B,BAK1,MYC,GRM4,PTK2,AKR1B1,ATF4,MAPK14,NTRK2,TOMM22,PUF60,NRBP2,PLA2G6,SOX10,PIM1,ZC3HC1,SMO,HSF1,IRF5,CDKN2A,ZNF16,TEK,BAG1,CNTFR,SLC25A27,KIT,SLC1A1,FAM32A,TNFRSF21,NCK2,FHL2,TFAP2B,SPTLC1,GADD45G,SEMA4D,GAPDH,TMEM14A,PDCL3,HINT2,NINJ1,FBXO10,SHB,ZNF268,CAT,DNAJA1,PRKCE,EPCAM,MSH2,TFPT,RTN4,PPP2R1A,PHIP,GSDME,HOXA13,PPT1,ALB,SLC46A2,NOD1,GGCT,AQP1,CASP8AP2,PELI1,WDR92,ANXA4,EPHA7,TNFSF15,TGFA,PTN,KLF11,MET,YWHAZ,POU3F3,EGFR,ING3,TRIM32,TRAF1,BCL2L12,SFRP4,DKKL1,VPS35,ATG5,SLC7A11,OSR1,FOXO3,NTF4,CDK19,FAF1,FGF21,BRAF,BCAP29,TRAF3IP2,SPHK2,CDCA7,HIGD1A,SPRY1,FOXE3,HDAC2,DNMT3A,BMI1,NDNF,C5AR1,ARMC10,PHB,SOX9,TOPAZ1,ERCC2,ERCC3,DDIAS,PDIA3,PLK3,FASTK,MLH1,GLI2,RALB,DEDD2,STEAP3,GRIK5,RAF1,XRCC2,MYD88,ZFAND6,PRDX3,UBE2O,EGLN2,CSRNP1,ACER3,POU4F1,FBH1,SPRY2,CIDEC,WNT11,ALK,AKT2,ARRB1,TIMM50,TGFBR2,USP36,CBX4,RELT,CHD8,SIRT2,ZMYND11,RARB,TCIM,JDO1,PAWR,SRA1,TMTC4,DPF1,EIF2AK2,PRNP,DUSP6,BAG4,ARHGEF7,BTG1,SEMA3A,UNC5D,RNF122,AIMP1,PDK1,TFDP1,DDRGK1,SH3RF2,WRN,NCKAP1L,GAS6,RYBP,PPP2CB,FOXP1,MITF,TAF10,RASSF7,ARL6IP5,PRKDC,IRF7,ERCC6,TRAF6,NR1H4,APIP,KCNIP3,SLC5A8,TRIB3,PLK2,MAL,RET,HCK,NSMAF,ASAH1,ZC3H8,IL1A,DRAM1,GPI,PAX8,NR4A1,ACVR1B,FAIM,	grey	VSMC_M10

GO:0000910	1.00	0.00	51	141	cytokinesis	BP	1	VPS4B,TRIM36,SEPT8,SEPT3,WASHC5,MYH9,SEPT10,EFHC1,MITD1,CHMP2A,PRKCE,SPTBN1,PLK3,PLK2,KIF3B,CSPP1,DCDC1,CHMP2B,CHMP4C,RTKN,SEPT11,CHMP7,BIN3,ZFYVE19,KIF13A,KLHDC8B,SEPT2,SETD2,EFHC2,AHCTF1,SEPT1,CNTROB,RAB11A,MYH10,NOX5,CALM1,KLHL13,UNC119,FSD1,KLHL21,SPIRE2,CHMP1A,CDC14A,SH3GLB1,VPS4A,RHOA,AURKC,PLK5,STAMBP,APC,PDXP	grey	VSMC_M10
GO:0009719	1.00	0.00	570	1202	response to endogenous stimulus	BP	1	SLC39A5,FECH,ONECUT2,ARPC3,LRP1,AP3S1,MARS,PIP4K2C,CYP27B1,USP15,ESR1,FRS2,CNOT2,TPH2,SNW1,PRKN,AGER,PPARA,TNFRSF11B,PNPLA3,RXRB,TSPO,GDF9,SMAD5,LEMD2,PTK2,AKR1B1,ATF4,TAB1,NTRK2,MAPK13,GKAP1,KDM4C,SOX10,MICALL1,TXN2,HSF1,KCP,CCND3,FOXH1,GPT,RBFOX2,TEK,CRY1,SRF,STEAP2,GABRA1,KIT,SLC1A1,FHL2,TGFBRAP1,TFAP2B,ROR2,DLX5,PPAT,SOSTDC1,CAT,DNAJA1,PRKCE,CD109,PHIP,FPR2,HAS1,PNPT1,ME1,HOXA13,CXCL8,NOD1,AREG,BMP8A,CRHR2,AQP1,RRAGD,BMPER,PTN,ITGB1BP1,DDC,KLF11,GRB10,TNC,EGFR,LANCL2,FUZ,TLR4,GAB1,LPIN1,SFRP4,UCP1,VPS35,SDCBP,MGARP,TRPM4,FOXO3,PGRMC2,NTF4,WASF1,APOB,FGF21,SPRY1,HDAC2,SESN3,DNMT3A,BMI1,NDNF,SLC26A5,PIP4K2A,RAB10,PRKD2,HADHA,PHB,SOX9,CYSLTR2,GLB1,KHK,EIF2B3,EPM2AIP1,MEGF8,ECHDC3,ATP1A3,MYD88,TIMP4,ACVR2B,KLF5,TBC1D4,UBE2O,EGLN2,AANAT,FNDC4,HNMT,FBH1,SPRY2,ALK,TADA3,AKT2,EID2,TGFBR2,OVOL2,SNX5,ACVR2A,SIRT2,MKKS,RPTOR,RARB,NR1D2,SRA1,RYR1,FERMT1,SPRED3,CRLS1,SPINT2,PRNP,BAG4,TAF7,ASH2L,DIAPH1,BTG1,SPART,RNF14,KL,DDRGK1,LARS,PTPRA,FOXP1,LEPROTL1,ARID5A,PRKDC,CALCOCO1,NCOA4,NR1H4,SLC38A9,TUB,TRIB3,LMO2,HTR7,FAM107A,CYP7B1,DNMT3B,GPI,PAX8,FGFBP3,NR4A1,FER,IDE,UFSP2,SNX25,NCOA6,PIK3R1,LPXN,CASP3,NCOA2,DKK3,ING2,HPGD,P2RX3,ROBO2,ZNF366,CHRM5,IL17RD,RYR3,ARNTL,SORBS1,GPD1,MEF2C,P2RX7,CNOT1,SOX6,P2RY1,PTK2B,KMT2D,RAPGEF2,SLC33A1,NR1H3,FGF5,VEPH1,RIPK2,DDX54,STC1,NKX3-1,OPA1,SPIDR,LPIN3,NKX6-1,RAPGEF3,CHRM4,NR4A2,ACVR1C,SRSF6,SPINT1,CR	grey	VSMC_M10
GO:1900182	1.00	0.00	23	76	positive regulation of protein localization to nucleus	BP	1	MAPK14,SMO,MAVS,PIK3R1,TERT,HCLS1,PARP9,DTX3L,BAG3,LIMK2,MEPCE,MAPK1,PARP1,TARDBP,PSEN1,NGFR,KAT7,SMAD3,EFCAB7,PARK7,LAMTOR5,LIF,ZIC1	grey	VSMC_M10
GO:0044419	1.00	0.00	445	948	biological process involved in interspecies interaction between organisms	BP	1	CD226,VPS4B,SHMT2,YTHDC2,MAP3K5,TNFAIP3,CYP27B1,FUCA2,USP15,TRIM39,SNW1,HSPA1B,IGF2R,PRKN,RNF5,TSPO,BAK1,FER1L6,XRCC6,TRIB1,CXCL14,PTK2,C6orf106,LY6E,APOBEC3H,MAPK14,PLA2G6,EXOSC4,HSF1,IRF5,CDK6,GAPDH,PRDX1,ADH5,CHMP2A,SDHAF4,PRKCE,FPR2,GSDME,REL,ANKRD17,CXCL8,NOD1,AKIRIN2,AQP1,PELI1,LYPD8,RSAD2,NR1H2,EGFR,TRIM32,TLR4,IL15,ATG5,MGST2,PUM2,EPS15,APOB,CDK19,TRAF3IP2,HDAC2,HS3ST5,ZC3HAV1,RAB7A,C5AR1,NAPEPLD,PTGIR,KPNA3,PHB,CUBN,LACC1,NECTIN2,FBXL2,PVR,OPTN,MLH1,UNC13D,MYD88,PRDX3,TIMP4,RPSA,IRAK2,THBD,SEC14L1,SLC20A2,IKBKB,NFKBIB,SIRT2,NMI,ZMYND11,TMEM173,CLPB,ACTG1,NPLOC4,EIF2AK2,DCN,MAVS,AIMP1,GAS6,HPX,ULK1,FOXP1,ARID5A,PRKDC,IRF7,MFHAS1,TRAF6,PCBP2,NR1H4,TRIM44,THOC7,HCK,IL1A,IL37,NR4A1,FER,IDE,FLNB,OTUD4,CASP3,IRF2,CHMP2B,ERAP1,SAP30,HPGD,PLSCR4,MEF2C,NUGGC,P2RX7,AUP1,CHMP4C,PTK2B,RASGRP1,CCL17,EIF2AK4,NR1H3,TRAFD1,SERINC5,OAS3,NLRC5,RIPK2,OTULIN,TPCN1,IFNGR2,WRNIP1,F2RL1,F2R,ANO6,VPS18,POLR3D,ABCC2,CHID1,IFIT2,MAPKBP1,HERC5,NOD2,ITGB6,TOLLIP,CD40,GBF1,NFKB2,MX2,RAB7B,MAPKAPK3,CD96,IFIH1,OASL,HDAC1,HYAL1,RGS1,LCK,HYAL3,BANK1,SP100,CRCP,PDCD4,GPAM,FAM20A,ADARB1,DAG1,UNC93B1,POLR3C,ZNF639,SELPLG,CFL1,TLR5,NCF1,MAPKAPK2,FABP4,SCN7A,TIFA,HSPA8,ALPK1,YTHDF2,GRK2,ATG16L1,GPER1,SLAMF8,PARP9,DTX3L,PARP14,POU2F3,IRF9,IFI6,RNF26,FGR,PC,CBL,ACE2,NLRX1,ABCF3,TRAF3IP1,ITGB5,HTRA1,TRIM52,NECTIN4,COCH,XPR1,IL10RA,FCER1G,NCF2,PPP2R3C,SETD2,LYZL6,ADAM8,LRRC15,CADM1,F	grey	VSMC_M10
GO:0044770	1.00	0.00	185	426	cell cycle phase transition	BP	1	VPS4B,GLI1,MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,TAF2,MAPK15,MAPK14,FBXL6,CCND3,CDKN2A,ZNF16,FBXO7,CRY1,ABCB1,CDK14,CDK6,PPAT,CHMP2A,BRSK1,MSH2,ANKRD17,ETAA1,LSM10,KLF11,EGFR,CDK5RAP2,CCNY,TPRA1,TOPAZ1,XPC,ERCC2,ERCC3,CLASP2,PLK3,UBE2E2,PAXIP1,DYNC1LI1,PPME1,SIRT2,NEK10,RPTOR,TCIM,ANAPC15,PLCB1,IK,SIRT7,NEK11,USP44,TFDP1,DDRGK1,TAF10,MTA3,PRKDC,ERCC6,CEP63,STK33,PLK2,MOS,FAM107A,ACVR1B,RAD17,ATR,FBXW7,ANAPC5,PKIA,ANAPC7,CCNJ,RAD9B,CHMP4C,ADAMTS1,CCNG2,BACH1,EIF2AK4,NBN,USH1C,ABRAXAS1,CHMP7,DONSON,ZFYVE19,CCNJL,PIDD1,PKD2,NPM2,TAOK3,LZTS1,CDK18,FBXL15,HYAL1,PPP3CA,HECW2,CCND1,TERT,PPP2R2D,DYRK3,GIGYF2,CHEK2,PSME1,CACUL1,CDK15,ATRIP,EPS8,SYF2,CDKN1B,DLG1,OVOL1,MAP3K11,STOX1,SUSD2,DBF4B,MEN1,DDX3X,MEPCE,PTPN6,UPF1,ECD,PSME3,USP37,TIPRL,RHNO1,PIM2,AKAP8L,AKAP8,DDB1,PHF8,PRPF19,ANAPC4,RAD51B,UIMC1,FOXO4,PAGR1,FBXL22,CTC1,EME1,MUC1,TAOK2,TAF1,ESRRB,RAB11A,TIPIN,KDM8,LCMT1,FOXN3,CALM1,RAD51C,DNM2,DCUN1D3,SIN3A,CAMK2A,CCL2,PPP6C,CUL4B,PSMG2,TAOK1,FZR1,DOT1L,PKD1,MECP2,CDK10,FBXO31,CDC14A,GFI1,VPS4A,FBXL8,NAE1,MIR29A,MIR222,FBXL12,RPA4,PLK5,E2F6,RPS27L,SOX4,DUSP1,SPDYA,RGCC,APC,CDC26,ZFP36L2,BRCC3,CRADD,ARPP19,NABP1	grey	VSMC_M10

GO:0040007	1.00	0.00	339	742	growth	BP	1	ADNP2,NEDD4L,LRP1,SEMA6A,GLI1,CYP27B1,YEATS4,ESR1,RAB21,STK3,HSPA1B,RIMS2,EBAG9,PRKN,PPARA,GDF9,ROS1,FSTL4,H3F3C,PTCH1,LY6E,PLXNA4,MAPK14,CPNE5,SOX10,PI16,PIM1,EXOSC4,SMO,BNC2,TAF8,CDKN2A,LARGE1,PTK7,SRF,APBA1,TEC,SMARCA2,SEMA4D,NINJ1,SEMA4C,RIMS1,RTN4,PPP2R1A,PNPT1,RUFY3,PPT1,AREG,AKIRIN1,COL27A1,EPHA7,PTN,TNC,EGFR,ING3,TRIM32,SDCBP,NRCAM,FOXO3,WASF1,SPHK2,SPRY1,PLXNA1,ARMC10,PHB,SOX9,ERCC1,ERCC2,PTCH2,GOLGA4,KCTD21,GLI2,MEGF8,XRCC2,KLF5,WDR48,EGLN2,TSKU,SPRY2,WNT11,SERTAD3,CPNE9,TGFBR2,MKKS,RPTOR,RARB,HBEGF,SYT1,PLCB1,SLC23A2,ING1,DUSP6,SEMA3D,BTG1,SPART,SEMA3A,WRN,GAS6,ULK1,TAF10,PRKDC,ERCC6,RYK,PLAG1,TTL,FAM107A,KCTD6,ACVR1B,ING2,CDKN2AIP,PLS1,PLCE1,FMN1,IL17RB,PTPRJ,MEF2C,SEMA4F,IL7,HTRA2,NDUFS3,CELF1,TLL2,PTK2B,KMT2D,DPYSL2,EIF2AK4,TIAM1,SLIT1,NBN,STC1,NKX6-1,TBX5,ZFYVE27,ACVR1C,BIN3,PRDM11,FTO,SEMA3G,RTF1,SPP1,STK4,CYFIP1,ALCAM,SEMA4G,SALL1,NKD1,JARID2,SLC12A5,IGF2,BMPR1B,GAS2,DCAF1,BDNF,SLC4A10,KIAA0319,LGR6,SLC6A3,HYAL1,PPP3CA,CAPRIN2,SBDS,SEMA3F,TGFB2,GAP43,FBLN5,GPAM,IGSF11,EI24,PRKAR1A,HEPACAM,ADARB1,DAG1,AUTS2,ZNF639,HLX,GIGYF2,ADNP,SOX2,DISC1,SH3BP4,ARIH2,AGT,CIB1,IP6K2,SLC9A1,KDF1,SFN,SPTBN2,BNIPL,FZD7,RPS6KA1,OSM,ACTN3,KCNK2,MRGBP,CDKL5,CLIC4,ING5,CSPG5,FZD9,CDKN1B,APOD,YBX3,WNT3,POR,CREB1,SPG11,DUSP10,MAPT,SUPV3L1,BCL6,SEMA6D,ITGA4,DDX3X,TNR,RASGRP2,FN1,SAV1,DDX49,NIN,FLRT1,FKBP8,ING4,PPP3CB,MYOZ1,GDF15,FGFR3,S	grey	VSMC_M10
GO:0051493	1.00	0.00	198	457	regulation of cytoskeleton organization	BP	1	VPS4B,ARPC3,LRP1,TRIM36,AVIL,MDM1,ATAT1,HSPA1B,PRKN,MTSS1,WASHC5,PTK2,MAPK15,BAIAP2L2,PICK1,MPDZ,CDC42EP1,RAC2,TEK,LMOD2,CCL27,SLAIN2,NCK2,KIAA1211,BICD2,CHMP2A,TMOD1,PLEKHH2,PRKCE,SPTBN1,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,CDK5RAP2,EPHA1,CNTRL,MYLK3,FAM49A,MAPRE1,WASF1,EML2,SLC39A12,CLASP2,MAPRE3,TRIM54,MYCBP2,SLAIN1,WNT11,PLEKHG2,FCHSD2,MKKS,ACTG1,NAV3,RAC3,BAG4,ARHGEF7,DIAPH1,SPEF1,FCHSD1,NCKAP1L,ARFIP2,RASSF7,LMOD3,ATXN7,HCK,FAM107A,FER,CEP70,PIK3R1,HIP1R,CHMP2B,CLIP1,KATNBL1,FMN1,LIMA1,P2RX7,CHMP4C,KATNB1,PTK2B,RND1,ALMS1,TMEM67,RAPGEF3,RHOBTB2,F2RL1,IQGAP2,CYFIP1,DMTN,STMND1,MAGEL2,PXN,CARMIL1,PPFIA1,LMOD1,ADD3,TRPV4,TTBK2,SSH1,HCLS1,ARHGAP6,AP1AR,CIB1,WASF2,SLC9A1,SPTBN2,CCDC84,TRAF3IP1,TMOD4,PHLDB1,EPS8,CLIC4,RHOBTB1,INPP5J,GRHL3,WHAMM,CDKN1B,DLG1,CAPZA1,CDC42EP2,MAPT,ABL2,TOGARAM1,DIXDC1,NCKAP1,AFAP1,NIN,WNT4,RNF4,MARK2,ARPC1A,BST1,MAPK1,WAS,TMOD2,ARHGEF19,SPTB,SYDE1,PFN3,TAOK2,MAPK3,AC138894.1,HAX1,SMAD3,CORO2B,S100A8,TRIM37,BCAS3,ARHGAP44,EVL,CAPN6,CSF1R,CAMSAP3,CDK5R1,PTGER4,TAOK1,NUBP1,SSH2,FSD1,CRK,INPP5K,SERPINF2,MLST8,PKD1,MECP2,APC2,PLXNA3,CAMSAP1,SPIRE2,CDK10,CHMP1A,PSRC1,GPSM2,TSC1,WDR63,CARMIL2,FHOD1,MIR21,RHOA,VASP,GMFG,ASAP3,RND3,RGS4,CCSAP,GRB2,RGCC,APC,HRAS,PFN4,PDXP,MAP1A,COTL1,DRG1,MAP6D1	grey	VSMC_M10
GO:0009891	1.00	0.00	738	1533	positive regulation of biosynthetic process	BP	1	NFATC1,ZNF407,SMARCC2,ONECUT2,TCF4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,RMND1,YEATS4,ESR1,MYRFL,CNOT6,OSR2,PRR16,PABPC1,SNW1,ARID1B,EIF3E,ZBED4,MAP3K4,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,JMJD4,AGO2,HABP4,PTCH1,ATF4,MAPK15,MAPK14,PLA2G6,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,GUCA1B,GPT,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,EPCAM,ZNF462,PHIP,HMGN3,NFYC,PPP4R3B,HOXA2,HOXA7,HOXA13,REL,CREB5,CXCL8,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,IL15,TEAD2,SETD7,MYCN,ELF2,OSR1,FOXO3,ZXDC,SSBP1,FAF1,MAMSTR,ATAD2B,SPHK2,KDM7A,ZNF438,HDAC2,PHF10,MAML2,MLLT10,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,MAPRE3,UTF1,SUMO2,EPM2AIP1,CDC123,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,SS18L2,WNT11,TADA3,SERTAD3,KLF6,AKT2,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,PAWR,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,CEP290,NSD3,ING1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,RYBP,SIRT3,MITF,RBPMS,UPF3A,MTA3,PRKDC,IRF7,ERCC6,HOXC13,CALCOCO1,ST18,RASL11A,NCOA4,TRAF6,NR1H4,TRIM44,TCF15,SOX12,PLAG1,USF2,RET,CYP	grey	VSMC_M10
GO:1902850	1.00	0.00	47	133	microtubule cytoskeleton organization involved in mitosis	BP	1	VPS4B,ZNF207,HSPA1B,SUN2,EFHC1,CHMP2A,CDK5RAP2,SPRY1,CCDC61,CLASP2,PIBF1,SPRY2,NSFL1C,PLK2,KIF3B,CHMP2B,CHMP4C,MCPH1,ABRAXAS1,AC112128.1,SBDS,INTS13,TBCE,CHEK2,ABRAXAS2,SETD2,TOGARAM1,EFHC2,HTT,TUBG1,CEP126,KPNB1,NDEL1,RAB11A,CEP192,FSD1,PKD1,MECP2,WRAP73,SAPCD2,CHMP1A,PSRC1,GPSM2,RHOA,AURKC,CCSAP,DRG1	grey	VSMC_M10

GO:0022607	1.00	0.00	1098	2230	cellular component assembly	BP	1	TIMM21,VPS4B,PAN2,ATP8B1,ONECUT2,MIP,ARPC3,BAZ2A,TCF4,MYO1A,LRP1,STX7,SHMT2,ATG12,TBPL1,PIP4K2C,AVIL,ATP23,TBC1D30,MDM1,ATAT1,CPSF6,ESR1,CNOT2,CNOT6,STK3,ZNF207,SNCAIP,MAPK8IP2,APOM,HSPA1B,SF3A3,TUBGCP6,EIF3E,LYRM7,KCNV1,TNXB,PRKN,RNF5,HLA-DRA,HLA-DOB,HLA-DMA,IL5,BRD2,PARVG,KIF3A,HLA-DPB1,SEPT8,SHROOM1,HSD17B8,ASF1A,HSPA4,TBC1D32,RRP7A,NDUFA6,UBE2B,BAK1,MTSS1,WASHC5,ASAP1,LRRC6,OBSCN,AGO2,H3F3C,PTK2,FANCC,ISCA1,MAPK15,NTRK2,CBY1,DMC1,PUF60,PODXL,PSMD5,BAIAP2L2,PICK1,EIF3L,MPDZ,CDC42EP1,RAC2,GPAA1,TSPAN33,HSF1,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,GNMT,TRPM6,POT1,LMOD2,SRF,TTBK1,CFAP69,GABRA1,APBA1,FZD1,C12orf45,PGM5,SLAIN2,RFX3,KIT,ADGRF1,NCK2,TLN1,SEMA4D,KIAA1211,PTPDC1,NINJ1,FGD3,COA5,CHMP2A,ADGRL3,RPS14,TMOD1,RAB23,DYNC2LI1,STX17,CLDN19,SDHAF4,PRKCE,EPS8L1,RIMS1,PRPF31,SPTBN1,RTN4,PPP2R1A,HAS1,MPP6,YTHDC1,PNPT1,SKAP2,SHANK1,LPAR1,CEP162,ECPAS,SRSF10,MDN1,TMEM17,GJA10,AKIRIN1,PXDN,WDR92,TRAPPC12,PLEK,LRRN3,EPHA7,NR1H2,ITGB1BP1,MED25,MET,ADD2,AGO1,YWHAZ,FUZ,ARHGEF5,TLR4,CDK5RAP2,EPHA1,IQUB,TRAF1,CCDC155,MYLK3,VPS35,TEAD2,ATG5,SDCBP,FAM49A,NRCAM,TRPM4,ARMC2,MAPRE1,PUM2,FIG4,WASF1,ARMC4,EPS15,SSBP1,APOB,FAF1,NDUFB2,INTU,SPATA6,HIGD1A,UBN2,MTMR2,TTC26,NAPA,BBS7,RAB7A,PIP4K2A,AP2S1,VSTM5,ARHGEF4,MSRB2,ATPAF1,KCNRG,KPNA3,DRC1,CCDC61,SOX9,RSPH6A,MYO7B,EML2,ERCC1,NDUFB6,ERCC2,SLC39A12,LCP1,TMEM126B,CLASP2,APOC	grey	VSMC_M10
GO:0033045	1.00	0.00	18	64	regulation of sister chromatid segregation	BP	1	ZNF207,MAPK15,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,MOS,ANAPC5,ANAPC7,HECW2,ANAPC4,LCMT1,PSMG2,RMI2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0090130	1.00	0.00	108	266	tissue migration	BP	1	PTK2,PTP4A3,MYH9,TEK,SRF,KIT,MEOX2,SVBP,PRKCE,RTN4,EPB41L4B,EMC10,BMPER,PTN,ITGB1BP1,MET,PRKD2,IQSEC1,SOX9,CLASP2,PAXIP1,RIN2,TGFBR2,HBEGF,FERMT1,DCN,SEMA3A,FOXP1,PLK2,GPI,NR4A1,PIK3CB,LPXN,ATP5F1A,ROBO1,FBXW7,MEF2C,VEGFC,PTK2B,ACTG2,DOCK5,STC1,HDAC7,LOXL2,RREB1,ADTRP,CD40,PXN,GPLD1,FAP,HYAL1,SP100,TGFB2,PDCD6,PRKX,EGF,AGT,CIB1,ACTC1,MAP3K3,DOCK1,PATZ1,GLUL,NFE2L2,MIA3,DUSP10,CTSH,EPHB4,S100P,PDCD10,RHOJ,SYNJ2BP,SEMA4A,RAB25,FGF18,ITGA3,EFNA1,VASH1,RAB11A,MAP2K5,BCAS3,EVL,AMOT,PDPK1,MECP2,FOXF1,LCN2,MARVELD3,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,DPP4,ACVRL1,NANOS1,ZNF580,WNT5A,GADD45A,RGCC,FGF1,S100A2	grey	VSMC_M10
GO:0032956	1.00	0.00	125	304	regulation of actin cytoskeleton organization	BP	1	ARPC3,LRP1,AVIL,PRKN,MTSS1,WASHC5,BAIAP2L2,PICK1,CDC42EP1,RAC2,TEK,LMOD2,CCL27,NCK2,KIAA1211,TMOD1,PLEKHH2,PRKCE,SPTBN1,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,EPHA1,MYLK3,FAM49A,WASF1,CLASP2,WNT11,PLEKHG2,FCHSD2,MKKS,ACTG1,RAC3,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FAM107A,FER,PIK3R1,HIP1R,FMN1,LIMA1,PTK2B,RND1,ALMS1,RAPGEF3,RHOBTB2,F2RL1,IQGAP2,CYFIP1,DMTN,MAGEL2,PXN,CARMIL1,PPFIA1,LMOD1,ADD3,SSH1,HCLS1,ARHGAP6,AP1AR,WASF2,SLC9A1,SPTBN2,TMOD4,EPS8,RHOBTB1,GRHL3,WHAMM,DLG1,CAPZA1,CDC42EP2,ABL2,DIXDC1,NCKAP1,WNT4,ARPC1A,BST1,WAS,TMOD2,ARHGEF19,SPTB,PFN3,TAOK2,HAX1,SMAD3,CORO2B,BCAS3,ARHGAP44,EVL,CSF1R,CDK5R1,PTGER4,TAOK1,SSH2,CRK,INPP5K,SERPINF2,MLST8,SPIRE2,CDK10,TSC1,WDR63,CARMIL2,FHOD1,MIR21,RHOA,VASP,GMFG,ASAP3,RND3,RGS4,GRB2,RGCC,HRAS,PFN4,PDXP,COTL1	grey	VSMC_M10
GO:0040012	1.00	0.00	365	796	regulation of locomotion	BP	1	ONECUT2,LRP1,SEMA6A,SRGAP1,AGER,GPSM3,FBLN1,TRIB1,AGO2,PTK2,MAPK15,PLXNA4,SUN2,PODXL,RAC2,SMO,TEK,FBXO7,SRF,CFAP69,CCL27,CDK6,KIT,ROR2,SEMA4D,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,RNF20,PRKCE,EPCAM,RTN4,FPR2,HAS1,EPB41L4B,RUFY3,HOXA7,EMC10,CXCL8,BMPER,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,BVES,GAB1,SDCBP,FOXO3,FGF21,PLXNA1,LAMA4,C5AR2,C5AR1,SLC26A5,PRKD2,IQSEC1,SOX9,BEX4,CLASP2,MEGF8,RAF1,MYD88,OXSR1,DACH1,MYCBP2,CYGB,SPRY2,WNT11,RIN2,AKT2,TGFBR2,SRGAP3,JAG1,MKKS,ACTG1,NAV3,HBEGF,PLCB1,FERMT1,SPINT2,CNN2,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,PLXNC1,SEMA3A,UNC5D,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,DPYSL3,FLT1,RYK,PLK2,MTUS1,RET,AL359736.1,FAM107A,GPI,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,ATP5F1A,ROBO1,ROBO2,FBXW7,PTPRJ,MEF2C,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,IGSF10,ADAMTS1,PTK2B,RAPGEF2,TIAM1,FGF5,DOCK5,SLC8B1,STC1,HDAC7,NKX6-1,TBX5,CHRM4,ACVR1C,F2RL1,F2R,ANO6,TP53INP1,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,ADTRP,NOD2,NKD1,CD40,LDB1,SRGAP2C,GPLD1,DOCK10,CD200,SLK,LGR6,DNM1L,CARMIL1,HYAL1,PPP3CA,SINHCAF,SP100,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,ADARB1,CD99,GNA13,PRKX,DAG1,TTBK2,PRSS56,SSH1,AJUBA,CMKLR1,SNAI1,EGF,ABHD2,AP1AR,SORL1,GPER1,SLAMF8,CFAP45,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,CERS2,HDAC4,LAMA5,YTHDF1,PTPRO,CHRD,CLIC4,MAP3K3,DOCK1,PATZ1,GLUL,ELP6,LRIG2,APOD,ADAM8,WNT3,LRRC15,FRMD5,NFE2L2,TBCCD	grey	VSMC_M10

GO:0043412	1.00	0.00	1511	3029	macromolecule modification	BP	1	PHLPP1,ERBB3,NEDD4L,BAZ2A,RNMT,LRP1,SHMT2,EYA4,ATG12,FEM1C,PGGT1B,TRIM36,B4GALT7,RMND5B,CLK4,MAP3K5,TNFAIP3,AGAP2,ADAT2,ATP23,USP15,FBXO30,RXYLT1,MAML1,MRNIP,TRIM39,ATAT1,ARMT1,YEATS4,GFPT2,STK3,FBXO43,SNW1,TFB1M,MARCH3,ABHD16A,ADM2,ZDHHC14,HSPA1B,TULP4,SELENOO,MOV10L1,ALG12,BRD1,TNXB,MAP3K4,PRRT1,PPT2,PRKN,RNF5,AGER,TRMU,FBLN1,P4HA2,MED30,IL5,BRD2,TSPO,GDF9,ROS1,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,TRMT11,RNF146,TRIB1,MYC,SMAD5,KLHL3,OBSCN,JMJD4,PTK2,KDM3B,PTP4A3,TAB1,MAPK15,RPAP2,AGTPBP1,APOBEC3H,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,C9orf64,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,PIM1,CMTR1,ZC3HC1,EXOSC4,GPAA1,ZDHHC21,HSF1,FBXL6,OARD1,ADCK5,USP49,CCND3,OPN1SW,PPP1R16A,CDKN2A,CHRNA3,TEK,LARGE1,GNMT,TRPM6,FBXO7,KLHDC3,ASB15,PRDM4,CRY1,PTK7,ABHD17B,TTBK1,NFX1,NUAK1,PTAR1,CDK14,DCAF12,TEC,CWH43,CDK6,SUPT3H,USP46,LNX1,KIT,SLC1A1,ST6GAL2,SRD5A3,NCK2,ROR2,SEMA4D,GAPDH,CDK20,PDCL3,C1GALT1,PTPDC1,HINT2,WNK2,PHF14,LIPT1,KLHL31,ADH5,FBXO10,EXOSC3,DCAF10,KANSL3,SVBP,ALG2,CLDN19,CAMKMT,RIMKLA,DNAJA1,IL11,BRSK1,TMEM246,RNF20,PRKCE,EPAS1,PIGF,STPG4,MTO1,CD109,ASB3,SPTBN1,FKTN,PPP2R1A,PHIP,FPR2,ELP1,PPP4R3B,IBTK,UBE3D,ACP4,MOB1B,VRK2,FANCL,PUS10,PPT1,TRIT1,SLC35A1,EPGN,AREG,BMP8A,RNGTT,MINDY4,FKBP9,PELI1,BMPER,AGBL3,FKBP15,CNOT4,ETAA1,BSPRY,RSPO1,AAK1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,YWHAZ,EGFR,ING3,HECW1,USP45,ARHGEF5	grey	VSMC_M10
GO:0031328	1.00	0.00	722	1503	positive regulation of cellular biosynthetic process	BP	1	NFATC1,ZNF407,SMARCC2,ONECUT2,TCF4,GLI1,MARS,MAP3K5,PLAGL1,MAML1,RMND1,YEATS4,ESR1,MYRFL,CNOT6,OSR2,PRR16,PABPC1,SNW1,ARID1B,EIF3E,ZBED4,MAP3K4,PRKN,PPARA,MED30,IL5,RXRB,VGLL2,HSF2,XRCC6,NCOA7,PITX1,MYC,SMAD5,JMJD4,AGO2,HABP4,PTCH1,ATF4,MAPK15,MAPK14,PLA2G6,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,FOXH1,GUCA1B,GPT,IFT74,BICRAL,POT1,RORB,ZNF300,PRDM4,DMTF1,SRF,ZNF318,FZD1,SUPT3H,SMARCA2,RFX3,NCK2,TFAP2B,ROR2,NFIL3,DLX5,IPPK,ETV1,MEOX2,KANSL3,ZNF268,MACC1,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,EPCAM,ZNF462,PHIP,HMGN3,NFYC,PPP4R3B,HOXA2,HOXA7,HOXA13,REL,CREB5,CXCL8,AKIRIN2,AKIRIN1,MTF1,PCBP1,NR1H2,AKNA,ITGB1BP1,GRHL1,MED25,MET,IL4I1,AGO1,POU3F3,EGFR,TRIM32,TLR4,CCNC,CDK5RAP2,BCL2L12,LPIN1,IL15,TEAD2,SETD7,MYCN,ELF2,OSR1,FOXO3,ZXDC,SSBP1,FAF1,MAMSTR,ATAD2B,SPHK2,KDM7A,ZNF438,HDAC2,PHF10,MAML2,MLLT10,PRKD2,CNBP,PHB,FOXA3,SOX9,ZNF786,ZNF746,ERCC1,GPBP1L1,XPC,MAPRE3,UTF1,SUMO2,EPM2AIP1,CDC123,GLI2,RSF1,CAND2,ZNF513,ZNF574,RAF1,KLF5,KLF12,FOXJ1,PAXIP1,CSRNP1,METTL23,POU4F1,SS18L2,WNT11,TADA3,SERTAD3,KLF6,AKT2,ARRB1,DYRK1B,OVOL2,SNX5,ZNF219,ACVR2A,EOMES,IKBKB,TASP1,CHD8,JAG1,NFKBIB,SIRT2,RPTOR,TMEM173,RARB,NR1D2,PAWR,SRA1,PLCB1,NUP98,SIRT7,MAFG,DPF1,ALX1,CEP290,NSD3,ING1,TAF7,LUM,DCN,MAVS,RNF14,TFDP1,DDRGK1,RYBP,SIRT3,MITF,RBPMS,UPF3A,MTA3,PRKDC,IRF7,ERCC6,HOXC13,CALCOCO1,ST18,RASL11A,NCOA4,TRAF6,NR1H4,TRIM44,TCF15,SOX12,PLAG1,USF2,RET,LM	grey	VSMC_M10
GO:0051130	1.00	0.00	401	870	positive regulation of cellular component organization	BP	1	NME1,VPS4B,NEDD4L,PAN2,ARPC3,LRP1,PIP4K2C,AVIL,PPP1R10,ATAT1,ESR1,CNOT2,RAB21,CNOT6,TIAM2,HSPA1B,MAP3K4,PRKN,IL5,UBE2B,BAK1,MTSS1,WASHC5,ASAP1,JMJD4,MAPK15,PLXNA4,MAPK14,NTRK2,PLA2G6,BAIAP2L2,PICK1,CDC42EP1,RAC2,HSF1,TEK,LINGO2,POT1,FBXO7,LMOD2,PTK7,SRF,TTBK1,FZD1,CCL27,SLAIN2,KIT,NCK2,ROR2,SEMA4D,KIAA1211,CLDN19,PRKCE,EPS8L1,TMEM30A,PHIP,RUFY3,HOXA13,LPAR1,PPT1,EPGN,AKIRIN1,PLEK,LRRN3,NR1H2,TGFA,PTN,ITGB1BP1,MED25,MET,FUZ,ARHGEF5,TLR4,CDK5RAP2,EPHA1,SFRP4,MYLK3,VPS35,SDCBP,MGARP,MAPRE1,FIG4,WASF1,SSBP1,FAF1,PLXNA1,NDNF,PIP4K2A,VSTM5,SETDB2,IQSEC1,SOX9,ERCC1,LCP1,CLASP2,GOLGA4,MEGF8,RALB,MYD88,SLAIN1,SS18L2,WNT11,ALK,AKT2,ARRB1,FCHSD2,SIRT2,ANK1,NAV3,SYT1,TMEM106B,PLCB1,FERMT1,DDHD2,BAG4,ARHGEF7,DCN,PLXNC1,FCHSD1,NRG1,NCKAP1L,ULK1,ARFIP2,LMOD3,DPYSL3,SYT9,PAN3,EPHB1,NPHP1,RET,HCK,TOX,IL1A,CBFA2T2,FER,ANKRD27,OSBP,PIK3R1,CLSTN2,HIP1R,ATR,TRABD2A,CLIP1,ROBO1,ROBO2,KATNBL1,PLCE1,SLF1,FAM208A,TENM3,FMN1,HMBOX1,PTPRJ,ENC1,ANAPC5,HTRA2,P2RX7,CNOT1,ANAPC7,CUX2,KATNB1,PTK2B,CNOT6L,FNIP2,RAPGEF2,MAPKAPK5,TIAM1,NBN,SYNJ1,OPA1,SPIDR,CDH17,RAPGEF3,TBX5,AMIGO2,ZFYVE27,F2RL1,IQGAP2,ANO6,RREB1,ITPKA,CYFIP1,SLF2,NPM2,PPHLN1,CNTN1,IGF2,MAGEL2,BDNF,PXN,NEURL1,DNM1L,CARMIL1,HYAL1,ZMYND10,LMOD1,PPP3CA,CAPRIN2,TRPV4,TGFB2,COL16A1,ZDHHC6,DAG1,AUTS2,AMIGO3,SSH1,AJUBA,EGF,HCLS1,ADNP,AP1AR,DISC1,C2CD5,GPER1,DGKD,AGT,CBL,WASF2,ACE2,DVL3,CIDEB,AP2M1,PHLDB1,HDAC4,SS	grey	VSMC_M10

GO:0070887	1.00	0.00	1096	2230	cellular response to chemical stimulus	BP	1	ADNP2,ZNF236,NME1,SLC39A5,FECH,ONECUT2,ARPC3,RNMT,LRP1,SEMA6A,AP3S1,MARS,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,LTC4S,ESR1,FRS2,GFPT2,CNOT2,TPH2,SNW1,APOM,SLC12A2,HSPA1B,PRKN,PACRG,AGPAT1,RNF5,AGER,PPARA,GPSM3,IL5,PNPLA3,RXRB,TSPO,GDF9,DERL1,TCF7,TNFRSF13C,BAK1,XRCC6,NCOA7,PMM1,TRIB1,CXCL14,MYC,SMAD5,LEMD2,PRXL2C,PTK2,ERCC6L2,KDM3B,PTP4A3,PTCH1,FANCC,LY6E,AKR1B1,ATF4,TAB1,SYNGR1,PLXNA4,MAPK14,NTRK2,MAPK13,CPNE5,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,MICALL1,PIM1,RAC2,SMO,HSF1,IRF5,KCP,CCND3,FOXH1,GPT,ZNF16,RBFOX2,CHRNA3,GPR37,FBXO7,RORB,ALDH1A1,CRY1,PTK7,SRF,GABRA1,CNTFR,TXNRD1,CCL27,KIT,SLC1A1,TNFRSF21,NCK2,TGFBRAP1,ERMP1,IL1R2,TFAP2B,ROR2,NFIL3,GAPDH,DLX5,PPAT,NINJ1,PRDX1,ADH5,SOSTDC1,CAT,DNAJA1,PRKCE,EPAS1,CD109,RAD23B,PHIP,FPR2,HMGN3,HAS1,GSDME,PNPT1,VRK2,HOXA2,ADAMTS3,HOXA13,LPAR1,ALB,CXCL8,NOD1,BMP8A,CRHR2,AQP1,RRAGD,BMPER,AKIRIN1,HERPUD2,PXDN,BSPRY,MTF1,ZNF277,NR1H2,PTN,ITGB1BP1,DDC,KLF11,MET,GRB10,TNC,EGFR,LANCL2,TSPAN12,FUZ,TRIM32,TLR4,TRAF1,GAB1,LPIN1,IL15,SFRP4,MYLK3,UCP1,VPS35,TEAD2,ATG5,MGST2,SDCBP,MGARP,TRPM4,SLC7A11,OSR1,FOXO3,PGRMC2,NTF4,WASF1,TXNRD3,APOB,BCAT2,CDK19,FGF21,BRAF,TRAF3IP2,SPHK2,DHFR,SPRY1,HDAC2,ADCY3,SESN3,DNMT3A,BMI1,NDNF,C5AR2,C5AR1,PIP4K2A,RAB10,PRKD2,PHB,SOX9,CYSLTR2,NUDT15,ESD,DLG2,AKR1A1,CD300LF,GSTK1,PDIA3,SUV39H2,PLK3,OPTN,GLI2,MEGF8,RALB,ECHDC3,GRIK5,RAF1,ATP1A3,MYD88,OXSR1,ZFAND6,PRDX3,ACVR2B,KLF5,TBC1	grey	VSMC_M10
GO:0032970	1.00	0.00	140	337	regulation of actin filament-based process	BP	1	ARPC3,LRP1,AVIL,PRKN,MTSS1,WASHC5,BAIAP2L2,PICK1,CDC42EP1,RAC2,MYH9,TEK,LMOD2,CCL27,NCK2,KIAA1211,TMOD1,PLEKHH2,PRKCE,SPTBN1,SHANK1,LPAR1,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,EPHA1,MYLK3,FAM49A,TRPM4,WASF1,CLASP2,SCN5A,WNT11,PLEKHG2,FCHSD2,MKKS,ACTG1,RAC3,CNN2,BAG4,FCHSD1,NCKAP1L,ARFIP2,LMOD3,HCK,FAM107A,FER,PIK3R1,HIP1R,FMN1,LIMA1,PTK2B,RND1,ALMS1,STC1,RAPGEF3,RHOBTB2,F2RL1,IQGAP2,TNNC1,DSP,CYFIP1,DMTN,RYR2,MAGEL2,PXN,PKP2,CARMIL1,PPFIA1,LMOD1,ADD3,KCNJ2,SSH1,HCLS1,ARHGAP6,AP1AR,ANK2,WASF2,ATP1A2,SLC9A1,SPTBN2,TMOD4,EPS8,RHOBTB1,GRHL3,WHAMM,DLG1,CAPZA1,CDC42EP2,ABL2,DIXDC1,NCKAP1,WNT4,ARPC1A,BST1,WAS,TMOD2,ARHGEF19,SPTB,PFN3,TAOK2,HAX1,ATP2A1,SMAD3,CORO2B,BCAS3,ARHGAP44,EVL,DSG2,CSF1R,CDK5R1,PTGER4,TAOK1,SSH2,CRK,INPP5K,SERPINF2,MLST8,SPIRE2,CDK10,TSC1,WDR63,CARMIL2,FHOD1,MIR21,RHOA,VASP,GMFG,ASAP3,RND3,RGS4,GRB2,RGCC,HRAS,PFN4,HCN4,PDXP,COTL1	grey	VSMC_M10
GO:0007091	1.00	0.00	15	57	metaphase/anaphase transition of mitotic cell cycle	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,ANAPC5,ANAPC7,HECW2,ANAPC4,LCMT1,PSMG2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0001933	1.00	0.00	112	276	negative regulation of protein phosphorylation	BP	1	LRP1,TNFAIP3,PRKN,FBLN1,UBE2B,BAK1,TRIB1,STK38,CDKN2A,FBXO7,NCK2,SEMA4D,KLHL31,DNAJA1,CD109,PPP2R1A,IBTK,ACP4,ITGB1BP1,EPHA1,PRKAR2B,SPRY1,PRKAG2,PIBF1,SPRY2,GPD1L,ARRB1,SIRT2,PTPRQ,PRNP,DUSP6,TAF7,PRKDC,TRIB3,CEBPA,PIK3CB,SNX25,CASP3,PTPRJ,PKIA,PAQR3,DBNDD2,DMTN,DTNBP1,LRRK1,PDCD4,PRKAR1A,ADARB1,FABP4,UBASH3B,SORL1,RTRAF,PARP14,AGT,CIB1,CBL,SFN,TRAF3IP1,CAMK2N2,PTPRO,INPP5J,MLXIPL,SNX6,CDKN1B,AIDA,YWHAG,DUSP10,HEXIM2,MEN1,DNAJC10,DUSP19,PTPN6,FKBP8,ZFYVE28,SOCS4,RGS14,DGKQ,TARDBP,PSEN1,PYDC1,CALM1,BDKRB1,SMCR8,SUZ12,PTPN2,SOCS1,INPP5K,PDPK1,PRKCZ,PARK7,DBNDD1,PIP5KL1,ENG,DAB2IP,MIR27B,MIR24-1,DMD,MIR125A,IMPACT,NOG,SMYD3,THY1,GADD45A,DUSP26,DUSP1,APC,DUSP22,LAX1,CADM4,LDLRAD4,PARD6A,PRKRIP1	grey	VSMC_M10
GO:0035295	1.00	0.00	390	849	tube development	BP	1	LRP1,SEMA6A,GLI1,TNFAIP3,HECA,ESR1,RIDA,STK3,ADM2,SLC12A2,FZD6,QKI,BRD2,VPS52,TBC1D32,CCDC134,BAK1,MTSS1,RSPO3,MYC,SMAD5,KLHL3,AGO2,PTK2,PTCH1,AKR1B1,TAB1,MAPK14,NTRK2,PODXL,SOX10,SMO,MYH9,FOXH1,TEK,PTK7,CEMIP2,SRF,KIT,SLC1A1,TFAP2B,PDCL3,C1GALT1,NINJ1,SEMA4C,SHB,MEOX2,SOSTDC1,CAT,SIX2,TNNI3,EPAS1,EPCAM,HOXA7,HOXA13,EMC10,CXCL8,EPGN,AREG,AQP1,BMPER,EPHA7,TGFA,PTN,ITGB1BP1,MET,TNC,AGO1,YWHAZ,POU3F3,EGFR,TSPAN12,FUZ,EPHA1,GJB5,GAB1,TEAD2,MYCN,NRCAM,SLC7A11,OSR1,APOB,INTU,SPRY1,WISP3,BBS7,BMI1,NDNF,C5AR1,PRKD2,SETDB2,SOX9,SLC39A12,SLC4A2,GLI2,MEGF8,AQP11,KLF5,IFT172,FOXJ1,PAXIP1,WDR48,GZF1,SPRY2,WNT11,RIN2,TGFBR2,OVOL2,ISM1,CHD8,JAG1,MKKS,RARB,ACTG1,SPINT2,CEP290,DCN,PANK2,BTG1,AIMP1,CCKBR,FOXP1,FLT1,TRAF6,EPHB1,PLK2,RET,POFUT1,ASXL1,IL1A,PAX8,NR4A1,CEBPA,CBFA2T2,PIK3CB,CASP3,ERAP1,HAND2,ING2,HPGD,EYA1,PARVA,ROBO1,ROBO2,FBXW7,FMN1,FZD3,MEF2C,VEGFC,ADAMTS1,PTK2B,MME,RAPGEF2,OTULIN,VDR,NKX3-1,OPA1,HDAC7,RAPGEF3,LOXL2,TBX5,AP3B1,AGGF1,SRSF6,IFT52,ARHGAP24,SPINT1,RPGRIP1L,PKD2,STK4,HIF1AN,PAX2,SALL1,PRICKLE1,ADTRP,ITGB6,CD40,WARS2,RYR2,SUFU,GPLD1,FAP,IRX2,PKNOX1,HYAL1,SP100,TERT,TGFB2,PDCD6,ITPK1,PRKX,DAG1,HLX,KRAS,SPATA2,EGF,ENPEP,HSD11B1,AGT,MCAM,CIB1,WASF2,GBX2,DVL3,NFATC4,VASH2,LAMA5,CHRD,CLIC4,MAP3K3,GRHL3,EPHB3,GLUL,SP3,EFEMP2,APOLD1,E2F2,DLG1,LUZP1,APOD,SETD2,ADAM8,NFE2L2,CREB1,FZD5,MIA3,STOX1,PLOD3,CPS1,CTSH,EPHB4,IL12A,AB	grey	VSMC_M10

GO:0010631	1.00	0.00	105	261	epithelial cell migration	BP	1	PTK2,PTP4A3,MYH9,TEK,SRF,KIT,MEOX2,SVBP,PRKCE,RTN4,EPB41L4B,EMC10,BMPER,PTN,ITGB1BP1,MET,PRKD2,IQSEC1,SOX9,CLASP2,PAXIP1,RIN2,TGFBR2,HBEGF,FERMT1,DCN,SEMA3A,FOXP1,PLK2,GPI,NR4A1,PIK3CB,LPXN,ATP5F1A,ROBO1,FBXW7,MEF2C,VEGFC,PTK2B,DOCK5,STC1,HDAC7,LOXL2,RREB1,ADTRP,CD40,PXN,GPLD1,FAP,HYAL1,SP100,TGFB2,PDCD6,PRKX,EGF,AGT,CIB1,MAP3K3,DOCK1,PATZ1,GLUL,NFE2L2,MIA3,DUSP10,CTSH,EPHB4,S100P,PDCD10,RHOJ,SYNJ2BP,SEMA4A,RAB25,FGF18,ITGA3,EFNA1,VASH1,RAB11A,MAP2K5,BCAS3,EVL,AMOT,PDPK1,MECP2,LCN2,MARVELD3,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,DPP4,ACVRL1,NANOS1,ZNF580,WNT5A,GADD45A,RGCC,FGF1,S100A2	grey	VSMC_M10
GO:0071897	1.00	0.00	54	150	DNA biosynthetic process	BP	1	POLI,MAP3K4,MYC,MAPK15,POT1,REV1,REV3L,PRKD2,PHB,DACH1,TFDP1,WRN,PARP4,PRIMPOL,ATR,POLE4,HMBOX1,PTK2B,MAPKAPK5,WRNIP1,SYCP1,POLL,TENT4B,STN1,TERT,GAR1,POLG2,POLG,SPRTN,KCNK2,TEX12,MEN1,XRCC5,POLN,MAPK1,ZBTB1,NVL,GNL3L,FGFR4,WRAP53,SMG5,CTC1,PIF1,MAPK3,LIG3,PARN,TERF2,ACVRL1,TINF2,TEN1,DUSP1,CHRAC1,RGCC,MAP2K7	grey	VSMC_M10
GO:0001568	1.00	0.00	255	576	blood vessel development	BP	1	LRP1,SEMA6A,TNFAIP3,ADM2,SLC12A2,QKI,CCDC134,BAK1,RSPO3,AGO2,PTK2,TAB1,MAPK14,NTRK2,SMO,MYH9,FOXH1,TEK,PTK7,CEMIP2,SRF,SLC1A1,TFAP2B,PDCL3,C1GALT1,NINJ1,SHB,MEOX2,TNNI3,EPAS1,HOXA7,HOXA13,EMC10,ANKRD17,CXCL8,EPGN,AQP1,BMPER,TGFA,PTN,ITGB1BP1,AGO1,YWHAZ,TSPAN12,EPHA1,CNTRL,GAB1,TEAD2,NRCAM,OSR1,APOB,SPHK2,WISP3,NDNF,C5AR1,PRKD2,SLC39A12,MEGF8,ACVR2B,KLF5,PAXIP1,SPRY2,WNT11,RIN2,TGFBR2,OVOL2,ISM1,JAG1,ACTG1,DCN,PANK2,BTG1,AIMP1,FLT1,EPHB1,PLK2,POFUT1,IL1A,NR4A1,PIK3CB,ERAP1,HAND2,HPGD,EYA1,PARVA,ROBO1,ROBO2,FBXW7,MEF2C,VEGFC,ADAMTS1,PTK2B,RAPGEF2,OTULIN,NKX3-1,HDAC7,RAPGEF3,LOXL2,TBX5,AGGF1,ARHGAP24,SPINT1,PKD2,STK4,HIF1AN,PRICKLE1,ADTRP,CD40,WARS2,SUFU,GPLD1,FAP,PKNOX1,HYAL1,SLC2A10,SP100,TERT,TGFB2,TCF7L2,PDCD6,PRKX,DAG1,EGF,ENPEP,GPER1,AGT,MCAM,CIB1,WASF2,GBX2,NFATC4,VASH2,MMP21,MAP3K3,EPHB3,GLUL,EFEMP2,APOLD1,E2F2,LUZP1,APOD,SETD2,ADAM8,NFE2L2,FZD5,MIA3,CTSH,EPHB4,IL12A,FN1,PDCD10,CXCR2,WNT4,CALCRL,HSPG2,RAMP2,STAT3,MAPK1,RHOJ,BMPR1A,RBPJ,MED1,ALDH1A2,PLXDC1,SYNJ2BP,ANXA2,NAXE,PSEN1,SEMA4A,FGF18,FOXO4,NGFR,DLX3,PGF,EFNA1,VASH1,CITED1,IL6R,MAP2K1,TMEM100,VEZF1,MAP2K5,NOX5,TNMD,LDLR,PRKCB,DCTN5,TBX4,TBX2,BCAS3,STRA6,ANGPTL6,TNFAIP2,MAPK7,AMOT,GATA6,MIB1,AP2B1,CCL2,ESM1,ISL1,ZBTB14,LAMA1,LEPR,JAK1,C3,GPC3,JUN,SERPINF2,PDPK1,PKD1,MECP2,BSG,COL5A1,FOXF1,VAV3,ENG,GLMN,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR125B1,MIR22,MIR27	grey	VSMC_M10
GO:0045765	1.00	0.00	90	229	regulation of angiogenesis	BP	1	SEMA6A,TNFAIP3,ADM2,SLC12A2,AGO2,TEK,CEMIP2,PDCL3,NINJ1,EMC10,CXCL8,AQP1,BMPER,PTN,AGO1,TSPAN12,EPHA1,GAB1,WISP3,C5AR1,PRKD2,SLC39A12,SPRY2,TGFBR2,ISM1,DCN,BTG1,FLT1,PLK2,IL1A,PIK3CB,ERAP1,VEGFC,ADAMTS1,PTK2B,RAPGEF3,AGGF1,CD40,HYAL1,SP100,TERT,TGFB2,PDCD6,AGT,VASH2,GLUL,E2F2,NFE2L2,CTSH,CXCR2,HSPG2,RAMP2,STAT3,RHOJ,SYNJ2BP,NAXE,SEMA4A,FGF18,FOXO4,PGF,EFNA1,VASH1,TNMD,PRKCB,MAPK7,AMOT,GATA6,ISL1,JAK1,C3,PDPK1,MECP2,ENG,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR125B1,MIR27B,MIR24-1,ACVRL1,FOXJ2,MIR125A,MIR99B,WNT5A,GADD45A,ZNF304,RGCC,FGF1	grey	VSMC_M10
GO:1905818	1.00	0.00	18	65	regulation of chromosome separation	BP	1	ZNF207,MAPK15,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,MOS,ANAPC5,ANAPC7,CSNK2A2,HECW2,ANAPC4,LCMT1,PSMG2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0051306	1.00	0.00	16	60	mitotic sister chromatid separation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,ANAPC5,ANAPC7,HECW2,DIS3L2,ANAPC4,LCMT1,PSMG2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0090132	1.00	0.00	105	262	epithelium migration	BP	1	PTK2,PTP4A3,MYH9,TEK,SRF,KIT,MEOX2,SVBP,PRKCE,RTN4,EPB41L4B,EMC10,BMPER,PTN,ITGB1BP1,MET,PRKD2,IQSEC1,SOX9,CLASP2,PAXIP1,RIN2,TGFBR2,HBEGF,FERMT1,DCN,SEMA3A,FOXP1,PLK2,GPI,NR4A1,PIK3CB,LPXN,ATP5F1A,ROBO1,FBXW7,MEF2C,VEGFC,PTK2B,DOCK5,STC1,HDAC7,LOXL2,RREB1,ADTRP,CD40,PXN,GPLD1,FAP,HYAL1,SP100,TGFB2,PDCD6,PRKX,EGF,AGT,CIB1,MAP3K3,DOCK1,PATZ1,GLUL,NFE2L2,MIA3,DUSP10,CTSH,EPHB4,S100P,PDCD10,RHOJ,SYNJ2BP,SEMA4A,RAB25,FGF18,ITGA3,EFNA1,VASH1,RAB11A,MAP2K5,BCAS3,EVL,AMOT,PDPK1,MECP2,LCN2,MARVELD3,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,DPP4,ACVRL1,NANOS1,ZNF580,WNT5A,GADD45A,RGCC,FGF1,S100A2	grey	VSMC_M10
GO:1901342	1.00	0.00	91	232	regulation of vasculature development	BP	1	SEMA6A,TNFAIP3,ADM2,SLC12A2,AGO2,TEK,CEMIP2,PDCL3,NINJ1,EMC10,CXCL8,AQP1,BMPER,PTN,AGO1,TSPAN12,EPHA1,GAB1,WISP3,C5AR1,PRKD2,SLC39A12,SPRY2,TGFBR2,ISM1,DCN,BTG1,FLT1,PLK2,IL1A,PIK3CB,ERAP1,VEGFC,ADAMTS1,PTK2B,RAPGEF3,AGGF1,CD40,HYAL1,SP100,TERT,TGFB2,PDCD6,AGT,VASH2,GLUL,E2F2,NFE2L2,CTSH,CXCR2,WNT4,HSPG2,RAMP2,STAT3,RHOJ,SYNJ2BP,NAXE,SEMA4A,FGF18,FOXO4,PGF,EFNA1,VASH1,TNMD,PRKCB,MAPK7,AMOT,GATA6,ISL1,JAK1,C3,PDPK1,MECP2,ENG,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR125B1,MIR27B,MIR24-1,ACVRL1,FOXJ2,MIR125A,MIR99B,WNT5A,GADD45A,ZNF304,RGCC,FGF1	grey	VSMC_M10

GO:0010965	1.00	0.00	15	58	regulation of mitotic sister chromatid separation	BP	1	ZNF207,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,ANAPC5,ANAPC7,HECW2,ANAPC4,LCMT1,PSMG2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0009057	1.00	0.00	518	1102	macromolecule catabolic process	BP	1	VPS4B,NEDD4L,PAN2,LRP1,FEM1C,RMND5B,TNFAIP3,AGAP2,USP15,CANX,TRIM39,CNOT2,CNOT6,RIDA,PABPC1,PHAX,HSPA1B,SKIV2L,DXO,EIF3E,PNLDC1,PRKN,RNF5,PSMB8,DERL1,SKP1,UBE2B,RNF217,CSDC2,RNF146,TRIB1,KLHL3,AGO2,PTK2,TNRC6B,TUT7,AGTPBP1,GTPBP1,MAPK14,CSNK1E,EXOSC4,FOXRED2,HSF1,FBXL6,USP49,FBXO7,KLHDC3,ABHD17B,CEMIP2,DCAF12,USP46,LNX1,CNOT11,RGP1,PDCL3,FBXO10,EXOSC3,LRPPRC,SEC61B,RNF20,RAD23B,UBE3D,PNPT1,ECPAS,PPT1,XPO1,PELI1,WDR91,CNOT4,RNASEH1,FBXO48,AGO1,EGFR,HECW1,USP45,TRIM32,ASCC3,HACE1,USP38,VPS35,ZYG11B,SDCBP,TUT4,PUM2,MGAM,MFSD8,APOB,FAF1,TRAF3IP2,MTPAP,MTMR2,ZC3HAV1,BBS7,RAB7A,DHX34,FBXL13,PHB,SOX9,PYGB,NUDT15,FBXL2,GLB1,KCTD2,PLK3,SUMO2,FASTK,MLH1,USP35,KBTBD6,KCTD21,DEDD2,AQP11,MYD88,DMAC2,TIMP4,EGLN2,MYCBP2,UBXN4,UBE3C,SPOPL,FBH1,TNRC6C,PPP1CB,UBE2E1,KLHL40,ARRB1,SNX5,UGGT2,USP36,FBXO17,SIRT2,DNAJC18,NPLOC4,TMEM106B,UBAC2,NHLRC3,LSM1,NUDT16,RNF14,RNF122,NRG1,USP44,DDRGK1,SH3RF2,RYBP,TRIM3,PPP2CB,UBXN8,PKP3,UPF3A,PPP1R3B,PAN3,NSFL1C,PCBP2,PSMF1,PSMD6,TRIB3,PLK2,LYPLA1,ERCC8,KCTD6,CEBPA,IDE,NUDT12,ARMC8,SNX25,FOXL2,SPSB4,RNF7,TAF9,UBE2L6,ZCCHC8,FBXO8,TRPC4AP,TTC37,SH3D19,ARNTL,FBXW7,USP25,TRIM2,ENC1,ANAPC5,HTRA2,AUP1,CNOT1,ANAPC7,CELF1,CHMP4C,CSNK2A2,CTSO,USP16,PTK2B,CNOT6L,FAM192A,PFKM,TENT2,TMEM67,AMFR,RNFT2,FBXO21,RIPK1,FTO,MARCH7,KCNE2,ERLIN1,TTC3,PRICKLE1,NKD1,TENT5C,MYLIP,FBXW4,TENT4B,RBM24,TOLLIP,SIAH1,LONP2,NHLRC1,FBXL15,RNF1	grey	VSMC_M10
GO:0051052	1.00	0.00	121	297	regulation of DNA metabolic process	BP	1	EYA4,MRNIP,HELB,PPP1R10,MAP3K4,UBE2B,MYC,MAPK15,HSF1,POT1,EXOSC3,STPG4,MSH2,CYREN,EGFR,HMCES,PRKD2,ERCC1,ERCC2,XRCC1,MLH1,DACH1,ZRANB3,PAXIP1,WDR48,FBH1,KPNA2,RNF169,FAM168A,SIRT7,SHLD1,TFDP1,WRN,PPP4R2,TEX15,PRKDC,ERCC6,TOX,ERCC8,PARP4,OTUD4,ATR,EYA1,SLF1,HMBOX1,PTK2B,MAPKAPK5,NBN,ABRAXAS1,SPIDR,WRNIP1,SLF2,NPM2,TENT4B,CD40,STN1,AXIN2,POLG2,EYA3,PARP9,DTX3L,KCNK2,CD28,RNF168,RTEL1,MGMT,SETD2,STOX1,BCL6,MEN1,XRCC5,ZCWPW1,UPF1,MAPK1,WAS,DDX11,RAD52,FOXP3,PARP1,SHLD2,NVL,GNL3L,FGFR4,UIMC1,TBX21,WRAP53,SMG5,KAT7,YLPM1,CTC1,PIF1,MAPK3,OTUB2,SMCHD1,IL7R,SUPT6H,PARN,ERCC4,RMI2,MBD1,NUDT16L1,PAM16,SLX4,MECP2,WDR18,SPIRE2,TERF2,MIR29A,OOEP,ACVRL1,TINF2,TEN1,TIGAR,DUSP1,RNF8,RGCC,UBE2N,BRCC3,MAP2K7,CBX8,NMNAT1	grey	VSMC_M10
GO:0008152	1.00	0.00	4415	8467	metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,CD226,NME1,SERPINB8,SERPINB2,RDH5,VPS4B,KDSR,PHLPP1,ORMDL2,SUOX,ERBB3,SEC11C,ZC3H10,SMARCC2,NEDD4L,PAN2,APOF,ATP8B1,FECH,ONECUT2,GLS2,BAZ2A,TCF4,RDH16,POLI,HSD17B4,TNFAIP8,RNMT,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,ALDH8A1,GLI1,HBS1L,MARS,B4GALT7,RMND5B,PDE7B,CLK4,PIP4K2C,MAP3K5,PEX7,B4GALNT1,RPA3,TNFAIP3,AGAP2,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,AIG1,ADAT2,FUCA2,ATP23,PLAGL1,USP15,EPM2A,FBXO30,RXYLT1,CANX,MAML1,LTC4S,MRNIP,ENPP3,ATP5MGL,HELB,TRIM39,RPP21,PPP1R10,ATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,TSPAN8,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,SNCAIP,FBXO43,MIOX,PABPC1,SNW1,TFB1M,ZNF706,CPT1B,ALDH7A1,PHAX,MARCH3,APOM,ABHD16A,ARID1B,ADM2,ZDHHC14,HSPA1B,SYNJ2,SERAC1,TULP4,FZD6,RIMS2,ZBTB12,DPYS,SKIV2L,SF3A3,SELENOO,DXO,MOV10L1,EIF3E,SLC27A6,ALG12,CYP21A2,ZBED4,TMEM74,BRD1,ADAMTS19,LYRM7,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,AGPAT4,PPT2,PRKN,AGPAT1,QKI,RNF5,AGER,TRMU,PPARA,GPSM3,PDE10A,ACSL6,HLA-DRA,FBLN1,HLA-DOB,UTP23,P4HA2,MED30,PSMB8,SLC22A4,HLA-DMA,IL5,BRD2,TAF2,PNPLA3,PNPLA5,SULT4A1,HLA-DPB1,ZUP1,RXRB,TSPO,GDF9,MCAT,UQCRQ,VGLL2,ROS1,HSD17B8,MCM9,ASF1A,MRPL13,A4GALT,RPS18,RRP7A,HSF2,DERL1,NDUFA6,TCF7,SKP1,PHF1,SMPDL3A,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,RNF146,ECHDC1,AL096711.2,ACO2,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,KLHL3,	grey	VSMC_M10

GO:0030334	1.00	0.00	332	735	regulation of cell migration	BP	1	ONECUT2,LRP1,SEMA6A,SRGAP1,AGER,GPSM3,TRIB1,AGO2,PTK2,MAPK15,PLXNA4,SUN2,PODXL,RAC2,SMO,TEK,SRF,CCL27,KIT,ROR2,SEMA4D,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,RNF20,PRKCE,RTN4,FPR2,HAS1,EPB41L4B,RUFY3,HOXA7,EMC10,CXCL8,BMPER,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,GAB1,SDCBP,FOXO3,FGF21,PLXNA1,LAMA4,C5AR2,C5AR1,PRKD2,IQSEC1,SOX9,BEX4,CLASP2,MYD88,OXSR1,DACH1,CYGB,SPRY2,WNT11,RIN2,AKT2,TGFBR2,SRGAP3,JAG1,ACTG1,NAV3,HBEGF,PLCB1,FERMT1,CNN2,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,PLXNC1,SEMA3A,UNC5D,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,DPYSL3,FLT1,PLK2,MTUS1,RET,AL359736.1,FAM107A,GPI,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,ATP5F1A,ROBO1,FBXW7,PTPRJ,MEF2C,ELP3,SEMA4F,VEGFC,JAM2,IGSF10,ADAMTS1,PTK2B,RAPGEF2,TIAM1,FGF5,DOCK5,SLC8B1,STC1,HDAC7,NKX6-1,TBX5,ACVR1C,F2RL1,F2R,ANO6,TP53INP1,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,ADTRP,NOD2,NKD1,CD40,LDB1,SRGAP2C,GPLD1,DOCK10,CD200,SLK,LGR6,DNM1L,CARMIL1,HYAL1,PPP3CA,SINHCAF,SP100,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,ADARB1,CD99,GNA13,PRKX,DAG1,TTBK2,PRSS56,SSH1,AJUBA,CMKLR1,SNAI1,EGF,ABHD2,SORL1,GPER1,SLAMF8,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,CERS2,HDAC4,LAMA5,CHRD,CLIC4,MAP3K3,DOCK1,PATZ1,GLUL,ELP6,LRIG2,APOD,ADAM8,LRRC15,FRMD5,NFE2L2,TBCCD1,MIA3,DUSP10,CCAR1,CEMIP,SEMA6D,TRIP6,CTSH,ITGA2B,ITGA4,IL12A,FN1,VSIR,MCU,PDCD10,TNFSF18,FERMT3,CXCR2,WNT4,COL3A1,STAT3,VCL,BST1,	grey	VSMC_M10
GO:0051270	1.00	0.00	379	830	regulation of cellular component movement	BP	1	ONECUT2,LRP1,SEMA6A,SRGAP1,AGER,GPSM3,FBLN1,TRIB1,AGO2,PTK2,MAPK15,PLXNA4,SUN2,PODXL,RAC2,SMO,TEK,SRF,CFAP69,CCL27,CDK6,KIT,ROR2,SEMA4D,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,RNF20,PRKCE,EPCAM,DNAH11,RTN4,FPR2,HAS1,EPB41L4B,RUFY3,HOXA7,EMC10,CXCL8,BMPER,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,GAB1,SDCBP,TRPM4,FOXO3,ARMC4,FGF21,PLXNA1,LAMA4,C5AR2,C5AR1,SLC26A5,PRKD2,DRC1,IQSEC1,SOX9,BEX4,CLASP2,RAF1,MYD88,OXSR1,DACH1,SCN5A,MYCBP2,CYGB,SPRY2,WNT11,RIN2,AKT2,TGFBR2,SRGAP3,JAG1,MKKS,ACTG1,NAV3,HBEGF,PLCB1,FERMT1,SPINT2,CNN2,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,PLXNC1,SEMA3A,UNC5D,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,DPYSL3,FLT1,PLK2,MTUS1,RET,AL359736.1,FAM107A,GPI,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,ATP5F1A,ROBO1,FBXW7,PTPRJ,MEF2C,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,IGSF10,ADAMTS1,PTK2B,RAPGEF2,CCDC65,TIAM1,FGF5,DOCK5,SLC8B1,STC1,HDAC7,NKX6-1,TBX5,ACVR1C,F2RL1,F2R,ANO6,TNNC1,TP53INP1,SEMA3G,RREB1,DSP,STK4,GCNT2,DMTN,SEMA4G,ADTRP,NOD2,NKD1,CD40,LDB1,RYR2,SRGAP2C,GPLD1,DOCK10,CD200,PKP2,SLK,LGR6,DNM1L,CARMIL1,CFAP43,HYAL1,PPP3CA,SINHCAF,SP100,KCNJ2,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,ADARB1,CD99,GNA13,PRKX,DAG1,TTBK2,PRSS56,SSH1,AJUBA,CMKLR1,SNAI1,EGF,ABHD2,TTC21B,AP1AR,SORL1,ANK2,GPER1,SLAMF8,CFAP45,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,ATP1A2,CERS2,HDAC4,LAMA5,YTHDF1,PTPRO,CNIH2,CHRD,CLIC4,MAP3K3,DOCK1,PATZ1,GLUL,ELP6,	grey	VSMC_M10
GO:0034504	1.00	0.00	96	244	protein localization to nucleus	BP	1	PPP1R10,SKP1,FAM53C,C6orf106,SUN2,MAPK14,SMO,TAF8,RAB23,SIX2,XPO1,TRAF3IP2,KPNA3,SOX9,IPO13,TAF3,GCKR,KPNA2,TMCO6,NUP98,FERMT1,ING1,MAVS,WRN,MFHAS1,NUP58,IPO11,POLR1A,PIK3R1,DCLK2,TNPO1,PKIA,NUP54,ARL2BP,CRY2,MORC3,PRICKLE1,SUFU,CABP1,RPL23,PPP3CA,IPO9,SP100,TERT,TBRG1,INTS13,HCLS1,OTUD7B,PARP9,DTX3L,AGT,BAG3,TOR1AIP1,LIMK2,GLUL,EIF4ENIF1,RPL11,POM121,APOD,PIKFYVE,MEPCE,FAM53A,STAT3,MAPK1,ATP13A2,MAGED1,PARP1,NVL,MED1,KPNB1,WRAP53,TARDBP,PSEN1,NGFR,RANBP17,KAT7,TNPO2,SMAD3,SIN3A,EFCAB7,ABCA7,PARK7,BANP,NUP214,LAMTOR5,TOR1B,NXT2,SUPT7L,CNEP1R1,SIX1,RASSF5,HIKESHI,TXN,LIF,PTTG1IP,ZIC1	grey	VSMC_M10
GO:2000145	1.00	0.00	350	772	regulation of cell motility	BP	1	ONECUT2,LRP1,SEMA6A,SRGAP1,AGER,GPSM3,FBLN1,TRIB1,AGO2,PTK2,MAPK15,PLXNA4,SUN2,PODXL,RAC2,SMO,TEK,SRF,CFAP69,CCL27,CDK6,KIT,ROR2,SEMA4D,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,RNF20,PRKCE,EPCAM,RTN4,FPR2,HAS1,EPB41L4B,RUFY3,HOXA7,EMC10,CXCL8,BMPER,AKIRIN1,PTN,ITGB1BP1,MET,EGFR,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,GAB1,SDCBP,FOXO3,FGF21,PLXNA1,LAMA4,C5AR2,C5AR1,SLC26A5,PRKD2,IQSEC1,SOX9,BEX4,CLASP2,RAF1,MYD88,OXSR1,DACH1,CYGB,SPRY2,WNT11,RIN2,AKT2,TGFBR2,SRGAP3,JAG1,MKKS,ACTG1,NAV3,HBEGF,PLCB1,FERMT1,SPINT2,CNN2,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,PLXNC1,SEMA3A,UNC5D,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,DPYSL3,FLT1,PLK2,MTUS1,RET,AL359736.1,FAM107A,GPI,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,ATP5F1A,ROBO1,FBXW7,PTPRJ,MEF2C,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,IGSF10,ADAMTS1,PTK2B,RAPGEF2,TIAM1,FGF5,DOCK5,SLC8B1,STC1,HDAC7,NKX6-1,TBX5,ACVR1C,F2RL1,F2R,ANO6,TP53INP1,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,ADTRP,NOD2,NKD1,CD40,LDB1,SRGAP2C,GPLD1,DOCK10,CD200,SLK,LGR6,DNM1L,CARMIL1,HYAL1,PPP3CA,SINHCAF,SP100,TERT,TRPV4,SEMA3F,TGFB2,ADRA2A,PDCD6,ADARB1,CD99,GNA13,PRKX,DAG1,TTBK2,PRSS56,SSH1,AJUBA,CMKLR1,SNAI1,EGF,ABHD2,AP1AR,SORL1,GPER1,SLAMF8,CFAP45,MOSPD2,CASS4,AGT,FGR,MCAM,CIB1,CERS2,HDAC4,LAMA5,CHRD,CLIC4,MAP3K3,DOCK1,PATZ1,GLUL,ELP6,LRIG2,APOD,ADAM8,LRRC15,FRMD5,NFE2L2,TBCCD1,MIA3,DUSP10,DUOX1,CCAR1,CEMIP,ABL2,SEMA6D,TRIP6,CTSH,ITGA2B,ITGA4,IL12	grey	VSMC_M10

GO:0008283	1.00	0.00	689	1442	cell population proliferation	BP	1	NME1,ERBB3,SLC39A5,C18orf54,LRP1,SHMT2,PGGT1B,GLI1,B4GALT7,MAP3K5,RPA3,TNFAIP3,TSPAN31,CYP27B1,ENPP3,ESR1,FRS2,CNOT6,RIDA,STK3,OSR2,SNW1,HSPA1B,FZD6,AGER,FBLN1,IL5,HLA-DPB1,TSPO,GDF9,TNFRSF13C,BAK1,XRCC6,MTSS1,TRIB1,MYC,TOB2,H3F3C,PTK2,PTCH1,AKR1B1,MAPK15,AGTPBP1,MAPK14,NTRK2,C6orf89,KDM4C,SOX10,PIM1,RAC2,SMO,HSF1,CCND3,TAF8,CDKN2A,ZNF16,RBFOX2,IFT74,TEK,SRF,ABCB1,NUAK1,CNTFR,TXNRD1,CDK6,SMARCA2,SLC25A27,KIT,TNFRSF21,NCK2,TFAP2B,ROR2,DLX5,S1PR3,TBC1D8,PDCL3,WNK2,OGN,PRDX1,ZNF268,CLDN19,SIX2,IL11,EPCAM,CD109,FKTN,RTN4,PHIP,GSDME,SKAP2,FANCL,EMC10,CXCL8,EPGN,AREG,ORC3,AKIRIN2,AQP1,PELI1,BMPER,AKIRIN1,AKNA,TGFA,PTN,ITGB1BP1,MED25,KLF11,TNC,IL4I1,POU3F3,EGFR,FUZ,TRIM32,TLR4,ASCC3,EPHA1,IL15,SFRP4,SDCBP,MYCN,TRPM4,SLC7A11,OSR1,FOXO3,EPS15,FGF21,INTU,SPHK2,CDCA7,SPRY1,WISP3,FOXE3,HDAC2,BMI1,C5AR2,C5AR1,RAB10,PRKD2,PTGIR,CNBP,PHB,ABI1,SOX9,BEX4,ERCC1,ERCC2,GAB2,CDC123,GLI2,AQP11,RAF1,MYD88,DACH1,PRDX3,KLF5,IFT172,FOXJ1,SCN5A,WDR48,NUMBL,ACER3,SPRY2,THAP12,WNT11,ALK,AKT2,HOOK3,RBBP9,ARRB1,THAP1,ABCC4,EID2,TGFBR2,OVOL2,ACVR2A,JAG1,SIRT2,NMI,RPTOR,RARB,PURA,HBEGF,PAWR,PLCL2,MAP4K1,MAFG,RASGRP4,FERMT1,CHTOP,SPINT2,CNN2,EIF2AK2,PRNP,ADRA1D,ING1,ASH2L,BTG1,MAB21L1,AIMP1,PDK1,NRG1,TFDP1,CCKBR,DDRGK1,NCKAP1L,GAS6,FOXP1,MITF,MTA3,PRKDC,ALKBH3,SLC7A1,FLT1,RYK,ST18,CIAO1,TMEM127,SDCBP2,TRAF6,EPHB1,GAPT,PLAG1,SDR16C5,LGI4,HCK,TOX,IL1A,CYP7B1,NR4A1,CEBPA,FE	grey	VSMC_M10
GO:0001525	1.00	0.00	182	428	angiogenesis	BP	1	SEMA6A,TNFAIP3,ADM2,SLC12A2,CCDC134,RSPO3,AGO2,PTK2,MAPK14,MYH9,TEK,CEMIP2,SRF,PDCL3,C1GALT1,NINJ1,SHB,MEOX2,EPAS1,HOXA7,EMC10,CXCL8,EPGN,AQP1,BMPER,TGFA,PTN,ITGB1BP1,AGO1,YWHAZ,TSPAN12,EPHA1,GAB1,NRCAM,WISP3,NDNF,C5AR1,PRKD2,SLC39A12,KLF5,SPRY2,TGFBR2,OVOL2,ISM1,JAG1,ACTG1,DCN,PANK2,BTG1,AIMP1,FLT1,EPHB1,PLK2,POFUT1,IL1A,NR4A1,PIK3CB,ERAP1,HAND2,PARVA,ROBO1,FBXW7,VEGFC,ADAMTS1,PTK2B,OTULIN,HDAC7,RAPGEF3,LOXL2,AGGF1,ARHGAP24,STK4,ADTRP,CD40,GPLD1,FAP,PKNOX1,HYAL1,SP100,TERT,TGFB2,PDCD6,PRKX,DAG1,EGF,ENPEP,AGT,MCAM,CIB1,WASF2,GBX2,NFATC4,VASH2,MAP3K3,EPHB3,GLUL,APOLD1,E2F2,APOD,SETD2,ADAM8,NFE2L2,FZD5,MIA3,CTSH,EPHB4,IL12A,FN1,PDCD10,CXCR2,CALCRL,HSPG2,RAMP2,STAT3,RHOJ,RBPJ,MED1,PLXDC1,SYNJ2BP,ANXA2,NAXE,SEMA4A,FGF18,FOXO4,NGFR,PGF,EFNA1,VASH1,TMEM100,VEZF1,MAP2K5,NOX5,TNMD,PRKCB,TBX4,BCAS3,ANGPTL6,TNFAIP2,MAPK7,AMOT,GATA6,CCL2,ESM1,ISL1,LEPR,JAK1,C3,JUN,PDPK1,MECP2,BSG,VAV3,ENG,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR125B1,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,ADGRG1,CASP8,ACVRL1,FOXJ2,MIR125A,MIR99B,HOXB3,THY1,WNT5A,GADD45A,CSPG4,ZNF304,RGCC,EREG,FGF1,HOXA3,COL8A2	grey	VSMC_M10
GO:0048514	1.00	0.00	220	508	blood vessel morphogenesis	BP	1	LRP1,SEMA6A,TNFAIP3,ADM2,SLC12A2,QKI,CCDC134,BAK1,RSPO3,AGO2,PTK2,MAPK14,NTRK2,SMO,MYH9,FOXH1,TEK,CEMIP2,SRF,SLC1A1,TFAP2B,PDCL3,C1GALT1,NINJ1,SHB,MEOX2,TNNI3,EPAS1,HOXA7,HOXA13,EMC10,CXCL8,EPGN,AQP1,BMPER,TGFA,PTN,ITGB1BP1,AGO1,YWHAZ,TSPAN12,EPHA1,GAB1,TEAD2,NRCAM,APOB,WISP3,NDNF,C5AR1,PRKD2,SLC39A12,KLF5,PAXIP1,SPRY2,WNT11,RIN2,TGFBR2,OVOL2,ISM1,JAG1,ACTG1,DCN,PANK2,BTG1,AIMP1,FLT1,EPHB1,PLK2,POFUT1,IL1A,NR4A1,PIK3CB,ERAP1,HAND2,HPGD,EYA1,PARVA,ROBO1,FBXW7,VEGFC,ADAMTS1,PTK2B,RAPGEF2,OTULIN,HDAC7,RAPGEF3,LOXL2,TBX5,AGGF1,ARHGAP24,PKD2,STK4,HIF1AN,ADTRP,CD40,WARS2,GPLD1,FAP,PKNOX1,HYAL1,SP100,TERT,TGFB2,PDCD6,PRKX,DAG1,EGF,ENPEP,AGT,MCAM,CIB1,WASF2,GBX2,NFATC4,VASH2,MAP3K3,EPHB3,GLUL,EFEMP2,APOLD1,E2F2,APOD,SETD2,ADAM8,NFE2L2,FZD5,MIA3,CTSH,EPHB4,IL12A,FN1,PDCD10,CXCR2,WNT4,CALCRL,HSPG2,RAMP2,STAT3,RHOJ,BMPR1A,RBPJ,MED1,PLXDC1,SYNJ2BP,ANXA2,NAXE,SEMA4A,FGF18,FOXO4,NGFR,PGF,EFNA1,VASH1,CITED1,TMEM100,VEZF1,MAP2K5,NOX5,TNMD,LDLR,PRKCB,TBX4,TBX2,BCAS3,STRA6,ANGPTL6,TNFAIP2,MAPK7,AMOT,GATA6,CCL2,ESM1,ISL1,LAMA1,LEPR,JAK1,C3,JUN,SERPINF2,PDPK1,MECP2,BSG,FOXF1,VAV3,ENG,GLMN,DAB2IP,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR125B1,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,ADGRG1,SOX4,CASP8,ACVRL1,FOXJ2,MIR125A,MIR99B,HOXB3,NOG,THY1,WNT5A,GADD45A,SIX1,CSPG4,ZNF304,RGCC,EREG,NKX2-5,FGF1,HEY2,HOXA3,COL8A2	grey	VSMC_M10

GO:0010563	1.00	0.00	148	356	negative regulation of phosphorus metabolic process	BP	1	LRP1,PIP4K2C,TNFAIP3,PRKN,PPARA,FBLN1,UBE2B,BAK1,TRIB1,STK38,CDKN2A,FBXO7,NCK2,SEMA4D,KLHL31,DNAJA1,CD109,PPP2R1A,IBTK,ACP4,PLEK,ITGB1BP1,GRB10,EPHA1,PRKAR2B,SPRY1,PIP4K2A,APOC1,PRKAG2,PRDX3,PIBF1,GCKR,SPRY2,GPD1L,ARRB1,IKBKB,SIRT2,PTPRQ,PRNP,DUSP6,BAG4,TAF7,NCKAP1L,PRKDC,MFHAS1,TRIB3,CEBPA,PIK3CB,SNX25,CASP3,PTPRJ,PKIA,PAQR3,CRY2,DBNDD2,DMTN,DTNBP1,LPCAT1,LRRK1,PDCD4,TGFB2,PRKAR1A,ADARB1,AJUBA,FABP4,UBASH3B,SORL1,RTRAF,PARP14,AGT,CIB1,CBL,SFN,PPP2R5A,TRAF3IP1,ACTN3,HDAC4,CAMK2N2,RUBCN,PTPRO,INPP5J,MLXIPL,PIK3IP1,SNX6,CDKN1B,AIDA,YWHAG,DUSP10,MAPT,HEXIM2,MEN1,DNAJC10,DUSP19,PTPN6,FKBP8,ZFYVE28,SOCS4,STAT3,TIPRL,SLC27A1,INHA,PARP1,RGS14,DGKQ,TARDBP,BOD1L2,PSEN1,PYDC1,COX11,CALM1,PPP4R4,BDKRB1,NCOR1,SMCR8,SUZ12,PTPN2,SOCS1,INPP5K,PDPK1,PRKCZ,PARK7,DBNDD1,PIP5KL1,ENG,DAB2IP,MIR27B,MIR24-1,DMD,MIR125A,PDZD3,IMPACT,NOG,SMYD3,THY1,TIGAR,GADD45A,DUSP26,DUSP1,PPP1R15A,APC,DUSP22,LAX1,CADM4,LDLRAD4,PARD6A,TMEM225B,PRKRIP1,ARPP19	grey	VSMC_M10
GO:0045936	1.00	0.00	148	356	negative regulation of phosphate metabolic process	BP	1	LRP1,PIP4K2C,TNFAIP3,PRKN,PPARA,FBLN1,UBE2B,BAK1,TRIB1,STK38,CDKN2A,FBXO7,NCK2,SEMA4D,KLHL31,DNAJA1,CD109,PPP2R1A,IBTK,ACP4,PLEK,ITGB1BP1,GRB10,EPHA1,PRKAR2B,SPRY1,PIP4K2A,APOC1,PRKAG2,PRDX3,PIBF1,GCKR,SPRY2,GPD1L,ARRB1,IKBKB,SIRT2,PTPRQ,PRNP,DUSP6,BAG4,TAF7,NCKAP1L,PRKDC,MFHAS1,TRIB3,CEBPA,PIK3CB,SNX25,CASP3,PTPRJ,PKIA,PAQR3,CRY2,DBNDD2,DMTN,DTNBP1,LPCAT1,LRRK1,PDCD4,TGFB2,PRKAR1A,ADARB1,AJUBA,FABP4,UBASH3B,SORL1,RTRAF,PARP14,AGT,CIB1,CBL,SFN,PPP2R5A,TRAF3IP1,ACTN3,HDAC4,CAMK2N2,RUBCN,PTPRO,INPP5J,MLXIPL,PIK3IP1,SNX6,CDKN1B,AIDA,YWHAG,DUSP10,MAPT,HEXIM2,MEN1,DNAJC10,DUSP19,PTPN6,FKBP8,ZFYVE28,SOCS4,STAT3,TIPRL,SLC27A1,INHA,PARP1,RGS14,DGKQ,TARDBP,BOD1L2,PSEN1,PYDC1,COX11,CALM1,PPP4R4,BDKRB1,NCOR1,SMCR8,SUZ12,PTPN2,SOCS1,INPP5K,PDPK1,PRKCZ,PARK7,DBNDD1,PIP5KL1,ENG,DAB2IP,MIR27B,MIR24-1,DMD,MIR125A,PDZD3,IMPACT,NOG,SMYD3,THY1,TIGAR,GADD45A,DUSP26,DUSP1,PPP1R15A,APC,DUSP22,LAX1,CADM4,LDLRAD4,PARD6A,TMEM225B,PRKRIP1,ARPP19	grey	VSMC_M10
GO:0040011	1.00	0.00	637	1349	locomotion	BP	1	ONECUT2,ARPC3,LRP1,SEMA6A,KIF5A,TNFAIP3,SRGAP1,SLC12A2,AGER,GPSM3,FBLN1,TSPO,CEP85L,UBE2B,CATSPER3,TRIB1,CXCL14,LRRC6,AGO2,GFRA3,PTK2,PTP4A3,PTCH1,ANKS1A,MAPK15,PLXNA4,SUN2,MAPK14,NTRK2,PODXL,PLA2G6,SOX10,RAC2,STRIP2,SMO,MYH9,RBFOX2,TEK,GPR37,FBXO7,ZFAND5,PTK7,SRF,CFAP69,CCL27,CDK6,RFX3,KIT,NCK2,PLGRKT,ROR2,SEMA4D,DLX5,EFHC1,NINJ1,ETV1,ADGRL3,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,SIX2,DNAJA1,RNF20,PRKCE,EPCAM,MBOAT7,DNAH11,RTN4,FPR2,HAS1,EPB41L4B,CABS1,RUFY3,HOXA2,HOXA7,EMC10,LPAR1,CXCL8,AVL9,BMPER,AKIRIN1,EPHA7,PTN,ITGB1BP1,MET,ADD2,GRB10,POU3F3,EGFR,USP45,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,BVES,GAB1,SDCBP,NRCAM,TRPM4,FOXO3,ARMC2,MAPRE1,APOB,FGF21,PLXNA1,LAMA4,PODXL2,ADCY3,NDNF,C5AR2,C5AR1,SLC26A5,PRKD2,DRC1,IQSEC1,SOX9,RSPH6A,BEX4,LCP1,CLASP2,GLI2,MEGF8,RAF1,MYD88,OXSR1,DACH1,FOXJ1,PAXIP1,PTPRF,TTC21A,MYCBP2,CYGB,POU4F1,SPRY2,PLAT,WNT11,TTLL3,RIN2,ACKR2,AKT2,CMTM7,CMTM8,TGFBR2,OVOL2,SRGAP3,KIF5C,JAG1,MKKS,ACTG1,FSCN2,NAV3,HBEGF,PLCB1,FEZ2,FERMT1,SPINT2,CNN2,ALX1,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,BTG1,SPEF1,PLXNC1,SEMA3A,CHL1,UNC5D,AIMP1,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,FAM19A4,DPYSL3,FLT1,RYK,EPHB1,PLK2,MTUS1,RET,AL359736.1,HCK,FAM107A,CYP7B1,GPI,NR4A1,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,LPXN,HAND2,ATP5F1A,ING2,PARVA,ROBO1,DNAH6,ROBO2,WDR66,FBXW7,LIMA1,PTPRJ,FZD3,MEF2C,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,IGSF10,ADAMTS1,P2RY1,PTK2B,RAP	grey	VSMC_M10

GO:0031399	1.00	0.00	555	1182	regulation of protein modification process	BP	1	ERBB3,LRP1,MAP3K5,TNFAIP3,AGAP2,MRNIP,STK3,SNW1,HSPA1B,TNXB,MAP3K4,PRKN,AGER,FBLN1,IL5,TSPO,GDF9,DERL1,SKP1,PHF1,UBE2B,BAK1,XRCC6,NCOA7,TRIB1,PTK2,TAB1,NTRK2,STK38,PLA2G6,C6orf89,HSF1,CCND3,PPP1R16A,CDKN2A,CHRNA3,TEK,FBXO7,CRY1,TTBK1,NUAK1,TEC,KIT,SLC1A1,NCK2,ROR2,SEMA4D,PDCL3,HINT2,KLHL31,SVBP,CLDN19,DNAJA1,IL11,RNF20,PRKCE,EPAS1,CD109,FKTN,PPP2R1A,PHIP,FPR2,IBTK,ACP4,MOB1B,EPGN,AREG,BMP8A,PELI1,BMPER,ETAA1,RSPO1,EPHA7,TNFSF15,TGFA,ITGB1BP1,VRK3,EGFR,ARHGEF5,TLR4,EPHA1,IL15,CCNY,ATG5,SETD7,SDCBP,NTF4,FGF21,BRAF,PRKAR2B,SPHK2,SPRY1,HDAC2,SLC8A2,BMI1,CSAR1,MOB3C,PRKD2,PHB,ABI1,SOX9,SYMPK,BEX4,IWS1,MAPRE3,CRTAP,XRCC1,RALB,KDM4A,PRKAG2,RAF1,PIBF1,PAXIP1,WDR48,MYCBP2,SPOPL,FBH1,SPRY2,WNT11,TADA3,KLHL40,AKT2,GPD1L,ARRB1,TGFBR2,ACVR2A,IKBKB,SIRT2,NMI,NEK10,RPTOR,TCIM,HBEGF,PTPRQ,ASPSCR1,PLCL2,SIRT7,CHTOP,NSD3,PRNP,DUSP6,BAG4,TAF7,MAVS,NRG1,USP44,DDRGK1,SH3RF2,NCKAP1L,GAS6,HPX,RBPMS,PRKDC,ERCC6,MFHAS1,FLT1,ADRA2B,TRAF6,TRIM44,TRIB3,SDR16C5,RET,FAM107A,DNMT3B,ACVR1B,CEBPA,FER,PIK3CB,SNX25,OSBP,OTUD4,SPSB4,ZFP91,HPF1,CDK7,CASP3,TRABD2A,ING2,ROBO1,PLCE1,ARNTL,FBXW7,PTPRJ,PKIA,IL7,CCNH,VEGFC,CCNJ,P2RY1,ATG10,MADD,PTK2B,RASGRP1,CCNG2,FNIP2,RAPGEF2,MOB1A,PRKAG1,EIF2AK4,ARL2BP,TIAM1,PAQR3,FGF5,RIPK2,NBN,NKX3-1,RAPGEF3,RIPK1,CRY2,CCNJL,CDYL,MARCH7,CDK2AP1,RTF1,PKD2,STK4,DBNDD2,DMTN,PRICKLE1,ADTRP,HERC5,NOD2,PRMT3,CNTN1,ZNF335,JARID2,DTNBP	grey	VSMC_M10
GO:0035239	1.00	0.00	312	699	tube morphogenesis	BP	1	LRP1,SEMA6A,GLI1,TNFAIP3,ESR1,STK3,ADM2,SLC12A2,FZD6,QKI,BRD2,CCDC134,BAK1,MTSS1,RSPO3,MYC,KLHL3,AGO2,PTK2,PTCH1,MAPK14,NTRK2,PODXL,SOX10,SMO,MYH9,FOXH1,TEK,PTK7,CEMIP2,SRF,SLC1A1,TFAP2B,PDCL3,C1GALT1,NINJ1,SEMA4C,SHB,MEOX2,SOSTDC1,SIX2,TNNI3,EPAS1,HOXA7,HOXA13,EMC10,CXCL8,EPGN,AREG,AQP1,BMPER,EPHA7,TGFA,PTN,ITGB1BP1,MET,TNC,AGO1,YWHAZ,TSPAN12,FUZ,EPHA1,GAB1,TEAD2,MYCN,NRCAM,OSR1,APOB,SPRY1,WISP3,BBS7,NDNF,C5AR1,PRKD2,SETDB2,SOX9,SLC39A12,GLI2,MEGF8,KLF5,IFT172,PAXIP1,GZF1,SPRY2,WNT11,RIN2,TGFBR2,OVOL2,ISM1,JAG1,MKKS,ACTG1,SPINT2,CEP290,DCN,PANK2,BTG1,AIMP1,FOXP1,FLT1,TRAF6,EPHB1,PLK2,RET,POFUT1,IL1A,PAX8,NR4A1,PIK3CB,CASP3,ERAP1,HAND2,HPGD,EYA1,PARVA,ROBO1,FBXW7,FMN1,FZD3,MEF2C,VEGFC,ADAMTS1,PTK2B,RAPGEF2,OTULIN,VDR,NKX3-1,OPA1,HDAC7,RAPGEF3,LOXL2,TBX5,AGGF1,IFT52,ARHGAP24,SPINT1,PKD2,STK4,HIF1AN,PAX2,SALL1,PRICKLE1,ADTRP,CD40,WARS2,RYR2,SUFU,GPLD1,FAP,IRX2,PKNOX1,HYAL1,SP100,TERT,TGFB2,PDCD6,PRKX,DAG1,HLX,KRAS,EGF,ENPEP,AGT,MCAM,CIB1,WASF2,GBX2,DVL3,NFATC4,VASH2,LAMA5,CLIC4,MAP3K3,GRHL3,EPHB3,GLUL,EFEMP2,APOLD1,E2F2,DLG1,LUZP1,APOD,SETD2,ADAM8,NFE2L2,FZD5,MIA3,STOX1,CTSH,EPHB4,IL12A,FN1,PDCD10,CXCR2,WNT4,CALCRL,HSPG2,RAMP2,STAT3,TULP3,RHOJ,SDCCAG8,EPHA4,LIAS,MAGED1,DVL2,BMPR1A,TCAP,RBPJ,MED1,PLXDC1,SYNJ2BP,ANXA2,NAXE,PSEN1,SEMA4A,FGF18,FOXO4,NGFR,PGF,EFNA1,RBPMS2,VASH1,CITED1,TMEM100,SMAD3,NTN1,VEZF1,MAP2K5,MKS1,NOX5,TNM	grey	VSMC_M10
GO:0044237	1.00	0.00	4114	7918	cellular metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,NME1,SERPINB8,SERPINB2,RDH5,VPS4B,KDSR,PHLPP1,ORMDL2,SUOX,ERBB3,SEC11C,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,FECH,ONECUT2,GLS2,BAZ2A,TCF4,RDH16,POLI,HSD17B4,TNFAIP8,RNMT,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,ALDH8A1,GLI1,HBS1L,MARS,B4GALT7,RMND5B,PDE7B,CLK4,PIP4K2C,MAP3K5,PEX7,B4GALNT1,RPA3,TNFAIP3,AGAP2,CYP27B1,TSFM,AVIL,HIVEP2,AIG1,ADAT2,ATP23,PLAGL1,USP15,EPM2A,FBXO30,RXYLT1,CANX,MAML1,LTC4S,MRNIP,ENPP3,ATP5MGL,HELB,TRIM39,RPP21,PPP1R10,ATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,SNCAIP,FBXO43,MIOX,PABPC1,SNW1,TFB1M,ZNF706,CPT1B,ALDH7A1,PHAX,MARCH3,ABHD16A,ARID1B,ADM2,ZDHHC14,HSPA1B,SYNJ2,SERAC1,TULP4,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,SELENOO,DXO,MOV10L1,EIF3E,SLC27A6,ALG12,CYP21A2,ZBED4,TMEM74,BRD1,LYRM7,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,AGPAT4,PPT2,PRKN,AGPAT1,QKI,RNF5,AGER,TRMU,PPARA,PDE10A,ACSL6,FBLN1,UTP23,P4HA2,MED30,PSMB8,SLC22A4,IL5,BRD2,TAF2,PNPLA3,PNPLA5,SULT4A1,RXRB,TSPO,GDF9,MCAT,UQCRQ,VGLL2,ROS1,HSD17B8,MCM9,ASF1A,MRPL13,A4GALT,RPS18,RRP7A,HSF2,DERL1,NDUFA6,TCF7,SKP1,PHF1,SMPDL3A,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,RNF146,ECHDC1,AL096711.2,ACO2,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,KLHL3,MCHR1,OBSCN,MRPL55,JMJD4,AGO2,PRXL2C,HABP4,RPS10,PTK2,HSD17B3,ERCC6L2,C6orf106,KDM3B,PTP4A3,PTCH1,TNR	grey	VSMC_M10

GO:0006928	1.00	0.00	745	1565	movement of cell or subcellular component	BP	1	NEDD4L,ONECUT2,ARPC3,MYO1A,LRP1,SEMA6A,AP3S1,KIF5A,TNFAIP3,SRGAP1,RAB21,SLC12A2,AGER,GPSM3,FBLN1,KIF3A,TSPO,CEP85L,UBE2B,CATSPER3,TRIB1,CXCL14,LRRC6,AGO2,GFRA3,PTK2,PTP4A3,PTCH1,ANKS1A,MAPK15,AGTPBP1,PLXNA4,SUN2,NTRK2,PODXL,COPG2,SOX10,RAC2,STRIP2,SMO,MYH9,RBFOX2,IFT74,TEK,ZFAND5,PTK7,SRF,CFAP69,APBA1,CCL27,CDK6,RFX3,KIT,NCK2,ROR2,SEMA4D,DLX5,EFHC1,NINJ1,BICD2,ETV1,ADGRL3,SEMA4C,MEOX2,ZNF268,DYNC2LI1,SVBP,LRPPRC,CLDN19,SIX2,DNAJA1,RNF20,PRKCE,EPCAM,MBOAT7,DNAH11,RTN4,FPR2,HAS1,EPB41L4B,CABS1,RUFY3,HOXA2,HOXA7,EMC10,LPAR1,CXCL8,AVL9,MYH14,BMPER,AKIRIN1,EPHA7,PTN,ITGB1BP1,MET,ADD2,GRB10,POU3F3,EGFR,USP45,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,BVES,GAB1,SDCBP,NRCAM,MGARP,TRPM4,FOXO3,ARMC2,MAPRE1,WASF1,ARMC4,APOB,FGF21,PLXNA1,LAMA4,PODXL2,TCTE3,ADCY3,TTC26,NDNF,C5AR2,C5AR1,SLC26A5,KIF3C,ARHGAP21,COPG1,PRKD2,DRC1,IQSEC1,SOX9,RSPH6A,MYO7B,BEX4,CACNB2,LCP1,KLC3,CLASP2,DLG2,TCTEX1D4,GLI2,MEGF8,RAF1,MYD88,OXSR1,DACH1,IFT172,FOXJ1,SCN5A,SCN1A,PAXIP1,PTPRF,MYO7A,TTC21A,MYCBP2,CYGB,POU4F1,WDR60,SPRY2,CFAP61,PLAT,WNT11,TTLL3,RIN2,ACKR2,AKT2,DYNC1LI1,GPD1L,TGFBR2,OVOL2,SRGAP3,AP3M2,KIF5C,JAG1,MKKS,NEK10,ACTG1,PURA,FSCN2,NAV3,HBEGF,PLCB1,FEZ2,FERMT1,SPINT2,CNN2,ALX1,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,BTG1,SPEF1,PLXNC1,SEMA3A,CHL1,UNC5D,AIMP1,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,FAM19A4,DPYSL3,FLT1,RYK,TUB,EPHB1,PLK2,MTUS1,DNAH10,RET,AL359736.1,HCK,KIF3B,	grey	VSMC_M10
GO:0044772	1.00	0.00	145	350	mitotic cell cycle phase transition	BP	1	VPS4B,MRNIP,TRIM39,ZNF207,TAF2,FBXL6,CCND3,CDKN2A,FBXO7,ABCB1,CDK14,CDK6,PPAT,CHMP2A,BRSK1,ANKRD17,LSM10,KLF11,EGFR,CDK5RAP2,CCNY,TPRA1,XPC,ERCC2,ERCC3,CLASP2,PLK3,UBE2E2,DYNC1LI1,PPME1,SIRT2,RPTOR,ANAPC15,PLCB1,IK,SIRT7,NEK11,USP44,TFDP1,TAF10,MTA3,PRKDC,PLK2,FAM107A,ACVR1B,RAD17,ANAPC5,PKIA,ANAPC7,CCNJ,CHMP4C,ADAMTS1,CCNG2,BACH1,NBN,USH1C,ABRAXAS1,CHMP7,DONSON,ZFYVE19,CCNJL,PIDD1,PKD2,NPM2,TAOK3,LZTS1,CDK18,FBXL15,HYAL1,PPP3CA,HECW2,CCND1,TERT,PPP2R2D,GIGYF2,CHEK2,PSME1,CACUL1,CDK15,EPS8,SYF2,CDKN1B,DLG1,STOX1,DBF4B,DDX3X,MEPCE,PTPN6,ECD,PSME3,USP37,PIM2,DDB1,PHF8,ANAPC4,RAD51B,UIMC1,FOXO4,FBXL22,CTC1,MUC1,TAOK2,ESRRB,RAB11A,KDM8,LCMT1,FOXN3,CALM1,RAD51C,DNM2,DCUN1D3,SIN3A,CAMK2A,CCL2,PPP6C,CUL4B,PSMG2,TAOK1,FZR1,PKD1,MECP2,CDK10,FBXO31,CDC14A,GFI1,VPS4A,FBXL8,NAE1,MIR29A,MIR222,FBXL12,PLK5,E2F6,RPS27L,SOX4,DUSP1,SPDYA,RGCC,APC,CDC26,ZFP36L2,BRCC3,CRADD,ARPP19,NABP1	grey	VSMC_M10
GO:0010033	1.00	0.00	1112	2273	response to organic substance	BP	1	ADNP2,ZNF236,NME1,VPS4B,SLC39A5,FECH,ONECUT2,ARPC3,RNMT,LRP1,SEMA6A,SHMT2,AP3S1,PGGT1B,YTHDC2,MARS,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,CANX,ESR1,FRS2,GFPT2,CNOT2,TPH2,RIDA,SNW1,APOM,SLC12A2,HSPA1B,IGF2R,PRKN,PACRG,AGPAT1,RNF5,AGER,PPARA,TNFRSF11B,IL5,TAF2,PNPLA3,RXRB,TSPO,GDF9,HSPA4,DERL1,TCF7,TNFRSF13C,BAK1,PMM1,TRIB1,MYC,SMAD5,LEMD2,PTK2,PTP4A3,PTCH1,LY6E,AKR1B1,ATF4,TAB1,SYNGR1,MAPK14,NTRK2,MAPK13,PLA2G6,GKAP1,KDM4C,SOX10,MICALL1,PIM1,SMO,FOXRED2,TXN2,HSF1,PLIN2,IRF5,KCP,CCND3,FOXH1,GPT,MTAP,ZNF16,RBFOX2,CHRNA3,TEK,RORB,ALDH1A1,CRY1,PTK7,SRF,STEAP2,GABRA1,CNTFR,USP46,KIT,SLC1A1,CA9,TNFRSF21,NCK2,FHL2,TGFBRAP1,ERMP1,IL1R2,TFAP2B,ROR2,NFIL3,GAPDH,DLX5,PPAT,ADH5,SOSTDC1,CAT,SEC61B,ERP44,DNAJA1,PRKCE,CD109,PPP2R1A,RAD23B,PHIP,FPR2,HMGN3,HAS1,GSDME,PNPT1,VRK2,ME1,HOXA2,ADAMTS3,HOXA13,REL,ECPAS,CXCL8,NOD1,AREG,AKIRIN2,BMP8A,CRHR2,AQP1,RRAGD,PELI1,BMPER,HERPUD2,PXDN,BSPRY,NR1H2,PTN,ITGB1BP1,FOXP2,DDC,KLF11,GRB10,TNC,EGFR,LANCL2,TSPAN12,FUZ,TRIM32,TLR4,TRAF1,GAB1,LPIN1,IL15,SFRP4,MYLK3,UCP1,VPS35,TEAD2,MGST2,SETD7,SDCBP,MGARP,TRPM4,SLC7A11,OSR1,FOXO3,PGRMC2,NTF4,WASF1,APOB,BCAT2,CDK19,FGF21,PRKAR2B,HSPE1,TRAF3IP2,SPHK2,DHFR,SPRY1,HDAC2,ADCY3,TRPC3,SESN3,DNMT3A,BMI1,NDNF,C5AR1,PANX1,SLC26A5,PIP4K2A,RAB10,PRKD2,HADHA,PTGIR,PHB,SOX9,GIPR,CYSLTR2,ERCC1,ESD,AKR1A1,CD300LF,PDIA3,GLB1,KHK,EIF2B3,XRCC1,OPTN,EPM2AIP1,KBTBD6,GLI2,MEGF8,TMEM145,RALB,E	grey	VSMC_M10

GO:0000226	1.00	0.00	226	522	microtubule cytoskeleton organization	BP	1	VPS4B,CCDC68,TRIM36,MAP7,KATNA1,MDM1,ATAT1,CCDC170,ZNF207,HSPA1B,TUBGCP6,KIF3A,UBE2B,WASHC5,LRRC6,MAPK15,SUN2,MPDZ,CNTLN,MYH9,CFAP69,SLAIN2,HEPACAM2,GAPDH,EFHC1,BICD2,CHMP2A,NLRP5,BRSK1,XPO1,CEP68,WDR92,MET,CDK5RAP2,CCDC155,ARMC2,MAPRE1,ARMC4,SPRY1,TTC26,DRC1,CCDC61,RSPH6A,NINL,EML2,SLC39A12,CLASP2,MAPRE3,PLK3,MLH1,LLGL2,TRIM54,XRCC2,NCKAP5,PIBF1,IFT172,FOXJ1,SLAIN1,KIZ,SPRY2,CLIP4,TTLL3,CCDC13,DYNC1LI1,HOOK3,CEP295NL,NAV3,ARHGEF7,SPEF1,RASSF7,KATNAL1,CEP63,NSFL1C,ATXN7,PLK2,MOS,TTL,KIF3B,FAM107A,FER,CEP70,CHMP2B,DCLK2,CEP44,CLIP1,CEP250,CCDC66,CETN3,NCKAP5L,CHMP4C,MCPH1,KATNB1,CCDC65,ALMS1,ABRAXAS1,TMEM67,TUBB2A,TUBGCP5,PKD2,DNAH1,DNAH5,TUBA1A,STMND1,SRGAP2C,NEURL1,SLK,FIGN,CFAP43,ZMYND10,AC112128.1,TRPV4,SBDS,CFAP46,DAG1,TTBK2,INTS13,MARK1,TBCE,CFL1,JHY,DISC1,TBCEL,CHEK2,TTLL13P,TUBGCP4,CIB1,CCDC84,TRAF3IP1,PHLDB1,ABRAXAS2,KIAA1614,WDR73,INPP5J,LIMK2,CDKN1B,SIK3,DLG1,SAXO2,SLC16A1,PPP2R3C,SETD2,MAPT,TTC12,TOGARAM1,DIXDC1,DNAAF2,SPAG16,EFHC2,NIN,HTT,CEP152,RNF4,TUBG1,TTLL4,MARK2,CEP126,UXT,OBSL1,TTC25,CCDC120,CRMP1,SDCCAG8,DNAAF4,MNS1,TUBA8,RGS14,SEPT1,KPNB1,PEX14,CNTROB,TRIM46,TTLL5,NDEL1,HOOK2,RAB11A,CCDC151,CCDC88C,TRIM37,TUBD1,BCAS3,NCOR1,CAPN6,MARK3,CAMSAP3,CDK5R1,DOCK7,SPEF2,CEP192,TAOK1,NUBP1,FSD1,C16orf71,TLE6,PRKCZ,PKD1,MECP2,WRAP73,SAPCD2,APC2,TPGS1,CAMSAP1,TUBB3,SPIRE2,CHMP1A,PSRC1,GPSM2,CDC14A,HYDIN,TTLL11,WDR63,	grey	VSMC_M10
GO:0071310	1.00	0.00	859	1784	cellular response to organic substance	BP	1	ADNP2,ZNF236,NME1,SLC39A5,FECH,ONECUT2,ARPC3,RNMT,LRP1,SEMA6A,AP3S1,MARS,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,ESR1,FRS2,GFPT2,CNOT2,SNW1,SLC12A2,HSPA1B,PRKN,PACRG,AGPAT1,RNF5,AGER,PPARA,IL5,PNPLA3,RXRB,TSPO,GDF9,DERL1,TCF7,TNFRSF13C,BAK1,PMM1,TRIB1,SMAD5,LEMD2,PTK2,PTP4A3,PTCH1,AKR1B1,ATF4,TAB1,SYNGR1,MAPK14,NTRK2,MAPK13,PLA2G6,GKAP1,KDM4C,SOX10,MICALL1,PIM1,SMO,HSF1,IRF5,KCP,CCND3,FOXH1,GPT,ZNF16,RBFOX2,RORB,CRY1,PTK7,SRF,GABRA1,CNTFR,KIT,SLC1A1,TNFRSF21,NCK2,TGFBRAP1,ERMP1,IL1R2,TFAP2B,ROR2,NFIL3,GAPDH,DLX5,PPAT,SOSTDC1,CAT,DNAJA1,PRKCE,CD109,RAD23B,PHIP,FPR2,HMGN3,HAS1,GSDME,PNPT1,VRK2,HOXA2,ADAMTS3,HOXA13,CXCL8,NOD1,BMP8A,CRHR2,AQP1,RRAGD,BMPER,HERPUD2,PXDN,BSPRY,NR1H2,PTN,ITGB1BP1,DDC,KLF11,GRB10,TNC,EGFR,LANCL2,TSPAN12,FUZ,TRIM32,TLR4,TRAF1,GAB1,LPIN1,IL15,SFRP4,MYLK3,UCP1,VPS35,TEAD2,SDCBP,MGARP,TRPM4,OSR1,FOXO3,PGRMC2,NTF4,WASF1,APOB,BCAT2,CDK19,FGF21,TRAF3IP2,SPHK2,SPRY1,HDAC2,ADCY3,SESN3,DNMT3A,BMI1,NDNF,PIP4K2A,RAB10,PRKD2,PHB,SOX9,CYSLTR2,CD300LF,PDIA3,OPTN,GLI2,MEGF8,RALB,ECHDC3,GRIK5,RAF1,ATP1A3,MYD88,OXSR1,ZFAND6,ACVR2B,KLF5,TBC1D4,UBE2O,EGLN2,AANAT,NUMBL,IRAK2,POU4F1,IL15RA,IL17RE,SPRY2,WNT11,ALK,TADA3,ACKR2,AKT2,EID2,TGFBR2,OVOL2,SNX5,PFKP,UGGT2,ACVR2A,IKBKB,NFKBIB,SIRT2,MKKS,NMI,RPTOR,DNAJC18,TMEM173,RARB,ACTG1,NR1D2,SRA1,PLCB1,TMTC4,MAP4K1,RYR1,FERMT1,SPRED3,SPINT2,SLC23A2,EIF2AK2,PRNP,BAG4,TAF7,DCN,DIAPH1,MAVS,SP	grey	VSMC_M10
GO:0051983	1.00	0.00	22	78	regulation of chromosome segregation	BP	1	ZNF207,MAPK15,CDK5RAP2,PUM2,DYNC1LI1,SIRT2,ANAPC15,IK,USP44,MOS,ANAPC5,ANAPC7,CSNK2A2,HECW2,CCDC36,ANAPC4,LCMT1,PSMG2,RMI2,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0051173	1.00	0.00	1140	2331	positive regulation of nitrogen compound metabolic process	BP	1	NFATC1,ZNF407,ERBB3,SMARCC2,NEDD4L,PAN2,ONECUT2,TCF4,LRP1,EYA4,GLI1,MARS,MAP3K5,TNFAIP3,AGAP2,PLAGL1,MAML1,MRNIP,PPP1R10,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ARID1B,HSPA1B,DXO,EIF3E,ZBED4,PNLDC1,GRAMD4,MAP3K4,PRKN,AGER,PPARA,FBLN1,MED30,IL5,RXRB,GDF9,VGLL2,HSF2,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PITX1,TRIB1,MYC,SMAD5,JMJD4,AGO2,PRXL2C,HABP4,PTK2,PTCH1,TNRC6B,ATF4,TUT7,TAB1,MAPK15,AGTPBP1,GTPBP1,MAPK14,NTRK2,CSNK1E,PLA2G6,C6orf89,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,GUCA1B,IFT74,CHRNA3,TEK,BICRAL,POT1,GPR37,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,TTBK1,ZNF318,FZD1,TEC,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,NCK2,PLGRKT,TFAP2B,ROR2,NFIL3,SEMA4D,DLX5,IPPK,ETV1,EXOSC3,MEOX2,KANSL3,ZNF268,MACC1,CLDN19,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,STPG4,EPCAM,MSH2,ZNF462,TRA2A,PHIP,FPR2,HMGN3,NFYC,PNPT1,MOB1B,SLC4A4,HOXA2,HOXA7,HOXA13,REL,CREB5,EPGN,NOD1,AREG,AKIRIN2,BMP8A,CASP8AP2,PELI1,AKIRIN1,ETAA1,MTF1,RSPO1,PCBP1,EPHA7,NR1H2,AKNA,TNFSF15,TGFA,ITGB1BP1,GRHL1,MED25,MET,VRK3,IL4I1,AGO1,POU3F3,EGFR,HECW1,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,HACE1,BCL2L12,LPIN1,IL15,CCNY,VPS35,TEAD2,SETD7,ZYG11B,SDCBP,MYCN,ELF2,TUT4,OSR1,FOXO3,ZXDC,NTF4,FAF1,FGF21,BRAF,MAMSTR,ATAD2B,HSPE1,SPHK2,KDM7A,ZNF438,HDAC2,PHF10,MAML2,ZC3HAV1,BBS7,SLC8A2,MLLT10,RAB7A,HMCES,BMI1,MOB3C,PRKD2,CNBP,PHB,FOXA3,ABI1,SOX9,SYMPK,ZNF7	grey	VSMC_M10

GO:0007346	1.00	0.00	149	360	regulation of mitotic cell cycle	BP	1	VPS4B,YTHDC2,RPA3,HECA,MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,FBXO43,PTCH1,HSF1,CCND3,FBXO7,ZNF268,BRSK1,MSH2,PHIP,HOXA13,ANKRD17,EPGN,TGFA,LSM10,EGFR,CDK5RAP2,SDCBP,TPRA1,XPC,ERCC2,ERCC3,PLK3,UBE2E2,DYNC1LI1,THAP1,SIRT2,RPTOR,ANAPC15,SRA1,PLCB1,IK,NEK11,BTG1,USP44,TFDP1,MTA3,PRKDC,STK33,PLK2,TTL,FAM107A,IL1A,RAD17,FZD3,BTG3,ANAPC5,PKIA,ANAPC7,RAD9B,CHMP4C,ADAMTS1,NBN,NKX3-1,ABRAXAS1,DONSON,ZFYVE19,PIDD1,PKD2,NPM2,TAOK3,IGF2,GBF1,SIK1,HYAL1,HECW2,CCND1,TERT,INTS13,GIGYF2,EGF,CHEK2,PSME1,USP2,ANGEL2,CD28,SYF2,CDKN1B,DLG1,OVOL1,STOX1,BCL6,DBF4B,BRINP2,DDX3X,MEPCE,PTPN6,ECD,PSME3,STAT5B,OBSL1,PIM2,DDB1,ANAPC4,RAD51B,UIMC1,FOXO4,CTC1,EME1,MUC1,TAOK2,RAB11A,TIPIN,SMAD3,LCMT1,FOXN3,RAD51C,DCUN1D3,SIN3A,INSR,NLE1,CCL2,TOM1L2,PSMG2,TAOK1,FZR1,PKD1,MECP2,CDK10,FBXO31,CDC14A,VPS4A,NAE1,MIR29A,MIR21,MIR222,PLK5,RPS27L,FOXG1,SOX4,DUSP1,RGCC,NME6,APC,CDC26,ZFP36L2,BRCC3,EREG,CRADD,PDXP,NABP1	grey	VSMC_M10
GO:0044238	1.00	0.00	3960	7641	primary metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,NME1,SERPINB8,SERPINB2,RDH5,VPS4B,KDSR,PHLPP1,ORMDL2,ERBB3,SEC11C,ZC3H10,SMARCC2,NEDD4L,PAN2,APOF,ATP8B1,ONECUT2,GLS2,BAZ2A,TCF4,RDH16,POLI,HSD17B4,TNFAIP8,RNMT,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,ALDH8A1,GLI1,HBS1L,MARS,B4GALT7,RMND5B,PDE7B,CLK4,PIP4K2C,MAP3K5,PEX7,B4GALNT1,RPA3,TNFAIP3,AGAP2,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,AIG1,ADAT2,FUCA2,ATP23,PLAGL1,USP15,FBXO30,RXYLT1,CANX,MAML1,LTC4S,MRNIP,ENPP3,ATP5MGL,HELB,TRIM39,RPP21,PPP1R10,ATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,FBXO43,MIOX,PABPC1,SNW1,TFB1M,ZNF706,CPT1B,PHAX,MARCH3,APOM,ABHD16A,ARID1B,ADM2,ZDHHC14,HSPA1B,SYNJ2,SERAC1,TULP4,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,SELENOO,DXO,MOV10L1,EIF3E,SLC27A6,ALG12,CYP21A2,ZBED4,BRD1,ADAMTS19,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,AGPAT4,PPT2,PRKN,AGPAT1,QKI,RNF5,AGER,TRMU,PPARA,PDE10A,ACSL6,FBLN1,UTP23,P4HA2,MED30,PSMB8,SLC22A4,IL5,BRD2,TAF2,PNPLA3,PNPLA5,SULT4A1,ZUP1,RXRB,TSPO,GDF9,MCAT,VGLL2,ROS1,HSD17B8,MCM9,ASF1A,MRPL13,A4GALT,RPS18,RRP7A,HSF2,DERL1,TCF7,SKP1,PHF1,SMPDL3A,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,RNF146,ECHDC1,ACO2,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,KLHL3,XPNPEP3,OBSCN,MRPL55,JMJD4,AGO2,PRXL2C,HABP4,RPS10,PTK2,HSD17B3,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,AKR1B1,ZC3H3,ATF4,PYCR3,TUT7,T	grey	VSMC_M10
GO:0097435	1.00	0.00	273	622	supramolecular fiber organization	BP	1	ARPC3,MYO1A,B4GALT7,AVIL,ZNF207,HSPA1B,TUBGCP6,TNXB,PRKN,COL11A2,SHROOM1,COL14A1,MTSS1,WASHC5,OBSCN,BAIAP2L2,PICK1,CDC42EP1,RAC2,LMOD2,SRF,PGM5,SLAIN2,NCK2,KIAA1211,TMOD1,PLEKHH2,NLRP5,PRKCE,SPTBN1,RUFY3,SHANK1,ADAMTS3,LPAR1,PXDN,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,CDK5RAP2,EPHA1,CCDC155,MYLK3,FAM49A,MAPRE1,WASF1,ARHGAP12,KPTN,MSRB2,ABI1,MYO7B,EML2,SLC39A12,LCP1,CLASP2,MAPRE3,CRTAP,PLK3,TRIM54,NCKAP5,IFT172,MYO7A,SLAIN1,CLIP4,WNT11,CCDC13,HOOK3,ARRB1,BFSP1,PLEKHG2,FCHSD2,MKKS,ACTG1,FSCN2,NAV3,PAWR,RAC3,BAG4,ARHGEF7,LUM,DIAPH1,SPEF1,FCHSD1,NCKAP1L,ARFIP2,LMOD3,DPYSL3,TTC17,ATXN7,PFDN5,HCK,FAM107A,FER,PIK3R1,HIP1R,PLS1,CLIP1,FMN1,LIMA1,SORBS1,NCKAP5L,TLL2,KATNB1,PTK2B,RND1,ALMS1,USH1C,NEFM,RAPGEF3,LOXL2,RHOBTB2,BIN3,F2RL1,IQGAP2,RIPK1,LOXL4,DSP,TUBGCP5,CYFIP1,DMTN,STMND1,SIAH1,GAS2,MAGEL2,PXN,RAP1GDS1,ELMO2,PKP2,SLK,CARMIL1,PPFIA1,LMOD1,ADD3,TRPV4,TGFB2,FBLN5,PRKAR1A,TTBK2,SSH1,CFL1,SHROOM2,HCLS1,ARHGAP6,AP1AR,HSPA8,KLHL24,CASS4,SPATC1L,TUBGCP4,CIB1,WASF2,ACTC1,SLC9A1,SPTBN2,MYOZ2,CASQ1,ITGB5,TMOD4,EPS8,WDR73,RHOBTB1,INPP5J,LIMK2,BACE1,WHAMM,EFEMP2,CDKN1B,DLG1,CAPZA1,MYPN,CDC42EP2,MAPT,PLOD3,COL13A1,TOGARAM1,TTN,MMP11,NCKAP1,MCU,NIN,WNT4,COL3A1,COL5A2,MYOZ1,TUBG1,ARPC1A,CEP126,DES,WAS,TMOD2,OBSL1,TPM4,P3H4,SHROOM4,LDB3,SPTB,TCAP,PFN3,PFDN4,WASHC3,KPNB1,ANXA2,PSEN1,KCTD13,NDEL1,HOOK2,VIPAS39,HAX1,RAB11A,SMAD3,GAS7,CORO2B,	grey	VSMC_M10
GO:0016032	1.00	0.00	132	325	viral process	BP	1	VPS4B,YTHDC2,CANX,PABPC1,SNW1,HSPA1B,IGF2R,PRKN,PPARA,LY6E,APOBEC3H,EIF3L,CHMP2A,CXCL8,RSAD2,PCBP1,EGFR,TRIM32,ATG5,EPS15,HS3ST5,ZC3HAV1,RAB7A,KPNA3,PHB,NECTIN2,FBXL2,PVR,RSF1,RPSA,ST6GALNAC2,KPNA2,SLC20A2,ATG16L2,RAB5A,EIF2AK2,MAVS,GAS6,IRF7,PCBP2,USF2,IDE,CHMP2B,FAM208A,MOGS,CHMP4C,EIF2AK4,SPCS1,OAS3,TPCN1,CHMP7,ANO6,VPS18,ITGB6,EIF2D,IFIH1,OASL,HDAC1,TMEM39A,ADARB1,NR5A2,DAG1,ZNF639,SELPLG,CFL1,STAU1,HSPA8,GRK2,ATG16L1,PARP9,POU2F3,PC,ACE2,DDX6,ITGB5,USF1,NECTIN4,XPR1,RAB1B,CD28,MGAT1,VPS37D,LRRC15,PIKFYVE,MGAT2,DDX3X,PI4KA,SLC3A2,DDB1,PSMC3,TARDBP,HACD3,LDLR,LARP1,GALNT1,TNIP1,CD74,INSR,CCL5,NPC1,CCL2,MCTS1,JUN,CIITA,FMR1,INPP5K,HCFC1,BSG,CHMP1A,RXRA,LAMTOR5,ST6GALNAC4,ST3GAL2,GFI1,MVB12B,WWP2,VPS4A,MIR222,HTATSF1,HAVCR1,SETDB1,OAS1,TRIM68,DPP4,TRIM34,CD46,CLDN1,TBC1D20,ZNF502,EFNB3,FAM111A,PARD6A	grey	VSMC_M10

GO:0048513	1.00	0.00	1238	2529	animal organ development	BP	1	NFATC1,NME1,ITGA7,ERBB3,SLC39A5,ATP8B1,ONECUT2,HSD17B4,LRP1,SEMA6A,EYA4,STAC3,GLI1,TNFAIP3,HECA,CYP27B1,ADGRG6,MAML1,MDM1,ATAT1,ESR1,FRS2,RIDA,STK3,OSR2,MPIG6B,HSPA1B,SYNJ2,FZD6,IGF2R,BRD1,MAP3K4,AGER,PPARA,HLA-DRA,TNFRSF11B,IL5,COL11A2,TSPO,GDF9,UQCRQ,VGLL2,VPS52,TBC1D32,TCF7,CCDC134,BAK1,XRCC6,MTSS1,PITX1,RSPO3,ACO2,TRIB1,MYC,TOB2,SMAD5,LRRC6,L3MBTL3,KLHL3,LEMD2,H3F3C,PTK2,HSD17B3,PTCH1,FANCC,LY6E,AKR1B1,EXOC4,ATF4,TAB1,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,CBY1,DMC1,PODXL,CSNK1E,SOX10,PI16,PIM1,CKB,MFNG,SMO,ZDHHC21,BNC2,HSF1,DAAM2,MDFI,TFEB,KCP,MYH9,FOXH1,ZNF16,RBFOX2,IFT74,TEK,PRPH2,LARGE1,FBXO7,RORB,ZFAND5,PTK7,SRF,TTBK1,FZD1,CNTFR,FANCG,CDK6,SLC25A27,RFX3,KIT,SLC1A1,SGCE,FHL2,TFAP2B,ROR2,NFIL3,SEMA4D,DLX5,EFHC1,PPAT,C1GALT1,CCIN,OMD,ETV1,ADGRL3,SEMA4C,RPS14,CNNM4,TDRD7,MEOX2,SOSTDC1,TMOD1,RAB23,ANKS6,CAT,SIX2,HIVEP3,TMEM190,IL11,COL9A1,SMAP1,TNNI3,EPAS1,RDH13,EPCAM,ABCB5,MSH2,CD109,MBOAT7,DNAH11,FKTN,RTN4,RAD23B,KCNQ4,GSDME,PNPT1,KLK4,UTP3,ACP4,HOXA2,HOXA4,HOXA6,HOXA7,HOXA13,PPT1,PTBP3,MYCL,CXCL8,SLC46A2,MTURN,AREG,BMP8A,AQP1,MYH14,BPGM,BMPER,AKIRIN1,CNOT4,PLEK,RSAD2,COL27A1,EPHA7,AKNA,WHRN,MBOAT2,TGFA,PTN,ITGB1BP1,FOXP2,GRHL1,MET,ADD2,TNC,CTTNBP2,IL4I1,YWHAZ,POU3F3,EGFR,TSPAN12,USP45,FUZ,TLR4,CDK5RAP2,BVES,CNTRL,GJB5,LPIN1,IL15,SFRP4,KEL,MYLK3,TEAD2,ATG5,SDCBP,MYCN,SOBP,TRPM4,SLC7A11,OSTM1,OSR1,FOXO3,PGRMC2,MATN3,ZBTB24,	grey	VSMC_M10
GO:0007088	1.00	0.00	29	96	regulation of mitotic nuclear division	BP	1	ZNF207,FBXO43,PHIP,HOXA13,EPGN,TGFA,CDK5RAP2,DYNC1LI1,ANAPC15,IK,USP44,IL1A,ANAPC5,ANAPC7,IGF2,EGF,CD28,OBSL1,ANAPC4,LCMT1,INSR,TOM1L2,PSMG2,DUSP1,RGCC,NME6,APC,EREG,PDXP	grey	VSMC_M10
GO:0044092	1.00	0.00	367	806	negative regulation of molecular function	BP	1	SERPINB8,SERPINB2,NEDD4L,TNFAIP8,LRP1,PIP4K2C,TNFAIP3,CYP27B1,PPP1R10,ESR1,FZD6,PRKN,PPARA,GOPC,TRIB1,HABP4,C6orf106,PTCH1,LY6E,STK38,CSNK1E,PI16,PIM1,SMO,MDFI,FOXH1,LRRC14,CDKN2A,POT1,FBXO7,TTBK1,NFKBIE,SEMA4D,GAPDH,MITD1,GABBR2,CAT,DNAJA1,PRKCE,TNNI3,PPP1R12C,CD109,ZNF462,IBTK,ACP4,MTURN,AQP1,PELI1,ANXA4,PTN,ITGB1BP1,MET,HECW1,TCAF2,EPHA1,BCL2L12,NOSIP,SFRP4,DKKL1,OSR1,FAF1,PRKAR2B,SPHK2,SPRY1,HDAC2,PIP4K2A,KCNRG,CST7,SYMPK,SSPO,PPP1R37,APOC1,RALB,RSF1,PRKAG2,RAF1,OXSR1,PRDX3,TIMP4,TAF3,FOXJ1,PAXIP1,PTPRF,UBE2O,IRAK2,GCKR,FBH1,SPRY2,ARRB1,EOMES,IKBKB,PPME1,BHLHE40,NFKBIB,MKKS,RPTOR,PURA,PDE6G,PTPRQ,EFHB,GPS1,SPINT2,PRNP,BAG4,TAF7,USP44,SH3RF2,NCKAP1L,GAS6,PSMF1,TRIB3,GPI,NR4A1,BTAF1,PXK,CEBPA,PIK3CB,CASP3,DKK3,HAND2,PARVA,FBXW7,ADGRV1,SCG5,PTPRJ,PKIA,IL7,TMBIM6,SETD6,RTKN,P2RY1,FNIP2,FAM192A,EIF2AK4,PAQR3,NLRC5,OTULIN,SERPINB1,IQGAP2,TESC,SPINT1,CRY2,KCNE2,PKD2,PLA2R1,IFIT2,DBNDD2,PAX2,CASQ2,NOD2,DTNBP1,TAOK3,GRM2,MTRR,APLP2,SUFU,CABP1,CD200,RPL23,SIK1,PPP3CA,HECW2,SP100,PDCD4,TGFB2,ADRA2A,PRKAR1A,TCF7L2,ADARB1,DKK2,PDE6D,OXA1L,TTBK2,AJUBA,FICD,CMKLR1,FABP4,ADNP,UBASH3B,DISC1,SORL1,RTRAF,SAG,PARP9,DTX3L,SH3BP4,IFI6,AGT,CIB1,CBL,ACE2,ATP1A2,COL6A3,SFN,PPP2R5A,NFATC4,COL7A1,RPS6KA1,HES6,PER2,C4orf3,PEX19,HDAC4,CAMK2N2,RUBCN,PTPRO,PDE6H,PIK3IP1,CST6,RPL11,SNX6,CDKN1B,POR,AIDA,YWHAG,DUSP10,CTTNBP2NL,RASA4,MAPT,MBIP,HEXIM2,GEMIN2,GMIP,ITGA4,MEN1,VCPKMT,DD	grey	VSMC_M10
GO:0010604	1.00	0.00	1270	2586	positive regulation of macromolecule metabolic process	BP	1	NFATC1,ZNF407,CD226,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ONECUT2,TCF4,LRP1,EYA4,GLI1,MARS,MAP3K5,TNFAIP3,AGAP2,PLAGL1,MAML1,MRNIP,PPP1R10,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ARID1B,ADM2,HSPA1B,RIMS2,DXO,EIF3E,ZBED4,PNLDC1,GRAMD4,MAP3K4,PRKN,AGPAT1,QKI,AGER,PPARA,GPSM3,FBLN1,MED30,IL5,HLA-DPB1,RXRB,GDF9,VGLL2,HSF2,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PITX1,TRIB1,MYC,SMAD5,JMJD4,AGO2,HABP4,PTK2,PTCH1,TNRC6B,ATF4,TUT7,TAB1,MAPK15,AGTPBP1,GTPBP1,MAPK14,NTRK2,MAPK13,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,IFT74,CHRNA3,TEK,BICRAL,POT1,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,TTBK1,ZNF318,FZD1,TEC,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,NCK2,PLGRKT,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,DLX5,PDCL3,IPPK,ETV1,EXOSC3,MEOX2,KANSL3,ZNF268,MACC1,CLDN19,SIX2,FOXJ3,HIVEP3,IL11,RNF20,EPAS1,RIMS1,STPG4,EPCAM,MSH2,SPTBN1,ZNF462,TRA2A,PHIP,FPR2,HMGN3,NFYC,EPB41L4B,PNPT1,MOB1B,HOXA2,HOXA7,HOXA13,REL,CREB5,CXCL8,EPGN,NOD1,AREG,AKIRIN2,BMP8A,CASP8AP2,PELI1,AKIRIN1,ETAA1,MTF1,RSPO1,RSAD2,PCBP1,EPHA7,NR1H2,AKNA,WHRN,TNFSF15,TGFA,ITGB1BP1,GRHL1,MED25,MET,VRK3,TNC,IL4I1,AGO1,POU3F3,EGFR,HECW1,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,HACE1,BCL2L12,BVES,LPIN1,IL15,SFRP4,CCNY,VPS35,TEAD2,SETD7,ZYG11B,SDCBP,MYCN,ELF2,TUT4,OSR1,FOXO3,ZXDC,NTF4,EPS15,SSBP1,APOB,FAF1,FGF21,BR	grey	VSMC_M10

GO:0009893	1.00	0.00	1388	2815	positive regulation of metabolic process	BP	1	NFATC1,ZNF407,CD226,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ONECUT2,TCF4,LRP1,EYA4,GLI1,MARS,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,PLAGL1,EPM2A,MAML1,MRNIP,PPP1R10,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ARID1B,ADM2,HSPA1B,RIMS2,DXO,EIF3E,ZBED4,PNLDC1,GRAMD4,MAP3K4,PRKN,AGPAT1,QKI,AGER,PPARA,GPSM3,FBLN1,MED30,IL5,HLA-DPB1,RXRB,TSPO,GDF9,VGLL2,ROS1,HSF2,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PITX1,TRIB1,MYC,SMAD5,JMJD4,AGO2,PRXL2C,HABP4,PTK2,PTCH1,TNRC6B,ATF4,TUT7,TAB1,MAPK15,AGTPBP1,GTPBP1,MAPK14,NTRK2,MAPK13,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,GUCA1B,GPT,ZNF16,IFT74,CHRNA3,TEK,BICRAL,POT1,GPR37,FBXO7,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,TTBK1,ZNF318,FZD1,TEC,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,NCK2,PLGRKT,TFAP2B,SPTLC1,ROR2,NFIL3,GADD45G,SEMA4D,GAPDH,DLX5,PDCL3,IPPK,ETV1,EXOSC3,MEOX2,KANSL3,ZNF268,MACC1,CLDN19,SIX2,FOXJ3,HIVEP3,IL11,RNF20,PRKCE,EPAS1,RIMS1,STPG4,EPCAM,MSH2,SPTBN1,ZNF462,TRA2A,PHIP,FPR2,HMGN3,NFYC,EPB41L4B,PPP4R3B,PNPT1,MOB1B,SLC4A4,HOXA2,HOXA7,HOXA13,REL,CREB5,CXCL8,EPGN,NOD1,AREG,AKIRIN2,BMP8A,CASP8AP2,PELI1,AKIRIN1,ETAA1,MTF1,PLEK,RSPO1,RSAD2,PCBP1,EPHA7,NR1H2,AKNA,WHRN,TNFSF15,TGFA,ITGB1BP1,GRHL1,MED25,MET,VRK3,GRB10,TNC,IL4I1,AGO1,POU3F3,EGFR,HECW1,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,EPHA1,HACE1,BCL2L12,BVES,LPIN1,IL15,SFRP4,CC	grey	VSMC_M10
GO:0006464	1.00	0.00	1410	2859	cellular protein modification process	BP	1	PHLPP1,ERBB3,NEDD4L,BAZ2A,LRP1,SHMT2,EYA4,ATG12,FEM1C,PGGT1B,TRIM36,B4GALT7,RMND5B,CLK4,MAP3K5,TNFAIP3,AGAP2,ATP23,USP15,FBXO30,RXYLT1,MAML1,MRNIP,TRIM39,ATAT1,ARMT1,YEATS4,GFPT2,STK3,FBXO43,SNW1,MARCH3,ADM2,ZDHHC14,HSPA1B,TULP4,SELENOO,ALG12,BRD1,TNXB,MAP3K4,PRRT1,PRKN,RNF5,AGER,FBLN1,P4HA2,MED30,IL5,BRD2,TSPO,GDF9,ROS1,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,RNF146,TRIB1,SMAD5,KLHL3,OBSCN,JMJD4,PTK2,KDM3B,PTP4A3,TAB1,MAPK15,RPAP2,AGTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,PIM1,ZC3HC1,GPAA1,ZDHHC21,HSF1,FBXL6,OARD1,ADCK5,USP49,CCND3,OPN1SW,PPP1R16A,CDKN2A,CHRNA3,TEK,LARGE1,GNMT,TRPM6,FBXO7,KLHDC3,ASB15,PRDM4,CRY1,PTK7,ABHD17B,TTBK1,NFX1,NUAK1,PTAR1,CDK14,DCAF12,TEC,CWH43,CDK6,SUPT3H,USP46,LNX1,KIT,SLC1A1,ST6GAL2,SRD5A3,NCK2,ROR2,SEMA4D,GAPDH,CDK20,PDCL3,C1GALT1,PTPDC1,HINT2,WNK2,PHF14,LIPT1,KLHL31,ADH5,FBXO10,DCAF10,KANSL3,SVBP,ALG2,CLDN19,CAMKMT,RIMKLA,DNAJA1,IL11,BRSK1,TMEM246,RNF20,PRKCE,EPAS1,PIGF,CD109,ASB3,SPTBN1,FKTN,PPP2R1A,PHIP,FPR2,PPP4R3B,IBTK,UBE3D,ACP4,MOB1B,VRK2,FANCL,PPT1,SLC35A1,EPGN,AREG,BMP8A,RNGTT,MINDY4,FKBP9,PELI1,BMPER,AGBL3,FKBP15,CNOT4,ETAA1,BSPRY,RSPO1,AAK1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,YWHAZ,EGFR,ING3,HECW1,USP45,ARHGEF5,TRIM32,TLR4,FBXW2,EPHA1,TRAF1,HACE1,NOSIP,USP38,IL15,CCNY,MYLK3,ATG5,SETD7,SDCBP,TRPM4,DLD,NTF4,CDK19,FGF21,BRAF,PRKAR2B,T	grey	VSMC_M10
GO:0036211	1.00	0.00	1410	2859	protein modification process	BP	1	PHLPP1,ERBB3,NEDD4L,BAZ2A,LRP1,SHMT2,EYA4,ATG12,FEM1C,PGGT1B,TRIM36,B4GALT7,RMND5B,CLK4,MAP3K5,TNFAIP3,AGAP2,ATP23,USP15,FBXO30,RXYLT1,MAML1,MRNIP,TRIM39,ATAT1,ARMT1,YEATS4,GFPT2,STK3,FBXO43,SNW1,MARCH3,ADM2,ZDHHC14,HSPA1B,TULP4,SELENOO,ALG12,BRD1,TNXB,MAP3K4,PRRT1,PRKN,RNF5,AGER,FBLN1,P4HA2,MED30,IL5,BRD2,TSPO,GDF9,ROS1,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,RNF146,TRIB1,SMAD5,KLHL3,OBSCN,JMJD4,PTK2,KDM3B,PTP4A3,TAB1,MAPK15,RPAP2,AGTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,PIM1,ZC3HC1,GPAA1,ZDHHC21,HSF1,FBXL6,OARD1,ADCK5,USP49,CCND3,OPN1SW,PPP1R16A,CDKN2A,CHRNA3,TEK,LARGE1,GNMT,TRPM6,FBXO7,KLHDC3,ASB15,PRDM4,CRY1,PTK7,ABHD17B,TTBK1,NFX1,NUAK1,PTAR1,CDK14,DCAF12,TEC,CWH43,CDK6,SUPT3H,USP46,LNX1,KIT,SLC1A1,ST6GAL2,SRD5A3,NCK2,ROR2,SEMA4D,GAPDH,CDK20,PDCL3,C1GALT1,PTPDC1,HINT2,WNK2,PHF14,LIPT1,KLHL31,ADH5,FBXO10,DCAF10,KANSL3,SVBP,ALG2,CLDN19,CAMKMT,RIMKLA,DNAJA1,IL11,BRSK1,TMEM246,RNF20,PRKCE,EPAS1,PIGF,CD109,ASB3,SPTBN1,FKTN,PPP2R1A,PHIP,FPR2,PPP4R3B,IBTK,UBE3D,ACP4,MOB1B,VRK2,FANCL,PPT1,SLC35A1,EPGN,AREG,BMP8A,RNGTT,MINDY4,FKBP9,PELI1,BMPER,AGBL3,FKBP15,CNOT4,ETAA1,BSPRY,RSPO1,AAK1,EPHA7,TNFSF15,TGFA,ITGB1BP1,MET,VRK3,YWHAZ,EGFR,ING3,HECW1,USP45,ARHGEF5,TRIM32,TLR4,FBXW2,EPHA1,TRAF1,HACE1,NOSIP,USP38,IL15,CCNY,MYLK3,ATG5,SETD7,SDCBP,TRPM4,DLD,NTF4,CDK19,FGF21,BRAF,PRKAR2B,T	grey	VSMC_M10

GO:0071704	1.00	0.00	4197	8083	organic substance metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,CD226,NME1,SERPINB8,SERPINB2,RDH5,VPS4B,KDSR,PHLPP1,ORMDL2,ERBB3,SEC11C,ZC3H10,SMARCC2,NEDD4L,PAN2,APOF,ATP8B1,FECH,ONECUT2,GLS2,BAZ2A,TCF4,RDH16,POLI,HSD17B4,TNFAIP8,RNMT,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,ALDH8A1,GLI1,HBS1L,MARS,B4GALT7,RMND5B,PDE7B,CLK4,PIP4K2C,MAP3K5,PEX7,B4GALNT1,RPA3,TNFAIP3,AGAP2,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,AIG1,ADAT2,FUCA2,ATP23,PLAGL1,USP15,FBXO30,RXYLT1,CANX,MAML1,LTC4S,MRNIP,ENPP3,ATP5MGL,HELB,TRIM39,RPP21,PPP1R10,ATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,TSPAN8,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,SNCAIP,FBXO43,MIOX,PABPC1,SNW1,TFB1M,ZNF706,CPT1B,ALDH7A1,PHAX,MARCH3,APOM,ABHD16A,ARID1B,ADM2,ZDHHC14,HSPA1B,SYNJ2,SERAC1,TULP4,FZD6,RIMS2,ZBTB12,DPYS,SKIV2L,SF3A3,SELENOO,DXO,MOV10L1,EIF3E,SLC27A6,ALG12,CYP21A2,ZBED4,BRD1,ADAMTS19,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,AGPAT4,PPT2,PRKN,AGPAT1,QKI,RNF5,AGER,TRMU,PPARA,GPSM3,PDE10A,ACSL6,HLA-DRA,FBLN1,HLA-DOB,UTP23,P4HA2,MED30,PSMB8,SLC22A4,HLA-DMA,IL5,BRD2,TAF2,PNPLA3,PNPLA5,SULT4A1,HLA-DPB1,ZUP1,RXRB,TSPO,GDF9,MCAT,VGLL2,ROS1,HSD17B8,MCM9,ASF1A,MRPL13,A4GALT,RPS18,RRP7A,HSF2,DERL1,TCF7,SKP1,PHF1,SMPDL3A,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,RNF146,ECHDC1,ACO2,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,KLHL3,XPNPEP3,OBSCN,MRPL55,JMJ	grey	VSMC_M10
GO:0001944	1.00	0.00	265	607	vasculature development	BP	1	NFATC1,LRP1,SEMA6A,TNFAIP3,ADM2,SLC12A2,QKI,CCDC134,BAK1,RSPO3,AGO2,PTK2,TAB1,MAPK14,NTRK2,SMO,MYH9,FOXH1,TEK,ZFAND5,PTK7,CEMIP2,SRF,KIT,SLC1A1,TFAP2B,PDCL3,C1GALT1,NINJ1,SHB,MEOX2,TNNI3,EPAS1,HOXA7,HOXA13,EMC10,ANKRD17,CXCL8,EPGN,AQP1,BMPER,TGFA,PTN,ITGB1BP1,AGO1,YWHAZ,TSPAN12,EPHA1,CNTRL,GAB1,TEAD2,NRCAM,OSR1,APOB,SPHK2,WISP3,NDNF,C5AR1,PRKD2,SLC39A12,MEGF8,ACVR2B,KLF5,PAXIP1,SPRY2,WNT11,RIN2,TGFBR2,OVOL2,ISM1,JAG1,ACTG1,DCN,PANK2,BTG1,AIMP1,FLT1,EPHB1,PLK2,POFUT1,IL1A,NR4A1,PIK3CB,ERAP1,HAND2,HPGD,EYA1,PARVA,ROBO1,ROBO2,FBXW7,MEF2C,VEGFC,ADAMTS1,PTK2B,RAPGEF2,OTULIN,NKX3-1,HDAC7,RAPGEF3,LOXL2,TBX5,AGGF1,ARHGAP24,SPINT1,PKD2,STK4,HIF1AN,PRICKLE1,ADTRP,CD40,WARS2,SUFU,GPLD1,FAP,PKNOX1,HYAL1,SLC2A10,SP100,TERT,PDCD4,TGFB2,TCF7L2,PDCD6,PRKX,DAG1,EGF,ENPEP,GPER1,AGT,MCAM,CIB1,WASF2,GBX2,NFATC4,VASH2,MMP21,CLIC4,MAP3K3,EPHB3,GLUL,EFEMP2,APOLD1,E2F2,LUZP1,APOD,SETD2,ADAM8,NFE2L2,FZD5,MIA3,CTSH,EPHB4,IL12A,FN1,PDCD10,CXCR2,WNT4,CALCRL,HSPG2,PPP3CB,RAMP2,STAT3,MAPK1,RHOJ,ROM1,BMPR1A,RBPJ,MED1,ALDH1A2,PLXDC1,SYNJ2BP,ANXA2,NAXE,PSEN1,SEMA4A,FGF18,FOXO4,NGFR,DLX3,PGF,EFNA1,VASH1,CITED1,IL6R,MAP2K1,TMEM100,VEZF1,MAP2K5,NOX5,TNMD,LDLR,PRKCB,DCTN5,TBX4,TBX2,BCAS3,STRA6,ANGPTL6,TNFAIP2,MAPK7,AMOT,GATA6,MIB1,AP2B1,CCL2,ESM1,ISL1,ZBTB14,LAMA1,LEPR,JAK1,C3,GPC3,JUN,SERPINF2,PDPK1,PKD1,MECP2,BSG,COL5A1,FOXF1,VAV3,TMEM2	grey	VSMC_M10
GO:0007051	1.00	0.00	58	165	spindle organization	BP	1	VPS4B,TRIM36,ZNF207,HSPA1B,TUBGCP6,WASHC5,MAPK15,SUN2,MYH9,EFHC1,CHMP2A,CCDC155,MAPRE1,CCDC61,CLASP2,MAPRE3,MLH1,PIBF1,KIZ,CEP63,PLK2,MOS,KIF3B,CHMP2B,CHMP4C,ABRAXAS1,TUBGCP5,AC112128.1,SBDS,INTS13,TBCE,CHEK2,TUBGCP4,ABRAXAS2,LIMK2,DLG1,TOGARAM1,EFHC2,RNF4,TUBG1,CEP126,RGS14,SEPT1,KPNB1,RAB11A,NCOR1,CEP192,FSD1,PKD1,MECP2,WRAP73,CHMP1A,PSRC1,GPSM2,RHOA,AURKC,CCSAP,DRG1	grey	VSMC_M10
GO:0031400	1.00	0.00	179	426	negative regulation of protein modification process	BP	1	LRP1,TNFAIP3,HSPA1B,PRKN,FBLN1,TSPO,PHF1,UBE2B,BAK1,NCOA7,TRIB1,STK38,CDKN2A,FBXO7,CRY1,NCK2,SEMA4D,HINT2,KLHL31,SVBP,DNAJA1,PRKCE,CD109,PPP2R1A,IBTK,ACP4,ITGB1BP1,EPHA1,ATG5,PRKAR2B,SPHK2,SPRY1,HDAC2,BEX4,CRTAP,XRCC1,KDM4A,PRKAG2,PIBF1,SPOPL,SPRY2,KLHL40,GPD1L,ARRB1,IKBKB,SIRT2,PTPRQ,SIRT7,PRNP,DUSP6,TAF7,USP44,SH3RF2,NCKAP1L,PRKDC,MFHAS1,TRIM44,TRIB3,SDR16C5,DNMT3B,CEBPA,PIK3CB,SNX25,CASP3,PTPRJ,PKIA,PAQR3,CRY2,CDYL,MARCH7,DBNDD2,DMTN,PRMT3,JARID2,DTNBP1,RPL23,LRRK1,HDAC1,PDCD4,PKAR1A,ADARB1,PIAS3,FABP4,UBASH3B,SORL1,RTRAF,DTX3L,PARP14,AGT,CIB1,CBL,SFN,PER2,TRAF3IP1,CAMK2N2,PTPRO,INPP5J,MLXIPL,RPL11,SNX6,CDKN1B,SENP2,AIDA,YWHAG,IVNS1ABP,DUSP10,MAPT,HEXIM2,BCOR,MEN1,DNAJC10,DUSP19,PTPN6,FKBP8,ZFYVE28,SOCS4,TIPRL,KDM5A,FOXP3,GPS2,RGS14,GNL3L,DGKQ,TARDBP,BOD1L2,PSEN1,PYDC1,TAF1,OGT,CALM1,OTUB2,PPP4R4,BDKRB1,DCUN1D3,SIN3A,SMCR8,SUZ12,SUPT6H,PTPN2,SOCS1,INPP5K,PDPK1,PRKCZ,SKI,PARK7,DBNDD1,PIP5KL1,ENG,MTF2,GLMN,DAB2IP,MIR27B,MIR24-1,PRMT6,DMD,SOX4,TINF2,MIR125A,BAG2,IMPACT,NOG,SMYD3,THY1,GADD45A,ACER2,CAMLG,DUSP26,DUSP1,PPP1R15A,APC,DUSP22,LAX1,CADM4,PRR7,LDLRAD4,PARD6A,PRKRIP1,ARPP19,RASD2	grey	VSMC_M10

GO:0008150	1.00	0.00	6446	12183	biological_process	BP	1	ADNP2,NFATC1,ATP9B,ZNF236,ZNF407,CNDP1,TIMM21,MTCH2,CD226,NME1,SERPINB8,SERPINB2,ITGA7,RDH5,VPS4B,KDSR,PHLPP1,ORMDL2,SUOX,ERBB3,SEC11C,ZC3H10,SMARCC2,SLC39A5,NEDD4L,PAN2,APOF,ATP8B1,FECH,ONECUT2,MIP,SPRYD4,GLS2,ARPC3,BAZ2A,TCF4,CCDC68,C18orf54,RDH16,STARD6,POLI,TAC3,MYO1A,HSD17B4,NEMP1,TNFAIP8,RNMT,FAM210A,LRP1,STX7,SLC18B1,RPS12,SEMA6A,SHMT2,EYA4,LVRN,STAC3,AP3S1,ATG12,TBPL1,FEM1C,SLC2A12,PGGT1B,TRIM36,ALDH8A1,GLI1,YTHDC2,ARHGAP9,HBS1L,MARS,B4GALT7,N4BP3,RMND5B,KIF5A,PDE7B,MAP7,CLK4,PIP4K2C,MAP3K5,SLC26A10,PEX7,B4GALNT1,RPA3,TNFAIP3,AGAP2,HEBP2,NHSL1,TSPAN31,REPS1,HECA,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,AIG1,ADAT2,PEX3,FUCA2,ATP23,SLC16A7,PLAGL1,SERF2,USP15,EPM2A,FBXO30,RXYLT1,SRGAP1,CANX,MAML1,LTC4S,TBC1D30,MRNIP,ENPP3,ATP5MGL,HELB,TBC1D9B,KATNA1,TRIM39,RPP21,PPP1R10,MDM1,AATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,CCDC170,ESR1,FRS2,GFPT2,MYRFL,CNOT2,MDC1,IER3,TSPAN8,ZFC3H1,RAB21,TPH2,CNOT6,RIDA,MUCL3,C6orf15,NIPAL2,STK3,ZNF207,OSR2,PRR16,SNCAIP,PRRC2A,SNX24,FBXO43,MIOX,SNX31,PABPC1,MAPK8IP2,SNW1,TIAM2,TFB1M,ZNF706,CPT1B,ALDH7A1,PHAX,MARCH3,APOM,ABHD16A,ARID1B,ADM2,MPIG6B,ZDHHC14,DENND6B,VWA7,SLC12A2,HSPA1B,SYNJ2,SERAC1,TULP4,FZD6,RIMS2,ZBTB12,DPYS,SKIV2L,SF3A3,TUBGCP6,IGF2R,SELENOO,DXO,MOV10L1,EIF3E,SLC27A6,ALG12,CYP21A2,EMC2,ZBED4,TMEM74,BRD1,NUDCD1,ADAMTS19,LYRM7,CDC42SE2,EBAG9,PNLDC1,KCNV1,TNXB,GRAMD4,MAP3K4,PRRT1,AGPAT4,PPT2	grey	VSMC_M10
GO:0098813	1.00	0.00	87	230	nuclear chromosome segregation	BP	1	VPS4B,ZNF207,UBE2B,MAPK15,DMC1,CHMP2A,MCMBP,TRAPPC12,CDK5RAP2,CCDC155,MLH1,PIBF1,CCNB1IP1,DYNC1LI1,SIRT2,ANAPC15,IK,SIRT7,USP44,TEX15,CHAMP1,MOS,TTL,CHMP2B,SLF1,FBXW7,ANAPC5,M1AP,ANAPC7,CHMP4C,KATNB1,ABRAXAS1,CHMP7,SYCP1,SLF2,AC112128.1,HECW2,DIS3L2,AXIN2,CCDC36,KLHDC8B,SPO11,NSL1,HORMAD2,POGZ,ABRAXAS2,TEX12,MAJIN,TTN,MAU2,ZCWPW1,STAG3,TUBG1,DDX11,P3H4,AKAP8L,AKAP8,ANAPC4,SEPT1,KPNB1,EME1,SYCE2,RAB11A,LCMT1,RAD51C,SFPQ,ERCC4,PSMG2,RMI2,SLX4,NAA10,WRAP73,MEIOB,CHMP1A,PSRC1,VPS4A,CTCF,MSH4,AURKC,RNF212B,AGO4,SYCE1L,DUSP1,APC,CDC26,CENPX,GEM	grey	VSMC_M10
GO:0001667	1.00	0.00	147	360	ameboidal-type cell migration	BP	1	SEMA6A,AGO2,PTK2,PTP4A3,SOX10,SMO,MYH9,TEK,ZFAND5,SRF,KIT,SEMA4D,SEMA4C,MEOX2,SVBP,PRKCE,RTN4,HAS1,EPB41L4B,EMC10,BMPER,PTN,ITGB1BP1,MET,PRKD2,IQSEC1,SOX9,CLASP2,MEGF8,PAXIP1,CYGB,WNT11,RIN2,TGFBR2,OVOL2,HBEGF,FERMT1,ALX1,BAG4,ARHGEF7,SEMA3D,DCN,SEMA3A,FOXP1,PLK2,RET,GPI,NR4A1,ACVR1B,FER,PIK3CB,LPXN,HAND2,ATP5F1A,ROBO1,FBXW7,MEF2C,SEMA4F,VEGFC,PTK2B,DOCK5,STC1,HDAC7,LOXL2,ACVR1C,SEMA3G,RREB1,DMTN,SEMA4G,ADTRP,CD40,PXN,GPLD1,FAP,HYAL1,SP100,SEMA3F,TGFB2,PDCD6,PRKX,EGF,AGT,CIB1,WASF2,GBX2,LAMA5,MAP3K3,DOCK1,PATZ1,GLUL,NFE2L2,MIA3,DUSP10,SEMA6D,CTSH,EPHB4,ITGA4,S100P,FN1,PDCD10,RHOJ,RADIL,SYDE1,SYNJ2BP,SEMA4A,RAB25,FGF18,ITGA3,EFNA1,AC138894.1,VASH1,RAB11A,MAP2K5,BCAS3,EVL,AMOT,ISL1,GPC3,PDPK1,ARHGAP4,MECP2,SOX8,LCN2,MARVELD3,DAB2IP,CAP1,MIR29A,MIR199A1,MIR21,MIR222,MIR23A,MIR22,MIR27B,MIR24-1,MIR27A,RHOA,C5orf30,DPP4,ACVRL1,NANOS1,ZNF580,WNT5A,GADD45A,LAMTOR2,RGCC,FGF1,S100A2	grey	VSMC_M10
GO:0023051	1.00	0.00	1232	2524	regulation of signaling	BP	1	NFATC1,CD226,PHLPP1,ERBB3,ONECUT2,LRP1,RPS12,SEMA6A,EYA4,GLI1,ARHGAP9,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,EPM2A,TRIM39,PPP1R10,ESR1,FRS2,CNOT2,STK3,SNCAIP,MAPK8IP2,SNW1,TIAM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,PDE10A,FBLN1,IL5,GDF9,ROS1,RGL2,FSTL4,SYNGAP1,UBE2B,BAK1,RSPO3,RNF146,TRIB1,MYC,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,ZC3H3,ATF4,TAB1,SYNGR1,MAPK14,NTRK2,CBY1,STK38,CSNK1E,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,BTBD9,ZC3HC1,MFNG,SMO,DAAM2,MDFI,KCP,CCND3,FOXH1,LRRC14,CHRNA3,TEK,LRRC4,GRM8,CHRNA5,GPR37,CRY1,RIC8B,PTK7,SRF,DLK2,NUAK1,APBA1,CDK14,LRRD1,PHF24,SLC35B2,OCIAD1,USP46,RFX3,KIT,SLC1A1,NCK2,FHL2,IL1R2,TFAP2B,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,TMEM14A,WNK2,NINJ1,FGD3,KLHL31,PRDX1,SEMA4C,SOSTDC1,BEND6,CAT,CAMKMT,DNAJA1,IL11,BRSK1,PRKCE,EPS8L1,RIMS1,CD109,SPTBN1,FKTN,RTN4,PPP2R1A,PHIP,FPR2,HMGN3,GSDME,RIMS3,KLK14,ACP4,SHANK1,VRK2,ADAMTS3,HOXA13,EMC10,LPAR1,REL,ANKRD17,CXCL8,SLC46A2,MTURN,EPGN,NOD1,AREG,BMP8A,CRHR2,RRAGD,PELI1,BMPER,PXDN,ETAA1,PLEK,RSPO1,RSAD2,AAK1,EPHA7,NR1H2,TGFA,PTN,ITGB1BP1,DGKI,MET,VRK3,GRB10,YWHAZ,ATP6V1C2,EGFR,LANCL2,TSPAN12,HECW1,FUZ,ARHGEF5,TRIM32,TLR4,NCDN,CDK5RAP2,GRIK2,TRAF1,BCL2L12,BVES,DLGAP3,SFRP4,CCNY,DKKL1,VPS35,SDCBP,TRPM4,SLC7A11,FOXO3,PPFIA3,NTF4,PUM2,WASF1,EPS15,FAF1,FGF21,BRAF,INTU,PRKAR2B,TRAF3IP2,SPHK2,SPRY1,	grey	VSMC_M10

GO:0048583	1.00	0.00	1394	2834	regulation of response to stimulus	BP	1	NFATC1,CD226,SERPINB2,PHLPP1,ERBB3,ONECUT2,LRP1,STX7,RPS12,SEMA6A,EYA4,GLI1,ARHGAP9,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,EPM2A,MRNIP,ENPP3,HELB,TRIM39,PPP1R10,ARMT1,ESR1,FRS2,CNOT2,IER3,TSPAN8,STK3,MAPK8IP2,SNW1,TIAM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,GPSM3,PDE10A,HLA-DRA,FBLN1,IL5,HLA-DPB1,GDF9,ROS1,RGL2,FSTL4,SYNGAP1,UBE2B,BAK1,XRCC6,NCOA7,RSPO3,RNF146,TRIB1,MYC,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,PTK2,C6orf106,GPR20,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,ZC3H3,ATF4,TAB1,PLXNA4,MAPK14,NTRK2,MAPK13,CBY1,STK38,CSNK1E,PLA2G6,GKAP1,KDM4C,SOX10,PI16,ZC3HC1,MFNG,RAC2,SMO,HSF1,DAAM2,MDFI,KCP,CCND3,FOXH1,LRRC14,CDKN2A,TEK,POT1,GPR37,FBXO7,CRY1,RIC8B,PTK7,ABCB1,TTBK1,DLK2,NUAK1,CDK14,TEC,LRRD1,CCL27,PHF24,SLC35B2,OCIAD1,CDK6,ENPP4,KIT,TNFRSF21,NCK2,FHL2,IL1R2,TFAP2B,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,TMEM14A,WNK2,NINJ1,FGD3,KLHL31,PRDX1,EXOSC3,SEMA4C,SOSTDC1,BEND6,CAT,CLDN19,CAMKMT,DNAJA1,IL11,PRKCE,EPS8L1,RIMS1,MSH2,CD109,SPTBN1,FKTN,RTN4,PPP2R1A,PHIP,FPR2,GSDME,KLK14,PNPT1,ACP4,SHANK1,VRK2,ADAMTS3,HOXA13,EMC10,LPAR1,REL,NT5E,ANKRD17,CXCL8,SLC46A2,MTURN,EPGN,NOD1,AREG,AKIRIN2,BMP8A,RRAGD,PELI1,BMPER,CYREN,AKIRIN1,PXDN,ETAA1,PLEK,RSPO1,RSAD2,AAK1,ZNF277,EPHA7,NR1H2,AKNA,TGFA,PTN,ITGB1BP1,MET,VRK3,GRB10,IL4I1,YWHAZ,ATP6V1C2,EGFR,LANCL2,TSPAN12,HECW1,FUZ,ARHGEF5,TRIM32,TLR4,CDK5RAP2,TRAF1,BC	grey	VSMC_M10
GO:0032269	1.00	0.00	341	760	negative regulation of cellular protein metabolic process	BP	1	SERPINB8,SERPINB2,PAN2,TNFAIP8,LRP1,SHMT2,TNFAIP3,TRIM39,CNOT2,CNOT6,RIDA,PABPC1,HSPA1B,EIF3E,PNLDC1,PRKN,FBLN1,TSPO,MRPL13,PHF1,UBE2B,BAK1,NCOA7,TRIB1,AGO2,TNRC6B,ATF4,TUT7,STK38,PI16,CDKN2A,FBXO7,CRY1,NCK2,IL1R2,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,SVBP,DNAJA1,PRKCE,CD109,IGF2BP3,PPP2R1A,IBTK,PNPT1,ACP4,AQP1,NR1H2,ITGB1BP1,AGO1,EPHA1,BCL2L12,ATG5,SDCBP,TUT4,PRKAR2B,SPHK2,DHFR,SPRY1,HDAC2,CST7,BEX4,CRTAP,XRCC1,MLH1,KDM4A,AQP11,PRKAG2,RAF1,PRDX3,TIMP4,PIBF1,UBE2O,SPOPL,TNRC6C,SPRY2,PLAT,KLHL40,GPD1L,ARRB1,IKBKB,SIRT2,PURA,PTPRQ,SIRT7,SPINT2,EIF2AK2,PRNP,DUSP6,LSM1,TAF7,USP44,DDRGK1,SH3RF2,NCKAP1L,GAS6,RYBP,PRKDC,MFHAS1,PAN3,PSMF1,TRIM44,TRIB3,SDR16C5,DNMT3B,GPI,NR4A1,CEBPA,IDE,PIK3CB,SNX25,CASP3,TAF9,USP25,PTPRJ,ENC1,PKIA,CNOT1,CELF1,CSNK2A2,CNOT6L,FAM192A,EIF2AK4,NR1H3,EIF4E2,PAQR3,PAIP2B,SERPINB1,SPINT1,CRY2,CDYL,FTO,MARCH7,DBNDD2,PAX2,DMTN,PRMT3,JARID2,DTNBP1,TENT4B,RBM24,APLP2,SUFU,SIRT4,TM4SF20,RPL23,LRRK1,HDAC1,BANK1,CAPRIN2,PDCD4,PRKAR1A,ADARB1,DIS3L2,PIAS3,FABP4,GIGYF2,USP19,YTHDF2,UBASH3B,SORL1,RTRAF,DTX3L,PARP14,IFI6,AGT,CIB1,CBL,COL6A3,SFN,COL7A1,RPS6KA1,PER2,DDX6,TRAF3IP1,CAMK2N2,YTHDF1,PTPRO,INPP5J,MLXIPL,CST6,EIF4ENIF1,RPL11,SNX6,CDKN1B,SENP2,IGF2BP2,LRIG2,POR,AIDA,YWHAG,IVNS1ABP,DUSP10,MAPT,HEXIM2,EIF4EBP2,BCOR,MEN1,DDX3X,DNAJC10,SPOCK2,DUSP19,RC3H1,PTPN6,SERPINC1,UPF1,SERPINI1,FKBP8,ZFYVE28,SAMD4A,SOCS4,BIRC3,STAT3,TIPRL,ARL6IP1,POLR	grey	VSMC_M10
GO:0072359	1.00	0.00	407	902	circulatory system development	BP	1	NFATC1,ERBB3,LRP1,SEMA6A,GLI1,TNFAIP3,ADGRG6,MAML1,FRS2,STK3,ADM2,SLC12A2,QKI,PPARA,TBC1D32,CCDC134,BAK1,RSPO3,SMAD5,LEMD2,AGO2,PTK2,PTCH1,LY6E,TAB1,MAPK14,NTRK2,CBY1,PI16,PIM1,SMO,MYH9,FOXH1,IFT74,TEK,ZFAND5,PTK7,CEMIP2,SRF,KIT,SLC1A1,FHL2,TFAP2B,PDCL3,C1GALT1,NINJ1,SHB,MEOX2,ANKS6,TNNI3,EPAS1,DNAH11,RTN4,HOXA7,HOXA13,EMC10,ANKRD17,CXCL8,EPGN,AQP1,BMPER,TGFA,PTN,ITGB1BP1,AGO1,YWHAZ,EGFR,TSPAN12,EPHA1,BVES,CNTRL,GAB1,MYLK3,TEAD2,ATG5,NRCAM,OSR1,ARMC4,APOB,TRAF3IP2,SPHK2,SPRY1,WISP3,BBS7,NDNF,C5AR1,PRKD2,SETDB2,DRC1,SOX9,SLC39A12,GLI2,MEGF8,GALNT11,RAF1,ACVR2B,KLF5,IFT172,FOXJ1,SCN5A,PAXIP1,POU4F1,SPRY2,WNT11,RIN2,TGFBR2,OVOL2,ISM1,JAG1,MKKS,RARB,ACTG1,RYR1,FREM2,DUSP6,DCN,PANK2,BTG1,AIMP1,NRG1,PRKDC,FLT1,EPHB1,PLK2,SGCG,POFUT1,ASXL1,IL1A,PAX8,NR4A1,SMYD1,PIK3CB,NCOA6,TFDP2,CASP3,ERAP1,HAND2,HPGD,EYA1,PARVA,ROBO1,ROBO2,PLCE1,FBXW7,MEF2C,VEGFC,ADAMTS1,SOX6,PTK2B,RAPGEF2,NPY1R,OTULIN,NKX3-1,HDAC7,RAPGEF3,LOXL2,TBX5,AGGF1,IFT52,ARHGAP24,SPINT1,TNNC1,COL4A3BP,RPGRIP1L,DSP,PKD2,STK4,RIPPLY3,HIF1AN,SALL1,PRICKLE1,ADTRP,DNAH5,JARID2,RBM24,CD40,WARS2,RYR2,SUFU,GPLD1,FAP,PKP2,PKNOX1,SIK1,HYAL1,SLC2A10,SP100,TERT,TNNI1,PDCD4,TGFB2,TRIP11,POGLUT1,PRKAR1A,TCF7L2,COX17,PDCD6,PRKX,DAG1,AXIN2,SNAI1,EGF,ENPEP,MYH7,GRK2,ANK2,GPER1,AP1B1,AGT,MCAM,CIB1,WASF2,GBX2,ACTC1,SLC9A1,BICC1,NFATC4,VASH2,FZD7,KCNK2,MMP21,CLIC4,ALPK3,MAP3K3,EPHB3,GLUL,E	grey	VSMC_M10

GO:0031325	1.00	0.00	1212	2483	positive regulation of cellular metabolic process	BP	1	NFATC1,ZNF407,ERBB3,SMARCC2,PAN2,ONECUT2,TCF4,LRP1,EYA4,GLI1,MARS,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,PLAGL1,EPM2A,MAML1,MRNIP,PPP1R10,RMND1,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ARID1B,HSPA1B,DXO,EIF3E,ZBED4,PNLDC1,GRAMD4,MAP3K4,PRKN,AGER,PPARA,FBLN1,MED30,IL5,RXRB,TSPO,GDF9,VGLL2,ROS1,HSF2,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PITX1,TRIB1,MYC,SMAD5,JMJD4,AGO2,PRXL2C,HABP4,PTK2,PTCH1,TNRC6B,ATF4,TUT7,TAB1,MAPK15,AGTPBP1,GTPBP1,MAPK14,NTRK2,CSNK1E,PLA2G6,PICK1,C6orf89,SOX10,PIM1,NRF1,TMPRSS6,SMO,HSF1,NFYA,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,GUCA1B,GPT,ZNF16,IFT74,CHRNA3,TEK,BICRAL,POT1,GPR37,FBXO7,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,TTBK1,ZNF318,FZD1,TEC,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,NCK2,PLGRKT,TFAP2B,SPTLC1,ROR2,NFIL3,SEMA4D,DLX5,IPPK,ETV1,EXOSC3,MEOX2,KANSL3,ZNF268,MACC1,CLDN19,SIX2,FOXJ3,HIVEP3,IL11,RNF20,PRKCE,EPAS1,STPG4,EPCAM,MSH2,ZNF462,TRA2A,PHIP,FPR2,HMGN3,NFYC,PPP4R3B,PNPT1,MOB1B,SLC4A4,HOXA2,HOXA7,HOXA13,REL,CREB5,CXCL8,EPGN,NOD1,AREG,AKIRIN2,BMP8A,CASP8AP2,PELI1,AKIRIN1,ETAA1,MTF1,PLEK,RSPO1,PCBP1,EPHA7,NR1H2,AKNA,TNFSF15,TGFA,ITGB1BP1,GRHL1,MED25,MET,VRK3,IL4I1,AGO1,POU3F3,EGFR,ARHGEF5,TRIM32,TLR4,CCNC,CDK5RAP2,EPHA1,BCL2L12,BVES,LPIN1,IL15,SFRP4,CCNY,VPS35,TEAD2,SCOC,SETD7,ZYG11B,SDCBP,MYCN,ELF2,TUT4,OSR1,FOXO3,ZXDC,NTF4,EPS15,SSBP1,FAF1,FGF21,BRAF,MAMSTR,ATAD2B,HSPE1,SPHK2,KDM7A,ZNF438,HDAC2,PHF10,MAML2,ZC3	grey	VSMC_M10
GO:0031324	1.00	0.00	912	1896	negative regulation of cellular metabolic process	BP	1	SERPINB8,SERPINB2,ORMDL2,ZC3H10,SMARCC2,PAN2,ATP8B1,TNFAIP8,LRP1,SHMT2,PIP4K2C,TNFAIP3,CYP27B1,PLAGL1,HELB,TRIM39,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,PHAX,HSPA1B,ZBTB12,EIF3E,PNLDC1,PRKN,RNF5,PPARA,FBLN1,TSPO,MRPL13,TCF7,PHF1,UBE2B,BAK1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PTCH1,TNRC6B,ATF4,TUT7,CBX7,MAPK14,NTRK2,CBY1,NRBP2,STK38,SOX10,PI16,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,FBXO7,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,IL1R2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SVBP,LRPPRC,DNAJA1,SCMH1,RNF20,PRKCE,MSH2,CD109,IGF2BP3,RTN4,PPP2R1A,IBTK,NFE2L3,PNPT1,ACP4,HOXA2,HOXA7,JAZF1,PTBP3,XPO1,AKIRIN2,SRSF10,AQP1,CASP8AP2,BACH2,ZNF692,CYREN,PLEK,NR1H2,ZNF350,ITGB1BP1,FOXP2,MED25,KLF11,MET,GRB10,AGO1,POU3F3,LANCL2,FAM3C,EPHA1,BCL2L12,DKKL1,CREM,ATG5,SDCBP,MYCN,TUT4,OSR1,FOXO3,BEND5,PRKAR2B,TRAF3IP2,SPHK2,DHFR,SPRY1,HDAC2,PHF10,MTMR2,DNMT3A,BMI1,DHX34,ZC3H4,PIP4K2A,CST7,CNBP,SETDB2,PHB,SOX9,BEX4,ZNF746,ERCC1,EED,APOC1,CRTAP,DNAJC15,SUV39H2,ZNF404,PLK3,XRCC1,OPTN,MLH1,GLI2,DEDD2,RSF1,KDM4A,AQP11,PRKAG2,RAF1,MYD88,DACH1,PRDX3,TIMP4,SLC22A13,TAF3,PIBF1,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,UBE2O,SFMBT2,GZF1,GCKR,SPOPL,POU4F1,FBH1,TNRC6C,SPRY2,PLAT,WNT11,KLHL40,GPD1L,ARRB1,THAP1,EID2,OVOL2,RNF169,ZNF219,EOMES,USP36,IKBKB,CBX4,BHLHE40,CHD8,SI	grey	VSMC_M10
GO:0044085	1.00	0.00	1199	2454	cellular component biogenesis	BP	1	TIMM21,VPS4B,ORMDL2,PAN2,ATP8B1,ONECUT2,MIP,ARPC3,BAZ2A,TCF4,MYO1A,LRP1,STX7,SHMT2,ATG12,TBPL1,PIP4K2C,AVIL,PEX3,ATP23,TBC1D30,HELB,MDM1,ATAT1,CPSF6,ESR1,CNOT2,CNOT6,STK3,ZNF207,SNCAIP,MAPK8IP2,TFB1M,APOM,HSPA1B,SF3A3,TUBGCP6,EIF3E,LYRM7,KCNV1,TNXB,PRKN,RNF5,HLA-DRA,HLA-DOB,UTP23,HLA-DMA,IL5,BRD2,PARVG,KIF3A,HLA-DPB1,SEPT8,SHROOM1,HSD17B8,ASF1A,HSPA4,TBC1D32,RRP7A,NDUFA6,UBE2B,BAK1,MTSS1,WASHC5,ASAP1,LRRC6,OBSCN,AGO2,H3F3C,PTK2,FANCC,JSCA1,MAPK15,NTRK2,CBY1,DMC1,PUF60,PODXL,PSMD5,PLA2G6,BAIAP2L2,PICK1,EIF3L,MPDZ,CDC42EP1,RAC2,EXOSC4,GPAA1,TSPAN33,HSF1,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,GNMT,TRPM6,POT1,LMOD2,SRF,TTBK1,NOL6,CFAP69,GTPBP10,GABRA1,APBA1,FZD1,C12orf45,PGM5,SLAIN2,RFX3,KIT,ADGRF1,NCK2,TSR1,TLN1,SEMA4D,KIAA1211,PTPDC1,NINJ1,FGD3,COA5,CHMP2A,ADGRL3,EXOSC3,RPS14,TMOD1,RAB23,DYNC2LI1,STX17,CLDN19,SDHAF4,PRKCE,EPS8L1,RIMS1,PRPF31,SPTBN1,RTN4,PPP2R1A,HAS1,MPP6,YTHDC1,PNPT1,UTP3,SKAP2,SHANK1,LPAR1,CEP162,ECPAS,XPO1,SRSF10,MDN1,TMEM17,GJA10,AKIRIN1,PXDN,WDR92,TRAPPC12,PLEK,LRRN3,EPHA7,NR1H2,ITGB1BP1,MED25,MET,ADD2,AGO1,YWHAZ,FCF1,FUZ,ARHGEF5,TLR4,CDK5RAP2,EPHA1,IQUB,TRAF1,CCDC155,MYLK3,VPS35,TEAD2,ATG5,SDCBP,FAM49A,NRCAM,TRPM4,ARMC2,MAPRE1,PUM2,FIG4,WASF1,ARMC4,EPS15,SSBP1,APOB,FAF1,NDUFB2,INTU,SPATA6,SPHK2,HIGD1A,UBN2,MTMR2,TTC26,NAPA,BBS7,RAB7A,PIP4K2A,AP2S1,VSTM5,ARHGEF4,MSRB2,ATPAF1,KC	grey	VSMC_M10

GO:0048285	1.00	0.00	165	401	organelle fission	BP	1	VPS4B,ZNF207,FBXO43,HSPA1B,MOV10L1,PRKN,UBE2B,WASHC5,MAPK15,DMC1,KLHDC3,CHMP2A,FOXJ3,PHIP,HOXA13,EPGN,TGFA,CDK5RAP2,CCDC155,VPS35,CCDC61,CLASP2,MLH1,PIBF1,CCNB1IP1,DYNC1LI1,SIRT2,ANAPC15,PLCB1,IK,SIRT7,DDHD2,DCN,USP44,TEX15,CHAMP1,NSFL1C,MOS,KIF3B,IL1A,CHMP2B,ING2,SLF1,ANAPC5,M1AP,ANAPC7,CHMP4C,USP16,KATNB1,ABRAXAS1,OPA1,RAD54B,AP3B1,CHMP7,SYCP1,SLF2,SYCP2L,NPM2,IGF2,DNM1L,HSF2BP,AC112128.1,HECW2,PPP2R2D,PRKAR1A,DIS3L2,PEX11B,EGF,CCDC36,KLHDC8B,CHEK2,SPO11,GPR3,C11orf80,NSL1,HORMAD2,PEX19,POGZ,EPS8,MTFP1,ABRAXAS2,TDRKH,CD28,CDKN1B,MAPT,FIS1,TEX12,TOGARAM1,MAJIN,TTN,SEC16B,MAU2,C11orf65,ZCWPW1,MCU,STAG3,WNT4,DDHD1,TUBG1,PINK1,MUL1,OBSL1,P3H4,AKAP8L,AKAP8,ANAPC4,RAD51B,SEPT1,KPNB1,EME1,NDEL1,SYCE2,RAB11A,LCMT1,RAD51C,STAT2,COX10,INSR,PEX11G,MIEF2,RAD51D,TOM1L2,RALBP1,ERCC4,PSMG2,CEP192,FZR1,SLX4,NAA10,WRAP73,MEIOB,SPIRE2,CHMP1A,PSRC1,CDC14A,DHODH,VPS4A,MSH4,RHOA,AURKC,UBB,SYCP3,RNF212B,AGO4,OOEP,FOXJ2,ZSCAN21,SYCE1L,WNT5A,DUSP1,SPDYA,CCSAP,PEX11A,BCL2L11,RGCC,NME6,APC,RALA,LIF,CDC26,CENPX,MIEF1,EREG,PDXP,DRG1	grey	VSMC_M10
GO:0051172	1.00	0.00	846	1770	negative regulation of nitrogen compound metabolic process	BP	1	SERPINB8,SERPINB2,ORMDL2,ZC3H10,SMARCC2,PAN2,ATP8B1,TNFAIP8,LRP1,SHMT2,TNFAIP3,AGAP2,PLAGL1,HELB,TRIM39,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,PHAX,HSPA1B,ZBTB12,EIF3E,PNLDC1,PRKN,PPARA,FBLN1,TSPO,MRPL13,TCF7,PHF1,UBE2B,BAK1,XRCC6,NCOA7,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,PTCH1,TNRC6B,ATF4,TUT7,CBX7,MAPK14,NTRK2,CBY1,STK38,SOX10,PI16,TMPRSS6,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,FBXO7,RORB,CRY1,SRF,ZNF318,NFX1,SMARCA2,RFX3,NCK2,FHL2,IL1R2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SVBP,LRPPRC,DNAJA1,SCMH1,RNF20,PRKCE,MSH2,CD109,IGF2BP3,RTN4,PPP2R1A,IBTK,NFE2L3,PNPT1,ACP4,HOXA2,HOXA7,JAZF1,PTBP3,XPO1,AKIRIN2,SRSF10,AQP1,CASP8AP2,BACH2,ZNF692,CYREN,NR1H2,ZNF350,ITGB1BP1,FOXP2,MED25,KLF11,AGO1,POU3F3,EGFR,LANCL2,EPHA1,BCL2L12,CREM,ATG5,SDCBP,TUT4,OSR1,FOXO3,BEND5,PRKAR2B,TRAF3IP2,SPHK2,DHFR,SPRY1,HDAC2,PHF10,DNMT3A,BMI1,DHX34,ZC3H4,CST7,CNBP,SETDB2,PHB,SOX9,BEX4,ZNF746,ERCC1,EED,APOC1,CRTAP,SUV39H2,ZNF404,PLK3,XRCC1,MLH1,GLI2,DEDD2,RSF1,KDM4A,AQP11,PRKAG2,RAF1,MYD88,DACH1,PRDX3,TIMP4,TAF3,PIBF1,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,UBE2O,MYCBP2,SFMBT2,GZF1,SPOPL,POU4F1,FBH1,TNRC6C,SPRY2,PLAT,WNT11,KLHL40,GPD1L,ARRB1,THAP1,EID2,OVOL2,RNF169,ZNF219,EOMES,IKBKB,CBX4,BHLHE40,CHD8,SIRT2,ZMYND11,RARB,PURA,HBEGF,NR1D2,PAWR,PTPRQ,PLCB1,SIRT7,SPINT2,DPF1,ALX1,SHLD1,EIF2AK2,PRNP,	grey	VSMC_M10
GO:0010646	1.00	0.00	1222	2513	regulation of cell communication	BP	1	NFATC1,CD226,PHLPP1,ERBB3,ONECUT2,LRP1,RPS12,SEMA6A,EYA4,GLI1,ARHGAP9,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,EPM2A,TRIM39,PPP1R10,ESR1,FRS2,CNOT2,STK3,SNCAIP,MAPK8IP2,SNW1,TIAM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,PDE10A,FBLN1,IL5,GDF9,ROS1,RGL2,FSTL4,SYNGAP1,UBE2B,BAK1,RSPO3,RNF146,TRIB1,MYC,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,ZC3H3,ATF4,TAB1,SYNGR1,MAPK14,NTRK2,CBY1,STK38,CSNK1E,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,BTBD9,ZC3HC1,MFNG,SMO,DAAM2,MDFI,KCP,CCND3,FOXH1,LRRC14,CHRNA3,TEK,LRRC4,GRM8,CHRNA5,GPR37,CRY1,RIC8B,PTK7,SRF,DLK2,NUAK1,APBA1,CDK14,LRRD1,PHF24,SLC35B2,OCIAD1,USP46,RFX3,KIT,SLC1A1,NCK2,FHL2,IL1R2,TFAP2B,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,TMEM14A,WNK2,NINJ1,FGD3,KLHL31,PRDX1,SEMA4C,SOSTDC1,BEND6,CAT,CAMKMT,DNAJA1,IL11,BRSK1,PRKCE,EPS8L1,RIMS1,CD109,SPTBN1,FKTN,RTN4,PPP2R1A,PHIP,FPR2,HMGN3,GSDME,RIMS3,KLK14,ACP4,SHANK1,VRK2,ADAMTS3,HOXA13,EMC10,LPAR1,REL,ANKRD17,CXCL8,SLC46A2,MTURN,EPGN,NOD1,AREG,BMP8A,CRHR2,RRAGD,PELI1,BMPER,PXDN,ETAA1,PLEK,RSPO1,RSAD2,AAK1,EPHA7,NR1H2,TGFA,PTN,ITGB1BP1,DGKI,MET,VRK3,GRB10,YWHAZ,ATP6V1C2,EGFR,LANCL2,TSPAN12,HECW1,FUZ,ARHGEF5,TRIM32,TLR4,NCDN,CDK5RAP2,GRIK2,TRAF1,BCL2L12,DLGAP3,SFRP4,CCNY,DKKL1,VPS35,SDCBP,TRPM4,SLC7A11,FOXO3,PPFIA3,NTF4,PUM2,WASF1,FAF1,FGF21,BRAF,INTU,PRKAR2B,TRAF3IP2,SPHK2,SPRY1,GRIN2D,ARHG	grey	VSMC_M10

GO:0048870	1.00	0.00	571	1234	cell motility	BP	1	ONECUT2,ARPC3,LRP1,SEMA6A,TNFAIP3,SRGAP1,SLC12A2,AGER,GPSM3,FBLN1,TSPO,CEP85L,UBE2B,CATSPER3,TRIB1,CXCL14,LRRC6,AGO2,GFRA3,PTK2,PTP4A3,ANKS1A,MAPK15,PLXNA4,SUN2,NTRK2,PODXL,SOX10,RAC2,STRIP2,SMO,MYH9,RBFOX2,TEK,ZFAND5,PTK7,SRF,CFAP69,CCL27,CDK6,RFX3,KIT,NCK2,ROR2,SEMA4D,EFHC1,NINJ1,ADGRL3,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,SIX2,DNAJA1,RNF20,PRKCE,EPCAM,MBOAT7,DNAH11,RTN4,FPR2,HAS1,EPB41L4B,CABS1,RUFY3,HOXA7,EMC10,LPAR1,CXCL8,AVL9,BMPER,AKIRIN1,PTN,ITGB1BP1,MET,ADD2,GRB10,POU3F3,EGFR,USP45,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,BVES,GAB1,SDCBP,NRCAM,TRPM4,FOXO3,ARMC2,MAPRE1,APOB,FGF21,PLXNA1,LAMA4,PODXL2,ADCY3,NDNF,C5AR2,C5AR1,SLC26A5,PRKD2,DRC1,IQSEC1,SOX9,RSPH6A,BEX4,LCP1,CLASP2,MEGF8,RAF1,MYD88,OXSR1,DACH1,FOXJ1,PAXIP1,PTPRF,TTC21A,CYGB,POU4F1,SPRY2,PLAT,WNT11,TTLL3,RIN2,ACKR2,AKT2,TGFBR2,OVOL2,SRGAP3,JAG1,MKKS,ACTG1,FSCN2,NAV3,HBEGF,PLCB1,FERMT1,SPINT2,CNN2,ALX1,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,BTG1,SPEF1,PLXNC1,SEMA3A,UNC5D,AIMP1,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,FAM19A4,DPYSL3,FLT1,EPHB1,PLK2,MTUS1,RET,AL359736.1,HCK,FAM107A,CYP7B1,GPI,NR4A1,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,LPXN,HAND2,ATP5F1A,ING2,PARVA,ROBO1,DNAH6,WDR66,FBXW7,LIMA1,PTPRJ,FZD3,MEF2C,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,IGSF10,ADAMTS1,P2RY1,PTK2B,RAPGEF2,CCL17,CCDC65,RND1,TIAM1,FGF5,DOCK5,SLC8B1,STC1,HDAC7,NKX6-1,LOXL2,TBX5,NR4A2,ACVR1C,BIN3,F2RL1,F2R,ARHG	grey	VSMC_M10
GO:0051674	1.00	0.00	571	1234	localization of cell	BP	1	ONECUT2,ARPC3,LRP1,SEMA6A,TNFAIP3,SRGAP1,SLC12A2,AGER,GPSM3,FBLN1,TSPO,CEP85L,UBE2B,CATSPER3,TRIB1,CXCL14,LRRC6,AGO2,GFRA3,PTK2,PTP4A3,ANKS1A,MAPK15,PLXNA4,SUN2,NTRK2,PODXL,SOX10,RAC2,STRIP2,SMO,MYH9,RBFOX2,TEK,ZFAND5,PTK7,SRF,CFAP69,CCL27,CDK6,RFX3,KIT,NCK2,ROR2,SEMA4D,EFHC1,NINJ1,ADGRL3,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,SIX2,DNAJA1,RNF20,PRKCE,EPCAM,MBOAT7,DNAH11,RTN4,FPR2,HAS1,EPB41L4B,CABS1,RUFY3,HOXA7,EMC10,LPAR1,CXCL8,AVL9,BMPER,AKIRIN1,PTN,ITGB1BP1,MET,ADD2,GRB10,POU3F3,EGFR,USP45,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,BVES,GAB1,SDCBP,NRCAM,TRPM4,FOXO3,ARMC2,MAPRE1,APOB,FGF21,PLXNA1,LAMA4,PODXL2,ADCY3,NDNF,C5AR2,C5AR1,SLC26A5,PRKD2,DRC1,IQSEC1,SOX9,RSPH6A,BEX4,LCP1,CLASP2,MEGF8,RAF1,MYD88,OXSR1,DACH1,FOXJ1,PAXIP1,PTPRF,TTC21A,CYGB,POU4F1,SPRY2,PLAT,WNT11,TTLL3,RIN2,ACKR2,AKT2,TGFBR2,OVOL2,SRGAP3,JAG1,MKKS,ACTG1,FSCN2,NAV3,HBEGF,PLCB1,FERMT1,SPINT2,CNN2,ALX1,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,BTG1,SPEF1,PLXNC1,SEMA3A,UNC5D,AIMP1,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,FAM19A4,DPYSL3,FLT1,EPHB1,PLK2,MTUS1,RET,AL359736.1,HCK,FAM107A,CYP7B1,GPI,NR4A1,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,LPXN,HAND2,ATP5F1A,ING2,PARVA,ROBO1,DNAH6,WDR66,FBXW7,LIMA1,PTPRJ,FZD3,MEF2C,ELP3,SEMA4F,CCDC25,VEGFC,JAM2,CFAP20,IGSF10,ADAMTS1,P2RY1,PTK2B,RAPGEF2,CCL17,CCDC65,RND1,TIAM1,FGF5,DOCK5,SLC8B1,STC1,HDAC7,NKX6-1,LOXL2,TBX5,NR4A2,ACVR1C,BIN3,F2RL1,F2R,ARHG	grey	VSMC_M10
GO:0006281	1.00	0.00	190	455	DNA repair	BP	1	POLI,EYA4,RPA3,ATP23,MRNIP,HELB,MDC1,MCM9,ASF1A,UBE2B,XRCC6,ERCC6L2,FANCC,DMC1,CSNK1E,HSF1,POT1,FANCG,REV1,MSH2,TFPT,RAD23B,FANCL,CYREN,ETAA1,EGFR,USP45,ASCC3,CCDC155,REV3L,HMCES,ERCC1,XPC,ERCC2,ERCC3,XRCC1,MLH1,MBD4,XRCC2,KIN,ZRANB3,PAXIP1,WDR48,FBH1,MGME1,RNF169,FAM168A,SIRT7,MCM8,SHLD1,AP5S1,WRN,PPP4R2,TEX15,PRKDC,POLR2I,ERCC6,ALKBH3,ERCC8,PARP4,HPF1,PRIMPOL,CDK7,RAD17,GTF2H2C,ATR,EYA1,SLF1,RAD9B,XRCC4,BACH1,DDB2,NBN,HELQ,ABRAXAS1,SPIDR,RAD54B,WRNIP1,PMS1,FTO,SYCP1,SLF2,HERC2,POLL,TAOK3,TEX264,FAN1,HSF2BP,IGHMBP2,ALKBH2,AXIN2,POLG2,POLG,SPRTN,CHEK2,EYA3,PARP9,DTX3L,SPO11,CIB1,RECQL,ATRIP,RNF168,RTEL1,MGMT,SETD2,NONO,TEX12,MEN1,APEX2,XRCC5,ASCC1,ZCWPW1,UPF1,POLN,IFFO1,WAS,PMS2,RHNO1,DDX11,RAD52,ZBTB1,PARP1,SHLD2,AP5Z1,DDB1,PRPF19,RAD51B,UIMC1,EXD2,RNF111,WRAP53,KAT7,PAGR1,EME1,PIF1,RNASEH2A,ALKBH1,SWSAP1,NSMCE1,TDP1,RAD51C,SFPQ,OTUB2,YY1,NEIL1,XAB2,RAD51D,LIG3,SMCHD1,CUL4B,ERCC4,TAOK1,RMI2,PIAS4,TREX2,NUDT16L1,FZR1,SLX4,DOT1L,NTHL1,MEIOB,PAXX,MUM1,PARK7,MPG,SPIRE2,GINS2,TERF2,MSH4,PRMT6,RPA4,SWI5,OOEP,FAAP24,TIGAR,GADD45A,FANCF,RNF8,NHEJ1,UBE2N,UBE2U,FAM111A,CENPX,BRCC3,SFR1,CBX8,CINP,GTF2H5,NABP1	grey	VSMC_M10

GO:0010564	1.00	0.00	218	515	regulation of cell cycle process	BP	1	VPS4B,GLI1,MRNIP,TRIM39,PPP1R10,MDM1,MDC1,ZNF207,FBXO43,HSPA1B,UBE2B,MAPK15,MAPK14,CCND3,ZNF16,FBXO7,CRY1,CHMP2A,BRSK1,PRKCE,MSH2,PHIP,HOXA13,ANKRD17,XPO1,EPGN,ETAA1,TGFA,LSM10,EGFR,CDK5RAP2,TPRA1,SOX9,TOPAZ1,XPC,ERCC2,ERCC3,PLK3,UBE2E2,DACH1,PAXIP1,DYNC1LI1,CEP295NL,SIRT2,NEK10,RPTOR,TCIM,ANAPC15,PLCB1,IK,NEK11,NUDT16,USP44,TFDP1,DDRGK1,MTA3,PRKDC,ERCC6,CEP63,NSFL1C,STK33,PLK2,MOS,TTL,KIF3B,FAM107A,IL1A,CSPP1,DCDC1,RAD17,CHMP2B,ATR,SLF1,CEP250,FBXW7,ANAPC5,NUGGC,PKIA,ANAPC7,RAD9B,CHMP4C,CSNK2A2,MCPH1,ADAMTS1,EIF2AK4,ALMS1,RPRD1B,NBN,ABRAXAS1,TMEM67,DONSON,ZFYVE19,PIDD1,PKD2,SLF2,NPM2,TAOK3,IGF2,KIF13A,HYAL1,AC112128.1,HECW2,CCND1,TERT,PRKAR1A,AXIN2,DYRK3,GIGYF2,EGF,USP19,CCDC36,YTHDF2,GPER1,CHEK2,PSME1,GPR3,CCDC84,ATRIP,TXLNG,CD28,SYF2,CDKN1B,DLG1,OVOL1,SETD2,STOX1,BCL6,SUSD2,PPP2R5B,DBF4B,MEN1,DDX3X,MEPCE,PTPN6,ECD,WNT4,PSME3,RNF4,TIPRL,RHNO1,OBSL1,DDX11,AHCTF1,DDB1,PRPF19,ANAPC4,MED1,RAD51B,UIMC1,SOX15,FOXO4,PAGR1,CTC1,EME1,MUC1,TAOK2,TAF1,RAB11A,TIPIN,LCMT1,FOXN3,CALM1,RAD51C,TRIM37,SFPQ,DCUN1D3,SIN3A,INSR,KLHL13,CCL2,TOM1L2,PSMG2,TAOK1,RMI2,NUBP1,FSD1,FZR1,NAA10,DOT1L,PKD1,MECP2,KLHL21,CDK10,CHMP1A,PSRC1,GPSM2,FBXO31,CDC14A,SH3GLB1,TERF2,VPS4A,DAB2IP,CTCF,NAE1,MIR29A,MIR222,RHOA,AURKC,RPA4,PLK5,RPS27L,OOEP,SOX4,WNT5A,DUSP1,CCSAP,RGCC,NME6,APC,LIF,CDC26,ZFP36L2,BRCC3,EREG,CRADD,PDXP,DRG1,NABP1	grey	VSMC_M10
GO:0031323	1.00	0.00	2202	4391	regulation of cellular metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,SERPINB8,SERPINB2,ORMDL2,ERBB3,ZC3H10,SMARCC2,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,TNFAIP8,LRP1,SHMT2,EYA4,GLI1,HBS1L,MARS,CLK4,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,EPM2A,MAML1,MRNIP,HELB,TRIM39,PPP1R10,ZBTB2,RMND1,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DXO,EIF3E,ZBED4,PNLDC1,TNXB,GRAMD4,MAP3K4,PRKN,QKI,RNF5,AGER,PPARA,FBLN1,MED30,IL5,BRD2,RXRB,TSPO,GDF9,VGLL2,ROS1,MRPL13,HSF2,DERL1,TCF7,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,CSDC2,PITX1,AL096711.2,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,PRXL2C,HABP4,PTK2,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,EXOC4,ATF4,TUT7,TAB1,MAPK15,RPAP2,AGTPBP1,CBX7,GTPBP1,MAPK14,NTRK2,CBY1,PUF60,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,SOX10,PI16,PIM1,NRF1,RAC2,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,GUCA1B,PPP1R16A,GPT,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,BICRAL,GNMT,POT1,GPR37,FBXO7,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,TTBK1,ZNF318,NFX1,NUAK1,CDK14,DCAF12,FZD1,MTERF1,NFXL1,TEC,NFKBIE,SUPT3H,SMARCA2,USP46,RFX3,KIT,SLC1A1,ADGRF1,NCK2,FHL2,TGFBRAP1,PLGRKT,IL1R2,TFAP2B,SPTLC1,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,RGP1,PDCL3,HINT2,PHF14,IPPK,KLHL31,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,SVBP,MACC1,LRPPRC,C	grey	VSMC_M10
GO:0006807	1.00	0.00	3755	7284	nitrogen compound metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,NME1,SERPINB8,SERPINB2,VPS4B,KDSR,PHLPP1,ORMDL2,ERBB3,SEC11C,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,FECH,ONECUT2,GLS2,BAZ2A,TCF4,POLI,HSD17B4,TNFAIP8,RNMT,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,ALDH8A1,GLI1,HBS1L,MARS,B4GALT7,RMND5B,PDE7B,CLK4,MAP3K5,B4GALNT1,RPA3,TNFAIP3,AGAP2,TSFM,ADGRG6,HIVEP2,ADAT2,ATP23,PLAGL1,USP15,FBXO30,RXYLT1,CANX,MAML1,MRNIP,ENPP3,ATP5MGL,HELB,TRIM39,RPP21,PPP1R10,ATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,ZFC3H1,TPH2,CNOT6,RIDA,STK3,OSR2,PRR16,SNCAIP,FBXO43,PABPC1,SNW1,TFB1M,ZNF706,CPT1B,ALDH7A1,PHAX,MARCH3,APOM,ABHD16A,ARID1B,ADM2,ZDHHC14,HSPA1B,TULP4,FZD6,ZBTB12,DPYS,SKIV2L,SF3A3,SELENOO,DXO,MOV10L1,EIF3E,ALG12,ZBED4,BRD1,ADAMTS19,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,PPT2,PRKN,QKI,RNF5,AGER,TRMU,PPARA,PDE10A,ACSL6,FBLN1,UTP23,P4HA2,MED30,PSMB8,SLC22A4,IL5,BRD2,TAF2,ZUP1,RXRB,TSPO,GDF9,VGLL2,ROS1,MCM9,ASF1A,MRPL13,A4GALT,RPS18,RRP7A,HSF2,DERL1,TCF7,SKP1,PHF1,SMPDL3A,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,RNF146,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,KLHL3,XPNPEP3,OBSCN,MRPL55,JMJD4,AGO2,PRXL2C,HABP4,RPS10,PTK2,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,LY6E,AKR1B1,ZC3H3,ATF4,PYCR3,TUT7,TAB1,ISCA1,MAPK15,RPAP2,AGTPBP1,CBX7,APOBEC3H,GTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,CBY1,DMC1,PUF60,C9orf64,NRBP2,STK38,CSNK1E,PLA2G6,P	grey	VSMC_M10

GO:0033043	1.00	0.00	429	950	regulation of organelle organization	BP	1	VPS4B,PAN2,ARPC3,LRP1,TRIM36,PIP4K2C,AVIL,TBC1D30,PPP1R10,MDM1,ATAT1,CNOT2,CNOT6,ZNF207,FBXO43,HSPA1B,MAP3K4,PRKN,RNF5,IL5,TSPO,UBE2B,BAK1,MTSS1,WASHC5,MYC,ASAP1,H3F3C,PTK2,MAPK15,PLA2G6,BAIAP2L2,PICK1,MPDZ,CDC42EP1,RAC2,TEK,POT1,FBXO7,LMOD2,CCL27,SLAIN2,NCK2,KIAA1211,TMEM14A,BICD2,CHMP2A,TMOD1,PLEKHH2,DYNC2LI1,PRKCE,SPTBN1,PHIP,SHANK1,HOXA13,LPAR1,EPGN,TRAPPC12,PLEK,TGFA,ITGB1BP1,MET,ADD2,FUZ,ARHGEF5,CDK5RAP2,EPHA1,CNTRL,MYLK3,VPS35,ATG5,SDCBP,FAM49A,MGARP,MAPRE1,WASF1,SSBP1,RAB7A,PIP4K2A,SETDB2,EML2,ERCC1,SLC39A12,LCP1,CLASP2,RBSN,MAPRE3,XRCC1,TRIM54,RALB,GRIK5,TBC1D4,MYCBP2,SLAIN1,WNT11,AKT2,DYNC1LI1,PLEKHG2,USP36,CEP295NL,LRFN1,FCHSD2,SIRT2,MKKS,ANK1,ACTG1,NAV3,SYT1,TMEM106B,ANAPC15,RAB5A,PLCB1,IK,SIRT7,FEZ2,RAC3,DDHD2,BAG4,ARHGEF7,DCN,DIAPH1,MAVS,SPEF1,FCHSD1,USP44,NCKAP1L,ULK1,ARFIP2,RASSF7,LMOD3,SYT9,PAN3,ATXN7,PLK2,MOS,HCK,FAM107A,IL1A,FER,ANKRD27,CEP70,OSBP,PIK3R1,HIP1R,CHMP2B,ATR,CLIP1,KATNBL1,SLF1,TBC1D12,FAM208A,FBXW7,FMN1,LIMA1,HMBOX1,ANAPC5,HTRA2,P2RX7,CNOT1,ANAPC7,CHMP4C,CSNK2A2,MCPH1,KATNB1,PTK2B,CNOT6L,MAPKAPK5,RND1,ALMS1,NBN,SYNJ1,TMEM67,OPA1,RAPGEF3,RHOBTB2,F2RL1,IQGAP2,CYFIP1,SLF2,DMTN,NPM2,PPHLN1,TENT4B,STMND1,ARMH3,IGF2,MAGEL2,PXN,STN1,DNM1L,CARMIL1,PPFIA1,ZMYND10,AC112128.1,LMOD1,HECW2,ADD3,SEC22B,TRPV4,GAP43,TMEM39A,ZDHHC6,PRKAR1A,ADPRH,USP30,TTBK2,AXIN2,SSH1,EGF,HCLS1,ARHGAP6,AP1AR,C2CD5,GPER1,CIB1,W	grey	VSMC_M10
GO:0051248	1.00	0.00	364	813	negative regulation of protein metabolic process	BP	1	SERPINB8,SERPINB2,PAN2,TNFAIP8,LRP1,SHMT2,TNFAIP3,AGAP2,TRIM39,CNOT2,CNOT6,RIDA,PABPC1,HSPA1B,EIF3E,PNLDC1,PRKN,FBLN1,TSPO,MRPL13,PHF1,UBE2B,BAK1,NCOA7,TRIB1,AGO2,TNRC6B,ATF4,TUT7,NTRK2,STK38,PI16,CDKN2A,FBXO7,CRY1,NCK2,IL1R2,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,SVBP,DNAJA1,PRKCE,CD109,IGF2BP3,RTN4,PPP2R1A,IBTK,PNPT1,ACP4,AQP1,NR1H2,ITGB1BP1,AGO1,EGFR,EPHA1,BCL2L12,ATG5,SDCBP,TUT4,PRKAR2B,SPHK2,DHFR,SPRY1,HDAC2,CST7,PHB,BEX4,CRTAP,XRCC1,MLH1,KDM4A,AQP11,PRKAG2,RAF1,PRDX3,TIMP4,PIBF1,UBE2O,MYCBP2,SPOPL,TNRC6C,SPRY2,PLAT,KLHL40,GPD1L,ARRB1,IKBKB,SIRT2,PURA,HBEGF,PTPRQ,SIRT7,SPINT2,EIF2AK2,PRNP,DUSP6,LSM1,TAF7,NRG1,USP44,DDRGK1,SH3RF2,NCKAP1L,GAS6,RYBP,PRKDC,MFHAS1,PAN3,PSMF1,TRIM44,TRIB3,PFDN5,SDR16C5,DNMT3B,GPI,NR4A1,CEBPA,IDE,PIK3CB,SNX25,CASP3,TAF9,USP25,PTPRJ,ENC1,PKIA,CNOT1,CELF1,CSNK2A2,CNOT6L,FAM192A,EIF2AK4,NR1H3,EIF4E2,PAQR3,PAIP2B,SERPINB1,SPINT1,CRY2,CDYL,FTO,MARCH7,DBNDD2,PAX2,DMTN,PRMT3,JARID2,DTNBP1,TENT4B,RBM24,APLP2,SUFU,SIRT4,AZIN2,TM4SF20,RPL23,LRRK1,HDAC1,SLC2A10,BANK1,CAPRIN2,PDCD4,PRKAR1A,ADARB1,DIS3L2,PIAS3,FABP4,GIGYF2,USP19,YTHDF2,UBASH3B,SORL1,RTRAF,DTX3L,PARP14,IFI6,AGT,CIB1,CBL,COL6A3,SFN,COL7A1,RPS6KA1,PER2,DDX6,TRAF3IP1,CAMK2N2,DEDD,YTHDF1,PTPRO,INPP5J,MLXIPL,CST6,EIF4ENIF1,RPL11,SNX6,CDKN1B,SENP2,IGF2BP2,LRIG2,APOD,POR,AIDA,YWHAG,IVNS1ABP,DUSP10,MAPT,HEXIM2,EIF4EBP2,BCOR,MEN1,DDX3X,DNAJC10,SPOCK2,DUSP19,RC3H1,PT	grey	VSMC_M10
GO:0006974	1.00	0.00	307	699	cellular response to DNA damage stimulus	BP	1	POLI,EYA4,RPA3,ATP23,MRNIP,HELB,TRIM39,PPP1R10,ARMT1,MDC1,IER3,SNW1,MCM9,ASF1A,PHF1,UBE2B,BAK1,XRCC6,MYC,ERCC6L2,FANCC,MAPK15,MAPK14,DMC1,CSNK1E,HSF1,OARD1,POT1,CRY1,NUAK1,FANCG,MRPS9,REV1,DNAJA1,BRSK1,MSH2,TFPT,RAD23B,FANCL,CYREN,ETAA1,EGFR,USP45,TRIM32,ASCC3,CCDC155,SETD7,FOXO3,CHCHD6,REV3L,HMCES,ERCC1,XPC,ERCC2,ERCC3,DDIAS,PLK3,XRCC1,MLH1,MBD4,UBE2E2,XRCC2,KIN,ZRANB3,PAXIP1,WDR48,FBH1,CCDC13,MGME1,RNF169,FAM168A,SIRT7,MCM8,SHLD1,NEK11,ASH2L,AP5S1,WRN,PPP4R2,MRPS26,TEX15,FOXP1,PRKDC,IRF7,POLR2I,ERCC6,ALKBH3,CEP63,TRAF6,STK33,PLK2,ERCC8,PARP4,NCOA6,PIK3R1,HPF1,PRIMPOL,CDK7,CASP3,TAF9,RAD17,GTF2H2C,ATR,ING2,CDKN2AIP,EYA1,SLF1,HTRA2,RAD9B,USP16,XRCC4,FNIP2,BACH1,EIF2AK4,DDB2,NBN,NKX3-1,HELQ,ABRAXAS1,SPIDR,RAD54B,WRNIP1,DONSON,PMS1,FTO,MARCH7,PIDD1,PLA2R1,SYCP1,SLF2,HERC2,POLL,TAOK3,RBM24,RBBP5,TEX264,NUPR2,SIRT4,FAN1,HSF2BP,CCND1,SP100,IGHMBP2,MAP2K6,MRPS35,ALKBH2,AXIN2,DYRK3,MAPKAPK2,GIGYF2,SNAI1,MRPS11,AEN,POLG2,POLG,SPRTN,CHEK2,EYA3,PARP9,DTX3L,SPO11,MCL1,CIB1,CBL,RECQL,CIDEB,SFN,NFATC4,ATRIP,SYF2,RNF168,RTEL1,BAZ1B,EGLN3,CDKN1B,MGMT,SETD2,MAPT,NONO,BCL6,BCL2A1,TEX12,MEN1,APEX2,XRCC5,ASCC1,ZCWPW1,UPF1,ZBTB40,ALKBH8,ING4,POLN,IFFO1,TIPRL,MAPK1,WAS,PMS2,RHNO1,DDX11,RAD52,ZBTB1,PARP1,SHLD2,AP5Z1,DDB1,TNFRSF1B,PRPF19,RAD51B,UIMC1,EXD2,SUSD6,RNF111,FXR2,WRAP53,PSEN1,CBX1,FOXO4,KAT7,PAGR1,CTC1,EME1,MUC1,TAOK2,BATF,TAF1,PIF1,MAPK3	grey	VSMC_M10

GO:0032879	1.00	0.00	995	2074	regulation of localization	BP	1	VPS4B,ERBB3,NEDD4L,ATP8B1,ONECUT2,LRP1,STX7,SEMA6A,STAC3,SRGAP1,CPSF6,RAB21,SNCAIP,MAPK8IP2,SLC12A2,RIMS2,KCNV1,PRRT1,PRKN,AGER,PPARA,GPSM3,FBLN1,TSPO,GDF9,GOPC,BAK1,CATSPER3,TRIB1,EPB41L2,MCHR1,AGO2,PTK2,C6orf106,PTP4A3,PTCH1,MAPK15,PLXNA4,SUN2,MAPK14,PODXL,KCNJ4,CSNK1E,PLA2G6,PICK1,PIM1,MEST,BTBD9,RAC2,SMO,TTC39B,PLIN2,CHRNA3,TEK,CHRNA5,CRY1,ABHD17B,SRF,ABCB1,CFAP69,APBA1,CCL27,CDK6,USP46,CLIC5,SLC25A27,RFX3,KIT,SLC1A1,TFAP2B,ROR2,SEMA4D,TMEM14A,WNK2,CHMP2A,SEMA4C,MEOX2,TSPAN13,ZNF268,RAB23,NLRP5,ABCG5,SVBP,ABCG8,CLDN19,DNAJA1,IL11,BRSK1,RNF20,PRKCE,SMAP1,RIMS1,EPCAM,TMEM30A,DNAH11,SPTBN1,RTN4,FPR2,HMGN3,HAS1,KCNQ4,RIMS3,EPB41L4B,IBTK,RUFY3,SHANK1,HOXA7,EMC10,PPT1,CXCL8,XPO1,BMP8A,AQP1,BMPER,AKIRIN1,SLC31A2,TRAPPC12,RSPO1,RSAD2,AAK1,NR1H2,PTN,ITGB1BP1,MET,GRB10,EGFR,HECW1,FUZ,ARHGEF5,TRIM32,TLR4,TCAF2,EPHA1,HACE1,BVES,GAB1,CLCN1,IL15,SFRP4,KEL,VPS35,ATG5,SDCBP,TRPM4,SLC7A11,OSR1,FOXO3,ARMC4,APOB,FGF21,BRAF,SPHK2,PLXNA1,KCNJ14,LAMA4,MTMR2,DNAJC27,TRPC3,RAB7A,C5AR2,C5AR1,SLC26A5,AP2S1,RAB10,PRKD2,KCNRG,DRC1,IQSEC1,SOX9,GIPR,BEX4,ABHD5,CACNB2,IWS1,LCP1,CLASP2,CD300LF,APOC1,PLK3,FRMD4A,STAC,GAB2,LLGL2,RALB,PRKAG2,GRIK5,UNC13D,RAF1,MYD88,OXSR1,DACH1,TBC1D4,SCN5A,SCN1A,MYCBP2,CYGB,IL15RA,SPRY2,WNT11,RIN2,AKT2,GPD1L,ARRB1,TGFBR2,NEU3,SNX5,USP36,SRGAP3,C1QTNF1,JAG1,MKKS,ACTG1,NAV3,HBEGF,SYT1,CACNB4,UBAC2,RAB5A,EFHB,APBB3,ASPSCR1,PLCB1,DPH	grey	VSMC_M10
GO:0080090	1.00	0.00	2102	4206	regulation of primary metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,SERPINB8,SERPINB2,ORMDL2,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,TNFAIP8,LRP1,SHMT2,EYA4,GLI1,HBS1L,MARS,CLK4,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,MAML1,MRNIP,HELB,TRIM39,PPP1R10,ZBTB2,RMND1,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DXO,EIF3E,ZBED4,PNLDC1,TNXB,GRAMD4,MAP3K4,PRKN,QKI,AGER,PPARA,FBLN1,MED30,PSMB8,IL5,BRD2,RXRB,TSPO,GDF9,VGLL2,MRPL13,HSF2,DERL1,TCF7,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,PRXL2C,HABP4,PTK2,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,ATF4,TUT7,TAB1,MAPK15,GOLM1,RPAP2,AGTPBP1,CBX7,GTPBP1,MAPK14,NTRK2,CBY1,PUF60,STK38,CSNK1E,PLA2G6,C6orf89,KDM4C,SOX10,PI16,PIM1,NRF1,TMPRSS6,SMO,TTC39B,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,GUCA1B,PPP1R16A,GPT,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,BICRAL,GNMT,POT1,GPR37,FBXO7,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,TTBK1,ZNF318,NFX1,NUAK1,CDK14,FZD1,MTERF1,NFXL1,TEC,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,ADGRF1,NCK2,FHL2,TGFBRAP1,PLGRKT,IL1R2,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,RGP1,PDCL3,HINT2,PHF14,IPPK,KLHL31,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,SVBP,MACC1,LRPPRC,CLDN19,SIX2,DNAJA1,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1	grey	VSMC_M10
GO:0065009	1.00	0.00	1115	2307	regulation of molecular function	BP	1	NME1,SERPINB8,SERPINB2,ERBB3,NEDD4L,TNFAIP8,LRP1,STAC3,ARHGAP9,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,CYP27B1,SRGAP1,LTC4S,TBC1D30,MRNIP,TBC1D9B,PPP1R10,ESR1,FRS2,STK3,MAPK8IP2,TIAM2,DENND6B,HSPA1B,FZD6,EIF3E,TNXB,GRAMD4,MAP3K4,PRRT1,PRKN,AGER,PPARA,GPSM3,FBLN1,PSMB8,IL5,ROS1,GOPC,RGL2,DERL1,SKP1,SYNGAP1,BAK1,XRCC6,TRIB1,MYC,ASAP1,LRRC6,FAM13B,OBSCN,HABP4,PTK2,C6orf106,PTCH1,LY6E,SIL1,TAB1,MAPK15,PLXNA4,MAPK14,NTRK2,STK38,CSNK1E,PLA2G6,C6orf89,PI16,PIM1,TBC1D22B,MFNG,RAC2,SMO,ZDHHC21,HSF1,MDFI,CCND3,FOXH1,GUCA1B,PPP1R16A,LRRC14,CDKN2A,ZNF16,CHRNA3,TEK,POT1,FBXO7,ALDH1A1,RIC8B,SRF,ABCB1,TTBK1,BAG1,NUAK1,FZD1,NFKBIE,RCAN2,KIT,SLC1A1,ADGRF1,NCK2,ROR2,SEMA4D,GAPDH,TBC1D8,RGP1,WNK2,FGD3,MITD1,GABBR2,CAT,SVBP,DNAJA1,SDHAF4,PRKCE,SMAP1,TNNI3,PPP1R12C,EPS8L1,RIMS1,MSH2,CD109,RAPGEF5,PPP2R1A,ZNF462,FPR2,IBTK,ACP4,SHANK1,MOB1B,LPAR1,PPT1,MTURN,EPGN,NOD1,AREG,AKIRIN2,AQP1,CASP8AP2,PELI1,WDR91,ETAA1,PLEK,ZNF618,ANXA4,EPHA7,NR1H2,TNFSF15,TGFA,PTN,ASAP2,ITGB1BP1,MED25,MET,ADD2,VRK3,EGFR,HECW1,ARHGEF5,TRIM32,TLR4,CCNC,TCAF2,EPHA1,TRAF1,BCL2L12,BVES,DLGAP3,NOSIP,LPIN1,SFRP4,TBC1D9,CCNY,DKKL1,MGST2,OSR1,MAPRE1,SSBP1,FAF1,FGF21,PRKAR2B,HSPE1,SPHK2,DHFR,SPRY1,PLXNA1,ARHGAP12,HDAC2,NAPA,SLC8A2,BMI1,C5AR1,PIP4K2A,ARHGEF4,ARHGAP21,PRKD2,PTGIR,KCNRG,CST7,PHB,IQSEC1,ABI1,SYMPK,GIPR,CYSLTR2,ABHD5,EED,CACNB2,ERCC2,SSPO,PPP1R37,RSU1,APOC1,MAPRE3,DNAJC15,EIF2B3,XRCC1,STAC,EPM2AI	grey	VSMC_M10

GO:0043086	1.00	0.00	237	555	negative regulation of catalytic activity	BP	1	SERPINB8,SERPINB2,TNFAIP8,LRP1,PIP4K2C,TNFAIP3,CYP27B1,PPP1R10,PRKN,TRIB1,STK38,PI16,CDKN2A,POT1,FBXO7,SEMA4D,GAPDH,GABBR2,DNAJA1,TNNI3,PPP1R12C,CD109,IBTK,ACP4,AQP1,ANXA4,PTN,ITGB1BP1,EPHA1,BCL2L12,NOSIP,PRKAR2B,SPHK2,SPRY1,PIP4K2A,CST7,SSPO,PPP1R37,APOC1,PRKAG2,RAF1,PRDX3,TIMP4,UBE2O,GCKR,SPRY2,ARRB1,IKBKB,PPME1,MKKS,RPTOR,PDE6G,PTPRQ,GPS1,SPINT2,PRNP,BAG4,TAF7,USP44,SH3RF2,NCKAP1L,GAS6,PSMF1,TRIB3,GPI,NR4A1,PXK,CEBPA,PIK3CB,CASP3,PARVA,ADGRV1,SCG5,PTPRJ,PKIA,IL7,TMBIM6,RTKN,FNIP2,PAQR3,SERPINB1,IQGAP2,TESC,SPINT1,CRY2,PLA2R1,DBNDD2,PAX2,DTNBP1,TAOK3,GRM2,MTRR,APLP2,CABP1,RPL23,PDCD4,TGFB2,PRKAR1A,ADARB1,PDE6D,OXA1L,AJUBA,FICD,FABP4,UBASH3B,SORL1,RTRAF,SAG,PARP9,DTX3L,SH3BP4,IFI6,AGT,CIB1,CBL,COL6A3,SFN,PPP2R5A,COL7A1,RPS6KA1,CAMK2N2,RUBCN,PTPRO,PDE6H,PIK3IP1,CST6,RPL11,SNX6,CDKN1B,POR,AIDA,YWHAG,DUSP10,RASA4,MAPT,MBIP,HEXIM2,GMIP,MEN1,VCPKMT,DDX3X,SPOCK2,DUSP19,PPP1R2C,PTPN6,SERPINC1,SERPINI1,MYOZ1,ZFYVE28,SOCS4,BIRC3,TIPRL,ARL6IP1,KDM5A,SCGB1A1,GPS2,ANXA8,RGS14,ANXA2,SIMC1,BOD1L2,PSEN1,PAPLN,PYDC1,TMED10,PIF1,AC138894.1,WFIKKN2,COX11,MAP2K5,PPP4R4,GLA,BCAS3,NEIL1,CAMK2A,MAPK7,AMOT,PRPSAP2,SMCR8,NLE1,LEPR,C3,PTPN2,GPC3,SOCS1,INPP5K,APBA3,PAM16,SERPINF2,PDPK1,PRKCZ,OAZ1,WFIKKN1,PARK7,GPSM1,PALM,DBNDD1,GNAI3,TSC1,LAMTOR5,GFI1,NQO1,TERF2,DAB2IP,DUS2,MIR199A1,MIR21,MIR27B,MIR24-1,NOL3,SERPINB5,A2M,MIR339,PDZD3,GMFG,SERPI	grey	VSMC_M10
GO:1902531	1.00	0.00	606	1309	regulation of intracellular signal transduction	BP	1	PHLPP1,ERBB3,LRP1,SEMA6A,ARHGAP9,MAP3K5,TNFAIP3,USP15,EPM2A,TRIM39,PPP1R10,ESR1,FRS2,STK3,MAPK8IP2,TIAM2,HSPA1B,CDC42SE2,MAP3K4,PRKN,AGER,PPARA,PDE10A,FBLN1,ROS1,RGL2,SYNGAP1,UBE2B,MYC,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,TAB1,MAPK14,NTRK2,STK38,PLA2G6,TEK,GPR37,CRY1,NUAK1,LRRD1,SLC35B2,KIT,NCK2,FHL2,ROR2,GADD45G,SEMA4D,GAPDH,WNK2,FGD3,KLHL31,PRDX1,SEMA4C,CAT,DNAJA1,IL11,PRKCE,EPS8L1,FKTN,RTN4,FPR2,GSDME,VRK2,EMC10,LPAR1,REL,ANKRD17,SLC46A2,MTURN,EPGN,NOD1,RRAGD,PELI1,BMPER,ETAA1,PLEK,EPHA7,TGFA,ITGB1BP1,MET,VRK3,YWHAZ,EGFR,ARHGEF5,TRIM32,TLR4,CDK5RAP2,TRAF1,SDCBP,PUM2,FGF21,BRAF,TRAF3IP2,SPHK2,SPRY1,ARHGAP12,DNAJC27,KPTN,SESN3,SLC8A2,C5AR2,C5AR1,ARHGEF4,ARMC10,ARHGAP21,PRKD2,PHB,IQSEC1,SOX9,GIPR,PPM1N,DDIAS,FBXL2,PLK3,OPTN,KBTBD6,RAF1,MYD88,ZFAND6,SEC14L1,FBH1,SZT2,SPRY2,WNT11,ALK,PSD3,DYNC1LI1,GPD1L,ARRB1,PIP4P1,IKBKB,SRGAP3,C1QTNF1,NMI,NEK10,ZMYND11,RPTOR,TCIM,HBEGF,NPLOC4,PDE6G,ANAPC15,EFHB,PLCB1,RASGRP4,SPRED3,EIF2AK2,PRNP,ADRA1D,DUSP6,BAG4,DCN,MAVS,RELL2,SEMA3A,MCF2L,ARHGAP26,P2RX2,KL,NRG1,USP44,SH3RF2,NCKAP1L,GAS6,LARS,SIRT3,PPP2CB,RASA3,ARL6IP5,MFHAS1,FLT1,RYK,TMEM127,ADRA2B,TRAF6,NR1H4,TRIM44,SLC38A9,APIP,SETD9,TMEM9B,ST5,EPHB1,PLK2,AKIP1,MOS,RET,AL359736.1,PIK3CB,PREX2,RASA2,TAF9,ARHGAP10,HAND2,ATR,FBXO8,ING2,ROBO1,P2RX3,PLCE1,ARNTL,FBXW7,ADGRV1,ARHGEF28,PTPRJ,HTRA2,TMBIM6,P2RX7,NDUFS3,GUCY1A1,WDR54,SLA2,	grey	VSMC_M10
GO:0007154	1.00	0.00	2144	4300	cell communication	BP	1	NFATC1,CD226,ITGA7,PHLPP1,ERBB3,SLC39A5,ONECUT2,CCDC68,TAC3,LRP1,RPS12,SEMA6A,EYA4,LVRN,STAC3,AP3S1,GLI1,ARHGAP9,HBS1L,MARS,KIF5A,PDE7B,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,ADGRG6,USP15,EPM2A,SRGAP1,MAML1,MRNIP,TRIM39,PPP1R10,ESR1,FRS2,CNOT2,MDC1,RAB21,STK3,ZNF207,SNCAIP,MAPK8IP2,SNW1,TIAM2,ADM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,IGF2R,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,PDE10A,FBLN1,TNFRSF11B,IL5,HLA-DPB1,RXRB,GDF9,ROS1,TBC1D32,RGL2,FSTL4,DERL1,TCF7,TNFRSF13C,SYNGAP1,UBE2B,BAK1,MTSS1,RSPO3,RNF146,TRIB1,CXCL14,MYC,SMAD5,MCHR1,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,GFRA3,PTK2,GPR20,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,GRAP2,SCUBE3,ZC3H3,EXOC4,ATF4,TAB1,SYNGR1,MAPK15,PLXNA4,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,NRBP2,STK38,CSNK1E,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,PIM1,BTBD9,ZC3HC1,CDC42EP1,MFNG,RAC2,SMO,ZDHHC21,TXN2,HSF1,DAAM2,MDFI,TFEB,SLC39A4,IRF5,KCP,CCND3,OPN1SW,MYH9,FOXH1,GUCA1B,LRRC14,CDKN2A,OSTF1,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,GRM8,CHRNA5,GPR37,RORB,ASB15,CRY1,RIC8B,ZFAND5,PTK7,SRF,BAG1,DLK2,TCP11L2,NUAK1,GABRA1,APBA1,CDK14,FZD1,CNTFR,TEC,TXNRD1,LRRD1,CCL27,PHF24,SLC35B2,OCIAD1,USP46,ENPP5,RCAN2,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TGFBRAP1,INSL6,RLN1,ERMP1,IL1R2,TLN1,TFAP2B,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,S1PR3,TMEM14A,WNK2,NINJ1,FGD3,KLHL31,OGN,PRDX1,INPP4A,ADGRL3,SEMA4C,SHB,SOSTDC1,OXER1,BEND6,GABBR2,A	grey	VSMC_M10

GO:0043170	1.00	0.00	3614	7034	macromolecule metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,CD226,NME1,SERPINB8,SERPINB2,VPS4B,PHLPP1,ORMDL2,ERBB3,SEC11C,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,POLI,TNFAIP8,RNMT,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,GU1,HBS1L,MARS,B4GALT7,RMND5B,CLK4,MAP3K5,RPA3,TNFAIP3,AGAP2,TSFM,ADGRG6,HIVEP2,ADAT2,ATP23,PLAGL1,USP15,FBXO30,RXYLT1,CANX,MAML1,MRNIP,ENPP3,HELB,TRIM39,RPP21,PPP1R10,ATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,TSPAN8,ZFC3H1,CNOT6,RIDA,STK3,OSR2,PRR16,FBXO43,PABPC1,SNW1,TFB1M,ZNF706,PHAX,MARCH3,APOM,ABHD16A,ARID1B,ADM2,ZDHHC14,HSPA1B,TULP4,FZD6,RIMS2,ZBTB12,SKIV2L,SF3A3,SELENOO,DXO,MOV10L1,EIF3E,ALG12,ZBED4,BRD1,ADAMTS19,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,PPT2,PRKN,AGPAT1,QKI,RNF5,AGER,TRMU,PPARA,GPSM3,PDE10A,HLA-DRA,FBLN1,HLA-DOB,UTP23,P4HA2,MED30,PSMB8,HLA-DMA,IL5,BRD2,TAF2,HLA-DPB1,ZUP1,RXRB,TSPO,GDF9,VGLL2,ROS1,MCM9,ASF1A,MRPL13,RPS18,RRP7A,HSF2,DERL1,TCF7,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,RNF146,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,KLHL3,XPNPEP3,OBSCN,MRPL55,JMJD4,AGO2,HABP4,H3F3C,RPS10,PTK2,ERCC6L2,C6orf106,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,ZC3H3,ATF4,TUT7,TAB1,ISCA1,MAPK15,RPAP2,AGTPBP1,CBX7,APOBEC3H,GTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,CBY1,DMC1,PUF60,C9orf64,NRBP2,STK3	grey	VSMC_M10
GO:0023052	1.00	0.00	2120	4258	signaling	BP	1	NFATC1,CD226,ITGA7,PHLPP1,ERBB3,SLC39A5,ONECUT2,CCDC68,TAC3,LRP1,RPS12,SEMA6A,EYA4,LVRN,STAC3,AP3S1,GLI1,ARHGAP9,HBS1L,KIF5A,PDE7B,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,ADGRG6,USP15,EPM2A,SRGAP1,MAML1,MRNIP,TRIM39,PPP1R10,ESR1,FRS2,CNOT2,MDC1,RAB21,STK3,ZNF207,SNCAIP,MAPK8IP2,SNW1,TIAM2,ADM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,IGF2R,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,PDE10A,FBLN1,TNFRSF11B,IL5,HLA-DPB1,RXRB,GDF9,ROS1,TBC1D32,RGL2,FSTL4,DERL1,TCF7,TNFRSF13C,SYNGAP1,UBE2B,BAK1,MTSS1,RSPO3,RNF146,TRIB1,CXCL14,MYC,SMAD5,MCHR1,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,GFRA3,PTK2,GPR20,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,GRAP2,SCUBE3,ZC3H3,EXOC4,ATF4,TAB1,SYNGR1,MAPK15,PLXNA4,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,NRBP2,STK38,CSNK1E,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,PIM1,BTBD9,ZC3HC1,CDC42EP1,MFNG,RAC2,SMO,ZDHHC21,HSF1,DAAM2,MDFI,IRF5,KCP,CCND3,OPN1SW,MYH9,FOXH1,GUCA1B,LRRC14,CDKN2A,OSTF1,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,GRM8,CHRNA5,GPR37,RORB,ASB15,CRY1,RIC8B,ZFAND5,PTK7,SRF,BAG1,DLK2,TCP11L2,NUAK1,GABRA1,APBA1,CDK14,FZD1,CNTFR,TEC,TXNRD1,LRRD1,CCL27,PHF24,SLC35B2,OCIAD1,USP46,RCAN2,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TGFBRAP1,INSL6,RLN1,ERMP1,IL1R2,TLN1,TFAP2B,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,S1PR3,TMEM14A,WNK2,NINJ1,FGD3,KLHL31,OGN,PRDX1,INPP4A,ADGRL3,SEMA4C,SHB,SOSTDC1,OXER1,BEND6,GABBR2,ABCG5,CAT,MACC1,ABCG8,CL	grey	VSMC_M10
GO:0010605	1.00	0.00	1002	2090	negative regulation of macromolecule metabolic process	BP	1	NME1,SERPINB8,SERPINB2,ZC3H10,SMARCC2,PAN2,ATP8B1,BAZ2A,TNFAIP8,LRP1,SHMT2,PGGT1B,TNFAIP3,AGAP2,PLAGL1,HELB,TRIM39,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,PHAX,HSPA1B,ZBTB12,SKIV2L,DXO,MOV10L1,EIF3E,PNLDC1,PRKN,AGER,PPARA,FBLN1,TSPO,MRPL13,TCF7,PHF1,UBE2B,BAK1,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,H3F3C,C6orf106,PTCH1,TNRC6B,ATF4,TUT7,CBX7,GTPBP1,MAPK14,NTRK2,CBY1,STK38,SOX10,PI16,TMPRSS6,EXOSC4,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,FBXO7,RORB,CRY1,SRF,TTBK1,ZNF318,NFX1,XPO5,SMARCA2,RFX3,TNFRSF21,NCK2,FHL2,IL1R2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SVBP,LRPPRC,CLDN19,DNAJA1,SCMH1,RNF20,PRKCE,MSH2,CD109,IGF2BP3,RTN4,PPP2R1A,IBTK,NFE2L3,PNPT1,ACP4,HOXA2,HOXA7,REL,PUS10,JAZF1,PTBP3,CXCL8,XPO1,AKIRIN2,SRSF10,AQP1,CASP8AP2,BACH2,ZNF692,CYREN,SNIP1,ANXA4,NR1H2,ZNF350,ITGB1BP1,FOXP2,MED25,KLF11,AGO1,POU3F3,EGFR,LANCL2,TLR4,EPHA1,BCL2L12,CREM,ATG5,SDCBP,MYCN,TUT4,OSR1,FOXO3,PUM2,BEND5,PRKAR2B,TRAF3IP2,SPHK2,DHFR,SPRY1,MTPAP,HDAC2,PHF10,MTMR2,ZC3HAV1,DNMT3A,BMI1,DHX34,C5AR2,ZC3H4,CST7,CNBP,SETDB2,PHB,SOX9,BEX4,ZNF746,ERCC1,EED,CRTAP,SUV39H2,ZNF404,PLK3,FASTK,XRCC1,OPTN,MLH1,GLI2,DEDD2,RSF1,KDM4A,AQP11,PRKAG2,RAF1,MYD88,DACH1,PRDX3,TIMP4,TAF3,PIBF1,ACVR2B,KLF5,KLF12,FOXJ1,ZRANB3,UBE2O,MYCBP2,SFMBT2,GZF1,SPOPL,POU4F1,TSKU,FBH1,TNRC6C,SPRY2,PLAT,WNT	grey	VSMC_M10

GO:0007165	1.00	0.00	1943	3919	signal transduction	BP	1	NFATC1,CD226,ITGA7,PHLPP1,ERBB3,SLC39A5,ONECUT2,CCDC68,TAC3,LRP1,RPS12,SEMA6A,EYA4,LVRN,STAC3,AP3S1,GLI1,ARHGAP9,HBS1L,PDE7B,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,ADGRG6,USP15,EPM2A,SRGAP1,MAML1,MRNIP,TRIM39,PPP1R10,ESR1,FRS2,CNOT2,MDC1,RAB21,STK3,ZNF207,MAPK8IP2,SNW1,TIAM2,ADM2,MPIG6B,HSPA1B,FZD6,RIMS2,IGF2R,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,PDE10A,FBLN1,TNFRSF11B,IL5,HLA-DPB1,RXRB,GDF9,ROS1,TBC1D32,RGL2,FSTL4,DERL1,TCF7,TNFRSF13C,SYNGAP1,UBE2B,BAK1,MTSS1,RSPO3,RNF146,TRIB1,CXCL14,MYC,SMAD5,MCHR1,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,GFRA3,PTK2,GPR20,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,GRAP2,SCUBE3,ZC3H3,ATF4,TAB1,MAPK15,PLXNA4,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,NRBP2,STK38,CSNK1E,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,PIM1,ZC3HC1,CDC42EP1,MFNG,RAC2,SMO,ZDHHC21,HSF1,DAAM2,MDFI,IRF5,KCP,CCND3,OPN1SW,MYH9,FOXH1,GUCA1B,LRRC14,CDKN2A,OSTF1,RBFOX2,IFT74,CHRNA3,TEK,GRM8,CHRNA5,GPR37,RORB,ASB15,CRY1,RIC8B,ZFAND5,PTK7,BAG1,DLK2,TCP11L2,NUAK1,GABRA1,CDK14,FZD1,CNTFR,TEC,TXNRD1,LRRD1,CCL27,PHF24,SLC35B2,OCIAD1,RCAN2,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TGFBRAP1,INSL6,RLN1,ERMP1,IL1R2,TLN1,TFAP2B,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,S1PR3,TMEM14A,WNK2,NINJ1,FGD3,KLHL31,OGN,PRDX1,INPP4A,ADGRL3,SEMA4C,SHB,SOSTDC1,OXER1,BEND6,GABBR2,ABCG5,CAT,MACC1,ABCG8,CAMKMT,DNAJA1,PLPPR1,IL11,BRSK1,PRKCE,TNNI3,PPP1R12C,EPAS1,EPS8L1,RIMS1,EPCAM,MSH2,CD109,TF	grey	VSMC_M10
GO:0007010	1.00	0.00	535	1177	cytoskeleton organization	BP	1	VPS4B,ARPC3,CCDC68,MYO1A,LRP1,SEMA6A,TRIM36,MAP7,TNFAIP3,AGAP2,AVIL,KATNA1,MDM1,ATAT1,YEATS4,CCDC170,ZNF207,HSPA1B,TUBGCP6,TNXB,PRKN,PARVG,KIF3A,SHROOM1,UBE2B,MTSS1,WASHC5,LRRC6,EPB41L2,OBSCN,PTK2,MAPK15,SUN2,BAIAP2L2,PICK1,MPDZ,CDC42EP1,RAC2,STRIP2,DAAM2,CNTLN,FLNC,MYH9,TEK,LMOD2,PTK7,SRF,CFAP69,PGM5,CCL27,SLAIN2,HEPACAM2,KIT,NCK2,TLN1,GAPDH,KIAA1211,EFHC1,PDCL3,FGD3,CCIN,BICD2,CHMP2A,ZNF135,TMOD1,PLEKHH2,NLRP5,CLDN19,BRSK1,PRKCE,SPTBN1,ACTL7A,PHIP,EPB41L4B,RUFY3,SHANK1,LPAR1,XPO1,AQP1,EHBP1,MYH14,CEP68,WDR92,PLEK,ITGB1BP1,MET,ADD2,ARHGEF5,TRIM32,CDK5RAP2,EPHA1,ZMYM6,CNTRL,GAB1,CCDC155,MYLK3,SDCBP,FAM49A,ARMC2,MAPRE1,WASF1,ARMC4,SPRY1,ARHGAP12,TTC26,KPTN,MSRB2,DRC1,CCDC61,IQSEC1,ABI1,SOX9,RSPH6A,NINL,MYO7B,EML2,SLC39A12,LCP1,CLASP2,NECTIN2,MAPRE3,PLK3,MLH1,LLGL2,TRIM54,RAF1,XRCC2,NCKAP5,EVPL,PIBF1,IFT172,FOXJ1,MYO7A,MYCBP2,SLAIN1,KIZ,SPRY2,CLIP4,WNT11,TTLL3,CCDC13,DYNC1LI1,HOOK3,ARRB1,BFSP1,PLEKHG2,IKBKB,CEP295NL,FARP1,FCHSD2,MKKS,ANK1,ACTG1,FSCN2,NAV3,PAWR,RAC3,CNN2,BAG4,ARHGEF7,DIAPH1,SPEF1,FCHSD1,ARHGAP26,FGD6,NCKAP1L,ARFIP2,RASSF7,LMOD3,DPYSL3,KATNAL1,TTC17,CEP63,NSFL1C,ATXN7,PLK2,MOS,NPHP1,HCK,TTL,KIF3B,FAM107A,FER,MRAS,CEP70,MAST4,FLNB,PIK3R1,HIP1R,CHMP2B,ARHGAP10,DCLK2,CEP44,PARVA,PLS1,CLIP1,KATNBL1,PLCE1,SH3D19,CEP250,CCDC66,FMN1,LIMA1,SORBS1,CETN3,NCKAP5L,P2RX7,EPB41L1,CHMP4C,RTKN,SDAD1,MCPH1,KATNB1,PTK2B,DPYSL2,CCDC65,RND1,	grey	VSMC_M10
GO:0019222	1.00	0.00	2440	4858	regulation of metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,CD226,NME1,SERPINB8,SERPINB2,ORMDL2,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,TNFAIP8,LRP1,SHMT2,EYA4,PGGT1B,GLI1,HBS1L,MARS,CLK4,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,CYP27B1,TSFM,AVIL,HIVEP2,PLAGL1,EPM2A,MAML1,MRNIP,HELB,TRIM39,PPP1R10,ZBTB2,RMND1,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,TSPAN8,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,PHAX,ARID1B,ADM2,HSPA1B,FZD6,RIMS2,ZBTB12,SKIV2L,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,TNXB,GRAMD4,MAP3K4,PRKN,AGPAT1,QKI,RNF5,AGER,PPARA,GPSM3,FBLN1,MED30,PSMB8,IL5,BRD2,HLA-DPB1,ZUP1,RXRB,TSPO,GDF9,VGLL2,ROS1,MRPL13,HSF2,DERL1,TCF7,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,CSDC2,PITX1,AL096711.2,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,PRXL2C,HABP4,H3F3C,PTK2,C6orf106,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,EXOC4,ATF4,TUT7,TAB1,MAPK15,GOLM1,RPAP2,AGTPBP1,CBX7,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,PUF60,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,SOX10,PI16,PIM1,NRF1,RAC2,TMPRSS6,EXOSC4,SMO,TTC39B,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,GUCA1B,PPP1R16A,GPT,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,BICRAL,GNMT,POT1,GPR37,FBXO7,RORB,ZNF300,PRDM4,ALDH1A1,CRY1,DMTF1,SRF,SMU1,TTBK1,ZNF318,NFX1,NUAK1,XPO5,APBA1,CDK14,DCAF12,FZD1,MTERF1,NFXL1,TEC,NFKBIE,CDK6,SUPT3H,SMARCA2,USP46,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TGFBRAP1,PLGRKT,IL1R2,TF	grey	VSMC_M10

GO:0009892	1.00	0.00	1084	2254	negative regulation of metabolic process	BP	1	NME1,SERPINB8,SERPINB2,ORMDL2,ZC3H10,SMARCC2,PAN2,ATP8B1,BAZ2A,TNFAIP8,LRP1,SHMT2,PGGT1B,PIP4K2C,TNFAIP3,AGAP2,CYP27B1,PLAGL1,HELB,TRIM39,ZBTB2,ESR1,CNOT2,CNOT6,RIDA,OSR2,PABPC1,SNW1,ZNF706,PHAX,HSPA1B,ZBTB12,SKIV2L,DXO,MOV10L1,EIF3E,PNLDC1,PRKN,RNF5,AGER,PPARA,FBLN1,TSPO,MRPL13,TCF7,PHF1,UBE2B,BAK1,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,AGO2,H3F3C,C6orf106,PTCH1,TNRC6B,ATF4,TUT7,CBX7,GTPBP1,MAPK14,NTRK2,CBY1,NRBP2,STK38,SOX10,PI16,TMPRSS6,EXOSC4,SMO,HSF1,FOXP4,MDFI,CCND3,FOXH1,CDKN2A,RBFOX2,POT1,FBXO7,RORB,ALDH1A1,CRY1,SRF,TTBK1,ZNF318,NFX1,XPO5,SMARCA2,RFX3,TNFRSF21,NCK2,FHL2,IL1R2,TFAP2B,NFIL3,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,RPS14,ZNF550,BEND6,ZNF268,SVBP,LRPPRC,CLDN19,DNAJA1,SCMH1,RNF20,PRKCE,MSH2,CD109,IGF2BP3,RTN4,PPP2R1A,IBTK,NFE2L3,PNPT1,ACP4,HOXA2,HOXA7,REL,PUS10,JAZF1,PTBP3,CXCL8,XPO1,AKIRIN2,SRSF10,AQP1,CASP8AP2,BACH2,ZNF692,CYREN,PLEK,SNIP1,ANXA4,NR1H2,ZNF350,ITGB1BP1,FOXP2,MED25,KLF11,MET,GRB10,AGO1,POU3F3,EGFR,LANCL2,FAM3C,TLR4,EPHA1,BCL2L12,IL15,DKKL1,CREM,ATG5,SDCBP,MYCN,TUT4,OSR1,FOXO3,PUM2,BEND5,PRKAR2B,TRAF3IP2,SPHK2,DHFR,SPRY1,MTPAP,LAMA4,HDAC2,PHF10,MTMR2,ZC3HAV1,DNMT3A,BMI1,DHX34,C5AR2,ZC3H4,PIP4K2A,CST7,CNBP,SETDB2,PHB,SOX9,BEX4,ZNF746,ERCC1,EED,APOC1,CRTAP,DNAJC15,SUV39H2,ZNF404,PLK3,FASTK,XRCC1,OPTN,MLH1,GLI2,DEDD2,RSF1,KDM4A,AQP11,PRKAG2,RAF1,MYD88,DACH1,PRDX3,TIMP4,SLC22A13,T	grey	VSMC_M10
GO:0051171	1.00	0.00	2030	4082	regulation of nitrogen compound metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,SERPINB8,SERPINB2,ORMDL2,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,TNFAIP8,LRP1,SHMT2,EYA4,GLI1,HBS1L,MARS,CLK4,MAP3K5,TNFAIP3,AGAP2,TSFM,HIVEP2,PLAGL1,MAML1,MRNIP,HELB,TRIM39,PPP1R10,ZBTB2,RMND1,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,PHAX,ARID1B,HSPA1B,FZD6,ZBTB12,DXO,EIF3E,ZBED4,PNLDC1,TNXB,GRAMD4,MAP3K4,PRKN,QKI,AGER,PPARA,FBLN1,MED30,PSMB8,IL5,BRD2,RXRB,TSPO,GDF9,VGLL2,MRPL13,HSF2,DERL1,TCF7,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,PRXL2C,HABP4,PTK2,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,ATF4,TUT7,TAB1,MAPK15,RPAP2,AGTPBP1,CBX7,GTPBP1,MAPK14,NTRK2,CBY1,PUF60,STK38,CSNK1E,PLA2G6,C6orf89,KDM4C,SOX10,PI16,PIM1,NRF1,TMPRSS6,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,GUCA1B,PPP1R16A,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,BICRAL,POT1,GPR37,FBXO7,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,TTBK1,ZNF318,NFX1,NUAK1,CDK14,FZD1,MTERF1,NFXL1,TEC,NFKBIE,SUPT3H,SMARCA2,RFX3,KIT,SLC1A1,ADGRF1,NCK2,FHL2,TGFBRAP1,PLGRKT,IL1R2,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,RGP1,PDCL3,HINT2,PHF14,IPPK,KLHL31,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,MEOX2,ZNF550,KANSL3,BEND6,ZNF268,ZNF667,ZNF787,ZNF691,CAT,SVBP,MACC1,LRPPRC,CLDN19,SIX2,DNAJA1,FOXJ3,ZNF865,HIVEP3,IL11,SCMH1,ZNF189,RNF20,PRKCE,EPAS1,STPG4,EPCAM,MSH	grey	VSMC_M10
GO:0050790	1.00	0.00	863	1823	regulation of catalytic activity	BP	1	SERPINB8,SERPINB2,ERBB3,TNFAIP8,LRP1,ARHGAP9,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,CYP27B1,SRGAP1,LTC4S,TBC1D30,MRNIP,TBC1D9B,PPP1R10,ESR1,FRS2,STK3,TIAM2,DENND6B,TNXB,GRAMD4,MAP3K4,PRKN,AGER,GPSM3,FBLN1,PSMB8,ROS1,RGL2,SKP1,SYNGAP1,BAK1,XRCC6,TRIB1,MYC,ASAP1,FAM13B,OBSCN,PTK2,SIL1,TAB1,MAPK15,PLXNA4,MAPK14,NTRK2,STK38,C6orf89,PI16,TBC1D22B,RAC2,ZDHHC21,HSF1,CCND3,GUCA1B,PPP1R16A,CDKN2A,ZNF16,CHRNA3,TEK,POT1,FBXO7,ALDH1A1,RIC8B,TTBK1,BAG1,NUAK1,RCAN2,KIT,SLC1A1,NCK2,ROR2,SEMA4D,GAPDH,TBC1D8,RGP1,FGD3,GABBR2,SVBP,DNAJA1,SDHAF4,PRKCE,SMAP1,TNNI3,PPP1R12C,EPS8L1,RIMS1,MSH2,CD109,RAPGEF5,PPP2R1A,FPR2,IBTK,ACP4,MOB1B,LPAR1,PPT1,EPGN,NOD1,AREG,AKIRIN2,AQP1,CASP8AP2,WDR91,ETAA1,PLEK,ANXA4,EPHA7,NR1H2,TNFSF15,TGFA,PTN,ASAP2,ITGB1BP1,MET,VRK3,EGFR,ARHGEF5,TLR4,CCNC,EPHA1,BCL2L12,BVES,NOSIP,LPIN1,TBC1D9,CCNY,MGST2,SSBP1,FAF1,PRKAR2B,HSPE1,SPHK2,DHFR,SPRY1,PLXNA1,ARHGAP12,NAPA,SLC8A2,BMI1,C5AR1,PIP4K2A,ARHGEF4,ARHGAP21,PRKD2,PTGIR,CST7,PHB,IQSEC1,ABI1,GIPR,CYSLTR2,ABHD5,EED,SSPO,PPP1R37,RSU1,APOC1,MAPRE3,DNAJC15,EIF2B3,XRCC1,EPM2AIP1,LLGL2,RALB,PRKAG2,RAF1,PRDX3,TIMP4,PIBF1,TBC1D4,FOXJ1,UBE2O,MYCBP2,GCKR,SZT2,SPRY2,WNT11,ALK,PSD3,RIN2,AKT2,PITRM1,ARRB1,TGFBR2,ACVR2A,PLEKHG2,IKBKB,SRGAP3,PPME1,TBC1D16,FARP1,RINL,MKKS,NEK10,RPTOR,TCIM,HBEGF,PDE6G,TMEM106B,PTPRQ,PLCB1,RASGRP4,GPS1,CHTOP,SPINT2,EIF2AK2,PRNP,BAG4,TAF7,ARHGEF7,PLXNC1,MCF2L,ARHGAP26,FGD6,ARHGEF33,N	grey	VSMC_M10

GO:0033554	1.00	0.00	731	1561	cellular response to stress	BP	1	ADNP2,PHLPP1,POLI,LRP1,EYA4,MARS,MAP3K5,RPA3,TNFAIP3,ATP23,CANX,MRNIP,HELB,TRIM39,PPP1R10,ARMT1,MDC1,IER3,STK3,MAPK8IP2,SNW1,HSPA1B,MAP3K4,PRKN,PACRG,RNF5,AGER,PPARA,TSPO,MCM9,ASF1A,DERL1,PHF1,UBE2B,BAK1,XRCC6,NCOA7,MTSS1,TRIB1,MYC,ERCC6L2,FANCC,AKR1B1,ATF4,MAPK15,MAPK14,MAPK13,DMC1,CSNK1E,PLA2G6,PICK1,FOXRED2,HSF1,OARD1,TFEB,SLC39A4,CDKN2A,POT1,GPR37,FBXO7,CRY1,SRF,NUAK1,FANCG,CDK6,SLC1A1,NCK2,MRPS9,ERMP1,ROR2,GADD45G,PDCL3,REV1,KLHL31,PRDX1,SEMA4C,SEC61B,ERP44,DNAJA1,BRSK1,PRKCE,EPAS1,MSH2,TFPT,FKTN,RAD23B,PNPT1,VRK2,FANCL,EMC10,REL,ECPAS,ALB,CXCL8,MTURN,NOD1,AQP1,RRAGD,CYREN,HERPUD2,ETAA1,ZNF277,NR1H2,PTN,MET,TNC,EGFR,USP45,TRIM32,TLR4,ASCC3,VPS41,TRAF1,CCDC155,UCP1,ATG5,SETD7,SDCBP,MGARP,SLC7A11,FOXO3,FGF21,BRAF,CHCHD6,REV3L,DHFR,HDAC2,KPTN,SESN3,DNMT3A,HMCES,NDNF,FOXA3,ERCC1,NUDT15,XPC,ERCC2,ERCC3,DDIAS,PDIA3,DNAJC15,SUV39H2,PLK3,XRCC1,STAC,OPTN,MLH1,RALB,MBD4,AQP11,PRKAG2,UBE2E2,XRCC2,MYD88,OXSR1,PRDX3,KIN,ZRANB3,PAXIP1,WDR48,PTPRF,EGLN2,UBXN4,FBH1,SZT2,CCDC13,MGME1,RNF169,UGGT2,IKBKB,FAM168A,FBXO17,SIRT2,ZMYND11,RPTOR,DNAJC18,CLPB,TCIM,NPLOC4,PAWR,UBAC2,PLCB1,TMTC4,MAP4K1,SIRT7,GPS1,MCM8,SHLD1,EIF2AK2,NEK11,ASH2L,AP5S1,BRF2,RELL2,SEMA3A,CHL1,PDK1,DDRGK1,SH3RF2,WRN,PPP4R2,GAS6,LARS,MRPS26,ULK1,TEX15,PPP2CB,FOXP1,UBXN8,ARL6IP5,PRKDC,IRF7,POLR2I,ERCC6,ALKBH3,MFHAS1,STX2,CEP63,TRAF6,STK33,TRIB3,EPHB1,PLK2,COX4I2,ERCC8,IL1A,DN	grey	VSMC_M10
GO:0009966	1.00	0.00	1071	2237	regulation of signal transduction	BP	1	NFATC1,CD226,PHLPP1,ERBB3,ONECUT2,LRP1,RPS12,SEMA6A,EYA4,GLI1,ARHGAP9,PIP4K2C,MAP3K5,TNFAIP3,CYP27B1,USP15,EPM2A,TRIM39,PPP1R10,ESR1,FRS2,CNOT2,STK3,MAPK8IP2,SNW1,TIAM2,MPIG6B,HSPA1B,FZD6,RIMS2,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,PDE10A,FBLN1,IL5,GDF9,ROS1,RGL2,FSTL4,SYNGAP1,UBE2B,BAK1,RSPO3,RNF146,TRIB1,MYC,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,PTCH1,ANKS1A,LY6E,AKR1B1,ZC3H3,TAB1,MAPK14,NTRK2,CBY1,STK38,CSNK1E,PLA2G6,GKAP1,KDM4C,SOX10,ZC3HC1,MFNG,SMO,DAAM2,MDFI,KCP,CCND3,FOXH1,LRRC14,TEK,GPR37,CRY1,RIC8B,PTK7,DLK2,NUAK1,CDK14,LRRD1,PHF24,SLC35B2,OCIAD1,KIT,NCK2,FHL2,IL1R2,TFAP2B,ROR2,GADD45G,SEMA4D,GAPDH,DLX5,TMEM14A,WNK2,NINJ1,FGD3,KLHL31,PRDX1,SEMA4C,SOSTDC1,BEND6,CAT,CAMKMT,DNAJA1,IL11,PRKCE,EPS8L1,RIMS1,CD109,SPTBN1,FKTN,RTN4,PPP2R1A,PHIP,FPR2,GSDME,KLK14,ACP4,SHANK1,VRK2,ADAMTS3,HOXA13,EMC10,LPAR1,REL,ANKRD17,CXCL8,SLC46A2,MTURN,EPGN,NOD1,AREG,BMP8A,RRAGD,PELI1,BMPER,PXDN,ETAA1,PLEK,RSPO1,RSAD2,AAK1,EPHA7,NR1H2,TGFA,ITGB1BP1,MET,VRK3,GRB10,YWHAZ,ATP6V1C2,EGFR,LANCL2,TSPAN12,HECW1,FUZ,ARHGEF5,TRIM32,TLR4,CDK5RAP2,TRAF1,BCL2L12,DLGAP3,SFRP4,CCNY,DKKL1,VPS35,SDCBP,TRPM4,FOXO3,PUM2,WASF1,FAF1,FGF21,BRAF,INTU,TRAF3IP2,SPHK2,SPRY1,ARHGAP12,HDAC2,MTMR2,DNAJC27,KPTN,SESN3,SLC8A2,RAB7A,BMI1,C5AR2,C5AR1,PIP4K2A,ARHGEF4,ARMC10,ARHGAP21,PRKD2,PTGIR,PHB,IQSEC1,SOX9,GIPR,PPM1N,CD300LF,DDIAS,NECTIN2,FBXL2,PDI	grey	VSMC_M10
GO:0048856	1.00	0.00	2079	4193	anatomical structure development	BP	1	ADNP2,NFATC1,NME1,ITGA7,PHLPP1,ERBB3,SMARCC2,SLC39A5,NEDD4L,ATP8B1,ONECUT2,TCF4,HSD17B4,LRP1,SEMA6A,EYA4,STAC3,TBPL1,GLI1,YTHDC2,N4BP3,KIF5A,TNFAIP3,HECA,CYP27B1,ADGRG6,AVIL,MAML1,MDM1,ATAT1,CPM,ESR1,FRS2,CNOT2,IER3,RAB21,RIDA,STK3,OSR2,MAPK8IP2,SNW1,TIAM2,ARID1B,ADM2,MPIG6B,SLC12A2,HSPA1B,SYNJ2,FZD6,RIMS2,IGF2R,MOV10L1,BRD1,CDC42SE2,PNLDC1,MAP3K4,PRKN,PACRG,QKI,AGER,PPARA,HLA-DRA,FBLN1,TNFRSF11B,IL5,BRD2,PARVG,SULT4A1,COL11A2,RXRB,TSPO,SHROOM1,GDF9,UQCRQ,VGLL2,ROS1,CEP85L,ASF1A,VPS52,TBC1D32,RRP7A,FSTL4,TCF7,SYNGAP1,CCDC134,UBE2B,BAK1,XRCC6,MTSS1,CATSPER3,PITX1,RSPO3,WASHC5,ACO2,TRIB1,MYC,TOB2,SMAD5,ASAP1,LRRC6,L3MBTL3,KLHL3,OBSCN,LEMD2,AGO2,H3F3C,GFRA3,PTK2,HSD17B3,PTCH1,ANKS1A,FANCC,LY6E,AKR1B1,EXOC4,ATF4,TUT7,TAB1,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,CBY1,DMC1,PODXL,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,PI16,MICALL1,PIM1,MEST,CKB,CDC42EP1,MFNG,RAC2,STRIP2,SMO,ZDHHC21,BNC2,HSF1,DAAM2,FLNC,MDFI,TFEB,KCP,TAF8,MYH9,FOXH1,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,LARGE1,FBXO7,RORB,LMOD2,ZFAND5,PTK7,GDA,CEMIP2,SRF,TTBK1,ADAM22,CFAP69,GABRA1,APBA1,FZD1,PGM5,CNTFR,TEC,TXNRD1,FANCG,CDK6,SMARCA2,SLC25A27,RFX3,KIT,SLC1A1,ADGRF1,CA9,TNFRSF21,NCK2,SGCE,FHL2,C2orf49,TFAP2B,ROR2,NFIL3,SEMA4D,DLX5,S1PR3,EFHC1,PPAT,PDCL3,C1GALT1,NINJ1,FGD3,CCIN,VWDE,OMD,PRDX1,ETV1,ADGRL3,ZNF135,EXOSC3,SEMA4C,SHB,RPS14,CNNM4,TDRD7,MEOX2,SOSTDC1,TMO	grey	VSMC_M10

GO:0000280	1.00	0.00	138	355	nuclear division	BP	1	VPS4B,ZNF207,FBXO43,HSPA1B,MOV10L1,UBE2B,WASHC5,MAPK15,DMC1,KLHDC3,CHMP2A,FOXJ3,PHIP,HOXA13,EPGN,TGFA,CDK5RAP2,CCDC155,CCDC61,CLASP2,MLH1,PIBF1,CCNB1IP1,DYNC1LI1,SIRT2,ANAPC15,PLCB1,IK,SIRT7,USP44,TEX15,CHAMP1,NSFL1C,MOS,KIF3B,IL1A,CHMP2B,ING2,SLF1,ANAPC5,M1AP,ANAPC7,CHMP4C,USP16,KATNB1,ABRAXAS1,RAD54B,CHMP7,SYCP1,SLF2,SYCP2L,NPM2,IGF2,HSF2BP,AC112128.1,HECW2,PPP2R2D,PRKAR1A,DIS3L2,EGF,CCDC36,KLHDC8B,CHEK2,SPO11,GPR3,C11orf80,NSL1,HORMAD2,POGZ,EPS8,ABRAXAS2,TDRKH,CD28,CDKN1B,TEX12,TOGARAM1,MAJIN,TTN,MAU2,ZCWPW1,STAG3,WNT4,TUBG1,OBSL1,P3H4,AKAP8L,AKAP8,ANAPC4,RAD51B,SEPT1,KPNB1,EME1,NDEL1,SYCE2,RAB11A,LCMT1,RAD51C,INSR,RAD51D,TOM1L2,ERCC4,PSMG2,CEP192,FZR1,SLX4,NAA10,WRAP73,MEIOB,SPIRE2,CHMP1A,PSRC1,CDC14A,VPS4A,MSH4,RHOA,AURKC,UBB,SYCP3,RNF212B,AGO4,OOEP,FOXJ2,ZSCAN21,SYCE1L,WNT5A,DUSP1,SPDYA,CCSAP,BCL2L11,RGCC,NME6,APC,LIF,CDC26,CENPX,EREG,PDXP,DRG1	grey	VSMC_M10
GO:0060255	1.00	0.00	2229	4468	regulation of macromolecule metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,CD226,NME1,SERPINB8,SERPINB2,ORMDL2,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,TNFAIP8,LRP1,SHMT2,EYA4,PGGT1B,GLI1,HBS1L,MARS,CLK4,MAP3K5,TNFAIP3,AGAP2,TSFM,HIVEP2,PLAGL1,MAML1,MRNIP,HELB,TRIM39,PPP1R10,ZBTB2,RMND1,CPSF6,YEATS4,ESR1,MYRFL,CNOT2,TSPAN8,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,SNW1,ZNF706,PHAX,ARID1B,ADM2,HSPA1B,FZD6,RIMS2,ZBTB12,SKIV2L,DXO,MOV10L1,EIF3E,ZBED4,PNLDC1,TNXB,GRAMD4,MAP3K4,PRKN,AGPAT1,QKI,AGER,PPARA,GPSM3,FBLN1,MED30,PSMB8,IL5,BRD2,HLA-DPB1,ZUP1,RXRB,TSPO,GDF9,VGLL2,MRPL13,HSF2,DERL1,TCF7,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,JMJD4,AGO2,HABP4,H3F3C,PTK2,C6orf106,KDM3B,PTP4A3,PTCH1,TNRC6B,ZC3H3,ATF4,TUT7,TAB1,MAPK15,RPAP2,AGTPBP1,CBX7,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,PUF60,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,SOX10,PI16,PIM1,NRF1,TMPRSS6,EXOSC4,SMO,BNC2,HSF1,NFYA,FOXP4,MDFI,TFEB,IRF5,MED20,CCND3,MYH9,FOXH1,PPP1R16A,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,BICRAL,POT1,FBXO7,RORB,ZNF300,PRDM4,CRY1,DMTF1,SRF,SMU1,TTBK1,ZNF318,NFX1,NUAK1,XPO5,APBA1,CDK14,FZD1,MTERF1,NFXL1,TEC,NFKBIE,CDK6,SUPT3H,SMARCA2,USP46,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,FHL2,TGFBRAP1,PLGRKT,IL1R2,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,RFX8,DLX5,CNOT11,S1PR3,RGP1,PDCL3,HINT2,PHF14,IPPK,KLHL31,ETV1,ZNF135,EXOSC3,RPS14,ZNF154,TDRD7,MEOX2,ZNF550,	grey	VSMC_M10
GO:0035556	1.00	0.00	978	2063	intracellular signal transduction	BP	1	NFATC1,PHLPP1,ERBB3,CCDC68,LRP1,SEMA6A,STAC3,ARHGAP9,PDE7B,MAP3K5,TNFAIP3,ADGRG6,USP15,EPM2A,MRNIP,TRIM39,PPP1R10,ESR1,FRS2,MDC1,RAB21,STK3,ZNF207,MAPK8IP2,SNW1,TIAM2,HSPA1B,RIMS2,CDC42SE2,MAP3K4,PRKN,AGER,PPARA,PDE10A,FBLN1,ROS1,RGL2,SYNGAP1,UBE2B,BAK1,TRIB1,MYC,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,PTK2,GPR20,PTP4A3,AKR1B1,GRAP2,ATF4,TAB1,MAPK15,MAPK14,NTRK2,MAPK13,NRBP2,STK38,PLA2G6,CDC42EP1,RAC2,SMO,HSF1,CDKN2A,TEK,GPR37,ASB15,CRY1,NUAK1,TEC,LRRD1,SLC35B2,RCAN2,KIT,NCK2,FHL2,ROR2,GADD45G,SEMA4D,GAPDH,WNK2,FGD3,KLHL31,PRDX1,SEMA4C,CAT,DNAJA1,IL11,BRSK1,PRKCE,TNNI3,EPS8L1,MSH2,ASB3,RAPGEF5,FKTN,RTN4,PPP2R1A,IRAK1BP1,FPR2,GSDME,CTNNAL1,MOB1B,VRK2,EMC10,LPAR1,REL,ANKRD17,CXCL8,SLC46A2,MTURN,EPGN,NOD1,AQP1,RRAGD,PELI1,BMPER,ETAA1,PLEK,SNIP1,EPHA7,TNFSF15,TGFA,ITGB1BP1,DGKI,MET,VRK3,GRB10,YWHAZ,EGFR,ARHGEF5,TRIM32,TLR4,CDK5RAP2,TRAF1,HACE1,TEAD2,SDCBP,TRPM4,FOXO3,SMPD2,PUM2,WASF1,MFSD8,FGF21,BRAF,PRKAR2B,TRAF3IP2,SPHK2,FAT4,SPRY1,GRIN2D,ARHGAP12,ADCY3,DNAJC27,KPTN,SESN3,SLC8A2,NDNF,C5AR2,C5AR1,MKNK1,ARHGEF4,ARMC10,ARHGAP21,PRKD2,PHB,IQSEC1,SOX9,GIPR,PPM1N,XPC,LCP1,LACC1,DDIAS,FBXL2,PLK3,STAC,OPTN,GAB2,MLH1,KBTBD6,RALB,DEDD2,PRKAG2,RAF1,MYD88,OXSR1,ZFAND6,PAXIP1,IRAK2,SEC14L1,POU4F1,FBH1,SZT2,ASB13,PPP1CB,SPRY2,WNT11,ALK,PSD3,RIN2,ACKR2,AKT2,DYNC1LI1,GPD1L,ARRB1,PIP4P1,IKBKB,SRGAP3,C1QTNF1,SIRT2,NMI,NEK10,ZMYND11,RPTOR,CLPB,TCIM,HBEG	grey	VSMC_M10

GO:0016477	1.00	0.00	503	1120	cell migration	BP	1	ONECUT2,LRP1,SEMA6A,TNFAIP3,SRGAP1,SLC12A2,AGER,GPSM3,TSPO,CEP85L,TRIB1,CXCL14,AGO2,GFRA3,PTK2,PTP4A3,ANKS1A,MAPK15,PLXNA4,SUN2,NTRK2,PODXL,SOX10,RAC2,STRIP2,SMO,MYH9,RBFOX2,TEK,ZFAND5,PTK7,SRF,CCL27,KIT,NCK2,ROR2,SEMA4D,EFHC1,NINJ1,ADGRL3,SEMA4C,MEOX2,ZNF268,SVBP,CLDN19,SIX2,RNF20,PRKCE,MBOAT7,RTN4,FPR2,HAS1,EPB41L4B,RUFY3,HOXA7,EMC10,LPAR1,CXCL8,AVL9,BMPER,AKIRIN1,PTN,ITGB1BP1,MET,ADD2,GRB10,POU3F3,EGFR,USP45,FUZ,TRIM32,TLR4,TCAF2,EPHA1,HACE1,BVES,GAB1,SDCBP,NRCAM,TRPM4,FOXO3,MAPRE1,FGF21,PLXNA1,LAMA4,PODXL2,NDNF,C5AR2,C5AR1,PRKD2,IQSEC1,SOX9,BEX4,LCP1,CLASP2,MEGF8,MYD88,OXSR1,DACH1,FOXJ1,PAXIP1,PTPRF,CYGB,POU4F1,SPRY2,PLAT,WNT11,RIN2,ACKR2,AKT2,TGFBR2,OVOL2,SRGAP3,JAG1,ACTG1,FSCN2,NAV3,HBEGF,PLCB1,FERMT1,CNN2,ALX1,BAG4,ARHGEF7,SEMA3D,DCN,DIAPH1,BTG1,SPEF1,PLXNC1,SEMA3A,UNC5D,AIMP1,NRG1,DDRGK1,SH3RF2,NCKAP1L,GAS6,FOXP1,MITF,FAM19A4,DPYSL3,FLT1,EPHB1,PLK2,MTUS1,RET,AL359736.1,HCK,FAM107A,CYP7B1,GPI,NR4A1,ACVR1B,ABHD6,FER,PIK3CB,PIK3R1,LPXN,HAND2,ATP5F1A,PARVA,ROBO1,FBXW7,LIMA1,PTPRJ,FZD3,MEF2C,ELP3,SEMA4F,VEGFC,JAM2,IGSF10,ADAMTS1,P2RY1,PTK2B,RAPGEF2,CCL17,RND1,TIAM1,FGF5,DOCK5,SLC8B1,STC1,HDAC7,NKX6-1,LOXL2,TBX5,NR4A2,ACVR1C,BIN3,F2RL1,F2R,ARHGAP24,TUBB2A,ANO6,TP53INP1,SEMA3G,RREB1,STK4,GCNT2,DMTN,SEMA4G,ADTRP,NOD2,NKD1,ITGB6,CD40,LDB1,GBF1,SRGAP2C,PXN,GPLD1,DOCK10,ELMO2,FAP,KIAA0319,CD200,SLK,LGR6,DNM1L,CARMIL1,H	grey	VSMC_M10
GO:0000819	1.00	0.00	53	168	sister chromatid segregation	BP	1	VPS4B,ZNF207,MAPK15,CHMP2A,MCMBP,CDK5RAP2,PIBF1,DYNC1LI1,ANAPC15,IK,USP44,CHAMP1,MOS,CHMP2B,SLF1,FBXW7,ANAPC5,ANAPC7,CHMP4C,KATNB1,CHMP7,SLF2,HECW2,DIS3L2,AXIN2,NSL1,HORMAD2,POGZ,TTN,MAU2,STAG3,TUBG1,DDX11,AKAP8L,AKAP8,ANAPC4,KPNB1,RAB11A,LCMT1,RAD51C,SFPQ,PSMG2,RMI2,NAA10,WRAP73,CHMP1A,PSRC1,VPS4A,CTCF,AURKC,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0032501	1.00	0.00	2500	5003	multicellular organismal process	BP	1	ADNP2,NFATC1,CD226,NME1,SERPINB2,ITGA7,RDH5,PHLPP1,ERBB3,SMARCC2,SLC39A5,NEDD4L,ATP8B1,ONECUT2,MIP,TCF4,TAC3,MYO1A,HSD17B4,LRP1,SEMA6A,EYA4,LVRN,STAC3,TBPL1,GLI1,YTHDC2,N4BP3,KIF5A,B4GALNT1,TNFAIP3,HECA,CYP27B1,ADGRG6,AVIL,SLC16A7,MAML1,MDM1,ATAT1,ESR1,FRS2,CNOT2,TSPAN8,RAB21,RIDA,STK3,OSR2,MAPK8IP2,SNW1,TIAM2,ZNF706,ALDH7A1,APOM,ARID1B,ADM2,MPIG6B,SLC12A2,HSPA1B,SYNJ2,FZD6,RIMS2,IGF2R,MOV10L1,BRD1,PNLDC1,MAP3K4,PRRT1,PRKN,PACRG,AGPAT1,QKI,AGER,PPARA,GPSM3,HLA-DRA,FBLN1,MED30,TNFRSF11B,IL5,BRD2,SULT4A1,HLA-DPB1,COL11A2,TSPO,GDF9,UQCRQ,VGLL2,ROS1,CEP85L,MCM9,ASF1A,VPS52,TBC1D32,SNTB1,RRP7A,FSTL4,HSF2,TCF7,SYNGAP1,CCDC134,UBE2B,BAK1,XRCC6,MTSS1,CATSPER3,PITX1,RSPO3,WASHC5,ACO2,TRIB1,MYC,TOB2,SMAD5,ASAP1,LRRC6,L3MBTL3,KLHL3,XPNPEP3,LEMD2,AGO2,H3F3C,GFRA3,PTK2,HSD17B3,C6orf106,PTP4A3,PTCH1,ANKS1A,FANCC,LY6E,AKR1B1,EXOC4,ATF4,TUT7,TAB1,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,MAPK13,CBY1,DMC1,PODXL,NRBP2,CSNK1E,CPNE5,PLA2G6,PICK1,KDM4C,SOX10,PI16,MICALL1,PIM1,SPATA31D3,CKB,BTBD9,MFNG,RAC2,SMO,ZDHHC21,BNC2,HSF1,DAAM2,MDFI,TFEB,IRF5,KCP,TAF8,OPN1SW,MYH9,FOXH1,GUCA1B,ZNF16,OSTF1,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,GRM8,LARGE1,CHRNA5,FBXO7,RORB,LMOD2,ALDH1A1,CRY1,ZFAND5,PTK7,GDA,CEMIP2,SRF,ABCB1,TTBK1,ADAM22,CFAP69,GABRA1,CLDN12,APBA1,FZD1,CNGA1,CNTFR,TEC,TXNRD1,PHF24,FANCG,CDK6,SMARC	grey	VSMC_M10
GO:0048523	1.00	0.00	1793	3647	negative regulation of cellular process	BP	1	ADNP2,NFATC1,NME1,SERPINB8,SERPINB2,VPS4B,PHLPP1,ORMDL2,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,C18orf54,TNFAIP8,LRP1,SEMA6A,SHMT2,EYA4,GLI1,YTHDC2,B4GALT7,PIP4K2C,TNFAIP3,AGAP2,HECA,CYP27B1,AVIL,PLAGL1,EPM2A,SRGAP1,TBC1D30,MRNIP,ENPP3,HELB,TRIM39,PPP1R10,MDM1,ZBTB2,ESR1,FRS2,CNOT2,MDC1,IER3,CNOT6,RIDA,STK3,ZNF207,OSR2,FBXO43,PABPC1,MAPK8IP2,SNW1,ZNF706,PHAX,APOM,MPIG6B,HSPA1B,FZD6,ZBTB12,EIF3E,PNLDC1,GRAMD4,PRRT1,PRKN,PACRG,RNF5,AGER,PPARA,PDE10A,FBLN1,TSPO,GDF9,GOPC,MRPL13,RGL2,FSTL4,TCF7,PHF1,SYNGAP1,UBE2B,BAK1,XRCC6,NCOA7,MTSS1,PITX1,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,LEMD2,AGO2,H3F3C,PTK2,C6orf106,PTCH1,TNRC6B,AKR1B1,ATF4,TUT7,MAPK15,AGTPBP1,CBX7,APOBEC3H,PLXNA4,MAPK14,NTRK2,CBY1,PODXL,NRBP2,STK38,PLA2G6,PICK1,SOX10,PI16,PIM1,ZC3HC1,TMPRSS6,SMO,HSF1,DAAM2,FOXP4,MDFI,CCND3,MYH9,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,TEK,POT1,GPR37,FBXO7,RORB,LMOD2,CRY1,ABHD17B,SRF,BAG1,ZNF318,NFX1,ADAM22,DLK2,CNTFR,CDK6,SMARCA2,SLC25A27,RFX3,KIT,SLC1A1,TNFRSF21,NCK2,FHL2,IL1R2,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,CNOT11,KIAA1211,S1PR3,TMEM14A,RGP1,PDCL3,HINT2,WNK2,KLHL31,OGN,CHMP2A,EXOSC3,SEMA4C,RPS14,MEOX2,ZNF550,SOSTDC1,TMOD1,BEND6,ZNF268,RAB23,PLEKHH2,CAT,SVBP,LRPPRC,CLDN19,SIX2,DNAJA1,IL11,SCMH1,BRSK1,RNF20,PRKCE,EPCAM,MSH2,CD109,SPTBN1,IGF2BP3,FKTN,RTN4,PPP2R1A,PHIP,HAS1,GSDME,IBTK,NFE2L3,KLK14,PNPT1,RUFY3,ACP4,SKAP2,SHANK1,HOXA2,HOXA7,L	grey	VSMC_M10

GO:0065007	1.00	0.00	4301	8375	biological regulation	BP	1	ADNP2,NFATC1,ATP9B,ZNF236,ZNF407,CNDP1,MTCH2,CD226,NME1,SERPINB8,SERPINB2,ITGA7,RDH5,VPS4B,PHLPP1,ORMDL2,ERBB3,ZC3H10,SMARCC2,SLC39A5,NEDD4L,PAN2,ATP8B1,ONECUT2,MIP,GLS2,ARPC3,BAZ2A,TCF4,CCDC68,C18orf54,RDH16,TAC3,HSD17B4,TNFAIP8,LRP1,STX7,RPS12,SEMA6A,SHMT2,EYA4,LVRN,STAC3,AP3S1,PGGT1B,TRIM36,ALDH8A1,GLI1,YTHDC2,ARHGAP9,HBS1L,MARS,B4GALT7,PDE7B,CLK4,PIP4K2C,MAP3K5,RPA3,TNFAIP3,AGAP2,HEBP2,TSPAN31,HECA,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,FUCA2,PLAGL1,SERF2,USP15,EPM2A,SRGAP1,MAML1,LTC4S,TBC1D30,MRNIP,ENPP3,HELB,TBC1D9B,TRIM39,PPP1R10,MDM1,ATAT1,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,FRS2,MYRFL,CNOT2,MDC1,IER3,TSPAN8,RAB21,CNOT6,RIDA,STK3,ZNF207,OSR2,PRR16,SNCAIP,FBXO43,PABPC1,MAPK8IP2,SNW1,TIAM2,ZNF706,PHAX,APOM,ARID1B,ADM2,MPIG6B,DENND6B,SLC12A2,HSPA1B,FZD6,RIMS2,ZBTB12,SKIV2L,IGF2R,DXO,MOV10L1,EIF3E,CYP21A2,ZBED4,BRD1,CDC42SE2,EBAG9,PNLDC1,KCNV1,TNXB,GRAMD4,MAP3K4,PRRT1,PRKN,PACRG,AGPAT1,QKI,RNF5,AGER,PPARA,GPSM3,PDE10A,HLA-DRA,FBLN1,HLA-DOB,MED30,PSMB8,TNFRSF11B,SLC22A4,HLA-DMA,IL5,BRD2,PNPLA3,PNPLA5,HLA-DPB1,ZUP1,SEPT8,RXRB,TSPO,GDF9,VGLL2,ROS1,HSD17B8,GOPC,MRPL13,TBC1D32,RGL2,FSTL4,HSF2,DERL1,SMDT1,TCF7,SKP1,PHF1,TNFRSF13C,SYNGAP1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,MTSS1,CSDC2,CATSPER3,PITX1,RSPO3,RNF146,WASHC5,AL096711.2,TRIB1,CXCL14,MYC,TOB2,SMAD5,ASAP1,LRRC6,L3MBTL3,L3MBTL2,KLHL3,EPB41L2,MCHR1,AKAP7,FAM13B,	grey	VSMC_M10
GO:0032268	1.00	0.00	855	1819	regulation of cellular protein metabolic process	BP	1	CNDP1,SERPINB8,SERPINB2,ERBB3,PAN2,TNFAIP8,LRP1,SHMT2,HBS1L,MAP3K5,TNFAIP3,AGAP2,TSFM,MRNIP,TRIM39,RMND1,CNOT2,CNOT6,RIDA,STK3,PRR16,PABPC1,SNW1,ZNF706,HSPA1B,EIF3E,PNLDC1,TNXB,GRAMD4,MAP3K4,PRKN,QKI,AGER,FBLN1,IL5,TSPO,GDF9,MRPL13,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,TRIB1,MYC,JMJD4,AGO2,HABP4,PTK2,TNRC6B,ATF4,TUT7,TAB1,AGTPBP1,NTRK2,STK38,CSNK1E,PLA2G6,C6orf89,PI16,HSF1,CCND3,MYH9,PPP1R16A,CDKN2A,CHRNA3,TEK,FBXO7,CRY1,TTBK1,NUAK1,TEC,KIT,SLC1A1,NCK2,PLGRKT,IL1R2,ROR2,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,RPS14,SVBP,LRPPRC,CLDN19,DNAJA1,IL11,RNF20,PRKCE,EPAS1,CD109,IGF2BP3,FKTN,PPP2R1A,RAD23B,PHIP,FPR2,MTIF2,IBTK,PNPT1,ACP4,MOB1B,XPO1,EPGN,NOD1,AREG,AKIRIN2,BMP8A,PM20D2,AQP1,CASP8AP2,PELI1,BMPER,WDR91,ETAA1,RSPO1,EPHA7,NR1H2,TNFSF15,TGFA,ITGB1BP1,VRK3,AGO1,EGFR,ARHGEF5,TRIM32,TLR4,ASCC3,EPHA1,BCL2L12,IL15,CCNY,VPS35,ATG5,SETD7,ZYG11B,SDCBP,C6orf203,TUT4,FOXO3,NTF4,PUM2,MFSD8,FAF1,FGF21,BRAF,PRKAR2B,HSPE1,SPHK2,DHFR,SPRY1,HDAC2,BBS7,EEFSEC,SLC8A2,BMI1,C5AR1,MKNK1,MOB3C,PRKD2,CST7,CNBP,PHB,ABI1,SOX9,SYMPK,BEX4,NUDT15,IWS1,MAPRE3,CRTAP,PLK3,SUMO2,XRCC1,MLH1,CDC123,MTRF1,RALB,DPH2,KDM4A,AQP11,PRKAG2,RAF1,PRDX3,TIMP4,PIBF1,PAXIP1,WDR48,UBE2O,MYCBP2,SPOPL,FBH1,TNRC6C,SPRY2,PLAT,WNT11,TADA3,KLHL40,AKT2,GPD1L,ARRB1,TGFBR2,ACVR2A,IKBKB,SIRT2,NMI,NEK10,RPTOR,PURA,TCIM,HBEGF,PTPRQ,ASPSCR1,PLCL2,DPH3,SIRT7,CHTOP,SPINT2,EIF2AK2,NSD3,	grey	VSMC_M10
GO:1901564	1.00	0.00	2399	4789	organonitrogen compound metabolic process	BP	1	CNDP1,NME1,SERPINB8,SERPINB2,VPS4B,KDSR,PHLPP1,ORMDL2,ERBB3,SEC11C,NEDD4L,PAN2,FECH,GLS2,BAZ2A,HSD17B4,TNFAIP8,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,ALDH8A1,HBS1L,MARS,B4GALT7,RMND5B,PDE7B,CLK4,MAP3K5,B4GALNT1,TNFAIP3,AGAP2,TSFM,ADGRG6,ATP23,USP15,FBXO30,RXYLT1,CANX,MAML1,MRNIP,ENPP3,ATP5MGL,TRIM39,ATAT1,CPM,RMND1,ARMT1,YEATS4,GFPT2,MYRFL,CNOT2,TPH2,CNOT6,RIDA,STK3,PRR16,SNCAIP,FBXO43,PABPC1,SNW1,ZNF706,CPT1B,ALDH7A1,MARCH3,APOM,ABHD16A,ADM2,ZDHHC14,HSPA1B,TULP4,DPYS,SELENOO,EIF3E,ALG12,BRD1,ADAMTS19,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,PPT2,PRKN,QKI,RNF5,AGER,PPARA,PDE10A,ACSL6,FBLN1,P4HA2,MED30,PSMB8,SLC22A4,IL5,BRD2,ZUP1,TSPO,GDF9,ROS1,MRPL13,A4GALT,RPS18,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,RNF146,TRIB1,MYC,SMAD5,KLHL3,XPNPEP3,OBSCN,MRPL55,JMJD4,AGO2,PRXL2C,HABP4,RPS10,PTK2,KDM3B,PTP4A3,PTCH1,TNRC6B,LY6E,AKR1B1,ATF4,PYCR3,TUT7,TAB1,ISCA1,MAPK15,RPAP2,AGTPBP1,APOBEC3H,GTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,PI16,EIF3L,PIM1,CKB,BTBD9,ZC3HC1,TMPRSS6,GPAA1,ZDHHC21,TSPAN33,FOXRED2,HSF1,MOCS1,PSAT1,FBXL6,OARD1,ADCK5,USP49,CCND3,OPN1SW,MYH9,GUCA1B,PPP1R16A,GPT,IMPDH1,HACD4,MTAP,CDKN2A,APOL4,NMRK1,CARNMT1,APOL6,CHRNA3,TEK,LARGE1,GNMT,TRPM6,GPR37,FBXO7,KLHDC3,ASB15,PRDM4,ALDH1A1,CRY1,PTK7,GDA,ABHD17B,CEMIP2,CROT,TTBK1,NFX1,ADAM22,GNPDA2,NUAK1,PTAR1,	grey	VSMC_M10

GO:0007275	1.00	0.00	1871	3815	multicellular organism development	BP	1	ADNP2,NFATC1,NME1,ITGA7,PHLPP1,ERBB3,SMARCC2,SLC39A5,NEDD4L,ATP8B1,ONECUT2,TCF4,HSD17B4,LRP1,SEMA6A,EYA4,STAC3,GLI1,N4BP3,KIF5A,TNFAIP3,HECA,CYP27B1,ADGRG6,AVIL,MAML1,MDM1,ATAT1,ESR1,FRS2,CNOT2,RAB21,RIDA,STK3,OSR2,MAPK8IP2,SNW1,TIAM2,ARID1B,ADM2,MPIG6B,SLC12A2,HSPA1B,SYNJ2,FZD6,RIMS2,IGF2R,BRD1,PNLDC1,MAP3K4,PRKN,QKI,AGER,PPARA,HLA-DRA,FBLN1,TNFRSF11B,IL5,BRD2,SULT4A1,COL11A2,TSPO,GDF9,UQCRQ,VGLL2,ROS1,CEP85L,VPS52,TBC1D32,RRP7A,FSTL4,TCF7,SYNGAP1,CCDC134,UBE2B,BAK1,XRCC6,MTSS1,PITX1,RSPO3,WASHC5,ACO2,TRIB1,MYC,TOB2,SMAD5,ASAP1,LRRC6,L3MBTL3,KLHL3,LEMD2,AGO2,H3F3C,GFRA3,PTK2,HSD17B3,PTCH1,ANKS1A,FANCC,LY6E,AKR1B1,EXOC4,ATF4,TAB1,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,CBY1,DMC1,PODXL,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,PI16,MICALL1,PIM1,CKB,MFNG,RAC2,SMO,ZDHHC21,BNC2,HSF1,DAAM2,MDFI,TFEB,KCP,TAF8,MYH9,FOXH1,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,LARGE1,FBXO7,RORB,ZFAND5,PTK7,GDA,CEMIP2,SRF,TTBK1,ADAM22,GABRA1,APBA1,FZD1,CNTFR,TXNRD1,FANCG,CDK6,SMARCA2,SLC25A27,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,SGCE,FHL2,C2orf49,TFAP2B,ROR2,NFIL3,SEMA4D,DLX5,S1PR3,EFHC1,PPAT,PDCL3,C1GALT1,NINJ1,CCIN,OMD,PRDX1,ETV1,ADGRL3,EXOSC3,SEMA4C,SHB,RPS14,CNNM4,TDRD7,MEOX2,SOSTDC1,TMOD1,BEND6,RAB23,ANKS6,PHF3,DYNC2LI1,NLRP5,CAT,SVBP,SIX2,HIVEP3,PLPPR1,TMEM190,IL11,COL9A1,SCMH1,BRSK1,SMAP1,TNNI3,EPAS1,RDH13,RIMS1,STPG4,EPCAM,ABCB5,MSH2,CD109	grey	VSMC_M10
GO:0051726	1.00	0.00	358	827	regulation of cell cycle	BP	1	VPS4B,PGGT1B,TRIM36,GLI1,YTHDC2,RPA3,TNFAIP3,HECA,PLAGL1,MRNIP,TRIM39,PPP1R10,MDM1,MDC1,ZNF207,FBXO43,HSPA1B,UBE2B,BAK1,MYC,PTCH1,MAPK15,MAPK14,UHRF2,C6orf89,HSF1,FBXL6,CCND3,CDKN2A,ZNF16,FBXO7,CRY1,TTBK1,CDK14,CDK6,GADD45G,CDK20,CHMP2A,ZNF268,BRSK1,PRKCE,MSH2,PHIP,PNPT1,HOXA13,ANKRD17,CXCL8,XPO1,EPGN,ETAA1,TGFA,LSM10,MED25,EGFR,TRIM32,CDK5RAP2,CCNY,SDCBP,CDK19,FOXE3,TPRA1,SOX9,TOPAZ1,XPC,ERCC2,ERCC3,MAPRE3,PLK3,CDC123,UBE2E2,DACH1,PAXIP1,POU4F1,AKT2,DYNC1LI1,THAP1,CEP295NL,SIRT2,NEK10,RPTOR,TCIM,ANAPC15,SRA1,PLCB1,IK,NEK11,NUDT16,BTG1,CLIC1,CDKL4,USP44,TFDP1,DDRGK1,MTA3,PRKDC,ERCC6,CEP63,NSFL1C,STK33,PLK2,MOS,TTL,KIF3B,FAM107A,IL1A,NR4A1,CEBPA,CSPP1,DCDC1,TFDP2,CDK7,CASP3,RAD17,CHMP2B,ATR,HPGD,SLF1,CEP250,ARNTL,FBXW7,FZD3,BTG3,ANAPC5,NUGGC,PKIA,CCNH,HTRA2,ANAPC7,CELF1,CCNJ,RAD9B,CHMP4C,CSNK2A2,MCPH1,ADAMTS1,E2F5,USP16,MADD,CCNG2,EIF2AK4,ALMS1,RPRD1B,NBN,NKX3-1,ABRAXAS1,TMEM67,DONSON,ZFYVE19,PRDM11,CCNJL,TP53INP1,PIDD1,ZBED6,PKD2,SLF2,NPM2,HERC5,TAOK3,CDK18,IGF2,KIF13A,GBF1,MX2,NUPR2,FAP,RPL23,SIK1,HYAL1,AC112128.1,HECW2,CCND1,TERT,MAP2K6,PDCD4,TGFB2,PRKAR1A,TCF7L2,ADARB1,TBRG1,AXIN2,INTS13,DYRK3,GIGYF2,EGF,USP19,SOX2,HSPA8,CCDC36,YTHDF2,GPER1,CHEK2,PSME1,CCNDBP1,USP2,GPR3,TGM1,SFN,CDK15,ANGEL2,CCDC84,PER2,WDR12,ATRIP,TXLNG,CABLES2,CDKL5,CD28,SYF2,RUNX3,MLXIPL,UHMK1,FZD9,CDKN1B,E2F2,DLG1,OVOL1,SETD2,STOX1,HEXIM2,BCL6,SUSD2,PPP2R5B,DBF4	grey	VSMC_M10
GO:0032502	1.00	0.00	2277	4589	developmental process	BP	1	ADNP2,NFATC1,NME1,ITGA7,PHLPP1,ERBB3,SMARCC2,SLC39A5,NEDD4L,ATP8B1,ONECUT2,TCF4,HSD17B4,LRP1,SEMA6A,EYA4,STAC3,TBPL1,GLI1,YTHDC2,N4BP3,KIF5A,MAP3K5,B4GALNT1,TNFAIP3,NHSL1,HECA,CYP27B1,ADGRG6,AVIL,CANX,MAML1,MDM1,ATAT1,CPM,ESR1,FRS2,CNOT2,IER3,TSPAN8,RAB21,RIDA,STK3,OSR2,PRRC2A,MAPK8IP2,SNW1,TIAM2,ZNF706,ARID1B,ADM2,MPIG6B,SLC12A2,HSPA1B,SYNJ2,FZD6,RIMS2,IGF2R,MOV10L1,BRD1,CDC42SE2,PNLDC1,MAP3K4,PRKN,PACRG,QKI,AGER,PPARA,HLA-DRA,FBLN1,MED30,PSMB8,TNFRSF11B,IL5,BRD2,PARVG,PNPLA3,SULT4A1,COL11A2,RXRB,TSPO,SHROOM1,GDF9,UQCRQ,VGLL2,ROS1,CEP85L,ASF1A,VPS52,TBC1D32,RRP7A,FSTL4,HSF2,TCF7,SYNGAP1,ANXA13,CCDC134,UBE2B,BAK1,XRCC6,MTSS1,CATSPER3,PITX1,RSPO3,WASHC5,ACO2,TRIB1,MYC,TOB2,SMAD5,ASAP1,LRRC6,L3MBTL3,KLHL3,OBSCN,LEMD2,AGO2,H3F3C,GFRA3,PTK2,HSD17B3,PTCH1,ANKS1A,FANCC,LY6E,AKR1B1,EXOC4,ATF4,TUT7,TAB1,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,UHRF2,CBY1,DMC1,PODXL,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,PI16,MICALL1,PIM1,MEST,SPATA31D3,CKB,CDC42EP1,MFNG,RAC2,STRIP2,SMO,ZDHHC21,BNC2,HSF1,DAAM2,FLNC,MDFI,TFEB,KCP,TAF8,MYH9,FOXH1,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,LARGE1,FBXO7,RORB,LMOD2,ZFAND5,PTK7,GDA,CEMIP2,SRF,TTBK1,ADAM22,DLK2,YIPF3,CFAP69,NUAK1,GABRA1,APBA1,FZD1,PGM5,CNTFR,TEC,TXNRD1,OCIAD1,FANCG,CDK6,SMARCA2,SLC25A27,TDRD6,RFX3,KIT,SLC1A1,ADGRF1,CA9,TNFRSF21,NCK2,SGCE,FHL2,C2orf49,TFAP2B,ROR2,NFIL3,GADD45G,SEMA4D,DLX5,	grey	VSMC_M10

GO:0051276	1.00	0.00	287	682	chromosome organization	BP	1	VPS4B,SMARCC2,BAZ2A,RPA3,HELB,PPP1R10,ESR1,ZNF207,ARID1B,MAP3K4,BRD2,MCM9,ASF1A,PHF1,UBE2B,XRCC6,MYC,L3MBTL3,L3MBTL2,H3F3C,MAPK15,CBX7,DMC1,KDM4C,POT1,MTERF1,SMARCA2,CHMP2A,MCMBP,SCMH1,STPG4,MSH2,ZNF462,RAD23B,HMGN3,UTP3,TRAPPC12,ASCC3,CDK5RAP2,CCDC155,SETD7,SSBP1,HDAC2,UBN2,DNMT3A,SETDB2,RCBTB1,FOXA3,SOX9,HDAC11,ERCC1,XPC,ERCC2,ERCC3,GTF2F2,SUV39H2,XRCC1,MLH1,NUDT5,RSF1,KDM4A,PIBF1,ZRANB3,FBH1,CCNB1IP1,DYNC1LI1,CBX4,CHD8,SIRT2,ZMYND11,PURA,ANAPC15,IK,SIRT7,MCM8,USP44,WRN,TEX15,CHAMP1,PRKDC,ERCC6,ACTR6,MOS,TOX,SMYD1,CHMP2B,ATR,ING2,SLF1,FAM208A,FBXW7,HMBOX1,HLTF,SMARCD1,ANAPC5,M1AP,DQX1,ANAPC7,CHMP4C,MCPH1,KATNB1,MAPKAPK5,SFMBT1,TPRKB,TTI1,NBN,TOP1,PBRM1,HELQ,ABRAXAS1,BAHD1,RAD54B,LOXL2,CHMP7,WRNIP1,RSBN1,PHF21A,SPTY2D1,SYCP1,SLF2,NPM2,TWNK,PPHLN1,NAP1L5,JARID2,TENT4B,LDB1,RAD54L2,STN1,RBBP4,HDAC1,HECW2,LTO1,SP100,TERT,IGHMBP2,SATB2,TCF7L2,DIS3L2,AXIN2,SART3,ZNFX1,ACIN1,ARID4B,SNAI1,GAR1,SOX2,CCDC36,GPER1,SPO11,RCCD1,RECQL,ARID1A,NSL1,AEBP2,HORMAD2,VPS72,HDAC4,SS18L1,POGZ,RTEL1,BAZ1B,SETD2,MAPT,TET1,SUPV3L1,TEX12,H2AFY2,MAJIN,TTN,DDX3X,MAU2,TADA2B,XRCC5,ZCWPW1,STAG3,UPF1,HIRA,RNF4,TUBG1,MAPK1,DDX11,KDM5A,PADI2,P3H4,FOXP3,ACTB,ZBTB1,AKAP8L,TSPYL2,AKAP8,PARP1,KDM5C,PHF8,ANAPC4,GNL3L,SOX15,KPNB1,WRAP53,SETD1A,DPF3,KDM6B,SMG5,YLPM1,CTC1,SYCE2,PIF1,MAPK3,NAP1L2,RAB11A,LCMT1,NRDE2,RAD51C,SFPQ,G3BP1,YY1,NCOR1,RAD51D,METTL4,	grey	VSMC_M10
GO:0000070	1.00	0.00	41	143	mitotic sister chromatid segregation	BP	1	VPS4B,ZNF207,CHMP2A,CDK5RAP2,PIBF1,DYNC1LI1,ANAPC15,IK,USP44,CHAMP1,CHMP2B,SLF1,ANAPC5,ANAPC7,CHMP4C,KATNB1,CHMP7,SLF2,HECW2,DIS3L2,NSL1,POGZ,TTN,MAU2,TUBG1,AKAP8L,AKAP8,ANAPC4,KPNB1,RAB11A,LCMT1,PSMG2,NAA10,WRAP73,CHMP1A,PSRC1,VPS4A,AURKC,DUSP1,APC,CDC26	grey	VSMC_M10
GO:0048519	1.00	0.00	1952	3961	negative regulation of biological process	BP	1	ADNP2,NFATC1,NME1,SERPINB8,SERPINB2,VPS4B,PHLPP1,ORMDL2,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,BAZ2A,C18orf54,TNFAIP8,LRP1,SEMA6A,SHMT2,EYA4,PGGT1B,GLI1,YTHDC2,B4GALT7,PIP4K2C,TNFAIP3,AGAP2,HECA,CYP27B1,AVIL,PLAGL1,USP15,EPM2A,SRGAP1,TBC1D30,MRNIP,ENPP3,HELB,TRIM39,PPP1R10,MDM1,ZBTB2,ESR1,FRS2,CNOT2,MDC1,IER3,TSPAN8,CNOT6,RIDA,STK3,ZNF207,OSR2,FBXO43,PABPC1,MAPK8IP2,SNW1,ZNF706,PHAX,APOM,MPIG6B,SLC12A2,HSPA1B,FZD6,ZBTB12,SKIV2L,DXO,MOV10L1,EIF3E,PNLDC1,GRAMD4,PRRT1,PRKN,PACRG,RNF5,AGER,PPARA,PDE10A,FBLN1,HLA-DOB,TNFRSF11B,TSPO,GDF9,GOPC,MRPL13,RGL2,FSTL4,TCF7,PHF1,SYNGAP1,UBE2B,BAK1,XRCC6,NCOA7,MTSS1,CSDC2,PITX1,TRIB1,MYC,TOB2,SMAD5,ASAP1,L3MBTL3,L3MBTL2,LEMD2,AGO2,H3F3C,PTK2,C6orf106,PTCH1,TNRC6B,LY6E,AKR1B1,ATF4,TUT7,MAPK15,AGTPBP1,CBX7,APOBEC3H,PLXNA4,GTPBP1,MAPK14,NTRK2,CBY1,PODXL,NRBP2,STK38,PLA2G6,PICK1,SOX10,PI16,PIM1,ZC3HC1,TMPRSS6,EXOSC4,SMO,TTC39B,HSF1,DAAM2,FOXP4,MDFI,CCND3,MYH9,FOXH1,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,TEK,POT1,GPR37,FBXO7,RORB,LMOD2,ALDH1A1,CRY1,ABHD17B,SRF,TTBK1,BAG1,ZNF318,NFX1,ADAM22,DLK2,XPO5,CNTFR,CDK6,SMARCA2,SLC25A27,RFX3,KIT,SLC1A1,TNFRSF21,NCK2,FHL2,IL1R2,TFAP2B,ROR2,NFIL3,SEMA4D,GAPDH,CNOT11,KIAA1211,S1PR3,TMEM14A,RGP1,PDCL3,HINT2,WNK2,KLHL31,OGN,CHMP2A,EXOSC3,SEMA4C,RPS14,MEOX2,ZNF550,SOSTDC1,TMOD1,BEND6,ZNF268,RAB23,PLEKHH2,NLRP5,ABCG5,CAT,SVBP,ABCG8,LRPPRC,CLDN19,SIX2,DNAJA1,IL11,S	grey	VSMC_M10
GO:0048731	1.00	0.00	1732	3556	system development	BP	1	ADNP2,NFATC1,NME1,ITGA7,PHLPP1,ERBB3,SMARCC2,SLC39A5,NEDD4L,ATP8B1,ONECUT2,TCF4,HSD17B4,LRP1,SEMA6A,EYA4,STAC3,GLI1,N4BP3,KIF5A,TNFAIP3,HECA,CYP27B1,ADGRG6,AVIL,MAML1,MDM1,ATAT1,ESR1,FRS2,RAB21,RIDA,STK3,OSR2,MAPK8IP2,SNW1,TIAM2,ARID1B,ADM2,MPIG6B,SLC12A2,HSPA1B,SYNJ2,FZD6,RIMS2,IGF2R,BRD1,MAP3K4,PRKN,QKI,AGER,PPARA,HLA-DRA,TNFRSF11B,IL5,BRD2,SULT4A1,COL11A2,TSPO,GDF9,UQCRQ,VGLL2,CEP85L,VPS52,TBC1D32,FSTL4,TCF7,SYNGAP1,CCDC134,BAK1,XRCC6,MTSS1,PITX1,RSPO3,WASHC5,ACO2,TRIB1,MYC,TOB2,SMAD5,ASAP1,LRRC6,L3MBTL3,KLHL3,LEMD2,AGO2,H3F3C,GFRA3,PTK2,HSD17B3,PTCH1,ANKS1A,FANCC,LY6E,AKR1B1,EXOC4,ATF4,TAB1,AGTPBP1,PLXNA4,SUN2,MAPK14,NTRK2,CBY1,DMC1,PODXL,NRBP2,CSNK1E,CPNE5,PICK1,KDM4C,SOX10,PI16,MICALL1,PIM1,CKB,MFNG,RAC2,SMO,ZDHHC21,BNC2,HSF1,DAAM2,MDFI,TFEB,KCP,MYH9,FOXH1,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,LARGE1,FBXO7,RORB,ZFAND5,PTK7,GDA,CEMIP2,SRF,TTBK1,ADAM22,GABRA1,APBA1,FZD1,CNTFR,FANCG,CDK6,SMARCA2,SLC25A27,RFX3,KIT,SLC1A1,ADGRF1,TNFRSF21,NCK2,SGCE,FHL2,TFAP2B,ROR2,NFIL3,SEMA4D,DLX5,EFHC1,PPAT,PDCL3,C1GALT1,NINJ1,CCIN,OMD,PRDX1,ETV1,ADGRL3,EXOSC3,SEMA4C,SHB,RPS14,CNNM4,TDRD7,MEOX2,SOSTDC1,TMOD1,BEND6,RAB23,ANKS6,CAT,SVBP,SIX2,HIVEP3,PLPPR1,TMEM190,IL11,COL9A1,BRSK1,SMAP1,TNNI3,EPAS1,RDH13,RIMS1,EPCAM,ABCB5,MSH2,CD109,MBOAT7,TMEM30A,DNAH11,RAPGEF5,IGF2BP3,FKTN,RTN4,RAD23B,FPR2,KCNQ4,GSDME,PNPT1,KLK	grey	VSMC_M10

GO:0007059	1.00	0.00	102	288	chromosome segregation	BP	1	VPS4B,ZNF207,UBE2B,MAPK15,DMC1,CHMP2A,MCMBP,PPP2R1A,TRAPPC12,CDK5RAP2,CCDC155,PUM2,SETDB2,BEX4,ERCC2,MLH1,PIBF1,CCNB1IP1,DYNC1LI1,SIRT2,ANAPC15,IK,SIRT7,NEK11,USP44,TEX15,CHAMP1,CIAO1,MOS,TTL,CHMP2B,SLF1,FBXW7,ANAPC5,M1AP,ANAPC7,CHMP4C,CSNK2A2,KATNB1,TOP1,ABRAXAS1,CHMP7,SYCP1,SLF2,AC112128.1,HECW2,DIS3L2,AXIN2,CCDC36,KLHDC8B,SPO11,NSL1,HORMAD2,POGZ,ABRAXAS2,TEX12,MAJIN,TTN,DDX3X,MAU2,ZCWPW1,STAG3,TUBG1,DDX11,P3H4,AKAP8L,AKAP8,RGS14,ANAPC4,SEPT1,KPNB1,EME1,NDEL1,SYCE2,RAB11A,LCMT1,RAD51C,SFPQ,RIOK3,ERCC4,PSMG2,RMI2,SLX4,NAA60,NAA10,WRAP73,MEIOB,CHMP1A,PSRC1,VPS4A,CTCF,MSH4,CIAO2B,AURKC,RNF212B,AGO4,SYCE1L,DUSP1,APC,CDC26,CENPX,GEM	grey	VSMC_M10
GO:0048518	1.00	0.00	2248	4533	positive regulation of biological process	BP	1	ADNP2,NFATC1,ZNF407,MTCH2,CD226,NME1,VPS4B,ERBB3,ZC3H10,SMARCC2,NEDD4L,PAN2,ONECUT2,MIP,ARPC3,TCF4,TNFAIP8,LRP1,STX7,RPS12,SEMA6A,SHMT2,EYA4,STAC3,PGGT1B,GLI1,YTHDC2,MARS,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,HEBP2,TSPAN31,CYP27B1,AVIL,PLAGL1,USP15,EPM2A,MAML1,MRNIP,ENPP3,TRIM39,PPP1R10,ATAT1,RMND1,CPSF6,YEATS4,ESR1,FRS2,MYRFL,CNOT2,RAB21,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,MAPK8IP2,SNW1,TIAM2,ARID1B,ADM2,SLC12A2,HSPA1B,RIMS2,IGF2R,DXO,EIF3E,ZBED4,BRD1,PNLDC1,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,QKI,AGER,PPARA,GPSM3,HLA-DRA,FBLN1,HLA-DOB,MED30,HLA-DMA,IL5,HLA-DPB1,RXRB,TSPO,GDF9,VGLL2,ROS1,RGL2,HSF2,DERL1,SKP1,PHF1,TNFRSF13C,UBE2B,BAK1,RNF217,XRCC6,NCOA7,MTSS1,PITX1,RSPO3,RNF146,WASHC5,TRIB1,MYC,TOB2,SMAD5,ASAP1,EPB41L2,MCHR1,JMJD4,AGO2,PRXL2C,GRM4,HABP4,H3F3C,PTK2,GPR20,PTP4A3,PTCH1,TNRC6B,AKR1B1,ZC3H3,ATF4,TUT7,TAB1,MAPK15,AGTPBP1,PLXNA4,SUN2,GTPBP1,MAPK14,NTRK2,MAPK13,TOMM22,PODXL,CSNK1E,CPNE5,PLA2G6,GKAP1,BAIAP2L2,PICK1,C6orf89,KDM4C,SOX10,PIM1,CDC42EP1,MFNG,NRF1,RAC2,TMPRSS6,EXOSC4,SMO,HSF1,DAAM2,NFYA,TFEB,PLIN2,IRF5,MED20,KCP,CCND3,MYH9,FOXH1,GUCA1B,GPT,CDKN2A,ZNF16,IFT74,CHRNA3,TEK,BICRAL,LINGO2,POT1,GPR37,FBXO7,RORB,LMOD2,ZNF300,PRDM4,CRY1,PTK7,DMTF1,ABHD17B,SRF,ABCB1,TTBK1,ZNF318,CFAP69,XPO5,FZD1,CNTFR,TEC,LRRD1,CCL27,SLAIN2,SLC35B2,OCIAD1,CDK6,SUPT3H,SMARCA2,ENPP4,SLC25A27,RFX3,KIT,SLC1A1,TNFRSF21,NCK2,PLGRKT,TFAP2B,SPTLC1,R	grey	VSMC_M10
GO:0009987	1.00	0.00	6132	11676	cellular process	BP	1	ADNP2,NFATC1,ATP9B,ZNF236,ZNF407,CNDP1,TIMM21,MTCH2,CD226,NME1,SERPINB8,SERPINB2,ITGA7,RDH5,VPS4B,KDSR,PHLPP1,ORMDL2,SUOX,ERBB3,SEC11C,ZC3H10,SMARCC2,SLC39A5,NEDD4L,PAN2,ATP8B1,FECH,ONECUT2,MIP,GLS2,ARPC3,BAZ2A,TCF4,CCDC68,C18orf54,RDH16,POLI,TAC3,MYO1A,HSD17B4,NEMP1,TNFAIP8,RNMT,LRP1,STX7,SLC18B1,RPS12,SEMA6A,SHMT2,EYA4,LVRN,STAC3,AP3S1,ATG12,TBPL1,FEM1C,SLC2A12,PGGT1B,TRIM36,ALDH8A1,GLI1,YTHDC2,ARHGAP9,HBS1L,MARS,B4GALT7,RMND5B,KIF5A,PDE7B,MAP7,CLK4,PIP4K2C,MAP3K5,SLC26A10,PEX7,B4GALNT1,RPA3,TNFAIP3,AGAP2,HEBP2,NHSL1,TSPAN31,REPS1,HECA,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,AIG1,ADAT2,PEX3,ATP23,SLC16A7,PLAGL1,USP15,EPM2A,FBXO30,RXYLT1,SRGAP1,CANX,MAML1,LTC4S,TBC1D30,MRNIP,ENPP3,ATP5MGL,HELB,TBC1D9B,KATNA1,TRIM39,RPP21,PPP1R10,MDM1,ATAT1,CPM,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,CCDC170,ESR1,FRS2,GFPT2,MYRFL,CNOT2,MDC1,IER3,ZFC3H1,RAB21,TPH2,CNOT6,RIDA,C6orf15,NIPAL2,STK3,ZNF207,OSR2,PRR16,SNCAIP,PRRC2A,FBXO43,MIOX,SNX31,PABPC1,MAPK8IP2,SNW1,TIAM2,TFB1M,ZNF706,CPT1B,ALDH7A1,PHAX,MARCH3,APOM,ABHD16A,ARID1B,ADM2,MPIG6B,ZDHHC14,SLC12A2,HSPA1B,SYNJ2,SERAC1,TULP4,FZD6,RIMS2,ZBTB12,DPYS,SKIV2L,SF3A3,TUBGCP6,IGF2R,SELENOO,DXO,MOV10L1,EIF3E,SLC27A6,ALG12,CYP21A2,EMC2,ZBED4,TMEM74,BRD1,ADAMTS19,LYRM7,CDC42SE2,EBAG9,PNLDC1,KCNV1,TNXB,GRAMD4,MAP3K4,PRRT1,AGPAT4,PPT2,PRKN,PACRG,AGPAT1,QKI,RNF5,AGER,TRMU,PPARA,GPSM3,PDE10A,ACSL6,HLA-DRA,FBLN1,HLA-	grey	VSMC_M10
GO:0007049	1.00	0.00	601	1405	cell cycle	BP	1	VPS4B,SLC39A5,PGGT1B,TRIM36,GLI1,YTHDC2,RPA3,TNFAIP3,HECA,CYP27B1,PLAGL1,MRNIP,KATNA1,TRIM39,PPP1R10,MDM1,YEATS4,MDC1,RIDA,ZNF207,FBXO43,HSPA1B,TUBGCP6,MOV10L1,TAF2,KIF3A,SEPT8,SEPT3,UBE2B,BAK1,WASHC5,MYC,EPB41L2,PTCH1,MAPK15,SUN2,MAPK14,UHRF2,MAPK13,DMC1,C6orf89,PIM1,ZC3HC1,HSF1,CNTLN,FBXL6,CCND3,MYH9,CDKN2A,ZNF16,FBXO7,KLHDC3,CRY1,DMTF1,ABCB1,TTBK1,ZNF318,CDK14,SEPT10,CDK6,HEPACAM2,FAM32A,GADD45G,EFHC1,CDK20,PPAT,MITD1,CHMP2A,MCMBP,ZNF268,NLRP5,FOXJ3,BRSK1,PRKCE,MSH2,SPTBN1,PHIP,PNPT1,HOXA13,ANKRD17,CXCL8,XPO1,EPGN,CASP8AP2,CEP68,ETAA1,TRAPPC12,TGFA,LSM10,MED25,KLF11,EGFR,TRIM32,CDK5RAP2,HACE1,CNTRL,LPIN1,CCDC155,CCNY,SDCBP,MAPRE1,CDK19,SPRY1,FOXE3,TPRA1,DNMT3A,SETDB2,RCBTB1,CCDC61,SOX9,TOPAZ1,ERCC1,NUDT15,XPC,ERCC2,ERCC3,CLASP2,DDIAS,MAPRE3,SUV39H2,PLK3,MLH1,CDC123,LLGL2,RALB,STEAP3,UBE2E2,XRCC2,DACH1,PIBF1,PAXIP1,POU4F1,KIZ,PPP1CB,SPRY2,TADA3,CCNB1IP1,AKT2,DYNC1LI1,THAP1,CEP295NL,PPME1,SIRT2,NEK10,ZMYND11,RPTOR,TCIM,ANAPC15,SRA1,PLCB1,IK,SIRT7,MCM8,PRNP,ING1,NEK11,NUDT16,BTG1,WTAP,CLIC1,CDKL4,USP44,TFDP1,DDRGK1,WRN,TEX15,TAF10,CHAMP1,MTA3,PRKDC,ERCC6,CEP63,NSFL1C,STK33,PLK2,MOS,TTL,KIF3B,FAM107A,IL1A,NR4A1,ACVR1B,CEBPA,CSPP1,DCDC1,USP39,TFDP2,CDK7,CASP3,RAD17,CHMP2B,ATR,ING2,CEP44,HPGD,CLIP1,SLF1,CEP250,ARNTL,FBXW7,CETN3,FZD3,BTG3,ANAPC5,M1AP,NUGGC,PKIA,CCNH,HTRA2,ANAPC7,CELF1,CCNJ,RAD9B,GINS3,CHMP4C,CSNK2A2,RTKN,MCPH1,ADAMTS	grey	VSMC_M10

GO:0050794	1.00	0.00	3863	7581	regulation of cellular process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,MTCH2,CD226,NME1,SERPINB8,SERPINB2,ITGA7,VPS4B,PHLPP1,ORMDL2,ERBB3,ZC3H10,SMARCC2,SLC39A5,NEDD4L,PAN2,ATP8B1,ONECUT2,MIP,GLS2,ARPC3,BAZ2A,TCF4,CCDC68,C18orf54,TAC3,TNFAIP8,LRP1,STX7,RPS12,SEMA6A,SHMT2,EYA4,LVRN,STAC3,AP3S1,PGGT1B,TRIM36,GLI1,YTHDC2,ARHGAP9,HBS1L,MARS,B4GALT7,PDE7B,CLK4,PIP4K2C,MAP3K5,RPA3,TNFAIP3,AGAP2,HEBP2,TSPAN31,HECA,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,PLAGL1,USP15,EPM2A,SRGAP1,MAML1,TBC1D30,MRNIP,ENPP3,HELB,TRIM39,PPP1R10,MDM1,ATAT1,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,FRS2,MYRFL,CNOT2,MDC1,IER3,RAB21,CNOT6,RIDA,STK3,ZNF207,OSR2,PRR16,SNCAIP,FBXO43,PABPC1,MAPK8IP2,SNW1,TIAM2,ZNF706,PHAX,APOM,ARID1B,ADM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,ZBTB12,IGF2R,DXO,EIF3E,ZBED4,BRD1,CDC42SE2,EBAG9,PNLDC1,KCNV1,TNXB,GRAMD4,MAP3K4,PRRT1,PRKN,PACRG,AGPAT1,QKI,RNF5,AGER,PPARA,GPSM3,PDE10A,HLA-DRA,FBLN1,HLA-DOB,MED30,TNFRSF11B,HLA-DMA,IL5,BRD2,HLA-DPB1,SEPT8,RXRB,TSPO,GDF9,VGLL2,ROS1,GOPC,MRPL13,TBC1D32,RGL2,FSTL4,HSF2,DERL1,TCF7,SKP1,PHF1,TNFRSF13C,SYNGAP1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,MTSS1,CSDC2,CATSPER3,PITX1,RSPO3,RNF146,WASHC5,AL096711.2,TRIB1,CXCL14,MYC,TOB2,SMAD5,ASAP1,L3MBTL3,L3MBTL2,EPB41L2,MCHR1,AKAP7,FAM13B,OBSCN,JMJD4,LEMD2,AGO2,PRXL2C,GRM4,HABP4,H3F3C,GFRA3,PTK2,C6orf106,KDM3B,GPR20,PTP4A3,PTCH1,TNRC6B,ANKS1A,LY6E,AKR1B1,GRAP2,SCUBE3,ZC3H3,EXOC4,ATF4,TUT7,TAB1,SYN	grey	VSMC_M10
GO:0051301	1.00	0.00	185	525	cell division	BP	1	VPS4B,TRIM36,KATNA1,ZNF207,SEPT8,SEPT3,WASHC5,MYC,EPB41L2,PTCH1,ZC3HC1,CCND3,MYH9,ZNF16,CDK14,SEPT10,CDK6,HEPACAM2,KIT,EFHC1,CDK20,MITD1,CHMP2A,MCMBP,NLRP5,CAT,MACC1,PRKCE,SPTBN1,AKNA,TGFA,PTN,ITGB1BP1,POU3F3,CNTRL,CCNY,MAPRE1,INTU,TPRA1,BMI1,RAB10,SETDB2,TOPAZ1,ERCC2,CLASP2,MAPRE3,PLK3,CDC123,LLGL2,RALB,NUMBL,PPP1CB,DYNC1LI1,SIRT2,ANAPC15,SPART,USP44,CEP63,PLK2,KIF3B,IL1A,CSPP1,DCDC1,USP39,CDK7,CHMP2B,ING2,CETN3,ANAPC5,VEGFC,ANAPC7,CHMP4C,RTKN,USP16,KATNB1,SEPT11,CCNG2,FGF5,TOP1,NKX3-1,CHMP7,BIN3,ZFYVE19,SYCP1,TUBA1A,TENT4B,IGF2,KIF13A,PRDM15,FIGN,AC112128.1,CCND1,TGFB2,PPP2R2D,KLHL42,DIS3L2,INTS13,DYRK3,EPB41,KLHDC8B,YTHDF2,CHEK2,CIB1,KDF1,SFN,NSL1,FZD7,OSM,CABLES2,POGZ,ABRAXAS2,SEPT2,SENP5,SETD2,SSSCA1,HMCN1,STOX1,SUSD2,DIXDC1,MAU2,EFHC2,USP37,AHCTF1,RGS14,ANAPC4,SEPT1,BOD1L2,CNTROB,PGF,SYCE2,ESRRB,NAP1L2,RAB11A,MYH10,TIPIN,NOX5,NRDE2,CALM1,GAREM1,CABLES1,KLHL13,LIG3,EVI2B,UNC119,DOCK7,ZNF449,FSD1,FZR1,TLE6,SAPCD2,KLHL21,SPIRE2,CHMP1A,GNAI3,PSRC1,GPSM2,CDC14A,SPOUT1,SH3GLB1,VPS4A,RHOA,AURKC,SYCP3,PLK5,OOEP,STAMBP,ITGB3BP,POU3F2,CCSAP,RNF8,YBX1,APC,RALA,CDC26,ZFP36L2,CENPX,BRCC3,EREG,TUBA1C,PARD6A,PDXP,FGF1,CINP,PDGFD,ARPP19	grey	VSMC_M10
GO:0071840	1.00	0.00	2347	4827	cellular component organization or biogenesis	BP	1	ADNP2,ATP9B,TIMM21,NME1,VPS4B,ORMDL2,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,MIP,ARPC3,BAZ2A,TCF4,CCDC68,MYO1A,NEMP1,LRP1,STX7,SEMA6A,SHMT2,ATG12,TBPL1,TRIM36,B4GALT7,KIF5A,MAP7,PIP4K2C,PEX7,RPA3,TNFAIP3,AGAP2,HEBP2,CYP27B1,AVIL,PEX3,ATP23,TBC1D30,HELB,KATNA1,PPP1R10,MDM1,ATAT1,CPSF6,YEATS4,CCDC170,ESR1,CNOT2,RAB21,CNOT6,C6orf15,STK3,ZNF207,PRR16,SNCAIP,FBXO43,MAPK8IP2,TIAM2,TFB1M,APOM,ARID1B,SLC12A2,HSPA1B,SYNJ2,SERAC1,RIMS2,SF3A3,TUBGCP6,MOV10L1,EIF3E,EMC2,ADAMTS19,LYRM7,EBAG9,KCNV1,TNXB,MAP3K4,PRRT1,PRKN,RNF5,AGER,PPARA,HLA-DRA,FBLN1,HLA-DOB,UTP23,TNFRSF11B,HLA-DMA,IL5,BRD2,PARVG,PNPLA3,KIF3A,SULT4A1,HLA-DPB1,COL11A2,SEPT8,TSPO,SHROOM1,GDF9,ROS1,HSD17B8,COL14A1,MCM9,ASF1A,A4GALT,HSPA4,TBC1D32,RRP7A,FSTL4,NDUFA6,PHF1,SYNGAP1,UBE2B,BAK1,FAM91A1,FER1L6,XRCC6,MTSS1,WASHC5,MYC,ASAP1,LRRC6,L3MBTL3,L3MBTL2,EPB41L2,OBSCN,JMJD4,LEMD2,AGO2,HABP4,H3F3C,GFRA3,PTK2,PTCH1,TSNARE1,FANCC,EXOC4,ISCA1,SYNGR1,MAPK15,GOLM1,AGTPBP1,CBX7,PLXNA4,SUN2,MAPK14,NTRK2,TOMM22,CBY1,DMC1,PUF60,PODXL,PSMD5,CPNE5,PLA2G6,BAIAP2L2,PICK1,KDM4C,PI16,MICALL1,EIF3L,BTBD9,MPDZ,CDC42EP1,RAC2,TMPRSS6,STRIP2,EXOSC4,GPAA1,SMO,TSPAN33,HSF1,DAAM2,CNTLN,FLNC,TFEB,TAF8,MYH9,CDKN2A,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,GNMT,PEX6,TRPM6,POT1,FBXO7,KLHDC3,LMOD2,PTK7,ABHD17B,SRF,ABCB1,TTBK1,TJAP1,NOL6,CFAP69,GTPBP10,GABRA1,WASHC4,APBA1,FZD1,MTERF1,C12orf45,PGM5,CCL27,SLAIN	grey	VSMC_M10
GO:0140014	1.00	0.00	81	244	mitotic nuclear division	BP	1	VPS4B,ZNF207,FBXO43,HSPA1B,CHMP2A,PHIP,HOXA13,EPGN,TGFA,CDK5RAP2,CCDC61,CLASP2,PIBF1,DYNC1LI1,SIRT2,ANAPC15,IK,SIRT7,USP44,CHAMP1,NSFL1C,KIF3B,IL1A,CHMP2B,SLF1,ANAPC5,ANAPC7,CHMP4C,USP16,KATNB1,ABRAXAS1,CHMP7,SLF2,NPM2,IGF2,AC112128.1,HECW2,PPP2R2D,DIS3L2,EGF,KLHDC8B,CHEK2,NSL1,POGZ,EPS8,ABRAXAS2,CD28,CDKN1B,TOGARAM1,TTN,MAU2,TUBG1,OBSL1,AKAP8L,AKAP8,ANAPC4,KPNB1,NDEL1,RAB11A,LCMT1,INSR,TOM1L2,PSMG2,CEP192,NAA10,WRAP73,CHMP1A,PSRC1,CDC14A,VPS4A,RHOA,AURKC,DUSP1,CCSAP,RGCC,NME6,APC,CDC26,EREG,PDXP,DRG1	grey	VSMC_M10

GO:0000278	1.00	0.00	283	729	mitotic cell cycle	BP	1	VPS4B,TRIM36,YTHDC2,RPA3,HECA,MRNIP,TRIM39,PPP1R10,YEATS4,MDC1,ZNF207,FBXO43,HSPA1B,TUBGCP6,TAF2,PTCH1,SUN2,HSF1,FBXL6,CCND3,CDKN2A,FBXO7,ABCB1,CDK14,CDK6,EFHC1,PPAT,MITD1,CHMP2A,ZNF268,BRSK1,MSH2,SPTBN1,PHIP,HOXA13,ANKRD17,EPGN,TGFA,LSM10,KLF11,EGFR,CDK5RAP2,LPIN1,CCNY,SDCBP,SPRY1,TPRA1,DNMT3A,SETDB2,CCDC61,NUDT15,XPC,ERCC2,ERCC3,CLASP2,PLK3,UBE2E2,XRCC2,PIBF1,SPRY2,TADA3,DYNC1LI1,THAP1,PPME1,SIRT2,RPTOR,ANAPC15,SRA1,PLCB1,IK,SIRT7,NEK11,BTG1,USP44,TFDP1,TAF10,CHAMP1,MTA3,PRKDC,NSFL1C,STK33,PLK2,TTL,KIF3B,FAM107A,IL1A,ACVR1B,DCDC1,RAD17,CHMP2B,CLIP1,SLF1,CEP250,FZD3,BTG3,ANAPC5,PKIA,ANAPC7,CCNJ,RAD9B,GINS3,CHMP4C,RTKN,MCPH1,ADAMTS1,USP16,KATNB1,CCNG2,BACH1,NBN,USH1C,PBRM1,NKX3-1,ABRAXAS1,CHMP7,DONSON,TUBB2A,ZFYVE19,CCNJL,PIDD1,TUBGCP5,PKD2,SLF2,NPM2,TAOK3,TUBA1A,LZTS1,CDK18,IGF2,GBF1,FBXL15,SIK1,HYAL1,AC112128.1,PPP3CA,HECW2,CCND1,TERT,SBDS,PPP2R2D,DIS3L2,INTS13,TBCE,GIGYF2,EGF,KLHDC8B,CHEK2,PSME1,RTF2,CACUL1,USP2,TUBGCP4,CIB1,NSL1,CDK15,ANGEL2,POGZ,EPS8,ABRAXAS2,CD28,SYF2,RTEL1,CDKN1B,DLG1,OVOL1,SETD2,SSSCA1,STOX1,BCL6,TOGARAM1,TTN,DBF4B,BRINP2,MEN1,DDX3X,MAU2,MEPCE,PTPN6,EFHC2,ECD,HTT,PSME3,CLTCL1,USP37,TUBG1,CEP126,STAT5B,OBSL1,PIM2,AKAP8L,AKAP8,TUBA8,DDB1,PHF8,RGS14,ANAPC4,RAD51B,UIMC1,KPNB1,CNTROB,FOXO4,FBXL22,CTC1,EME1,MUC1,TAOK2,NDEL1,ESRRB,RAB11A,MYH10,TIPIN,SMAD3,KDM8,LCMT1,FOXN3,NRDE2,CALM1,RAD51C,PRKCB,DNM2,	grey	VSMC_M10
GO:1903047	1.00	0.00	231	608	mitotic cell cycle process	BP	1	VPS4B,TRIM36,MRNIP,TRIM39,PPP1R10,MDC1,ZNF207,FBXO43,HSPA1B,TAF2,SUN2,FBXL6,CCND3,CDKN2A,FBXO7,ABCB1,CDK14,CDK6,EFHC1,PPAT,MITD1,CHMP2A,BRSK1,MSH2,SPTBN1,PHIP,HOXA13,ANKRD17,EPGN,TGFA,LSM10,KLF11,EGFR,CDK5RAP2,LPIN1,CCNY,SPRY1,TPRA1,CCDC61,XPC,ERCC2,ERCC3,CLASP2,PLK3,UBE2E2,PIBF1,SPRY2,DYNC1LI1,PPME1,SIRT2,RPTOR,ANAPC15,PLCB1,IK,SIRT7,NEK11,USP44,TFDP1,TAF10,CHAMP1,MTA3,PRKDC,NSFL1C,STK33,PLK2,KIF3B,FAM107A,IL1A,ACVR1B,DCDC1,RAD17,CHMP2B,SLF1,ANAPC5,PKIA,ANAPC7,CCNJ,RAD9B,GINS3,CHMP4C,RTKN,MCPH1,ADAMTS1,USP16,KATNB1,CCNG2,BACH1,NBN,USH1C,ABRAXAS1,CHMP7,DONSON,ZFYVE19,CCNJL,PIDD1,PKD2,SLF2,NPM2,TAOK3,LZTS1,CDK18,IGF2,FBXL15,HYAL1,AC112128.1,PPP3CA,HECW2,CCND1,TERT,SBDS,PPP2R2D,DIS3L2,INTS13,TBCE,GIGYF2,EGF,KLHDC8B,CHEK2,PSME1,RTF2,CACUL1,NSL1,CDK15,POGZ,EPS8,ABRAXAS2,CD28,SYF2,RTEL1,CDKN1B,DLG1,SETD2,STOX1,BCL6,TOGARAM1,TTN,DBF4B,DDX3X,MAU2,MEPCE,PTPN6,EFHC2,ECD,HTT,PSME3,USP37,TUBG1,CEP126,OBSL1,PIM2,AKAP8L,AKAP8,DDB1,PHF8,ANAPC4,RAD51B,UIMC1,KPNB1,CNTROB,FOXO4,FBXL22,CTC1,EME1,MUC1,TAOK2,NDEL1,ESRRB,RAB11A,MYH10,TIPIN,KDM8,LCMT1,FOXN3,CALM1,RAD51C,PRKCB,DNM2,DCUN1D3,SIN3A,CAMK2A,INSR,CCL2,TOM1L2,PPP6C,CUL4B,UNC119,PSMG2,CEP192,TAOK1,FSD1,FZR1,NAA10,PKD1,MECP2,WRAP73,SAPCD2,CDK10,CHMP1A,PSRC1,GPSM2,FBXO31,CDC14A,GFI1,VPS4A,FBXL8,NAE1,MIR29A,MIR222,FBXL12,RHOA,AURKC,PLK5,E2F6,RPS27L,SOX4,STAMBP,DUSP1,SPDYA,CCSAP,RGCC,NME6,APC,CDC26,	grey	VSMC_M10
GO:0016043	1.00	0.00	2271	4652	cellular component organization	BP	1	ADNP2,ATP9B,TIMM21,NME1,VPS4B,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,MIP,ARPC3,BAZ2A,TCF4,CCDC68,MYO1A,NEMP1,LRP1,STX7,SEMA6A,SHMT2,ATG12,TBPL1,TRIM36,B4GALT7,KIF5A,MAP7,PIP4K2C,PEX7,RPA3,TNFAIP3,AGAP2,HEBP2,CYP27B1,AVIL,PEX3,ATP23,TBC1D30,HELB,KATNA1,PPP1R10,MDM1,ATAT1,CPSF6,YEATS4,CCDC170,ESR1,CNOT2,RAB21,CNOT6,C6orf15,STK3,ZNF207,PRR16,SNCAIP,FBXO43,MAPK8IP2,TIAM2,APOM,ARID1B,SLC12A2,HSPA1B,SYNJ2,SERAC1,RIMS2,SF3A3,TUBGCP6,MOV10L1,EIF3E,EMC2,ADAMTS19,LYRM7,EBAG9,KCNV1,TNXB,MAP3K4,PRRT1,PRKN,RNF5,AGER,PPARA,HLA-DRA,FBLN1,HLA-DOB,TNFRSF11B,HLA-DMA,IL5,BRD2,PARVG,PNPLA3,KIF3A,SULT4A1,HLA-DPB1,COL11A2,SEPT8,TSPO,SHROOM1,GDF9,ROS1,HSD17B8,COL14A1,MCM9,ASF1A,A4GALT,HSPA4,TBC1D32,RRP7A,FSTL4,NDUFA6,PHF1,SYNGAP1,UBE2B,BAK1,FAM91A1,FER1L6,XRCC6,MTSS1,WASHC5,MYC,ASAP1,LRRC6,L3MBTL3,L3MBTL2,EPB41L2,OBSCN,JMJD4,LEMD2,AGO2,HABP4,H3F3C,GFRA3,PTK2,PTCH1,TSNARE1,FANCC,EXOC4,ISCA1,SYNGR1,MAPK15,GOLM1,AGTPBP1,CBX7,PLXNA4,SUN2,MAPK14,NTRK2,TOMM22,CBY1,DMC1,PUF60,PODXL,PSMD5,CPNE5,PLA2G6,BAIAP2L2,PICK1,KDM4C,PI16,MICALL1,EIF3L,BTBD9,MPDZ,CDC42EP1,RAC2,TMPRSS6,STRIP2,EXOSC4,GPAA1,SMO,TSPAN33,HSF1,DAAM2,CNTLN,FLNC,TFEB,TAF8,MYH9,CDKN2A,RBFOX2,IFT74,CHRNA3,TEK,LRRC4,PRPH2,LINGO2,GNMT,PEX6,TRPM6,POT1,FBXO7,KLHDC3,LMOD2,PTK7,ABHD17B,SRF,ABCB1,TTBK1,TJAP1,CFAP69,GABRA1,WASHC4,APBA1,FZD1,MTERF1,C12orf45,PGM5,CCL27,SLAIN2,PEX1,FANCG,	grey	VSMC_M10

GO:0022402	1.00	0.00	399	951	cell cycle process	BP	1	VPS4B,SLC39A5,TRIM36,GLI1,YTHDC2,CYP27B1,MRNIP,TRIM39,PPP1R10,MDM1,MDC1,RIDA,ZNF207,FBXO43,HSPA1B,TUBGCP6,MOV10L1,TAF2,KIF3A,SEPT8,SEPT3,UBE2B,WASHC5,MAPK15,SUN2,MAPK14,DMC1,CNTLN,FBXL6,CCND3,MYH9,CDKN2A,ZNF16,FBXO7,KLHDC3,CRY1,ABCB1,CDK14,SEPT10,CDK6,HEPACAM2,EFHC1,PPAT,MITD1,CHMP2A,MCMBP,NLRP5,FOXJ3,BRSK1,PRKCE,MSH2,SPTBN1,PHIP,HOXA13,ANKRD17,XPO1,EPGN,CEP68,ETAA1,TRAPPC12,TGFA,LSM10,KLF11,EGFR,CDK5RAP2,LPIN1,CCDC155,CCNY,MAPRE1,SPRY1,TPRA1,CCDC61,SOX9,TOPAZ1,ERCC1,XPC,ERCC2,ERCC3,CLASP2,MAPRE3,PLK3,MLH1,LLGL2,UBE2E2,XRCC2,DACH1,PIBF1,PAXIP1,KIZ,SPRY2,CCNB1IP1,DYNC1LI1,CEP295NL,PPME1,SIRT2,NEK10,RPTOR,TCIM,ANAPC15,PLCB1,IK,SIRT7,NEK11,NUDT16,USP44,TFDP1,DDRGK1,WRN,TEX15,TAF10,CHAMP1,MTA3,PRKDC,ERCC6,CEP63,NSFL1C,STK33,PLK2,MOS,TTL,KIF3B,FAM107A,IL1A,ACVR1B,CSPP1,DCDC1,RAD17,CHMP2B,ATR,ING2,CEP44,SLF1,CEP250,FBXW7,CETN3,ANAPC5,M1AP,NUGGC,PKIA,ANAPC7,CCNJ,RAD9B,GINS3,CHMP4C,CSNK2A2,RTKN,MCPH1,ADAMTS1,USP16,KATNB1,SEPT11,CCNG2,BACH1,EIF2AK4,ALMS1,RPRD1B,NBN,USH1C,ABRAXAS1,TMEM67,RAD54B,CHMP7,BIN3,DONSON,ZFYVE19,CCNJL,PIDD1,TUBGCP5,PKD2,SYCP1,SLF2,SYCP2L,NPM2,TAOK3,LZTS1,CDK18,IGF2,KIF13A,FBXL15,HYAL1,HSF2BP,AC112128.1,PPP3CA,HECW2,CCND1,TERT,SBDS,PPP2R2D,PRKAR1A,DIS3L2,AXIN2,INTS13,TBCE,CFL1,DYRK3,GIGYF2,EGF,USP19,CCDC36,KLHDC8B,YTHDF2,GPER1,CHEK2,PSME1,RTF2,CACUL1,SPO11,TUBGCP4,GPR3,C11orf80,NSL1,CDK15,CCDC84,HORMAD2,ATRIP,TXLNG,POGZ,EPS	grey	VSMC_M10
GO:0019538	1.00	0.00	2023	4113	protein metabolic process	BP	1	CNDP1,SERPINB8,SERPINB2,VPS4B,PHLPP1,ERBB3,SEC11C,NEDD4L,PAN2,BAZ2A,TNFAIP8,LRP1,RPS12,SHMT2,EYA4,LVRN,ATG12,FEM1C,PGGT1B,TRIM36,HBS1L,MARS,B4GALT7,RMND5B,CLK4,MAP3K5,TNFAIP3,AGAP2,TSFM,ADGRG6,ATP23,USP15,FBXO30,RXYLT1,CANX,MAML1,MRNIP,TRIM39,ATAT1,CPM,RMND1,ARMT1,YEATS4,GFPT2,MYRFL,CNOT2,CNOT6,RIDA,STK3,PRR16,FBXO43,PABPC1,SNW1,ZNF706,MARCH3,APOM,ADM2,ZDHHC14,HSPA1B,TULP4,SELENOO,EIF3E,ALG12,BRD1,ADAMTS19,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,PRKN,QKI,RNF5,AGER,PPARA,FBLN1,P4HA2,MED30,PSMB8,IL5,BRD2,ZUP1,TSPO,GDF9,ROS1,MRPL13,RPS18,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,RNF146,TRIB1,MYC,SMAD5,KLHL3,XPNPEP3,OBSCN,MRPL55,JMJD4,AGO2,HABP4,RPS10,PTK2,KDM3B,PTP4A3,PTCH1,TNRC6B,ATF4,TUT7,TAB1,ISCA1,MAPK15,RPAP2,AGTPBP1,GTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,PI16,EIF3L,PIM1,ZC3HC1,TMPRSS6,GPAA1,ZDHHC21,TSPAN33,FOXRED2,HSF1,MOCS1,FBXL6,OARD1,ADCK5,USP49,CCND3,OPN1SW,MYH9,PPP1R16A,CDKN2A,APOL4,APOL6,CHRNA3,TEK,LARGE1,GNMT,TRPM6,FBXO7,KLHDC3,ASB15,PRDM4,CRY1,PTK7,ABHD17B,TTBK1,NFX1,ADAM22,NUAK1,PTAR1,CDK14,DCAF12,GTPBP2,TEC,CAPN11,CWH43,CDK6,SUPT3H,USP46,LNX1,KIT,SLC1A1,ST6GAL2,SRD5A3,NCK2,PLGRKT,MRPS9,ERMP1,IL1R2,ROR2,SEMA4D,GAPDH,CNOT11,CDK20,RGP1,PDCL3,C1GALT1,PTPDC1,CHST10,HINT2,WNK2,PHF14,LIPT1,KLHL31,ADH5,FBXO10,EXOSC3,DCAF10,RPS14,KANSL3,CAT,SVBP,LRPPRC,ALG2,SEC61B,CLDN19,E	grey	VSMC_M10
GO:0051716	1.00	0.00	2505	5042	cellular response to stimulus	BP	1	ADNP2,NFATC1,ZNF236,CD226,NME1,ITGA7,PHLPP1,ERBB3,SLC39A5,FECH,ONECUT2,ARPC3,CCDC68,POLI,TAC3,RNMT,LRP1,RPS12,SEMA6A,EYA4,LVRN,STAC3,AP3S1,GLI1,ARHGAP9,HBS1L,MARS,PDE7B,PIP4K2C,MAP3K5,RPA3,TNFAIP3,CYP27B1,ADGRG6,ATP23,USP15,EPM2A,SRGAP1,CANX,MAML1,LTC4S,MRNIP,HELB,TRIM39,PPP1R10,ARMT1,ESR1,FRS2,GFPT2,CNOT2,MDC1,IER3,RAB21,TPH2,STK3,ZNF207,MAPK8IP2,SNW1,TIAM2,APOM,ADM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,IGF2R,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,PACRG,AGPAT1,RNF5,AGER,PPARA,GPSM3,PDE10A,FBLN1,TNFRSF11B,IL5,PNPLA3,HLA-DPB1,RXRB,TSPO,GDF9,ROS1,MCM9,ASF1A,TBC1D32,RGL2,FSTL4,DERL1,TCF7,PHF1,TNFRSF13C,SYNGAP1,UBE2B,BAK1,XRCC6,NCOA7,PMM1,MTSS1,RSPO3,RNF146,TRIB1,CXCL14,MYC,SMAD5,MCHR1,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,HABP4,GFRA3,PTK2,ERCC6L2,KDM3B,GPR20,PTP4A3,PTCH1,ANKS1A,FANCC,LY6E,AKR1B1,GRAP2,SCUBE3,ZC3H3,ATF4,TAB1,SYNGR1,MAPK15,PLXNA4,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,DMC1,NRBP2,STK38,CSNK1E,CPNE5,PLA2G6,GKAP1,PICK1,KDM4C,SOX10,MICALL1,PIM1,ZC3HC1,CDC42EP1,MFNG,RAC2,SMO,ZDHHC21,FOXRED2,TXN2,HSF1,DAAM2,OARD1,MDFI,TFEB,SLC39A4,IRF5,KCP,CCND3,OPN1SW,MYH9,FOXH1,GUCA1B,GPT,LRRC14,CDKN2A,ZNF16,OSTF1,RBFOX2,IFT74,CHRNA3,TEK,GRM8,CHRNA5,POT1,GPR37,FBXO7,RORB,ASB15,ALDH1A1,CRY1,RIC8B,ZFAND5,PTK7,SRF,BAG1,DLK2,TCP11L2,NUAK1,GABRA1,CDK14,FZD1,CNTFR,TEC,TXNRD1,LRRD1,CCL27,PHF24,SLC35B2,OCIAD1,FANCG,CDK6,RCAN2,KIT,SLC1A1,ADGRF1,TNFRSF21,N	grey	VSMC_M10

GO:0044267	1.00	0.00	1824	3725	cellular protein metabolic process	BP	1	CNDP1,SERPINB8,SERPINB2,VPS4B,PHLPP1,ERBB3,SEC11C,NEDD4L,PAN2,BAZ2A,TNFAIP8,LRP1,RPS12,SHMT2,EYA4,ATG12,FEM1C,PGGT1B,TRIM36,HBS1L,MARS,B4GALT7,RMND5B,CLK4,MAP3K5,TNFAIP3,AGAP2,TSFM,ATP23,USP15,FBXO30,RXYLT1,CANX,MAML1,MRNIP,TRIM39,ATAT1,RMND1,ARMT1,YEATS4,GFPT2,CNOT2,CNOT6,RIDA,STK3,PRR16,FBXO43,PABPC1,SNW1,ZNF706,MARCH3,ADM2,ZDHHC14,HSPA1B,TULP4,SELENOO,EIF3E,ALG12,BRD1,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,PRKN,QKI,RNF5,AGER,FBLN1,P4HA2,MED30,PSMB8,IL5,BRD2,TSPO,GDF9,ROS1,MRPL13,RPS18,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,RNF146,TRIB1,MYC,SMAD5,KLHL3,OBSCN,MRPL55,JMJD4,AGO2,HABP4,RPS10,PTK2,KDM3B,PTP4A3,TNRC6B,ATF4,TUT7,TAB1,MAPK15,RPAP2,AGTPBP1,GTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,PI16,EIF3L,PIM1,ZC3HC1,GPAA1,ZDHHC21,FOXRED2,HSF1,MOCS1,FBXL6,OARD1,ADCK5,USP49,CCND3,OPN1SW,MYH9,PPP1R16A,CDKN2A,CHRNA3,TEK,LARGE1,GNMT,TRPM6,FBXO7,KLHDC3,ASB15,PRDM4,CRY1,PTK7,ABHD17B,TTBK1,NFX1,NUAK1,PTAR1,CDK14,DCAF12,GTPBP2,TEC,CWH43,CDK6,SUPT3H,USP46,LNX1,KIT,SLC1A1,ST6GAL2,SRD5A3,NCK2,PLGRKT,MRPS9,IL1R2,ROR2,SEMA4D,GAPDH,CNOT11,CDK20,RGP1,PDCL3,C1GALT1,PTPDC1,HINT2,WNK2,PHF14,LIPT1,KLHL31,ADH5,FBXO10,EXOSC3,DCAF10,RPS14,KANSL3,SVBP,LRPPRC,ALG2,SEC61B,CLDN19,CAMKMT,SRBD1,RIMKLA,DNAJA1,IL11,BRSK1,TMEM246,RNF20,PRKCE,EPAS1,PIGF,CD109,ASB3,SPTBN1,IGF2BP3,FKTN,PPP2R1A,RAD23B,PHIP,FPR2,MTIF2,	grey	VSMC_M10
GO:0006996	1.00	0.00	1414	2943	organelle organization	BP	1	TIMM21,VPS4B,SMARCC2,PAN2,ATP8B1,ONECUT2,ARPC3,BAZ2A,CCDC68,MYO1A,NEMP1,LRP1,STX7,SEMA6A,ATG12,TBPL1,TRIM36,MAP7,PIP4K2C,PEX7,RPA3,TNFAIP3,AGAP2,HEBP2,AVIL,PEX3,ATP23,TBC1D30,HELB,KATNA1,PPP1R10,MDM1,ATAT1,YEATS4,CCDC170,ESR1,CNOT2,CNOT6,ZNF207,FBXO43,ARID1B,HSPA1B,TUBGCP6,MOV10L1,EMC2,LYRM7,TNXB,MAP3K4,PRKN,RNF5,IL5,BRD2,PARVG,PNPLA3,KIF3A,SEPT8,TSPO,SHROOM1,MCM9,ASF1A,HSPA4,TBC1D32,RRP7A,NDUFA6,PHF1,SYNGAP1,UBE2B,BAK1,XRCC6,MTSS1,WASHC5,MYC,ASAP1,LRRC6,L3MBTL3,L3MBTL2,EPB41L2,OBSCN,LEMD2,HABP4,H3F3C,PTK2,TSNARE1,MAPK15,GOLM1,AGTPBP1,CBX7,SUN2,TOMM22,DMC1,PLA2G6,BAIAP2L2,PICK1,KDM4C,MPDZ,CDC42EP1,RAC2,STRIP2,DAAM2,CNTLN,FLNC,TFEB,MYH9,IFT74,TEK,LRRC4,PEX6,POT1,FBXO7,KLHDC3,LMOD2,PTK7,SRF,TJAP1,CFAP69,WASHC4,MTERF1,PGM5,CCL27,SLAIN2,PEX1,FANCG,HEPACAM2,SMARCA2,RFX3,KIT,NCK2,TGFBRAP1,TLN1,GAPDH,KIAA1211,EFHC1,TRAM2,TMEM14A,PDCL3,PTPDC1,FGD3,CCIN,BICD2,COA5,CHMP2A,ZNF135,RPS14,TMOD1,MCMBP,RAB23,PLEKHH2,DYNC2LI1,NLRP5,STX17,CLDN19,CAMKMT,FOXJ3,SCMH1,BRSK1,SDHAF4,PRKCE,EPAS1,STPG4,MSH2,SPTBN1,RTN4,ZNF462,RAD23B,ACTL7A,PHIP,HMGN3,MTIF2,EPB41L4B,PNPT1,UTP3,RUFY3,ACP4,SHANK1,HOXA13,EMC10,LPAR1,CEP162,PPT1,XPO1,EPGN,GGCT,AQP1,EHBP1,MDN1,TMEM17,MYH14,CEP68,WDR92,TRAPPC12,PLEK,TGFA,ITGB1BP1,MET,ADD2,YWHAZ,FUZ,ARHGEF5,TRIM32,ASCC3,CDK5RAP2,EPHA1,VPS41,IQUB,HACE1,ZMYM6,CNTRL,GAB1,LPIN1,CCDC155,MYLK3,VPS35,ATG5,SETD7,SDCBP,FAM49A	grey	VSMC_M10
GO:0050789	1.00	0.00	4033	7907	regulation of biological process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,MTCH2,CD226,NME1,SERPINB8,SERPINB2,ITGA7,VPS4B,PHLPP1,ORMDL2,ERBB3,ZC3H10,SMARCC2,SLC39A5,NEDD4L,PAN2,ATP8B1,ONECUT2,MIP,GLS2,ARPC3,BAZ2A,TCF4,CCDC68,C18orf54,TAC3,TNFAIP8,LRP1,STX7,RPS12,SEMA6A,SHMT2,EYA4,LVRN,STAC3,AP3S1,PGGT1B,TRIM36,GLI1,YTHDC2,ARHGAP9,HBS1L,MARS,B4GALT7,PDE7B,CLK4,PIP4K2C,MAP3K5,RPA3,TNFAIP3,AGAP2,HEBP2,TSPAN31,HECA,CYP27B1,TSFM,ADGRG6,AVIL,HIVEP2,FUCA2,PLAGL1,USP15,EPM2A,SRGAP1,MAML1,TBC1D30,MRNIP,ENPP3,HELB,TRIM39,PPP1R10,MDM1,ATAT1,ZBTB2,RMND1,CPSF6,ARMT1,YEATS4,ESR1,FRS2,MYRFL,CNOT2,MDC1,IER3,TSPAN8,RAB21,CNOT6,RIDA,STK3,ZNF207,OSR2,PRR16,SNCAIP,FBXO43,PABPC1,MAPK8IP2,SNW1,TIAM2,ZNF706,PHAX,APOM,ARID1B,ADM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,ZBTB12,SKIV2L,IGF2R,DXO,MOV10L1,EIF3E,ZBED4,BRD1,CDC42SE2,EBAG9,PNLDC1,KCNV1,TNXB,GRAMD4,MAP3K4,PRRT1,PRKN,PACRG,AGPAT1,QKI,RNF5,AGER,PPARA,GPSM3,PDE10A,HLA-DRA,FBLN1,HLA-DOB,MED30,PSMB8,TNFRSF11B,HLA-DMA,IL5,BRD2,HLA-DPB1,ZUP1,SEPT8,RXRB,TSPO,GDF9,VGLL2,ROS1,GOPC,MRPL13,TBC1D32,RGL2,FSTL4,HSF2,DERL1,TCF7,SKP1,PHF1,TNFRSF13C,SYNGAP1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,MTSS1,CSDC2,CATSPER3,PITX1,RSPO3,RNF146,WASHC5,AL096711.2,TRIB1,CXCL14,MYC,TOB2,SMAD5,ASAP1,L3MBTL3,L3MBTL2,EPB41L2,MCHR1,AKAP7,FAM13B,OBSCN,JMJD4,LEMD2,AGO2,PRXL2C,GRM4,HABP4,H3F3C,GFRA3,PTK2,C6orf106,KDM3B,GPR20,PTP4A3,PTCH1,TNRC6B,ANKS1A,LY6E,A	grey	VSMC_M10

GO:0050896	1.00	0.00	2949	5876	response to stimulus	BP	1	ADNP2,NFATC1,ZNF236,CD226,NME1,SERPINB2,ITGA7,RDH5,VPS4B,PHLPP1,ERBB3,SLC39A5,NEDD4L,FECH,ONECUT2,MIP,ARPC3,CCDC68,POLI,TAC3,RNMT,LRP1,STX7,RPS12,SEMA6A,SHMT2,EYA4,LVRN,STAC3,AP3S1,PGGT1B,GLI1,YTHDC2,ARHGAP9,HBS1L,MARS,KIF5A,PDE7B,MAP7,PIP4K2C,MAP3K5,RPA3,TNFAIP3,CYP27B1,ADGRG6,FUCA2,ATP23,USP15,EPM2A,SRGAP1,CANX,MAML1,LTC4S,MRNIP,ENPP3,HELB,TRIM39,PPP1R10,ARMT1,ESR1,FRS2,GFPT2,CNOT2,MDC1,IER3,TSPAN8,RAB21,TPH2,RIDA,STK3,ZNF207,MAPK8IP2,SNW1,TIAM2,CPT1B,APOM,ADM2,MPIG6B,SLC12A2,HSPA1B,FZD6,RIMS2,IGF2R,BRD1,CDC42SE2,GRAMD4,MAP3K4,PRRT1,PRKN,PACRG,AGPAT1,RNF5,AGER,PPARA,GPSM3,PDE10A,HLA-DRA,FBLN1,HLA-DOB,TAP1,TNFRSF11B,HLA-DMA,IL5,TAF2,PNPLA3,HLA-DPB1,RXRB,TSPO,GDF9,ROS1,MCM9,ASF1A,HSPA4,TBC1D32,RGL2,FSTL4,DERL1,NDUFA6,TCF7,PHF1,TNFRSF13C,SYNGAP1,UBE2B,BAK1,FER1L6,XRCC6,NCOA7,PMM1,MTSS1,RSPO3,RNF146,ACO2,TRIB1,CXCL14,MYC,SMAD5,MCHR1,PKD2L2,AKAP7,FAM13B,OBSCN,LEMD2,PRXL2C,GRM4,HABP4,GFRA3,PTK2,ERCC6L2,C6orf106,KDM3B,GPR20,PTP4A3,PTCH1,ANKS1A,FANCC,LY6E,AKR1B1,GRAP2,SCUBE3,ZC3H3,ATF4,TAB1,SYNGR1,MAPK15,APOBEC3H,PLXNA4,GTPBP1,MAPK14,NTRK2,MAPK13,CBY1,DMC1,NRBP2,STK38,CSNK1E,CPNE5,PLA2G6,GKAP1,PICK1,C6orf89,KDM4C,SOX10,PI16,MICALL1,PIM1,ZC3HC1,CDC42EP1,MFNG,RAC2,EXOSC4,SMO,ZDHHC21,FOXRED2,TXN2,HSF1,DAAM2,FBXL6,OARD1,MDFI,TFEB,PLIN2,SLC39A4,IRF5,KCP,CCND3,OPN1SW,MYH9,FOXH1,GUCA1B,GPT,LRRC14,	grey	VSMC_M10
GO:0044260	1.00	0.00	2976	5916	cellular macromolecule metabolic process	BP	1	ADNP2,NFATC1,ZNF236,ZNF407,CNDP1,NME1,SERPINB8,SERPINB2,VPS4B,PHLPP1,ERBB3,SEC11C,SMARCC2,NEDD4L,PAN2,ATP8B1,ONECUT2,BAZ2A,TCF4,POLI,TNFAIP8,RNMT,LRP1,RPS12,SHMT2,EYA4,ATG12,TBPL1,FEM1C,PGGT1B,TRIM36,GLI1,HBS1L,MARS,B4GALT7,RMND5B,CLK4,MAP3K5,RPA3,TNFAIP3,AGAP2,TSFM,HIVEP2,ATP23,PLAGL1,USP15,FBXO30,RXYLT1,CANX,MAML1,MRNIP,HELB,TRIM39,PPP1R10,ATAT1,ZBTB2,RMND1,ARMT1,YEATS4,ESR1,GFPT2,MYRFL,CNOT2,MDC1,CNOT6,RIDA,STK3,OSR2,PRR16,FBXO43,PABPC1,SNW1,TFB1M,ZNF706,PHAX,MARCH3,ARID1B,ADM2,ZDHHC14,HSPA1B,TULP4,FZD6,ZBTB12,SKIV2L,SELENOO,DXO,MOV10L1,EIF3E,ALG12,ZBED4,BRD1,PNLDC1,TNXB,GRAMD4,MAP3K4,PRRT1,PRKN,QKI,RNF5,AGER,PPARA,PDE10A,FBLN1,P4HA2,MED30,PSMB8,IL5,BRD2,TAF2,RXRB,TSPO,GDF9,VGLL2,ROS1,MCM9,ASF1A,MRPL13,RPS18,HSF2,DERL1,TCF7,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,PMM1,CSDC2,TRMT11,PITX1,RNF146,TRIB1,MYC,TOB2,SMAD5,L3MBTL3,L3MBTL2,KLHL3,OBSCN,MRPL55,JMJD4,AGO2,HABP4,RPS10,PTK2,ERCC6L2,KDM3B,PTP4A3,PTCH1,TNRC6B,FANCC,ATF4,TUT7,TAB1,MAPK15,RPAP2,AGTPBP1,CBX7,APOBEC3H,GTPBP1,MAPK14,JOSD1,NTRK2,UHRF2,MAPK13,CBY1,DMC1,NRBP2,STK38,CSNK1E,PLA2G6,PICK1,C6orf89,KDM4C,SOX10,PI16,EIF3L,PIM1,CMTR1,ZC3HC1,NRF1,TMPRSS6,EXOSC4,GPAA1,SMO,ZDHHC21,SNAPC3,FOXRED2,BNC2,HSF1,MOCS1,FBXL6,OARD1,NFYA,ADCK5,FOXP4,MDFI,TFEB,USP49,IRF5,MED20,CCND3,TAF8,OPN1SW,MYH9,FOXH1,PPP1R16A,LRRC14,CDKN2A,ZNF16,RBFOX2,IFT74,CHRNA3,TEK,BICRAL,LARGE1,GNMT,TRPM6,POT1,F	grey	VSMC_M10
GO:0048522	1.00	0.00	2072	4212	positive regulation of cellular process	BP	1	ADNP2,NFATC1,ZNF407,MTCH2,CD226,NME1,VPS4B,ERBB3,SMARCC2,NEDD4L,PAN2,ONECUT2,MIP,ARPC3,TCF4,TNFAIP8,LRP1,STX7,RPS12,SEMA6A,SHMT2,EYA4,STAC3,PGGT1B,GLI1,YTHDC2,MARS,PIP4K2C,MAP3K5,TNFAIP3,AGAP2,HEBP2,TSPAN31,CYP27B1,AVIL,PLAGL1,USP15,EPM2A,MAML1,MRNIP,TRIM39,PPP1R10,ATAT1,RMND1,CPSF6,YEATS4,ESR1,FRS2,MYRFL,CNOT2,RAB21,CNOT6,RIDA,STK3,OSR2,PRR16,PABPC1,MAPK8IP2,SNW1,TIAM2,ARID1B,SLC12A2,HSPA1B,RIMS2,IGF2R,DXO,EIF3E,ZBED4,BRD1,PNLDC1,GRAMD4,MAP3K4,PRRT1,PRKN,AGPAT1,AGER,PPARA,GPSM3,HLA-DRA,FBLN1,HLA-DOB,MED30,HLA-DMA,IL5,HLA-DPB1,RXRB,TSPO,GDF9,VGLL2,ROS1,RGL2,HSF2,DERL1,SKP1,PHF1,TNFRSF13C,UBE2B,BAK1,RNF217,XRCC6,NCOA7,MTSS1,PITX1,RSPO3,RNF146,WASHC5,TRIB1,MYC,SMAD5,ASAP1,EPB41L2,JMJD4,AGO2,PRXL2C,GRM4,HABP4,H3F3C,PTK2,GPR20,PTP4A3,PTCH1,TNRC6B,AKR1B1,ZC3H3,ATF4,TUT7,TAB1,MAPK15,AGTPBP1,PLXNA4,SUN2,GTPBP1,MAPK14,NTRK2,TOMM22,PODXL,CSNK1E,CPNE5,PLA2G6,GKAP1,BAIAP2L2,PICK1,C6orf89,KDM4C,SOX10,PIM1,CDC42EP1,MFNG,NRF1,RAC2,TMPRSS6,EXOSC4,SMO,HSF1,DAAM2,NFYA,TFEB,IRF5,MED20,KCP,CCND3,MYH9,FOXH1,GUCA1B,GPT,CDKN2A,ZNF16,IFT74,CHRNA3,TEK,BICRAL,LINGO2,POT1,GPR37,FBXO7,RORB,LMOD2,ZNF300,PRDM4,CRY1,PTK7,DMTF1,ABHD17B,SRF,ABCB1,TTBK1,ZNF318,CFAP69,FZD1,CNTFR,TEC,LRRD1,CCL27,SLAIN2,SLC35B2,OCIAD1,CDK6,SUPT3H,SMARCA2,SLC25A27,RFX3,KIT,SLC1A1,NCK2,PLGRKT,TFAP2B,SPTLC1,ROR2,NFIL3,GADD45G,SEMA4D,GAPDH,DLX5,KIAA	grey	VSMC_M10

GO:0006259	1.00	0.00	310	741	DNA metabolic process	BP	1	NME1,BAZ2A,POLI,EYA4,RPA3,ATP23,MRNIP,HELB,PPP1R10,MDC1,MOV10L1,MAP3K4,MCM9,ASF1A,TCF7,UBE2B,XRCC6,MYC,ERCC6L2,FANCC,MAPK15,APOBEC3H,UHRF2,DMC1,CSNK1E,PICK1,EXOSC4,HSF1,POT1,KLHDC3,FANCG,REV1,EXOSC3,STPG4,MSH2,TFPT,RAD23B,FANCL,NT5E,ORC3,CYREN,ETAA1,RNASEH1,EGFR,USP45,ASCC3,CCDC155,REV3L,ORC5,DNMT3A,HMCES,BMI1,PRKD2,CNBP,PHB,CDADC1,ERCC1,NUDT15,XPC,ERCC2,ERCC3,XRCC1,MLH1,MBD4,XRCC2,DACH1,KIN,ZRANB3,PAXIP1,WDR48,FBH1,KPNA2,CCNB1IP1,MGME1,RNF169,FAM168A,PURA,SIRT7,MCM8,SHLD1,AP5S1,TFDP1,WRN,PPP4R2,TEX15,PRKDC,POLR2I,ERCC6,ALKBH3,TOX,ERCC8,DNMT3B,PARP4,GIN1,FOXL2,OTUD4,HPF1,PRIMPOL,CDK7,RAD17,GTF2H2C,ATR,EYA1,NOC3L,SLF1,POLE4,HMBOX1,RAD9B,GINS3,XRCC4,PTK2B,BACH1,MAPKAPK5,TPRKB,DDB2,NBN,THAP9,TOP1,HELQ,ABRAXAS1,SPIDR,RAD54B,WRNIP1,DONSON,PMS1,FTO,SYCP1,SLF2,NPM2,HERC2,POLL,TAOK3,TENT4B,CD40,TEX264,MTRR,DCAF1,HEMK1,FAN1,STN1,CBSL,GLRX2,HSF2BP,LTO1,SP100,TERT,IGHMBP2,TCF7L2,ALKBH2,AXIN2,GAR1,CCDC36,ZGRF1,POLG2,POLG,SPRTN,CHEK2,EYA3,PARP9,RTF2,DTX3L,SPO11,ORC2,PGBD5,CIB1,RECQL,C11orf80,NYNRIN,ATRIP,KCNK2,TDRKH,CD28,RNF168,RTEL1,MGMT,SETD2,TET1,NONO,STOX1,SUPV3L1,BCL6,TEX12,MEN1,APEX2,XRCC5,ASCC1,ZCWPW1,UPF1,POLN,IFFO1,MAPK1,WAS,PMS2,RHNO1,DDX11,RAD52,FOXP3,ZBTB1,PARP1,SHLD2,AP5Z1,DDB1,NVL,PRPF19,GNL3L,RAD51B,FGFR4,UIMC1,EXD2,RNF111,TBX21,WRAP53,SMG5,KAT7,PAGR1,YLPM1,CTC1,EME1,FOS,BATF,KRBA2,PIF1,MAPK3,DNASE2,RNASEH2A,ALKBH1,TIPIN,S	grey	VSMC_M10
GO:0051246	1.00	0.00	913	1953	regulation of protein metabolic process	BP	1	CNDP1,SERPINB8,SERPINB2,ERBB3,NEDD4L,PAN2,TNFAIP8,LRP1,SHMT2,HBS1L,MAP3K5,TNFAIP3,AGAP2,TSFM,MRNIP,TRIM39,RMND1,CNOT2,CNOT6,RIDA,STK3,PRR16,PABPC1,SNW1,ZNF706,HSPA1B,EIF3E,PNLDC1,TNXB,GRAMD4,MAP3K4,PRKN,QKI,AGER,FBLN1,PSMB8,IL5,TSPO,GDF9,MRPL13,DERL1,SKP1,PHF1,UBE2B,BAK1,RNF217,XRCC6,NCOA7,TRIB1,MYC,JMJD4,AGO2,HABP4,PTK2,TNRC6B,ATF4,TUT7,TAB1,AGTPBP1,NTRK2,STK38,CSNK1E,PLA2G6,C6orf89,PI16,HSF1,CCND3,MYH9,PPP1R16A,CDKN2A,CHRNA3,TEK,FBXO7,CRY1,TTBK1,NUAK1,TEC,KIT,SLC1A1,NCK2,PLGRKT,IL1R2,ROR2,SEMA4D,GAPDH,CNOT11,RGP1,PDCL3,HINT2,KLHL31,EXOSC3,RPS14,SVBP,LRPPRC,CLDN19,DNAJA1,IL11,RNF20,PRKCE,EPAS1,CD109,IGF2BP3,FKTN,RTN4,PPP2R1A,RAD23B,PHIP,FPR2,MTIF2,IBTK,PNPT1,ACP4,MOB1B,XPO1,EPGN,NOD1,AREG,AKIRIN2,BMP8A,PM20D2,AQP1,CASP8AP2,PELI1,BMPER,WDR91,ETAA1,RSPO1,EPHA7,NR1H2,TNFSF15,TGFA,ITGB1BP1,VRK3,AGO1,EGFR,HECW1,ARHGEF5,TRIM32,TLR4,ASCC3,EPHA1,HACE1,BCL2L12,IL15,CCNY,VPS35,ATG5,SETD7,ZYG11B,SDCBP,C6orf203,TUT4,FOXO3,NTF4,PUM2,MFSD8,FAF1,FGF21,BRAF,PRKAR2B,HSPE1,SPHK2,DHFR,SPRY1,HDAC2,BBS7,EEFSEC,SLC8A2,RAB7A,BMI1,C5AR1,MKNK1,MOB3C,PRKD2,CST7,CNBP,PHB,ABI1,SOX9,SYMPK,BEX4,NUDT15,IWS1,SSPO,MAPRE3,CRTAP,PLK3,SUMO2,XRCC1,MLH1,CDC123,MTRF1,RALB,DPH2,KDM4A,AQP11,PRKAG2,RAF1,PRDX3,TIMP4,PIBF1,PAXIP1,WDR48,UBE2O,EGLN2,MYCBP2,SPOPL,FBH1,TNRC6C,SPRY2,PLAT,WNT11,TADA3,KLHL40,AKT2,GPD1L,ARRB1,TGFBR2,ACVR2A,IKBKB,SIRT2,NMI,NEK10,RPTOR,PURA,TCIM,HBEGF,PAWR,P	grey	VSMC_M10
GO:0051128	1.00	0.00	870	1877	regulation of cellular component organization	BP	1	ADNP2,NME1,VPS4B,NEDD4L,PAN2,ATP8B1,ARPC3,LRP1,SEMA6A,TRIM36,PIP4K2C,CYP27B1,AVIL,TBC1D30,PPP1R10,MDM1,ATAT1,ESR1,CNOT2,RAB21,CNOT6,ZNF207,SNCAIP,FBXO43,TIAM2,APOM,HSPA1B,RIMS2,EBAG9,MAP3K4,PRKN,RNF5,PPARA,IL5,SEPT8,TSPO,GDF9,ROS1,FSTL4,SYNGAP1,UBE2B,BAK1,MTSS1,WASHC5,MYC,ASAP1,JMJD4,H3F3C,PTK2,MAPK15,PLXNA4,MAPK14,NTRK2,PODXL,CPNE5,PLA2G6,BAIAP2L2,PICK1,PI16,BTBD9,MPDZ,CDC42EP1,RAC2,EXOSC4,HSF1,MYH9,CDKN2A,CHRNA3,TEK,LINGO2,POT1,FBXO7,LMOD2,PTK7,ABHD17B,SRF,TTBK1,FZD1,CCL27,SLAIN2,SMARCA2,USP46,KIT,NCK2,ROR2,SEMA4D,KIAA1211,TMEM14A,BICD2,CHMP2A,SEMA4C,TMOD1,PLEKHH2,DYNC2LI1,CLDN19,BRSK1,PRKCE,SMAP1,EPS8L1,RIMS1,TMEM30A,SPTBN1,RTN4,PPP2R1A,PHIP,RUFY3,ACP4,SHANK1,HOXA13,LPAR1,PPT1,XPO1,EPGN,AKIRIN1,TRAPPC12,PLEK,RSPO1,LRRN3,AAK1,EPHA7,NR1H2,TGFA,PTN,ITGB1BP1,MED25,MET,ADD2,CTTNBP2,YWHAZ,EGFR,HECW1,FUZ,ARHGEF5,TRIM32,TLR4,CDK5RAP2,EPHA1,CNTRL,SFRP4,KEL,MYLK3,VPS35,ATG5,SDCBP,FAM49A,RTN4IP1,NRCAM,MGARP,SLC7A11,MAPRE1,FIG4,WASF1,SSBP1,FAF1,SPHK2,PLXNA1,HDAC2,MTMR2,NAPA,RAB7A,NDNF,PIP4K2A,AP2S1,VSTM5,SETDB2,PHB,IQSEC1,SOX9,EML2,ERCC1,SLC39A12,LCP1,CLASP2,RBSN,APOC1,MAPRE3,DNAJC15,PTCH2,XRCC1,MTRF1,GOLGA4,MEGF8,TRIM54,PCDH8,RALB,GRIK5,RAF1,MYD88,KLF5,TBC1D4,PTPRF,EGLN2,MYCBP2,NAPB,SLAIN1,TSKU,SPRY2,SS18L2,WNT11,SLITRK5,ALK,SERTAD3,AKT2,DYNC1LI1,ARRB1,CPNE9,NEU3,PLEKHG2,USP36,IKBKB,CEP295NL,LRFN1,FARP1,FCHSD2,SIRT2,MKKS,ANK1,RPTOR,ACTG1,NA	grey	VSMC_M10

GO:0006950	1.00	0.00	1304	2715	response to stress	BP	1	ADNP2,CD226,SERPINB2,PHLPP1,ERBB3,POLI,LRP1,SHMT2,EYA4,GLI1,MARS,MAP7,MAP3K5,RPA3,TNFAIP3,CYP27B1,ATP23,USP15,CANX,MRNIP,ENPP3,HELB,TRIM39,PPP1R10,ARMT1,ESR1,MDC1,IER3,TSPAN8,STK3,MAPK8IP2,SNW1,MPIG6B,SLC12A2,HSPA1B,FZD6,BRD1,MAP3K4,PRKN,PACRG,RNF5,AGER,PPARA,GPSM3,FBLN1,TAP1,IL5,TSPO,MCM9,ASF1A,HSPA4,DERL1,NDUFA6,PHF1,UBE2B,BAK1,XRCC6,NCOA7,MTSS1,ACO2,TRIB1,MYC,PTK2,ERCC6L2,C6orf106,FANCC,AKR1B1,ATF4,MAPK15,APOBEC3H,MAPK14,MAPK13,DMC1,CSNK1E,PLA2G6,PICK1,C6orf89,EXOSC4,FOXRED2,TXN2,HSF1,OARD1,TFEB,SLC39A4,IRF5,MYH9,GPT,CDKN2A,TEK,POT1,GPR37,FBXO7,CRY1,PTK7,SRF,ABCB1,TTBK1,NFX1,NUAK1,TEC,FANCG,CDK6,USP46,ENPP4,SLC25A27,KIT,SLC1A1,CA9,NCK2,PLGRKT,MRPS9,ERMP1,IL1R2,TLN1,ROR2,GADD45G,GAPDH,S1PR3,PDCL3,REV1,NINJ1,KLHL31,PRDX1,ADH5,SEMA4C,RAB23,CAT,SEC61B,CLDN19,ERP44,DNAJA1,BRSK1,SDHAF4,PRKCE,EPAS1,MSH2,CD109,TFPT,FKTN,RAD23B,FPR2,EPB41L4B,PNPT1,VRK2,FANCL,EMC10,REL,ECPAS,NT5E,ANKRD17,ALB,CXCL8,MTURN,NOD1,AREG,AKIRIN2,AQP1,RRAGD,LYPD8,CYREN,HERPUD2,PXDN,ETAA1,MTF1,PLEK,RSAD2,ZNF277,NR1H2,AKNA,TGFA,PTN,DGKI,MET,TNC,EGFR,USP45,TRIM32,TLR4,ASCC3,VPS41,TRAF1,BVES,IL15,CCDC155,MYLK3,UCP1,VPS35,ATG5,MGST2,SETD7,SDCBP,MGARP,SLC7A11,FOXO3,PUM2,CDK19,FGF21,BRAF,CHCHD6,REV3L,HSPE1,TRAF3IP2,DHFR,HDAC2,ZC3HAV1,TRPC3,KPTN,SESN3,SLC8A2,DNMT3A,HMCES,NDNF,C5AR2,C5AR1,PANX1,SLC26A5,MSRB2,NAPEPLD,PTGIR,CST7,PHB,FOXA3,GIPR,ERCC1,NUDT15,XPC,ERCC2,ERCC3,CLASP2,LACC1,	grey	VSMC_M10
GO:0040011	0.00	1.00	91	1349	locomotion	BP	2.2E-10	TNFRSF11A,FLT4,MEGF10,CELSR1,ENPP2,IP6K3,PDGFB,MDGA1,DNAH8,ATP8A1,KDR,SYK,EPHA5,IL6,C5,SLC22A16,PIK3CG,NOVA2,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,GPC6,P2RY6,SFRP1,CNTN4,CFAP54,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,NKX2-3,SNCA,HYAL2,DPYSL4,ROBO4,NFATC2,CD34,PECAM1,BMP7,IGFBP3,PROX1,GPC1,JAML,ACE,LAMC2,CCRL2,TBX1,RGN,LGALS12,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,ABI3,PDE4B,SEMA6B,TNFRSF18,NOTCH1,S1PR1,LHX2,LHX6,CDH1,CDH5,ALOX12,MMP12,ATP1A4,SOX17,RELN,C3AR1,PDLIM1,VSTM2L,SOX18,GNA12,TRPM2,BAMBI,CCR7,MGAT3,MSMP	turquoise	VSMC_M6
GO:0048870	0.00	1.00	83	1234	cell motility	BP	1.3E-09	TNFRSF11A,FLT4,MEGF10,CELSR1,ENPP2,PDGFB,MDGA1,DNAH8,ATP8A1,KDR,SYK,IL6,C5,SLC22A16,PIK3CG,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,GPC6,P2RY6,SFRP1,CFAP54,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,NKX2-3,HYAL2,ROBO4,NFATC2,CD34,PECAM1,BMP7,IGFBP3,PROX1,GPC1,JAML,ACE,LAMC2,CCRL2,TBX1,RGN,LGALS12,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,ABI3,PDE4B,SEMA6B,TNFRSF18,NOTCH1,S1PR1,LHX6,CDH1,CDH5,ALOX12,MMP12,ATP1A4,SOX17,RELN,C3AR1,PDLIM1,SOX18,GNA12,TRPM2,BAMBI,CCR7,MGAT3,MSMP	turquoise	VSMC_M6
GO:0051674	0.00	1.00	83	1234	localization of cell	BP	1.3E-09	TNFRSF11A,FLT4,MEGF10,CELSR1,ENPP2,PDGFB,MDGA1,DNAH8,ATP8A1,KDR,SYK,IL6,C5,SLC22A16,PIK3CG,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,GPC6,P2RY6,SFRP1,CFAP54,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,NKX2-3,HYAL2,ROBO4,NFATC2,CD34,PECAM1,BMP7,IGFBP3,PROX1,GPC1,JAML,ACE,LAMC2,CCRL2,TBX1,RGN,LGALS12,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,ABI3,PDE4B,SEMA6B,TNFRSF18,NOTCH1,S1PR1,LHX6,CDH1,CDH5,ALOX12,MMP12,ATP1A4,SOX17,RELN,C3AR1,PDLIM1,SOX18,GNA12,TRPM2,BAMBI,CCR7,MGAT3,MSMP	turquoise	VSMC_M6
GO:0016477	0.00	1.00	78	1120	cell migration	BP	1.3E-09	TNFRSF11A,FLT4,MEGF10,CELSR1,ENPP2,PDGFB,MDGA1,ATP8A1,KDR,SYK,IL6,C5,PIK3CG,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,GPC6,P2RY6,SFRP1,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,NKX2-3,HYAL2,ROBO4,NFATC2,CD34,PECAM1,BMP7,IGFBP3,PROX1,GPC1,JAML,ACE,LAMC2,CCRL2,TBX1,LGALS12,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,ABI3,PDE4B,SEMA6B,TNFRSF18,NOTCH1,S1PR1,LHX6,CDH1,CDH5,ALOX12,MMP12,SOX17,RELN,C3AR1,PDLIM1,SOX18,GNA12,TRPM2,BAMBI,CCR7,MGAT3,MSMP	turquoise	VSMC_M6
GO:0022610	0.00	1.00	74	1050	biological adhesion	BP	2.4E-09	IL23A,MEGF10,CELSR1,NOTCH4,PDGFB,MDGA1,FREM1,KDR,IL1RL2,SYK,IL6,LRRC4B,PIK3CG,DLL1,LYPD3,CD177,ITGB4,TGFB1,CXCR4,CTNNB1,GPC6,SFRP1,CNTN4,PCDH12,CD36,NFKBID,KIRREL2,ADAMTS9,LYVE1,ANGPT2,THBS4,STAB1,MMRN1,CTNND2,SLC39A8,LSAMP,HFE,ROBO4,ESAM,LAPTM5,CD34,PECAM1,CD86,COL18A1,BMP7,JAML,LAMC2,LTF,CLDN16,CCDC88B,SELE,SELP,VWF,BAIAP2L1,PPM1F,KIF26B,COL4A6,DSC2,TNFRSF18,NRARP,EGFL7,NOTCH1,S1PR1,GBP1,CDH3,CDH1,CDH5,ALOX12,MMP12,RELN,PDLIM1,VSTM2L,CCR7,SCARF1	turquoise	VSMC_M6

GO:0007155	0.00	1.00	73	1044	cell adhesion	BP	4.3E-09	IL23A,MEGF10,CELSR1,NOTCH4,PDGFB,MDGA1,FREM1,KDR,IL1RL2,SYK,IL6,LRRC4B,PIK3CG,DLL1,LYPD3,CD177,ITGB4,TGFB1,CXCR4,CTNNB1,GPC6,SFRP1,CNTN4,PCDH12,CD36,NFKBID,KIRREL2,ADAMTS9,LYVE1,ANGPT2,THBS4,STAB1,MMRN1,CTNND2,SLC39A8,LSAMP,HFE,ROBO4,ESAM,LAPTM5,CD34,PECAM1,CD86,COL18A1,BMP7,JAML,LAMC2,CLDN16,CCDC88B,SELE,SELP,VWF,BAIAP2L1,PPM1F,KIF26B,COL4A6,DSC2,TNFRSF18,NRARP,EGFL7,NOTCH1,S1PR1,GBP1,CDH3,CDH1,CDH5,ALOX12,MMP12,RELN,PDLIM1,VSTM2L,CCR7,SCARF1	turquoise	VSMC_M6
GO:0001944	0.00	1.00	52	607	vasculature development	BP	6.2E-09	FLT4,NOTCH4,ENPP2,PDGFB,ADGRF5,KDR,SYK,THSD7A,IL6,C5,GJA4,RASIP1,PIK3CG,DLL1,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,PDE2A,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,ROBO4,NFATC2,CD34,PECAM1,COL18A1,BMP7,PROX1,TBX1,LGALS12,MMRN2,ARHGEF15,NPR1,LYL1,LRG1,NRARP,TMEM204,EGFL7,NOTCH1,S1PR1,CDH5,SOX17,C3AR1,SOX18	turquoise	VSMC_M6
GO:0003158	0.00	1.00	21	107	endothelium development	BP	7.6E-09	NOTCH4,KDR,GJA4,DLL1,CXCR4,CTNNB1,TIE1,PDE2A,CXCL10,PPP1R16B,ROBO4,CD34,PECAM1,COL18A1,PROX1,NOTCH1,S1PR1,CDH5,ALOX12,SOX17,SOX18	turquoise	VSMC_M6
GO:0006928	0.00	1.00	94	1565	movement of cell or subcellular component	BP	7.6E-09	TNFRSF11A,KCNN2,FLT4,MEGF10,SYBU,CELSR1,ENPP2,PDGFB,MDGA1,DNAH8,ATP8A1,KDR,SYK,EPHA5,IL6,C5,CFAP100,SLC22A16,PIK3CG,NOVA2,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,GPC6,P2RY6,SFRP1,CNTN4,CFAP54,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,NKX2-3,HYAL2,DPYSL4,ROBO4,NFATC2,CD34,PECAM1,BMP7,IGFBP3,PROX1,GPC1,JAML,ACE,LAMC2,CCRL2,TBX1,RGN,LGALS12,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,TTLL6,ABI3,DSC2,PDE4B,SEMA6B,TNFRSF18,NOTCH1,S1PR1,LHX2,LHX6,CDH1,CDH5,ALOX12,MMP12,ATP1A4,SOX17,RELN,C3AR1,PDLIM1,VSTM2L,SOX18,GNA12,TRPM2,BAMBI,CCR7,MGAT3,MSMP	turquoise	VSMC_M6
GO:0023052	0.00	1.00	188	4258	signaling	BP	2.9E-08	TNFRSF11A,IL23A,KCNN2,NMBR,FLT4,SYBU,CELSR1,NOTCH4,SYT17,DENND3,PDGFB,CSF2RB,MOB3B,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,ANKRD6,ARHGAP25,C5,GJA4,MAML3,RASIP1,PIK3CG,DLL1,CTSC,RAB38,SLC6A6,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,SYN2,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,RASGRP3,NOTUM,CNTN4,CD36,NFKBID,PRAG1,PRR5L,HHEX,SOX7,P2RY14,CXCL10,ANGPT2,SOGA1,ADGRG3,HUNK,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,STAB1,MAPK10,GOT1,BMP1,SNCA,CTNND2,SHANK2,HYAL2,ESRRG,NKD2,HFE,MCTP2,HCRTR1,LAPTM5,NFATC2,INPP5D,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,BMP7,IGFBP3,PROX1,GPC1,SRMS,PTPRE,CNKSR2,PRAME,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,LPAR2,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,ERAS,PRKCH,GRID2IP,TSPAN14,MMRN2,SNCG,PPP1R1B,LFNG,ARHGEF9,MTOR,GNGT2,ARHGEF15,MAST1,NPR1,BEX5,COL4A6,COL4A5,DSC2,KIF26A,PDE4B,SARM1,SEMA6B,LRG1,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,SSTR5,NOTCH1,S1PR1,SH2D3C,GBP1,CDH3,CDH1,ADGRL4,EXOC3L1,CDH5,DCDC2B,MMP12,PMAIP1,ATP1A4,SOX17,RELN,ACKR1,ALKAL1,C3AR1,NMUR1,NUCB1,GRAP,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,OR6N2,NSG2,MSMP,NMB,HPCAL4,RTN4RL2,GNG4,PDE1B	turquoise	VSMC_M6
GO:0007154	0.00	1.00	189	4300	cell communication	BP	3.4E-08	TNFRSF11A,IL23A,KCNN2,NMBR,FLT4,SYBU,CELSR1,NOTCH4,SYT17,DENND3,PDGFB,CSF2RB,FREM1,MOB3B,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,ANKRD6,ARHGAP25,C5,GJA4,MAML3,RASIP1,PIK3CG,DLL1,CTSC,RAB38,SLC6A6,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,SYN2,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,RASGRP3,NOTUM,CNTN4,CD36,NFKBID,PRAG1,PRR5L,HHEX,SOX7,P2RY14,CXCL10,ANGPT2,SOGA1,ADGRG3,HUNK,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,STAB1,MAPK10,GOT1,BMP1,SNCA,CTNND2,SHANK2,HYAL2,ESRRG,NKD2,HFE,MCTP2,HCRTR1,LAPTM5,NFATC2,INPP5D,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,BMP7,IGFBP3,PROX1,GPC1,SRMS,PTPRE,CNKSR2,PRAME,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,LPAR2,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,ERAS,PRKCH,GRID2IP,TSPAN14,MMRN2,SNCG,PPP1R1B,LFNG,ARHGEF9,MTOR,GNGT2,ARHGEF15,MAST1,NPR1,BEX5,COL4A6,COL4A5,DSC2,KIF26A,PDE4B,SARM1,SEMA6B,LRG1,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,SSTR5,NOTCH1,S1PR1,SH2D3C,GBP1,CDH3,CDH1,ADGRL4,EXOC3L1,CDH5,DCDC2B,MMP12,PMAIP1,ATP1A4,SOX17,RELN,ACKR1,ALKAL1,C3AR1,NMUR1,NUCB1,GRAP,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,OR6N2,NSG2,MSMP,NMB,HPCAL4,RTN4RL2,GNG4,PDE1B	turquoise	VSMC_M6
GO:0001568	0.00	1.00	48	576	blood vessel development	BP	6.8E-08	FLT4,NOTCH4,ENPP2,PDGFB,ADGRF5,KDR,SYK,THSD7A,IL6,C5,GJA4,RASIP1,PIK3CG,DLL1,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,PDE2A,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,ROBO4,CD34,PECAM1,COL18A1,BMP7,PROX1,TBX1,MMRN2,NPR1,LYL1,LRG1,NRARP,EGFL7,NOTCH1,S1PR1,CDH5,SOX17,C3AR1,SOX18	turquoise	VSMC_M6

GO:0032501	0.00	1.00	209	5003	multicellular organismal process	BP	1.2E-07	TNFRSF11A,IL23A,KCNN2,LYZ,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,PDGFB,ETV7,MDGA1,CSF2RB,FREM1,IREB2,ATP8A1,ADGRF5,KDR,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,C5,GJA4,SLC22A16,RASIP1,PIK3CG,DLL1,NOVA2,CTSC,SLC6A6,GRIP2,RARRES2,NOS3,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,GPC6,MAP6,SLCO2B1,P2RY2,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,PCDH12,CD36,CFAP54,NFKBID,PRAG1,ADAMTS9,ATP8A2,MALL,F11,KLKB1,HHEX,PROCR,SOX7,CXCL10,ANGPT2,SLC4A5,ADGRG3,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,STAB1,IRX6,NKX2-3,BMP1,SPATA25,IGSF3,SNCA,MMRN1,CTNND2,SHANK2,MTTP,HYAL2,SLC39A8,ESRRG,LSAMP,HFE,DPYSL4,ROBO4,NRAP,ESAM,LAPTM5,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,COL18A1,SLAMF9,BMP7,PROX1,MGST1,GPC1,OAZ3,ACE,LAMC2,HOXD10,PAX9,LTF,CLDN16,CCDC88B,TBX1,RGN,LGALS12,SELP,VWF,PLVAP,FGF23,CRACR2A,RCSD1,PPM1F,PRKCH,KIF26B,BCL6B,MMRN2,SNCG,PPP1R1B,LFNG,C19orf57,MTOR,BCKDK,ABI3,ARHGEF15,KLF1,MAST1,BEST2,NPR1,ISLR2,LYL1,B4GALT6,DSC2,GREB1L,KIF26A,HCN1,PDE4B,SARM1,SEMA6B,LRG1,NRARP,TMEM204,HES3,EGFL7,NOTCH1,IRF8,S1PR1,ENDOG,GBP1,LHX2,PTGS1,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,GGN,PKHD1L1,ATP1A4,SOX17,RELN,ACKR1,ALKAL1,C3AR1,OLIG2,PDLIM1,NMUR1,VSTM2L,GRAP,SOX18,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,OR6N2,MGAT3,HPCAL4,RTN4RL2,SCARF1,PDE1B,FLI1	turquoise	VSMC_M6
GO:0007165	0.00	1.00	173	3919	signal transduction	BP	2.9E-07	TNFRSF11A,IL23A,NMBR,FLT4,CELSR1,NOTCH4,DENND3,PDGFB,CSF2RB,MOB3B,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,ANKRD6,ARHGAP25,C5,MAML3,RASIP1,PIK3CG,DLL1,CTSC,RAB38,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,TIE1,GPC6,P2RY6,P2RY2,PDE2A,SFRP1,RASGRP3,NOTUM,CD36,NFKBID,PRAG1,PRR5L,HHEX,SOX7,P2RY14,CXCL10,ANGPT2,SOGA1,ADGRG3,HUNK,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,MAPK10,GOT1,BMP1,SNCA,CTNND2,SHANK2,HYAL2,ESRRG,NKD2,HFE,MCTP2,HCRTR1,LAPTM5,NFATC2,INPP5D,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,BMP7,IGFBP3,PROX1,GPC1,SRMS,PTPRE,CNKSR2,PRAME,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,LPAR2,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,ERAS,PRKCH,TSPAN14,MMRN2,PPP1R1B,LFNG,ARHGEF9,MTOR,GNGT2,ARHGEF15,MAST1,NPR1,BEX5,COL4A6,COL4A5,KIF26A,PDE4B,SARM1,SEMA6B,LRG1,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,SSTR5,NOTCH1,S1PR1,SH2D3C,GBP1,CDH3,ADGRL4,CDH5,DCDC2B,MMP12,PMAIP1,ATP1A4,SOX17,RELN,ACKR1,ALKAL1,C3AR1,NMUR1,NUCB1,GRAP,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,OR6N2,NSG2,MSMP,NMB,HPCAL4,RTN4RL2,GNG4,PDE1B	turquoise	VSMC_M6
GO:0001525	0.00	1.00	39	428	angiogenesis	BP	3.1E-07	FLT4,NOTCH4,ENPP2,KDR,SYK,THSD7A,IL6,C5,RASIP1,PIK3CG,DLL1,NOS3,PPARG,CXCR4,CTNNB1,TIE1,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,ROBO4,CD34,COL18A1,TBX1,MMRN2,NPR1,LRG1,NRARP,EGFL7,NOTCH1,S1PR1,CDH5,SOX17,C3AR1,SOX18	turquoise	VSMC_M6
GO:0098609	0.00	1.00	47	592	cell-cell adhesion	BP	3.9E-07	IL23A,MEGF10,CELSR1,NOTCH4,MDGA1,IL1RL2,SYK,IL6,LRRC4B,PIK3CG,CD177,TGFB1,CTNNB1,GPC6,CNTN4,PCDH12,NFKBID,KIRREL2,THBS4,CTNND2,SLC39A8,HFE,ROBO4,ESAM,LAPTM5,CD34,PECAM1,CD86,BMP7,JAML,CLDN16,CCDC88B,SELE,SELP,BAIAP2L1,PPM1F,KIF26B,DSC2,NRARP,NOTCH1,CDH3,CDH1,CDH5,ALOX12,PDLIM1,VSTM2L,CCR7	turquoise	VSMC_M6
GO:0007166	0.00	1.00	103	1935	cell surface receptor signaling pathway	BP	3.9E-07	TNFRSF11A,IL23A,FLT4,CELSR1,NOTCH4,PDGFB,CSF2RB,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,ANKRD6,C5,MAML3,DLL1,GRIP2,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TMC8,TIE1,GPC6,P2RY6,P2RY2,SFRP1,NOTUM,CD36,NFKBID,PRAG1,HHEX,SOX7,P2RY14,CXCL10,ANGPT2,SOGA1,ADGRG3,COL2A1,MAPK10,GOT1,SNCA,CTNND2,HYAL2,NKD2,HFE,LAPTM5,NFATC2,INPP5D,PECAM1,CD86,BMP7,IGFBP3,GPC1,SRMS,PTPRE,ADGRA1,LTF,CCRL2,TSPAN15,CDA,PLVAP,BAIAP2L1,FGF23,PRKCH,TSPAN14,MMRN2,LFNG,NPR1,COL4A6,COL4A5,PDE4B,SEMA6B,LRG1,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,NOTCH1,GBP1,CDH3,ADGRL4,CDH5,MMP12,PMAIP1,ATP1A4,SOX17,RELN,ACKR1,C3AR1,SHANK3,BAMBI,CCR7,RTN4RL2	turquoise	VSMC_M6
GO:0045446	0.00	1.00	17	91	endothelial cell differentiation	BP	9.3E-07	NOTCH4,KDR,DLL1,CXCR4,CTNNB1,TIE1,PDE2A,PPP1R16B,ROBO4,PECAM1,COL18A1,PROX1,NOTCH1,S1PR1,CDH5,SOX17,SOX18	turquoise	VSMC_M6
GO:0048514	0.00	1.00	42	508	blood vessel morphogenesis	BP	9.3E-07	FLT4,NOTCH4,ENPP2,ADGRF5,KDR,SYK,THSD7A,IL6,C5,RASIP1,PIK3CG,DLL1,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,ROBO4,CD34,COL18A1,PROX1,TBX1,MMRN2,NPR1,LRG1,NRARP,EGFL7,NOTCH1,S1PR1,CDH5,SOX17,C3AR1,SOX18	turquoise	VSMC_M6

GO:0051270	0.00	1.00	56	830	regulation of cellular component movement	BP	2.5E-06	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,C5,PIK3CG,NOVA2,RARRES2,NOS3,PPARG,TGFB1,CXCR4,TIE1,P2RY6,SFRP1,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,HYAL2,ROBO4,PECAM1,BMP7,IGFBP3,PROX1,ACE,LAMC2,RGN,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,TTLL6,ABI3,DSC2,PDE4B,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH1,CDH5,ALOX12,RELN,C3AR1,GNA12,CCR7,MGAT3	turquoise	VSMC_M6
GO:0050896	0.00	1.00	230	5876	response to stimulus	BP	2.5E-06	TNFRSF11A,IL23A,NMBR,LYZ,FLT4,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,DENND3,PDGFB,CSF2RB,MOB3B,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,ANKRD6,ARHGAP25,C5,GJA4,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,TIE1,GPC6,P2RY6,P2RY2,PDE2A,SFRP1,RASGRP3,NOTUM,CNTN4,SLC4A11,CD36,NFKBID,PRAG1,PRR5L,ATP8A2,F11,BPIFB3,KLKB1,HHEX,LYVE1,PROCR,SOX7,TSC22D2,P2RY14,CXCL10,ANGPT2,SOGA1,ADGRG3,HUNK,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,GSTA4,STAB1,MAPK10,GOT1,NKX2-3,BMP1,SNCA,MMRN1,CTNND2,ANO3,SHANK2,MTTP,HYAL2,ESRRG,NKD2,UPK1B,HFE,MCTP2,DPYSL4,HCRTR1,ROBO4,LAPTM5,ISG20,NFATC2,INPP5D,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,COL18A1,SLAMF9,BMP7,IGFBP3,ASCC2,PROX1,MGST1,GPC1,JAML,SRMS,PTPRE,CNKSR2,LAMC2,PRAME,PAX9,ST6GAL1,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,LPAR2,CCDC88B,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,RCSD1,PPM1F,ERAS,PRKCH,TSPAN14,BCL6B,MMRN2,PPP1R1B,LFNG,ARHGEF9,C19orf57,MTOR,GNGT2,ABI3,ARHGEF15,KLF1,MAST1,NPR1,BEX5,COL4A6,COL4A5,KIF26A,HCN1,PDE4B,SARM1,SEMA6B,LRG1,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,PTGS1,CDH3,CDH1,ADGRL4,CDH5,ALOX12,DCDC2B,MMP12,PMAIP1,GGN,RUFY4,PKHD1L1,TRIM43,ATP1A4,SOX17,RELN,ACKR1,ALKAL1,C3AR1,PDLIM1,NMUR1,VSTM2L,NUCB1,GRAP,GNA12,SH	turquoise	VSMC_M6
GO:0040012	0.00	1.00	54	796	regulation of locomotion	BP	3.8E-06	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,C5,PIK3CG,NOVA2,RARRES2,NOS3,PPARG,TGFB1,CXCR4,TIE1,P2RY6,SFRP1,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,SNCA,HYAL2,ROBO4,PECAM1,BMP7,IGFBP3,PROX1,ACE,LAMC2,RGN,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,ABI3,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH1,CDH5,ALOX12,RELN,C3AR1,GNA12,CCR7,MGAT3	turquoise	VSMC_M6
GO:0035239	0.00	1.00	49	699	tube morphogenesis	BP	6.9E-06	FLT4,CELSR1,NOTCH4,ENPP2,ADGRF5,KDR,SYK,THSD7A,IL6,C5,RASIP1,PIK3CG,DLL1,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,NKX2-3,ROBO4,CD34,COL18A1,BMP7,PROX1,TBX1,KIF26B,MMRN2,NPR1,GREB1L,LRG1,NRARP,EGFL7,NOTCH1,S1PR1,LHX2,CDH5,ALOX12,SOX17,C3AR1,SOX18	turquoise	VSMC_M6
GO:0042592	0.00	1.00	74	1295	homeostatic process	BP	7.5E-06	TNFRSF11A,LYZ,MYCT1,SYBU,IREB2,STEAP4,ADGRF5,KDR,SYK,EPHA5,IL6,PIK3CG,DLL1,NOVA2,RAB38,NOS3,PPARG,CXCR4,EDNRB,CTNNB1,TMC8,P2RY6,P2RY2,SLC4A11,CD36,MALL,CP,CXCL10,SLC4A5,ATP6V0D2,CYP26B1,COL2A1,GOT1,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,HFE,HCRTR1,ESAM,INPP5D,CD34,PECAM1,ERN1,LTF,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,FGF23,HEPH,KLF1,NPR1,PDE4B,SSTR5,NOTCH1,S1PR1,ENDOG,CDH3,CDH5,ALOX12,PMAIP1,ATP1A4,C3AR1,SHANK3,LPAR6,TRPM2,CCR7,NMB,RBP1,EMCN	turquoise	VSMC_M6
GO:2000145	0.00	1.00	52	772	regulation of cell motility	BP	7.9E-06	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,C5,PIK3CG,RARRES2,NOS3,PPARG,TGFB1,CXCR4,TIE1,P2RY6,SFRP1,PRAG1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,HYAL2,ROBO4,PECAM1,BMP7,IGFBP3,PROX1,ACE,LAMC2,RGN,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,ABI3,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH1,CDH5,ALOX12,RELN,C3AR1,GNA12,CCR7,MGAT3	turquoise	VSMC_M6
GO:0006935	0.00	1.00	36	426	chemotaxis	BP	7.9E-06	TNFRSF11A,ENPP2,PDGFB,KDR,SYK,EPHA5,IL6,C5,PIK3CG,NOVA2,RARRES2,TGFB1,CXCR4,EDNRB,CNTN4,CXCL10,ANGPT2,THBS4,DPYSL4,ROBO4,BMP7,JAML,LAMC2,CCRL2,PPM1F,PDE4B,SEMA6B,NOTCH1,S1PR1,LHX2,RELN,C3AR1,VSTM2L,TRPM2,CCR7,MSMP	turquoise	VSMC_M6
GO:0042330	0.00	1.00	36	427	taxis	BP	8E-06	TNFRSF11A,ENPP2,PDGFB,KDR,SYK,EPHA5,IL6,C5,PIK3CG,NOVA2,RARRES2,TGFB1,CXCR4,EDNRB,CNTN4,CXCL10,ANGPT2,THBS4,DPYSL4,ROBO4,BMP7,JAML,LAMC2,CCRL2,PPM1F,PDE4B,SEMA6B,NOTCH1,S1PR1,LHX2,RELN,C3AR1,VSTM2L,TRPM2,CCR7,MSMP	turquoise	VSMC_M6

GO:0065008	0.00	1.00	128	2770	regulation of biological quality	BP	8E-06	TNFRSF11A,KCNN2,LYZ,MYCT1,SYBU,PDGFB,MDGA1,IREB2,ATP8A1,STEAP4,ADGRF5,KDR,SYK,EPHA5,IL6,LRRC4B,RASIP1,PIK3CG,DLL1,NOVA2,RAB38,GRIP2,FGD5,RARRES2,NOS3,PPARG,SYN2,TGFB1,CXCR4,EDNRB,CTNNB1,TMC8,SPTBN4,GPC6,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,CNTN4,SLC4A11,CD36,PRAG1,ATP8A2,MALL,F11,KLKB1,PROCR,CP,CXCL10,SLC4A5,ATP6V0D2,CYP26B1,COL2A1,MAPK10,GOT1,NKX2-3,SNCA,MMRN1,ANO3,SHANK2,MTTP,HYAL2,SLC39A8,ESRRG,HFE,MCTP2,HCRTR1,ESAM,LAPTM5,INPP5D,CD34,PECAM1,ERN1,SLCO4A1,ACE,LTF,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,SELP,VWF,PLVAP,BAIAP2L1,FGF23,GRID2IP,SNCG,PPP1R1B,HEPH,MTOR,ABI3,ARHGEF15,KLF1,BEST2,NPR1,ISLR2,DSC2,HCN1,PDE4B,SEMA6B,SSTR5,NOTCH1,S1PR1,ENDOG,PALMD,PTGS1,CDH3,EXOC3L1,CDH5,ALOX12,PMAIP1,ATP1A4,SOX17,RELN,C3AR1,KANK3,GNA12,SHANK3,LPAR6,TRPM2,BAMBI,CCR7,NMB,FLI1,RBP1,EMCN	turquoise	VSMC_M6
GO:0009605	0.00	1.00	92	1770	response to external stimulus	BP	8.3E-06	TNFRSF11A,IL23A,LYZ,ENPP2,PDGFB,CSF2RB,KDR,IL18RAP,IL1RL2,SYK,EPHA5,IL6,C5,PIK3CG,NOVA2,CTSC,RAB38,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,PDE2A,SFRP1,CNTN4,CD36,ATP8A2,F11,BPIFB3,KLKB1,CXCL10,ANGPT2,THBS4,CYP26B1,STAB1,GOT1,SNCA,ANO3,HYAL2,UPK1B,HFE,DPYSL4,ROBO4,ISG20,TLR7,CD34,CD86,BMP7,PROX1,MGST1,JAML,SRMS,LAMC2,LTF,CCRL2,CCDC88B,SELE,SELP,BAIAP2L1,FGF23,PPM1F,BCL6B,MTOR,GNGT2,KIF26A,PDE4B,SARM1,SEMA6B,LRG1,NOTCH1,IRF8,S1PR1,ENDOG,GBP1,LHX2,CDH5,ALOX12,MMP12,PMAIP1,TRIM43,RELN,C3AR1,VSTM2L,SHANK3,TRPM2,TRIM62,CCR7,MSMP,SCARF1	turquoise	VSMC_M6
GO:0050900	0.00	1.00	26	245	leukocyte migration	BP	9.2E-06	TNFRSF11A,PDGFB,SYK,IL6,C5,PIK3CG,RARRES2,CD177,CXCR4,EDNRB,CXCL10,THBS4,NKX2-3,CD34,PECAM1,JAML,SELE,SELP,PLVAP,PDE4B,TNFRSF18,S1PR1,C3AR1,TRPM2,CCR7,MSMP	turquoise	VSMC_M6
GO:0030334	0.00	1.00	50	735	regulation of cell migration	BP	9.2E-06	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,C5,PIK3CG,RARRES2,NOS3,PPARG,TGFB1,CXCR4,TIE1,P2RY6,SFRP1,ADAMTS9,PRR5L,CXCL10,ANGPT2,ADGRG3,THBS4,HYAL2,ROBO4,PECAM1,BMP7,IGFBP3,PROX1,ACE,LAMC2,SELE,SELP,PLVAP,FGF23,PPM1F,MMRN2,MTOR,ABI3,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH1,CDH5,ALOX12,RELN,C3AR1,GNA12,CCR7,MGAT3	turquoise	VSMC_M6
GO:0048731	0.00	1.00	154	3556	system development	BP	9.2E-06	TNFRSF11A,IL23A,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,PDGFB,ETV7,MDGA1,FREM1,IREB2,ADGRF5,KDR,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,C5,GJA4,RASIP1,PIK3CG,DLL1,NOVA2,CTSC,RARRES2,NOS3,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,GPC6,MAP6,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,PCDH12,NFKBID,PRAG1,ADAMTS9,ATP8A2,MALL,HHEX,CXCL10,ANGPT2,SLC4A5,ADGRG3,PRDM8,THBS4,CYP26B1,PPP1R16B,COL2A1,STAB1,IRX6,NKX2-3,BMP1,IGSF3,SNCA,CTNND2,SHANK2,HYAL2,LSAMP,HFE,DPYSL4,ROBO4,NRAP,NFATC2,INPP5D,EAF2,CD34,PECAM1,CD86,COL18A1,BMP7,PROX1,MGST1,GPC1,ACE,LAMC2,HOXD10,PAX9,LTF,TBX1,RGN,LGALS12,FGF23,CRACR2A,PRKCH,KIF26B,MMRN2,LFNG,MTOR,ABI3,ARHGEF15,KLF1,MAST1,NPR1,ISLR2,LYL1,B4GALT6,GREB1L,KIF26A,HCN1,SARM1,SEMA6B,LRG1,NRARP,TMEM204,HES3,EGFL7,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,SOX17,RELN,ALKAL1,C3AR1,OLIG2,PDLIM1,VSTM2L,SOX18,SHANK3,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,HPCAL4,RTN4RL2,SCARF1,PDE1B,FLI1	turquoise	VSMC_M6
GO:0030154	0.00	1.00	134	2966	cell differentiation	BP	1E-05	TNFRSF11A,IL23A,FLT4,MEGF10,CELSR1,NOTCH4,SYT17,PDGFB,ETV7,MDGA1,IREB2,STEAP4,ADGRF5,KDR,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,BCL11A,SLC22A16,RASIP1,DLL1,NOVA2,RAB38,SLC6A6,RARRES2,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,MAP6,SNAP25,PDE2A,SFRP1,ZIC2,CNTN4,PCDH12,SLC4A11,CD36,CFAP54,NFKBID,PRAG1,ATP8A2,HHEX,SOX7,CXCL10,ANGPT2,SLC4A5,ADGRG3,PRDM8,CYP26B1,PPP1R16B,COL2A1,IRX6,GOT1,NKX2-3,BMP1,SPATA25,CTNND2,HYAL2,UPK1B,DPYSL4,ROBO4,NRAP,NFATC2,INPP5D,CD34,PECAM1,CD86,COL18A1,BMP7,IGFBP3,PROX1,MGST1,GPC1,SRMS,ACE,LAMC2,HOXD10,PRAME,LTF,TBX1,LGALS12,FGF23,CRACR2A,PRKCH,BCL6B,LFNG,MTOR,ABI3,KLF1,ISLR2,LYL1,B4GALT6,HCN1,SARM1,SEMA6B,LRG1,NRARP,TMEM204,HES3,EGFL7,NOTCH1,IRF8,S1PR1,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,GGN,SOX17,RELN,ALKAL1,OLIG2,VSTM2L,SOX18,SHANK3,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,RTN4RL2,SCARF1,PDE1B,FLI1	turquoise	VSMC_M6
GO:0072359	0.00	1.00	57	902	circulatory system development	BP	1E-05	FLT4,NOTCH4,ENPP2,PDGFB,ADGRF5,KDR,SYK,THSD7A,IL6,C5,GJA4,RASIP1,PIK3CG,DLL1,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,PDE2A,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,COL2A1,STAB1,ROBO4,NRAP,NFATC2,CD34,PECAM1,COL18A1,BMP7,PROX1,TBX1,LGALS12,MMRN2,MTOR,ARHGEF15,NPR1,LYL1,GREB1L,LRG1,NRARP,TMEM204,EGFL7,NOTCH1,S1PR1,CDH5,SOX17,C3AR1,PDLIM1,SOX18	turquoise	VSMC_M6

GO:0048869	0.00	1.00	136	3033	cellular developmental process	BP	1.1E-05	TNFRSF11A,IL23A,FLT4,MEGF10,CELSR1,NOTCH4,ENPP2,SYT17,PDGFB,ETV7,MDGA1,IREB2,STEAP4,ADGRF5,KDR,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,BCL11A,SLC22A16,RASIP1,DLL1,NOVA2,RAB38,SLC6A6,RARRES2,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,MAP6,SNAP25,PDE2A,SFRP1,ZIC2,CNTN4,PCDH12,SLC4A11,CD36,CFAP54,NFKBID,PRAG1,ATP8A2,HHEX,SOX7,CXCL10,ANGPT2,SLC4A5,ADGRG3,PRDM8,CYP26B1,PPP1R16B,COL2A1,MAPK10,IRX6,GOT1,NKX2-3,BMP1,SPATA25,CTNND2,HYAL2,UPK1B,DPYSL4,ROBO4,NRAP,NFATC2,INPP5D,CD34,PECAM1,CD86,COL18A1,BMP7,IGFBP3,PROX1,MGST1,GPC1,SRMS,ACE,LAMC2,HOXD10,PRAME,LTF,TBX1,LGALS12,FGF23,CRACR2A,PRKCH,BCL6B,LFNG,MTOR,ABI3,KLF1,ISLR2,LYL1,B4GALT6,HCN1,SARM1,SEMA6B,LRG1,NRARP,TMEM204,HES3,EGFL7,NOTCH1,IRF8,S1PR1,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,GGN,SOX17,RELN,ALKAL1,OLIG2,VSTM2L,SOX18,SHANK3,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,RTN4RL2,SCARF1,PDE1B,FLI1	turquoise	VSMC_M6
GO:0002376	0.00	1.00	87	1656	immune system process	BP	1.1E-05	TNFRSF11A,IL23A,LYZ,FLT4,NOTCH4,ENPP2,PDGFB,IREB2,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,IL6,C5,PIK3CG,DLL1,CTSC,RARRES2,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SFRP1,CD36,NFKBID,BPIFB3,HHEX,CXCL10,ADGRG3,THBS4,CYP26B1,STAB1,MAPK10,NKX2-3,SNCA,HYAL2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,TLR7,CD34,PECAM1,CD86,SLAMF9,JAML,SRMS,ACE,ST6GAL1,LTF,CCRL2,CCDC88B,TBX1,SELE,SELP,PLVAP,CRACR2A,PRKCH,BCL6B,LFNG,MTOR,KLF1,LYL1,PDE4B,SARM1,TNFRSF18,NRARP,NOTCH1,IRF8,S1PR1,GBP1,MMP12,PMAIP1,PKHD1L1,TRIM43,C3AR1,TRPM2,TRIM62,CCR7,MSMP,PDE1B,FLI1	turquoise	VSMC_M6
GO:0007186	0.00	1.00	37	458	G protein-coupled receptor signaling pathway	BP	1.2E-05	NMBR,CELSR1,ADGRF5,C5,PIK3CG,PPARG,HTR5A,CXCR4,EDNRB,P2RY6,P2RY2,PDE2A,P2RY14,CXCL10,ADGRG3,PLCB2,SNCA,HCRTR1,GPR146,ADGRA1,CCRL2,LPAR2,GNGT2,NPR1,PDE4B,SSTR5,S1PR1,ADGRL4,ACKR1,C3AR1,NMUR1,GNA12,LPAR6,CCR7,OR6N2,NMB,GNG4	turquoise	VSMC_M6
GO:0006811	0.00	1.00	62	1026	ion transport	BP	1.2E-05	TNFRSF11A,KCNN2,SYT17,PDGFB,SLC16A8,IREB2,ATP8A1,STEAP4,SYK,NDUFA4,GJA4,KCNA7,SLC22A16,PIK3CG,SLC6A6,CXCR4,CTNNB1,TMC6,TMC8,SPTBN4,SLCO2B1,P2RY6,SNAP25,SLC4A11,CD36,SLCO2A1,SLCO5A1,CP,CXCL10,SLC4A5,ATP6V0D2,CLIC6,SNCA,ANO3,MTTP,SLC39A8,HFE,MGST1,SLCO4A1,ACE,LTF,CLDN16,ATP13A1,RGN,FGF23,CRACR2A,SNCG,SLC25A18,HEPH,MTOR,BEST2,HCN1,PDE4B,ATP1A4,RELN,KCNU1,NMUR1,SHANK3,TRPM2,CCR7,NMB,FXYD6	turquoise	VSMC_M6
GO:0048646	0.00	1.00	55	877	anatomical structure formation involved in morphogenesis	BP	2.1E-05	FLT4,CELSR1,NOTCH4,ENPP2,KDR,SYK,THSD7A,IL6,C5,RASIP1,PIK3CG,DLL1,NOS3,ITGB4,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,SFRP1,CD36,ADAMTS9,ATP8A2,HHEX,SOX7,CXCL10,ANGPT2,THBS4,PPP1R16B,COL2A1,STAB1,ROBO4,NRAP,NFATC2,CD34,COL18A1,BMP7,PROX1,GPC1,TBX1,KIF26B,MMRN2,LFNG,NPR1,LRG1,NRARP,EGFL7,NOTCH1,S1PR1,LHX2,CDH5,SOX17,RELN,C3AR1,SOX18	turquoise	VSMC_M6
GO:0048583	0.00	1.00	128	2834	regulation of response to stimulus	BP	2.2E-05	TNFRSF11A,IL23A,FLT4,DENND3,PDGFB,MOB3B,KDR,IL18RAP,IL1RL2,SYK,BARX1,IL6,ANKRD6,ARHGAP25,C5,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,FGD5,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TMC8,GPC6,P2RY6,PDE2A,SFRP1,NOTUM,CD36,NFKBID,PRAG1,PRR5L,F11,KLKB1,HHEX,SOX7,CXCL10,ANGPT2,ADGRG3,THBS4,CYP26B1,PPP1R16B,COL2A1,MAPK10,GOT1,SNCA,CTNND2,SHANK2,HYAL2,NKD2,HFE,HCRTR1,LAPTM5,NFATC2,INPP5D,TLR7,CD34,CD86,ERN1,BMP7,IGFBP3,PROX1,GPC1,SRMS,PTPRE,CNKSR2,PRAME,LTF,ARHGAP27,TSPAN15,TBX1,GUCY1A2,RGN,SELE,SELP,VWF,BAIAP2L1,FGF23,CRACR2A,PPM1F,PRKCH,TSPAN14,BCL6B,MMRN2,LFNG,ARHGEF9,MTOR,ABI3,ARHGEF15,NPR1,KIF26A,PDE4B,SARM1,SEMA6B,LRG1,NRARP,TMEM204,EGFL7,NOTCH1,S1PR1,ENDOG,GBP1,CDH3,CDH5,ALOX12,MMP12,PMAIP1,SOX17,RELN,ALKAL1,C3AR1,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,GNG4,SCARF1	turquoise	VSMC_M6
GO:0050793	0.00	1.00	93	1852	regulation of developmental process	BP	2.3E-05	IL23A,FLT4,MEGF10,CELSR1,NOTCH4,ENPP2,SYT17,PDGFB,KDR,IL1RL2,SYK,IL6,BCL11A,LRRC4B,ANKRD6,C5,DLL1,CTSC,SLC6A6,FGD5,RARRES2,NOS3,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,GPC6,MAP6,SFRP1,NOTUM,CNTN4,SLC4A11,CD36,NFKBID,PRAG1,ADAMTS9,ATP8A2,HHEX,CXCL10,ANGPT2,THBS4,CYP26B1,PPP1R16B,STAB1,BMP1,NFATC2,INPP5D,EAF2,CD34,CD86,BMP7,IGFBP3,PROX1,GPC1,PRAME,PAX9,LTF,TBX1,RGN,LGALS12,FGF23,PRKCH,BCL6B,LFNG,MTOR,ABI3,ARHGEF15,NPR1,ISLR2,SARM1,SEMA6B,LRG1,NRARP,HES3,NOTCH1,S1PR1,PALMD,GBP1,LHX2,CDH3,CDH5,ALOX12,SOX17,RELN,C3AR1,OLIG2,SHANK3,TRIM62,BAMBI,SCARF1	turquoise	VSMC_M6
GO:0050801	0.00	1.00	40	542	ion homeostasis	BP	3.4E-05	IREB2,STEAP4,KDR,PIK3CG,RAB38,CXCR4,EDNRB,TMC8,P2RY6,P2RY2,SLC4A11,CD36,CP,CXCL10,SLC4A5,ATP6V0D2,GOT1,SNCA,HYAL2,SLC39A8,HFE,HCRTR1,LTF,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,FGF23,HEPH,NPR1,S1PR1,CDH5,ALOX12,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0098742	0.00	1.00	19	152	cell-cell adhesion via plasma-membrane adhesion molecules	BP	3.6E-05	CELSR1,MDGA1,LRRC4B,CD177,GPC6,CNTN4,PCDH12,ROBO4,ESAM,PECAM1,JAML,CLDN16,SELE,SELP,DSC2,CDH3,CDH1,CDH5,VSTM2L	turquoise	VSMC_M6

GO:0035295	0.00	1.00	53	849	tube development	BP	3.9E-05	FLT4,CELSR1,NOTCH4,ENPP2,ADGRF5,KDR,SYK,THSD7A,IL6,C5,RASIP1,PIK3CG,DLL1,RARRES2,NOS3,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,COL2A1,STAB1,NKX2-3,ROBO4,CD34,COL18A1,BMP7,PROX1,TBX1,KIF26B,MMRN2,NPR1,GREB1L,LRG1,NRARP,EGFL7,NOTCH1,S1PR1,LHX2,CDH5,ALOX12,MMP12,SOX17,C3AR1,SOX18	turquoise	VSMC_M6
GO:0009653	0.00	1.00	99	2050	anatomical structure morphogenesis	BP	4.3E-05	FLT4,CELSR1,NOTCH4,ENPP2,SYT17,ETV7,FREM1,ADGRF5,KDR,SYK,THSD7A,EPHA5,IL6,BCL11A,ANKRD6,C5,RASIP1,PIK3CG,DLL1,NOVA2,FGD5,NOS3,ITGB4,PPARG,TGFB1,CXCR4,CTNNB1,SPTBN4,TIE1,GPC6,MAP6,SFRP1,CNTN4,CD36,PRAG1,ADAMTS9,ATP8A2,HHEX,LYVE1,SOX7,CXCL10,ANGPT2,THBS4,CYP26B1,PPP1R16B,COL2A1,STAB1,NKX2-3,BMP1,CTNND2,HYAL2,DPYSL4,ROBO4,NRAP,NFATC2,CD34,COL18A1,BMP7,PROX1,GPC1,LAMC2,HOXD10,PAX9,LTF,TBX1,LGALS12,FGF23,KIF26B,MMRN2,LFNG,MTOR,ABI3,ARHGEF15,NPR1,ISLR2,B4GALT6,GREB1L,HCN1,SARM1,SEMA6B,LRG1,NRARP,EGFL7,NOTCH1,S1PR1,PALMD,GBP1,LHX2,CDH5,ALOX12,MMP12,SOX17,RELN,C3AR1,VSTM2L,SOX18,SHANK3,BAMBI,FLI1	turquoise	VSMC_M6
GO:0051716	0.00	1.00	198	5042	cellular response to stimulus	BP	4.5E-05	TNFRSF11A,IL23A,NMBR,FLT4,SYBU,CELSR1,NOTCH4,SYT17,DENND3,PDGFB,CSF2RB,MOB3B,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,ANKRD6,ARHGAP25,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,CTSC,RAB38,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,TIE1,GPC6,P2RY6,P2RY2,PDE2A,SFRP1,RASGRP3,NOTUM,SLC4A11,CD36,NFKBID,PRAG1,PRR5L,HHEX,SOX7,P2RY14,CXCL10,ANGPT2,SOGA1,ADGRG3,HUNK,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,GSTA4,MAPK10,GOT1,BMP1,SNCA,CTNND2,SHANK2,HYAL2,ESRRG,NKD2,HFE,MCTP2,HCRTR1,LAPTM5,NFATC2,INPP5D,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,BMP7,IGFBP3,ASCC2,PROX1,MGST1,GPC1,JAML,SRMS,PTPRE,CNKSR2,PRAME,PAX9,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,LPAR2,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,RCSD1,PPM1F,ERAS,PRKCH,TSPAN14,MMRN2,PPP1R1B,LFNG,ARHGEF9,C19orf57,MTOR,GNGT2,ABI3,ARHGEF15,KLF1,MAST1,NPR1,BEX5,COL4A6,COL4A5,KIF26A,HCN1,PDE4B,SARM1,SEMA6B,LRG1,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,PTGS1,CDH3,CDH1,ADGRL4,CDH5,ALOX12,DCDC2B,MMP12,PMAIP1,GGN,RUFY4,ATP1A4,SOX17,RELN,ACKR1,ALKAL1,C3AR1,NMUR1,NUCB1,GRAP,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,OR6N2,NSG2,MGAT3,MSMP,NMB,HPCAL4,RTN4RL2,GNG4,SCARF1,GPX3,PDE1B	turquoise	VSMC_M6
GO:0007275	0.00	1.00	159	3815	multicellular organism development	BP	4.5E-05	TNFRSF11A,IL23A,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,PDGFB,ETV7,MDGA1,FREM1,IREB2,ADGRF5,KDR,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,C5,GJA4,RASIP1,PIK3CG,DLL1,NOVA2,CTSC,RARRES2,NOS3,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,GPC6,MAP6,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,PCDH12,NFKBID,PRAG1,ADAMTS9,ATP8A2,MALL,HHEX,SOX7,CXCL10,ANGPT2,SLC4A5,ADGRG3,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,COL2A1,STAB1,IRX6,NKX2-3,BMP1,IGSF3,SNCA,CTNND2,SHANK2,HYAL2,LSAMP,HFE,DPYSL4,ROBO4,NRAP,NFATC2,INPP5D,EAF2,CD34,PECAM1,CD86,COL18A1,BMP7,PROX1,MGST1,GPC1,ACE,LAMC2,HOXD10,PAX9,LTF,TBX1,RGN,LGALS12,FGF23,CRACR2A,PRKCH,KIF26B,MMRN2,LFNG,C19orf57,MTOR,ABI3,ARHGEF15,KLF1,MAST1,NPR1,ISLR2,LYL1,B4GALT6,GREB1L,KIF26A,HCN1,SARM1,SEMA6B,LRG1,NRARP,TMEM204,HES3,EGFL7,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,SOX17,RELN,ALKAL1,C3AR1,OLIG2,PDLIM1,VSTM2L,SOX18,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,HPCAL4,RTN4RL2,SCARF1,PDE1B,FLI1	turquoise	VSMC_M6
GO:0048878	0.00	1.00	52	832	chemical homeostasis	BP	4.6E-05	SYBU,IREB2,STEAP4,ADGRF5,KDR,EPHA5,IL6,PIK3CG,RAB38,PPARG,CXCR4,EDNRB,TMC8,P2RY6,P2RY2,SLC4A11,CD36,MALL,CP,CXCL10,SLC4A5,ATP6V0D2,CYP26B1,GOT1,SNCA,MTTP,HYAL2,SLC39A8,HFE,HCRTR1,ERN1,LTF,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,FGF23,HEPH,NPR1,SSTR5,S1PR1,ENDOG,CDH5,ALOX12,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB,RBP1	turquoise	VSMC_M6
GO:0032101	0.00	1.00	44	646	regulation of response to external stimulus	BP	6.1E-05	TNFRSF11A,IL23A,PDGFB,KDR,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,NOVA2,CTSC,RARRES2,NOS3,PPARG,TGFB1,CXCR4,EDNRB,PDE2A,CD36,F11,KLKB1,CXCL10,ANGPT2,THBS4,SNCA,HYAL2,TLR7,CD34,LTF,SELE,PPM1F,BCL6B,MTOR,SEMA6B,NOTCH1,S1PR1,CDH5,ALOX12,MMP12,C3AR1,TRIM62,CCR7,SCARF1	turquoise	VSMC_M6

GO:0032502	0.00	1.00	183	4589	developmental process	BP	6.2E-05	TNFRSF11A,IL23A,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,PDGFB,ETV7,MDGA1,FREM1,IREB2,STEAP4,ADGRF5,KDR,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,C5,GJA4,SLC22A16,RASIP1,PIK3CG,DLL1,NOVA2,CTSC,RAB38,SLC6A6,FGD5,RARRES2,NOS3,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,GPC6,MAP6,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,PCDH12,SLC4A11,CD36,CFAP54,NFKBID,PRAG1,ADAMTS9,ATP8A2,MALL,HHEX,LYVE1,SOX7,CXCL10,ANGPT2,SLC4A5,ADGRG3,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,COL2A1,STAB1,MAPK10,IRX6,GOT1,NKX2-3,BMP1,SPATA25,IGSF3,SNCA,CTNND2,SHANK2,HYAL2,LSAMP,UPK1B,HFE,DPYSL4,ROBO4,NRAP,NFATC2,INPP5D,EAF2,CD34,PECAM1,CD86,COL18A1,BMP7,IGFBP3,PROX1,MGST1,GPC1,OAZ3,SRMS,ACE,LAMC2,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,LGALS12,PLVAP,FGF23,CRACR2A,PRKCH,KIF26B,BCL6B,MMRN2,LFNG,C19orf57,MTOR,BCKDK,ABI3,ARHGEF15,KLF1,MAST1,NPR1,ISLR2,LYL1,B4GALT6,GREB1L,KIF26A,HCN1,SARM1,SEMA6B,LRG1,NRARP,TMEM204,HES3,EGFL7,NOTCH1,IRF8,S1PR1,ENDOG,PALMD,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,GGN,ATP1A4,SOX17,RELN,ALKAL1,C3AR1,OLIG2,PDLIM1,VSTM2L,SOX18,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,HPCAL4,RTN4RL2,SCARF1,PDE1B,FLI1	turquoise	VSMC_M6
GO:0006954	0.00	1.00	37	497	inflammatory response	BP	7.9E-05	TNFRSF11A,IL23A,LYZ,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,CTSC,RARRES2,PPARG,TGFB1,CXCR4,EDNRB,PDE2A,CD36,NFKBID,KLKB1,CXCL10,CYP26B1,STAB1,SNCA,HYAL2,HFE,TLR7,CCRL2,SELE,SELP,BCL6B,NOTCH1,PTGS1,CDH5,ACKR1,C3AR1,CCR7,MSMP	turquoise	VSMC_M6
GO:0045765	0.00	1.00	23	229	regulation of angiogenesis	BP	9.7E-05	ENPP2,KDR,IL6,C5,DLL1,NOS3,PPARG,CXCR4,CTNNB1,TIE1,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,CD34,NPR1,LRG1,CDH5,C3AR1	turquoise	VSMC_M6
GO:0048584	0.00	1.00	77	1488	positive regulation of response to stimulus	BP	9.7E-05	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,IL18RAP,SYK,IL6,ANKRD6,C5,PIK3CG,DLL1,KDM4D,CTSC,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,CTNNB1,P2RY6,PDE2A,SFRP1,CD36,NFKBID,PRAG1,PRR5L,HHEX,CXCL10,THBS4,GOT1,SNCA,HYAL2,HFE,HCRTR1,LAPTM5,NFATC2,INPP5D,TLR7,CD86,ERN1,BMP7,PROX1,LTF,TBX1,GUCY1A2,SELP,VWF,FGF23,CRACR2A,PPM1F,PRKCH,TSPAN14,MTOR,ABI3,NPR1,PDE4B,LRG1,NRARP,NOTCH1,S1PR1,ENDOG,GBP1,CDH3,CDH5,MMP12,PMAIP1,RELN,ALKAL1,C3AR1,SHANK3,LPAR6,TRIM62,BAMBI,CCR7,SCARF1	turquoise	VSMC_M6
GO:0001945	0.00	1.00	8	25	lymph vessel development	BP	1E-04	FLT4,SYK,TIE1,PROX1,TBX1,LGALS12,TMEM204,SOX18	turquoise	VSMC_M6
GO:0006873	0.00	1.00	34	444	cellular ion homeostasis	BP	0.00011	IREB2,STEAP4,PIK3CG,RAB38,CXCR4,EDNRB,P2RY6,P2RY2,SLC4A11,CD36,CP,CXCL10,SLC4A5,ATP6V0D2,GOT1,SNCA,SLC39A8,HFE,HCRTR1,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,FGF23,HEPH,S1PR1,CDH5,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:1901342	0.00	1.00	23	232	regulation of vasculature development	BP	0.00011	ENPP2,KDR,IL6,C5,DLL1,NOS3,PPARG,CXCR4,CTNNB1,TIE1,SFRP1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,CD34,NPR1,LRG1,CDH5,C3AR1	turquoise	VSMC_M6
GO:0051239	0.00	1.00	93	1937	regulation of multicellular organismal process	BP	0.00012	TNFRSF11A,IL23A,KCNN2,FLT4,NOTCH4,ENPP2,PDGFB,KDR,IL1RL2,SYK,IL6,BCL11A,LRRC4B,C5,PIK3CG,DLL1,NOVA2,CTSC,NOS3,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,MAP6,P2RY2,SFRP1,NOTUM,CD36,NFKBID,ADAMTS9,ATP8A2,F11,KLKB1,HHEX,PROCR,CXCL10,ANGPT2,THBS4,CYP26B1,PPP1R16B,STAB1,BMP1,HYAL2,ESRRG,HFE,LAPTM5,INPP5D,EAF2,TLR7,CD34,CD86,BMP7,PROX1,ACE,LTF,CCDC88B,RGN,FGF23,PPM1F,PRKCH,BCL6B,MMRN2,LFNG,MTOR,NPR1,ISLR2,DSC2,PDE4B,SEMA6B,LRG1,NRARP,HES3,NOTCH1,IRF8,S1PR1,GBP1,LHX2,CDH3,CDH5,ALOX12,MMP12,SOX17,RELN,ACKR1,C3AR1,OLIG2,SHANK3,TRIM62,BAMBI,CCR7	turquoise	VSMC_M6
GO:0022603	0.00	1.00	48	761	regulation of anatomical structure morphogenesis	BP	0.00012	FLT4,CELSR1,ENPP2,SYT17,KDR,IL6,BCL11A,ANKRD6,C5,DLL1,FGD5,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,GPC6,MAP6,SFRP1,PRAG1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,PPP1R16B,STAB1,CD34,BMP7,PAX9,TBX1,LFNG,ABI3,NPR1,ISLR2,SARM1,SEMA6B,LRG1,NOTCH1,PALMD,GBP1,CDH5,ALOX12,RELN,C3AR1,SHANK3,BAMBI	turquoise	VSMC_M6
GO:0030595	0.00	1.00	18	150	leukocyte chemotaxis	BP	0.00013	TNFRSF11A,PDGFB,SYK,IL6,C5,PIK3CG,RARRES2,CXCR4,EDNRB,CXCL10,THBS4,JAML,PDE4B,S1PR1,C3AR1,TRPM2,CCR7,MSMP	turquoise	VSMC_M6
GO:0019932	0.00	1.00	22	218	second-messenger-mediated signaling	BP	0.00014	KDR,SYK,EPHA5,NOS3,HTR5A,CXCR4,EDNRB,PDE2A,CD36,MCTP2,NFATC2,CCRL2,GUCY1A2,RGN,SELE,SELP,MTOR,NPR1,GBP1,NMUR1,TRPM2,CCR7	turquoise	VSMC_M6

GO:0010646	0.00	1.00	113	2513	regulation of cell communication	BP	0.00014	TNFRSF11A,IL23A,FLT4,SYBU,DENND3,PDGFB,MOB3B,KDR,SYK,BARX1,EPHA5,IL6,ANKRD6,ARHGAP25,RASIP1,PIK3CG,DLL1,CTSC,SLC6A6,FGD5,NOS3,CD177,PPARG,TGFB1,CXCR4,CTNNB1,TMC8,GPC6,P2RY6,SNAP25,PDE2A,SFRP1,NOTUM,CNTN4,CD36,PRAG1,PRR5L,HHEX,SOX7,ADGRG3,CYP26B1,PPP1R16B,COL2A1,GOT1,SNCA,CTNND2,SHANK2,HYAL2,NKD2,HFE,MCTP2,HCRTR1,LAPTM5,INPP5D,TLR7,CD86,ERN1,BMP7,IGFBP3,PROX1,GPC1,SRMS,PTPRE,CNKSR2,PRAME,LTF,ARHGAP27,TSPAN15,TBX1,GUCY1A2,RGN,SELP,VWF,BAIAP2L1,FGF23,CRACR2A,PRKCH,GRID2IP,TSPAN14,MMRN2,SNCG,LFNG,ARHGEF9,MTOR,ARHGEF15,NPR1,KIF26A,PDE4B,SARM1,LRG1,NRARP,TMEM204,EGFL7,SSTR5,NOTCH1,GBP1,CDH3,CDH1,CDH5,MMP12,PMAIP1,SOX17,RELN,ALKAL1,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,NMB,GNG4	turquoise	VSMC_M6
GO:0051241	0.00	1.00	47	743	negative regulation of multicellular organismal process	BP	0.00015	IL23A,PDGFB,IL6,BCL11A,PIK3CG,DLL1,NOVA2,CTSC,NOS3,PPARG,TGFB1,CTNNB1,SPTBN4,TIE1,SFRP1,ADAMTS9,F11,KLKB1,HHEX,PROCR,CXCL10,ANGPT2,THBS4,STAB1,HFE,LAPTM5,INPP5D,EAF2,CD34,BMP7,LTF,RGN,FGF23,MMRN2,MTOR,NPR1,PDE4B,SEMA6B,NRARP,NOTCH1,GBP1,LHX2,CDH3,ALOX12,SOX17,TRIM62,CCR7	turquoise	VSMC_M6
GO:0055080	0.00	1.00	36	494	cation homeostasis	BP	0.00015	IREB2,STEAP4,PIK3CG,RAB38,CXCR4,EDNRB,TMC8,P2RY6,SLC4A11,CD36,CP,CXCL10,SLC4A5,ATP6V0D2,GOT1,SNCA,HYAL2,SLC39A8,HFE,HCRTR1,LTF,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,HEPH,NPR1,S1PR1,CDH5,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0023051	0.00	1.00	113	2524	regulation of signaling	BP	0.00016	TNFRSF11A,IL23A,FLT4,SYBU,DENND3,PDGFB,MOB3B,KDR,SYK,BARX1,EPHA5,IL6,ANKRD6,ARHGAP25,RASIP1,PIK3CG,DLL1,CTSC,SLC6A6,FGD5,NOS3,CD177,PPARG,TGFB1,CXCR4,CTNNB1,TMC8,GPC6,P2RY6,SNAP25,PDE2A,SFRP1,NOTUM,CNTN4,CD36,PRAG1,PRR5L,HHEX,SOX7,ADGRG3,CYP26B1,PPP1R16B,COL2A1,GOT1,SNCA,CTNND2,SHANK2,HYAL2,NKD2,HFE,MCTP2,HCRTR1,LAPTM5,INPP5D,TLR7,CD86,ERN1,BMP7,IGFBP3,PROX1,GPC1,SRMS,PTPRE,CNKSR2,PRAME,LTF,ARHGAP27,TSPAN15,TBX1,GUCY1A2,RGN,SELP,VWF,BAIAP2L1,FGF23,CRACR2A,PRKCH,GRID2IP,TSPAN14,MMRN2,SNCG,LFNG,ARHGEF9,MTOR,ARHGEF15,NPR1,KIF26A,PDE4B,SARM1,LRG1,NRARP,TMEM204,EGFL7,SSTR5,NOTCH1,GBP1,CDH3,CDH1,CDH5,MMP12,PMAIP1,SOX17,RELN,ALKAL1,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,NMB,GNG4	turquoise	VSMC_M6
GO:0060326	0.00	1.00	21	206	cell chemotaxis	BP	0.0002	TNFRSF11A,PDGFB,KDR,SYK,IL6,C5,PIK3CG,RARRES2,CXCR4,EDNRB,CXCL10,THBS4,JAML,CCRL2,PDE4B,NOTCH1,S1PR1,C3AR1,TRPM2,CCR7,MSMP	turquoise	VSMC_M6
GO:0098771	0.00	1.00	36	502	inorganic ion homeostasis	BP	0.0002	IREB2,STEAP4,PIK3CG,RAB38,CXCR4,EDNRB,TMC8,P2RY6,CD36,CP,CXCL10,SLC4A5,ATP6V0D2,GOT1,SNCA,HYAL2,SLC39A8,HFE,HCRTR1,LTF,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,FGF23,HEPH,NPR1,S1PR1,CDH5,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0001667	0.00	1.00	29	360	ameboidal-type cell migration	BP	0.00024	FLT4,ENPP2,PDGFB,KDR,PIK3CG,NOS3,ITGB4,PPARG,TGFB1,EDNRB,ADAMTS9,PRR5L,ANGPT2,HYAL2,BMP7,PROX1,TBX1,LGALS12,PPM1F,MMRN2,MTOR,SEMA6B,NOTCH1,CDH5,ALOX12,SOX17,PDLIM1,SOX18,GNA12	turquoise	VSMC_M6
GO:0097529	0.00	1.00	17	142	myeloid leukocyte migration	BP	0.00024	TNFRSF11A,PDGFB,SYK,IL6,C5,PIK3CG,RARRES2,CD177,EDNRB,CXCL10,THBS4,PECAM1,JAML,PDE4B,C3AR1,CCR7,MSMP	turquoise	VSMC_M6
GO:0010562	0.00	1.00	43	669	positive regulation of phosphorus metabolic process	BP	0.00031	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,ADGRF5,KDR,SYK,EPHA5,IL6,PIK3CG,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,TIE1,P2RY6,CD36,PRR5L,THBS4,PPP1R16B,SNCA,HFE,PECAM1,CD86,ERN1,BMP7,PROX1,ACE,LTF,TBX1,RGN,FGF23,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0045937	0.00	1.00	43	669	positive regulation of phosphate metabolic process	BP	0.00031	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,ADGRF5,KDR,SYK,EPHA5,IL6,PIK3CG,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,TIE1,P2RY6,CD36,PRR5L,THBS4,PPP1R16B,SNCA,HFE,PECAM1,CD86,ERN1,BMP7,PROX1,ACE,LTF,TBX1,RGN,FGF23,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0032103	0.00	1.00	25	286	positive regulation of response to external stimulus	BP	0.00031	TNFRSF11A,IL23A,PDGFB,KDR,IL18RAP,SYK,IL6,PIK3CG,CTSC,RARRES2,TGFB1,CXCR4,PDE2A,CXCL10,THBS4,SNCA,HYAL2,TLR7,PPM1F,S1PR1,MMP12,C3AR1,TRIM62,CCR7,SCARF1	turquoise	VSMC_M6
GO:0006955	0.00	1.00	57	1012	immune response	BP	0.00038	TNFRSF11A,IL23A,LYZ,ENPP2,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,DLL1,CTSC,RARRES2,CD177,PPARG,TGFB1,CXCR4,CD36,NFKBID,BPIFB3,CXCL10,STAB1,MAPK10,NKX2-3,SNCA,HYAL2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,TLR7,CD86,SLAMF9,SRMS,ST6GAL1,LTF,CCRL2,CCDC88B,SELP,CRACR2A,PRKCH,BCL6B,LFNG,MTOR,PDE4B,SARM1,NOTCH1,IRF8,GBP1,MMP12,PMAIP1,PKHD1L1,TRIM43,C3AR1,TRIM62,CCR7	turquoise	VSMC_M6
GO:0055082	0.00	1.00	38	564	cellular chemical homeostasis	BP	0.00041	SYBU,IREB2,STEAP4,EPHA5,PIK3CG,RAB38,CXCR4,EDNRB,P2RY6,P2RY2,SLC4A11,CD36,CP,CXCL10,SLC4A5,ATP6V0D2,GOT1,SNCA,SLC39A8,HFE,HCRTR1,ERN1,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,FGF23,HEPH,S1PR1,ENDOG,CDH5,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0030003	0.00	1.00	32	434	cellular cation homeostasis	BP	0.00042	IREB2,STEAP4,PIK3CG,RAB38,CXCR4,EDNRB,P2RY6,SLC4A11,CD36,CP,CXCL10,SLC4A5,ATP6V0D2,GOT1,SNCA,SLC39A8,HFE,HCRTR1,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,HEPH,S1PR1,CDH5,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6

GO:0008284	0.00	1.00	43	681	positive regulation of cell population proliferation	BP	0.00047	TNFRSF11A,IL23A,FLT4,MEGF10,PDGFB,KDR,SYK,IL6,DLL1,TGFB1,EDNRB,CTNNB1,P2RY6,SFRP1,CXCL10,THBS4,PPP1R16B,SHANK2,NFATC2,CD86,ERN1,PROX1,JAML,LAMC2,PRAME,LTF,CCDC88B,TBX1,FGF23,PRKCH,MTOR,LRG1,MATK,NRARP,EGFL7,NOTCH1,S1PR1,LHX2,CDH3,ALOX12,MMP12,BAMBI,NMB	turquoise	VSMC_M6
GO:0003013	0.00	1.00	32	437	circulatory system process	BP	0.00047	KCNN2,PDGFB,ATP8A1,PIK3CG,DLL1,SLC6A6,GRIP2,RARRES2,NOS3,PPARG,TGFB1,CXCR4,EDNRB,SPTBN4,SLCO2B1,P2RY2,PDE2A,CD36,CXCL10,SLC4A5,CD34,ACE,PLVAP,MTOR,NPR1,DSC2,PDE4B,PTGS1,CDH5,ATP1A4,C3AR1,FLI1	turquoise	VSMC_M6
GO:0055065	0.00	1.00	32	438	metal ion homeostasis	BP	0.00049	IREB2,STEAP4,PIK3CG,CXCR4,EDNRB,TMC8,P2RY6,CD36,CP,CXCL10,GOT1,SNCA,HYAL2,SLC39A8,HFE,HCRTR1,LTF,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,HEPH,NPR1,S1PR1,CDH5,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0019725	0.00	1.00	41	638	cellular homeostasis	BP	0.0005	SYBU,IREB2,STEAP4,EPHA5,IL6,PIK3CG,RAB38,NOS3,CXCR4,EDNRB,P2RY6,P2RY2,SLC4A11,CD36,CP,CXCL10,SLC4A5,ATP6V0D2,GOT1,SNCA,SLC39A8,HFE,HCRTR1,ERN1,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,FGF23,HEPH,S1PR1,ENDOG,CDH5,ATP1A4,C3AR1,SHANK3,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0042127	0.00	1.00	65	1230	regulation of cell population proliferation	BP	0.0005	TNFRSF11A,IL23A,FLT4,MEGF10,PDGFB,KDR,SYK,IL6,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,TIE1,P2RY6,SFRP1,ATP8A2,HHEX,SOX7,CXCL10,THBS4,PPP1R16B,NKX2-3,SHANK2,NFATC2,INPP5D,EAF2,CD86,ERN1,COL18A1,BMP7,IGFBP3,PROX1,JAML,ACE,LAMC2,PRAME,LTF,CCDC88B,TBX1,RGN,FGF23,PRKCH,BCL6B,MTOR,NPR1,LRG1,MATK,NRARP,EGFL7,SSTR5,NOTCH1,S1PR1,LHX2,PTGS1,CDH3,CDH5,ALOX12,MMP12,SOX17,SOX18,GNA12,BAMBI,NMB	turquoise	VSMC_M6
GO:0032879	0.00	1.00	96	2074	regulation of localization	BP	0.0005	PARD6G,TNFRSF11A,KCNN2,FLT4,SYBU,ENPP2,SYT17,PDGFB,ATP8A1,KDR,SYK,EPHA5,IL6,NDUFA4,C5,KCNA7,PIK3CG,DLL1,NOVA2,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,GPC6,P2RY6,P2RY2,SNAP25,SFRP1,CD36,PRAG1,ADAMTS9,PRR5L,ATP8A2,CXCL10,ANGPT2,ADGRG3,THBS4,CLIC6,SNCA,HYAL2,NKD2,HFE,MCTP2,ROBO4,PECAM1,BMP7,IGFBP3,PROX1,GPC1,OAZ3,ACE,LAMC2,RGN,SELE,SELP,PLVAP,FGF23,CRACR2A,PPM1F,PRKCH,MMRN2,SNCG,MTOR,TTLL6,ABI3,NPR1,DSC2,HCN1,PDE4B,SEMA6B,TNFRSF18,SSTR5,NOTCH1,S1PR1,GBP1,CDH3,CDH1,CDH5,ALOX12,RELN,C3AR1,KCNU1,NUCB1,GNA12,SHANK3,TRPM2,CCR7,MGAT3,NMB,FXYD6	turquoise	VSMC_M6
GO:0050673	0.00	1.00	26	316	epithelial cell proliferation	BP	0.00051	FLT4,PDGFB,KDR,IL6,PPARG,TGFB1,EDNRB,CTNNB1,TIE1,SFRP1,THBS4,PPP1R16B,EAF2,CD34,ERN1,PROX1,JAML,TBX1,RGN,MTOR,LRG1,NRARP,EGFL7,NOTCH1,CDH3,MMP12	turquoise	VSMC_M6
GO:0048871	0.00	1.00	29	378	multicellular organismal homeostasis	BP	0.00053	TNFRSF11A,LYZ,ADGRF5,SYK,IL6,DLL1,NOVA2,NOS3,CXCR4,EDNRB,CTNNB1,CD36,CYP26B1,COL2A1,HYAL2,SLC39A8,ESRRG,HFE,ESAM,INPP5D,CD34,PECAM1,LTF,NOTCH1,S1PR1,CDH3,CDH5,ALOX12,TRPM2	turquoise	VSMC_M6
GO:0050679	0.00	1.00	17	154	positive regulation of epithelial cell proliferation	BP	0.00059	FLT4,PDGFB,KDR,CTNNB1,SFRP1,THBS4,PPP1R16B,PROX1,JAML,TBX1,MTOR,LRG1,NRARP,EGFL7,NOTCH1,CDH3,MMP12	turquoise	VSMC_M6
GO:0048856	0.00	1.00	166	4193	anatomical structure development	BP	0.00067	TNFRSF11A,IL23A,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,PDGFB,ETV7,MDGA1,FREM1,IREB2,ADGRF5,KDR,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,C5,GJA4,RASIP1,PIK3CG,DLL1,NOVA2,CTSC,FGD5,RARRES2,NOS3,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,GPC6,MAP6,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,PCDH12,CD36,NFKBID,PRAG1,ADAMTS9,ATP8A2,MALL,HHEX,LYVE1,SOX7,CXCL10,ANGPT2,SLC4A5,ADGRG3,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,COL2A1,STAB1,IRX6,NKX2-3,BMP1,IGSF3,SNCA,CTNND2,SHANK2,HYAL2,LSAMP,UPK1B,HFE,DPYSL4,ROBO4,NRAP,NFATC2,INPP5D,EAF2,CD34,PECAM1,CD86,COL18A1,BMP7,IGFBP3,PROX1,MGST1,GPC1,ACE,LAMC2,HOXD10,PAX9,LTF,TBX1,RGN,LGALS12,FGF23,CRACR2A,PRKCH,KIF26B,MMRN2,LFNG,C19orf57,MTOR,ABI3,ARHGEF15,KLF1,MAST1,NPR1,ISLR2,LYL1,B4GALT6,GREB1L,KIF26A,HCN1,SARM1,SEMA6B,LRG1,NRARP,TMEM204,HES3,EGFL7,NOTCH1,IRF8,S1PR1,ENDOG,PALMD,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,SOX17,RELN,ALKAL1,C3AR1,OLIG2,PDLIM1,VSTM2L,SOX18,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,HPCAL4,RTN4RL2,SCARF1,PDE1B,FLI1	turquoise	VSMC_M6
GO:2000026	0.00	1.00	56	1014	regulation of multicellular organismal development	BP	0.00071	IL23A,NOTCH4,ENPP2,KDR,IL1RL2,SYK,IL6,LRRC4B,C5,DLL1,CTSC,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,MAP6,SFRP1,NOTUM,NFKBID,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,CYP26B1,PPP1R16B,STAB1,BMP1,INPP5D,CD34,CD86,BMP7,PROX1,LTF,RGN,FGF23,PRKCH,MTOR,NPR1,ISLR2,SEMA6B,LRG1,NRARP,HES3,NOTCH1,S1PR1,LHX2,CDH3,CDH5,SOX17,RELN,C3AR1,OLIG2,SHANK3	turquoise	VSMC_M6

GO:0009966	0.00	1.00	101	2237	regulation of signal transduction	BP	0.00072	TNFRSF11A,IL23A,FLT4,DENND3,PDGFB,MOB3B,KDR,SYK,BARX1,IL6,ANKRD6,ARHGAP25,RASIP1,PIK3CG,DLL1,CTSC,FGD5,NOS3,CD177,PPARG,TGFB1,CXCR4,CTNNB1,TMC8,GPC6,P2RY6,PDE2A,SFRP1,NOTUM,CD36,PRAG1,PRR5L,HHEX,SOX7,ADGRG3,CYP26B1,PPP1R16B,COL2A1,GOT1,SNCA,CTNND2,SHANK2,HYAL2,NKD2,HFE,HCRTR1,LAPTM5,INPP5D,TLR7,CD86,ERN1,BMP7,IGFBP3,PROX1,GPC1,SRM5,PTPRE,CNKSR2,PRAME,LTF,ARHGAP27,TSPAN15,TBX1,GUCY1A2,RGN,SELP,VWF,BAIAP2L1,FGF23,CRACR2A,PRKCH,TSPAN14,MMRN2,LFNG,ARHGEF9,MTOR,ARHGEF15,NPR1,KIF26A,PDE4B,SARM1,LRG1,NRARP,TMEM204,EGFL7,NOTCH1,GBP1,CDH3,CDH5,MMP12,PMAIP1,SOX17,RELN,ALKAL1,GNA12,SHANK3,LPAR6,TRIM62,BAMBI,CCR7,GNG4	turquoise	VSMC_M6
GO:0034103	0.00	1.00	10	57	regulation of tissue remodeling	BP	0.00104	TNFRSF11A,IL23A,FLT4,SYK,IL6,TGFB1,SFRP1,THBS4,INPP5D,S1PR1	turquoise	VSMC_M6
GO:0050678	0.00	1.00	23	275	regulation of epithelial cell proliferation	BP	0.00133	FLT4,PDGFB,KDR,PPARG,TGFB1,EDNRB,CTNNB1,TIE1,SFRP1,THBS4,PPP1R16B,EAF2,PROX1,JAML,TBX1,RGN,MTOR,LRG1,NRARP,EGFL7,NOTCH1,CDH3,MMP12	turquoise	VSMC_M6
GO:0001775	0.00	1.00	42	692	cell activation	BP	0.00145	IL23A,MEGF10,PDGFB,ADGRF5,IL18RAP,IL1RL2,SYK,IL6,PIK3CG,DLL1,CTSC,NOS3,CD177,TGFB1,CTNNB1,SFRP1,NFKBID,HHEX,CXCL10,ADGRG3,CYP26B1,NKX2-3,SNCA,HYAL2,HFE,LAPTM5,NFATC2,INPP5D,CD86,SLAMF9,JAML,CCDC88B,SELP,VWF,CRACR2A,LFNG,MTOR,LYL1,NRARP,IRF8,ALOX12,CCR7	turquoise	VSMC_M6
GO:0030335	0.00	1.00	31	443	positive regulation of cell migration	BP	0.00146	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,PIK3CG,RARRES2,NOS3,TGFB1,CXCR4,P2RY6,CXCL10,THBS4,PECAM1,BMP7,PROX1,LAMC2,SELP,PLVAP,PPM1F,MTOR,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH5,ALOX12,RELN,C3AR1,CCR7	turquoise	VSMC_M6
GO:1903131	0.00	1.00	24	297	mononuclear cell differentiation	BP	0.00151	IL23A,IL1RL2,SYK,IL6,DLL1,PPARG,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,INPP5D,CD86,CRACR2A,LFNG,MTOR,LYL1,NRARP,IRF8,TRPM2,CCR7,PDE1B	turquoise	VSMC_M6
GO:0051272	0.00	1.00	32	466	positive regulation of cellular component movement	BP	0.00151	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,PIK3CG,RARRES2,NOS3,TGFB1,CXCR4,P2RY6,CXCL10,THBS4,PECAM1,BMP7,PROX1,LAMC2,SELP,PLVAP,PPM1F,MTOR,TTLL6,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH5,ALOX12,RELN,C3AR1,CCR7	turquoise	VSMC_M6
GO:0006875	0.00	1.00	28	381	cellular metal ion homeostasis	BP	0.00155	IREB2,STEAP4,PIK3CG,CXCR4,EDNRB,P2RY6,CD36,CP,CXCL10,GOT1,SNCA,SLC39A8,HFE,HCRTR1,CCRL2,CLDN16,ATP13A1,LPAR2,RGN,HEPH,S1PR1,CDH5,ATP1A4,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0048534	0.00	1.00	40	649	hematopoietic or lymphoid organ development	BP	0.00155	TNFRSF11A,IL23A,FLT4,NOTCH4,IREB2,ADGRF5,KDR,IL1RL2,SYK,BARX1,IL6,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,HYAL2,INPP5D,CD34,CD86,ACE,LTF,TBX1,CRACR2A,LFNG,MTOR,KLF1,LYL1,NRARP,NOTCH1,IRF8,TRPM2,CCR7,PDE1B,FLI1	turquoise	VSMC_M6
GO:0050920	0.00	1.00	17	167	regulation of chemotaxis	BP	0.00156	PDGFB,KDR,IL6,C5,NOVA2,RARRES2,TGFB1,CXCR4,CXCL10,ANGPT2,THBS4,PPM1F,SEMA6B,NOTCH1,S1PR1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0006820	0.00	1.00	25	319	anion transport	BP	0.00163	TNFRSF11A,SLC16A8,SYK,SLC6A6,SLCO2B1,P2RY6,SLC4A11,CD36,SLCO2A1,SLCO5A1,SLC4A5,CLIC6,SNCA,ANO3,MTTP,SLC39A8,MGST1,SLCO4A1,ACE,FGF23,SLC25A18,MTOR,BEST2,NMUR1,NMB	turquoise	VSMC_M6
GO:0021700	0.00	1.00	19	204	developmental maturation	BP	0.00163	SYBU,BCL11A,RAB38,PPARG,EDNRB,CTNNB1,SPTBN4,LTF,MTOR,ARHGEF15,LYL1,B4GALT6,S1PR1,LHX6,CDH3,CDH5,RELN,SOX18,SCARF1	turquoise	VSMC_M6
GO:0051093	0.00	1.00	41	676	negative regulation of developmental process	BP	0.00163	NOTCH4,PDGFB,IL6,BCL11A,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,TIE1,SFRP1,CNTN4,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,STAB1,NFATC2,INPP5D,EAF2,BMP7,PRAME,LTF,TBX1,RGN,FGF23,ARHGEF15,NPR1,SEMA6B,NRARP,HES3,NOTCH1,GBP1,LHX2,CDH3,SOX17,OLIG2,TRIM62,BAMBI	turquoise	VSMC_M6
GO:0001932	0.00	1.00	48	845	regulation of protein phosphorylation	BP	0.00163	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,IL6,RASIP1,PIK3CG,KDM4D,RARRES2,PPARG,TGFB1,EDNRB,SPTBN4,SFRP1,CD36,KIRREL2,PRR5L,HHEX,THBS4,SNCA,HYAL2,HFE,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,ACE,LTF,TBX1,RGN,FGF23,PPM1F,PPP1R1B,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0003160	0.00	1.00	4	6	endocardium morphogenesis	BP	0.00163	PROX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0002521	0.00	1.00	28	383	leukocyte differentiation	BP	0.00166	TNFRSF11A,IL23A,IREB2,IL1RL2,SYK,IL6,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,INPP5D,CD86,LTF,CRACR2A,LFNG,MTOR,LYL1,NRARP,IRF8,TRPM2,CCR7,PDE1B	turquoise	VSMC_M6
GO:0030155	0.00	1.00	35	541	regulation of cell adhesion	BP	0.00183	IL23A,MEGF10,NOTCH4,PDGFB,MDGA1,KDR,IL1RL2,SYK,IL6,PIK3CG,DLL1,TGFB1,CXCR4,SFRP1,CD36,NFKBID,ANGPT2,HFE,LAPTM5,CD86,BMP7,CCDC88B,SELE,SELP,PPM1F,KIF26B,TNFRSF18,NRARP,NOTCH1,S1PR1,GBP1,CDH1,ALOX12,MMP12,CCR7	turquoise	VSMC_M6
GO:0006952	0.00	1.00	52	949	defense response	BP	0.00187	TNFRSF11A,IL23A,LYZ,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,CTSC,RARRES2,CD177,PPARG,TGFB1,CXCR4,EDNRB,PDE2A,CD36,NFKBID,BPIFB3,KLKB1,CXCL10,CYP26B1,STAB1,SNCA,HYAL2,HFE,LAPTM5,ISG20,TLR7,SRM5,LTF,CCRL2,CCDC88B,SELE,SELP,BCL6B,ABI3,SARM1,NOTCH1,IRF8,GBP1,PTGS1,CDH5,MMP12,PMAIP1,TRIM43,ACKR1,C3AR1,TRIM62,CCR7,MSMP	turquoise	VSMC_M6
GO:0001894	0.00	1.00	18	189	tissue homeostasis	BP	0.00197	TNFRSF11A,LYZ,ADGRF5,SYK,IL6,NOS3,CTNNB1,COL2A1,SLC39A8,ESAM,INPP5D,CD34,PECAM1,LTF,NOTCH1,S1PR1,CDH3,CDH5	turquoise	VSMC_M6
GO:2000147	0.00	1.00	31	455	positive regulation of cell motility	BP	0.00212	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,PIK3CG,RARRES2,NOS3,TGFB1,CXCR4,P2RY6,CXCL10,THBS4,PECAM1,BMP7,PROX1,LAMC2,SELP,PLVAP,PPM1F,MTOR,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH5,ALOX12,RELN,C3AR1,CCR7	turquoise	VSMC_M6

GO:0051094	0.00	1.00	53	982	positive regulation of developmental process	BP	0.00212	IL23A,ENPP2,SYT17,PDGFB,KDR,IL1RL2,SYK,IL6,LRRC4B,C5,DLL1,SLC6A6,RARRES2,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,SPTBN4,TIE1,MAP6,SFRP1,CD36,NFKBID,ATP8A2,ANGPT2,CYP26B1,BMP1,NFATC2,INPP5D,CD34,CD86,BMP7,IGFBP3,PROX1,GPC1,LTF,TBX1,PRKCH,MTOR,ABI3,ISLR2,LRG1,NOTCH1,CDH5,ALOX12,SOX17,RELN,C3AR1,OLIG2,SHANK3,BAMBI,SCARF1	turquoise	VSMC_M6
GO:0007219	0.00	1.00	15	138	Notch signaling pathway	BP	0.00213	NOTCH4,MAML3,DLL1,GRIP2,NOS3,PRAG1,GOT1,BMP7,TSPAN15,TSPAN14,LFNG,NRARP,HES3,EGFL7,NOTCH1	turquoise	VSMC_M6
GO:0008015	0.00	1.00	27	369	blood circulation	BP	0.00213	KCNN2,PDGFB,PIK3CG,DLL1,GRIP2,RARRES2,NOS3,PPARG,TGFB1,CXCR4,EDNRB,SPTBN4,P2RY2,PDE2A,CXCL10,SLC4A5,CD34,ACE,PLVAP,MTOR,NPR1,DSC2,PDE4B,PTGS1,CDH5,C3AR1,FLI1	turquoise	VSMC_M6
GO:0060429	0.00	1.00	46	810	epithelium development	BP	0.0022	CELSR1,NOTCH4,PDGFB,KDR,BARX1,ANKRD6,GJA4,RASIP1,DLL1,PPARG,TGFB1,CXCR4,CTNNB1,TIE1,GPC6,PDE2A,SFRP1,CXCL10,SLC4A5,CYP26B1,PPP1R16B,COL2A1,UPK1B,ROBO4,CD34,PECAM1,COL18A1,BMP7,PROX1,TBX1,PRKCH,KIF26B,LFNG,MTOR,GREB1L,NRARP,NOTCH1,S1PR1,LHX2,CDH3,CDH5,ALOX12,MMP12,SOX17,SOX18,HRASLS	turquoise	VSMC_M6
GO:0001935	0.00	1.00	14	123	endothelial cell proliferation	BP	0.0023	FLT4,PDGFB,KDR,PPARG,TIE1,THBS4,PPP1R16B,CD34,ERN1,PROX1,MTOR,LRG1,NRARP,EGFL7	turquoise	VSMC_M6
GO:0030097	0.00	1.00	38	618	hemopoiesis	BP	0.00235	TNFRSF11A,IL23A,FLT4,NOTCH4,IREB2,ADGRF5,KDR,IL1RL2,SYK,IL6,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,HYAL2,INPP5D,CD34,CD86,ACE,LTF,CRACR2A,LFNG,MTOR,KLF1,LYL1,NRARP,NOTCH1,IRF8,TRPM2,CCR7,PDE1B,FLI1	turquoise	VSMC_M6
GO:0007202	0.00	1.00	6	20	activation of phospholipase C activity	BP	0.00249	P2RY6,PLCB2,CD86,LPAR2,SELE,NMUR1	turquoise	VSMC_M6
GO:0010647	0.00	1.00	63	1251	positive regulation of cell communication	BP	0.00258	TNFRSF11A,IL23A,FLT4,SYBU,PDGFB,KDR,SYK,IL6,ANKRD6,PIK3CG,DLL1,CTSC,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,P2RY6,SNAP25,SFRP1,CD36,PRAG1,PRR5L,HHEX,GOT1,SNCA,SHANK2,HYAL2,HFE,HCRTR1,LAPTM5,TLR7,CD86,ERN1,BMP7,PROX1,LTF,TBX1,GUCY1A2,SELP,VWF,FGF23,CRACR2A,PRKCH,TSPAN14,MTOR,NPR1,LRG1,NRARP,NOTCH1,CDH3,CDH5,MMP12,PMAIP1,RELN,ALKAL1,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,NMB	turquoise	VSMC_M6
GO:0040017	0.00	1.00	31	462	positive regulation of locomotion	BP	0.00264	FLT4,ENPP2,PDGFB,ATP8A1,KDR,IL6,PIK3CG,RARRES2,NOS3,TGFB1,CXCR4,P2RY6,CXCL10,THBS4,PECAM1,BMP7,PROX1,LAMC2,SELP,PLVAP,PPM1F,MTOR,SEMA6B,TNFRSF18,NOTCH1,S1PR1,CDH5,ALOX12,RELN,C3AR1,CCR7	turquoise	VSMC_M6
GO:0050878	0.00	1.00	22	273	regulation of body fluid levels	BP	0.00289	PDGFB,SYK,IL6,PIK3CG,NOS3,EDNRB,P2RY2,CD36,F11,KLKB1,PROCR,SLC4A5,CYP26B1,MMRN1,HYAL2,CD34,SELP,VWF,NPR1,ALOX12,GNA12,FLI1	turquoise	VSMC_M6
GO:0022407	0.00	1.00	23	293	regulation of cell-cell adhesion	BP	0.00289	IL23A,MEGF10,NOTCH4,MDGA1,IL1RL2,SYK,IL6,TGFB1,NFKBID,HFE,LAPTM5,CD86,BMP7,CCDC88B,SELE,SELP,PPM1F,KIF26B,NRARP,NOTCH1,CDH1,ALOX12,CCR7	turquoise	VSMC_M6
GO:0071674	0.00	1.00	14	126	mononuclear cell migration	BP	0.00289	TNFRSF11A,PDGFB,IL6,PIK3CG,RARRES2,CXCR4,CXCL10,PECAM1,JAML,S1PR1,C3AR1,TRPM2,CCR7,MSMP	turquoise	VSMC_M6
GO:0019220	0.00	1.00	56	1074	regulation of phosphate metabolic process	BP	0.00289	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,ADGRF5,KDR,SYK,EPHA5,IL6,RASIP1,PIK3CG,KDM4D,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,SPTBN4,TIE1,P2RY6,SFRP1,CD36,KIRREL2,PRR5L,HHEX,THBS4,PPP1R16B,SNCA,HYAL2,HFE,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,ACE,LTF,TBX1,RGN,CDA,FGF23,PPM1F,PPP1R1B,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0051174	0.00	1.00	56	1074	regulation of phosphorus metabolic process	BP	0.00289	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,ADGRF5,KDR,SYK,EPHA5,IL6,RASIP1,PIK3CG,KDM4D,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,SPTBN4,TIE1,P2RY6,SFRP1,CD36,KIRREL2,PRR5L,HHEX,THBS4,PPP1R16B,SNCA,HYAL2,HFE,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,ACE,LTF,TBX1,RGN,CDA,FGF23,PPM1F,PPP1R1B,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0023056	0.00	1.00	63	1258	positive regulation of signaling	BP	0.00289	TNFRSF11A,IL23A,FLT4,SYBU,PDGFB,KDR,SYK,IL6,ANKRD6,PIK3CG,DLL1,CTSC,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,P2RY6,SNAP25,SFRP1,CD36,PRAG1,PRR5L,HHEX,GOT1,SNCA,SHANK2,HYAL2,HFE,HCRTR1,LAPTM5,TLR7,CD86,ERN1,BMP7,PROX1,LTF,TBX1,GUCY1A2,SELP,VWF,FGF23,CRACR2A,PRKCH,TSPAN14,MTOR,NPR1,LRG1,NRARP,NOTCH1,CDH3,CDH5,MMP12,PMAIP1,RELN,ALKAL1,SHANK3,LPAR6,TRPM2,TRIM62,BAMBI,CCR7,NMB	turquoise	VSMC_M6
GO:0009611	0.00	1.00	29	422	response to wounding	BP	0.00301	NOTCH4,PDGFB,KDR,SYK,IL6,PIK3CG,NOS3,ITGB4,TGFB1,CXCR4,CD36,F11,KLKB1,HHEX,LYVE1,PROCR,MMRN1,CD34,JAML,SELP,VWF,MTOR,SARM1,CDH3,ALOX12,MMP12,GNA12,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0048771	0.00	1.00	14	129	tissue remodeling	BP	0.00359	TNFRSF11A,IL23A,FLT4,SYK,IL6,NOS3,TGFB1,CTNNB1,TIE1,SFRP1,THBS4,INPP5D,ACE,S1PR1	turquoise	VSMC_M6
GO:0019722	0.00	1.00	15	147	calcium-mediated signaling	BP	0.00378	KDR,SYK,CXCR4,EDNRB,MCTP2,NFATC2,CCRL2,RGN,SELE,SELP,MTOR,GBP1,NMUR1,TRPM2,CCR7	turquoise	VSMC_M6
GO:0009617	0.00	1.00	26	362	response to bacterium	BP	0.0038	TNFRSF11A,IL23A,LYZ,CSF2RB,SYK,IL6,RARRES2,NOS3,TGFB1,EDNRB,CD36,CXCL10,STAB1,SNCA,UPK1B,CD86,MGST1,LTF,SELE,SELP,BAIAP2L1,PDE4B,LRG1,NOTCH1,IRF8,CCR7	turquoise	VSMC_M6
GO:0030098	0.00	1.00	21	259	lymphocyte differentiation	BP	0.00384	IL23A,IL1RL2,SYK,IL6,DLL1,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,INPP5D,CD86,CRACR2A,LFNG,MTOR,LYL1,NRARP,IRF8,CCR7	turquoise	VSMC_M6
GO:0009607	0.00	1.00	47	856	response to biotic stimulus	BP	0.00396	TNFRSF11A,IL23A,LYZ,CSF2RB,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CD36,BPIFB3,CXCL10,STAB1,SNCA,HYAL2,UPK1B,LAPTM5,ISG20,TLR7,CD86,MGST1,SRMS,LTF,CCDC88B,SELE,SELP,BAIAP2L1,ABI3,PDE4B,SARM1,LRG1,NOTCH1,IRF8,GBP1,MMP12,PMAIP1,TRIM43,TRIM62,CCR7	turquoise	VSMC_M6

GO:0030855	0.00	1.00	29	430	epithelial cell differentiation	BP	0.00396	NOTCH4,PDGFB,KDR,BARX1,DLL1,PPARG,CXCR4,CTNNB1,TIE1,PDE2A,SLC4A5,CYP26B1,PPP1R16B,UPK1B,ROBO4,CD34,PECAM1,COL18A1,BMP7,PROX1,TBX1,PRKCH,NOTCH1,S1PR1,CDH3,CDH5,SOX17,SOX18,HRASLS	turquoise	VSMC_M6
GO:0001934	0.00	1.00	34	543	positive regulation of protein phosphorylation	BP	0.00402	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,IL6,PIK3CG,RARRES2,PPARG,TGFB1,EDNRB,CD36,PRR5L,THBS4,SNCA,HFE,PECAM1,CD86,ERN1,BMP7,PROX1,ACE,LTF,TBX1,FGF23,MTOR,TNFRSF18,SH2D3C,RELN,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0006468	0.00	1.00	61	1223	protein phosphorylation	BP	0.00408	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,RASIP1,PIK3CG,KDM4D,RARRES2,PPARG,TGFB1,EDNRB,SPTBN4,TIE1,SFRP1,CD36,KIRREL2,STK35,PRAG1,PRR5L,HHEX,HUNK,THBS4,MAPK10,SNCA,HYAL2,HFE,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,SRMS,ACE,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,PPP1R1B,MTOR,BCKDK,MAST1,NPR1,MATK,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0007599	0.00	1.00	16	166	hemostasis	BP	0.00412	PDGFB,SYK,IL6,PIK3CG,NOS3,CD36,F11,KLKB1,PROCR,MMRN1,CD34,SELP,VWF,ALOX12,GNA12,FLI1	turquoise	VSMC_M6
GO:0009888	0.00	1.00	67	1389	tissue development	BP	0.00437	MEGF10,CELSR1,NOTCH4,PDGFB,KDR,BARX1,IL6,ANKRD6,GJA4,RASIP1,DLL1,NOS3,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,GPC6,PDE2A,SFRP1,NOTUM,ADAMTS9,SOX7,CXCL10,SLC4A5,CYP26B1,PPP1R16B,COL2A1,NKX2-3,BMP1,HYAL2,UPK1B,ROBO4,NRAP,CD34,PECAM1,COL18A1,BMP7,PROX1,GPC1,LAMC2,HOXD10,PAX9,LTF,TBX1,FGF23,PRKCH,KIF26B,LFNG,MTOR,GREB1L,SEMA6B,NRARP,NOTCH1,S1PR1,LHX2,CDH3,CDH5,ALOX12,MMP12,SOX17,SOX18,TRIM62,BAMBI,HRASLS	turquoise	VSMC_M6
GO:0070887	0.00	1.00	97	2230	cellular response to chemical stimulus	BP	0.00437	TNFRSF11A,FLT4,SYBU,SYT17,PDGFB,CSF2RB,KDR,IL18RAP,IL1RL2,SYK,EPHA5,IL6,BCL11A,C5,PIK3CG,DLL1,RARRES2,NOS3,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,SLC4A11,CD36,PRR5L,HHEX,CXCL10,ANGPT2,SOGA1,THBS4,CYP26B1,COL2A1,GSTA4,MAPK10,GOT1,SNCA,HYAL2,ESRRG,HFE,LAPTM5,CD34,CD86,ERN1,BMP7,MGST1,GPC1,JAML,PTPRE,PAX9,LTF,CCRL2,TBX1,PLVAP,BAIAP2L1,FGF23,RCSD1,PPM1F,MMRN2,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,LRG1,TNFRSF18,TMEM204,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,GBP1,PTGS1,CDH1,CDH5,ALOX12,MMP12,PMAIP1,RUFY4,SOX17,ACKR1,C3AR1,TRPM2,BAMBI,CCR7,NSG2,MGAT3,MSMP,GPX3,PDE1B	turquoise	VSMC_M6
GO:0001570	0.00	1.00	10	71	vasculogenesis	BP	0.00488	KDR,RASIP1,TGFB1,CTNNB1,TIE1,CD34,EGFL7,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0072012	0.00	1.00	6	23	glomerulus vasculature development	BP	0.00488	PDGFB,ANGPT2,CD34,PECAM1,BMP7,NOTCH1	turquoise	VSMC_M6
GO:0002673	0.00	1.00	6	23	regulation of acute inflammatory response	BP	0.00488	TNFRSF11A,IL6,PIK3CG,EDNRB,KLKB1,CCR7	turquoise	VSMC_M6
GO:0002520	0.00	1.00	40	694	immune system development	BP	0.005	TNFRSF11A,IL23A,FLT4,NOTCH4,IREB2,ADGRF5,KDR,IL1RL2,SYK,BARX1,IL6,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,HYAL2,INPP5D,CD34,CD86,ACE,LTF,TBX1,CRACR2A,LFNG,MTOR,KLF1,LYL1,NRARP,NOTCH1,IRF8,TRPM2,CCR7,PDE1B,FLI1	turquoise	VSMC_M6
GO:0009967	0.00	1.00	57	1127	positive regulation of signal transduction	BP	0.00501	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,SYK,IL6,ANKRD6,PIK3CG,DLL1,CTSC,NOS3,PPARG,TGFB1,CXCR4,CTNNB1,P2RY6,SFRP1,CD36,PRAG1,PRR5L,HHEX,GOT1,HYAL2,HFE,HCRTR1,LAPTM5,TLR7,CD86,ERN1,BMP7,PROX1,LTF,TBX1,GUCY1A2,SELP,VWF,FGF23,CRACR2A,PRKCH,TSPAN14,MTOR,NPR1,LRG1,NRARP,NOTCH1,CDH3,CDH5,MMP12,PMAIP1,RELN,ALKAL1,SHANK3,LPAR6,TRIM62,BAMBI,CCR7	turquoise	VSMC_M6
GO:0051240	0.00	1.00	54	1050	positive regulation of multicellular organismal process	BP	0.00514	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,IL1RL2,SYK,IL6,LRRC4B,C5,PIK3CG,DLL1,NOS3,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,MAP6,P2RY2,CD36,NFKBID,ATP8A2,ANGPT2,BMP1,HYAL2,ESRRG,LAPTM5,INPP5D,TLR7,CD34,CD86,BMP7,PROX1,LTF,CCDC88B,PRKCH,MTOR,NPR1,JSLR2,PDE4B,LRG1,NOTCH1,IRF8,CDH5,ALOX12,MMP12,RELN,C3AR1,OLIG2,SHANK3,BAMBI,CCR7	turquoise	VSMC_M6
GO:0018108	0.00	1.00	22	287	peptidyl-tyrosine phosphorylation	BP	0.00514	IL23A,FLT4,ENPP2,PDGFB,KDR,SYK,EPHA5,IL6,TGFB1,TIE1,SFRP1,CD36,THBS4,HYAL2,PECAM1,SRMS,ACE,MTOR,MATK,TNFRSF18,RELN,ALKAL1	turquoise	VSMC_M6
GO:0006812	0.00	1.00	44	796	cation transport	BP	0.00527	KCNN2,SYT17,PDGFB,IREB2,ATP8A1,STEAP4,SYK,NDUFA4,GJA4,KCNA7,SLC22A16,PIK3CG,SLC6A6,CXCR4,CTNNB1,SPTBN4,P2RY6,SNAP25,SLC4A11,CP,CXCL10,SLC4A5,ATP6V0D2,SNCA,SLC39A8,HFE,LTF,CLDN16,ATP13A1,RGN,CRACR2A,SNCG,SLC25A18,HEPH,HCN1,PDE4B,ATP1A4,RELN,KCNU1,NMUR1,SHANK3,TRPM2,CCR7,FXYD6	turquoise	VSMC_M6
GO:0007156	0.00	1.00	11	88	homophilic cell adhesion via plasma membrane adhesion molecules	BP	0.00527	CELSR1,CNTN4,PCDH12,ROBO4,ESAM,PECAM1,DSC2,CDH3,CDH1,CDH5,VSTM2L	turquoise	VSMC_M6
GO:0043207	0.00	1.00	45	820	response to external biotic stimulus	BP	0.00529	TNFRSF11A,IL23A,LYZ,CSF2RB,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CD36,BPIFB3,CXCL10,STAB1,SNCA,HYAL2,UPK1B,ISG20,TLR7,CD86,MGST1,SRMS,LTF,CCDC88B,SELE,SELP,BAIAP2L1,PDE4B,SARM1,LRG1,NOTCH1,IRF8,GBP1,MMP12,PMAIP1,TRIM43,TRIM62,CCR7	turquoise	VSMC_M6
GO:0051707	0.00	1.00	45	820	response to other organism	BP	0.00529	TNFRSF11A,IL23A,LYZ,CSF2RB,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CD36,BPIFB3,CXCL10,STAB1,SNCA,HYAL2,UPK1B,ISG20,TLR7,CD86,MGST1,SRMS,LTF,CCDC88B,SELE,SELP,BAIAP2L1,PDE4B,SARM1,LRG1,NOTCH1,IRF8,GBP1,MMP12,PMAIP1,TRIM43,TRIM62,CCR7	turquoise	VSMC_M6

GO:0003008	0.00	1.00	61	1240	system process	BP	0.00538	KCNN2,FLT4,PDGFB,IREB2,ATP8A1,ADGRF5,PIK3CG,DLL1,CTSC,SLC6A6,GRIP2,RARRES2,NOS3,PPARG,TGFB1,CXCR4,EDNRB,SPTBN4,SLCO2B1,P2RY2,SNAP25,PDE2A,ZIC2,CD36,ATP8A2,CXCL10,SLC4A5,PLCB2,COL2A1,SNCA,SHANK2,HYAL2,CD34,COL18A1,ACE,HOXD10,CLDN16,TBX1,PLVAP,RCSD1,PPP1R1B,MTOR,BEST2,NPR1,DSC2,PDE4B,NOTCH1,S1PR1,PTGS1,CDH3,CDH5,PKHD1L1,ATP1A4,RELN,C3AR1,NMUR1,GRAP,SHANK3,OR6N2,MGAT3,FLI1	turquoise	VSMC_M6
GO:0050731	0.00	1.00	14	136	positive regulation of peptidyl-tyrosine phosphorylation	BP	0.00546	IL23A,ENPP2,PDGFB,SYK,IL6,TGFB1,CD36,THBS4,PECAM1,ACE,MTOR,TNFRSF18,RELN,ALKAL1	turquoise	VSMC_M6
GO:0045165	0.00	1.00	16	172	cell fate commitment	BP	0.00546	IL23A,NOTCH4,IL6,DLL1,PPARG,CTNNB1,SFRP1,CYP26B1,PROX1,HOXD10,TBX1,MTOR,NOTCH1,SOX17,OLIG2,SOX18	turquoise	VSMC_M6
GO:0060562	0.00	1.00	21	269	epithelial tube morphogenesis	BP	0.00546	CELSR1,NOTCH4,KDR,RASIP1,DLL1,TGFB1,CXCR4,CTNNB1,TIE1,SFRP1,CXCL10,BMP7,PROX1,KIF26B,GREB1L,NRARP,NOTCH1,LHX2,ALOX12,SOX17,SOX18	turquoise	VSMC_M6
GO:0018212	0.00	1.00	22	290	peptidyl-tyrosine modification	BP	0.00564	IL23A,FLT4,ENPP2,PDGFB,KDR,SYK,EPHA5,IL6,TGFB1,TIE1,SFRP1,CD36,THBS4,HYAL2,PECAM1,SRMS,ACE,MTOR,MATK,TNFRSF18,RELN,ALKAL1	turquoise	VSMC_M6
GO:0051179	0.00	1.00	173	4586	localization	BP	0.00582	PARD6G,TNFRSF11A,KCNN2,FLT4,MEGF10,SYBU,CELSR1,ENPP2,SYT17,DENND3,PDGFB,SLC16A8,MDGA1,DNAH8,IREB2,ATP8A1,STEAP4,KDR,SYK,EPHA5,IL6,OSBPL3,NDUFA4,ARHGAP25,C5,GJA4,KCNA7,SLC22A16,PIK3CG,DLL1,NOVA2,RAB38,SLC6A6,GRIP2,EXOC3L2,RARRES2,NOS3,CD177,ITGB4,PPARG,SYN2,TGFB1,CXCR4,EDNRB,CTNNB1,TMC6,TMC8,SPTBN4,TIE1,GPC6,MAP6,SLCO2B1,P2RY6,P2RY2,SNAP25,SFRP1,SLC4A11,CD36,CFAP54,SLCO2A1,PRAG1,ADAMTS9,PRR5L,ATP8A2,HHEX,REEP1,SLCO5A1,CP,CXCL10,ANGPT2,SLC4A5,ADGRG3,ATP6V0D2,THBS4,STAB1,MAPK10,NKX2-3,CLIC6,SNCA,MFSD4A,ANO3,MTTP,HYAL2,SLC39A8,NKD2,HFE,MCTP2,ROBO4,ESAM,LAPTM5,NFATC2,CD34,PECAM1,BMP7,IGFBP3,PROX1,MGST1,GPC1,SLCO4A1,JAML,OAZ3,ACE,LAMC2,SSC4D,LTF,ARHGAP27,CCRL2,TSPAN15,SYTL5,CLDN16,ATP13A1,CCDC88B,TBX1,RGN,LGALS12,SELE,SELP,PLVAP,FGF23,CRACR2A,PPM1F,PITPNM3,PRKCH,TSPAN14,MMRN2,SNCG,SLC25A18,HEPH,MTOR,SLC49A3,TTLL6,ABI3,BEST2,NPR1,DSC2,HCN1,PDE4B,SEMA6B,TNFRSF18,SSTR5,NOTCH1,IRF8,S1PR1,GBP1,LHX6,CDH3,CDH1,EXOC3L1,CDH5,ALOX12,MMP12,PMAIP1,ATP1A4,SOX17,RELN,C3AR1,KCNU1,PDLIM1,NMUR1,NUCB1,SOX18,GNA12,SHANK3,TRPM2,BAMBI,CCR7,NSG2,MGAT3,MSMP,NMB,TMEM50B,SCARF1,FXYD6	turquoise	VSMC_M6
GO:1990266	0.00	1.00	10	74	neutrophil migration	BP	0.00654	SYK,PIK3CG,CD177,CXCL10,THBS4,PECAM1,JAML,PDE4B,C3AR1,CCR7	turquoise	VSMC_M6
GO:0048513	0.00	1.00	106	2529	animal organ development	BP	0.00676	TNFRSF11A,IL23A,FLT4,MEGF10,CELSR1,NOTCH4,PDGFB,ETV7,MDGA1,FREM1,IREB2,ADGRF5,KDR,IL1RL2,SYK,BARX1,EPHA5,IL6,ANKRD6,DLL1,RARRES2,NOS3,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TIE1,GPC6,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,PCDH12,NFKBID,ADAMTS9,ATP8A2,HHEX,CXCL10,ANGPT2,SLC4A5,ADGRG3,CYP26B1,COL2A1,NKX2-3,BMP1,IGSF3,HYAL2,HFE,NRAP,INPP5D,EAF2,CD34,PECAM1,CD86,COL18A1,BMP7,PROX1,MGST1,GPC1,ACE,LAMC2,HOXD10,PAX9,LTF,TBX1,RGN,FGF23,CRACR2A,PRKCH,KIF26B,LFNG,MTOR,ARHGEF15,KLF1,MAST1,LYL1,GREB1L,HCN1,SEMA6B,NRARP,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH3,CDH1,ALOX12,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,SHANK3,TRPM2,TRIM62,BAMBI,CCR7,HRASLS,PDE1B,FLI1	turquoise	VSMC_M6
GO:0045321	0.00	1.00	35	586	leukocyte activation	BP	0.00695	IL23A,ADGRF5,IL18RAP,IL1RL2,SYK,IL6,PIK3CG,DLL1,CTSC,CD177,TGFB1,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,SNCA,HYAL2,HFE,LAPTM5,NFATC2,INPP5D,CD86,SLAMF9,JAML,CCDC88B,CRACR2A,LFNG,MTOR,LYL1,NRARP,IRF8,CCR7	turquoise	VSMC_M6
GO:0008283	0.00	1.00	68	1442	cell population proliferation	BP	0.00703	TNFRSF11A,IL23A,FLT4,MEGF10,PDGFB,KDR,IL18RAP,SYK,IL6,PIK3CG,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,TIE1,P2RY6,SFRP1,ATP8A2,HHEX,SOX7,CXCL10,THBS4,PPP1R16B,NKX2-3,SHANK2,NFATC2,INPP5D,EAF2,CD34,CD86,ERN1,COL18A1,BMP7,IGFBP3,PROX1,JAML,ACE,LAMC2,PRAME,LTF,CCDC88B,TBX1,RGN,FGF23,PRKCH,BCL6B,MTOR,NPR1,LRG1,MATK,NRARP,EGFL7,SSTR5,NOTCH1,S1PR1,LHX2,PTGS1,CDH3,CDH5,ALOX12,MMP12,SOX17,SOX18,GNA12,BAMBI,NMB	turquoise	VSMC_M6
GO:0061437	0.00	1.00	6	25	renal system vasculature development	BP	0.00703	PDGFB,ANGPT2,CD34,PECAM1,BMP7,NOTCH1	turquoise	VSMC_M6
GO:0061440	0.00	1.00	6	25	kidney vasculature development	BP	0.00703	PDGFB,ANGPT2,CD34,PECAM1,BMP7,NOTCH1	turquoise	VSMC_M6
GO:0042327	0.00	1.00	36	612	positive regulation of phosphorylation	BP	0.00703	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,PIK3CG,RARRES2,PPARG,TGFB1,EDNRB,TIE1,CD36,PRR5L,THBS4,SNCA,HFE,PECAM1,CD86,ERN1,BMP7,PROX1,ACE,LTF,TBX1,FGF23,MTOR,TNFRSF18,SH2D3C,RELN,ALKAL1,CCR7	turquoise	VSMC_M6

GO:0042221	0.00	1.00	119	2921	response to chemical	BP	0.00725	TNFRSF11A,FLT4,SYBU,ENPP2,SYT17,PDGFB,CSF2RB,KDR,IL18RAP,IL1RL2,SYK,EPHA5,IL6,BCL11A,C5,PIK3CG,DLL1,NOVA2,CTSC,RARRES2,NOS3,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TIE1,P2RY6,P2RY2,PDE2A,SFRP1,CNTN4,SLC4A11,CD36,PRR5L,HHEX,CXCL10,ANGPT2,SOGA1,THBS4,CYP26B1,COL2A1,GSTA4,MAPK10,GOT1,SNCA,MTTP,HYAL2,ESRRG,HFE,DPYSL4,ROBO4,LAPTM5,NFATC2,CD34,CD86,ERN1,COL18A1,BMP7,MGST1,GPC1,JAML,PTPRE,LAMC2,PAX9,LTF,CCRL2,TBX1,SELE,SELP,PLVAP,BAIAP2L1,FGF23,RCSD1,PPM1F,MMRN2,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,SARM1,SEMA6B,LRG1,TNFRSF18,TMEM204,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,GBP1,LHX2,PTGS1,CDH3,CDH1,CDH5,ALOX12,MMP12,PMAIP1,RUFY4,SOX17,RELN,ACKR1,C3AR1,VSTM2L,NUCB1,GNA12,TRPM2,BAMBI,CCR7,OR6N2,NSG2,MGAT3,MSMP,GPX3,PDE1B	turquoise	VSMC_M6
GO:0097530	0.00	1.00	11	91	granulocyte migration	BP	0.00764	SYK,PIK3CG,RARRES2,CD177,CXCL10,THBS4,PECAM1,JAML,PDE4B,C3AR1,CCR7	turquoise	VSMC_M6
GO:0008593	0.00	1.00	10	76	regulation of Notch signaling pathway	BP	0.00765	DLL1,NOS3,PRAG1,BMP7,TSPAN15,TSPAN14,LFNG,NRARP,EGFL7,NOTCH1	turquoise	VSMC_M6
GO:0042325	0.00	1.00	50	967	regulation of phosphorylation	BP	0.00769	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,RASIP1,PIK3CG,KDM4D,RARRES2,PPARG,TGFB1,EDNRB,SPTBN4,TIE1,SFRP1,CD36,KIRREL2,PRR5L,HHEX,THBS4,SNCA,HYAL2,HFE,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,ACE,LTF,TBX1,RGN,FGF23,PPM1F,PPP1R1B,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0048660	0.00	1.00	13	124	regulation of smooth muscle cell proliferation	BP	0.00769	PDGFB,IL6,PPARG,TGFB1,CTNNB1,P2RY6,ERN1,IGFBP3,MTOR,NPR1,S1PR1,ALOX12,GNA12	turquoise	VSMC_M6
GO:0043252	0.00	1.00	4	9	sodium-independent organic anion transport	BP	0.00813	SLCO2B1,SLCO2A1,SLCO5A1,SLCO4A1	turquoise	VSMC_M6
GO:0060249	0.00	1.00	18	218	anatomical structure homeostasis	BP	0.00834	TNFRSF11A,LYZ,ADGRF5,SYK,IL6,NOS3,CTNNB1,COL2A1,SLC39A8,ESAM,INPP5D,CD34,PECAM1,LTF,NOTCH1,S1PR1,CDH3,CDH5	turquoise	VSMC_M6
GO:0032735	0.00	1.00	6	26	positive regulation of interleukin-12 production	BP	0.00861	IL23A,SYK,CD36,LAPTM5,IRF8,CCR7	turquoise	VSMC_M6
GO:0050921	0.00	1.00	12	109	positive regulation of chemotaxis	BP	0.00861	PDGFB,KDR,IL6,RARRES2,TGFB1,CXCR4,CXCL10,THBS4,PPM1F,S1PR1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0001938	0.00	1.00	10	78	positive regulation of endothelial cell proliferation	BP	0.00893	FLT4,PDGFB,KDR,THBS4,PPP1R16B,PROX1,MTOR,LRG1,NRARP,EGFL7	turquoise	VSMC_M6
GO:0071695	0.00	1.00	15	163	anatomical structure maturation	BP	0.00926	BCL11A,PPARG,EDNRB,CTNNB1,SPTBN4,LTF,MTOR,LYL1,B4GALT6,S1PR1,LHX6,CDH3,CDH5,SOX18,SCARF1	turquoise	VSMC_M6
GO:0001936	0.00	1.00	12	111	regulation of endothelial cell proliferation	BP	0.00985	FLT4,PDGFB,KDR,PPARG,TIE1,THBS4,PPP1R16B,PROX1,MTOR,LRG1,NRARP,EGFL7	turquoise	VSMC_M6
GO:0050819	0.00	1.00	7	38	negative regulation of coagulation	BP	0.00995	PDGFB,NOS3,F11,KLKB1,PROCR,CD34,ALOX12	turquoise	VSMC_M6
GO:0007596	0.00	1.00	15	164	blood coagulation	BP	0.00995	PDGFB,SYK,IL6,PIK3CG,NOS3,CD36,F11,KLKB1,PROCR,MMRN1,CD34,SELP,VWF,ALOX12,GNA12	turquoise	VSMC_M6
GO:0048659	0.00	1.00	13	128	smooth muscle cell proliferation	BP	0.00999	PDGFB,IL6,PPARG,TGFB1,CTNNB1,P2RY6,ERN1,IGFBP3,MTOR,NPR1,S1PR1,ALOX12,GNA12	turquoise	VSMC_M6
GO:0065007	0.00	1.00	283	8375	biological regulation	BP	0.01092	PARD6G,TNFRSF11A,IL23A,KCNN2,NMBR,LYZ,FLT4,MYCT1,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,DENND3,PDGFB,ETV7,MDGA1,CSF2RB,MOB3B,IREB2,ATP8A1,STEAP4,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,NDUFA4,ARHGAP25,C5,MAML3,KCNA7,KIAA1147,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,SLC6A6,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,SYN2,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,MAP6,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,ZIC2,RASGRP3,NOTUM,CNTN4,SLC4A11,CD36,NFKBID,KIRREL2,PRAG1,ADAMTS9,PRR5L,ATP8A2,MALL,F11,KLKB1,HHEX,PROCR,SOX7,CP,TSC22D2,P2RY14,CXCL10,ANGPT2,SOGA1,SLC4A5,ADGRG3,ATP6V0D2,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,STAB1,TOX2,MAPK10,IRX6,GOT1,NKX2-3,CLIC6,BMP1,SNCA,MMRN1,CTNND2,ANO3,SHANK2,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,MCTP2,HCRTR1,ROBO4,ESAM,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,COL18A1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,SLCO4A1,JAML,OAZ3,SRMS,FANK1,ACE,PTPRE,CNKSR2,LAMC2,HOXD10,PRAME,PAX9,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,CLDN16,ATP13A1,LPAR2,AGFG2,CCDC88B,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,ERAS,PRKCH,GRID2IP,KIF26B,TSPAN14,BCL6B,MMRN2,SNCG,PPP1R1B,LFNG,ARHGEF9,HEPH,MTOR,BCKDK,TTLL6,GNGT2,ABI3,ARHGEF15,KLF1,MAST1,BEST2,NPR1,BEX5,ISLR2,LYL1,COL4A6,COL4A5,DSC2,KIF26A,HCN1,PDE4B,SARM1,SEMA6B,LRG1,MATK,TNFRSF18,NRARP,TMEM	turquoise	VSMC_M6
GO:0030183	0.00	1.00	11	96	B cell differentiation	BP	0.01114	SYK,IL6,DLL1,SFRP1,HHEX,ADGRG3,NKX2-3,INPP5D,LFNG,LYL1,IRF8	turquoise	VSMC_M6
GO:0050817	0.00	1.00	15	166	coagulation	BP	0.01115	PDGFB,SYK,IL6,PIK3CG,NOS3,CD36,F11,KLKB1,PROCR,MMRN1,CD34,SELP,VWF,ALOX12,GNA12	turquoise	VSMC_M6
GO:0042060	0.00	1.00	23	329	wound healing	BP	0.01115	NOTCH4,PDGFB,KDR,SYK,IL6,PIK3CG,NOS3,TGFB1,CXCR4,CD36,F11,KLKB1,PROCR,MMRN1,CD34,JAML,SELP,VWF,MTOR,CDH3,ALOX12,MMP12,GNA12	turquoise	VSMC_M6
GO:0032496	0.00	1.00	18	225	response to lipopolysaccharide	BP	0.0119	TNFRSF11A,CSF2RB,IL6,NOS3,TGFB1,EDNRB,CD36,CXCL10,SNCA,CD86,MGST1,LTF,SELE,SELP,PDE4B,NOTCH1,IRF8,CCR7	turquoise	VSMC_M6
GO:0002313	0.00	1.00	5	18	mature B cell differentiation involved in immune response	BP	0.012	IL6,DLL1,NKX2-3,LFNG,IRF8	turquoise	VSMC_M6
GO:0072672	0.00	1.00	4	10	neutrophil extravasation	BP	0.01201	PIK3CG,CD177,PECAM1,JAML	turquoise	VSMC_M6
GO:0030001	0.00	1.00	34	587	metal ion transport	BP	0.01262	KCNN2,PDGFB,IREB2,STEAP4,GJA4,KCNA7,PIK3CG,SLC6A6,CXCR4,CTNNB1,SPTBN4,P2RY6,SNAP25,SLC4A11,CP,CXCL10,SLC4A5,SNCA,SLC39A8,HFE,LTF,CLDN16,ATP13A1,RGN,CRACR2A,HEPH,HCN1,PDE4B,ATP1A4,KCNU1,NMUR1,TRPM2,CCR7,FXYD6	turquoise	VSMC_M6
GO:0016525	0.00	1.00	10	82	negative regulation of angiogenesis	BP	0.01268	PPARG,CTNNB1,TIE1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,STAB1,NPR1	turquoise	VSMC_M6
GO:0001885	0.00	1.00	8	53	endothelial cell development	BP	0.01268	NOTCH4,PDE2A,PPP1R16B,ROBO4,PECAM1,COL18A1,CDH5,SOX18	turquoise	VSMC_M6

GO:0044093	0.00	1.00	56	1151	positive regulation of molecular function	BP	0.01268	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,IL18RAP,SYK,EPHA5,IL6,NDUFA4,ARHGAP25,PIK3CG,KDM4D,NOS3,PPARG,TGFB1,CTNNB1,TIE1,P2RY6,SFRP1,ZIC2,CD36,SOX7,PLCB2,SNCA,HFE,LAPTM5,CD86,ERN1,PROX1,FANK1,ACE,LTF,ARHGAP27,LPAR2,RGN,SELE,FGF23,CRACR2A,PPM1F,PRKCH,MTOR,ARHGEF15,S1PR1,CDH3,ALOX12,PRSS22,PMAIP1,RELN,ALKAL1,NMUR1,SHANK3,PKIB,TRIM62,BAMBI,CCR7	turquoise	VSMC_M6
GO:0007200	0.00	1.00	8	53	phospholipase C-activating G protein-coupled receptor signaling pathway	BP	0.01309	NMBR,EDNRB,P2RY6,P2RY2,S1PR1,C3AR1,NMUR1,LPAR6	turquoise	VSMC_M6
GO:1901700	0.00	1.00	59	1234	response to oxygen-containing compound	BP	0.01309	TNFRSF11A,SYBU,PDGFB,CSF2RB,IL18RAP,EPHA5,IL6,BCL11A,PIK3CG,RARRES2,NOS3,PPARG,TGFB1,HTR5A,EDNRB,CTNNB1,TIE1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,HHEX,CXCL10,ANGPT2,SOGA1,CYP26B1,MAPK10,GOT1,SNCA,HYAL2,CD86,ERN1,COL18A1,BMP7,MGST1,PTPRE,LTF,TBX1,SELE,SELP,BAIAP2L1,FGF23,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,SARM1,NOTCH1,IRF8,ENDOG,CDH1,MMP12,TRPM2,CCR7,NSG2,GPX3	turquoise	VSMC_M6
GO:0015711	0.00	1.00	18	228	organic anion transport	BP	0.01337	TNFRSF11A,SLC16A8,SYK,SLC6A6,SLCO2B1,SLC4A11,CD36,SLCO2A1,SLCO5A1,SLC4A5,SNCA,MTTP,SLC39A8,MGST1,SLCO4A1,ACE,SLC25A18,NMB	turquoise	VSMC_M6
GO:2000181	0.00	1.00	10	83	negative regulation of blood vessel morphogenesis	BP	0.01369	PPARG,CTNNB1,TIE1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,STAB1,NPR1	turquoise	VSMC_M6
GO:0046649	0.00	1.00	29	470	lymphocyte activation	BP	0.0137	IL23A,IL1RL2,SYK,IL6,PIK3CG,DLL1,TGFB1,CTNNB1,SFRP1,NFKBID,HHEX,ADGRG3,CYP26B1,NKX2-3,HFE,LAPTM5,NFATC2,INPP5D,CD86,SLAMF9,JAML,CCDC88B,CRACR2A,LFNG,MTOR,LYL1,NRARP,IRF8,CCR7	turquoise	VSMC_M6
GO:0010863	0.00	1.00	6	29	positive regulation of phospholipase C activity	BP	0.01398	P2RY6,PLCB2,CD86,LPAR2,SELE,NMUR1	turquoise	VSMC_M6
GO:0050818	0.00	1.00	8	54	regulation of coagulation	BP	0.01449	PDGFB,NOS3,CD36,F11,KLKB1,PROCR,CD34,ALOX12	turquoise	VSMC_M6
GO:1901343	0.00	1.00	10	84	negative regulation of vasculature development	BP	0.01482	PPARG,CTNNB1,TIE1,ADAMTS9,HHEX,CXCL10,ANGPT2,THBS4,STAB1,NPR1	turquoise	VSMC_M6
GO:0051480	0.00	1.00	17	212	regulation of cytosolic calcium ion concentration	BP	0.01493	PIK3CG,CXCR4,EDNRB,P2RY6,CD36,CXCL10,GOT1,SNCA,HCRTR1,CCRL2,LPAR2,S1PR1,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0003157	0.00	1.00	4	11	endocardium development	BP	0.01653	PROX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0050730	0.00	1.00	16	193	regulation of peptidyl-tyrosine phosphorylation	BP	0.0166	IL23A,ENPP2,PDGFB,SYK,IL6,TGFB1,SFRP1,CD36,THBS4,HYAL2,PECAM1,ACE,MTOR,TNFRSF18,RELN,ALKAL1	turquoise	VSMC_M6
GO:0010543	0.00	1.00	6	30	regulation of platelet activation	BP	0.01666	PDGFB,SYK,IL6,NOS3,SELP,ALOX12	turquoise	VSMC_M6
GO:0001709	0.00	1.00	6	30	cell fate determination	BP	0.01666	NOTCH4,DLL1,CTNNB1,CYP26B1,PROX1,SOX17	turquoise	VSMC_M6
GO:0033002	0.00	1.00	15	174	muscle cell proliferation	BP	0.01673	MEGF10,PDGFB,IL6,PPARG,TGFB1,CTNNB1,P2RY6,ERN1,IGFBP3,MTOR,NPR1,NOTCH1,S1PR1,ALOX12,GNA12	turquoise	VSMC_M6
GO:0050865	0.00	1.00	25	385	regulation of cell activation	BP	0.01703	IL23A,PDGFB,ADGRF5,IL1RL2,SYK,IL6,CTSC,NOS3,CD177,TGFB1,CTNNB1,SFRP1,NFKBID,CYP26B1,SNCA,HFE,LAPTM5,NFATC2,INPP5D,CD86,CCDC88B,SELP,NRARP,ALOX12,CCR7	turquoise	VSMC_M6
GO:0071310	0.00	1.00	78	1784	cellular response to organic substance	BP	0.01754	TNFRSF11A,FLT4,SYBU,PDGFB,CSF2RB,KDR,IL18RAP,IL1RL2,SYK,EPHA5,IL6,BCL11A,PIK3CG,DLL1,RARRES2,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,HHEX,CXCL10,ANGPT2,SOGA1,CYP26B1,COL2A1,GOT1,SNCA,HYAL2,ESRRG,HFE,LAPTM5,CD86,ERN1,BMP7,MGST1,GPC1,PTPRE,PAX9,LTF,CCRL2,TBX1,PLVAP,BAIAP2L1,FGF23,MMRN2,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,LRG1,TNFRSF18,TMEM204,SSTR5,NOTCH1,IRF8,ENDOG,GBP1,CDH1,CDH5,ALOX12,MMP12,RUFY4,SOX17,ACKR1,TRPM2,BAMBI,CCR7,NSG2,PDE1B	turquoise	VSMC_M6
GO:0043542	0.00	1.00	16	195	endothelial cell migration	BP	0.01793	FLT4,PDGFB,KDR,PIK3CG,NOS3,PPARG,TGFB1,ADAMTS9,ANGPT2,PROX1,LGALS12,MMRN2,NOTCH1,CDH5,ALOX12,SOX18	turquoise	VSMC_M6
GO:0001816	0.00	1.00	30	504	cytokine production	BP	0.01827	IL23A,FLT4,IL1RL2,SYK,IL6,C5,PIK3CG,DLL1,TGFB1,CD36,HYAL2,HFE,LAPTM5,NFATC2,INPP5D,TLR7,CD34,CD86,SLAMF9,LTF,CCDC88B,BCL6B,PDE4B,IRF8,GBP1,CDH3,MMP12,ACKR1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0002237	0.00	1.00	18	236	response to molecule of bacterial origin	BP	0.0187	TNFRSF11A,CSF2RB,IL6,NOS3,TGFB1,EDNRB,CD36,CXCL10,SNCA,CD86,MGST1,LTF,SELE,SELP,PDE4B,NOTCH1,IRF8,CCR7	turquoise	VSMC_M6
GO:0010628	0.00	1.00	42	803	positive regulation of gene expression	BP	0.01872	IL23A,FLT4,PDGFB,IL1RL2,SYK,IL6,BCL11A,C5,PIK3CG,DLL1,NOS3,PPARG,TGFB1,CTNNB1,PDE2A,CD36,KLKB1,CYP26B1,HYAL2,NKD2,HFE,LAPTM5,NFATC2,TLR7,CD34,CD86,ERN1,BMP7,CCDC88B,FGF23,PPM1F,MTOR,PDE4B,NOTCH1,IRF8,CDH3,CDH5,ALOX12,MMP12,SOX17,C3AR1,CCR7	turquoise	VSMC_M6
GO:0072507	0.00	1.00	22	323	divalent inorganic cation homeostasis	BP	0.01883	PIK3CG,CXCR4,EDNRB,TMC8,P2RY6,CD36,CXCL10,GOT1,SNCA,SLC39A8,HCRTR1,CCRL2,ATP13A1,LPAR2,RGN,S1PR1,CDH5,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:1900274	0.00	1.00	6	31	regulation of phospholipase C activity	BP	0.01886	P2RY6,PLCB2,CD86,LPAR2,SELE,NMUR1	turquoise	VSMC_M6
GO:0008217	0.00	1.00	12	122	regulation of blood pressure	BP	0.02016	PDGFB,DLL1,GRIP2,RARRES2,NOS3,PPARG,EDNRB,SLC4A5,CD34,ACE,NPR1,PTGS1	turquoise	VSMC_M6
GO:0045595	0.00	1.00	55	1153	regulation of cell differentiation	BP	0.02055	IL23A,MEGF10,NOTCH4,PDGFB,KDR,IL1RL2,SYK,IL6,BCL11A,DLL1,SLC6A6,RARRES2,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,MAP6,SFRP1,CNTN4,SLC4A11,CD36,NFKBID,CXCL10,CYP26B1,NFATC2,INPP5D,CD34,CD86,BMP7,IGFBP3,PROX1,GPC1,PRAME,LTF,TBX1,LGALS12,FGF23,PRKCH,BCL6B,MTOR,ISLR2,SEMA6B,NRARP,HES3,NOTCH1,GBP1,LHX2,CDH5,SOX17,RELN,OLIG2,SHANK3,TRIM62,BAMBI	turquoise	VSMC_M6
GO:0036303	0.00	1.00	5	21	lymph vessel morphogenesis	BP	0.02085	FLT4,TIE1,PROX1,LGALS12,SOX18	turquoise	VSMC_M6
GO:0050727	0.00	1.00	18	239	regulation of inflammatory response	BP	0.02094	TNFRSF11A,IL23A,IL1RL2,SYK,IL6,PIK3CG,CTSC,PPARG,EDNRB,PDE2A,KLKB1,SNCA,HYAL2,TLR7,SELE,BCL6B,CDH5,CCR7	turquoise	VSMC_M6
GO:0010631	0.00	1.00	19	261	epithelial cell migration	BP	0.02127	FLT4,ENPP2,PDGFB,KDR,PIK3CG,NOS3,PPARG,TGFB1,ADAMTS9,ANGPT2,PROX1,LGALS12,PPM1F,MMRN2,MTOR,NOTCH1,CDH5,ALOX12,SOX18	turquoise	VSMC_M6
GO:0006874	0.00	1.00	20	283	cellular calcium ion homeostasis	BP	0.02127	PIK3CG,CXCR4,EDNRB,P2RY6,CD36,CXCL10,GOT1,SNCA,HCRTR1,CCRL2,ATP13A1,LPAR2,RGN,S1PR1,CDH5,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6

GO:0090132	0.00	1.00	19	262	epithelium migration	BP	0.02217	FLT4,ENPP2,PDGFB,KDR,PIK3CG,NOS3,PPARG,TGFB1,ADAMTS9,ANGPT2,PROX1,LGALS12,PPM1F,MMRN2,MTOR,NOTCH1,CDH5,ALOX12,SOX18	turquoise	VSMC_M6
GO:0050829	0.00	1.00	6	32	defense response to Gram-negative bacterium	BP	0.02217	IL23A,LYZ,IL6,RARRES2,LTF,SELP	turquoise	VSMC_M6
GO:0072503	0.00	1.00	21	306	cellular divalent inorganic cation homeostasis	BP	0.02217	PIK3CG,CXCR4,EDNRB,P2RY6,CD36,CXCL10,GOT1,SNCA,SLC39A8,HCRTR1,CCRL2,ATP13A1,LPAR2,RGN,S1PR1,CDH5,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0035556	0.00	1.00	87	2063	intracellular signal transduction	BP	0.02217	TNFRSF11A,IL23A,FLT4,CELSR1,DENND3,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,ANKRD6,ARHGAP25,RASIP1,PIK3CG,RAB38,FGD5,NOS3,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,P2RY6,PDE2A,SFRP1,RASGRP3,CD36,PRAG1,PRR5L,ADGRG3,HUNK,PPP1R16B,PLCB2,MAPK10,SHANK2,HYAL2,MCTP2,HCRTR1,LAPTM5,NFATC2,INPP5D,TLR7,CD86,ERN1,BMP7,PROX1,CNKSR2,LTF,ARHGAP27,CCRL2,TBX1,GUCY1A2,RGN,LGALS12,SELE,SELP,VWF,PLVAP,FGF23,CRACR2A,PPM1F,ERAS,PRKCH,PPP1R1B,ARHGEF9,MTOR,ARHGEF15,MAST1,NPR1,NOTCH1,SH2D3C,GBP1,DCDC2B,PMAIP1,RELN,ALKAL1,NMUR1,NUCB1,GRAP,GNA12,SHANK3,LPAR6,TRPM2,TRIM62,CCR7	turquoise	VSMC_M6
GO:0048729	0.00	1.00	29	490	tissue morphogenesis	BP	0.02222	CELSR1,NOTCH4,KDR,ANKRD6,RASIP1,DLL1,NOS3,ITGB4,TGFB1,CXCR4,CTNNB1,TIE1,GPC6,SFRP1,CXCL10,BMP7,PROX1,TBX1,KIF26B,MTOR,GREB1L,NRARP,NOTCH1,S1PR1,LHX2,ALOX12,MMP12,SOX17,SOX18	turquoise	VSMC_M6
GO:0010718	0.00	1.00	7	45	positive regulation of epithelial to mesenchymal transition	BP	0.02271	IL6,TGFB1,CTNNB1,BMP7,MTOR,NOTCH1,BAMBI	turquoise	VSMC_M6
GO:0043269	0.00	1.00	27	444	regulation of ion transport	BP	0.02382	TNFRSF11A,KCNN2,SYT17,PDGFB,SYK,NDUFA4,KCNA7,PIK3CG,CXCR4,CTNNB1,SPTBN4,P2RY6,CXCL10,CLIC6,SNCA,HFE,RGN,FGF23,CRACR2A,SNCG,MTOR,HCN1,PDE4B,RELN,KCNU1,SHANK3,FXYD6	turquoise	VSMC_M6
GO:0045597	0.00	1.00	35	639	positive regulation of cell differentiation	BP	0.02447	IL23A,KDR,IL1RL2,SYK,IL6,SLC6A6,RARRES2,PPARG,TGFB1,CXCR4,CTNNB1,MAP6,SFRP1,CD36,NFKBID,CYP26B1,INPP5D,CD34,CD86,BMP7,IGFBP3,PROX1,GPC1,LTF,TBX1,PRKCH,MTOR,ISLR2,NOTCH1,CDH5,SOX17,RELN,OLIG2,SHANK3,BAMBI	turquoise	VSMC_M6
GO:0043534	0.00	1.00	11	108	blood vessel endothelial cell migration	BP	0.02452	PDGFB,KDR,NOS3,PPARG,TGFB1,ANGPT2,MMRN2,NOTCH1,CDH5,ALOX12,SOX18	turquoise	VSMC_M6
GO:0045746	0.00	1.00	6	33	negative regulation of Notch signaling pathway	BP	0.02568	DLL1,BMP7,TSPAN15,LFNG,NRARP,EGFL7	turquoise	VSMC_M6
GO:0090130	0.00	1.00	19	266	tissue migration	BP	0.02568	FLT4,ENPP2,PDGFB,KDR,PIK3CG,NOS3,PPARG,TGFB1,ADAMTS9,ANGPT2,PROX1,LGALS12,PPM1F,MMRN2,MTOR,NOTCH1,CDH5,ALOX12,SOX18	turquoise	VSMC_M6
GO:0030593	0.00	1.00	8	60	neutrophil chemotaxis	BP	0.02569	SYK,PIK3CG,CXCL10,THBS4,JAML,PDE4B,C3AR1,CCR7	turquoise	VSMC_M6
GO:0071621	0.00	1.00	9	76	granulocyte chemotaxis	BP	0.02756	SYK,PIK3CG,RARRES2,CXCL10,THBS4,JAML,PDE4B,C3AR1,CCR7	turquoise	VSMC_M6
GO:0043085	0.00	1.00	44	875	positive regulation of catalytic activity	BP	0.02773	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,SYK,EPHA5,NDUFA4,ARHGAP25,PIK3CG,NOS3,PPARG,TGFB1,CTNNB1,TIE1,P2RY6,SFRP1,SOX7,PLCB2,SNCA,LAPTM5,CD86,ERN1,PROX1,ACE,LTF,ARHGAP27,LPAR2,RGN,SELE,FGF23,PPM1F,MTOR,ARHGEF15,S1PR1,CDH3,ALOX12,PRSS22,PMAIP1,RELN,ALKAL1,NMUR1,PKIB,CCR7	turquoise	VSMC_M6
GO:0055074	0.00	1.00	20	291	calcium ion homeostasis	BP	0.02854	PIK3CG,CXCR4,EDNRB,P2RY6,CD36,CXCL10,GOT1,SNCA,HCRTR1,CCRL2,ATP13A1,LPAR2,RGN,S1PR1,CDH5,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0050729	0.00	1.00	10	93	positive regulation of inflammatory response	BP	0.02904	TNFRSF11A,IL23A,IL6,PIK3CG,CTSC,PDE2A,SNCA,HYAL2,TLR7,CCR7	turquoise	VSMC_M6
GO:0001708	0.00	1.00	8	62	cell fate specification	BP	0.03027	DLL1,CTNNB1,HOXD10,TBX1,NOTCH1,SOX17,OLIG2,SOX18	turquoise	VSMC_M6
GO:0010575	0.00	1.00	5	23	positive regulation of vascular endothelial growth factor production	BP	0.03091	FLT4,IL6,C5,TGFB1,C3AR1	turquoise	VSMC_M6
GO:0010632	0.00	1.00	16	208	regulation of epithelial cell migration	BP	0.03091	FLT4,ENPP2,PDGFB,KDR,PIK3CG,NOS3,PPARG,TGFB1,ADAMTS9,ANGPT2,PROX1,PPM1F,MMRN2,MTOR,NOTCH1,ALOX12	turquoise	VSMC_M6
GO:0002252	0.00	1.00	23	360	immune effector process	BP	0.03091	IL23A,IL18RAP,SYK,IL6,C5,PIK3CG,DLL1,CTSC,CD177,TGFB1,CD36,NFKBID,NKX2-3,HFE,LAPTM5,INPP5D,CD86,SLAMF9,ACE,CRACR2A,LFNG,MTOR,IRF8	turquoise	VSMC_M6
GO:0014015	0.00	1.00	7	48	positive regulation of gliogenesis	BP	0.03091	IL6,TGFB1,CXCR4,PRKCH,MTOR,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0048384	0.00	1.00	5	23	retinoic acid receptor signaling pathway	BP	0.03091	PPARG,CYP26B1,ESRRG,PRAME,TBX1	turquoise	VSMC_M6
GO:0002335	0.00	1.00	5	23	mature B cell differentiation	BP	0.03097	IL6,DLL1,NKX2-3,LFNG,IRF8	turquoise	VSMC_M6
GO:0006826	0.00	1.00	7	48	iron ion transport	BP	0.03148	IREB2,STEAP4,CP,SLC39A8,HFE,LTF,HEPH	turquoise	VSMC_M6
GO:0034329	0.00	1.00	21	318	cell junction assembly	BP	0.03219	MDGA1,KDR,LRRC4B,GJA4,ITGB4,CTNNB1,GPC6,SFRP1,SNCA,CTNND2,SHANK2,ESAM,PECAM1,ACE,CLDN16,PPM1F,PRKCH,ABI3,CDH1,CDH5,SHANK3	turquoise	VSMC_M6
GO:0030195	0.00	1.00	6	35	negative regulation of blood coagulation	BP	0.03258	PDGFB,NOS3,F11,KLKB1,CD34,ALOX12	turquoise	VSMC_M6
GO:1901701	0.00	1.00	44	887	cellular response to oxygen-containing compound	BP	0.03373	SYBU,PDGFB,IL18RAP,EPHA5,IL6,BCL11A,PIK3CG,RARRES2,NOS3,PPARG,TGFB1,HTR5A,EDNRB,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,CXCL10,SOGA1,CYP26B1,GOT1,SNCA,CD86,ERN1,BMP7,MGST1,PTPRE,LTF,TBX1,BAIAP2L1,FGF23,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,IRF8,ENDOG,CDH1,TRPM2,NSG2	turquoise	VSMC_M6
GO:0009887	0.00	1.00	40	784	animal organ morphogenesis	BP	0.03373	CELSR1,ETV7,FREM1,SYK,IL6,ANKRD6,DLL1,NOS3,ITGB4,TGFB1,CTNNB1,GPC6,SFRP1,ATP8A2,CYP26B1,COL2A1,NKX2-3,BMP1,HYAL2,CD34,COL18A1,BMP7,PROX1,LAMC2,HOXD10,PAX9,LTF,TBX1,FGF23,KIF26B,LFNG,MTOR,GREB1L,HCN1,NOTCH1,S1PR1,SOX17,SOX18,SHANK3,FLI1	turquoise	VSMC_M6
GO:0000165	0.00	1.00	32	579	MAPK cascade	BP	0.03373	TNFRSF11A,FLT4,PDGFB,KDR,SYK,IL6,ANKRD6,PIK3CG,PPARG,TGFB1,CTNNB1,P2RY6,SFRP1,RASGRP3,CD36,MAPK10,HYAL2,HCRTR1,LAPTM5,TLR7,ERN1,BMP7,TBX1,PLVAP,FGF23,CRACR2A,NOTCH1,SH2D3C,GBP1,ALKAL1,SHANK3,CCR7	turquoise	VSMC_M6
GO:0002009	0.00	1.00	25	412	morphogenesis of an epithelium	BP	0.03491	CELSR1,NOTCH4,KDR,ANKRD6,RASIP1,DLL1,TGFB1,CXCR4,CTNNB1,TIE1,GPC6,SFRP1,CXCL10,BMP7,PROX1,KIF26B,MTOR,GREB1L,NRARP,NOTCH1,LHX2,ALOX12,MMP12,SOX17,SOX18	turquoise	VSMC_M6

GO:0010717	0.00	1.00	9	80	regulation of epithelial to mesenchymal transition	BP	0.03542	IL6,TGFB1,CTNNB1,SFRP1,BMP7,MTOR,NOTCH1,TRIM62,BAMBI	turquoise	VSMC_M6
GO:0002682	0.00	1.00	45	915	regulation of immune system process	BP	0.03577	IL23A,ADGRF5,IL18RAP,IL1RL2,SYK,IL6,C5,DLL1,CTSC,RARRES2,CD177,PPARG,TGFB1,CTNNB1,SFRP1,CD36,NFKBID,CXCL10,THBS4,CYP26B1,MAPK10,SNCA,HFE,LAPTM5,NFATC2,INPP5D,TLR7,CD86,LTF,CCDC88B,SELE,SELP,PLVAP,PRKCH,BCL6B,MTOR,PDE4B,SARM1,TNFRSF18,NRARP,GBP1,MMP12,C3AR1,TRIM62,CCR7	turquoise	VSMC_M6
GO:1900047	0.00	1.00	6	36	negative regulation of hemostasis	BP	0.03693	PDGFB,NOS3,F11,KLKB1,CD34,ALOX12	turquoise	VSMC_M6
GO:0002675	0.00	1.00	4	14	positive regulation of acute inflammatory response	BP	0.03693	TNFRSF11A,IL6,PIK3CG,CCR7	turquoise	VSMC_M6
GO:0002064	0.00	1.00	14	173	epithelial cell development	BP	0.03715	NOTCH4,PDGFB,DLL1,CXCR4,PDE2A,SLC4A5,PPP1R16B,ROBO4,PECAM1,COL18A1,PROX1,NOTCH1,CDH5,SOX18	turquoise	VSMC_M6
GO:0010517	0.00	1.00	7	50	regulation of phospholipase activity	BP	0.03835	P2RY6,PLCB2,SNCA,CD86,LPAR2,SELE,NMUR1	turquoise	VSMC_M6
GO:0007159	0.00	1.00	17	234	leukocyte cell-cell adhesion	BP	0.03842	IL23A,IL1RL2,SYK,IL6,CD177,NFKBID,SLC39A8,HFE,LAPTM5,PECAM1,CD86,BMP7,CCDC88B,SELE,SELP,NRARP,CCR7	turquoise	VSMC_M6
GO:0007204	0.00	1.00	15	194	positive regulation of cytosolic calcium ion concentration	BP	0.03842	PIK3CG,CXCR4,EDNRB,P2RY6,CD36,CXCL10,SNCA,CCRL2,LPAR2,S1PR1,C3AR1,LPAR6,TRPM2,CCR7,NMB	turquoise	VSMC_M6
GO:0045123	0.00	1.00	7	50	cellular extravasation	BP	0.03842	PIK3CG,CD177,PECAM1,JAML,SELE,SELP,PLVAP	turquoise	VSMC_M6
GO:0030193	0.00	1.00	7	50	regulation of blood coagulation	BP	0.03842	PDGFB,NOS3,CD36,F11,KLKB1,CD34,ALOX12	turquoise	VSMC_M6
GO:0042113	0.00	1.00	15	193	B cell activation	BP	0.03865	SYK,IL6,DLL1,TGFB1,SFRP1,HHEX,ADGRG3,NKX2-3,LAPTM5,NFATC2,INPP5D,CD86,LFNG,LYL1,IRF8	turquoise	VSMC_M6
GO:0002573	0.00	1.00	13	154	myeloid leukocyte differentiation	BP	0.04002	TNFRSF11A,IL23A,IREB2,PPARG,TGFB1,CTNNB1,SFRP1,NKX2-3,INPP5D,LTF,MTOR,CCR7,PDE1B	turquoise	VSMC_M6
GO:0045596	0.00	1.00	28	489	negative regulation of cell differentiation	BP	0.04003	NOTCH4,PDGFB,IL6,BCL11A,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,SFRP1,CNTN4,CXCL10,NFATC2,INPP5D,BMP7,PRAME,LTF,TBX1,FGF23,SEMA6B,NRARP,HES3,NOTCH1,GBP1,LHX2,OLIG2,TRIM62,BAMBI	turquoise	VSMC_M6
GO:0015718	0.00	1.00	8	66	monocarboxylic acid transport	BP	0.0425	TNFRSF11A,SLC16A8,SYK,SLCO2B1,CD36,SLCO2A1,ACE,NMB	turquoise	VSMC_M6
GO:1900046	0.00	1.00	7	51	regulation of hemostasis	BP	0.0426	PDGFB,NOS3,CD36,F11,KLKB1,CD34,ALOX12	turquoise	VSMC_M6
GO:0050794	0.00	1.00	256	7581	regulation of cellular process	BP	0.04332	PARD6G,TNFRSF11A,IL23A,KCNN2,NMBR,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,DENND3,PDGFB,ETV7,MDGA1,CSF2RB,MOB3B,IREB2,ATP8A1,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,NDUFA4,ARHGAP25,C5,MAML3,KCNA7,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,SLC6A6,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,MAP6,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,ZIC2,RASGRP3,NOTUM,CNTN4,SLC4A11,CD36,NFKBID,KIRREL2,PRAG1,ADAMTS9,PRR5L,ATP8A2,KLKB1,HHEX,SOX7,TSC22D2,P2RY14,CXCL10,ANGPT2,SOGA1,ADGRG3,ATP6V0D2,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,TOX2,MAPK10,IRX6,GOT1,NKX2-3,CLIC6,BMP1,SNCA,CTNND2,SHANK2,HYAL2,SLC39A8,ESRRG,NKD2,HFE,MCTP2,HCRTR1,ROBO4,ESAM,LAPTM5,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,COL18A1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,JAML,OAZ3,SRMS,FANK1,ACE,PTPRE,CNKSR2,LAMC2,HOXD10,PRAME,PAX9,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,LPAR2,CCDC88B,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,ERAS,PRKCH,GRID2IP,KIF26B,TSPAN14,BCL6B,MMRN2,SNCG,PPP1R1B,LFNG,ARHGEF9,MTOR,BCKDK,TTLL6,GNGT2,ABI3,ARHGEF15,KLF1,MAST1,NPR1,BEX5,ISLR2,LYL1,COL4A6,COL4A5,DSC2,KIF26A,HCN1,PDE4B,SARM1,SEMA6B,LRG1,MATK,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,PTGS1,LHX6,CDH3,CDH1,ADGRL4,CDH5,ALOX12,DCDC2B,M	turquoise	VSMC_M6
GO:0001819	0.00	1.00	20	304	positive regulation of cytokine production	BP	0.04488	IL23A,FLT4,IL1RL2,SYK,IL6,C5,PIK3CG,TGFB1,CD36,HYAL2,LAPTM5,TLR7,CD34,CD86,CCDC88B,PDE4B,IRF8,MMP12,C3AR1,CCR7	turquoise	VSMC_M6
GO:0001817	0.00	1.00	28	492	regulation of cytokine production	BP	0.04488	IL23A,FLT4,IL1RL2,SYK,IL6,C5,PIK3CG,DLL1,TGFB1,CD36,HYAL2,HFE,LAPTM5,INPP5D,TLR7,CD34,CD86,LTF,CCDC88B,BCL6B,PDE4B,IRF8,GBP1,CDH3,MMP12,ACKR1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0061028	0.00	1.00	6	38	establishment of endothelial barrier	BP	0.04488	PDE2A,PPP1R16B,ROBO4,PECAM1,CDH5,SOX18	turquoise	VSMC_M6
GO:0001763	0.00	1.00	13	157	morphogenesis of a branching structure	BP	0.04488	CELSR1,NOTCH4,KDR,BCL11A,RASIP1,CTNNB1,TIE1,SFRP1,BMP7,PROX1,GREB1L,NRARP,NOTCH1	turquoise	VSMC_M6
GO:0072109	0.00	1.00	4	15	glomerular mesangium development	BP	0.04488	PDGFB,CD34,BMP7,NOTCH1	turquoise	VSMC_M6
GO:0042551	0.00	1.00	6	38	neuron maturation	BP	0.04488	BCL11A,EDNRB,SPTBN4,MTOR,B4GALT6,SCARF1	turquoise	VSMC_M6
GO:0002407	0.00	1.00	4	15	dendritic cell chemotaxis	BP	0.04488	PIK3CG,CXCR4,TRPM2,CCR7	turquoise	VSMC_M6
GO:0010594	0.00	1.00	13	157	regulation of endothelial cell migration	BP	0.04488	FLT4,PDGFB,KDR,PIK3CG,NOS3,PPARG,TGFB1,ADAMTS9,ANGPT2,PROX1,MMRN2,NOTCH1,ALOX12	turquoise	VSMC_M6
GO:0046850	0.00	1.00	6	38	regulation of bone remodeling	BP	0.04488	TNFRSF11A,SYK,IL6,SFRP1,INPP5D,S1PR1	turquoise	VSMC_M6
GO:0032615	0.00	1.00	6	38	interleukin-12 production	BP	0.04488	IL23A,SYK,CD36,LAPTM5,IRF8,CCR7	turquoise	VSMC_M6
GO:0032655	0.00	1.00	6	38	regulation of interleukin-12 production	BP	0.04488	IL23A,SYK,CD36,LAPTM5,IRF8,CCR7	turquoise	VSMC_M6
GO:0031349	0.00	1.00	14	177	positive regulation of defense response	BP	0.04504	TNFRSF11A,IL23A,IL18RAP,SYK,IL6,PIK3CG,CTSC,PDE2A,SNCA,HYAL2,TLR7,MMP12,TRIM62,CCR7	turquoise	VSMC_M6
GO:0031401	0.00	1.00	38	747	positive regulation of protein modification process	BP	0.04504	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,IL6,PIK3CG,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,CD36,PRR5L,THBS4,PPP1R16B,SNCA,HFE,LAPTM5,PECAM1,CD86,ERN1,BMP7,PROX1,ACE,LTF,TBX1,FGF23,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,CCR7	turquoise	VSMC_M6

GO:0050789	0.00	1.00	265	7907	regulation of biological process	BP	0.04561	PARD6G,TNFRSF11A,IL23A,KCNN2,NMBR,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,DENND3,PDGFB,ETV7,MDGA1,CSF2RB,MOB3B,IREB2,ATP8A1,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,NDUFA4,ARHGAP25,C5,MAML3,KCNA7,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,SLC6A6,GRIP2,FGD5,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,MAP6,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,ZIC2,RASGRP3,NOTUM,CNTN4,SLC4A11,CD36,NFKBID,KIRREL2,PRAG1,ADAMTS9,PRR5L,ATP8A2,F11,KLKB1,HHEX,PROCR,SOX7,TSC22D2,P2RY14,CXCL10,ANGPT2,SOGA1,SLC4A5,ADGRG3,ATP6V0D2,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,STAB1,TOX2,MAPK10,IRX6,GOT1,NKX2-3,CLIC6,BMP1,SNCA,CTNND2,SHANK2,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,MCTP2,HCRTR1,ROBO4,ESAM,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,COL18A1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,JAML,OAZ3,SRMS,FANK1,ACE,PTPRE,CNKSR2,LAMC2,HOXD10,PRAME,PAX9,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,LPAR2,CCDC88B,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,ERAS,PRKCH,GRID2IP,KIF26B,TSPAN14,BCL6B,MMRN2,SNCG,PPP1R1B,LFNG,ARHGEF9,MTOR,BCKDK,TTLL6,GNGT2,ABI3,ARHGEF15,KLF1,MAST1,NPR1,BEX5,ISLR2,LYL1,COL4A6,COL4A5,DSC2,KIF26A,HCN1,PDE4B,SARM1,SEMA6B,LRG1,MATK,TNFRSF18,NRARP,TMEM204,HES3,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,PALMD,SH2D3C,GBP1,LHX2,PTGS1,LHX6,CDH3,CDH1,ADGRL4,CDH	turquoise	VSMC_M6
GO:0006959	0.00	1.00	9	84	humoral immune response	BP	0.04561	LYZ,IL6,C5,RARRES2,CXCL10,ST6GAL1,LTF,NOTCH1,CCR7	turquoise	VSMC_M6
GO:0030316	0.00	1.00	8	68	osteoclast differentiation	BP	0.04561	TNFRSF11A,IL23A,IREB2,CTNNB1,SFRP1,INPP5D,LTF,MTOR	turquoise	VSMC_M6
GO:0003018	0.00	1.00	15	200	vascular process in circulatory system	BP	0.04741	ATP8A1,SLC6A6,GRIP2,NOS3,TGFB1,EDNRB,SLCO2B1,P2RY2,PDE2A,CD36,ACE,PLVAP,NPR1,CDH5,ATP1A4	turquoise	VSMC_M6
GO:0030217	0.00	1.00	14	179	T cell differentiation	BP	0.04741	IL23A,IL1RL2,SYK,IL6,CTNNB1,NFKBID,CYP26B1,NKX2-3,CD86,CRACR2A,LFNG,MTOR,NRARP,CCR7	turquoise	VSMC_M6
GO:0046849	0.00	1.00	8	69	bone remodeling	BP	0.04966	TNFRSF11A,SYK,IL6,TGFB1,CTNNB1,SFRP1,INPP5D,S1PR1	turquoise	VSMC_M6
GO:0042110	0.00	1.00	20	310	T cell activation	BP	0.05085	IL23A,IL1RL2,SYK,IL6,PIK3CG,CTNNB1,NFKBID,CYP26B1,NKX2-3,HFE,LAPTM5,CD86,SLAMF9,JAML,CCDC88B,CRACR2A,LFNG,MTOR,NRARP,CCR7	turquoise	VSMC_M6
GO:0045685	0.00	1.00	7	54	regulation of glial cell differentiation	BP	0.05115	IL6,TGFB1,CXCR4,CTNNB1,MTOR,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0000041	0.00	1.00	9	86	transition metal ion transport	BP	0.0512	IREB2,STEAP4,CP,SLC39A8,HFE,LTF,ATP13A1,HEPH,TRPM2	turquoise	VSMC_M6
GO:0021510	0.00	1.00	8	70	spinal cord development	BP	0.0512	MDGA1,DLL1,PROX1,HOXD10,MTOR,NOTCH1,RELN,OLIG2	turquoise	VSMC_M6
GO:0001946	0.00	1.00	4	16	lymphangiogenesis	BP	0.0512	FLT4,TIE1,PROX1,SOX18	turquoise	VSMC_M6
GO:0002366	0.00	1.00	14	181	leukocyte activation involved in immune response	BP	0.0512	IL23A,SYK,IL6,PIK3CG,DLL1,CD177,TGFB1,NFKBID,NKX2-3,CD86,CRACR2A,LFNG,MTOR,IRF8	turquoise	VSMC_M6
GO:0048468	0.00	1.00	68	1587	cell development	BP	0.0512	MEGF10,NOTCH4,SYT17,PDGFB,ADGRF5,EPHA5,IL6,BCL11A,DLL1,NOVA2,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,MAP6,SNAP25,PDE2A,SFRP1,CNTN4,PCDH12,PRAG1,ATP8A2,ANGPT2,SLC4A5,PRDM8,PPP1R16B,IRX6,CTNND2,DPYSL4,ROBO4,NRAP,NFATC2,PECAM1,COL18A1,BMP7,PROX1,LAMC2,HOXD10,LTF,TBX1,PRKCH,MTOR,ABI3,ISLR2,B4GALT6,HCN1,SARM1,SEMA6B,HES3,NOTCH1,GBP1,LHX2,LHX6,CDH1,CDH5,SOX17,RELN,ALKAL1,OLIG2,VSTM2L,SOX18,SHANK3,RTN4RL2,SCARF1,FLI1	turquoise	VSMC_M6
GO:0048713	0.00	1.00	5	27	regulation of oligodendrocyte differentiation	BP	0.0512	CXCR4,CTNNB1,MTOR,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0006801	0.00	1.00	7	54	superoxide metabolic process	BP	0.05135	SYK,NOS3,CD177,TGFB1,CD36,BMP7,ALOX12	turquoise	VSMC_M6
GO:0033194	0.00	1.00	4	16	response to hydroperoxide	BP	0.05135	CD36,MGST1,TRPM2,GPX3	turquoise	VSMC_M6
GO:0010574	0.00	1.00	5	27	regulation of vascular endothelial growth factor production	BP	0.05176	FLT4,IL6,C5,TGFB1,C3AR1	turquoise	VSMC_M6
GO:1902533	0.00	1.00	37	731	positive regulation of intracellular signal transduction	BP	0.05225	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,SYK,IL6,ANKRD6,PIK3CG,TGFB1,CTNNB1,P2RY6,CD36,PRAG1,PRR5L,HCRTR1,LAPTM5,TLR7,CD86,ERN1,PROX1,LTF,TBX1,GUCY1A2,SELP,VWF,FGF23,CRACR2A,MTOR,NPR1,NOTCH1,PMAIP1,RELN,ALKAL1,LPAR6,TRIM62,CCR7	turquoise	VSMC_M6
GO:0090322	0.00	1.00	5	27	regulation of superoxide metabolic process	BP	0.05248	SYK,CD177,TGFB1,CD36,BMP7	turquoise	VSMC_M6
GO:0043535	0.00	1.00	9	87	regulation of blood vessel endothelial cell migration	BP	0.05265	PDGFB,KDR,NOS3,PPARG,TGFB1,ANGPT2,MMRN2,NOTCH1,ALOX12	turquoise	VSMC_M6
GO:0001822	0.00	1.00	17	248	kidney development	BP	0.05624	PDGFB,DLL1,CTNNB1,SFRP1,ANGPT2,CYP26B1,HYAL2,CD34,PECAM1,BMP7,PROX1,ACE,RGN,KIF26B,GREB1L,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0033993	0.00	1.00	34	657	response to lipid	BP	0.05637	TNFRSF11A,CSF2RB,SYK,IL6,NOS3,PPARG,TGFB1,HTR5A,EDNRB,CTNNB1,TIE1,SFRP1,CD36,CXCL10,CYP26B1,GOT1,SNCA,ESRRG,CD86,BMP7,MGST1,LTF,TBX1,SELE,SELP,FGF23,PDE4B,SSTR5,NOTCH1,IRF8,ENDOG,ALOX12,CCR7,GPX3	turquoise	VSMC_M6
GO:0044419	0.00	1.00	45	948	biological process involved in interspecies interaction between organisms	BP	0.05855	TNFRSF11A,IL23A,LYZ,CSF2RB,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CD36,BPIFB3,CXCL10,STAB1,SNCA,HYAL2,UPK1B,ISG20,TLR7,CD86,MGST1,SRMS,LTF,CCDC88B,SELE,SELP,BAIAP2L1,PDE4B,SARM1,LRG1,NOTCH1,IRF8,GBP1,MMP12,PMAIP1,TRIM43,TRIM62,CCR7	turquoise	VSMC_M6
GO:0010518	0.00	1.00	6	41	positive regulation of phospholipase activity	BP	0.05894	P2RY6,PLCB2,CD86,LPAR2,SELE,NMUR1	turquoise	VSMC_M6
GO:0002263	0.00	1.00	14	185	cell activation involved in immune response	BP	0.06059	IL23A,SYK,IL6,PIK3CG,DLL1,CD177,TGFB1,NFKBID,NKX2-3,CD86,CRACR2A,LFNG,MTOR,IRF8	turquoise	VSMC_M6
GO:0043367	0.00	1.00	7	56	CD4-positive, alpha-beta T cell differentiation	BP	0.06059	IL23A,IL6,NFKBID,NKX2-3,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0055072	0.00	1.00	8	72	iron ion homeostasis	BP	0.06115	IREB2,STEAP4,CP,HYAL2,SLC39A8,HFE,LTF,HEPH	turquoise	VSMC_M6

GO:0048585	0.00	1.00	55	1229	negative regulation of response to stimulus	BP	0.06134	PDGFB,SYK,BARX1,IL6,ANKRD6,ARHGAP25,C5,RASIP1,DLL1,NOS3,PPARG,CTNNB1,PDE2A,SFRP1,NOTUM,PRR5L,F11,KLKB1,HHEX,ANGPT2,ADGRG3,CYP26B1,COL2A1,SNCA,SHANK2,HYAL2,NKD2,HFE,LAPTM5,INPP5D,CD34,BMP7,IGFBP3,GPC1,SRMS,PTPRE,PRAME,LTF,TSPAN15,MMRN2,LFNG,MTOR,KIF26A,PDE4B,SARM1,SEMA6B,NRARP,EGFL7,NOTCH1,GBP1,CDH5,ALOX12,MMP12,SOX17,BAMBI	turquoise	VSMC_M6
GO:0070374	0.00	1.00	12	145	positive regulation of ERK1 and ERK2 cascade	BP	0.06134	TNFRSF11A,FLT4,PDGFB,KDR,TGFB1,P2RY6,CD36,HCRTR1,FGF23,NOTCH1,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0007267	0.00	1.00	52	1146	cell-cell signaling	BP	0.06134	TNFRSF11A,KCNN2,SYBU,CELSR1,SYT17,PDGFB,SYK,BARX1,EPHA5,IL6,ANKRD6,GJA4,DLL1,SLC6A6,SYN2,TGFB1,HTR5A,CTNNB1,GPC6,SNAP25,SFRP1,NOTUM,CNTN4,HHEX,SOX7,CXCL10,STAB1,SNCA,CTNND2,SHANK2,NKD2,HFE,MCTP2,HCRTR1,CD34,FGF23,GRID2IP,SNCG,MTOR,NRARP,SSTR5,NOTCH1,CDH3,CDH1,EXOC3L1,SOX17,RELN,GRAP,SHANK3,TRPM2,BAMBI,NMB	turquoise	VSMC_M6
GO:0045216	0.00	1.00	12	146	cell-cell junction organization	BP	0.06189	GJA4,CD177,TGFB1,CTNNB1,CTNND2,ESAM,PECAM1,ACE,CLDN16,PRKCH,CDH1,CDH5	turquoise	VSMC_M6
GO:0048641	0.00	1.00	4	17	regulation of skeletal muscle tissue development	BP	0.06189	MEGF10,DLL1,TGFB1,CTNNB1	turquoise	VSMC_M6
GO:0045662	0.00	1.00	4	17	negative regulation of myoblast differentiation	BP	0.06189	DLL1,TGFB1,CXCL10,NOTCH1	turquoise	VSMC_M6
GO:0006525	0.00	1.00	4	17	arginine metabolic process	BP	0.06189	NOS3,SLC39A8,ART4,AGMAT	turquoise	VSMC_M6
GO:0014013	0.00	1.00	8	73	regulation of gliogenesis	BP	0.06338	IL6,TGFB1,CXCR4,CTNNB1,PRKCH,MTOR,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0045670	0.00	1.00	6	42	regulation of osteoclast differentiation	BP	0.06414	IL23A,CTNNB1,SFRP1,INPP5D,LTF,MTOR	turquoise	VSMC_M6
GO:0002285	0.00	1.00	11	127	lymphocyte activation involved in immune response	BP	0.0645	IL23A,IL6,DLL1,TGFB1,NFKBID,NKX2-3,CD86,CRACR2A,LFNG,MTOR,IRF8	turquoise	VSMC_M6
GO:0061138	0.00	1.00	12	147	morphogenesis of a branching epithelium	BP	0.06491	CELSR1,NOTCH4,KDR,RASIP1,CTNNB1,TIE1,SFRP1,BMP7,PROX1,GREB1L,NRARP,NOTCH1	turquoise	VSMC_M6
GO:0042742	0.00	1.00	10	109	defense response to bacterium	BP	0.06766	IL23A,LYZ,SYK,IL6,RARRES2,CD36,STAB1,LTF,SELP,IRF8	turquoise	VSMC_M6
GO:0070167	0.00	1.00	8	74	regulation of biomineral tissue development	BP	0.06766	NOS3,TGFB1,NOTUM,BMP7,LTF,FGF23,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0034330	0.00	1.00	29	541	cell junction organization	BP	0.06784	SYBU,MDGA1,KDR,LRRC4B,GJA4,CD177,ITGB4,TGFB1,CTNNB1,GPC6,SFRP1,SNCA,CTNND2,SHANK2,ESAM,PECAM1,ACE,CNKSR2,CLDN16,PPM1F,PRKCH,SNCG,ABI3,ARHGEF15,COL4A5,CDH1,CDH5,RELN,SHANK3	turquoise	VSMC_M6
GO:0046632	0.00	1.00	8	74	alpha-beta T cell differentiation	BP	0.06867	IL23A,SYK,IL6,NFKBID,NKX2-3,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0003170	0.00	1.00	7	58	heart valve development	BP	0.06962	NOS3,TGFB1,TIE1,PDE2A,ADAMTS9,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0002526	0.00	1.00	7	58	acute inflammatory response	BP	0.07073	TNFRSF11A,IL6,PIK3CG,EDNRB,KLKB1,HFE,CCR7	turquoise	VSMC_M6
GO:0110149	0.00	1.00	8	75	regulation of biomineralization	BP	0.07269	NOS3,TGFB1,NOTUM,BMP7,LTF,FGF23,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0072001	0.00	1.00	17	256	renal system development	BP	0.07269	PDGFB,DLL1,CTNNB1,SFRP1,ANGPT2,CYP26B1,HYAL2,CD34,PECAM1,BMP7,PROX1,ACE,RGN,KIF26B,GREB1L,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0010648	0.00	1.00	48	1047	negative regulation of cell communication	BP	0.07347	BARX1,IL6,ANKRD6,ARHGAP25,RASIP1,DLL1,NOS3,PPARG,CTNNB1,PDE2A,SFRP1,NOTUM,PRR5L,HHEX,ADGRG3,CYP26B1,COL2A1,SNCA,SHANK2,HYAL2,NKD2,LAPTM5,INPP5D,BMP7,IGFBP3,GPC1,SRMS,PTPRE,PRAME,LTF,TSPAN15,FGF23,GRID2IP,MMRN2,LFNG,MTOR,KIF26A,PDE4B,SARM1,NRARP,EGFL7,NOTCH1,GBP1,MMP12,SOX17,SHANK3,BAMBI,NMB	turquoise	VSMC_M6
GO:0009952	0.00	1.00	12	150	anterior/posterior pattern specification	BP	0.0741	BARX1,DLL1,CTNNB1,SFRP1,HHEX,HOXD10,TBX1,LFNG,NRARP,HES3,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0002684	0.00	1.00	29	542	positive regulation of immune system process	BP	0.07417	IL23A,IL18RAP,IL1RL2,SYK,IL6,C5,CTSC,RARRES2,CD177,TGFB1,CD36,NFKBID,CXCL10,THBS4,LAPTM5,NFATC2,INPP5D,CD86,CCDC88B,SELP,PLVAP,PRKCH,PDE4B,TNFRSF18,GBP1,MMP12,C3AR1,TRIM62,CCR7	turquoise	VSMC_M6
GO:0023057	0.00	1.00	48	1048	negative regulation of signaling	BP	0.07428	BARX1,IL6,ANKRD6,ARHGAP25,RASIP1,DLL1,NOS3,PPARG,CTNNB1,PDE2A,SFRP1,NOTUM,PRR5L,HHEX,ADGRG3,CYP26B1,COL2A1,SNCA,SHANK2,HYAL2,NKD2,LAPTM5,INPP5D,BMP7,IGFBP3,GPC1,SRMS,PTPRE,PRAME,LTF,TSPAN15,FGF23,GRID2IP,MMRN2,LFNG,MTOR,KIF26A,PDE4B,SARM1,NRARP,EGFL7,NOTCH1,GBP1,MMP12,SOX17,SHANK3,BAMBI,NMB	turquoise	VSMC_M6
GO:0036336	0.00	1.00	4	18	dendritic cell migration	BP	0.07428	PIK3CG,CXCR4,TRPM2,CCR7	turquoise	VSMC_M6
GO:0010573	0.00	1.00	5	30	vascular endothelial growth factor production	BP	0.07534	FLT4,IL6,C5,TGFB1,C3AR1	turquoise	VSMC_M6
GO:0071715	0.00	1.00	5	30	icosanoid transport	BP	0.07625	TNFRSF11A,SYK,SLCO2A1,ACE,NMB	turquoise	VSMC_M6
GO:0042093	0.00	1.00	6	44	T-helper cell differentiation	BP	0.07712	IL23A,IL6,NFKBID,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0010001	0.00	1.00	13	173	glial cell differentiation	BP	0.08352	IL6,DLL1,ITGB4,TGFB1,CXCR4,CTNNB1,PRDM8,GPC1,MTOR,B4GALT6,NOTCH1,RELN,OLIG2	turquoise	VSMC_M6
GO:0015698	0.00	1.00	10	113	inorganic anion transport	BP	0.08354	P2RY6,SLC4A11,SLC4A5,CLIC6,ANO3,SLC39A8,FGF23,MTOR,BEST2,NMUR1	turquoise	VSMC_M6
GO:0001655	0.00	1.00	18	283	urogenital system development	BP	0.08367	PDGFB,DLL1,CTNNB1,SFRP1,ANGPT2,CYP26B1,HYAL2,EAF2,CD34,PECAM1,BMP7,PROX1,ACE,RGN,KIF26B,GREB1L,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0045687	0.00	1.00	5	31	positive regulation of glial cell differentiation	BP	0.08447	TGFB1,CXCR4,MTOR,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0002294	0.00	1.00	6	45	CD4-positive, alpha-beta T cell differentiation involved in immune response	BP	0.08447	IL23A,IL6,NFKBID,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0098542	0.00	1.00	30	574	defense response to other organism	BP	0.08447	IL23A,LYZ,IL18RAP,IL1RL2,SYK,IL6,C5,PIK3CG,RARRES2,CD177,PPARG,CD36,BPIFB3,CXCL10,STAB1,SNCA,HYAL2,ISG20,TLR7,SRMS,LTF,CCDC88B,SELP,SARM1,IRF8,GBP1,MMP12,PMAIP1,TRIM43,TRIM62	turquoise	VSMC_M6
GO:0002694	0.00	1.00	21	352	regulation of leukocyte activation	BP	0.08447	IL23A,ADGRF5,IL1RL2,SYK,IL6,CTSC,CD177,TGFB1,CTNNB1,SFRP1,NFKBID,CYP26B1,SNCA,HFE,LAPTM5,NFATC2,INPP5D,CD86,CCDC88B,NRARP,CCR7	turquoise	VSMC_M6
GO:0045766	0.00	1.00	11	133	positive regulation of angiogenesis	BP	0.08447	KDR,C5,DLL1,NOS3,CXCR4,TIE1,ANGPT2,CD34,LRG1,CDH5,C3AR1	turquoise	VSMC_M6
GO:1904018	0.00	1.00	11	133	positive regulation of vasculature development	BP	0.08447	KDR,C5,DLL1,NOS3,CXCR4,TIE1,ANGPT2,CD34,LRG1,CDH5,C3AR1	turquoise	VSMC_M6
GO:0045785	0.00	1.00	19	306	positive regulation of cell adhesion	BP	0.08447	IL23A,MEGF10,PDGFB,KDR,IL1RL2,SYK,IL6,SFRP1,CD36,NFKBID,CD86,BMP7,CCDC88B,SELE,SELP,PPM1F,KIF26B,TNFRSF18,CCR7	turquoise	VSMC_M6
GO:0045671	0.00	1.00	4	19	negative regulation of osteoclast differentiation	BP	0.0855	CTNNB1,SFRP1,INPP5D,LTF	turquoise	VSMC_M6

GO:0050778	0.00	1.00	19	306	positive regulation of immune response	BP	0.08601	IL23A,IL18RAP,SYK,IL6,C5,CD177,TGFB1,NFKBID,LAPTM5,NFATC2,INPP5D,CD86,PRKCH,PDE4B,GBP1,MMP12,C3AR1,TRIM62,CCR7	turquoise	VSMC_M6
GO:0019934	0.00	1.00	4	19	cGMP-mediated signaling	BP	0.08637	EDNRB,PDE2A,CD36,NPR1	turquoise	VSMC_M6
GO:0003159	0.00	1.00	4	19	morphogenesis of an endothelium	BP	0.0865	CXCR4,CTNNB1,CXCL10,ALOX12	turquoise	VSMC_M6
GO:0061154	0.00	1.00	4	19	endothelial tube morphogenesis	BP	0.0865	CXCR4,CTNNB1,CXCL10,ALOX12	turquoise	VSMC_M6
GO:0048661	0.00	1.00	8	78	positive regulation of smooth muscle cell proliferation	BP	0.08958	PDGFB,IL6,TGFB1,P2RY6,ERN1,MTOR,S1PR1,ALOX12	turquoise	VSMC_M6
GO:0061041	0.00	1.00	9	96	regulation of wound healing	BP	0.08995	PDGFB,NOS3,CXCR4,CD36,F11,KLKB1,CD34,MTOR,ALOX12	turquoise	VSMC_M6
GO:0051147	0.00	1.00	10	115	regulation of muscle cell differentiation	BP	0.09109	MEGF10,PDGFB,DLL1,TGFB1,CYP26B1,NFATC2,PROX1,TBX1,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0051703	0.00	1.00	5	32	biological process involved in intraspecies interaction between organisms	BP	0.09109	SHANK2,LTF,TBX1,MTOR,SHANK3	turquoise	VSMC_M6
GO:0002287	0.00	1.00	6	46	alpha-beta T cell activation involved in immune response	BP	0.09117	IL23A,IL6,NFKBID,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0002293	0.00	1.00	6	46	alpha-beta T cell differentiation involved in immune response	BP	0.09117	IL23A,IL6,NFKBID,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0043410	0.00	1.00	21	356	positive regulation of MAPK cascade	BP	0.09117	TNFRSF11A,FLT4,PDGFB,KDR,SYK,IL6,ANKRD6,PIK3CG,TGFB1,CTNNB1,P2RY6,CD36,HCRTR1,LAPTM5,ERN1,TBX1,FGF23,CRACR2A,NOTCH1,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0060193	0.00	1.00	6	46	positive regulation of lipase activity	BP	0.0914	P2RY6,PLCB2,CD86,LPAR2,SELE,NMUR1	turquoise	VSMC_M6
GO:0008037	0.00	1.00	9	97	cell recognition	BP	0.09376	MEGF10,CXCR4,CNTN4,PCDH12,CD36,ROBO4,PECAM1,VSTM2L,CCR7	turquoise	VSMC_M6
GO:0022409	0.00	1.00	13	176	positive regulation of cell-cell adhesion	BP	0.09376	IL23A,MEGF10,IL1RL2,SYK,IL6,NFKBID,CD86,BMP7,CDC88B,SELE,SELP,KIF26B,CCR7	turquoise	VSMC_M6
GO:0045124	0.00	1.00	5	32	regulation of bone resorption	BP	0.09376	TNFRSF11A,SYK,IL6,INPP5D,S1PR1	turquoise	VSMC_M6
GO:0046631	0.00	1.00	9	97	alpha-beta T cell activation	BP	0.0938	IL23A,SYK,IL6,NFKBID,NKX2-3,HFE,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0048469	0.00	1.00	10	116	cell maturation	BP	0.09394	BCL11A,PPARG,EDNRB,CTNNB1,SPTBN4,MTOR,B4GALT6,LHX6,SOX18,SCARF1	turquoise	VSMC_M6
GO:0032613	0.00	1.00	5	32	interleukin-10 production	BP	0.09398	IL23A,SYK,IL6,DLL1,CD34	turquoise	VSMC_M6
GO:0032653	0.00	1.00	5	32	regulation of interleukin-10 production	BP	0.09398	IL23A,SYK,IL6,DLL1,CD34	turquoise	VSMC_M6
GO:0060284	0.00	1.00	22	384	regulation of cell development	BP	0.09743	IL6,BCL11A,DLL1,TGFB1,CXCR4,EDNRB,CTNNB1,MAP6,BMP7,LTF,PRKCH,MTOR,ISLR2,SEMA6B,HES3,NOTCH1,GBP1,LHX2,CDH5,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0048265	0.00	1.00	4	20	response to pain	BP	0.09834	GJA4,EDNRB,THBS4,RELN	turquoise	VSMC_M6
GO:0060191	0.00	1.00	7	63	regulation of lipase activity	BP	0.10026	P2RY6,PLCB2,SNCA,CD86,LPAR2,SELE,NMUR1	turquoise	VSMC_M6
GO:0072006	0.00	1.00	10	118	nephron development	BP	0.10072	PDGFB,DLL1,CTNNB1,ANGPT2,CD34,PECAM1,BMP7,KIF26B,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0016310	0.00	1.00	61	1440	phosphorylation	BP	0.10074	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,RASIP1,PIK3CG,KDM4D,RARRES2,PPARG,TGFB1,EDNRB,SPTBN4,TIE1,SFRP1,CD36,KIRREL2,STK35,PRAG1,PRR5L,HHEX,HUNK,THBS4,MAPK10,SNCA,HYAL2,HFE,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,SRMS,ACE,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,PPP1R1B,MTOR,BCKDK,MAST1,NPR1,MATK,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0007043	0.00	1.00	9	99	cell-cell junction assembly	BP	0.10108	GJA4,CTNNB1,CTNND2,ESAM,PECAM1,ACE,CLDN16,PRKCH,CDH5	turquoise	VSMC_M6
GO:0043537	0.00	1.00	5	33	negative regulation of blood vessel endothelial cell migration	BP	0.10108	PPARG,TGFB1,ANGPT2,MMRN2,NOTCH1	turquoise	VSMC_M6
GO:0045058	0.00	1.00	5	33	T cell selection	BP	0.10135	IL23A,SYK,IL6,MTOR,CCR7	turquoise	VSMC_M6
GO:0010596	0.00	1.00	6	48	negative regulation of endothelial cell migration	BP	0.10476	PPARG,TGFB1,ADAMTS9,ANGPT2,MMRN2,NOTCH1	turquoise	VSMC_M6
GO:0048518	0.00	1.00	161	4533	positive regulation of biological process	BP	0.10885	TNFRSF11A,IL23A,FLT4,MEGF10,SYBU,NOTCH4,ENPP2,SYT17,PDGFB,MOB3B,ATP8A1,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,EPHA5,IL6,BCL11A,LRRC4B,ANKRD6,NDUFA4,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,CTSC,RAB38,SLC6A6,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,MAP6,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,ZIC2,CD36,NFKBID,PRAG1,PRR5L,ATP8A2,F11,KLKB1,HHEX,SOX7,CXCL10,ANGPT2,THBS4,CYP26B1,PPP1R16B,TOX2,IRX6,GOT1,NKX2-3,BMP1,SNCA,SHANK2,HYAL2,ESRRG,NKD2,HFE,HCRTR1,LAPTM5,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,GPC1,JAML,OAZ3,FANK1,ACE,LAMC2,HOXD10,PRAME,PAX9,LTF,CCDC88B,TBX1,GUCY1A2,RGN,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,PRKCH,KIF26B,TSPAN14,MTOR,TTLL6,ABI3,ARHGEF15,KLF1,NPR1,ISLR2,LYL1,PDE4B,SARM1,SEMA6B,LRG1,MATK,TNFRSF18,NRARP,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,RUFY4,SOX17,RELN,ALKAL1,C3AR1,OLIG2,PDLIM1,SOX18,SHANK3,LPAR6,TRPM2,PKIB,TRIM62,BAMBI,CCR7,MGAT3,NMB,SCARF1,FLI1	turquoise	VSMC_M6
GO:0030099	0.00	1.00	18	293	myeloid cell differentiation	BP	0.10951	TNFRSF11A,IL23A,IREB2,ADGRF5,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,NKX2-3,INPP5D,LTF,MTOR,KLF1,IRF8,CCR7,PDE1B,FLI1	turquoise	VSMC_M6

GO:0048522	0.00	1.00	151	4212	positive regulation of cellular process	BP	0.10951	TNFRSF11A,IL23A,FLT4,MEGF10,SYBU,NOTCH4,ENPP2,SYT17,PDGFB,MOB3B,ATP8A1,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,EPHA5,IL6,LRRC4B,ANKRD6,NDUFA4,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,CTSC,RAB38,SLC6A6,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,MAP6,P2RY6,SNAP25,SFRP1,ZIC2,CD36,NFKBID,PRAG1,PRR5L,ATP8A2,KLKB1,HHEX,SOX7,CXCL10,THBS4,CYP26B1,PPP1R16B,TOX2,IRX6,GOT1,NKX2-3,SNCA,SHANK2,HYAL2,ESRRG,NKD2,HFE,HCRTR1,LAPTM5,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,GPC1,JAML,OAZ3,FANK1,ACE,LAMC2,HOXD10,PRAME,PAX9,LTF,CCDC88B,TBX1,GUCY1A2,RGN,SELE,SELP,VWF,PLVAP,BAIAP2L1,FGF23,CRACR2A,PPM1F,PRKCH,KIF26B,TSPAN14,MTOR,TTLL6,ABI3,ARHGEF15,KLF1,NPR1,ISLR2,LYL1,SARM1,SEMA6B,LRG1,MATK,TNFRSF18,NRARP,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,RUFY4,SOX17,RELN,ALKAL1,C3AR1,OLIG2,PDLIM1,SOX18,SHANK3,LPAR6,TRPM2,PKIB,TRIM62,BAMBI,CCR7,MGAT3,NMB,SCARF1,FLI1	turquoise	VSMC_M6
GO:0031589	0.00	1.00	18	294	cell-substrate adhesion	BP	0.11027	PDGFB,FREM1,KDR,LYPD3,ITGB4,CTNNB1,SFRP1,CD36,ADAMTS9,LYVE1,ANGPT2,CD34,VWF,PPM1F,NOTCH1,GBP1,MMP12,CCR7	turquoise	VSMC_M6
GO:0051049	0.00	1.00	55	1276	regulation of transport	BP	0.11195	TNFRSF11A,KCNN2,SYBU,SYT17,PDGFB,ATP8A1,SYK,EPHA5,IL6,NDUFA4,KCNA7,PIK3CG,DLL1,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,P2RY6,P2RY2,SNAP25,SFRP1,CD36,PRR5L,ATP8A2,CXCL10,CLIC6,SNCA,HYAL2,HFE,MCTP2,OAZ3,RGN,SELE,FGF23,CRACR2A,PPM1F,SNCG,MTOR,NPR1,HCN1,PDE4B,SSTR5,NOTCH1,CDH3,CDH1,RELN,KCNU1,NUCB1,SHANK3,TRPM2,NMB,FXYD6	turquoise	VSMC_M6
GO:0035710	0.00	1.00	7	65	CD4-positive, alpha-beta T cell activation	BP	0.1126	IL23A,IL6,NFKBID,NKX2-3,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0006953	0.00	1.00	4	21	acute-phase response	BP	0.11335	TNFRSF11A,IL6,EDNRB,HFE	turquoise	VSMC_M6
GO:0002687	0.00	1.00	9	101	positive regulation of leukocyte migration	BP	0.11521	IL6,RARRES2,CXCL10,THBS4,SELP,PLVAP,TNFRSF18,C3AR1,CCR7	turquoise	VSMC_M6
GO:0071417	0.00	1.00	25	466	cellular response to organonitrogen compound	BP	0.11521	BCL11A,PIK3CG,RARRES2,PPARG,HTR5A,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,SOGA1,GOT1,SNCA,PTPRE,BAIAP2L1,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,CDH1,TRPM2,NSG2	turquoise	VSMC_M6
GO:0048754	0.00	1.00	10	121	branching morphogenesis of an epithelial tube	BP	0.11586	CELSR1,NOTCH4,KDR,RASIP1,CTNNB1,TIE1,BMP7,GREB1L,NRARP,NOTCH1	turquoise	VSMC_M6
GO:1902531	0.00	1.00	56	1309	regulation of intracellular signal transduction	BP	0.11691	TNFRSF11A,IL23A,FLT4,DENND3,PDGFB,MOB3B,KDR,SYK,IL6,ANKRD6,ARHGAP25,RASIP1,PIK3CG,FGD5,PPARG,TGFB1,CTNNB1,P2RY6,PDE2A,SFRP1,CD36,PRAG1,PRR5L,ADGRG3,PPP1R16B,SHANK2,HYAL2,HCRTR1,LAPTM5,TLR7,CD86,ERN1,BMP7,PROX1,LTF,ARHGAP27,TBX1,GUCY1A2,RGN,SELP,VWF,FGF23,CRACR2A,ARHGEF9,MTOR,ARHGEF15,NPR1,NOTCH1,GBP1,PMAIP1,RELN,ALKAL1,GNA12,LPAR6,TRIM62,CCR7	turquoise	VSMC_M6
GO:0009968	0.00	1.00	44	973	negative regulation of signal transduction	BP	0.1212	BARX1,IL6,ANKRD6,ARHGAP25,RASIP1,DLL1,NOS3,PPARG,CTNNB1,PDE2A,SFRP1,NOTUM,PRR5L,HHEX,ADGRG3,CYP26B1,COL2A1,SNCA,SHANK2,HYAL2,NKD2,LAPTM5,INPP5D,BMP7,IGFBP3,GPC1,SRMS,PTPRE,PRAME,LTF,TSPAN15,MMRN2,LFNG,MTOR,KIF26A,PDE4B,SARM1,NRARP,EGFL7,NOTCH1,GBP1,MMP12,SOX17,BAMBI	turquoise	VSMC_M6
GO:0071363	0.00	1.00	28	545	cellular response to growth factor stimulus	BP	0.1212	FLT4,PDGFB,KDR,DLL1,PPARG,TGFB1,CTNNB1,PDE2A,SFRP1,HHEX,ANGPT2,COL2A1,GOT1,SNCA,HYAL2,HFE,ERN1,BMP7,GPC1,PAX9,TBX1,FGF23,MMRN2,LRG1,TMEM204,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0003179	0.00	1.00	6	50	heart valve morphogenesis	BP	0.12381	NOS3,TGFB1,TIE1,ADAMTS9,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0002292	0.00	1.00	6	50	T cell differentiation involved in immune response	BP	0.12465	IL23A,IL6,NFKBID,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0045453	0.00	1.00	6	50	bone resorption	BP	0.12578	TNFRSF11A,SYK,IL6,CTNNB1,INPP5D,S1PR1	turquoise	VSMC_M6
GO:0090100	0.00	1.00	8	85	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.12736	PPARG,TGFB1,GOT1,HFE,BMP7,LRG1,NOTCH1,CDH5	turquoise	VSMC_M6
GO:0048709	0.00	1.00	7	67	oligodendrocyte differentiation	BP	0.12736	CXCR4,CTNNB1,PRDM8,MTOR,B4GALT6,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0010634	0.00	1.00	11	143	positive regulation of epithelial cell migration	BP	0.12736	FLT4,ENPP2,PDGFB,KDR,PIK3CG,NOS3,TGFB1,PROX1,PPM1F,MTOR,ALOX12	turquoise	VSMC_M6
GO:0044331	0.00	1.00	4	22	cell-cell adhesion mediated by cadherin	BP	0.12736	NOTCH4,PPM1F,NOTCH1,CDH5	turquoise	VSMC_M6
GO:0070168	0.00	1.00	4	22	negative regulation of biomineral tissue development	BP	0.12736	NOS3,TGFB1,FGF23,NOTCH1	turquoise	VSMC_M6
GO:0110150	0.00	1.00	4	22	negative regulation of biomineralization	BP	0.12736	NOS3,TGFB1,FGF23,NOTCH1	turquoise	VSMC_M6
GO:1903034	0.00	1.00	10	123	regulation of response to wounding	BP	0.12736	PDGFB,NOS3,CXCR4,CD36,F11,KLKB1,CD34,MTOR,ALOX12,SCARF1	turquoise	VSMC_M6
GO:0099174	0.00	1.00	4	22	regulation of presynapse organization	BP	0.12736	MDGA1,LRRC4B,GPC6,SNCA	turquoise	VSMC_M6
GO:1905606	0.00	1.00	4	22	regulation of presynapse assembly	BP	0.12736	MDGA1,LRRC4B,GPC6,SNCA	turquoise	VSMC_M6
GO:0048546	0.00	1.00	5	36	digestive tract morphogenesis	BP	0.13626	CTNNB1,SFRP1,NKX2-3,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0045664	0.00	1.00	11	145	regulation of neuron differentiation	BP	0.13645	BCL11A,DLL1,EDNRB,SFRP1,CNTN4,BMP7,PROX1,MTOR,HES3,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0032270	0.00	1.00	47	1066	positive regulation of cellular protein metabolic process	BP	0.14164	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,IL6,PIK3CG,CTSC,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,CD36,PRR5L,KLKB1,SOX7,THBS4,PPP1R16B,SNCA,NKD2,HFE,LAPTM5,PECAM1,CD86,ERN1,BMP7,PROX1,ACE,LTF,TBX1,RGN,FGF23,PPM1F,MTOR,TNFRSF18,SH2D3C,CDH5,ALOX12,PRSS22,PMAIP1,RELN,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0032835	0.00	1.00	6	52	glomerulus development	BP	0.14293	PDGFB,ANGPT2,CD34,PECAM1,BMP7,NOTCH1	turquoise	VSMC_M6
GO:0034220	0.00	1.00	36	765	ion transmembrane transport	BP	0.14351	KCNN2,SLC16A8,ATP8A1,NDUFA4,KCNA7,SLC22A16,PIK3CG,SLC6A6,TMC6,TMC8,P2RY6,SNAP25,SLC4A11,CXCL10,SLC4A5,ATP6V0D2,CLIC6,SNCA,ANO3,SLC39A8,HFE,CLDN16,ATP13A1,RGN,CRACR2A,SLC25A18,MTOR,HCN1,PDE4B,ATP1A4,RELN,KCNU1,SHANK3,TRPM2,CCR7,FXYD6	turquoise	VSMC_M6
GO:0045665	0.00	1.00	6	52	negative regulation of neuron differentiation	BP	0.14446	DLL1,CNTN4,BMP7,HES3,NOTCH1,OLIG2	turquoise	VSMC_M6

GO:0031399	0.00	1.00	51	1182	regulation of protein modification process	BP	0.14506	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,IL6,RASIP1,PIK3CG,KDM4D,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,SFRP1,CD36,KIRREL2,PRR5L,HHEX,THBS4,PPP1R16B,SNCA,HYAL2,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,ACE,LTF,TBX1,RGN,FGF23,PPM1F,PPP1R1B,MTOR,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0061045	0.00	1.00	6	52	negative regulation of wound healing	BP	0.14506	PDGFB,NOS3,F11,KLKB1,CD34,ALOX12	turquoise	VSMC_M6
GO:0043408	0.00	1.00	26	502	regulation of MAPK cascade	BP	0.14671	TNFRSF11A,FLT4,PDGFB,KDR,SYK,IL6,ANKRD6,PIK3CG,PPARG,TGFB1,CTNNB1,P2RY6,SFRP1,CD36,HYAL2,HCRTR1,LAPTM5,ERN1,BMP7,TBX1,FGF23,CRACR2A,NOTCH1,GBP1,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0070372	0.00	1.00	14	211	regulation of ERK1 and ERK2 cascade	BP	0.14671	TNFRSF11A,FLT4,PDGFB,KDR,SYK,TGFB1,P2RY6,CD36,HCRTR1,FGF23,NOTCH1,GBP1,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0032989	0.00	1.00	30	609	cellular component morphogenesis	BP	0.14785	ENPP2,SYT17,EPHA5,BCL11A,NOVA2,ITGB4,CXCR4,CTNNB1,SPTBN4,MAP6,CNTN4,ATP8A2,CTNND2,DPYSL4,ROBO4,NRAP,BMP7,PROX1,GPC1,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L,SHANK3	turquoise	VSMC_M6
GO:0002446	0.00	1.00	4	23	neutrophil mediated immunity	BP	0.14841	SYK,IL6,CD177,ACE	turquoise	VSMC_M6
GO:1901136	0.00	1.00	10	126	carbohydrate derivative catabolic process	BP	0.14906	TGFB1,PDE2A,ADAMTS9,LYVE1,HYAL2,GPC1,CDA,PDE4B,MMP12,NUDT4B	turquoise	VSMC_M6
GO:0030850	0.00	1.00	5	37	prostate gland development	BP	0.15111	CTNNB1,SFRP1,EAF2,BMP7,NOTCH1	turquoise	VSMC_M6
GO:0051155	0.00	1.00	5	37	positive regulation of striated muscle cell differentiation	BP	0.15189	TGFB1,CYP26B1,PROX1,TBX1,MTOR	turquoise	VSMC_M6
GO:0000902	0.00	1.00	37	799	cell morphogenesis	BP	0.15393	NOTCH4,ENPP2,SYT17,KDR,EPHA5,BCL11A,NOVA2,FGD5,CXCR4,CTNNB1,SPTBN4,MAP6,CNTN4,PRAG1,ATP8A2,CTNND2,DPYSL4,ROBO4,COL18A1,BMP7,PROX1,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,PALMD,GBP1,LHX2,CDH5,SOX17,RELN,VSTM2L,SHANK3,BAMBI	turquoise	VSMC_M6
GO:0055076	0.00	1.00	9	107	transition metal ion homeostasis	BP	0.15455	IREB2,STEAP4,TMC8,CP,HYAL2,SLC39A8,HFE,LTF,HEPH	turquoise	VSMC_M6
GO:0019221	0.00	1.00	18	306	cytokine-mediated signaling pathway	BP	0.15724	TNFRSF11A,PDGFB,CSF2RB,IL18RAP,IL1RL2,SYK,IL6,PPARG,CXCR4,CXCL10,LAPTM5,CCRL2,PLVAP,TNFRSF18,NOTCH1,MMP12,ACKR1,CCR7	turquoise	VSMC_M6
GO:0007160	0.00	1.00	13	192	cell-matrix adhesion	BP	0.15801	FREM1,KDR,LYPD3,ITGB4,CTNNB1,SFRP1,CD36,ADAMTS9,LYVE1,CD34,PPM1F,MMP12,CCR7	turquoise	VSMC_M6
GO:2000027	0.00	1.00	9	108	regulation of animal organ morphogenesis	BP	0.15946	CELSR1,ANKRD6,CTNNB1,GPC6,SFRP1,CD34,BMP7,PAX9,TBX1	turquoise	VSMC_M6
GO:0043549	0.00	1.00	30	612	regulation of kinase activity	BP	0.16108	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,SYK,EPHA5,RASIP1,PIK3CG,PPARG,TGFB1,TIE1,SFRP1,HHEX,SNCA,HYAL2,CD86,ERN1,BMP7,PROX1,ACE,LTF,RGN,PPM1F,PPP1R1B,MTOR,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0050767	0.00	1.00	17	285	regulation of neurogenesis	BP	0.16108	IL6,DLL1,TGFB1,CXCR4,CTNNB1,MAP6,BMP7,PRKCH,MTOR,ISLR2,SEMA6B,HES3,NOTCH1,LHX2,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0042552	0.01	1.00	9	109	myelination	BP	0.16259	CTSC,ITGB4,CXCR4,CTNNB1,MALL,GPC1,MTOR,B4GALT6,OLIG2	turquoise	VSMC_M6
GO:0045667	0.01	1.00	9	109	regulation of osteoblast differentiation	BP	0.16259	IL6,PPARG,CTNNB1,SFRP1,BMP7,LTF,FGF23,NOTCH1,BAMBI	turquoise	VSMC_M6
GO:0032309	0.01	1.00	4	24	icosanoid secretion	BP	0.1627	TNFRSF11A,SYK,ACE,NMB	turquoise	VSMC_M6
GO:1902105	0.01	1.00	13	193	regulation of leukocyte differentiation	BP	0.16326	IL23A,IL1RL2,SYK,TGFB1,CTNNB1,SFRP1,NFKBID,CYP26B1,INPP5D,CD86,LTF,MTOR,NRARP	turquoise	VSMC_M6
GO:0010721	0.01	1.00	10	130	negative regulation of cell development	BP	0.16466	IL6,BCL11A,EDNRB,CTNNB1,BMP7,LTF,SEMA6B,NOTCH1,GBP1,LHX2	turquoise	VSMC_M6
GO:0007272	0.01	1.00	9	110	ensheathment of neurons	BP	0.1679	CTSC,ITGB4,CXCR4,CTNNB1,MALL,GPC1,MTOR,B4GALT6,OLIG2	turquoise	VSMC_M6
GO:0008366	0.01	1.00	9	110	axon ensheathment	BP	0.1679	CTSC,ITGB4,CXCR4,CTNNB1,MALL,GPC1,MTOR,B4GALT6,OLIG2	turquoise	VSMC_M6
GO:0022408	0.01	1.00	10	130	negative regulation of cell-cell adhesion	BP	0.16968	NOTCH4,TGFB1,HFE,LAPTM5,CD86,PPM1F,NRARP,NOTCH1,CDH1,ALOX12	turquoise	VSMC_M6
GO:0051153	0.01	1.00	7	72	regulation of striated muscle cell differentiation	BP	0.16988	DLL1,TGFB1,CYP26B1,PROX1,TBX1,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0007167	0.01	1.00	35	752	enzyme linked receptor protein signaling pathway	BP	0.17001	FLT4,PDGFB,KDR,SYK,EPHA5,DLL1,RARRES2,PPARG,TGFB1,CTNNB1,TIE1,SFRP1,HHEX,ANGPT2,SOGA1,GOT1,SNCA,HFE,BMP7,IGFBP3,GPC1,SRMS,PTPRE,BAIAP2L1,FGF23,MMRN2,NPR1,COL4A6,COL4A5,LRG1,TMEM204,NOTCH1,CDH3,CDH5,BAMBI	turquoise	VSMC_M6
GO:0030278	0.01	1.00	8	91	regulation of ossification	BP	0.17081	TGFB1,SFRP1,NOTUM,BMP7,LTF,FGF23,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0051247	0.01	1.00	49	1140	positive regulation of protein metabolic process	BP	0.17126	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,KDR,SYK,IL6,PIK3CG,CTSC,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,CD36,PRR5L,KLKB1,SOX7,THBS4,PPP1R16B,SNCA,NKD2,HFE,LAPTM5,PECAM1,CD86,ERN1,BMP7,PROX1,OAZ3,ACE,LTF,TBX1,RGN,FGF23,PPM1F,MTOR,TNFRSF18,SH2D3C,CDH5,ALOX12,PRSS22,PMAIP1,SOX17,RELN,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0051249	0.01	1.00	17	287	regulation of lymphocyte activation	BP	0.17408	IL23A,IL1RL2,SYK,IL6,TGFB1,CTNNB1,SFRP1,NFKBID,CYP26B1,HFE,LAPTM5,NFATC2,INPP5D,CD86,CCDC88B,NRARP,CCR7	turquoise	VSMC_M6
GO:0001837	0.01	1.00	10	131	epithelial to mesenchymal transition	BP	0.17409	NOTCH4,IL6,TGFB1,CTNNB1,SFRP1,BMP7,MTOR,NOTCH1,TRIM62,BAMBI	turquoise	VSMC_M6
GO:0045859	0.01	1.00	26	513	regulation of protein kinase activity	BP	0.17504	TNFRSF11A,IL23A,PDGFB,SYK,RASIP1,PIK3CG,PPARG,TGFB1,SFRP1,HHEX,SNCA,HYAL2,CD86,ERN1,BMP7,PROX1,ACE,LTF,RGN,PPM1F,PPP1R1B,MTOR,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0045661	0.01	1.00	5	39	regulation of myoblast differentiation	BP	0.17511	DLL1,TGFB1,CXCL10,IGFBP3,NOTCH1	turquoise	VSMC_M6
GO:0072538	0.01	1.00	4	25	T-helper 17 type immune response	BP	0.1775	IL23A,IL6,NFKBID,NOTCH1	turquoise	VSMC_M6
GO:0097106	0.01	1.00	4	25	postsynaptic density organization	BP	0.17757	LRRC4B,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0003007	0.01	1.00	13	197	heart morphogenesis	BP	0.17796	DLL1,NOS3,TGFB1,CTNNB1,COL2A1,BMP7,PROX1,TBX1,MTOR,NOTCH1,S1PR1,SOX17,SOX18	turquoise	VSMC_M6
GO:0002685	0.01	1.00	11	152	regulation of leukocyte migration	BP	0.17796	IL6,C5,RARRES2,CXCL10,THBS4,SELE,SELP,PLVAP,TNFRSF18,C3AR1,CCR7	turquoise	VSMC_M6
GO:0060251	0.01	1.00	4	25	regulation of glial cell proliferation	BP	0.178	IL6,PRKCH,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0010742	0.01	1.00	4	25	macrophage derived foam cell differentiation	BP	0.17805	PPARG,TGFB1,CD36,PRKCH	turquoise	VSMC_M6
GO:0090077	0.01	1.00	4	25	foam cell differentiation	BP	0.17805	PPARG,TGFB1,CD36,PRKCH	turquoise	VSMC_M6
GO:0061311	0.01	1.00	4	25	cell surface receptor signaling pathway involved in heart development	BP	0.17805	TGFB1,CTNNB1,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0001569	0.01	1.00	4	25	branching involved in blood vessel morphogenesis	BP	0.17805	NOTCH4,KDR,CTNNB1,NRARP	turquoise	VSMC_M6

GO:0006308	0.01	1.00	4	25	DNA catabolic process	BP	0.17805	IL6,ISG20,RGN,ENDOG	turquoise	VSMC_M6
GO:0046903	0.01	1.00	32	673	secretion	BP	0.17805	TNFRSF11A,SYBU,SYT17,SYK,EPHA5,IL6,SLC22A16,PIK3CG,EXOC3L2,CD177,SYN2,TGFB1,EDNRB,P2RY2,SNAP25,SFRP1,SLC4A5,SNCA,MTTP,NKD2,HFE,MCTP2,ACE,SYTL5,FGF23,SNCG,NPR1,SSTR5,NOTCH1,EXOC3L1,TRPM2,NMB	turquoise	VSMC_M6
GO:0009954	0.01	1.00	4	25	proximal/distal pattern formation	BP	0.17805	DLL1,CTNNB1,CYP26B1,HOXD10	turquoise	VSMC_M6
GO:0120039	0.01	1.00	26	517	plasma membrane bounded cell projection morphogenesis	BP	0.17805	ENPP2,SYT17,EPHA5,BCL11A,NOVA2,CXCR4,CTNNB1,SPTBN4,MAP6,CNTN4,ATP8A2,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L,SHANK3	turquoise	VSMC_M6
GO:0032733	0.01	1.00	4	25	positive regulation of interleukin-10 production	BP	0.17805	IL23A,SYK,IL6,CD34	turquoise	VSMC_M6
GO:0010033	0.01	1.00	87	2273	response to organic substance	BP	0.17933	TNFRSF11A,FLT4,SYBU,PDGFB,CSF2RB,KDR,IL18RAP,IL1RL2,SYK,EPHA5,IL6,BCL11A,PIK3CG,DLL1,CTSC,RARRES2,NOS3,PPARG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,TIE1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,HHEX,CXCL10,ANGPT2,SOGA1,THBS4,CYP26B1,COL2A1,GOT1,SNCA,HYAL2,ESRRG,HFE,LAPTM5,CD86,ERN1,BMP7,MGST1,GPC1,PTPRE,PAX9,LTF,CCRL2,TBX1,SELE,SELP,PLVAP,BAIAP2L1,FGF23,MMRN2,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,SARM1,LRG1,TNFRSF18,TMEM204,SSTR5,NOTCH1,IRF8,ENDOG,GBP1,CDH1,CDH5,ALOX12,MMP12,PMAIP1,RUFY4,SOX17,ACKR1,TRPM2,BAMBI,CCR7,NSG2,GPX3,PDE1B	turquoise	VSMC_M6
GO:0070848	0.01	1.00	28	570	response to growth factor	BP	0.18078	FLT4,PDGFB,KDR,DLL1,PPARG,TGFB1,CTNNB1,PDE2A,SFRP1,HHEX,ANGPT2,COL2A1,GOT1,SNCA,HYAL2,HFE,ERN1,BMP7,GPC1,PAX9,TBX1,FGF23,MMRN2,LRG1,TMEM204,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0001656	0.01	1.00	7	74	metanephros development	BP	0.18078	PDGFB,CTNNB1,CD34,BMP7,KIF26B,GREB1L,SOX17	turquoise	VSMC_M6
GO:0043114	0.01	1.00	5	40	regulation of vascular permeability	BP	0.18128	TGFB1,PDE2A,PLVAP,NPR1,CDH5	turquoise	VSMC_M6
GO:0006879	0.01	1.00	6	56	cellular iron ion homeostasis	BP	0.18154	IREB2,STEAP4,CP,SLC39A8,HFE,HEPH	turquoise	VSMC_M6
GO:0048762	0.01	1.00	13	198	mesenchymal cell differentiation	BP	0.18177	NOTCH4,IL6,TGFB1,EDNRB,CTNNB1,SFRP1,BMP7,TBX1,MTOR,SEMA6B,NOTCH1,TRIM62,BAMBI	turquoise	VSMC_M6
GO:0022029	0.01	1.00	5	40	telencephalon cell migration	BP	0.18251	MDGA1,CXCR4,CTNNB1,LHX6,RELN	turquoise	VSMC_M6
GO:0098655	0.01	1.00	30	623	cation transmembrane transport	BP	0.18251	KCNN2,ATP8A1,NDUFA4,KCNA7,SLC22A16,PIK3CG,SLC6A6,P2RY6,SNAP25,SLC4A11,CXCL10,SLC4A5,ATP6V0D2,SNCA,SLC39A8,HFE,CLDN16,ATP13A1,RGN,CRACR2A,SLC25A18,HCN1,PDE4B,ATP1A4,RELN,KCNU1,SHANK3,TRPM2,CCR7,FXYD6	turquoise	VSMC_M6
GO:0003014	0.01	1.00	7	74	renal system process	BP	0.18353	PDGFB,ADGRF5,EDNRB,SLC4A5,HYAL2,CD34,NPR1	turquoise	VSMC_M6
GO:0030182	0.01	1.00	46	1067	neuron differentiation	BP	0.18353	SYT17,MDGA1,EPHA5,IL6,BCL11A,DLL1,NOVA2,CXCR4,EDNRB,CTNNB1,SPTBN4,MAP6,SNAP25,SFRP1,CNTN4,PCDH12,PRAG1,ATP8A2,IRX6,CTNND2,DPYSL4,ROBO4,BMP7,PROX1,LAMC2,HOXD10,MTOR,ABI3,ISLR2,B4GALT6,HCN1,SARM1,SEMA6B,HES3,NOTCH1,S1PR1,LHX2,LHX6,CDH1,RELN,ALKAL1,OLIG2,VSTM2L,SHANK3,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0070098	0.01	1.00	5	40	chemokine-mediated signaling pathway	BP	0.18374	CXCR4,CXCL10,CCRL2,ACKR1,CCR7	turquoise	VSMC_M6
GO:0071901	0.01	1.00	8	93	negative regulation of protein serine/threonine kinase activity	BP	0.18382	RASIP1,PPARG,SFRP1,HHEX,HYAL2,BMP7,PPP1R1B,PKIB	turquoise	VSMC_M6
GO:0051345	0.01	1.00	23	440	positive regulation of hydrolase activity	BP	0.18391	SYK,ARHGAP25,PPARG,P2RY6,SFRP1,SOX7,PLCB2,SNCA,LAPTM5,CD86,ARHGAP27,LPAR2,RGN,SELE,PPM1F,MTOR,ARHGEF15,S1PR1,ALOX12,PRSS22,PMAIP1,NMUR1,CCR7	turquoise	VSMC_M6
GO:0002548	0.01	1.00	5	40	monocyte chemotaxis	BP	0.18444	TNFRSF11A,PDGFB,IL6,CXCL10,MSMP	turquoise	VSMC_M6
GO:0002250	0.01	1.00	15	244	adaptive immune response	BP	0.18444	TNFRSF11A,IL23A,SYK,IL6,C5,PIK3CG,CTSC,TGFB1,NFKBID,HFE,INPP5D,CD86,CRACR2A,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0048858	0.01	1.00	26	520	cell projection morphogenesis	BP	0.18444	ENPP2,SYT17,EPHA5,BCL11A,NOVA2,CXCR4,CTNNB1,SPTBN4,MAP6,CNTN4,ATP8A2,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L,SHANK3	turquoise	VSMC_M6
GO:0019935	0.01	1.00	6	57	cyclic-nucleotide-mediated signaling	BP	0.18979	EPHA5,HTR5A,EDNRB,PDE2A,CD36,NPR1	turquoise	VSMC_M6
GO:2000379	0.01	1.00	6	57	positive regulation of reactive oxygen species metabolic process	BP	0.19149	PDGFB,SYK,CD177,TGFB1,CD36,SNCA	turquoise	VSMC_M6
GO:0051145	0.01	1.00	6	57	smooth muscle cell differentiation	BP	0.19195	PDGFB,EDNRB,CTNNB1,NFATC2,TMEM204,NOTCH1	turquoise	VSMC_M6
GO:0021799	0.01	1.00	4	26	cerebral cortex radially oriented cell migration	BP	0.19322	MDGA1,CTNNB1,LHX6,RELN	turquoise	VSMC_M6
GO:0098660	0.01	1.00	28	574	inorganic ion transmembrane transport	BP	0.19496	KCNN2,NDUFA4,KCNA7,PIK3CG,SLC6A6,P2RY6,SNAP25,SLC4A11,CXCL10,SLC4A5,ATP6V0D2,SNCA,ANO3,SLC39A8,HFE,CLDN16,ATP13A1,RGN,CRACR2A,SLC25A18,MTOR,HCN1,PDE4B,ATP1A4,KCNU1,TRPM2,CCR7,FXYD6	turquoise	VSMC_M6
GO:0051960	0.01	1.00	19	344	regulation of nervous system development	BP	0.19708	IL6,LRRC4B,DLL1,CTSC,TGFB1,CXCR4,CTNNB1,MAP6,BMP7,PRKCH,MTOR,ISLR2,SEMA6B,HES3,NOTCH1,LHX2,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0045668	0.01	1.00	5	41	negative regulation of osteoblast differentiation	BP	0.19734	PPARG,SFRP1,FGF23,NOTCH1,BAMBI	turquoise	VSMC_M6
GO:0006950	0.01	0.99	101	2715	response to stress	BP	0.2004	TNFRSF11A,IL23A,LYZ,FLT4,NOTCH4,PDGFB,KDR,IL18RAP,IL1RL2,SYK,IL6,ANKRD6,C5,GJA4,PIK3CG,KDM4D,CTSC,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,PDE2A,SFRP1,SLC4A11,CD36,NFKBID,PRR5L,F11,BPIFB3,KLKB1,HHEX,LYVE1,PROCR,TSC22D2,CXCL10,ANGPT2,THBS4,CYP26B1,STAB1,MAPK10,GOT1,SNCA,MMRN1,HYAL2,HFE,LAPTM5,ISG20,NFATC2,TLR7,CD34,ERN1,COL18A1,BMP7,ASCC2,MGST1,JAML,SRMS,LTF,CCRL2,CCDC88B,SELE,SELP,VWF,CRACR2A,RCSD1,BCL6B,C19orf57,MTOR,ABI3,SARM1,NOTCH1,IRF8,ENDOG,SH2D3C,GBP1,PTGS1,CDH3,CDH5,ALOX12,MMP12,PMAIP1,GGN,TRIM43,RELN,ACKR1,C3AR1,PDLIM1,GNA12,TRPM2,TRIM62,CCR7,MGAT3,MSMP,RTN4RL2,SCARF1,GPX3	turquoise	VSMC_M6
GO:0072073	0.01	1.00	9	115	kidney epithelium development	BP	0.20083	DLL1,CTNNB1,SFRP1,CD34,PECAM1,BMP7,KIF26B,GREB1L,NOTCH1	turquoise	VSMC_M6

GO:0048666	0.01	1.00	39	877	neuron development	BP	0.20178	SYT17,EPHA5,IL6,BCL11A,NOVA2,CXCR4,EDNRB,CTNNB1,SPTBN4,MAP6,SNAP25,SFRP1,CNTN4,PCDH12,PRAG1,ATP8A2,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,HOXD10,MTOR,ABI3,ISLR2,B4GALT6,HCN1,SARM1,SEMA6B,NOTCH1,LHX2,LHX6,CDH1,RELN,ALKAL1,VSTM2L,SHANK3,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0021953	0.01	1.00	9	116	central nervous system neuron differentiation	BP	0.20654	MDGA1,NOVA2,SPTBN4,PROX1,HOXD10,B4GALT6,LHX6,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0050866	0.01	1.00	10	136	negative regulation of cell activation	BP	0.20654	PDGFB,ADGRF5,NOS3,SFRP1,HFE,LAPTM5,INPP5D,CD86,NRARP,ALOX12	turquoise	VSMC_M6
GO:0007169	0.01	1.00	25	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	0.20873	FLT4,PDGFB,KDR,SYK,EPHA5,DLL1,RARRES2,TGFB1,CTNNB1,TIE1,HHEX,ANGPT2,SOGA1,SNCA,IGFBP3,GPC1,SRMS,PTPRE,BAIAP2L1,FGF23,MMRN2,COL4A6,COL4A5,TMEM204,CDH3	turquoise	VSMC_M6
GO:0002768	0.01	1.00	11	158	immune response-regulating cell surface receptor signaling pathway	BP	0.2099	SYK,NFKBID,MAPK10,LAPTM5,NFATC2,INPP5D,PRKCH,PDE4B,GBP1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0055085	0.01	1.00	45	1047	transmembrane transport	BP	0.2099	KCNN2,SLC16A8,ATP8A1,NDUFA4,GJA4,KCNA7,SLC22A16,PIK3CG,SLC6A6,TMC6,TMC8,SLCO2B1,P2RY6,SNAP25,SLC4A11,CD36,SLCO2A1,SLCO5A1,CXCL10,SLC4A5,ATP6V0D2,CLIC6,SNCA,MFSD4A,ANO3,SLC39A8,HFE,SLCO4A1,OAZ3,CLDN16,ATP13A1,RGN,CRACR2A,SLC25A18,MTOR,SLC49A3,HCN1,PDE4B,ATP1A4,RELN,KCNU1,SHANK3,TRPM2,CCR7,FXYD6	turquoise	VSMC_M6
GO:0008038	0.01	1.00	5	42	neuron recognition	BP	0.2099	CXCR4,CNTN4,PCDH12,ROBO4,VSTM2L	turquoise	VSMC_M6
GO:0050769	0.01	1.00	12	181	positive regulation of neurogenesis	BP	0.21002	IL6,TGFB1,CXCR4,CTNNB1,MAP6,PRKCH,MTOR,ISLR2,NOTCH1,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0099084	0.01	1.00	4	27	postsynaptic specialization organization	BP	0.21004	LRRC4B,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0003151	0.01	1.00	6	59	outflow tract morphogenesis	BP	0.21004	CTNNB1,BMP7,TBX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0030168	0.01	1.00	8	96	platelet activation	BP	0.21014	PDGFB,SYK,IL6,PIK3CG,NOS3,SELP,VWF,ALOX12	turquoise	VSMC_M6
GO:0043280	0.01	1.00	8	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	0.21162	SYK,PPARG,SOX7,SNCA,LAPTM5,PPM1F,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0051050	0.01	1.00	31	660	positive regulation of transport	BP	0.21256	TNFRSF11A,SYBU,PDGFB,ATP8A1,SYK,NDUFA4,DLL1,CD177,PPARG,TGFB1,EDNRB,P2RY6,P2RY2,CD36,PRR5L,ATP8A2,CXCL10,SNCA,HYAL2,HFE,OAZ3,RGN,SELE,CRACR2A,NPR1,CDH3,CDH1,RELN,SHANK3,TRPM2,NMB	turquoise	VSMC_M6
GO:0010633	0.01	1.00	6	59	negative regulation of epithelial cell migration	BP	0.21256	PPARG,TGFB1,ADAMTS9,ANGPT2,MMRN2,NOTCH1	turquoise	VSMC_M6
GO:0034097	0.01	1.00	31	659	response to cytokine	BP	0.21256	TNFRSF11A,PDGFB,CSF2RB,IL18RAP,IL1RL2,SYK,IL6,PPARG,CXCR4,PDE2A,SFRP1,CXCL10,SNCA,HYAL2,LAPTM5,CCRL2,SELE,SELP,PLVAP,FGF23,TNFRSF18,NOTCH1,IRF8,ENDOG,GBP1,MMP12,RUFY4,SOX17,ACKR1,CCR7,PDE1B	turquoise	VSMC_M6
GO:0050867	0.01	1.00	14	226	positive regulation of cell activation	BP	0.21256	IL23A,IL1RL2,SYK,IL6,CTSC,CD177,TGFB1,NFKBID,NFATC2,INPP5D,CD86,CCDC88B,SELP,CCR7	turquoise	VSMC_M6
GO:0097485	0.01	1.00	12	182	neuron projection guidance	BP	0.21256	EPHA5,NOVA2,CNTN4,DPYSL4,ROBO4,BMP7,LAMC2,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L	turquoise	VSMC_M6
GO:0048246	0.01	1.00	4	27	macrophage chemotaxis	BP	0.21256	C5,RARRES2,EDNRB,C3AR1	turquoise	VSMC_M6
GO:0009620	0.01	1.00	4	27	response to fungus	BP	0.21256	SYK,RARRES2,LTF,TRIM62	turquoise	VSMC_M6
GO:0031347	0.01	1.00	21	397	regulation of defense response	BP	0.21256	TNFRSF11A,IL23A,IL18RAP,IL1RL2,SYK,IL6,PIK3CG,CTSC,PPARG,EDNRB,PDE2A,KLKB1,SNCA,HYAL2,TLR7,SELE,BCL6B,CDH5,MMP12,TRIM62,CCR7	turquoise	VSMC_M6
GO:0003002	0.01	1.00	15	251	regionalization	BP	0.21305	BARX1,DLL1,CTNNB1,SFRP1,HHEX,CYP26B1,HOXD10,TBX1,LFNG,NRARP,HES3,NOTCH1,LHX2,SOX17,RELN	turquoise	VSMC_M6
GO:0051091	0.01	1.00	13	204	positive regulation of DNA-binding transcription factor activity	BP	0.21305	TNFRSF11A,IL18RAP,EPHA5,IL6,PPARG,CTNNB1,ZIC2,CD36,FANK1,LTF,PRKCH,RELN,TRIM62	turquoise	VSMC_M6
GO:0032609	0.01	1.00	6	59	interferon-gamma production	BP	0.21305	IL23A,LAPTM5,TLR7,PDE4B,IRF8,CCR7	turquoise	VSMC_M6
GO:0032649	0.01	1.00	6	59	regulation of interferon-gamma production	BP	0.21305	IL23A,LAPTM5,TLR7,PDE4B,IRF8,CCR7	turquoise	VSMC_M6
GO:0048812	0.01	1.00	25	503	neuron projection morphogenesis	BP	0.21305	SYT17,EPHA5,BCL11A,NOVA2,CXCR4,CTNNB1,SPTBN4,MAP6,CNTN4,ATP8A2,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L,SHANK3	turquoise	VSMC_M6
GO:0033674	0.01	1.00	20	373	positive regulation of kinase activity	BP	0.21325	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,SYK,EPHA5,PIK3CG,TGFB1,TIE1,SNCA,CD86,ERN1,PROX1,ACE,LTF,MTOR,RELN,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0070371	0.01	1.00	14	227	ERK1 and ERK2 cascade	BP	0.21404	TNFRSF11A,FLT4,PDGFB,KDR,SYK,TGFB1,P2RY6,CD36,HCRTR1,FGF23,NOTCH1,GBP1,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0090288	0.01	1.00	7	78	negative regulation of cellular response to growth factor stimulus	BP	0.21427	PPARG,SFRP1,HHEX,GPC1,MMRN2,NOTCH1,BAMBI	turquoise	VSMC_M6
GO:0050851	0.01	1.00	9	117	antigen receptor-mediated signaling pathway	BP	0.21427	SYK,NFKBID,LAPTM5,NFATC2,INPP5D,PRKCH,PDE4B,GBP1,CCR7	turquoise	VSMC_M6
GO:0045619	0.01	1.00	9	117	regulation of lymphocyte differentiation	BP	0.21456	IL23A,IL1RL2,SYK,SFRP1,NFKBID,CYP26B1,INPP5D,CD86,NRARP	turquoise	VSMC_M6
GO:0043255	0.01	1.00	7	78	regulation of carbohydrate biosynthetic process	BP	0.21456	PDGFB,TGFB1,P2RY6,SOGA1,SNCA,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0071900	0.01	1.00	17	300	regulation of protein serine/threonine kinase activity	BP	0.21456	TNFRSF11A,PDGFB,SYK,RASIP1,PIK3CG,PPARG,TGFB1,SFRP1,HHEX,SNCA,HYAL2,ERN1,BMP7,PROX1,LTF,PPP1R1B,PKIB	turquoise	VSMC_M6
GO:0001933	0.01	1.00	16	276	negative regulation of protein phosphorylation	BP	0.21504	RASIP1,PPARG,TGFB1,SFRP1,KIRREL2,PRR5L,HHEX,SNCA,HYAL2,BMP7,IGFBP3,RGN,PPM1F,PPP1R1B,MTOR,PKIB	turquoise	VSMC_M6
GO:0006109	0.01	1.00	10	139	regulation of carbohydrate metabolic process	BP	0.21723	PDGFB,TGFB1,P2RY6,SOGA1,SNCA,RGN,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0021885	0.01	1.00	5	43	forebrain cell migration	BP	0.21781	MDGA1,CXCR4,CTNNB1,LHX6,RELN	turquoise	VSMC_M6
GO:0090287	0.01	1.00	14	230	regulation of cellular response to growth factor stimulus	BP	0.21877	DLL1,PPARG,TGFB1,CTNNB1,SFRP1,HHEX,GOT1,GPC1,MMRN2,LRG1,TMEM204,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0023061	0.01	1.00	18	325	signal release	BP	0.21877	TNFRSF11A,SYBU,SYT17,SYK,EPHA5,IL6,SYN2,SNAP25,SFRP1,SNCA,HFE,MCTP2,FGF23,SNCG,SSTR5,EXOC3L1,TRPM2,NMB	turquoise	VSMC_M6
GO:0032623	0.01	1.00	5	43	interleukin-2 production	BP	0.21888	LAPTM5,CD34,CD86,PDE4B,GBP1	turquoise	VSMC_M6
GO:0032663	0.01	1.00	5	43	regulation of interleukin-2 production	BP	0.21888	LAPTM5,CD34,CD86,PDE4B,GBP1	turquoise	VSMC_M6
GO:0070555	0.01	1.00	8	98	response to interleukin-1	BP	0.22038	TNFRSF11A,IL1RL2,IL6,SFRP1,SNCA,HYAL2,SELE,GBP1	turquoise	VSMC_M6
GO:0015908	0.01	1.00	6	60	fatty acid transport	BP	0.22042	TNFRSF11A,SYK,PPARG,CD36,ACE,NMB	turquoise	VSMC_M6
GO:0035051	0.01	1.00	9	119	cardiocyte differentiation	BP	0.22126	DLL1,TGFB1,NRAP,BMP7,PROX1,MTOR,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:1903037	0.01	1.00	13	206	regulation of leukocyte cell-cell adhesion	BP	0.22136	IL23A,IL1RL2,SYK,IL6,NFKBID,HFE,LAPTM5,CD86,CCDC88B,SELE,SELP,NRARP,CCR7	turquoise	VSMC_M6

GO:0035909	0.01	1.00	4	28	aorta morphogenesis	BP	0.22138	ADAMTS9,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0042063	0.01	1.00	14	230	gliogenesis	BP	0.22138	IL6,DLL1,ITGB4,TGFB1,CXCR4,CTNNB1,PRDM8,GPC1,PRKCH,MTOR,B4GALT6,NOTCH1,RELN,OLIG2	turquoise	VSMC_M6
GO:0050863	0.01	1.00	13	206	regulation of T cell activation	BP	0.22158	IL23A,IL1RL2,SYK,IL6,CTNNB1,NFKBID,CYP26B1,HFE,LAPTM5,CD86,CCDC88B,NRARP,CCR7	turquoise	VSMC_M6
GO:0080134	0.01	0.99	42	970	regulation of response to stress	BP	0.22158	TNFRSF11A,IL23A,FLT4,PDGFB,IL18RAP,IL1RL2,SYK,IL6,ANKRD6,PIK3CG,KDM4D,CTSC,NOS3,PPARG,CXCR4,EDNRB,CTNNB1,PDE2A,SFRP1,CD36,F11,KLKB1,SNCA,HYAL2,TLR7,CD34,ERN1,BMP7,SELE,CRACR2A,BCL6B,MTOR,ABI3,ENDOG,CDH5,ALOX12,MMP12,PMAIP1,TRPM2,TRIM62,CCR7,SCARF1	turquoise	VSMC_M6
GO:0014812	0.01	1.00	7	79	muscle cell migration	BP	0.22199	MEGF10,PDGFB,P2RY6,THBS4,IGFBP3,ACE,GNA12	turquoise	VSMC_M6
GO:1904894	0.01	1.00	4	28	positive regulation of receptor signaling pathway via STAT	BP	0.2226	IL23A,IL6,TGFB1,NOTCH1	turquoise	VSMC_M6
GO:0016202	0.01	1.00	4	28	regulation of striated muscle tissue development	BP	0.2226	MEGF10,DLL1,TGFB1,CTNNB1	turquoise	VSMC_M6
GO:0055123	0.01	1.00	8	99	digestive system development	BP	0.2226	BARX1,RARRES2,EDNRB,CTNNB1,SFRP1,NKX2-3,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0019730	0.01	1.00	4	28	antimicrobial humoral response	BP	0.2226	LYZ,RARRES2,CXCL10,LTF	turquoise	VSMC_M6
GO:0048699	0.01	0.99	49	1177	generation of neurons	BP	0.22327	CELSR1,SYT17,MDGA1,EPHA5,IL6,BCL11A,DLL1,NOVA2,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,MAP6,SNAP25,SFRP1,CNTN4,PCDH12,PRAG1,ATP8A2,IRX6,CTNND2,DPYSL4,ROBO4,BMP7,PROX1,LAMC2,HOXD10,PRKCH,MTOR,ABI3,ISLR2,B4GALT6,HCN1,SARM1,SEMA6B,HES3,NOTCH1,S1PR1,LHX2,LHX6,CDH1,RELN,ALKAL1,OLIG2,VSTM2L,SHANK3,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0051090	0.01	1.00	18	328	regulation of DNA-binding transcription factor activity	BP	0.22433	TNFRSF11A,IL18RAP,SYK,EPHA5,IL6,PPARG,CTNNB1,ZIC2,CD36,ADGRG3,MAPK10,BMP7,PROX1,FANK1,LTF,PRKCH,RELN,TRIM62	turquoise	VSMC_M6
GO:1901699	0.01	1.00	25	508	cellular response to nitrogen compound	BP	0.22433	BCL11A,PIK3CG,RARRES2,PPARG,HTR5A,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,SOGA1,GOT1,SNCA,PTPRE,BAIAP2L1,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,CDH1,TRPM2,NSG2	turquoise	VSMC_M6
GO:0032990	0.01	0.99	26	536	cell part morphogenesis	BP	0.22529	ENPP2,SYT17,EPHA5,BCL11A,NOVA2,CXCR4,CTNNB1,SPTBN4,MAP6,CNTN4,ATP8A2,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L,SHANK3	turquoise	VSMC_M6
GO:0070830	0.01	1.00	5	44	bicellular tight junction assembly	BP	0.22637	ESAM,PECAM1,CLDN16,PRKCH,CDH5	turquoise	VSMC_M6
GO:0030500	0.01	1.00	6	62	regulation of bone mineralization	BP	0.23641	TGFB1,NOTUM,BMP7,LTF,FGF23,S1PR1	turquoise	VSMC_M6
GO:0060828	0.01	1.00	13	210	regulation of canonical Wnt signaling pathway	BP	0.23886	ANKRD6,TGFB1,SFRP1,NOTUM,HHEX,SOX7,CTNND2,NKD2,NRARP,NOTCH1,CDH3,SOX17,BAMBI	turquoise	VSMC_M6
GO:0002699	0.01	1.00	10	142	positive regulation of immune effector process	BP	0.23899	IL23A,IL18RAP,SYK,IL6,CD177,TGFB1,CD36,NFKBID,LAPTM5,CD86	turquoise	VSMC_M6
GO:0045601	0.01	1.00	4	29	regulation of endothelial cell differentiation	BP	0.24036	NOTCH4,CTNNB1,NOTCH1,CDH5	turquoise	VSMC_M6
GO:0003180	0.01	1.00	4	29	aortic valve morphogenesis	BP	0.24036	NOS3,TGFB1,TIE1,NOTCH1	turquoise	VSMC_M6
GO:0010563	0.01	1.00	19	356	negative regulation of phosphorus metabolic process	BP	0.24036	PDGFB,RASIP1,PPARG,TGFB1,SFRP1,KIRREL2,PRR5L,HHEX,PPP1R16B,SNCA,HYAL2,BMP7,IGFBP3,RGN,CDA,PPM1F,PPP1R1B,MTOR,PKIB	turquoise	VSMC_M6
GO:0045936	0.01	1.00	19	356	negative regulation of phosphate metabolic process	BP	0.24036	PDGFB,RASIP1,PPARG,TGFB1,SFRP1,KIRREL2,PRR5L,HHEX,PPP1R16B,SNCA,HYAL2,BMP7,IGFBP3,RGN,CDA,PPM1F,PPP1R1B,MTOR,PKIB	turquoise	VSMC_M6
GO:0048634	0.01	1.00	4	29	regulation of muscle organ development	BP	0.24139	MEGF10,DLL1,TGFB1,CTNNB1	turquoise	VSMC_M6
GO:0032755	0.01	1.00	6	62	positive regulation of interleukin-6 production	BP	0.24139	IL1RL2,SYK,IL6,CD36,HYAL2,TLR7	turquoise	VSMC_M6
GO:2000146	0.01	1.00	14	234	negative regulation of cell motility	BP	0.24143	C5,PPARG,TGFB1,TIE1,SFRP1,ADAMTS9,ANGPT2,HYAL2,IGFBP3,RGN,MMRN2,NOTCH1,CDH1,GNA12	turquoise	VSMC_M6
GO:1903539	0.01	1.00	4	29	protein localization to postsynaptic membrane	BP	0.24145	GRIP2,GPC6,SNAP25,MAPK10	turquoise	VSMC_M6
GO:0022008	0.01	0.99	52	1272	neurogenesis	BP	0.24333	CELSR1,SYT17,MDGA1,EPHA5,IL6,BCL11A,DLL1,NOVA2,ITGB4,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,MAP6,SNAP25,SFRP1,CNTN4,PCDH12,PRAG1,ATP8A2,PRDM8,IRX6,CTNND2,DPYSL4,ROBO4,BMP7,PROX1,GPC1,LAMC2,HOXD10,PRKCH,MTOR,ABI3,ISLR2,B4GALT6,HCN1,SARM1,SEMA6B,HES3,NOTCH1,S1PR1,LHX2,LHX6,CDH1,RELN,ALKAL1,OLIG2,VSTM2L,SHANK3,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0009893	0.01	0.99	103	2815	positive regulation of metabolic process	BP	0.24333	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,MOB3B,ADGRF5,KDR,IL1RL2,SYK,EPHA5,IL6,BCL11A,C5,MAML3,PIK3CG,DLL1,KDM4D,CTSC,RAB38,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TIE1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,PRR5L,KLKB1,HHEX,SOX7,CXCL10,THBS4,CYP26B1,PPP1R16B,TOX2,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NKD2,HFE,LAPTM5,NFATC2,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,PROX1,OAZ3,FANK1,ACE,HOXD10,PAX9,LTF,CCDC88B,TBX1,RGN,SELE,FGF23,PPM1F,MTOR,KLF1,LYL1,PDE4B,TNFRSF18,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,RUFY4,SOX17,RELN,ALKAL1,C3AR1,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0062197	0.01	1.00	16	282	cellular response to chemical stress	BP	0.24333	IL18RAP,IL6,NOS3,CTNNB1,SLC4A11,CD36,PRR5L,MAPK10,SNCA,ERN1,BMP7,MGST1,RCSD1,ENDOG,TRPM2,MGAT3	turquoise	VSMC_M6
GO:0007519	0.01	1.00	9	122	skeletal muscle tissue development	BP	0.24333	MEGF10,DLL1,TGFB1,CTNNB1,CYP26B1,GPC1,HOXD10,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0034599	0.01	1.00	14	234	cellular response to oxidative stress	BP	0.24469	IL18RAP,IL6,NOS3,CTNNB1,SLC4A11,CD36,PRR5L,SNCA,ERN1,BMP7,MGST1,ENDOG,TRPM2,MGAT3	turquoise	VSMC_M6
GO:0050776	0.01	0.99	26	538	regulation of immune response	BP	0.24499	IL23A,IL18RAP,SYK,IL6,C5,CD177,PPARG,TGFB1,CD36,NFKBID,MAPK10,HFE,LAPTM5,NFATC2,INPP5D,TLR7,CD86,LTF,PRKCH,PDE4B,SARM1,GBP1,MMP12,C3AR1,TRIM62,CCR7	turquoise	VSMC_M6
GO:1903039	0.01	1.00	10	143	positive regulation of leukocyte cell-cell adhesion	BP	0.2455	IL23A,IL1RL2,SYK,IL6,NFKBID,CD86,CCDC88B,SELE,SELP,CCR7	turquoise	VSMC_M6
GO:0060485	0.01	1.00	14	235	mesenchyme development	BP	0.24604	NOTCH4,IL6,NOS3,TGFB1,EDNRB,CTNNB1,SFRP1,BMP7,TBX1,MTOR,SEMA6B,NOTCH1,TRIM62,BAMBI	turquoise	VSMC_M6
GO:0051046	0.01	0.99	22	434	regulation of secretion	BP	0.24769	TNFRSF11A,SYBU,SYT17,SYK,EPHA5,IL6,CD177,TGFB1,EDNRB,P2RY2,SNAP25,SFRP1,SNCA,HFE,MCTP2,FGF23,SNCG,NPR1,SSTR5,NOTCH1,TRPM2,NMB	turquoise	VSMC_M6

GO:1902414	0.01	1.00	7	82	protein localization to cell junction	BP	0.24806	GRIP2,GPC6,SNAP25,MAPK10,PECAM1,CDH5,RELN	turquoise	VSMC_M6
GO:0098662	0.01	0.99	26	541	inorganic cation transmembrane transport	BP	0.24939	KCNN2,NDUFA4,KCNA7,PIK3CG,SLC6A6,P2RY6,SNAP25,SLC4A11,CXCL10,SLC4A5,ATP6V0D2,SNCA,SLC39A8,HFE,CLDN16,ATP13A1,RGN,CRACR2A,SLC25A18,HCN1,PDE4B,ATP1A4,KCNU1,TRPM2,CCR7,FXYD6	turquoise	VSMC_M6
GO:0021515	0.01	1.00	4	30	cell differentiation in spinal cord	BP	0.25231	MDGA1,HOXD10,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0032885	0.01	1.00	4	30	regulation of polysaccharide biosynthetic process	BP	0.25429	PDGFB,TGFB1,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0040013	0.01	1.00	15	261	negative regulation of locomotion	BP	0.2564	C5,PPARG,TGFB1,TIE1,SFRP1,ADAMTS9,ANGPT2,HYAL2,IGFBP3,RGN,MMRN2,SEMA6B,NOTCH1,CDH1,GNA12	turquoise	VSMC_M6
GO:0010761	0.01	1.00	5	46	fibroblast migration	BP	0.25728	TGFB1,PRR5L,HYAL2,PDLIM1,GNA12	turquoise	VSMC_M6
GO:0097120	0.01	1.00	5	46	receptor localization to synapse	BP	0.25732	GRIP2,GPC6,SNAP25,MAPK10,RELN	turquoise	VSMC_M6
GO:1901861	0.01	1.00	4	30	regulation of muscle tissue development	BP	0.25815	MEGF10,DLL1,TGFB1,CTNNB1	turquoise	VSMC_M6
GO:0033280	0.01	1.00	4	30	response to vitamin D	BP	0.25815	SFRP1,CXCL10,BMP7,FGF23	turquoise	VSMC_M6
GO:0042554	0.01	1.00	4	30	superoxide anion generation	BP	0.25821	SYK,CD177,TGFB1,ALOX12	turquoise	VSMC_M6
GO:0031325	0.01	0.99	92	2483	positive regulation of cellular metabolic process	BP	0.25821	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,MOB3B,ADGRF5,KDR,SYK,EPHA5,IL6,MAML3,PIK3CG,DLL1,KDM4D,CTSC,RAB38,RARRES2,NOS3,CD177,PPARG,TGFB1,EDNRB,CTNNB1,TIE1,P2RY6,SFRP1,ZIC2,CD36,PRR5L,KLKB1,HHEX,SOX7,CXCL10,THBS4,PPP1R16B,TOX2,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NKD2,HFE,LAPTM5,NFATC2,EAF2,TLR7,PECAM1,CD86,ERN1,BMP7,PROX1,FANK1,ACE,HOXD10,PAX9,LTF,TBX1,RGN,SELE,FGF23,PPM1F,MTOR,KLF1,LYL1,TNFRSF18,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,RUFY4,SOX17,RELN,ALKAL1,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0062237	0.01	1.00	4	30	protein localization to postsynapse	BP	0.25853	GRIP2,GPC6,SNAP25,MAPK10	turquoise	VSMC_M6
GO:0015909	0.01	1.00	5	46	long-chain fatty acid transport	BP	0.25868	SYK,PPARG,CD36,ACE,NMB	turquoise	VSMC_M6
GO:1903035	0.01	1.00	6	64	negative regulation of response to wounding	BP	0.26018	PDGFB,NOS3,F11,KLKB1,CD34,ALOX12	turquoise	VSMC_M6
GO:0002312	0.01	1.00	6	64	B cell activation involved in immune response	BP	0.26206	IL6,DLL1,TGFB1,NKX2-3,LFNG,IRF8	turquoise	VSMC_M6
GO:0002367	0.01	1.00	6	64	cytokine production involved in immune response	BP	0.2627	IL6,TGFB1,CD36,HFE,LAPTM5,SLAMF9	turquoise	VSMC_M6
GO:0043405	0.01	1.00	10	146	regulation of MAP kinase activity	BP	0.26279	TNFRSF11A,PDGFB,SYK,PIK3CG,PPARG,TGFB1,SFRP1,HYAL2,ERN1,BMP7	turquoise	VSMC_M6
GO:0032970	0.01	0.99	18	337	regulation of actin filament-based process	BP	0.26318	CELSR1,EPHA5,SPTBN4,SFRP1,ESAM,PROX1,BAIAP2L1,PPM1F,MTOR,ABI3,ARHGEF15,DSC2,PDE4B,S1PR1,KANK3,SHANK3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0007162	0.01	0.99	13	215	negative regulation of cell adhesion	BP	0.26446	NOTCH4,TGFB1,ANGPT2,HFE,LAPTM5,CD86,PPM1F,NRARP,NOTCH1,GBP1,CDH1,ALOX12,MMP12	turquoise	VSMC_M6
GO:0051962	0.01	0.99	13	216	positive regulation of nervous system development	BP	0.26564	IL6,LRRC4B,TGFB1,CXCR4,CTNNB1,MAP6,PRKCH,MTOR,ISLR2,NOTCH1,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0035176	0.01	1.00	4	31	social behavior	BP	0.26564	SHANK2,TBX1,MTOR,SHANK3	turquoise	VSMC_M6
GO:0035306	0.01	1.00	5	47	positive regulation of dephosphorylation	BP	0.26564	TGFB1,PPP1R16B,RGN,MTOR,CDH5	turquoise	VSMC_M6
GO:0071772	0.01	1.00	9	126	response to BMP	BP	0.26564	PPARG,TGFB1,SFRP1,COL2A1,HFE,BMP7,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0071773	0.01	1.00	9	126	cellular response to BMP stimulus	BP	0.26564	PPARG,TGFB1,SFRP1,COL2A1,HFE,BMP7,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0050918	0.01	1.00	5	47	positive chemotaxis	BP	0.26565	PDGFB,KDR,CXCL10,ANGPT2,S1PR1	turquoise	VSMC_M6
GO:0098773	0.01	1.00	6	65	skin epidermis development	BP	0.26642	DLL1,CTNNB1,NOTCH1,LHX2,CDH3,SOX18	turquoise	VSMC_M6
GO:0051347	0.01	0.99	22	441	positive regulation of transferase activity	BP	0.26702	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,SYK,EPHA5,PIK3CG,TGFB1,CTNNB1,TIE1,SNCA,CD86,ERN1,PROX1,ACE,LTF,MTOR,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0002286	0.01	1.00	6	65	T cell activation involved in immune response	BP	0.26707	IL23A,IL6,NFKBID,CD86,CRACR2A,MTOR	turquoise	VSMC_M6
GO:0071345	0.01	0.99	27	574	cellular response to cytokine stimulus	BP	0.2705	TNFRSF11A,PDGFB,CSF2RB,IL18RAP,IL1RL2,SYK,IL6,PPARG,CXCR4,PDE2A,SFRP1,CXCL10,HYAL2,LAPTM5,CCRL2,PLVAP,FGF23,TNFRSF18,NOTCH1,IRF8,GBP1,MMP12,RUFY4,SOX17,ACKR1,CCR7,PDE1B	turquoise	VSMC_M6
GO:0031214	0.01	1.00	9	126	biomineral tissue development	BP	0.27064	NOS3,TGFB1,NOTUM,BMP7,LTF,TBX1,FGF23,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0010604	0.01	0.99	95	2586	positive regulation of macromolecule metabolic process	BP	0.27064	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,MOB3B,KDR,IL1RL2,SYK,IL6,BCL11A,C5,MAML3,PIK3CG,DLL1,KDM4D,CTSC,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,KLKB1,HHEX,SOX7,CXCL10,THBS4,CYP26B1,PPP1R16B,TOX2,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NKD2,HFE,LAPTM5,NFATC2,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,PROX1,OAZ3,FANK1,ACE,HOXD10,PAX9,LTF,CCDC88B,TBX1,RGN,SELE,FGF23,PPM1F,MTOR,KLF1,LYL1,PDE4B,TNFRSF18,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,SOX17,RELN,ALKAL1,C3AR1,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0030857	0.01	1.00	4	31	negative regulation of epithelial cell differentiation	BP	0.27064	NOTCH4,DLL1,CTNNB1,NOTCH1	turquoise	VSMC_M6
GO:0043588	0.01	1.00	11	171	skin development	BP	0.27163	DLL1,ITGB4,CTNNB1,ATP8A2,CYP26B1,PRKCH,NOTCH1,LHX2,CDH3,ALOX12,SOX18	turquoise	VSMC_M6
GO:0010595	0.01	1.00	8	105	positive regulation of endothelial cell migration	BP	0.2724	FLT4,PDGFB,KDR,PIK3CG,NOS3,TGFB1,PROX1,ALOX12	turquoise	VSMC_M6
GO:0051271	0.01	0.99	14	241	negative regulation of cellular component movement	BP	0.2724	C5,PPARG,TGFB1,TIE1,SFRP1,ADAMTS9,ANGPT2,HYAL2,IGFBP3,RGN,MMRN2,NOTCH1,CDH1,GNA12	turquoise	VSMC_M6
GO:2001056	0.01	1.00	8	105	positive regulation of cysteine-type endopeptidase activity	BP	0.2724	SYK,PPARG,SOX7,SNCA,LAPTM5,PPM1F,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0002429	0.01	1.00	10	148	immune response-activating cell surface receptor signaling pathway	BP	0.2724	SYK,NFKBID,LAPTM5,NFATC2,INPP5D,PRKCH,PDE4B,GBP1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0002757	0.01	1.00	10	148	immune response-activating signal transduction	BP	0.2724	SYK,NFKBID,LAPTM5,NFATC2,INPP5D,PRKCH,PDE4B,GBP1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0071222	0.01	1.00	9	126	cellular response to lipopolysaccharide	BP	0.2724	IL6,TGFB1,EDNRB,CD36,CXCL10,CD86,LTF,PDE4B,IRF8	turquoise	VSMC_M6
GO:0048863	0.01	0.99	11	171	stem cell differentiation	BP	0.27465	EDNRB,CTNNB1,SFRP1,SLC4A11,BMP7,ACE,TBX1,SEMA6B,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0021543	0.01	1.00	9	127	pallium development	BP	0.27465	MDGA1,EPHA5,HTR5A,CTNNB1,PROX1,SEMA6B,LHX2,LHX6,RELN	turquoise	VSMC_M6
GO:0001756	0.01	1.00	5	48	somitogenesis	BP	0.27668	DLL1,SFRP1,LFNG,NRARP,NOTCH1	turquoise	VSMC_M6
GO:0110148	0.01	1.00	9	127	biomineralization	BP	0.27702	NOS3,TGFB1,NOTUM,BMP7,LTF,TBX1,FGF23,NOTCH1,S1PR1	turquoise	VSMC_M6

GO:0032102	0.01	0.99	15	266	negative regulation of response to external stimulus	BP	0.27755	PDGFB,SYK,C5,NOS3,PPARG,F11,KLKB1,ANGPT2,CD34,LTF,SEMA6B,NOTCH1,CDH5,ALOX12,MMP12	turquoise	VSMC_M6
GO:0120192	0.01	1.00	5	48	tight junction assembly	BP	0.27831	ESAM,PECAM1,CLDN16,PRKCH,CDH5	turquoise	VSMC_M6
GO:0035914	0.01	1.00	5	48	skeletal muscle cell differentiation	BP	0.27933	MEGF10,CYP26B1,GPC1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0048010	0.01	1.00	5	48	vascular endothelial growth factor receptor signaling pathway	BP	0.28034	FLT4,KDR,HHEX,MMRN2,TMEM204	turquoise	VSMC_M6
GO:1990868	0.01	1.00	5	48	response to chemokine	BP	0.28034	CXCR4,CXCL10,CCRL2,ACKR1,CCR7	turquoise	VSMC_M6
GO:1990869	0.01	1.00	5	48	cellular response to chemokine	BP	0.28034	CXCR4,CXCL10,CCRL2,ACKR1,CCR7	turquoise	VSMC_M6
GO:0006469	0.01	0.99	11	172	negative regulation of protein kinase activity	BP	0.28037	RASIP1,PPARG,SFRP1,HHEX,SNCA,HYAL2,BMP7,RGN,PPM1F,PPP1R1B,PKIB	turquoise	VSMC_M6
GO:0002696	0.01	0.99	13	218	positive regulation of leukocyte activation	BP	0.2832	IL23A,IL1RL2,SYK,IL6,CTSC,CD177,TGFB1,NFKBID,NFATC2,INPP5D,CD86,CCDC88B,CCR7	turquoise	VSMC_M6
GO:0001818	0.01	0.99	12	195	negative regulation of cytokine production	BP	0.28487	IL23A,IL6,DLL1,TGFB1,HFE,LAPTM5,INPP5D,CD34,LTF,GBP1,CDH3,CCR7	turquoise	VSMC_M6
GO:0002761	0.01	1.00	7	86	regulation of myeloid leukocyte differentiation	BP	0.28659	IL23A,TGFB1,CTNNB1,SFRP1,INPP5D,LTF,MTOR	turquoise	VSMC_M6
GO:0044344	0.01	1.00	7	86	cellular response to fibroblast growth factor stimulus	BP	0.28682	CTNNB1,SFRP1,SNCA,HYAL2,GPC1,TBX1,FGF23	turquoise	VSMC_M6
GO:0035633	0.01	1.00	4	32	maintenance of blood-brain barrier	BP	0.2897	IL6,ESAM,PECAM1,CDH5	turquoise	VSMC_M6
GO:0021795	0.01	1.00	4	32	cerebral cortex cell migration	BP	0.28974	MDGA1,CTNNB1,LHX6,RELN	turquoise	VSMC_M6
GO:0010862	0.01	1.00	4	32	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	0.29048	PPARG,TGFB1,HFE,BMP7	turquoise	VSMC_M6
GO:0045445	0.01	1.00	6	67	myoblast differentiation	BP	0.29185	MEGF10,DLL1,TGFB1,CXCL10,IGFBP3,NOTCH1	turquoise	VSMC_M6
GO:0002460	0.01	0.99	11	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	0.29408	IL23A,IL6,C5,CTSC,TGFB1,NFKBID,HFE,INPP5D,CRACR2A,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0046942	0.01	0.99	11	173	carboxylic acid transport	BP	0.29408	TNFRSF11A,SLC16A8,SYK,SLC6A6,SLCO2B1,CD36,SLCO2A1,SNCA,ACE,SLC25A18,NMB	turquoise	VSMC_M6
GO:0098869	0.01	1.00	6	67	cellular oxidant detoxification	BP	0.2956	NOS3,CD36,BMP7,MGST1,PTGS1,GPX3	turquoise	VSMC_M6
GO:0001954	0.01	1.00	5	49	positive regulation of cell-matrix adhesion	BP	0.29633	KDR,SFRP1,CD36,PPM1F,CCR7	turquoise	VSMC_M6
GO:0007188	0.01	0.99	9	129	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	BP	0.2968	HTR5A,PDE2A,CXCL10,ADGRG3,LPAR2,PDE4B,S1PR1,ADGRL4,GNA12	turquoise	VSMC_M6
GO:0002443	0.02	0.99	13	221	leukocyte mediated immunity	BP	0.30597	IL23A,IL18RAP,SYK,IL6,C5,PIK3CG,CTSC,CD177,TGFB1,HFE,INPP5D,SLAMF9,ACE	turquoise	VSMC_M6
GO:0009187	0.02	1.00	4	33	cyclic nucleotide metabolic process	BP	0.30975	PDE2A,GUCY1A2,NPR1,PDE4B	turquoise	VSMC_M6
GO:0032881	0.02	1.00	4	33	regulation of polysaccharide metabolic process	BP	0.31073	PDGFB,TGFB1,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0035904	0.02	1.00	5	50	aorta development	BP	0.31179	PDE2A,ADAMTS9,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0009612	0.02	0.99	11	176	response to mechanical stimulus	BP	0.31273	CXCR4,CTNNB1,PDE2A,ATP8A2,CXCL10,ANGPT2,GOT1,ANO3,TLR7,ENDOG,SHANK3	turquoise	VSMC_M6
GO:0030336	0.02	0.99	13	223	negative regulation of cell migration	BP	0.31273	C5,PPARG,TGFB1,TIE1,SFRP1,ADAMTS9,ANGPT2,HYAL2,IGFBP3,MMRN2,NOTCH1,CDH1,GNA12	turquoise	VSMC_M6
GO:0045747	0.02	1.00	4	33	positive regulation of Notch signaling pathway	BP	0.31273	DLL1,NOS3,TSPAN14,NOTCH1	turquoise	VSMC_M6
GO:0010830	0.02	1.00	4	33	regulation of myotube differentiation	BP	0.31472	CYP26B1,TBX1,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0045598	0.02	0.99	8	109	regulation of fat cell differentiation	BP	0.31498	IL6,RARRES2,PPARG,TGFB1,SFRP1,BMP7,LGALS12,MTOR	turquoise	VSMC_M6
GO:0030308	0.02	0.99	10	153	negative regulation of cell growth	BP	0.31533	BCL11A,TGFB1,SFRP1,HYAL2,EAF2,CDA,NPR1,SEMA6B,SOX17,GNG4	turquoise	VSMC_M6
GO:0045834	0.02	0.99	8	109	positive regulation of lipid metabolic process	BP	0.31548	PDGFB,ADGRF5,RAB38,PPARG,TGFB1,RGN,MTOR,CCR7	turquoise	VSMC_M6
GO:0051353	0.02	1.00	5	50	positive regulation of oxidoreductase activity	BP	0.3161	NDUFA4,SNCA,RGN,FGF23,CDH3	turquoise	VSMC_M6
GO:0050830	0.02	1.00	4	33	defense response to Gram-positive bacterium	BP	0.31614	LYZ,IL6,RARRES2,CD36	turquoise	VSMC_M6
GO:0072593	0.02	0.99	11	176	reactive oxygen species metabolic process	BP	0.31837	PDGFB,SYK,NOS3,CD177,TGFB1,CD36,SNCA,BMP7,ALOX12,PMAIP1,GPX3	turquoise	VSMC_M6
GO:0034765	0.02	0.99	17	323	regulation of ion transmembrane transport	BP	0.31837	KCNN2,NDUFA4,KCNA7,PIK3CG,P2RY6,CXCL10,CLIC6,SNCA,RGN,CRACR2A,MTOR,HCN1,PDE4B,RELN,KCNU1,SHANK3,FXYD6	turquoise	VSMC_M6
GO:0072009	0.02	1.00	7	89	nephron epithelium development	BP	0.31859	DLL1,CTNNB1,CD34,PECAM1,KIF26B,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0000904	0.02	0.99	26	562	cell morphogenesis involved in differentiation	BP	0.31876	NOTCH4,EPHA5,NOVA2,CTNNB1,SPTBN4,MAP6,CNTN4,ATP8A2,CTNND2,ROBO4,COL18A1,BMP7,PROX1,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,GBP1,LHX2,SOX17,RELN,VSTM2L,SHANK3	turquoise	VSMC_M6
GO:0031175	0.02	0.99	34	784	neuron projection development	BP	0.31876	SYT17,EPHA5,IL6,BCL11A,NOVA2,CXCR4,CTNNB1,SPTBN4,MAP6,SNAP25,SFRP1,CNTN4,PRAG1,ATP8A2,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,MTOR,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,LHX2,CDH1,RELN,ALKAL1,VSTM2L,SHANK3,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0060538	0.02	0.99	9	132	skeletal muscle organ development	BP	0.31876	MEGF10,DLL1,TGFB1,CTNNB1,CYP26B1,GPC1,HOXD10,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0060070	0.02	0.99	14	250	canonical Wnt signaling pathway	BP	0.32552	ANKRD6,TGFB1,CTNNB1,SFRP1,NOTUM,HHEX,SOX7,CTNND2,NKD2,NRARP,NOTCH1,CDH3,SOX17,BAMBI	turquoise	VSMC_M6
GO:0001974	0.02	1.00	4	34	blood vessel remodeling	BP	0.32552	FLT4,NOS3,TGFB1,ACE	turquoise	VSMC_M6
GO:0030534	0.02	0.99	7	90	adult behavior	BP	0.32552	SPTBN4,SNCA,SHANK2,HOXD10,SNCG,PPP1R1B,SHANK3	turquoise	VSMC_M6
GO:0072210	0.02	1.00	4	34	metanephric nephron development	BP	0.32649	PDGFB,CTNNB1,CD34,KIF26B	turquoise	VSMC_M6
GO:0030198	0.02	0.99	14	250	extracellular matrix organization	BP	0.32649	IL6,TGFB1,TIE1,ADAMTS9,COL2A1,BMP1,SLC39A8,COL18A1,THSD4,COL4A6,COL4A5,NOTCH1,COL24A1,MMP12	turquoise	VSMC_M6
GO:0003176	0.02	1.00	4	34	aortic valve development	BP	0.32737	NOS3,TGFB1,TIE1,NOTCH1	turquoise	VSMC_M6
GO:2000249	0.02	1.00	4	34	regulation of actin cytoskeleton reorganization	BP	0.32737	ESAM,BAIAP2L1,ABI3,TRPM2	turquoise	VSMC_M6
GO:0061756	0.02	1.00	4	34	leukocyte adhesion to vascular endothelial cell	BP	0.32737	IL6,SLC39A8,SELE,SELP	turquoise	VSMC_M6
GO:0048663	0.02	1.00	4	34	neuron fate commitment	BP	0.32747	DLL1,HOXD10,NOTCH1,OLIG2	turquoise	VSMC_M6
GO:0046638	0.02	1.00	4	34	positive regulation of alpha-beta T cell differentiation	BP	0.32986	IL23A,SYK,NFKBID,CD86	turquoise	VSMC_M6
GO:0014070	0.02	0.99	31	703	response to organic cyclic compound	BP	0.3315	PDGFB,IL6,PIK3CG,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,CXCL10,ANGPT2,GOT1,SNCA,ESRRG,BMP7,FGF23,PPP1R1B,MTOR,HCN1,PDE4B,SSTR5,NOTCH1,ENDOG,CDH1,PMAIP1,TRPM2,NSG2	turquoise	VSMC_M6
GO:0043062	0.02	0.99	14	251	extracellular structure organization	BP	0.3315	IL6,TGFB1,TIE1,ADAMTS9,COL2A1,BMP1,SLC39A8,COL18A1,THSD4,COL4A6,COL4A5,NOTCH1,COL24A1,MMP12	turquoise	VSMC_M6
GO:0045229	0.02	0.99	14	251	external encapsulating structure organization	BP	0.3315	IL6,TGFB1,TIE1,ADAMTS9,COL2A1,BMP1,SLC39A8,COL18A1,THSD4,COL4A6,COL4A5,NOTCH1,COL24A1,MMP12	turquoise	VSMC_M6
GO:0071219	0.02	0.99	9	133	cellular response to molecule of bacterial origin	BP	0.33204	IL6,TGFB1,EDNRB,CD36,CXCL10,CD86,LTF,PDE4B,IRF8	turquoise	VSMC_M6

GO:0048639	0.02	0.99	9	134	positive regulation of developmental growth	BP	0.33328	SYT17,DLL1,CXCR4,SPTBN4,ATP8A2,PROX1,MTOR,ISLR2,NOTCH1	turquoise	VSMC_M6
GO:1901698	0.02	0.99	36	845	response to nitrogen compound	BP	0.33861	SYK,IL6,BCL11A,PIK3CG,RARRES2,PPARG,HTR5A,CXCR4,EDNRB,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,HHEX,SOGA1,GOT1,SNCA,BMP7,MGST1,PTPRE,BAIAP2L1,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,NOTCH1,CDH1,MMP12,PMAIP1,TRPM2,CCR7,NSG2	turquoise	VSMC_M6
GO:0034109	0.02	1.00	6	71	homotypic cell-cell adhesion	BP	0.3415	MEGF10,SYK,IL6,PIK3CG,DSC2,ALOX12	turquoise	VSMC_M6
GO:0043297	0.02	1.00	5	52	apical junction assembly	BP	0.3415	ESAM,PECAM1,CLDN16,PRKCH,CDH5	turquoise	VSMC_M6
GO:0071774	0.02	0.99	7	91	response to fibroblast growth factor	BP	0.34154	CTNNB1,SFRP1,SNCA,HYAL2,GPC1,TBX1,FGF23	turquoise	VSMC_M6
GO:0007411	0.02	0.99	11	181	axon guidance	BP	0.3431	EPHA5,NOVA2,CNTN4,ROBO4,BMP7,LAMC2,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L	turquoise	VSMC_M6
GO:0007389	0.02	0.99	17	329	pattern specification process	BP	0.34502	BARX1,DLL1,CTNNB1,SFRP1,HHEX,CYP26B1,BMP7,HOXD10,TBX1,LFNG,NRARP,HES3,NOTCH1,LHX2,SOX17,RELN,SOX18	turquoise	VSMC_M6
GO:0099054	0.02	1.00	4	35	presynapse assembly	BP	0.34636	MDGA1,LRRC4B,GPC6,SNCA	turquoise	VSMC_M6
GO:0002690	0.02	0.99	6	71	positive regulation of leukocyte chemotaxis	BP	0.34636	IL6,RARRES2,CXCL10,THBS4,C3AR1,CCR7	turquoise	VSMC_M6
GO:0071216	0.02	0.99	10	157	cellular response to biotic stimulus	BP	0.34768	SYK,IL6,TGFB1,EDNRB,CD36,CXCL10,CD86,LTF,PDE4B,IRF8	turquoise	VSMC_M6
GO:0051338	0.02	0.99	31	706	regulation of transferase activity	BP	0.34768	TNFRSF11A,IL23A,FLT4,PDGFB,KDR,SYK,EPHA5,RASIP1,PIK3CG,PPARG,TGFB1,CTNNB1,TIE1,SFRP1,HHEX,SNCA,HYAL2,CD86,ERN1,BMP7,PROX1,ACE,LTF,RGN,PPM1F,PPP1R1B,MTOR,RELN,ALKAL1,PKIB,CCR7	turquoise	VSMC_M6
GO:0002762	0.02	1.00	4	35	negative regulation of myeloid leukocyte differentiation	BP	0.34949	CTNNB1,SFRP1,INPP5D,LTF	turquoise	VSMC_M6
GO:0048565	0.02	0.99	7	92	digestive tract development	BP	0.34957	RARRES2,EDNRB,CTNNB1,SFRP1,NKX2-3,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0045087	0.02	0.99	22	459	innate immune response	BP	0.35036	IL23A,IL18RAP,IL1RL2,SYK,C5,PIK3CG,RARRES2,CD177,PPARG,BPIFB3,CXCL10,SNCA,ISG20,TLR7,SRMS,LTF,SARM1,IRF8,GBP1,MMP12,TRIM43,TRIM62	turquoise	VSMC_M6
GO:0002764	0.02	0.99	15	278	immune response-regulating signaling pathway	BP	0.35036	SYK,CD36,NFKBID,MAPK10,LAPTM5,NFATC2,INPP5D,TLR7,LTF,PRKCH,PDE4B,SARM1,GBP1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0032956	0.02	0.99	16	304	regulation of actin cytoskeleton organization	BP	0.35046	CELSR1,EPHA5,SPTBN4,SFRP1,ESAM,PROX1,BAIAP2L1,PPM1F,MTOR,ABI3,ARHGEF15,S1PR1,KANK3,SHANK3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0035307	0.02	1.00	4	35	positive regulation of protein dephosphorylation	BP	0.35046	TGFB1,PPP1R16B,MTOR,CDH5	turquoise	VSMC_M6
GO:0048872	0.02	0.99	13	229	homeostasis of number of cells	BP	0.3518	MYCT1,IREB2,ADGRF5,IL6,NOS3,NKX2-3,INPP5D,KLF1,PDE4B,NOTCH1,PMAIP1,CCR7,EMCN	turquoise	VSMC_M6
GO:0032729	0.02	1.00	4	35	positive regulation of interferon-gamma production	BP	0.3518	IL23A,TLR7,PDE4B,IRF8	turquoise	VSMC_M6
GO:0010762	0.02	1.00	4	35	regulation of fibroblast migration	BP	0.35244	TGFB1,PRR5L,HYAL2,GNA12	turquoise	VSMC_M6
GO:0010243	0.02	0.99	34	793	response to organonitrogen compound	BP	0.3571	SYK,IL6,BCL11A,PIK3CG,RARRES2,PPARG,HTR5A,CXCR4,EDNRB,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,HHEX,SOGA1,GOT1,SNCA,BMP7,MGST1,PTPRE,BAIAP2L1,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,NOTCH1,CDH1,MMP12,TRPM2,NSG2	turquoise	VSMC_M6
GO:0002688	0.02	0.99	7	92	regulation of leukocyte chemotaxis	BP	0.35731	IL6,C5,RARRES2,CXCL10,THBS4,C3AR1,CCR7	turquoise	VSMC_M6
GO:0034767	0.02	0.99	8	114	positive regulation of ion transmembrane transport	BP	0.35829	NDUFA4,P2RY6,CXCL10,SNCA,RGN,CRACR2A,RELN,SHANK3	turquoise	VSMC_M6
GO:0002040	0.02	0.99	8	114	sprouting angiogenesis	BP	0.35829	FLT4,KDR,DLL1,ADAMTS9,PPP1R16B,MMRN2,NRARP,NOTCH1	turquoise	VSMC_M6
GO:0043536	0.02	1.00	5	53	positive regulation of blood vessel endothelial cell migration	BP	0.35829	PDGFB,KDR,NOS3,TGFB1,ALOX12	turquoise	VSMC_M6
GO:0045860	0.02	0.99	16	305	positive regulation of protein kinase activity	BP	0.35829	TNFRSF11A,IL23A,PDGFB,SYK,PIK3CG,TGFB1,SNCA,CD86,ERN1,PROX1,ACE,LTF,MTOR,RELN,ALKAL1,CCR7	turquoise	VSMC_M6
GO:0045621	0.02	0.99	6	72	positive regulation of lymphocyte differentiation	BP	0.35829	IL23A,IL1RL2,SYK,NFKBID,INPP5D,CD86	turquoise	VSMC_M6
GO:0010675	0.02	0.99	8	114	regulation of cellular carbohydrate metabolic process	BP	0.35829	P2RY6,SOGA1,SNCA,RGN,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0051149	0.02	1.00	5	53	positive regulation of muscle cell differentiation	BP	0.35829	TGFB1,CYP26B1,PROX1,TBX1,MTOR	turquoise	VSMC_M6
GO:0010720	0.02	0.99	13	231	positive regulation of cell development	BP	0.35829	IL6,TGFB1,CXCR4,CTNNB1,MAP6,PRKCH,MTOR,ISLR2,NOTCH1,CDH5,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:1904705	0.02	1.00	5	53	regulation of vascular associated smooth muscle cell proliferation	BP	0.35829	PDGFB,PPARG,P2RY6,ERN1,GNA12	turquoise	VSMC_M6
GO:0050864	0.02	0.99	7	93	regulation of B cell activation	BP	0.36038	SYK,IL6,TGFB1,SFRP1,LAPTM5,NFATC2,INPP5D	turquoise	VSMC_M6
GO:0006810	0.02	0.98	116	3300	transport	BP	0.36207	TNFRSF11A,KCNN2,MEGF10,SYBU,ENPP2,SYT17,DENND3,PDGFB,SLC16A8,IREB2,ATP8A1,STEAP4,SYK,EPHA5,IL6,OSBPL3,NDUFA4,ARHGAP25,GJA4,KCNA7,SLC22A16,PIK3CG,DLL1,RAB38,SLC6A6,GRIP2,EXOC3L2,CD177,PPARG,SYN2,TGFB1,CXCR4,EDNRB,CTNNB1,TMC6,TMC8,SPTBN4,MAP6,SLCO2B1,P2RY6,P2RY2,SNAP25,SFRP1,SLC4A11,CD36,SLCO2A1,ADAMTS9,PRR5L,ATP8A2,HHEX,SLCO5A1,CP,CXCL10,SLC4A5,ATP6V0D2,STAB1,MAPK10,CLIC6,SNCA,MFSD4A,ANO3,MTTP,HYAL2,SLC39A8,NKD2,HFE,MCTP2,LAPTM5,PECAM1,MGST1,SLCO4A1,OAZ3,ACE,SSC4D,LTF,ARHGAP27,SYTL5,CLDN16,ATP13A1,CCDC88B,RGN,SELE,FGF23,CRACR2A,PPM1F,PITPNM3,SNCG,SLC25A18,HEPH,MTOR,SLC49A3,BEST2,NPR1,HCN1,PDE4B,SSTR5,NOTCH1,IRF8,CDH3,CDH1,EXOC3L1,MMP12,PMAIP1,ATP1A4,RELN,KCNU1,NMUR1,NUCB1,SHANK3,TRPM2,CCR7,NSG2,NMB,TMEM50B,SCARF1,FXYD6	turquoise	VSMC_M6
GO:0006979	0.02	0.99	18	357	response to oxidative stress	BP	0.36207	IL18RAP,IL6,NOS3,CTNNB1,SLC4A11,CD36,PRR5L,SNCA,HYAL2,ERN1,BMP7,MGST1,ENDOG,PTGS1,PDLIM1,TRPM2,MGAT3,GPX3	turquoise	VSMC_M6
GO:0021537	0.02	0.99	11	184	telencephalon development	BP	0.36463	MDGA1,EPHA5,HTR5A,CXCR4,CTNNB1,PROX1,SEMA6B,LHX2,LHX6,RELN,SHANK3	turquoise	VSMC_M6
GO:0120193	0.02	1.00	5	54	tight junction organization	BP	0.36567	ESAM,PECAM1,CLDN16,PRKCH,CDH5	turquoise	VSMC_M6
GO:0035418	0.02	0.99	5	54	protein localization to synapse	BP	0.3677	GRIP2,GPC6,SNAP25,MAPK10,RELN	turquoise	VSMC_M6
GO:0007218	0.02	1.00	4	36	neuropeptide signaling pathway	BP	0.3678	HCRTR1,SSTR5,NMUR1,NMB	turquoise	VSMC_M6
GO:0030509	0.02	0.99	8	116	BMP signaling pathway	BP	0.36972	PPARG,TGFB1,SFRP1,HFE,BMP7,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:1905517	0.02	1.00	4	36	macrophage migration	BP	0.36972	C5,RARRES2,EDNRB,C3AR1	turquoise	VSMC_M6

GO:0032940	0.02	0.99	26	574	secretion by cell	BP	0.36972	TNFRSF11A,SYBU,SYT17,SYK,EPHA5,IL6,PIK3CG,EXOC3L2,CD177,SYN2,TGFB1,SNAP25,SFRP1,SNCA,MTTP,NKD2,HFE,MCTP2,SYTL5,FGF23,SNCG,SSTR5,NOTCH1,EXOC3L1,TRPM2,NMB	turquoise	VSMC_M6
GO:1990874	0.02	0.99	5	54	vascular associated smooth muscle cell proliferation	BP	0.36972	PDGFB,PPARG,P2RY6,ERN1,GNA12	turquoise	VSMC_M6
GO:0051173	0.02	0.98	85	2331	positive regulation of nitrogen compound metabolic process	BP	0.37275	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,MOB3B,KDR,SYK,IL6,MAML3,PIK3CG,DLL1,KDM4D,CTSC,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SFRP1,ZIC2,CD36,PRR5L,KLKB1,HHEX,SOX7,CXCL10,THBS4,PPP1R16B,TOX2,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NKD2,HFE,LAPTM5,NFATC2,EAF2,TLR7,PECAM1,CD86,ERN1,BMP7,PROX1,OAZ3,FANK1,ACE,HOXD10,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,MTOR,KLF1,LYL1,TNFRSF18,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,SOX17,RELN,ALKAL1,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0035304	0.02	0.99	6	74	regulation of protein dephosphorylation	BP	0.37334	TGFB1,PPP1R16B,RGN,PPP1R1B,MTOR,CDH5	turquoise	VSMC_M6
GO:1903706	0.02	0.99	14	258	regulation of hemopoiesis	BP	0.37604	IL23A,IL1RL2,SYK,DLL1,TGFB1,CTNNB1,SFRP1,NFKBID,CYP26B1,INPP5D,CD86,LTF,MTOR,NRARP	turquoise	VSMC_M6
GO:0022612	0.02	0.99	7	95	gland morphogenesis	BP	0.37876	IL6,TGFB1,SFRP1,NKX2-3,BMP7,PROX1,NOTCH1	turquoise	VSMC_M6
GO:0099172	0.02	1.00	4	37	presynapse organization	BP	0.38111	MDGA1,LRRC4B,GPC6,SNCA	turquoise	VSMC_M6
GO:0035050	0.02	0.99	5	55	embryonic heart tube development	BP	0.38111	DLL1,CTNNB1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:1904427	0.02	0.99	5	55	positive regulation of calcium ion transmembrane transport	BP	0.38111	P2RY6,CXCL10,SNCA,RGN,CRACR2A	turquoise	VSMC_M6
GO:0051057	0.02	0.99	5	55	positive regulation of small GTPase mediated signal transduction	BP	0.38111	PIK3CG,PRAG1,NOTCH1,RELN,LPAR6	turquoise	VSMC_M6
GO:0048705	0.02	0.99	11	186	skeletal system morphogenesis	BP	0.38111	FREM1,CTNNB1,SFRP1,CYP26B1,COL2A1,BMP1,HYAL2,BMP7,HOXD10,LTF,TBX1	turquoise	VSMC_M6
GO:0048483	0.02	1.00	4	37	autonomic nervous system development	BP	0.3813	EDNRB,CTNNB1,TBX1,KIF26A	turquoise	VSMC_M6
GO:1905314	0.02	1.00	4	37	semi-lunar valve development	BP	0.3822	NOS3,TGFB1,TIE1,NOTCH1	turquoise	VSMC_M6
GO:0006809	0.02	0.99	5	55	nitric oxide biosynthetic process	BP	0.3822	NOS3,CD36,CD34,RGN,MTOR	turquoise	VSMC_M6
GO:0042326	0.02	0.99	16	311	negative regulation of phosphorylation	BP	0.38378	RASIP1,PPARG,TGFB1,SFRP1,KIRREL2,PRR5L,HHEX,SNCA,HYAL2,BMP7,IGFBP3,RGN,PPM1F,PPP1R1B,MTOR,PKIB	turquoise	VSMC_M6
GO:0006796	0.02	0.98	79	2150	phosphate-containing compound metabolic process	BP	0.38378	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,PDGFB,MOB3B,ADGRF5,KDR,SYK,EPHA5,IL6,RASIP1,PIK3CG,KDM4D,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,SPTBN4,TIE1,P2RY6,PDE2A,SFRP1,CD36,KIRREL2,STK35,PRAG1,PRR5L,HHEX,HUNK,THBS4,PPP1R16B,PLCB2,MAPK10,SNCA,HYAL2,HFE,INPP5D,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,SRMS,ACE,PTPRE,LTF,PALD1,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PITPNM3,PRKCH,PPP1R1B,MTOR,BCKDK,MAST1,NPR1,PDE4B,SARM1,MATK,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PPP1R3C,PKIB,CCR7,HRASLS,NUDT4B	turquoise	VSMC_M6
GO:0042102	0.02	0.99	5	55	positive regulation of T cell proliferation	BP	0.38378	IL23A,SYK,IL6,CD86,CCDC88B	turquoise	VSMC_M6
GO:0051251	0.02	0.99	11	186	positive regulation of lymphocyte activation	BP	0.38378	IL23A,IL1RL2,SYK,IL6,TGFB1,NFKBID,NFATC2,INPP5D,CD86,CCDC88B,CCR7	turquoise	VSMC_M6
GO:1901222	0.02	0.99	6	75	regulation of NIK/NF-kappaB signaling	BP	0.38378	IL23A,ADGRG3,LAPTM5,TLR7,CD86,BMP7	turquoise	VSMC_M6
GO:0051128	0.02	0.98	70	1877	regulation of cellular component organization	BP	0.38378	CELSR1,ENPP2,SYT17,PDGFB,MDGA1,ATP8A1,KDR,SYK,EPHA5,IL6,BCL11A,LRRC4B,RASIP1,DLL1,CD177,PPARG,TGFB1,CXCR4,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,MAP6,SNAP25,PDE2A,SFRP1,CD36,PRAG1,ATP8A2,CXCL10,PPP1R16B,SNCA,HYAL2,HFE,ESAM,NFATC2,EAF2,BMP7,PROX1,ACE,CDA,SELE,SELP,BAIAP2L1,PPM1F,PRKCH,MTOR,ABI3,ARHGEF15,NPR1,ISLR2,KIF26A,SARM1,SEMA6B,NOTCH1,S1PR1,CDH5,PMAIP1,SOX17,RELN,ALKAL1,KANK3,SHANK3,TRPM2,PKIB,CCR7,RTN4RL2,GNG4,SCARF1	turquoise	VSMC_M6
GO:0048519	0.02	0.98	136	3961	negative regulation of biological process	BP	0.38378	IL23A,FLT4,NOTCH4,PDGFB,ETV7,IREB2,ADGRF5,KDR,SYK,BARX1,IL6,BCL11A,ANKRD6,ARHGAP25,C5,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,TMC8,SPTBN4,TIE1,P2RY6,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,CD36,KIRREL2,PRAG1,ADAMTS9,PRR5L,ATP8A2,F11,KLKB1,HHEX,PROCR,SOX7,CXCL10,ANGPT2,SOGA1,ADGRG3,THBS4,CYP26B1,PPP1R16B,COL2A1,STAB1,MAPK10,GOT1,SNCA,SHANK2,HYAL2,NKD2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,CD34,CD86,ERN1,COL18A1,BMP7,IGFBP3,PROX1,GPC1,OAZ3,SRMS,FANK1,ACE,PTPRE,PRAME,PAX9,LTF,TSPAN15,TBX1,RGN,CDA,FGF23,PPM1F,PRKCH,GRID2IP,BCL6B,MMRN2,PPP1R1B,LFNG,MTOR,BCKDK,ABI3,ARHGEF15,NPR1,KIF26A,PDE4B,SARM1,SEMA6B,TNFRSF18,NRARP,HES3,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,GBP1,LHX2,CDH3,CDH1,CDH5,ALOX12,MMP12,SOX17,MIR1307,OLIG2,VSTM2L,SOX18,KANK3,GNA12,SHANK3,TRPM2,PKIB,TRIM62,BAMBI,CCR7,MGAT3,NMB,RTN4RL2,GNG4	turquoise	VSMC_M6
GO:0002244	0.02	0.99	7	96	hematopoietic progenitor cell differentiation	BP	0.38378	FLT4,KDR,TGFB1,SFRP1,HYAL2,ACE,NOTCH1	turquoise	VSMC_M6
GO:0051047	0.02	0.99	12	211	positive regulation of secretion	BP	0.38378	TNFRSF11A,SYBU,SYK,CD177,TGFB1,EDNRB,P2RY2,SNCA,HFE,NPR1,TRPM2,NMB	turquoise	VSMC_M6
GO:0010942	0.02	0.99	22	470	positive regulation of cell death	BP	0.38378	SYK,IL6,CTSC,SLC6A6,PPARG,CTNNB1,SFRP1,CD36,SNCA,HYAL2,LAPTM5,INPP5D,BMP7,IGFBP3,FANK1,MTOR,SARM1,NOTCH1,ENDOG,ALOX12,PMAIP1,TRPM2	turquoise	VSMC_M6
GO:0060415	0.02	0.99	5	56	muscle tissue morphogenesis	BP	0.38378	TGFB1,PROX1,TBX1,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0032635	0.02	0.99	7	96	interleukin-6 production	BP	0.38378	IL1RL2,SYK,IL6,CD36,HYAL2,INPP5D,TLR7	turquoise	VSMC_M6
GO:0032675	0.02	0.99	7	96	regulation of interleukin-6 production	BP	0.38378	IL1RL2,SYK,IL6,CD36,HYAL2,INPP5D,TLR7	turquoise	VSMC_M6
GO:0001659	0.02	0.99	9	141	temperature homeostasis	BP	0.38378	TNFRSF11A,SYK,NOVA2,CXCR4,EDNRB,CD36,ESRRG,NOTCH1,TRPM2	turquoise	VSMC_M6
GO:0046847	0.02	0.99	5	56	filopodium assembly	BP	0.38378	FGD5,ITGB4,PPP1R16B,TRPM2,CCR7	turquoise	VSMC_M6
GO:0009914	0.02	0.99	12	212	hormone transport	BP	0.38378	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,SLCO4A1,FGF23,SSTR5,EXOC3L1,TRPM2,NMB	turquoise	VSMC_M6
GO:0045444	0.03	0.99	11	188	fat cell differentiation	BP	0.38378	STEAP4,ADGRF5,IL6,RARRES2,PPARG,TGFB1,SFRP1,BMP7,LGALS12,MTOR,LRG1	turquoise	VSMC_M6

GO:1905330	0.03	0.99	5	56	regulation of morphogenesis of an epithelium	BP	0.38378	CTNNB1,SFRP1,CXCL10,BMP7,ALOX12	turquoise	VSMC_M6
GO:1901888	0.03	0.99	10	165	regulation of cell junction assembly	BP	0.38378	MDGA1,KDR,LRRC4B,GPC6,SFRP1,SNCA,ACE,PPM1F,PRKCH,ABI3	turquoise	VSMC_M6
GO:0014009	0.03	0.99	4	38	glial cell proliferation	BP	0.38378	IL6,PRKCH,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0043030	0.03	0.99	4	38	regulation of macrophage activation	BP	0.38378	ADGRF5,IL6,CTSC,SNCA	turquoise	VSMC_M6
GO:0010959	0.03	0.99	14	263	regulation of metal ion transport	BP	0.38378	KCNN2,PDGFB,PIK3CG,CXCR4,CTNNB1,SPTBN4,P2RY6,CXCL10,SNCA,HFE,RGN,CRACR2A,PDE4B,FXYD6	turquoise	VSMC_M6
GO:0010952	0.03	0.99	9	142	positive regulation of peptidase activity	BP	0.38378	SYK,PPARG,SOX7,SNCA,LAPTM5,PPM1F,ALOX12,PRSS22,PMAIP1	turquoise	VSMC_M6
GO:0048844	0.03	0.99	5	57	artery morphogenesis	BP	0.38378	ADGRF5,ADAMTS9,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0014823	0.03	0.99	5	57	response to activity	BP	0.38378	IL6,RARRES2,CXCR4,ANGPT2,MTOR	turquoise	VSMC_M6
GO:0045913	0.03	0.99	5	57	positive regulation of carbohydrate metabolic process	BP	0.38378	PDGFB,P2RY6,SNCA,RGN,PMAIP1	turquoise	VSMC_M6
GO:0030514	0.03	0.99	4	39	negative regulation of BMP signaling pathway	BP	0.38378	PPARG,SFRP1,NOTCH1,BAMBI	turquoise	VSMC_M6
GO:0045580	0.03	0.99	7	98	regulation of T cell differentiation	BP	0.38378	IL23A,IL1RL2,SYK,NFKBID,CYP26B1,CD86,NRARP	turquoise	VSMC_M6
GO:0044070	0.03	0.99	5	57	regulation of anion transport	BP	0.38378	TNFRSF11A,SYK,SNCA,FGF23,MTOR	turquoise	VSMC_M6
GO:0002683	0.03	0.99	15	290	negative regulation of immune system process	BP	0.38378	ADGRF5,SYK,C5,PPARG,TGFB1,CTNNB1,SFRP1,HFE,LAPTM5,INPP5D,CD86,LTF,NRARP,GBP1,MMP12	turquoise	VSMC_M6
GO:0033673	0.03	0.99	11	191	negative regulation of kinase activity	BP	0.38378	RASIP1,PPARG,SFRP1,HHEX,SNCA,HYAL2,BMP7,RGN,PPM1F,PPP1R1B,PKIB	turquoise	VSMC_M6
GO:0050994	0.03	0.99	4	39	regulation of lipid catabolic process	BP	0.38378	PIK3CG,RARRES2,LGALS12,MTOR	turquoise	VSMC_M6
GO:2000179	0.03	0.99	4	39	positive regulation of neural precursor cell proliferation	BP	0.38378	CTNNB1,PROX1,NOTCH1,LHX2	turquoise	VSMC_M6
GO:0085029	0.03	0.99	4	39	extracellular matrix assembly	BP	0.38378	TGFB1,TIE1,THSD4,NOTCH1	turquoise	VSMC_M6
GO:0002253	0.03	0.99	11	191	activation of immune response	BP	0.38378	SYK,C5,NFKBID,LAPTM5,NFATC2,INPP5D,PRKCH,PDE4B,GBP1,C3AR1,CCR7	turquoise	VSMC_M6
GO:0006793	0.03	0.98	79	2169	phosphorus metabolic process	BP	0.38378	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,PDGFB,MOB3B,ADGRF5,KDR,SYK,EPHA5,IL6,RASIP1,PIK3CG,KDM4D,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,SPTBN4,TIE1,P2RY6,PDE2A,SFRP1,CD36,KIRREL2,STK35,PRAG1,PRR5L,HHEX,HUNK,THBS4,PPP1R16B,PLCB2,MAPK10,SNCA,HYAL2,HFE,INPP5D,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,SRMS,ACE,PTPRE,LTF,PALD1,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PITPNM3,PRKCH,PPP1R1B,MTOR,BCKDK,MAST1,NPR1,PDE4B,SARM1,MATK,TNFRSF18,SH2D3C,CDH5,RELN,ALKAL1,PPP1R3C,PKIB,CCR7,HRASLS,NUDT4B	turquoise	VSMC_M6
GO:0001906	0.03	0.99	6	78	cell killing	BP	0.38378	IL23A,LYZ,IL18RAP,SYK,CTSC,LTF	turquoise	VSMC_M6
GO:0031100	0.03	0.99	5	58	animal organ regeneration	BP	0.38378	IL6,ANGPT2,HFE,RGN,NOTCH1	turquoise	VSMC_M6
GO:0007399	0.03	0.98	69	1867	nervous system development	BP	0.38378	SYBU,CELSR1,SYT17,MDGA1,EPHA5,IL6,BCL11A,LRRC4B,DLL1,NOVA2,CTSC,ITGB4,TGFB1,HTR5A,CXCR4,EDNRB,CTNNB1,SPTBN4,GPC6,MAP6,SNAP25,SFRP1,ZIC2,CNTN4,PCDH12,PRAG1,ATP8A2,MALL,PRDM8,COL2A1,IRX6,SNCA,CTNND2,SHANK2,LSAMP,DPYSL4,ROBO4,BMP7,PROX1,GPC1,LAMC2,HOXD10,TBX1,PRKCH,MTOR,ABI3,ARHGEF15,MAST1,ISLR2,B4GALT6,KIF26A,HCN1,SARM1,SEMA6B,HES3,NOTCH1,S1PR1,LHX2,LHX6,CDH1,SOX17,RELN,ALKAL1,OLIG2,VSTM2L,SHANK3,HPCAL4,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0007600	0.03	0.99	16	320	sensory perception	BP	0.38378	CXCR4,EDNRB,SPTBN4,ZIC2,CD36,ATP8A2,PLCB2,COL2A1,COL18A1,TBX1,MTOR,BEST2,CDH3,PKHD1L1,GRAP,OR6N2	turquoise	VSMC_M6
GO:0140352	0.03	0.98	27	618	export from cell	BP	0.38378	TNFRSF11A,SYBU,SYT17,SYK,EPHA5,IL6,PIK3CG,EXOC3L2,CD177,SYN2,TGFB1,SNAP25,SFRP1,SNCA,MTTP,NKD2,HFE,MCTP2,SYTL5,FGF23,SNCG,SSTR5,NOTCH1,EXOC3L1,ATP1A4,TRPM2,NMB	turquoise	VSMC_M6
GO:0007492	0.03	0.99	5	59	endoderm development	BP	0.38378	CTNNB1,SOX7,PAX9,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0061383	0.03	0.99	4	40	trabecula morphogenesis	BP	0.38378	SFRP1,BMP7,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:1903530	0.03	0.98	19	399	regulation of secretion by cell	BP	0.3842	TNFRSF11A,SYBU,SYT17,SYK,EPHA5,IL6,CD177,TGFB1,SNAP25,SFRP1,SNCA,HFE,MCTP2,FGF23,SNCG,SSTR5,NOTCH1,TRPM2,NMB	turquoise	VSMC_M6
GO:0050877	0.03	0.98	29	678	nervous system process	BP	0.38486	ATP8A1,CTSC,NOS3,CXCR4,EDNRB,SPTBN4,SNAP25,ZIC2,CD36,ATP8A2,PLCB2,COL2A1,SNCA,SHANK2,COL18A1,HOXD10,TBX1,RCSD1,PPP1R1B,MTOR,BEST2,S1PR1,CDH3,PKHD1L1,RELN,GRAP,SHANK3,OR6N2,MGAT3	turquoise	VSMC_M6
GO:0010676	0.03	0.99	4	40	positive regulation of cellular carbohydrate metabolic process	BP	0.38505	P2RY6,SNCA,RGN,PMAIP1	turquoise	VSMC_M6
GO:0021766	0.03	0.99	5	59	hippocampus development	BP	0.38506	EPHA5,HTR5A,PROX1,SEMA6B,RELN	turquoise	VSMC_M6
GO:0009798	0.03	0.99	5	59	axis specification	BP	0.3864	DLL1,CTNNB1,SFRP1,NRARP,NOTCH1	turquoise	VSMC_M6
GO:1990748	0.03	0.99	6	79	cellular detoxification	BP	0.38755	NOS3,CD36,BMP7,MGST1,PTGS1,GPX3	turquoise	VSMC_M6
GO:1904892	0.03	0.99	5	59	regulation of receptor signaling pathway via STAT	BP	0.39014	IL23A,IL6,PPARG,TGFB1,NOTCH1	turquoise	VSMC_M6
GO:0009064	0.03	0.99	5	59	glutamine family amino acid metabolic process	BP	0.39142	NOS3,GOT1,SLC39A8,ART4,AGMAT	turquoise	VSMC_M6
GO:0032414	0.03	0.99	6	80	positive regulation of ion transmembrane transporter activity	BP	0.3955	NDUFA4,P2RY6,RGN,CRACR2A,RELN,SHANK3	turquoise	VSMC_M6
GO:0007189	0.03	0.99	6	80	adenylate cyclase-activating G protein-coupled receptor signaling pathway	BP	0.39712	CXCL10,ADGRG3,LPAR2,PDE4B,S1PR1,ADGRL4	turquoise	VSMC_M6
GO:0007417	0.03	0.98	33	795	central nervous system development	BP	0.3975	CELSR1,MDGA1,EPHA5,IL6,DLL1,NOVA2,TGFB1,HTR5A,CXCR4,CTNNB1,SPTBN4,SFRP1,ZIC2,CNTN4,PRDM8,COL2A1,BMP7,PROX1,HOXD10,TBX1,MTOR,MAST1,B4GALT6,SEMA6B,NOTCH1,S1PR1,LHX2,LHX6,CDH1,RELN,OLIG2,SHANK3,HPCAL4	turquoise	VSMC_M6
GO:0045926	0.03	0.99	11	195	negative regulation of growth	BP	0.399	BCL11A,TGFB1,SFRP1,HYAL2,EAF2,CDA,NPR1,SEMA6B,NOTCH1,SOX17,GNG4	turquoise	VSMC_M6
GO:0034614	0.03	0.99	8	124	cellular response to reactive oxygen species	BP	0.40527	IL18RAP,IL6,NOS3,CD36,ERN1,BMP7,ENDOG,TRPM2	turquoise	VSMC_M6
GO:0014910	0.03	0.99	5	60	regulation of smooth muscle cell migration	BP	0.40784	PDGFB,P2RY6,IGFBP3,ACE,GNA12	turquoise	VSMC_M6
GO:0003073	0.03	0.99	5	60	regulation of systemic arterial blood pressure	BP	0.41097	PDGFB,RARRES2,NOS3,SLC4A5,ACE	turquoise	VSMC_M6
GO:0046209	0.03	0.99	5	60	nitric oxide metabolic process	BP	0.41097	NOS3,CD36,CD34,RGN,MTOR	turquoise	VSMC_M6
GO:0006821	0.03	0.99	5	60	chloride transport	BP	0.41097	P2RY6,CLIC6,ANO3,BEST2,NMUR1	turquoise	VSMC_M6
GO:0035850	0.03	0.99	4	41	epithelial cell differentiation involved in kidney development	BP	0.4111	PDGFB,CTNNB1,CD34,NOTCH1	turquoise	VSMC_M6
GO:0060840	0.03	0.99	6	81	artery development	BP	0.41118	ADGRF5,PDE2A,ADAMTS9,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0051924	0.03	0.99	10	172	regulation of calcium ion transport	BP	0.41138	PDGFB,PIK3CG,CXCR4,CTNNB1,P2RY6,CXCL10,SNCA,RGN,CRACR2A,PDE4B	turquoise	VSMC_M6
GO:0045582	0.03	0.99	5	60	positive regulation of T cell differentiation	BP	0.41409	IL23A,IL1RL2,SYK,NFKBID,CD86	turquoise	VSMC_M6

GO:0046635	0.03	0.99	4	41	positive regulation of alpha-beta T cell activation	BP	0.4154	IL23A,SYK,NFKBID,CD86	turquoise	VSMC_M6
GO:0071622	0.03	0.99	4	41	regulation of granulocyte chemotaxis	BP	0.4154	RARRES2,THBS4,C3AR1,CCR7	turquoise	VSMC_M6
GO:0032757	0.03	0.99	4	41	positive regulation of interleukin-8 production	BP	0.4154	SYK,IL6,HYAL2,TLR7	turquoise	VSMC_M6
GO:1904064	0.03	0.99	7	103	positive regulation of cation transmembrane transport	BP	0.41624	P2RY6,CXCL10,SNCA,RGN,CRACR2A,RELN,SHANK3	turquoise	VSMC_M6
GO:0006869	0.03	0.98	14	273	lipid transport	BP	0.41778	TNFRSF11A,ATP8A1,SYK,OSBPL3,PPARG,SLCO2B1,CD36,SLCO2A1,ATP8A2,ANO3,MTTP,ACE,PITPNM3,NMB	turquoise	VSMC_M6
GO:0048644	0.03	0.99	5	61	muscle organ morphogenesis	BP	0.41778	TGFB1,PROX1,TBX1,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0061564	0.03	0.98	18	380	axon development	BP	0.41875	EPHA5,NOVA2,SPTBN4,MAP6,CNTN4,ATP8A2,ROBO4,BMP7,LAMC2,ISLR2,B4GALT6,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0001942	0.03	0.99	5	61	hair follicle development	BP	0.42043	CTNNB1,NOTCH1,LHX2,CDH3,SOX18	turquoise	VSMC_M6
GO:0007612	0.03	0.99	7	104	learning	BP	0.42084	ATP8A1,SNAP25,SHANK2,PPP1R1B,MTOR,RELN,SHANK3	turquoise	VSMC_M6
GO:2001057	0.03	0.99	5	61	reactive nitrogen species metabolic process	BP	0.42227	NOS3,CD36,CD34,RGN,MTOR	turquoise	VSMC_M6
GO:0050871	0.03	0.99	5	61	positive regulation of B cell activation	BP	0.4237	SYK,IL6,TGFB1,NFATC2,INPP5D	turquoise	VSMC_M6
GO:0045807	0.03	0.99	6	82	positive regulation of endocytosis	BP	0.42395	SYK,DLL1,CD36,SNCA,HFE,SELE	turquoise	VSMC_M6
GO:0060042	0.03	0.99	4	42	retina morphogenesis in camera-type eye	BP	0.4254	DLL1,ATP8A2,PROX1,HCN1	turquoise	VSMC_M6
GO:0033555	0.04	0.99	4	42	multicellular organismal response to stress	BP	0.42736	GJA4,EDNRB,THBS4,RELN	turquoise	VSMC_M6
GO:0045927	0.04	0.98	11	199	positive regulation of growth	BP	0.42815	SYT17,DLL1,CXCR4,SPTBN4,SFRP1,ATP8A2,PROX1,PPM1F,MTOR,ISLR2,NOTCH1	turquoise	VSMC_M6
GO:0046883	0.04	0.98	10	174	regulation of hormone secretion	BP	0.42983	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,FGF23,SSTR5,TRPM2,NMB	turquoise	VSMC_M6
GO:0043647	0.04	0.99	4	42	inositol phosphate metabolic process	BP	0.43023	IP6K3,P2RY6,SNCA,NUDT4B	turquoise	VSMC_M6
GO:0050671	0.04	0.99	6	82	positive regulation of lymphocyte proliferation	BP	0.43039	IL23A,SYK,IL6,NFATC2,CD86,CCDC88B	turquoise	VSMC_M6
GO:1902041	0.04	0.99	4	42	regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	0.43244	NOS3,TMC8,SFRP1,PMAIP1	turquoise	VSMC_M6
GO:0010810	0.04	0.98	10	175	regulation of cell-substrate adhesion	BP	0.43244	PDGFB,KDR,SFRP1,CD36,ANGPT2,PPM1F,NOTCH1,GBP1,MMP12,CCR7	turquoise	VSMC_M6
GO:0060688	0.04	0.99	4	42	regulation of morphogenesis of a branching structure	BP	0.43244	BCL11A,CTNNB1,SFRP1,BMP7	turquoise	VSMC_M6
GO:0060560	0.04	0.98	11	200	developmental growth involved in morphogenesis	BP	0.43498	SYT17,BCL11A,CXCR4,CTNNB1,SFRP1,KIF26B,ISLR2,SEMA6B,NOTCH1,S1PR1,LHX2	turquoise	VSMC_M6
GO:0010950	0.04	0.99	8	127	positive regulation of endopeptidase activity	BP	0.4353	SYK,PPARG,SOX7,SNCA,LAPTM5,PPM1F,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0040008	0.04	0.98	23	518	regulation of growth	BP	0.43571	SYT17,BCL11A,DLL1,TGFB1,CXCR4,TMC8,SPTBN4,SFRP1,ATP8A2,HYAL2,EAF2,PROX1,PRAME,CDA,PPM1F,MTOR,NPR1,ISLR2,KIF26A,SEMA6B,NOTCH1,SOX17,GNG4	turquoise	VSMC_M6
GO:0042391	0.04	0.98	15	302	regulation of membrane potential	BP	0.43754	KCNN2,KDR,SLC4A11,CD36,GOT1,SNCA,SLC39A8,BEST2,DSC2,HCN1,ALOX12,PMAIP1,ATP1A4,RELN,SHANK3	turquoise	VSMC_M6
GO:0050808	0.04	0.98	16	329	synapse organization	BP	0.4376	SYBU,MDGA1,LRRC4B,CTNNB1,GPC6,SNCA,CTNND2,SHANK2,CNKSR2,SNCG,ABI3,ARHGEF15,COL4A5,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0042692	0.04	0.98	15	303	muscle cell differentiation	BP	0.43793	MEGF10,PDGFB,DLL1,TGFB1,EDNRB,CTNNB1,CXCL10,CYP26B1,NRAP,NFATC2,PROX1,TBX1,MTOR,TMEM204,NOTCH1	turquoise	VSMC_M6
GO:0035924	0.04	0.99	5	62	cellular response to vascular endothelial growth factor stimulus	BP	0.43929	FLT4,KDR,DLL1,ERN1,NOTCH1	turquoise	VSMC_M6
GO:0007264	0.04	0.98	20	437	small GTPase mediated signal transduction	BP	0.43929	CELSR1,DENND3,ARHGAP25,RASIP1,PIK3CG,RAB38,FGD5,RASGRP3,PRAG1,ARHGAP27,ERAS,ARHGEF9,ARHGEF15,NOTCH1,SH2D3C,RELN,NUCB1,GRAP,GNA12,LPAR6	turquoise	VSMC_M6
GO:0060291	0.04	0.99	5	62	long-term synaptic potentiation	BP	0.43974	SNAP25,SNCA,SHANK2,RELN,SHANK3	turquoise	VSMC_M6
GO:0006941	0.04	0.99	8	128	striated muscle contraction	BP	0.43974	KCNN2,PIK3CG,CXCR4,ATP8A2,RCSD1,MTOR,DSC2,PDE4B	turquoise	VSMC_M6
GO:0030111	0.04	0.98	14	277	regulation of Wnt signaling pathway	BP	0.44461	BARX1,ANKRD6,TGFB1,SFRP1,NOTUM,HHEX,SOX7,CTNND2,NKD2,NRARP,NOTCH1,CDH3,SOX17,BAMBI	turquoise	VSMC_M6
GO:2000241	0.04	0.99	7	105	regulation of reproductive process	BP	0.44461	EDNRB,CTNNB1,SFRP1,EAF2,BMP7,RGN,NOTCH1	turquoise	VSMC_M6
GO:0032946	0.04	0.99	6	83	positive regulation of mononuclear cell proliferation	BP	0.44461	IL23A,SYK,IL6,NFATC2,CD86,CCDC88B	turquoise	VSMC_M6
GO:0019216	0.04	0.98	13	251	regulation of lipid metabolic process	BP	0.44768	PDGFB,ADGRF5,PIK3CG,RAB38,RARRES2,PPARG,TGFB1,SNCA,PROX1,RGN,LGALS12,MTOR,CCR7	turquoise	VSMC_M6
GO:0099072	0.04	0.99	4	43	regulation of postsynaptic membrane neurotransmitter receptor levels	BP	0.45128	GRIP2,GPC6,SNAP25,MAPK10	turquoise	VSMC_M6
GO:0045428	0.04	0.99	4	43	regulation of nitric oxide biosynthetic process	BP	0.45345	CD36,CD34,RGN,MTOR	turquoise	VSMC_M6
GO:0007606	0.04	0.99	4	43	sensory perception of chemical stimulus	BP	0.45355	CD36,PLCB2,BEST2,OR6N2	turquoise	VSMC_M6
GO:0050854	0.04	0.99	4	43	regulation of antigen receptor-mediated signaling pathway	BP	0.45371	LAPTM5,PRKCH,GBP1,CCR7	turquoise	VSMC_M6
GO:1903053	0.04	0.99	4	43	regulation of extracellular matrix organization	BP	0.45371	IL6,TGFB1,TIE1,NOTCH1	turquoise	VSMC_M6
GO:0061053	0.04	0.99	5	63	somite development	BP	0.45501	DLL1,SFRP1,LFNG,NRARP,NOTCH1	turquoise	VSMC_M6
GO:0070661	0.04	0.98	11	201	leukocyte proliferation	BP	0.45501	IL23A,SYK,IL6,PIK3CG,CTNNB1,HHEX,NFATC2,INPP5D,CD86,ACE,CCDC88B	turquoise	VSMC_M6
GO:0035148	0.04	0.99	8	129	tube formation	BP	0.45501	CELSR1,TGFB1,CTNNB1,SFRP1,BMP7,PROX1,NOTCH1,LHX2	turquoise	VSMC_M6
GO:0043009	0.04	0.98	23	522	chordate embryonic development	BP	0.45501	CELSR1,PDGFB,ADGRF5,C5,DLL1,TGFB1,CTNNB1,TIE1,SFRP1,PCDH12,COL2A1,BMP7,PROX1,HOXD10,TBX1,LFNG,NRARP,NOTCH1,ENDOG,LHX2,SOX17,SOX18,LPAR6	turquoise	VSMC_M6
GO:0022404	0.04	0.99	5	63	molting cycle process	BP	0.45717	CTNNB1,NOTCH1,LHX2,CDH3,SOX18	turquoise	VSMC_M6
GO:0022405	0.04	0.99	5	63	hair cycle process	BP	0.45717	CTNNB1,NOTCH1,LHX2,CDH3,SOX18	turquoise	VSMC_M6
GO:0046634	0.04	0.99	5	63	regulation of alpha-beta T cell activation	BP	0.4627	IL23A,SYK,NFKBID,HFE,CD86	turquoise	VSMC_M6
GO:0002718	0.04	0.99	5	63	regulation of cytokine production involved in immune response	BP	0.46287	IL6,TGFB1,CD36,HFE,LAPTM5	turquoise	VSMC_M6
GO:0070663	0.04	0.98	9	153	regulation of leukocyte proliferation	BP	0.46451	IL23A,SYK,IL6,CTNNB1,HHEX,NFATC2,INPP5D,CD86,CCDC88B	turquoise	VSMC_M6
GO:0021915	0.04	0.98	8	130	neural tube development	BP	0.46641	CELSR1,TGFB1,SFRP1,BMP7,PROX1,NOTCH1,LHX2,SOX17	turquoise	VSMC_M6
GO:0032411	0.04	0.99	6	85	positive regulation of transporter activity	BP	0.46988	NDUFA4,P2RY6,RGN,CRACR2A,RELN,SHANK3	turquoise	VSMC_M6
GO:0014706	0.04	0.98	15	307	striated muscle tissue development	BP	0.46988	MEGF10,DLL1,TGFB1,CTNNB1,ADAMTS9,CYP26B1,NRAP,BMP7,PROX1,GPC1,HOXD10,TBX1,MTOR,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0016358	0.04	0.98	11	204	dendrite development	BP	0.46988	BCL11A,MAP6,CTNND2,BMP7,LAMC2,MTOR,ABI3,SARM1,RELN,SHANK3,SCARF1	turquoise	VSMC_M6
GO:0015849	0.04	0.98	11	203	organic acid transport	BP	0.46988	TNFRSF11A,SLC16A8,SYK,SLC6A6,PPARG,SLCO2B1,CD36,SNCA,ACE,SLC25A18,NMB	turquoise	VSMC_M6

GO:0050870	0.04	0.98	8	130	positive regulation of T cell activation	BP	0.46988	IL23A,IL1RL2,SYK,IL6,NFKBID,CD86,CCDC88B,CCR7	turquoise	VSMC_M6
GO:0060393	0.04	0.99	4	44	regulation of pathway-restricted SMAD protein phosphorylation	BP	0.46988	PPARG,TGFB1,HFE,BMP7	turquoise	VSMC_M6
GO:0050852	0.04	0.99	6	85	T cell receptor signaling pathway	BP	0.46988	NFKBID,LAPTM5,INPP5D,PDE4B,GBP1,CCR7	turquoise	VSMC_M6
GO:0030900	0.04	0.98	14	282	forebrain development	BP	0.46988	MDGA1,EPHA5,HTR5A,CXCR4,CTNNB1,PROX1,SEMA6B,NOTCH1,LHX2,LHX6,CDH1,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0060041	0.04	0.99	7	108	retina development in camera-type eye	BP	0.46988	DLL1,ATP8A2,SLC4A5,PROX1,ARHGEF15,HCN1,LHX2	turquoise	VSMC_M6
GO:0046637	0.04	0.99	4	44	regulation of alpha-beta T cell differentiation	BP	0.46988	IL23A,SYK,NFKBID,CD86	turquoise	VSMC_M6
GO:0061098	0.04	0.99	4	44	positive regulation of protein tyrosine kinase activity	BP	0.46988	PDGFB,ACE,RELN,ALKAL1	turquoise	VSMC_M6
GO:0045638	0.04	0.99	5	64	negative regulation of myeloid cell differentiation	BP	0.46988	DLL1,CTNNB1,SFRP1,INPP5D,LTF	turquoise	VSMC_M6
GO:0048662	0.04	0.99	4	44	negative regulation of smooth muscle cell proliferation	BP	0.46988	PPARG,IGFBP3,NPR1,GNA12	turquoise	VSMC_M6
GO:0097237	0.04	0.99	6	85	cellular response to toxic substance	BP	0.46988	NOS3,CD36,BMP7,MGST1,PTGS1,GPX3	turquoise	VSMC_M6
GO:0006816	0.04	0.98	14	282	calcium ion transport	BP	0.47106	PDGFB,GJA4,PIK3CG,CXCR4,CTNNB1,P2RY6,CXCL10,SNCA,RGN,CRACR2A,PDE4B,NMUR1,TRPM2,CCR7	turquoise	VSMC_M6
GO:0015850	0.04	0.98	10	179	organic hydroxy compound transport	BP	0.47128	SYT17,SLC16A8,SYK,OSBPL3,PPARG,SLCO2B1,CD36,SNCA,MTTP,SNCG	turquoise	VSMC_M6
GO:0032602	0.04	0.99	5	64	chemokine production	BP	0.47223	SYK,IL6,C5,TLR7,ACKR1	turquoise	VSMC_M6
GO:0032642	0.04	0.99	5	64	regulation of chemokine production	BP	0.47223	SYK,IL6,C5,TLR7,ACKR1	turquoise	VSMC_M6
GO:0098657	0.04	0.98	9	155	import into cell	BP	0.47372	STEAP4,SLC6A6,SNAP25,CD36,SNCA,SLC39A8,HFE,ATP1A4,TRPM2	turquoise	VSMC_M6
GO:0032943	0.04	0.98	10	179	mononuclear cell proliferation	BP	0.47416	IL23A,SYK,IL6,PIK3CG,CTNNB1,NFATC2,INPP5D,CD86,ACE,CCDC88B	turquoise	VSMC_M6
GO:0014902	0.04	0.99	6	86	myotube differentiation	BP	0.47496	CXCL10,CYP26B1,NFATC2,TBX1,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0048732	0.04	0.98	16	335	gland development	BP	0.4756	TNFRSF11A,NOTCH4,IL6,TGFB1,CTNNB1,SFRP1,NKX2-3,IGSF3,HFE,EAF2,BMP7,PROX1,TBX1,RGN,NOTCH1,CDH1	turquoise	VSMC_M6
GO:0016051	0.04	0.98	9	155	carbohydrate biosynthetic process	BP	0.47598	PDGFB,TGFB1,P2RY6,SOGA1,GOT1,SNCA,RGN,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0014066	0.04	0.99	6	86	regulation of phosphatidylinositol 3-kinase signaling	BP	0.47674	PDGFB,KDR,PRR5L,PPP1R16B,SELP,RELN	turquoise	VSMC_M6
GO:0051928	0.04	0.99	6	86	positive regulation of calcium ion transport	BP	0.47711	PDGFB,P2RY6,CXCL10,SNCA,RGN,CRACR2A	turquoise	VSMC_M6
GO:0007416	0.04	0.98	8	132	synapse assembly	BP	0.47711	MDGA1,LRRC4B,GPC6,SNCA,SHANK2,ABI3,CDH1,SHANK3	turquoise	VSMC_M6
GO:0110020	0.04	0.99	6	86	regulation of actomyosin structure organization	BP	0.47741	SFRP1,PROX1,PPM1F,MTOR,ARHGEF15,S1PR1	turquoise	VSMC_M6
GO:0007626	0.04	0.98	8	132	locomotory behavior	BP	0.4787	SPTBN4,SNAP25,SNCA,HOXD10,SNCG,PPP1R1B,MTOR,RELN	turquoise	VSMC_M6
GO:0065009	0.04	0.97	82	2307	regulation of molecular function	BP	0.47876	TNFRSF11A,IL23A,FLT4,DENND3,PDGFB,KDR,IL18RAP,SYK,EPHA5,IL6,NDUFA4,ARHGAP25,C5,KIAA1147,RASIP1,PIK3CG,KDM4D,FGD5,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,TMC8,TIE1,P2RY6,SFRP1,ZIC2,RASGRP3,CD36,HHEX,SOX7,CXCL10,ADGRG3,PPP1R16B,PLCB2,MAPK10,SNCA,HYAL2,HFE,LAPTM5,CD86,ERN1,BMP7,IGFBP3,PROX1,OAZ3,FANK1,ACE,LTF,ARHGAP27,LPAR2,AGFG2,RGN,SELE,FGF23,CRACR2A,PPM1F,PRKCH,PPP1R1B,ARHGEF9,MTOR,ARHGEF15,PDE4B,NOTCH1,S1PR1,SH2D3C,LHX2,CDH3,ALOX12,PRSS22,PMAIP1,RELN,ALKAL1,NMUR1,NUCB1,SHANK3,PKIB,TRIM62,BAMBI,CCR7,FXYD6	turquoise	VSMC_M6
GO:0048667	0.04	0.98	20	446	cell morphogenesis involved in neuron differentiation	BP	0.48414	EPHA5,NOVA2,SPTBN4,MAP6,CNTN4,ATP8A2,CTNND2,ROBO4,BMP7,LAMC2,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L,SHANK3	turquoise	VSMC_M6
GO:0046916	0.04	0.99	6	86	cellular transition metal ion homeostasis	BP	0.48414	IREB2,STEAP4,CP,SLC39A8,HFE,HEPH	turquoise	VSMC_M6
GO:0002274	0.04	0.98	9	156	myeloid leukocyte activation	BP	0.48907	ADGRF5,IL18RAP,SYK,IL6,PIK3CG,CTSC,CD177,SNCA,HYAL2	turquoise	VSMC_M6
GO:0001947	0.04	0.99	4	45	heart looping	BP	0.49335	DLL1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0080164	0.04	0.99	4	45	regulation of nitric oxide metabolic process	BP	0.4935	CD36,CD34,RGN,MTOR	turquoise	VSMC_M6
GO:0046879	0.04	0.98	11	206	hormone secretion	BP	0.49532	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,FGF23,SSTR5,EXOC3L1,TRPM2,NMB	turquoise	VSMC_M6
GO:0048015	0.04	0.98	8	133	phosphatidylinositol-mediated signaling	BP	0.49532	PDGFB,KDR,PIK3CG,PRR5L,PPP1R16B,PLCB2,SELP,RELN	turquoise	VSMC_M6
GO:0034612	0.04	0.98	10	181	response to tumor necrosis factor	BP	0.49532	TNFRSF11A,SYK,SFRP1,HYAL2,LAPTM5,SELE,PLVAP,TNFRSF18,ENDOG,GBP1	turquoise	VSMC_M6
GO:0002697	0.04	0.98	11	206	regulation of immune effector process	BP	0.49657	IL23A,IL18RAP,SYK,IL6,CD177,TGFB1,CD36,NFKBID,HFE,LAPTM5,CD86	turquoise	VSMC_M6
GO:0043270	0.05	0.98	10	182	positive regulation of ion transport	BP	0.50209	TNFRSF11A,PDGFB,NDUFA4,P2RY6,CXCL10,SNCA,RGN,CRACR2A,RELN,SHANK3	turquoise	VSMC_M6
GO:1903169	0.05	0.98	7	110	regulation of calcium ion transmembrane transport	BP	0.50272	PIK3CG,P2RY6,CXCL10,SNCA,RGN,CRACR2A,PDE4B	turquoise	VSMC_M6
GO:0010876	0.05	0.98	15	311	lipid localization	BP	0.50307	TNFRSF11A,ATP8A1,SYK,IL6,OSBPL3,PPARG,SLCO2B1,CD36,SLCO2A1,ATP8A2,ANO3,MTTP,ACE,PITPNM3,NMB	turquoise	VSMC_M6
GO:0051234	0.05	0.96	117	3429	establishment of localization	BP	0.50377	TNFRSF11A,KCNN2,MEGF10,SYBU,ENPP2,SYT17,DENND3,PDGFB,SLC16A8,IREB2,ATP8A1,STEAP4,SYK,EPHA5,IL6,OSBPL3,NDUFA4,ARHGAP25,GJA4,KCNA7,SLC22A16,PIK3CG,DLL1,RAB38,SLC6A6,GRIP2,EXOC3L2,CD177,PPARG,SYN2,TGFB1,CXCR4,EDNRB,CTNNB1,TMC6,TMC8,SPTBN4,MAP6,SLCO2B1,P2RY6,P2RY2,SNAP25,SFRP1,SLC4A11,CD36,SLCO2A1,ADAMTS9,PRR5L,ATP8A2,HHEX,REEP1,SLCO5A1,CP,CXCL10,SLC4A5,ATP6V0D2,STAB1,MAPK10,CLIC6,SNCA,MFSD4A,ANO3,MTTP,HYAL2,SLC39A8,NKD2,HFE,MCTP2,LAPTM5,PECAM1,MGST1,SLCO4A1,OAZ3,ACE,SSC4D,LTF,ARHGAP27,SYTL5,CLDN16,ATP13A1,CCDC88B,RGN,SELE,FGF23,CRACR2A,PPM1F,PITPNM3,SNCG,SLC25A18,HEPH,MTOR,SLC49A3,BEST2,NPR1,HCN1,PDE4B,SSTR5,NOTCH1,IRF8,CDH3,CDH1,EXOC3L1,MMP12,PMAIP1,ATP1A4,RELN,KCNU1,NMUR1,NUCB1,SHANK3,TRPM2,CCR7,NSG2,NMB,TMEM50B,SCARF1,FXYD6	turquoise	VSMC_M6
GO:0071407	0.05	0.97	20	448	cellular response to organic cyclic compound	BP	0.50444	PDGFB,PIK3CG,TGFB1,HTR5A,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,SNCA,ESRRG,BMP7,FGF23,PPP1R1B,HCN1,PDE4B,SSTR5,CDH1,TRPM2,NSG2	turquoise	VSMC_M6

GO:0014068	0.05	0.99	5	66	positive regulation of phosphatidylinositol 3-kinase signaling	BP	0.50449	PDGFB,KDR,PRR5L,SELP,RELN	turquoise	VSMC_M6
GO:1905114	0.05	0.97	20	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	0.50634	CELSR1,BARX1,ANKRD6,TGFB1,CTNNB1,GPC6,SFRP1,NOTUM,HHEX,SOX7,SNCA,CTNND2,NKD2,NRARP,NOTCH1,CDH3,SOX17,RELN,SHANK3,BAMBI	turquoise	VSMC_M6
GO:1902107	0.05	0.98	7	110	positive regulation of leukocyte differentiation	BP	0.51152	IL23A,IL1RL2,SYK,TGFB1,NFKBID,INPP5D,CD86	turquoise	VSMC_M6
GO:1903708	0.05	0.98	7	110	positive regulation of hemopoiesis	BP	0.51152	IL23A,IL1RL2,SYK,TGFB1,NFKBID,INPP5D,CD86	turquoise	VSMC_M6
GO:0001558	0.05	0.97	16	339	regulation of cell growth	BP	0.51297	SYT17,BCL11A,TGFB1,CXCR4,TMC8,SFRP1,HYAL2,EAF2,CDA,MTOR,NPR1,ISLR2,KIF26A,SEMA6B,SOX17,GNG4	turquoise	VSMC_M6
GO:1900407	0.05	0.99	5	66	regulation of cellular response to oxidative stress	BP	0.51297	CTNNB1,CD36,BMP7,ENDOG,TRPM2	turquoise	VSMC_M6
GO:0007254	0.05	0.98	8	134	JNK cascade	BP	0.51374	FLT4,ANKRD6,SFRP1,MAPK10,TLR7,CRACR2A,SH2D3C,CCR7	turquoise	VSMC_M6
GO:0051881	0.05	0.99	5	66	regulation of mitochondrial membrane potential	BP	0.51511	KDR,SLC4A11,GOT1,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0050922	0.05	0.99	4	46	negative regulation of chemotaxis	BP	0.51516	C5,ANGPT2,SEMA6B,NOTCH1	turquoise	VSMC_M6
GO:0014065	0.05	0.98	7	111	phosphatidylinositol 3-kinase signaling	BP	0.51516	PDGFB,KDR,PIK3CG,PRR5L,PPP1R16B,SELP,RELN	turquoise	VSMC_M6
GO:0019751	0.05	0.98	6	88	polyol metabolic process	BP	0.51707	IP6K3,P2RY6,GOT1,SNCA,DEGS2,NUDT4B	turquoise	VSMC_M6
GO:0007409	0.05	0.97	16	341	axonogenesis	BP	0.51775	EPHA5,NOVA2,SPTBN4,MAP6,CNTN4,ATP8A2,ROBO4,BMP7,LAMC2,ISLR2,B4GALT6,SEMA6B,NOTCH1,LHX2,RELN,VSTM2L	turquoise	VSMC_M6
GO:0043506	0.05	0.99	4	46	regulation of JUN kinase activity	BP	0.51854	TNFRSF11A,SYK,SFRP1,ERN1	turquoise	VSMC_M6
GO:0071396	0.05	0.97	19	422	cellular response to lipid	BP	0.51987	SYK,IL6,TGFB1,EDNRB,SFRP1,CD36,CXCL10,CYP26B1,ESRRG,CD86,BMP7,MGST1,LTF,TBX1,FGF23,PDE4B,SSTR5,IRF8,ALOX12	turquoise	VSMC_M6
GO:0048568	0.05	0.97	16	341	embryonic organ development	BP	0.52206	PDGFB,KDR,DLL1,RARRES2,TGFB1,CTNNB1,PCDH12,ATP8A2,COL2A1,BMP7,PROX1,HOXD10,TBX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0014909	0.05	0.99	5	67	smooth muscle cell migration	BP	0.52448	PDGFB,P2RY6,IGFBP3,ACE,GNA12	turquoise	VSMC_M6
GO:0034762	0.05	0.97	18	396	regulation of transmembrane transport	BP	0.52726	KCNN2,NDUFA4,KCNA7,PIK3CG,P2RY6,CXCL10,CLIC6,SNCA,OAZ3,RGN,CRACR2A,MTOR,HCN1,PDE4B,RELN,KCNU1,SHANK3,FXYD6	turquoise	VSMC_M6
GO:0003229	0.05	0.99	4	47	ventricular cardiac muscle tissue development	BP	0.53077	TGFB1,ADAMTS9,PROX1,NOTCH1	turquoise	VSMC_M6
GO:0042886	0.05	0.98	11	210	amide transport	BP	0.53437	SYBU,EPHA5,IL6,SNAP25,SFRP1,MTTP,HFE,MGST1,SSTR5,EXOC3L1,TRPM2	turquoise	VSMC_M6
GO:0009880	0.05	0.99	4	47	embryonic pattern specification	BP	0.53676	DLL1,CTNNB1,BMP7,NRARP	turquoise	VSMC_M6
GO:0001755	0.05	0.99	4	47	neural crest cell migration	BP	0.53724	EDNRB,BMP7,TBX1,SEMA6B	turquoise	VSMC_M6
GO:0009792	0.05	0.97	23	537	embryo development ending in birth or egg hatching	BP	0.53724	CELSR1,PDGFB,ADGRF5,C5,DLL1,TGFB1,CTNNB1,TIE1,SFRP1,PCDH12,COL2A1,BMP7,PROX1,HOXD10,TBX1,LFNG,NRARP,NOTCH1,ENDOG,LHX2,SOX17,SOX18,LPAR6	turquoise	VSMC_M6
GO:0061371	0.05	0.99	4	47	determination of heart left/right asymmetry	BP	0.53724	DLL1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0043407	0.05	0.99	4	47	negative regulation of MAP kinase activity	BP	0.53724	PPARG,SFRP1,HYAL2,BMP7	turquoise	VSMC_M6
GO:0060389	0.05	0.99	4	47	pathway-restricted SMAD protein phosphorylation	BP	0.53724	PPARG,TGFB1,HFE,BMP7	turquoise	VSMC_M6
GO:0051496	0.05	0.99	4	47	positive regulation of stress fiber assembly	BP	0.53724	SFRP1,PPM1F,MTOR,ARHGEF15	turquoise	VSMC_M6
GO:0048017	0.05	0.98	8	137	inositol lipid-mediated signaling	BP	0.53724	PDGFB,KDR,PIK3CG,PRR5L,PPP1R16B,PLCB2,SELP,RELN	turquoise	VSMC_M6
GO:0031400	0.05	0.97	19	426	negative regulation of protein modification process	BP	0.53724	RASIP1,KDM4D,PPARG,TGFB1,CTNNB1,SFRP1,KIRREL2,PRR5L,HHEX,PPP1R16B,SNCA,HYAL2,BMP7,IGFBP3,RGN,PPM1F,PPP1R1B,MTOR,PKIB	turquoise	VSMC_M6
GO:0015833	0.05	0.98	10	186	peptide transport	BP	0.53724	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,MGST1,SSTR5,EXOC3L1,TRPM2	turquoise	VSMC_M6
GO:0016049	0.05	0.97	18	399	cell growth	BP	0.53724	SYT17,BCL11A,TGFB1,CXCR4,CTNNB1,TMC8,SFRP1,HYAL2,EAF2,CDA,MTOR,NPR1,ISLR2,KIF26A,SEMA6B,LHX2,SOX17,GNG4	turquoise	VSMC_M6
GO:0098754	0.05	0.98	6	90	detoxification	BP	0.53724	NOS3,CD36,BMP7,MGST1,PTGS1,GPX3	turquoise	VSMC_M6
GO:0050670	0.05	0.98	8	137	regulation of lymphocyte proliferation	BP	0.53724	IL23A,SYK,IL6,CTNNB1,NFATC2,INPP5D,CD86,CCDC88B	turquoise	VSMC_M6
GO:0016055	0.05	0.97	17	373	Wnt signaling pathway	BP	0.53724	CELSR1,BARX1,ANKRD6,TGFB1,CTNNB1,GPC6,SFRP1,NOTUM,HHEX,SOX7,CTNND2,NKD2,NRARP,NOTCH1,CDH3,SOX17,BAMBI	turquoise	VSMC_M6
GO:0060071	0.05	0.99	4	48	Wnt signaling pathway, planar cell polarity pathway	BP	0.53724	CELSR1,ANKRD6,GPC6,SFRP1	turquoise	VSMC_M6
GO:0048523	0.05	0.96	123	3647	negative regulation of cellular process	BP	0.53724	FLT4,NOTCH4,PDGFB,ETV7,IREB2,ADGRF5,KDR,BARX1,IL6,BCL11A,ANKRD6,ARHGAP25,C5,RASIP1,PIK3CG,DLL1,KDM4D,CTSC,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,TMC8,SPTBN4,TIE1,P2RY6,PDE2A,SFRP1,ZIC2,NOTUM,CNTN4,CD36,KIRREL2,PRAG1,ADAMTS9,PRR5L,ATP8A2,HHEX,SOX7,CXCL10,ANGPT2,SOGA1,ADGRG3,CYP26B1,PPP1R16B,COL2A1,MAPK10,SNCA,SHANK2,HYAL2,NKD2,HFE,LAPTM5,NFATC2,INPP5D,EAF2,CD34,CD86,COL18A1,BMP7,IGFBP3,PROX1,GPC1,OAZ3,SRMS,FANK1,ACE,PTPRE,PRAME,PAX9,LTF,TSPAN15,TBX1,RGN,CDA,FGF23,PPM1F,PRKCH,GRID2IP,BCL6B,MMRN2,PPP1R1B,LFNG,MTOR,BCKDK,ABI3,ARHGEF15,NPR1,KIF26A,PDE4B,SARM1,SEMA6B,TNFRSF18,NRARP,HES3,EGFL7,SSTR5,NOTCH1,IRF8,S1PR1,GBP1,LHX2,CDH1,CDH5,ALOX12,MMP12,SOX17,OLIG2,VSTM2L,SOX18,KANK3,GNA12,SHANK3,TRPM2,PKIB,TRIM62,BAMBI,CCR7,MGAT3,NMB,RTN4RL2,GNG4	turquoise	VSMC_M6
GO:1902106	0.05	0.98	5	69	negative regulation of leukocyte differentiation	BP	0.53724	CTNNB1,SFRP1,INPP5D,LTF,NRARP	turquoise	VSMC_M6
GO:0032722	0.05	0.99	4	48	positive regulation of chemokine production	BP	0.53724	SYK,IL6,C5,TLR7	turquoise	VSMC_M6
GO:0032944	0.05	0.98	8	138	regulation of mononuclear cell proliferation	BP	0.53724	IL23A,SYK,IL6,CTNNB1,NFATC2,INPP5D,CD86,CCDC88B	turquoise	VSMC_M6
GO:0042116	0.05	0.98	5	69	macrophage activation	BP	0.53724	ADGRF5,SYK,IL6,CTSC,SNCA	turquoise	VSMC_M6
GO:0198738	0.05	0.97	17	374	cell-cell signaling by wnt	BP	0.53724	CELSR1,BARX1,ANKRD6,TGFB1,CTNNB1,GPC6,SFRP1,NOTUM,HHEX,SOX7,CTNND2,NKD2,NRARP,NOTCH1,CDH3,SOX17,BAMBI	turquoise	VSMC_M6
GO:0015844	0.05	0.99	4	48	monoamine transport	BP	0.53724	SYT17,SYK,SNCA,SNCG	turquoise	VSMC_M6
GO:0120036	0.05	0.96	45	1193	plasma membrane bounded cell projection organization	BP	0.53724	ENPP2,SYT17,DNAH8,EPHA5,IL6,BCL11A,CFAP100,NOVA2,FGD5,ITGB4,CXCR4,CTNNB1,SPTBN4,MAP6,DNAJB13,SNAP25,SFRP1,CNTN4,CFAP54,PRAG1,ATP8A2,PPP1R16B,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,MTOR,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,S1PR1,LHX2,CDH1,RELN,ALKAL1,VSTM2L,SHANK3,TRPM2,CCR7,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0071706	0.06	0.98	7	115	tumor necrosis factor superfamily cytokine production	BP	0.53724	IL23A,SYK,IL6,CD36,CD34,CD86,LTF	turquoise	VSMC_M6

GO:1903555	0.06	0.98	7	115	regulation of tumor necrosis factor superfamily cytokine production	BP	0.53724	IL23A,SYK,IL6,CD36,CD34,CD86,LTF	turquoise	VSMC_M6
GO:0090263	0.06	0.98	6	92	positive regulation of canonical Wnt signaling pathway	BP	0.53724	TGFB1,SFRP1,HHEX,NRARP,CDH3,BAMBI	turquoise	VSMC_M6
GO:0051017	0.06	0.98	8	139	actin filament bundle assembly	BP	0.53724	SFRP1,BAIAP2L1,PPM1F,MTOR,ARHGEF15,S1PR1,PDLIM1,SHANK3	turquoise	VSMC_M6
GO:0032231	0.06	0.98	6	92	regulation of actin filament bundle assembly	BP	0.53724	SFRP1,PPM1F,MTOR,ARHGEF15,S1PR1,SHANK3	turquoise	VSMC_M6
GO:1904062	0.06	0.97	12	241	regulation of cation transmembrane transport	BP	0.53724	KCNN2,NDUFA4,PIK3CG,P2RY6,CXCL10,SNCA,RGN,CRACR2A,PDE4B,RELN,SHANK3,FXYD6	turquoise	VSMC_M6
GO:0010975	0.06	0.97	17	376	regulation of neuron projection development	BP	0.53724	BCL11A,MAP6,SNAP25,SFRP1,PRAG1,ATP8A2,BMP7,MTOR,ABI3,ISLR2,SARM1,SEMA6B,RELN,ALKAL1,SHANK3,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0150104	0.06	0.98	5	70	transport across blood-brain barrier	BP	0.53724	ATP8A1,SLC6A6,SLCO2B1,CD36,ATP1A4	turquoise	VSMC_M6
GO:0015914	0.06	0.98	5	70	phospholipid transport	BP	0.53724	ATP8A1,ATP8A2,ANO3,MTTP,PITPNM3	turquoise	VSMC_M6
GO:0061005	0.06	0.99	4	49	cell differentiation involved in kidney development	BP	0.53724	PDGFB,CTNNB1,CD34,NOTCH1	turquoise	VSMC_M6
GO:0046579	0.06	0.99	4	49	positive regulation of Ras protein signal transduction	BP	0.53724	PIK3CG,PRAG1,NOTCH1,LPAR6	turquoise	VSMC_M6
GO:0006885	0.06	0.98	5	70	regulation of pH	BP	0.53724	RAB38,EDNRB,SLC4A5,ATP6V0D2,ATP1A4	turquoise	VSMC_M6
GO:0002444	0.06	0.98	5	70	myeloid leukocyte mediated immunity	BP	0.53724	SYK,IL6,PIK3CG,CD177,ACE	turquoise	VSMC_M6
GO:0072175	0.06	0.98	7	116	epithelial tube formation	BP	0.53724	CELSR1,TGFB1,CTNNB1,SFRP1,BMP7,PROX1,LHX2	turquoise	VSMC_M6
GO:0046173	0.06	0.99	4	49	polyol biosynthetic process	BP	0.53724	IP6K3,P2RY6,GOT1,SNCA	turquoise	VSMC_M6
GO:0060537	0.06	0.97	15	323	muscle tissue development	BP	0.53724	MEGF10,DLL1,TGFB1,CTNNB1,ADAMTS9,CYP26B1,NRAP,BMP7,PROX1,GPC1,HOXD10,TBX1,MTOR,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0090276	0.06	0.98	8	140	regulation of peptide hormone secretion	BP	0.53724	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,SSTR5,TRPM2	turquoise	VSMC_M6
GO:0043406	0.06	0.98	6	93	positive regulation of MAP kinase activity	BP	0.53724	TNFRSF11A,PDGFB,SYK,PIK3CG,TGFB1,ERN1	turquoise	VSMC_M6
GO:0071495	0.06	0.96	39	1018	cellular response to endogenous stimulus	BP	0.53724	BCL11A,PIK3CG,RARRES2,PPARG,TGFB1,HTR5A,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,SOGA1,COL2A1,GOT1,SNCA,HYAL2,ESRRG,HFE,BMP7,GPC1,PTPRE,TBX1,BAIAP2L1,FGF23,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,LRG1,SSTR5,NOTCH1,CDH1,CDH5,TRPM2,BAMBI,NSG2	turquoise	VSMC_M6
GO:0010232	0.06	0.98	5	71	vascular transport	BP	0.53923	ATP8A1,SLC6A6,SLCO2B1,CD36,ATP1A4	turquoise	VSMC_M6
GO:0070665	0.06	0.98	6	93	positive regulation of leukocyte proliferation	BP	0.53923	IL23A,SYK,IL6,NFATC2,CD86,CCDC88B	turquoise	VSMC_M6
GO:0055008	0.06	0.98	4	50	cardiac muscle tissue morphogenesis	BP	0.54237	TGFB1,PROX1,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0061572	0.06	0.98	8	141	actin filament bundle organization	BP	0.54259	SFRP1,BAIAP2L1,PPM1F,MTOR,ARHGEF15,S1PR1,PDLIM1,SHANK3	turquoise	VSMC_M6
GO:0062012	0.06	0.97	12	243	regulation of small molecule metabolic process	BP	0.54288	NOS3,PPARG,P2RY6,SOGA1,SNCA,PROX1,RGN,CDA,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0003143	0.06	0.98	4	50	embryonic heart tube morphogenesis	BP	0.54513	DLL1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0002011	0.06	0.98	4	50	morphogenesis of an epithelial sheet	BP	0.54625	BMP7,MTOR,NOTCH1,MMP12	turquoise	VSMC_M6
GO:0031532	0.06	0.98	6	94	actin cytoskeleton reorganization	BP	0.54673	THSD7A,ESAM,BAIAP2L1,ABI3,S1PR1,TRPM2	turquoise	VSMC_M6
GO:0031016	0.06	0.98	4	50	pancreas development	BP	0.54673	IL6,DLL1,CTNNB1,PROX1	turquoise	VSMC_M6
GO:0006898	0.06	0.97	10	192	receptor-mediated endocytosis	BP	0.54801	SYK,DLL1,SNAP25,CD36,STAB1,SNCA,HFE,ARHGAP27,SELE,SCARF1	turquoise	VSMC_M6
GO:0051130	0.06	0.96	34	870	positive regulation of cellular component organization	BP	0.54886	ENPP2,PDGFB,ATP8A1,KDR,SYK,IL6,LRRC4B,RASIP1,DLL1,TGFB1,CTNNB1,MAP6,SFRP1,CD36,ATP8A2,SNCA,HFE,NFATC2,BMP7,PROX1,SELE,BAIAP2L1,PPM1F,MTOR,ARHGEF15,ISLR2,CDH5,PMAIP1,RELN,ALKAL1,SHANK3,PKIB,CCR7,SCARF1	turquoise	VSMC_M6
GO:0010035	0.06	0.96	19	435	response to inorganic substance	BP	0.54889	SYT17,KDR,IL18RAP,IL6,NOS3,CD36,MAPK10,GOT1,SNCA,MTTP,HFE,ERN1,COL18A1,BMP7,FGF23,ENDOG,CDH1,TRPM2,CCR7	turquoise	VSMC_M6
GO:0009719	0.06	0.96	45	1202	response to endogenous stimulus	BP	0.55105	SYK,IL6,BCL11A,PIK3CG,RARRES2,NOS3,PPARG,TGFB1,HTR5A,EDNRB,CTNNB1,P2RY6,P2RY2,PDE2A,SFRP1,CD36,HHEX,SOGA1,COL2A1,GOT1,SNCA,HYAL2,ESRRG,HFE,BMP7,GPC1,PTPRE,TBX1,BAIAP2L1,FGF23,PPP1R1B,MTOR,KLF1,COL4A6,HCN1,PDE4B,LRG1,SSTR5,NOTCH1,CDH1,CDH5,TRPM2,BAMBI,CCR7,NSG2	turquoise	VSMC_M6
GO:0090092	0.06	0.97	10	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.55105	PPARG,TGFB1,SFRP1,GOT1,HFE,BMP7,LRG1,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0002791	0.06	0.97	8	142	regulation of peptide secretion	BP	0.559	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,SSTR5,TRPM2	turquoise	VSMC_M6
GO:1905952	0.06	0.98	7	118	regulation of lipid localization	BP	0.55962	TNFRSF11A,ATP8A1,SYK,IL6,PPARG,CD36,ATP8A2	turquoise	VSMC_M6
GO:2000116	0.06	0.97	9	167	regulation of cysteine-type endopeptidase activity	BP	0.56213	SYK,PPARG,SOX7,SNCA,LAPTM5,LTF,PPM1F,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0051348	0.06	0.97	11	219	negative regulation of transferase activity	BP	0.5642	RASIP1,PPARG,SFRP1,HHEX,SNCA,HYAL2,BMP7,RGN,PPM1F,PPP1R1B,PKIB	turquoise	VSMC_M6
GO:0002695	0.06	0.98	7	118	negative regulation of leukocyte activation	BP	0.56422	ADGRF5,SFRP1,HFE,LAPTM5,INPP5D,CD86,NRARP	turquoise	VSMC_M6
GO:1903707	0.06	0.98	5	72	negative regulation of hemopoiesis	BP	0.56439	CTNNB1,SFRP1,INPP5D,LTF,NRARP	turquoise	VSMC_M6
GO:1903557	0.06	0.98	5	72	positive regulation of tumor necrosis factor superfamily cytokine production	BP	0.56476	IL23A,SYK,IL6,CD36,CD86	turquoise	VSMC_M6
GO:0072676	0.06	0.98	5	72	lymphocyte migration	BP	0.56476	PIK3CG,CXCL10,S1PR1,CCR7,MSMP	turquoise	VSMC_M6
GO:0051336	0.06	0.96	30	754	regulation of hydrolase activity	BP	0.56476	SYK,EPHA5,ARHGAP25,C5,RASIP1,FGD5,PPARG,P2RY6,SFRP1,RASGRP3,SOX7,PLCB2,SNCA,LAPTM5,CD86,LTF,ARHGAP27,LPAR2,RGN,SELE,PPM1F,PPP1R1B,MTOR,ARHGEF15,S1PR1,ALOX12,PRSS22,PMAIP1,NMUR1,CCR7	turquoise	VSMC_M6
GO:0030038	0.06	0.98	6	95	contractile actin filament bundle assembly	BP	0.56476	SFRP1,PPM1F,MTOR,ARHGEF15,S1PR1,PDLIM1	turquoise	VSMC_M6
GO:0043149	0.06	0.98	6	95	stress fiber assembly	BP	0.56476	SFRP1,PPM1F,MTOR,ARHGEF15,S1PR1,PDLIM1	turquoise	VSMC_M6
GO:0042476	0.06	0.98	6	95	odontogenesis	BP	0.56476	CTNNB1,NKX2-3,CD34,BMP7,PAX9,TBX1	turquoise	VSMC_M6
GO:0010565	0.06	0.98	6	95	regulation of cellular ketone metabolic process	BP	0.56476	PPARG,SNCA,PROX1,RGN,MTOR,BCKDK	turquoise	VSMC_M6
GO:0030072	0.06	0.97	9	168	peptide hormone secretion	BP	0.56476	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,SSTR5,EXOC3L1,TRPM2	turquoise	VSMC_M6
GO:0090175	0.06	0.98	4	51	regulation of establishment of planar polarity	BP	0.56476	CELSR1,ANKRD6,GPC6,SFRP1	turquoise	VSMC_M6
GO:0070527	0.06	0.98	4	51	platelet aggregation	BP	0.56516	SYK,IL6,PIK3CG,ALOX12	turquoise	VSMC_M6
GO:1901224	0.06	0.98	4	51	positive regulation of NIK/NF-kappaB signaling	BP	0.5658	IL23A,LAPTM5,TLR7,CD86	turquoise	VSMC_M6
GO:0071456	0.06	0.97	7	119	cellular response to hypoxia	BP	0.56668	SFRP1,CD34,BMP7,MTOR,NOTCH1,ENDOG,PMAIP1	turquoise	VSMC_M6
GO:0001503	0.07	0.96	15	328	ossification	BP	0.57274	TNFRSF11A,IL6,PPARG,TGFB1,CTNNB1,SFRP1,NOTUM,COL2A1,BMP1,BMP7,LTF,FGF23,NOTCH1,S1PR1,BAMBI	turquoise	VSMC_M6
GO:0048593	0.07	0.98	6	96	camera-type eye morphogenesis	BP	0.57528	DLL1,CTNNB1,ATP8A2,BMP7,PROX1,HCN1	turquoise	VSMC_M6
GO:1905954	0.07	0.98	5	73	positive regulation of lipid localization	BP	0.57528	TNFRSF11A,ATP8A1,PPARG,CD36,ATP8A2	turquoise	VSMC_M6

GO:0014031	0.07	0.98	5	73	mesenchymal cell development	BP	0.57664	EDNRB,BMP7,TBX1,SEMA6B,NOTCH1	turquoise	VSMC_M6
GO:0035725	0.07	0.97	7	120	sodium ion transmembrane transport	BP	0.57665	SLC6A6,SLC4A11,SLC4A5,HCN1,ATP1A4,TRPM2,FXYD6	turquoise	VSMC_M6
GO:0010906	0.07	0.98	6	96	regulation of glucose metabolic process	BP	0.57934	SOGA1,RGN,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0090087	0.07	0.97	8	144	regulation of peptide transport	BP	0.57934	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,SSTR5,TRPM2	turquoise	VSMC_M6
GO:0062013	0.07	0.98	6	96	positive regulation of small molecule metabolic process	BP	0.5828	NOS3,PPARG,P2RY6,SNCA,RGN,PMAIP1	turquoise	VSMC_M6
GO:0050803	0.07	0.97	9	170	regulation of synapse structure or activity	BP	0.5863	SYBU,MDGA1,LRRC4B,GPC6,SNCA,ABI3,ARHGEF15,RELN,SHANK3	turquoise	VSMC_M6
GO:0071902	0.07	0.97	9	170	positive regulation of protein serine/threonine kinase activity	BP	0.58821	TNFRSF11A,PDGFB,SYK,PIK3CG,TGFB1,SNCA,ERN1,PROX1,LTF	turquoise	VSMC_M6
GO:0030510	0.07	0.98	5	74	regulation of BMP signaling pathway	BP	0.58822	PPARG,SFRP1,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:2000377	0.07	0.97	7	120	regulation of reactive oxygen species metabolic process	BP	0.58822	PDGFB,SYK,CD177,TGFB1,CD36,SNCA,BMP7	turquoise	VSMC_M6
GO:2001259	0.07	0.98	4	52	positive regulation of cation channel activity	BP	0.59232	P2RY6,CRACR2A,RELN,SHANK3	turquoise	VSMC_M6
GO:0009855	0.07	0.98	6	97	determination of bilateral symmetry	BP	0.59232	DLL1,CTNNB1,TBX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0018105	0.07	0.97	12	249	peptidyl-serine phosphorylation	BP	0.59308	PDGFB,SYK,IL6,TGFB1,SPTBN4,SNCA,ERN1,PPM1F,PRKCH,MTOR,MAST1,SH2D3C	turquoise	VSMC_M6
GO:0030282	0.07	0.97	6	97	bone mineralization	BP	0.5974	TGFB1,NOTUM,BMP7,LTF,FGF23,S1PR1	turquoise	VSMC_M6
GO:0035282	0.07	0.98	5	74	segmentation	BP	0.5974	DLL1,SFRP1,LFNG,NRARP,NOTCH1	turquoise	VSMC_M6
GO:0042306	0.07	0.98	4	52	regulation of protein import into nucleus	BP	0.5974	TGFB1,CD36,HYAL2,CDH1	turquoise	VSMC_M6
GO:0061097	0.07	0.98	5	74	regulation of protein tyrosine kinase activity	BP	0.60224	PDGFB,HYAL2,ACE,RELN,ALKAL1	turquoise	VSMC_M6
GO:0044106	0.07	0.98	5	74	cellular amine metabolic process	BP	0.60501	SNCA,OAZ3,AGMAT,BCKDK,NPR1	turquoise	VSMC_M6
GO:1902882	0.07	0.98	5	74	regulation of response to oxidative stress	BP	0.60501	CTNNB1,CD36,BMP7,ENDOG,TRPM2	turquoise	VSMC_M6
GO:0031032	0.07	0.97	9	172	actomyosin structure organization	BP	0.60784	FRMD3,SFRP1,NRAP,PROX1,PPM1F,MTOR,ARHGEF15,S1PR1,PDLIM1	turquoise	VSMC_M6
GO:0010817	0.07	0.96	15	331	regulation of hormone levels	BP	0.61133	SYBU,EPHA5,IL6,SNAP25,SFRP1,CYP26B1,HFE,SLCO4A1,ACE,FGF23,SSTR5,EXOC3L1,TRPM2,NMB,RBP1	turquoise	VSMC_M6
GO:0009799	0.07	0.97	6	98	specification of symmetry	BP	0.61133	DLL1,CTNNB1,TBX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0007507	0.07	0.96	20	474	heart development	BP	0.61325	PDGFB,DLL1,NOS3,TGFB1,CTNNB1,TIE1,PDE2A,ADAMTS9,COL2A1,NRAP,BMP7,PROX1,TBX1,MTOR,GREB1L,NOTCH1,S1PR1,SOX17,PDLIM1,SOX18	turquoise	VSMC_M6
GO:0032409	0.07	0.97	10	198	regulation of transporter activity	BP	0.61463	NDUFA4,PPARG,P2RY6,SNCA,RGN,CRACR2A,PDE4B,RELN,SHANK3,FXYD6	turquoise	VSMC_M6
GO:0008306	0.07	0.98	4	53	associative learning	BP	0.61473	SNAP25,PPP1R1B,MTOR,RELN	turquoise	VSMC_M6
GO:0072080	0.07	0.98	5	75	nephron tubule development	BP	0.61473	DLL1,CTNNB1,KIF26B,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0021761	0.07	0.98	5	75	limbic system development	BP	0.61473	EPHA5,HTR5A,PROX1,SEMA6B,RELN	turquoise	VSMC_M6
GO:0002790	0.07	0.97	9	172	peptide secretion	BP	0.61473	SYBU,EPHA5,IL6,SNAP25,SFRP1,HFE,SSTR5,EXOC3L1,TRPM2	turquoise	VSMC_M6
GO:0042303	0.07	0.98	5	75	molting cycle	BP	0.61473	CTNNB1,NOTCH1,LHX2,CDH3,SOX18	turquoise	VSMC_M6
GO:0042633	0.07	0.98	5	75	hair cycle	BP	0.61473	CTNNB1,NOTCH1,LHX2,CDH3,SOX18	turquoise	VSMC_M6
GO:0010812	0.07	0.98	4	53	negative regulation of cell-substrate adhesion	BP	0.61473	ANGPT2,NOTCH1,GBP1,MMP12	turquoise	VSMC_M6
GO:0071347	0.07	0.98	5	75	cellular response to interleukin-1	BP	0.61473	IL1RL2,IL6,SFRP1,HYAL2,GBP1	turquoise	VSMC_M6
GO:0048562	0.07	0.96	11	225	embryonic organ morphogenesis	BP	0.61473	DLL1,CTNNB1,ATP8A2,COL2A1,BMP7,PROX1,HOXD10,TBX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:0033273	0.07	0.98	5	75	response to vitamin	BP	0.61473	SFRP1,CXCL10,CYP26B1,BMP7,FGF23	turquoise	VSMC_M6
GO:1903036	0.07	0.98	4	53	positive regulation of response to wounding	BP	0.61546	CXCR4,CD36,MTOR,SCARF1	turquoise	VSMC_M6
GO:0033209	0.07	0.98	5	75	tumor necrosis factor-mediated signaling pathway	BP	0.61621	TNFRSF11A,SYK,LAPTM5,PLVAP,TNFRSF18	turquoise	VSMC_M6
GO:0045600	0.07	0.98	4	53	positive regulation of fat cell differentiation	BP	0.61628	RARRES2,PPARG,SFRP1,BMP7	turquoise	VSMC_M6
GO:0002702	0.07	0.98	5	75	positive regulation of production of molecular mediator of immune response	BP	0.61707	IL6,TGFB1,CD36,LAPTM5,CD86	turquoise	VSMC_M6
GO:1990778	0.07	0.96	13	279	protein localization to cell periphery	BP	0.6235	GRIP2,TGFB1,SPTBN4,GPC6,SNAP25,MAPK10,NKD2,TSPAN15,PRKCH,TSPAN14,ABI3,GBP1,CDH1	turquoise	VSMC_M6
GO:0007568	0.07	0.96	12	252	aging	BP	0.62762	CTSC,EDNRB,ATP8A2,MAPK10,SNCA,HYAL2,INPP5D,RGN,MTOR,ABI3,ENDOG,ALOX12	turquoise	VSMC_M6
GO:0038061	0.07	0.97	6	99	NIK/NF-kappaB signaling	BP	0.62847	IL23A,ADGRG3,LAPTM5,TLR7,CD86,BMP7	turquoise	VSMC_M6
GO:0051250	0.07	0.97	6	99	negative regulation of lymphocyte activation	BP	0.63293	SFRP1,HFE,LAPTM5,INPP5D,CD86,NRARP	turquoise	VSMC_M6
GO:0060997	0.08	0.98	4	54	dendritic spine morphogenesis	BP	0.63657	CTNND2,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0051607	0.08	0.96	9	174	defense response to virus	BP	0.63782	IL23A,IL6,CXCL10,HYAL2,ISG20,TLR7,GBP1,MMP12,PMAIP1	turquoise	VSMC_M6
GO:0140546	0.08	0.96	9	174	defense response to symbiont	BP	0.63782	IL23A,IL6,CXCL10,HYAL2,ISG20,TLR7,GBP1,MMP12,PMAIP1	turquoise	VSMC_M6
GO:0002705	0.08	0.97	5	76	positive regulation of leukocyte mediated immunity	BP	0.63782	IL23A,IL18RAP,IL6,CD177,TGFB1	turquoise	VSMC_M6
GO:0030177	0.08	0.97	7	124	positive regulation of Wnt signaling pathway	BP	0.63782	ANKRD6,TGFB1,SFRP1,HHEX,NRARP,CDH3,BAMBI	turquoise	VSMC_M6
GO:0072089	0.08	0.98	4	54	stem cell proliferation	BP	0.63782	CD34,ACE,SOX17,SOX18	turquoise	VSMC_M6
GO:0031644	0.08	0.97	6	100	regulation of nervous system process	BP	0.63782	CTSC,NOS3,EDNRB,MTOR,RELN,SHANK3	turquoise	VSMC_M6
GO:0002456	0.08	0.98	4	54	T cell mediated immunity	BP	0.63782	IL23A,IL6,CTSC,HFE	turquoise	VSMC_M6
GO:0060322	0.08	0.95	25	624	head development	BP	0.63782	MDGA1,EPHA5,DLL1,HTR5A,CXCR4,CTNNB1,SFRP1,ZIC2,CNTN4,COL2A1,BMP7,PROX1,PAX9,TBX1,MTOR,MAST1,SEMA6B,NOTCH1,S1PR1,LHX2,LHX6,CDH1,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0010811	0.08	0.97	6	100	positive regulation of cell-substrate adhesion	BP	0.63782	PDGFB,KDR,SFRP1,CD36,PPM1F,CCR7	turquoise	VSMC_M6
GO:0035150	0.08	0.97	6	100	regulation of tube size	BP	0.63782	GRIP2,NOS3,EDNRB,P2RY2,ACE,NPR1	turquoise	VSMC_M6
GO:0035296	0.08	0.97	6	100	regulation of tube diameter	BP	0.63782	GRIP2,NOS3,EDNRB,P2RY2,ACE,NPR1	turquoise	VSMC_M6
GO:0097746	0.08	0.97	6	100	blood vessel diameter maintenance	BP	0.63782	GRIP2,NOS3,EDNRB,P2RY2,ACE,NPR1	turquoise	VSMC_M6
GO:0030030	0.08	0.94	45	1226	cell projection organization	BP	0.63782	ENPP2,SYT17,DNAH8,EPHA5,IL6,BCL11A,CFAP100,NOVA2,FGD5,ITGB4,CXCR4,CTNNB1,SPTBN4,MAP6,DNAJB13,SNAP25,SFRP1,CNTN4,CFAP54,PRAG1,ATP8A2,PPP1R16B,CTNND2,DPYSL4,ROBO4,BMP7,LAMC2,MTOR,ABI3,ISLR2,B4GALT6,SARM1,SEMA6B,NOTCH1,S1PR1,LHX2,CDH1,RELN,ALKAL1,VSTM2L,SHANK3,TRPM2,CCR7,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0061326	0.08	0.97	5	77	renal tubule development	BP	0.63782	DLL1,CTNNB1,KIF26B,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0044087	0.08	0.95	31	801	regulation of cellular component biogenesis	BP	0.63782	MDGA1,KDR,SYK,LRRC4B,RASIP1,TGFB1,TMC8,SPTBN4,TIE1,GPC6,SFRP1,CD36,PPP1R16B,SNCA,ESAM,BMP7,ACE,SELP,BAIAP2L1,PPM1F,PRKCH,MTOR,ABI3,ARHGEF15,NOTCH1,S1PR1,CDH5,KANK3,SHANK3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0014033	0.08	0.97	5	77	neural crest cell differentiation	BP	0.63782	EDNRB,SFRP1,BMP7,TBX1,SEMA6B	turquoise	VSMC_M6

GO:0009891	0.08	0.94	55	1533	positive regulation of biosynthetic process	BP	0.63782	NOTCH4,PDGFB,ADGRF5,KDR,IL6,MAML3,DLL1,RAB38,NOS3,PPARG,TGFB1,CTNNB1,P2RY6,SFRP1,ZIC2,CD36,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,RGN,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,LHX2,CDH3,CDH1,MMP12,SOX17,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0050848	0.08	0.98	4	55	regulation of calcium-mediated signaling	BP	0.63782	SYK,RGN,MTOR,GBP1	turquoise	VSMC_M6
GO:0031328	0.08	0.94	54	1503	positive regulation of cellular biosynthetic process	BP	0.63782	NOTCH4,PDGFB,ADGRF5,IL6,MAML3,DLL1,RAB38,NOS3,PPARG,TGFB1,CTNNB1,P2RY6,SFRP1,ZIC2,CD36,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,RGN,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,LHX2,CDH3,CDH1,MMP12,SOX17,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0009308	0.08	0.97	5	77	amine metabolic process	BP	0.63782	SNCA,OAZ3,AGMAT,BCKDK,NPR1	turquoise	VSMC_M6
GO:0032370	0.08	0.98	4	55	positive regulation of lipid transport	BP	0.63782	TNFRSF11A,ATP8A1,PPARG,ATP8A2	turquoise	VSMC_M6
GO:0051148	0.08	0.98	4	55	negative regulation of muscle cell differentiation	BP	0.63782	PDGFB,DLL1,NFATC2,NOTCH1	turquoise	VSMC_M6
GO:1904589	0.08	0.98	4	55	regulation of protein import	BP	0.63782	TGFB1,CD36,HYAL2,CDH1	turquoise	VSMC_M6
GO:0050768	0.08	0.97	6	102	negative regulation of neurogenesis	BP	0.63782	IL6,CTNNB1,BMP7,SEMA6B,NOTCH1,LHX2	turquoise	VSMC_M6
GO:0001657	0.08	0.97	5	78	ureteric bud development	BP	0.63782	CTNNB1,SFRP1,BMP7,KIF26B,GREB1L	turquoise	VSMC_M6
GO:1901216	0.08	0.97	5	78	positive regulation of neuron death	BP	0.63782	CTNNB1,SNCA,MTOR,SARM1,TRPM2	turquoise	VSMC_M6
GO:0046651	0.08	0.96	9	177	lymphocyte proliferation	BP	0.63782	IL23A,SYK,IL6,PIK3CG,CTNNB1,NFATC2,INPP5D,CD86,CCDC88B	turquoise	VSMC_M6
GO:0000302	0.08	0.96	9	177	response to reactive oxygen species	BP	0.63782	IL18RAP,IL6,NOS3,CD36,HYAL2,ERN1,BMP7,ENDOG,TRPM2	turquoise	VSMC_M6
GO:0001539	0.08	0.97	5	79	cilium or flagellum-dependent cell motility	BP	0.63782	DNAH8,SLC22A16,CFAP54,RGN,ATP1A4	turquoise	VSMC_M6
GO:0060285	0.08	0.97	5	79	cilium-dependent cell motility	BP	0.63782	DNAH8,SLC22A16,CFAP54,RGN,ATP1A4	turquoise	VSMC_M6
GO:0051056	0.08	0.96	12	259	regulation of small GTPase mediated signal transduction	BP	0.63782	DENND3,ARHGAP25,RASIP1,PIK3CG,FGD5,PRAG1,ARHGAP27,ARHGEF9,ARHGEF15,NOTCH1,RELN,LPAR6	turquoise	VSMC_M6
GO:0008344	0.08	0.98	4	56	adult locomotory behavior	BP	0.63782	SPTBN4,SNCA,HOXD10,SNCG	turquoise	VSMC_M6
GO:0045669	0.08	0.98	4	56	positive regulation of osteoblast differentiation	BP	0.63782	IL6,CTNNB1,BMP7,LTF	turquoise	VSMC_M6
GO:0042129	0.08	0.97	6	102	regulation of T cell proliferation	BP	0.63782	IL23A,SYK,IL6,CTNNB1,CD86,CCDC88B	turquoise	VSMC_M6
GO:0045637	0.08	0.96	8	152	regulation of myeloid cell differentiation	BP	0.63782	IL23A,DLL1,TGFB1,CTNNB1,SFRP1,INPP5D,LTF,MTOR	turquoise	VSMC_M6
GO:0007517	0.08	0.95	12	259	muscle organ development	BP	0.63782	MEGF10,DLL1,TGFB1,CTNNB1,CXCL10,CYP26B1,PROX1,GPC1,HOXD10,TBX1,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0048645	0.08	0.97	4	56	animal organ formation	BP	0.63782	CTNNB1,BMP7,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0032233	0.08	0.97	4	56	positive regulation of actin filament bundle assembly	BP	0.63782	SFRP1,PPM1F,MTOR,ARHGEF15	turquoise	VSMC_M6
GO:0050796	0.08	0.96	7	127	regulation of insulin secretion	BP	0.63782	SYBU,EPHA5,IL6,SNAP25,SFRP1,SSTR5,TRPM2	turquoise	VSMC_M6
GO:0003341	0.09	0.97	6	103	cilium movement	BP	0.63782	CFAP100,SLC22A16,CFAP54,RGN,TTLL6,ATP1A4	turquoise	VSMC_M6
GO:0072163	0.09	0.97	5	79	mesonephric epithelium development	BP	0.63782	CTNNB1,SFRP1,BMP7,KIF26B,GREB1L	turquoise	VSMC_M6
GO:0072164	0.09	0.97	5	79	mesonephric tubule development	BP	0.63782	CTNNB1,SFRP1,BMP7,KIF26B,GREB1L	turquoise	VSMC_M6
GO:0050790	0.09	0.93	64	1823	regulation of catalytic activity	BP	0.63782	TNFRSF11A,IL23A,FLT4,DENND3,PDGFB,KDR,SYK,EPHA5,NDUFA4,ARHGAP25,C5,KIAA1147,RASIP1,PIK3CG,FGD5,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,TIE1,P2RY6,SFRP1,RASGRP3,HHEX,SOX7,CXCL10,PPP1R16B,PLCB2,SNCA,HYAL2,LAPTM5,CD86,ERN1,BMP7,IGFBP3,PROX1,OAZ3,ACE,LTF,ARHGAP27,LPAR2,AGFG2,RGN,SELE,FGF23,PPM1F,PPP1R1B,ARHGEF9,MTOR,ARHGEF15,NOTCH1,S1PR1,SH2D3C,CDH3,ALOX12,PRSS22,PMAIP1,RELN,ALKAL1,NMUR1,NUCB1,PKIB,CCR7	turquoise	VSMC_M6
GO:0051963	0.09	0.97	5	79	regulation of synapse assembly	BP	0.63782	MDGA1,LRRC4B,GPC6,SNCA,ABI3	turquoise	VSMC_M6
GO:0032677	0.09	0.97	4	56	regulation of interleukin-8 production	BP	0.63782	SYK,IL6,HYAL2,TLR7	turquoise	VSMC_M6
GO:0042098	0.09	0.96	7	127	T cell proliferation	BP	0.63782	IL23A,SYK,IL6,PIK3CG,CTNNB1,CD86,CCDC88B	turquoise	VSMC_M6
GO:0060048	0.09	0.97	6	103	cardiac muscle contraction	BP	0.63782	KCNN2,PIK3CG,CXCR4,MTOR,DSC2,PDE4B	turquoise	VSMC_M6
GO:0051341	0.09	0.97	5	79	regulation of oxidoreductase activity	BP	0.63782	NDUFA4,SNCA,RGN,FGF23,CDH3	turquoise	VSMC_M6
GO:0070301	0.09	0.97	5	79	cellular response to hydrogen peroxide	BP	0.63782	IL18RAP,IL6,ERN1,ENDOG,TRPM2	turquoise	VSMC_M6
GO:0051493	0.09	0.95	19	457	regulation of cytoskeleton organization	BP	0.63782	CELSR1,EPHA5,SPTBN4,MAP6,SFRP1,SNCA,ESAM,PROX1,BAIAP2L1,PPM1F,MTOR,ABI3,ARHGEF15,S1PR1,CDH5,KANK3,SHANK3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0043281	0.09	0.96	8	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	0.63782	SYK,PPARG,SOX7,SNCA,LAPTM5,PPM1F,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0030029	0.09	0.94	26	662	actin filament-based process	BP	0.63783	KCNN2,CELSR1,FRMD3,THSD7A,EPHA5,ARHGAP25,FGD5,SPTBN4,SFRP1,NRAP,ESAM,PROX1,SELE,BAIAP2L1,PPM1F,MTOR,ABI3,ARHGEF15,DSC2,PDE4B,S1PR1,PDLIM1,KANK3,SHANK3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0051492	0.09	0.97	5	80	regulation of stress fiber assembly	BP	0.64827	SFRP1,PPM1F,MTOR,ARHGEF15,S1PR1	turquoise	VSMC_M6
GO:0006919	0.09	0.97	4	57	activation of cysteine-type endopeptidase activity involved in apoptotic process	BP	0.64827	PPARG,SNCA,LAPTM5,PMAIP1	turquoise	VSMC_M6
GO:0033135	0.09	0.96	6	104	regulation of peptidyl-serine phosphorylation	BP	0.64827	IL6,TGFB1,SPTBN4,SNCA,PPM1F,SH2D3C	turquoise	VSMC_M6
GO:0036294	0.09	0.96	7	129	cellular response to decreased oxygen levels	BP	0.64827	SFRP1,CD34,BMP7,MTOR,NOTCH1,ENDOG,PMAIP1	turquoise	VSMC_M6
GO:0032637	0.09	0.97	4	57	interleukin-8 production	BP	0.64827	SYK,IL6,HYAL2,TLR7	turquoise	VSMC_M6
GO:0006606	0.09	0.96	7	129	protein import into nucleus	BP	0.64977	SYK,TGFB1,CD36,HYAL2,NOTCH1,CDH1,MMP12	turquoise	VSMC_M6
GO:0034764	0.09	0.96	8	155	positive regulation of transmembrane transport	BP	0.65113	NDUFA4,P2RY6,CXCL10,SNCA,RGN,CRACR2A,RELN,SHANK3	turquoise	VSMC_M6
GO:0001952	0.09	0.96	6	105	regulation of cell-matrix adhesion	BP	0.65757	KDR,SFRP1,CD36,PPM1F,MMP12,CCR7	turquoise	VSMC_M6
GO:0001823	0.09	0.97	5	81	mesonephros development	BP	0.66455	CTNNB1,SFRP1,BMP7,KIF26B,GREB1L	turquoise	VSMC_M6
GO:0032355	0.09	0.96	6	105	response to estradiol	BP	0.66635	TGFB1,HTR5A,CTNNB1,SFRP1,BMP7,ENDOG	turquoise	VSMC_M6
GO:0097696	0.09	0.96	6	105	receptor signaling pathway via STAT	BP	0.66706	IL23A,IL6,PPARG,TGFB1,TNFRSF18,NOTCH1	turquoise	VSMC_M6
GO:0000271	0.09	0.97	4	58	polysaccharide biosynthetic process	BP	0.66736	PDGFB,TGFB1,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0051209	0.09	0.97	5	82	release of sequestered calcium ion into cytosol	BP	0.67052	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0051961	0.09	0.96	6	106	negative regulation of nervous system development	BP	0.67348	IL6,CTNNB1,BMP7,SEMA6B,NOTCH1,LHX2	turquoise	VSMC_M6
GO:0015837	0.09	0.97	4	58	amine transport	BP	0.6754	SYT17,SLC22A16,SNCA,SNCG	turquoise	VSMC_M6
GO:0008285	0.09	0.94	22	548	negative regulation of cell population proliferation	BP	0.67743	IL6,DLL1,NOS3,PPARG,TGFB1,CTNNB1,SFRP1,ATP8A2,SOX7,INPP5D,EAF2,CD86,COL18A1,BMP7,IGFBP3,PROX1,RGN,NPR1,SSTR5,NOTCH1,CDH5,GNA12	turquoise	VSMC_M6
GO:0019827	0.09	0.96	6	106	stem cell population maintenance	BP	0.67743	DLL1,CTNNB1,SFRP1,BMP7,PROX1,NOTCH1	turquoise	VSMC_M6
GO:0043112	0.10	0.96	7	131	receptor metabolic process	BP	0.68219	SYK,TGFB1,SNAP25,CD36,SNCA,LAPTM5,SELE	turquoise	VSMC_M6
GO:0035303	0.10	0.96	6	106	regulation of dephosphorylation	BP	0.68248	TGFB1,PPP1R16B,RGN,PPP1R1B,MTOR,CDH5	turquoise	VSMC_M6

GO:0030856	0.10	0.96	6	106	regulation of epithelial cell differentiation	BP	0.68495	NOTCH4,DLL1,CTNNB1,PRKCH,NOTCH1,CDH5	turquoise	VSMC_M6
GO:0110053	0.10	0.95	11	237	regulation of actin filament organization	BP	0.68546	SPTBN4,SFRP1,ESAM,BAIAP2L1,PPM1F,MTOR,ARHGEF15,S1PR1,KANK3,SHANK3,CCR7	turquoise	VSMC_M6
GO:0042593	0.10	0.95	9	183	glucose homeostasis	BP	0.68546	SYBU,ADGRF5,EPHA5,IL6,PPARG,ERN1,SSTR5,ENDOG,NMB	turquoise	VSMC_M6
GO:0060411	0.10	0.97	4	59	cardiac septum morphogenesis	BP	0.68574	BMP7,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0002700	0.10	0.96	6	106	regulation of production of molecular mediator of immune response	BP	0.68829	IL6,TGFB1,CD36,HFE,LAPTM5,CD86	turquoise	VSMC_M6
GO:0051283	0.10	0.96	5	83	negative regulation of sequestering of calcium ion	BP	0.69118	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0033500	0.10	0.95	9	184	carbohydrate homeostasis	BP	0.69682	SYBU,ADGRF5,EPHA5,IL6,PPARG,ERN1,SSTR5,ENDOG,NMB	turquoise	VSMC_M6
GO:0090559	0.10	0.97	4	59	regulation of membrane permeability	BP	0.69841	RASIP1,LAPTM5,MTOR,PMAIP1	turquoise	VSMC_M6
GO:0051170	0.10	0.96	7	132	import into nucleus	BP	0.69841	SYK,TGFB1,CD36,HYAL2,NOTCH1,CDH1,MMP12	turquoise	VSMC_M6
GO:0001838	0.10	0.96	6	107	embryonic epithelial tube formation	BP	0.69841	CELSR1,TGFB1,CTNNB1,SFRP1,BMP7,LHX2	turquoise	VSMC_M6
GO:1904375	0.10	0.96	6	107	regulation of protein localization to cell periphery	BP	0.70023	TGFB1,GPC6,NKD2,PRKCH,ABI3,GBP1	turquoise	VSMC_M6
GO:0006887	0.10	0.95	12	266	exocytosis	BP	0.70167	SYT17,SYK,PIK3CG,EXOC3L2,CD177,SYN2,SNAP25,SNCA,NKD2,SYTL5,NOTCH1,EXOC3L1	turquoise	VSMC_M6
GO:0009582	0.10	0.96	5	83	detection of abiotic stimulus	BP	0.70362	CXCR4,CTNNB1,ATP8A2,ANO3,GNGT2	turquoise	VSMC_M6
GO:0120035	0.10	0.94	21	524	regulation of plasma membrane bounded cell projection organization	BP	0.70362	ENPP2,BCL11A,MAP6,SNAP25,SFRP1,PRAG1,ATP8A2,PPP1R16B,BMP7,MTOR,ABI3,ISLR2,SARM1,SEMA6B,RELN,ALKAL1,SHANK3,TRPM2,CCR7,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0005976	0.10	0.96	5	83	polysaccharide metabolic process	BP	0.70583	PDGFB,TGFB1,PCDH12,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0048704	0.10	0.96	5	83	embryonic skeletal system morphogenesis	BP	0.70583	CTNNB1,COL2A1,BMP7,HOXD10,TBX1	turquoise	VSMC_M6
GO:0018209	0.10	0.94	12	267	peptidyl-serine modification	BP	0.70835	PDGFB,SYK,IL6,TGFB1,SPTBN4,SNCA,ERN1,PPM1F,PRKCH,MTOR,MAST1,SH2D3C	turquoise	VSMC_M6
GO:0048738	0.10	0.95	9	186	cardiac muscle tissue development	BP	0.70854	DLL1,TGFB1,ADAMTS9,NRAP,BMP7,PROX1,MTOR,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0051282	0.10	0.96	5	84	regulation of sequestering of calcium ion	BP	0.70903	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0098727	0.10	0.96	6	108	maintenance of cell number	BP	0.70966	DLL1,CTNNB1,SFRP1,BMP7,PROX1,NOTCH1	turquoise	VSMC_M6
GO:0072657	0.10	0.94	19	466	protein localization to membrane	BP	0.71579	RAB38,GRIP2,TGFB1,SPTBN4,GPC6,SNAP25,REEP1,MAPK10,NKD2,GPC1,TSPAN15,ATP13A1,PRKCH,TSPAN14,ABI3,GBP1,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0022898	0.10	0.95	9	186	regulation of transmembrane transporter activity	BP	0.71837	NDUFA4,P2RY6,SNCA,RGN,CRACR2A,PDE4B,RELN,SHANK3,FXYD6	turquoise	VSMC_M6
GO:0055067	0.10	0.96	6	108	monovalent inorganic cation homeostasis	BP	0.71837	RAB38,EDNRB,SLC4A5,ATP6V0D2,NPR1,ATP1A4	turquoise	VSMC_M6
GO:0002449	0.10	0.95	8	159	lymphocyte mediated immunity	BP	0.71924	IL23A,IL18RAP,IL6,C5,CTSC,TGFB1,HFE,INPP5D	turquoise	VSMC_M6
GO:0009581	0.10	0.96	5	84	detection of external stimulus	BP	0.72646	CXCR4,CTNNB1,ATP8A2,ANO3,GNGT2	turquoise	VSMC_M6
GO:0014074	0.10	0.96	6	109	response to purine-containing compound	BP	0.72654	PIK3CG,P2RY6,P2RY2,PDE2A,HCN1,TRPM2	turquoise	VSMC_M6
GO:0009408	0.11	0.96	5	84	response to heat	BP	0.73312	NOS3,CXCL10,CD34,MTOR,TRPM2	turquoise	VSMC_M6
GO:0003205	0.11	0.95	7	135	cardiac chamber development	BP	0.73698	TGFB1,PDE2A,BMP7,PROX1,TBX1,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0006814	0.11	0.95	8	161	sodium ion transport	BP	0.73698	SLC6A6,SPTBN4,SLC4A11,SLC4A5,HCN1,ATP1A4,TRPM2,FXYD6	turquoise	VSMC_M6
GO:0021954	0.11	0.97	4	61	central nervous system neuron development	BP	0.73698	NOVA2,SPTBN4,B4GALT6,LHX6	turquoise	VSMC_M6
GO:0032268	0.11	0.92	63	1819	regulation of cellular protein metabolic process	BP	0.73698	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,IREB2,KDR,SYK,IL6,C5,RASIP1,PIK3CG,KDM4D,CTSC,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,SFRP1,CD36,KIRREL2,PRR5L,KLKB1,HHEX,SOX7,THBS4,PPP1R16B,SNCA,HYAL2,NKD2,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,ACE,LTF,TBX1,RGN,FGF23,PPM1F,PPP1R1B,MTOR,TNFRSF18,SH2D3C,CDH5,ALOX12,PRSS22,PMAIP1,RELN,ALKAL1,GNA12,PKIB,CCR7,MGAT3	turquoise	VSMC_M6
GO:0045862	0.11	0.94	13	297	positive regulation of proteolysis	BP	0.73698	SYK,CTSC,PPARG,KLKB1,SOX7,SNCA,NKD2,LAPTM5,RGN,PPM1F,ALOX12,PRSS22,PMAIP1	turquoise	VSMC_M6
GO:0048525	0.11	0.97	4	61	negative regulation of viral process	BP	0.73698	ISG20,PROX1,LTF,TRIM62	turquoise	VSMC_M6
GO:0009166	0.11	0.97	4	61	nucleotide catabolic process	BP	0.73698	PDE2A,PDE4B,SARM1,NUDT4B	turquoise	VSMC_M6
GO:0002708	0.11	0.97	4	61	positive regulation of lymphocyte mediated immunity	BP	0.73698	IL23A,IL18RAP,IL6,TGFB1	turquoise	VSMC_M6
GO:0046889	0.11	0.96	4	61	positive regulation of lipid biosynthetic process	BP	0.73698	ADGRF5,RAB38,RGN,MTOR	turquoise	VSMC_M6
GO:0031623	0.11	0.96	5	85	receptor internalization	BP	0.73698	SYK,SNAP25,CD36,SNCA,SELE	turquoise	VSMC_M6
GO:1902903	0.11	0.94	14	327	regulation of supramolecular fiber organization	BP	0.73698	SPTBN4,SFRP1,SNCA,ESAM,PROX1,BAIAP2L1,PPM1F,MTOR,ARHGEF15,S1PR1,CDH5,KANK3,SHANK3,CCR7	turquoise	VSMC_M6
GO:0021782	0.11	0.96	5	86	glial cell development	BP	0.73698	IL6,DLL1,ITGB4,PRDM8,B4GALT6	turquoise	VSMC_M6
GO:1904019	0.11	0.96	5	86	epithelial cell apoptotic process	BP	0.73698	KDR,IL6,PIK3CG,MTOR,CDH5	turquoise	VSMC_M6
GO:2000177	0.11	0.96	4	62	regulation of neural precursor cell proliferation	BP	0.73698	CTNNB1,PROX1,NOTCH1,LHX2	turquoise	VSMC_M6
GO:0002703	0.11	0.95	7	136	regulation of leukocyte mediated immunity	BP	0.73698	IL23A,IL18RAP,SYK,IL6,CD177,TGFB1,HFE	turquoise	VSMC_M6
GO:0045069	0.11	0.96	4	62	regulation of viral genome replication	BP	0.73698	ISG20,PROX1,LTF,NOTCH1	turquoise	VSMC_M6
GO:0014020	0.11	0.96	5	86	primary neural tube formation	BP	0.73698	CELSR1,TGFB1,SFRP1,BMP7,LHX2	turquoise	VSMC_M6
GO:0019217	0.11	0.96	4	62	regulation of fatty acid metabolic process	BP	0.73698	PPARG,SNCA,RGN,MTOR	turquoise	VSMC_M6
GO:0051208	0.11	0.96	5	87	sequestering of calcium ion	BP	0.73698	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0032640	0.11	0.95	6	111	tumor necrosis factor production	BP	0.73698	IL23A,SYK,IL6,CD36,CD34,LTF	turquoise	VSMC_M6
GO:0032680	0.11	0.95	6	111	regulation of tumor necrosis factor production	BP	0.73698	IL23A,SYK,IL6,CD36,CD34,LTF	turquoise	VSMC_M6
GO:0061061	0.11	0.93	20	504	muscle structure development	BP	0.73698	MEGF10,PDGFB,DLL1,TGFB1,EDNRB,CTNNB1,CXCL10,CYP26B1,NRAP,NFATC2,IGFBP3,PROX1,GPC1,HOXD10,TBX1,MTOR,TMEM204,NOTCH1,S1PR1,PDLIM1	turquoise	VSMC_M6
GO:0001649	0.11	0.94	9	190	osteoblast differentiation	BP	0.73698	IL6,PPARG,CTNNB1,SFRP1,BMP7,LTF,FGF23,NOTCH1,BAMBI	turquoise	VSMC_M6
GO:0071356	0.11	0.95	8	163	cellular response to tumor necrosis factor	BP	0.73698	TNFRSF11A,SYK,SFRP1,HYAL2,LAPTM5,PLVAP,TNFRSF18,GBP1	turquoise	VSMC_M6
GO:0007584	0.11	0.95	7	137	response to nutrient	BP	0.7383	PPARG,SFRP1,CXCL10,CYP26B1,BMP7,FGF23,MTOR	turquoise	VSMC_M6
GO:0009266	0.11	0.95	7	137	response to temperature stimulus	BP	0.73846	NOS3,CXCR4,CXCL10,ANO3,CD34,MTOR,TRPM2	turquoise	VSMC_M6
GO:0043069	0.11	0.92	26	681	negative regulation of programmed cell death	BP	0.73932	FLT4,KDR,IL6,PIK3CG,DLL1,NOS3,EDNRB,CTNNB1,SFRP1,COL2A1,SNCA,LAPTM5,BMP7,FANK1,PRAME,LTF,TBX1,RGN,PRKCH,MTOR,TNFRSF18,NOTCH1,CDH5,ALOX12,VSTM2L,CCR7	turquoise	VSMC_M6
GO:0021987	0.12	0.96	5	87	cerebral cortex development	BP	0.74196	MDGA1,CTNNB1,LHX2,LHX6,RELN	turquoise	VSMC_M6
GO:0060996	0.12	0.96	5	87	dendritic spine development	BP	0.74343	CTNND2,MTOR,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0042475	0.12	0.96	4	63	odontogenesis of dentin-containing tooth	BP	0.75072	CTNNB1,NKX2-3,BMP7,TBX1	turquoise	VSMC_M6
GO:0098586	0.12	0.96	4	63	cellular response to virus	BP	0.75175	IL6,CXCL10,TLR7,MMP12	turquoise	VSMC_M6
GO:0051781	0.12	0.96	4	63	positive regulation of cell division	BP	0.75195	PDGFB,TGFB1,THBS4,SSTR5	turquoise	VSMC_M6
GO:0001764	0.12	0.95	6	113	neuron migration	BP	0.75313	CELSR1,MDGA1,CXCR4,CTNNB1,LHX6,RELN	turquoise	VSMC_M6
GO:0050807	0.12	0.94	8	165	regulation of synapse organization	BP	0.75318	MDGA1,LRRC4B,GPC6,SNCA,ABI3,ARHGEF15,RELN,SHANK3	turquoise	VSMC_M6

GO:0002440	0.12	0.95	7	138	production of molecular mediator of immune response	BP	0.75318	IL6,TGFB1,CD36,HFE,LAPTM5,CD86,SLAMF9	turquoise	VSMC_M6
GO:0003279	0.12	0.95	5	88	cardiac septum development	BP	0.75589	PDE2A,BMP7,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0051146	0.12	0.94	10	220	striated muscle cell differentiation	BP	0.75589	DLL1,TGFB1,CXCL10,CYP26B1,NRAP,NFATC2,PROX1,TBX1,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0090090	0.12	0.95	6	113	negative regulation of canonical Wnt signaling pathway	BP	0.76027	ANKRD6,SFRP1,NOTUM,NKD2,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0001736	0.12	0.96	4	64	establishment of planar polarity	BP	0.76784	CELSR1,ANKRD6,GPC6,SFRP1	turquoise	VSMC_M6
GO:0007164	0.12	0.96	4	64	establishment of tissue polarity	BP	0.76784	CELSR1,ANKRD6,GPC6,SFRP1	turquoise	VSMC_M6
GO:0048736	0.12	0.94	7	140	appendage development	BP	0.76784	ITGB4,CTNNB1,CYP26B1,COL2A1,BMP7,HOXD10,NOTCH1	turquoise	VSMC_M6
GO:0060173	0.12	0.94	7	140	limb development	BP	0.76784	ITGB4,CTNNB1,CYP26B1,COL2A1,BMP7,HOXD10,NOTCH1	turquoise	VSMC_M6
GO:0031344	0.12	0.92	21	538	regulation of cell projection organization	BP	0.76786	ENPP2,BCL11A,MAP6,SNAP25,SFRP1,PRAG1,ATP8A2,PPP1R16B,BMP7,MTOR,ABI3,ISLR2,SARM1,SEMA6B,RELN,ALKAL1,SHANK3,TRPM2,CCR7,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0030641	0.12	0.96	4	64	regulation of cellular pH	BP	0.77093	RAB38,SLC4A5,ATP6V0D2,ATP1A4	turquoise	VSMC_M6
GO:0002824	0.12	0.96	4	64	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	0.77585	IL23A,IL6,TGFB1,NFKBID	turquoise	VSMC_M6
GO:0006576	0.12	0.96	4	64	cellular biogenic amine metabolic process	BP	0.77832	SNCA,OAZ3,AGMAT,NPR1	turquoise	VSMC_M6
GO:0045055	0.13	0.94	8	167	regulated exocytosis	BP	0.78643	SYT17,SYK,PIK3CG,CD177,SYN2,SNAP25,SNCA,NOTCH1	turquoise	VSMC_M6
GO:0035107	0.13	0.95	6	115	appendage morphogenesis	BP	0.78782	CTNNB1,CYP26B1,COL2A1,BMP7,HOXD10,NOTCH1	turquoise	VSMC_M6
GO:0035108	0.13	0.95	6	115	limb morphogenesis	BP	0.78782	CTNNB1,CYP26B1,COL2A1,BMP7,HOXD10,NOTCH1	turquoise	VSMC_M6
GO:0007498	0.13	0.95	5	89	mesoderm development	BP	0.78902	ITGB4,TIE1,BMP7,TBX1,LHX2	turquoise	VSMC_M6
GO:0045893	0.13	0.91	44	1244	positive regulation of transcription, DNA-templated	BP	0.79247	NOTCH4,PDGFB,IL6,MAML3,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,ZIC2,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,LHX2,CDH1,MMP12,SOX17,PDLIM1,SOX18,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:1903508	0.13	0.91	44	1244	positive regulation of nucleic acid-templated transcription	BP	0.79247	NOTCH4,PDGFB,IL6,MAML3,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,ZIC2,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,LHX2,CDH1,MMP12,SOX17,PDLIM1,SOX18,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0072028	0.13	0.96	4	65	nephron morphogenesis	BP	0.79487	CTNNB1,BMP7,KIF26B,GREB1L	turquoise	VSMC_M6
GO:0006112	0.13	0.96	4	65	energy reserve metabolic process	BP	0.79615	ADGRF5,PCDH12,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0043068	0.13	0.92	17	422	positive regulation of programmed cell death	BP	0.79645	SYK,IL6,CTSC,PPARG,CTNNB1,SFRP1,SNCA,HYAL2,LAPTM5,INPP5D,BMP7,IGFBP3,FANK1,NOTCH1,ENDOG,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0051099	0.13	0.94	7	141	positive regulation of binding	BP	0.79645	KDM4D,PPARG,TGFB1,CTNNB1,HFE,ACE,BAMBI	turquoise	VSMC_M6
GO:1904035	0.13	0.96	4	65	regulation of epithelial cell apoptotic process	BP	0.79645	KDR,IL6,MTOR,CDH5	turquoise	VSMC_M6
GO:0007368	0.13	0.95	5	90	determination of left/right symmetry	BP	0.79645	DLL1,TBX1,NOTCH1,SOX17,SOX18	turquoise	VSMC_M6
GO:1902680	0.13	0.90	44	1246	positive regulation of RNA biosynthetic process	BP	0.7986	NOTCH4,PDGFB,IL6,MAML3,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,ZIC2,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,LHX2,CDH1,MMP12,SOX17,PDLIM1,SOX18,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0018193	0.13	0.91	36	997	peptidyl-amino acid modification	BP	0.7986	IL23A,FLT4,ENPP2,PDGFB,KDR,SYK,EPHA5,IL6,BCL11A,KDM4D,TGFB1,CTNNB1,SPTBN4,TIE1,SFRP1,CD36,THBS4,SNCA,HYAL2,PECAM1,ERN1,BMP7,SRMS,ART4,ACE,ST6GAL1,PPM1F,PRKCH,MTOR,TTLL6,MAST1,MATK,TNFRSF18,SH2D3C,RELN,ALKAL1	turquoise	VSMC_M6
GO:1903076	0.13	0.95	5	90	regulation of protein localization to plasma membrane	BP	0.80504	TGFB1,NKD2,PRKCH,ABI3,GBP1	turquoise	VSMC_M6
GO:0071453	0.13	0.94	7	142	cellular response to oxygen levels	BP	0.80523	SFRP1,CD34,BMP7,MTOR,NOTCH1,ENDOG,PMAIP1	turquoise	VSMC_M6
GO:0030178	0.13	0.94	7	142	negative regulation of Wnt signaling pathway	BP	0.80592	BARX1,ANKRD6,SFRP1,NOTUM,NKD2,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0051899	0.13	0.95	4	66	membrane depolarization	BP	0.80602	KDR,GOT1,BEST2,ALOX12	turquoise	VSMC_M6
GO:1903532	0.13	0.93	9	196	positive regulation of secretion by cell	BP	0.81031	TNFRSF11A,SYBU,SYK,CD177,TGFB1,SNCA,HFE,TRPM2,NMB	turquoise	VSMC_M6
GO:0043066	0.13	0.91	25	662	negative regulation of apoptotic process	BP	0.81031	FLT4,KDR,IL6,PIK3CG,DLL1,NOS3,EDNRB,CTNNB1,SFRP1,COL2A1,SNCA,BMP7,FANK1,PRAME,LTF,TBX1,RGN,PRKCH,MTOR,TNFRSF18,NOTCH1,CDH5,ALOX12,VSTM2L,CCR7	turquoise	VSMC_M6
GO:0032272	0.13	0.95	4	66	negative regulation of protein polymerization	BP	0.81269	SPTBN4,SNCA,CDH5,KANK3	turquoise	VSMC_M6
GO:0071868	0.13	0.95	4	66	cellular response to monoamine stimulus	BP	0.81365	HTR5A,SNCA,PDE4B,NSG2	turquoise	VSMC_M6
GO:0071870	0.13	0.95	4	66	cellular response to catecholamine stimulus	BP	0.81365	HTR5A,SNCA,PDE4B,NSG2	turquoise	VSMC_M6
GO:0048167	0.13	0.94	7	143	regulation of synaptic plasticity	BP	0.81365	SNAP25,CNTN4,SNCA,SHANK2,GRID2IP,RELN,SHANK3	turquoise	VSMC_M6
GO:0002821	0.13	0.95	4	66	positive regulation of adaptive immune response	BP	0.81365	IL23A,IL6,TGFB1,NFKBID	turquoise	VSMC_M6
GO:0090596	0.13	0.93	9	198	sensory organ morphogenesis	BP	0.81365	DLL1,CTNNB1,ATP8A2,CYP26B1,COL2A1,BMP7,PROX1,TBX1,HCN1	turquoise	VSMC_M6
GO:0016042	0.14	0.93	10	225	lipid catabolic process	BP	0.81365	ENPP2,PIK3CG,RARRES2,CYP26B1,PLCB2,LGALS12,FGF23,MTOR,HRASLS,SCARF1	turquoise	VSMC_M6
GO:0071560	0.14	0.93	9	199	cellular response to transforming growth factor beta stimulus	BP	0.81365	PPARG,TGFB1,PDE2A,SFRP1,GOT1,HYAL2,LRG1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0048592	0.14	0.94	6	118	eye morphogenesis	BP	0.81365	DLL1,CTNNB1,ATP8A2,BMP7,PROX1,HCN1	turquoise	VSMC_M6
GO:1901019	0.14	0.95	4	67	regulation of calcium ion transmembrane transporter activity	BP	0.81365	P2RY6,RGN,CRACR2A,PDE4B	turquoise	VSMC_M6
GO:0001841	0.14	0.94	5	92	neural tube formation	BP	0.81365	CELSR1,TGFB1,SFRP1,BMP7,LHX2	turquoise	VSMC_M6
GO:0008625	0.14	0.95	4	67	extrinsic apoptotic signaling pathway via death domain receptors	BP	0.81365	NOS3,TMC8,SFRP1,PMAIP1	turquoise	VSMC_M6
GO:0031334	0.14	0.93	9	199	positive regulation of protein-containing complex assembly	BP	0.81365	SYK,RASIP1,TGFB1,CD36,SNCA,BAIAP2L1,MTOR,CDH5,CCR7	turquoise	VSMC_M6
GO:0071466	0.14	0.94	5	92	cellular response to xenobiotic stimulus	BP	0.81365	CXCR4,CYP26B1,GSTA4,PPM1F,PDE4B	turquoise	VSMC_M6
GO:0002706	0.14	0.94	5	92	regulation of lymphocyte mediated immunity	BP	0.81365	IL23A,IL18RAP,IL6,TGFB1,HFE	turquoise	VSMC_M6

GO:0060047	0.14	0.93	8	172	heart contraction	BP	0.81365	KCNN2,PIK3CG,CXCR4,SPTBN4,ACE,MTOR,DSC2,PDE4B	turquoise	VSMC_M6
GO:0006936	0.14	0.92	11	256	muscle contraction	BP	0.81365	KCNN2,PIK3CG,GRIP2,CXCR4,EDNRB,ATP8A2,RCSD1,MTOR,DSC2,PDE4B,NMUR1	turquoise	VSMC_M6
GO:0010941	0.14	0.89	43	1223	regulation of cell death	BP	0.81447	FLT4,KDR,SYK,IL6,PIK3CG,DLL1,CTSC,SLC6A6,NOS3,PPARG,CXCR4,EDNRB,CTNNB1,TMC8,SFRP1,CD36,CXCL10,COL2A1,SNCA,HYAL2,LAPTM5,INPP5D,CD34,BMP7,IGFBP3,FANK1,PRAME,LTF,TBX1,RGN,PRKCH,SNCG,MTOR,SARM1,TNFRSF18,NOTCH1,ENDOG,CDH5,ALOX12,PMAIP1,VSTM2L,TRPM2,CCR7	turquoise	VSMC_M6
GO:0060294	0.14	0.95	4	68	cilium movement involved in cell motility	BP	0.81494	SLC22A16,CFAP54,RGN,ATP1A4	turquoise	VSMC_M6
GO:0043087	0.14	0.92	12	285	regulation of GTPase activity	BP	0.8193	EPHA5,ARHGAP25,RASIP1,FGD5,SFRP1,RASGRP3,ARHGAP27,RGN,MTOR,ARHGEF15,S1PR1,CCR7	turquoise	VSMC_M6
GO:0001704	0.14	0.94	5	93	formation of primary germ layer	BP	0.8193	ITGB4,CTNNB1,SOX7,BMP7,SOX17	turquoise	VSMC_M6
GO:0006470	0.14	0.92	10	228	protein dephosphorylation	BP	0.8193	TGFB1,PPP1R16B,PTPRE,PALD1,RGN,PPM1F,PPP1R1B,MTOR,CDH5,PPP1R3C	turquoise	VSMC_M6
GO:0061008	0.14	0.94	6	119	hepaticobiliary system development	BP	0.8193	IL6,HFE,PROX1,RGN,NOTCH1,SOX17	turquoise	VSMC_M6
GO:0051246	0.14	0.89	66	1953	regulation of protein metabolic process	BP	0.8193	TNFRSF11A,IL23A,FLT4,ENPP2,PDGFB,MOB3B,IREB2,KDR,SYK,IL6,C5,RASIP1,PIK3CG,KDM4D,CTSC,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,SFRP1,CD36,KIRREL2,PRR5L,KLKB1,HHEX,SOX7,THBS4,PPP1R16B,SNCA,HYAL2,NKD2,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,OAZ3,ACE,LTF,TBX1,RGN,FGF23,PPM1F,PPP1R1B,MTOR,TNFRSF18,SH2D3C,CDH1,CDH5,ALOX12,PRSS22,PMAIP1,SOX17,RELN,ALKAL1,GNA12,PKIB,CCR7,MGAT3	turquoise	VSMC_M6
GO:0035567	0.14	0.95	4	68	non-canonical Wnt signaling pathway	BP	0.81991	CELSR1,ANKRD6,GPC6,SFRP1	turquoise	VSMC_M6
GO:0046330	0.14	0.95	4	68	positive regulation of JNK cascade	BP	0.82327	FLT4,ANKRD6,CRACR2A,CCR7	turquoise	VSMC_M6
GO:0006638	0.14	0.94	5	93	neutral lipid metabolic process	BP	0.82327	PIK3CG,NKX2-3,SNCA,MTTP,RGN	turquoise	VSMC_M6
GO:0048638	0.14	0.92	11	257	regulation of developmental growth	BP	0.82327	SYT17,BCL11A,DLL1,CXCR4,SPTBN4,ATP8A2,PROX1,MTOR,ISLR2,SEMA6B,NOTCH1	turquoise	VSMC_M6
GO:0050792	0.14	0.94	6	119	regulation of viral process	BP	0.82668	CXCR4,ISG20,PROX1,LTF,NOTCH1,TRIM62	turquoise	VSMC_M6
GO:0008544	0.14	0.92	9	201	epidermis development	BP	0.82699	DLL1,CTNNB1,CYP26B1,LAMC2,PRKCH,NOTCH1,LHX2,CDH3,SOX18	turquoise	VSMC_M6
GO:0001959	0.14	0.94	6	119	regulation of cytokine-mediated signaling pathway	BP	0.82737	SYK,IL6,PPARG,CXCR4,LAPTM5,MMP12	turquoise	VSMC_M6
GO:0051092	0.14	0.94	6	119	positive regulation of NF-kappaB transcription factor activity	BP	0.82746	TNFRSF11A,IL18RAP,CD36,LTF,PRKCH,TRIM62	turquoise	VSMC_M6
GO:0050954	0.14	0.93	6	120	sensory perception of mechanical stimulus	BP	0.82938	CXCR4,SPTBN4,COL2A1,TBX1,PKHD1L1,GRAP	turquoise	VSMC_M6
GO:0007015	0.14	0.91	15	373	actin filament organization	BP	0.8295	ARHGAP25,SPTBN4,SFRP1,NRAP,ESAM,PROX1,BAIAP2L1,PPM1F,MTOR,ARHGEF15,S1PR1,PDLIM1,KANK3,SHANK3,CCR7	turquoise	VSMC_M6
GO:0009410	0.14	0.91	13	314	response to xenobiotic stimulus	BP	0.82964	CXCR4,SFRP1,CYP26B1,GSTA4,SNCA,NFATC2,COL18A1,MGST1,PPM1F,PDE4B,CDH3,CDH1,GNA12	turquoise	VSMC_M6
GO:0044262	0.15	0.92	10	229	cellular carbohydrate metabolic process	BP	0.83467	P2RY6,PCDH12,SOGA1,GOT1,SNCA,RGN,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0007422	0.15	0.95	4	69	peripheral nervous system development	BP	0.8355	ITGB4,EDNRB,GPC1,HOXD10	turquoise	VSMC_M6
GO:1990138	0.15	0.93	7	147	neuron projection extension	BP	0.83642	SYT17,BCL11A,CXCR4,CTNNB1,ISLR2,SEMA6B,LHX2	turquoise	VSMC_M6
GO:0009913	0.15	0.93	6	120	epidermal cell differentiation	BP	0.83658	DLL1,CTNNB1,CYP26B1,PRKCH,NOTCH1,CDH3	turquoise	VSMC_M6
GO:0046683	0.15	0.94	5	94	response to organophosphorus	BP	0.84049	PIK3CG,P2RY6,P2RY2,PDE2A,HCN1	turquoise	VSMC_M6
GO:0097553	0.15	0.94	5	95	calcium ion transmembrane import into cytosol	BP	0.84381	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:1905475	0.15	0.93	7	147	regulation of protein localization to membrane	BP	0.84407	TGFB1,GPC6,NKD2,GPC1,PRKCH,ABI3,GBP1	turquoise	VSMC_M6
GO:0071867	0.15	0.95	4	69	response to monoamine	BP	0.84417	HTR5A,SNCA,PDE4B,NSG2	turquoise	VSMC_M6
GO:0071869	0.15	0.95	4	69	response to catecholamine	BP	0.84417	HTR5A,SNCA,PDE4B,NSG2	turquoise	VSMC_M6
GO:0014032	0.15	0.95	4	69	neural crest cell development	BP	0.84472	EDNRB,BMP7,TBX1,SEMA6B	turquoise	VSMC_M6
GO:0032760	0.15	0.95	4	69	positive regulation of tumor necrosis factor production	BP	0.84495	IL23A,SYK,IL6,CD36	turquoise	VSMC_M6
GO:1901292	0.15	0.95	4	69	nucleoside phosphate catabolic process	BP	0.84552	PDE2A,PDE4B,SARM1,NUDT4B	turquoise	VSMC_M6
GO:0050804	0.15	0.91	13	317	modulation of chemical synaptic transmission	BP	0.8485	SYBU,SLC6A6,SNAP25,CNTN4,SNCA,SHANK2,MCTP2,GRID2IP,SNCG,MTOR,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0060341	0.15	0.89	25	675	regulation of cellular localization	BP	0.85071	PARD6G,SYBU,SYK,EPHA5,TGFB1,CTNNB1,GPC6,P2RY6,CD36,PRR5L,CXCL10,SNCA,HYAL2,NKD2,HFE,GPC1,OAZ3,PPM1F,PRKCH,ABI3,GBP1,CDH3,CDH1,NUCB1,MGAT3	turquoise	VSMC_M6
GO:0061448	0.15	0.92	9	203	connective tissue development	BP	0.85296	PDGFB,TGFB1,CTNNB1,COL2A1,BMP1,HYAL2,CD34,BMP7,NOTCH1	turquoise	VSMC_M6
GO:2001236	0.15	0.93	6	121	regulation of extrinsic apoptotic signaling pathway	BP	0.85639	NOS3,TMC8,SFRP1,COL2A1,HYAL2,PMAIP1	turquoise	VSMC_M6
GO:0007420	0.15	0.90	22	587	brain development	BP	0.85828	MDGA1,EPHA5,DLL1,HTR5A,CXCR4,CTNNB1,SFRP1,ZIC2,CNTN4,BMP7,PROX1,MTOR,MAST1,SEMA6B,NOTCH1,S1PR1,LHX2,LHX6,CDH1,RELN,OLIG2,SHANK3	turquoise	VSMC_M6
GO:0032368	0.15	0.94	5	95	regulation of lipid transport	BP	0.85917	TNFRSF11A,ATP8A1,SYK,PPARG,ATP8A2	turquoise	VSMC_M6
GO:0099177	0.15	0.91	13	318	regulation of trans-synaptic signaling	BP	0.86059	SYBU,SLC6A6,SNAP25,CNTN4,SNCA,SHANK2,MCTP2,GRID2IP,SNCG,MTOR,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0097061	0.15	0.94	4	70	dendritic spine organization	BP	0.86322	CTNND2,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0022604	0.15	0.91	11	261	regulation of cell morphogenesis	BP	0.86534	ENPP2,SYT17,KDR,BCL11A,FGD5,CXCR4,PRAG1,PALMD,GBP1,RELN,BAMBI	turquoise	VSMC_M6
GO:0071559	0.15	0.92	9	205	response to transforming growth factor beta	BP	0.86797	PPARG,TGFB1,PDE2A,SFRP1,GOT1,HYAL2,LRG1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0030326	0.15	0.94	5	96	embryonic limb morphogenesis	BP	0.86887	CTNNB1,CYP26B1,BMP7,HOXD10,NOTCH1	turquoise	VSMC_M6
GO:0035113	0.15	0.94	5	96	embryonic appendage morphogenesis	BP	0.86887	CTNNB1,CYP26B1,BMP7,HOXD10,NOTCH1	turquoise	VSMC_M6
GO:0001776	0.15	0.94	4	70	leukocyte homeostasis	BP	0.8707	IL6,NKX2-3,PDE4B,PMAIP1	turquoise	VSMC_M6
GO:0006641	0.15	0.94	4	70	triglyceride metabolic process	BP	0.87131	PIK3CG,NKX2-3,MTTP,RGN	turquoise	VSMC_M6
GO:0055007	0.16	0.93	5	96	cardiac muscle cell differentiation	BP	0.87364	DLL1,TGFB1,NRAP,PROX1,MTOR	turquoise	VSMC_M6
GO:0030073	0.16	0.92	7	149	insulin secretion	BP	0.87904	SYBU,EPHA5,IL6,SNAP25,SFRP1,SSTR5,TRPM2	turquoise	VSMC_M6
GO:0055006	0.16	0.94	4	71	cardiac cell development	BP	0.8847	NRAP,PROX1,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0097306	0.16	0.94	4	71	cellular response to alcohol	BP	0.88633	CTNNB1,P2RY6,SFRP1,CDH1	turquoise	VSMC_M6
GO:0048598	0.16	0.90	18	469	embryonic morphogenesis	BP	0.88633	CELSR1,DLL1,ITGB4,TGFB1,CTNNB1,SFRP1,ATP8A2,SOX7,CYP26B1,COL2A1,BMP7,PROX1,HOXD10,TBX1,NOTCH1,LHX2,SOX17,SOX18	turquoise	VSMC_M6
GO:0106106	0.16	0.93	6	123	cold-induced thermogenesis	BP	0.88633	SYK,NOVA2,CXCR4,CD36,ESRRG,NOTCH1	turquoise	VSMC_M6
GO:0120161	0.16	0.93	6	123	regulation of cold-induced thermogenesis	BP	0.88633	SYK,NOVA2,CXCR4,CD36,ESRRG,NOTCH1	turquoise	VSMC_M6
GO:0098739	0.16	0.93	6	123	import across plasma membrane	BP	0.88633	SLC6A6,CD36,SLC39A8,HFE,ATP1A4,TRPM2	turquoise	VSMC_M6

GO:0040007	0.16	0.89	27	742	growth	BP	0.88633	SYT17,BCL11A,DLL1,TGFB1,CXCR4,CTNNB1,TMC8,SPTBN4,SFRP1,ATP8A2,HYAL2,EAF2,PROX1,PRAME,CDA,PPM1F,KIF26B,MTOR,NPR1,ISLR2,KIF26A,SEMA6B,NOTCH1,S1PR1,LHX2,SOX17,GNG4	turquoise	VSMC_M6
GO:0031099	0.16	0.92	7	150	regeneration	BP	0.88633	IL6,ANGPT2,HFE,RGN,NOTCH1,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0006970	0.16	0.94	4	71	response to osmotic stress	BP	0.88633	SLC4A11,TSC22D2,MAPK10,RCSD1	turquoise	VSMC_M6
GO:0032412	0.16	0.92	8	178	regulation of ion transmembrane transporter activity	BP	0.88633	NDUFA4,P2RY6,RGN,CRACR2A,PDE4B,RELN,SHANK3,FXYD6	turquoise	VSMC_M6
GO:0098659	0.16	0.94	4	71	inorganic cation import across plasma membrane	BP	0.88633	SLC39A8,HFE,ATP1A4,TRPM2	turquoise	VSMC_M6
GO:0099587	0.16	0.94	4	71	inorganic ion import across plasma membrane	BP	0.88633	SLC39A8,HFE,ATP1A4,TRPM2	turquoise	VSMC_M6
GO:0006766	0.16	0.94	4	71	vitamin metabolic process	BP	0.88633	CYP26B1,RGN,FGF23,RBP1	turquoise	VSMC_M6
GO:1901617	0.16	0.92	8	178	organic hydroxy compound biosynthetic process	BP	0.88633	IP6K3,OSBPL3,P2RY6,GOT1,SNCA,PROX1,CDH3,ALOX12	turquoise	VSMC_M6
GO:0099003	0.16	0.92	7	151	vesicle-mediated transport in synapse	BP	0.88633	GRIP2,SYN2,CTNNB1,SNAP25,MAPK10,SNCA,SNCG	turquoise	VSMC_M6
GO:0048864	0.17	0.94	4	72	stem cell development	BP	0.88633	EDNRB,BMP7,TBX1,SEMA6B	turquoise	VSMC_M6
GO:0003015	0.17	0.91	8	180	heart process	BP	0.88825	KCNN2,PIK3CG,CXCR4,SPTBN4,ACE,MTOR,DSC2,PDE4B	turquoise	VSMC_M6
GO:0099175	0.17	0.93	4	73	regulation of postsynapse organization	BP	0.90456	LRRC4B,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0048813	0.17	0.92	6	126	dendrite morphogenesis	BP	0.90469	MAP6,CTNND2,ABI3,SARM1,RELN,SHANK3	turquoise	VSMC_M6
GO:0006897	0.17	0.89	17	444	endocytosis	BP	0.90489	MEGF10,ENPP2,SYK,ARHGAP25,PIK3CG,DLL1,CD177,SNAP25,CD36,STAB1,SNCA,HFE,SSC4D,ARHGAP27,SELE,SNCG,SCARF1	turquoise	VSMC_M6
GO:0042472	0.17	0.93	4	73	inner ear morphogenesis	BP	0.90803	ATP8A2,COL2A1,PROX1,TBX1	turquoise	VSMC_M6
GO:0062014	0.17	0.93	4	73	negative regulation of small molecule metabolic process	BP	0.91045	SOGA1,PROX1,CDA,BCKDK	turquoise	VSMC_M6
GO:1903531	0.17	0.92	5	99	negative regulation of secretion by cell	BP	0.91253	SFRP1,SNCA,FGF23,NOTCH1,NMB	turquoise	VSMC_M6
GO:0070588	0.17	0.90	9	211	calcium ion transmembrane transport	BP	0.91694	PIK3CG,P2RY6,CXCL10,SNCA,RGN,CRACR2A,PDE4B,TRPM2,CCR7	turquoise	VSMC_M6
GO:0072659	0.18	0.90	10	239	protein localization to plasma membrane	BP	0.92338	GRIP2,TGFB1,SPTBN4,NKD2,TSPAN15,PRKCH,TSPAN14,ABI3,GBP1,CDH1	turquoise	VSMC_M6
GO:0030216	0.18	0.93	4	74	keratinocyte differentiation	BP	0.92627	CYP26B1,PRKCH,NOTCH1,CDH3	turquoise	VSMC_M6
GO:0016331	0.18	0.92	6	127	morphogenesis of embryonic epithelium	BP	0.93242	CELSR1,TGFB1,CTNNB1,SFRP1,BMP7,LHX2	turquoise	VSMC_M6
GO:0033138	0.18	0.93	4	74	positive regulation of peptidyl-serine phosphorylation	BP	0.93952	IL6,TGFB1,SNCA,SH2D3C	turquoise	VSMC_M6
GO:0030036	0.18	0.88	22	600	actin cytoskeleton organization	BP	0.93952	CELSR1,FRMD3,THSD7A,EPHA5,ARHGAP25,FGD5,SPTBN4,SFRP1,NRAP,ESAM,PROX1,BAIAP2L1,PPM1F,MTOR,ABI3,ARHGEF15,S1PR1,PDLIM1,KANK3,SHANK3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0046890	0.18	0.91	6	127	regulation of lipid biosynthetic process	BP	0.93991	PDGFB,ADGRF5,RAB38,PROX1,RGN,MTOR	turquoise	VSMC_M6
GO:0003231	0.18	0.92	5	101	cardiac ventricle development	BP	0.94222	TGFB1,PDE2A,PROX1,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0003206	0.18	0.92	5	101	cardiac chamber morphogenesis	BP	0.94222	TGFB1,BMP7,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0061024	0.18	0.87	22	599	membrane organization	BP	0.94639	MEGF10,ATP8A1,ARHGAP25,CXCR4,SPTBN4,TIE1,SNAP25,CD36,ATP8A2,REEP1,SNCA,ANO3,MTTP,HYAL2,NKD2,LAPTM5,SUN3,BAIAP2L1,PITPNM3,PMAIP1,RELN,SHANK3	turquoise	VSMC_M6
GO:0043010	0.18	0.89	10	242	camera-type eye development	BP	0.95382	DLL1,CTNNB1,ATP8A2,SLC4A5,BMP7,PROX1,ARHGEF15,HCN1,LHX2,HRASLS	turquoise	VSMC_M6
GO:0060759	0.18	0.91	6	128	regulation of response to cytokine stimulus	BP	0.95405	SYK,IL6,PPARG,CXCR4,LAPTM5,MMP12	turquoise	VSMC_M6
GO:0017015	0.18	0.92	5	102	regulation of transforming growth factor beta receptor signaling pathway	BP	0.95405	PPARG,TGFB1,GOT1,LRG1,BAMBI	turquoise	VSMC_M6
GO:0060548	0.18	0.87	27	754	negative regulation of cell death	BP	0.95405	FLT4,KDR,IL6,PIK3CG,DLL1,NOS3,EDNRB,CTNNB1,SFRP1,COL2A1,SNCA,LAPTM5,CD34,BMP7,FANK1,PRAME,LTF,TBX1,RGN,PRKCH,MTOR,TNFRSF18,NOTCH1,CDH5,ALOX12,VSTM2L,CCR7	turquoise	VSMC_M6
GO:0032880	0.18	0.87	25	693	regulation of protein localization	BP	0.95405	SYBU,EPHA5,IL6,TGFB1,CTNNB1,GPC6,SNAP25,SFRP1,CD36,PRR5L,HYAL2,NKD2,HFE,PECAM1,GPC1,OAZ3,PPM1F,PRKCH,ABI3,SSTR5,GBP1,CDH1,NUCB1,TRPM2,MGAT3	turquoise	VSMC_M6
GO:0007605	0.18	0.92	5	102	sensory perception of sound	BP	0.95405	SPTBN4,COL2A1,TBX1,PKHD1L1,GRAP	turquoise	VSMC_M6
GO:0032479	0.18	0.93	4	75	regulation of type I interferon production	BP	0.95405	SYK,TLR7,IRF8,MMP12	turquoise	VSMC_M6
GO:0032606	0.18	0.93	4	75	type I interferon production	BP	0.95405	SYK,TLR7,IRF8,MMP12	turquoise	VSMC_M6
GO:0032504	0.18	0.87	21	571	multicellular organism reproduction	BP	0.95405	SLC22A16,EDNRB,CTNNB1,SFRP1,CFAP54,ANGPT2,CYP26B1,SPATA25,OAZ3,ACE,RGN,PPP1R1B,C19orf57,MTOR,BCKDK,KLF1,NOTCH1,GGN,ATP1A4,SOX17,TRPM2	turquoise	VSMC_M6
GO:0015748	0.19	0.92	5	102	organophosphate ester transport	BP	0.95405	ATP8A1,ATP8A2,ANO3,MTTP,PITPNM3	turquoise	VSMC_M6
GO:0002822	0.19	0.92	5	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	0.95405	IL23A,IL6,TGFB1,NFKBID,HFE	turquoise	VSMC_M6
GO:0043254	0.19	0.88	14	361	regulation of protein-containing complex assembly	BP	0.95405	SYK,RASIP1,TGFB1,TMC8,SPTBN4,CD36,SNCA,ESAM,SELP,BAIAP2L1,MTOR,CDH5,KANK3,CCR7	turquoise	VSMC_M6
GO:0051254	0.19	0.85	46	1357	positive regulation of RNA metabolic process	BP	0.95405	NOTCH4,PDGFB,IL6,MAML3,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,ZIC2,PRR5L,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,LHX2,CDH1,MMP12,SOX17,PDLIM1,SOX18,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0060349	0.19	0.92	4	76	bone morphogenesis	BP	0.95405	FREM1,CYP26B1,COL2A1,LTF	turquoise	VSMC_M6
GO:0031503	0.19	0.90	8	186	protein-containing complex localization	BP	0.95405	GRIP2,EXOC3L2,GPC6,SNAP25,HHEX,MAPK10,EXOC3L1,RELN	turquoise	VSMC_M6
GO:0003012	0.19	0.88	13	332	muscle system process	BP	0.95405	KCNN2,PIK3CG,GRIP2,NOS3,CXCR4,EDNRB,ATP8A2,RCSD1,MTOR,DSC2,PDE4B,NOTCH1,NMUR1	turquoise	VSMC_M6
GO:0001666	0.19	0.89	10	244	response to hypoxia	BP	0.95405	CXCR4,SFRP1,ANGPT2,CD34,BMP7,MTOR,NOTCH1,ENDOG,PMAIP1,PDLIM1	turquoise	VSMC_M6
GO:0032091	0.19	0.92	4	76	negative regulation of protein binding	BP	0.95405	PDGFB,TMC8,HFE,ACE	turquoise	VSMC_M6
GO:0050868	0.19	0.92	4	76	negative regulation of T cell activation	BP	0.95405	HFE,LAPTM5,CD86,NRARP	turquoise	VSMC_M6
GO:1903844	0.19	0.91	5	104	regulation of cellular response to transforming growth factor beta stimulus	BP	0.96111	PPARG,TGFB1,GOT1,LRG1,BAMBI	turquoise	VSMC_M6
GO:0060993	0.19	0.92	4	77	kidney morphogenesis	BP	0.96754	CTNNB1,BMP7,KIF26B,GREB1L	turquoise	VSMC_M6
GO:0060419	0.19	0.92	4	77	heart growth	BP	0.96768	PROX1,MTOR,NOTCH1,S1PR1	turquoise	VSMC_M6

GO:0045935	0.19	0.85	50	1489	positive regulation of nucleobase-containing compound metabolic process	BP	0.96841	NOTCH4,PDGFB,IL6,MAML3,DLL1,KDM4D,NOS3,PPARG,TGFB1,CTNNB1,SFRP1,ZIC2,PRR5L,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,CDH1,MMP12,SOX17,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0071805	0.20	0.90	6	131	potassium ion transmembrane transport	BP	0.96854	KCNN2,KCNA7,SNAP25,HCN1,ATP1A4,KCNU1	turquoise	VSMC_M6
GO:1903827	0.20	0.87	17	454	regulation of cellular protein localization	BP	0.97027	TGFB1,CTNNB1,GPC6,CD36,PRR5L,HYAL2,NKD2,HFE,GPC1,OAZ3,PPM1F,PRKCH,ABI3,GBP1,CDH1,NUCB1,MGAT3	turquoise	VSMC_M6
GO:0046328	0.20	0.91	5	104	regulation of JNK cascade	BP	0.97711	FLT4,ANKRD6,SFRP1,CRACR2A,CCR7	turquoise	VSMC_M6
GO:0050806	0.20	0.91	5	104	positive regulation of synaptic transmission	BP	0.97878	SNAP25,SNCA,SHANK2,RELN,SHANK3	turquoise	VSMC_M6
GO:1903900	0.20	0.91	5	104	regulation of viral life cycle	BP	0.98037	ISG20,PROX1,LTF,NOTCH1,TRIM62	turquoise	VSMC_M6
GO:1990845	0.20	0.90	6	132	adaptive thermogenesis	BP	0.98218	SYK,NOVA2,CXCR4,CD36,ESRRG,NOTCH1	turquoise	VSMC_M6
GO:1901361	0.20	0.87	15	395	organic cyclic compound catabolic process	BP	0.98808	IL6,SLCO2B1,PDE2A,PRR5L,ISG20,ERN1,RGN,CDA,FGF23,MTOR,PDE4B,SARM1,ENDOG,NUDT4B,SCARF1	turquoise	VSMC_M6
GO:0106027	0.20	0.92	4	78	neuron projection organization	BP	0.99006	CTNND2,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0120162	0.20	0.92	4	78	positive regulation of cold-induced thermogenesis	BP	0.99305	SYK,CXCR4,CD36,ESRRG	turquoise	VSMC_M6
GO:0048706	0.20	0.91	5	105	embryonic skeletal system development	BP	0.99569	CTNNB1,COL2A1,BMP7,HOXD10,TBX1	turquoise	VSMC_M6
GO:0097581	0.20	0.92	4	78	lamellipodium organization	BP	0.99569	ENPP2,MTOR,ABI3,S1PR1	turquoise	VSMC_M6
GO:0032963	0.20	0.92	4	78	collagen metabolic process	BP	0.99847	IL6,TGFB1,GOT1,MMP12	turquoise	VSMC_M6
GO:0098656	0.20	0.89	7	161	anion transmembrane transport	BP	1	SLC16A8,SLC4A11,SLC4A5,ANO3,SLC39A8,SLC25A18,MTOR	turquoise	VSMC_M6
GO:0051403	0.21	0.89	8	190	stress-activated MAPK cascade	BP	1	FLT4,ANKRD6,SFRP1,MAPK10,TLR7,CRACR2A,SH2D3C,CCR7	turquoise	VSMC_M6
GO:0044057	0.21	0.86	15	398	regulation of system process	BP	1	KCNN2,PDGFB,PIK3CG,CTSC,NOS3,EDNRB,SPTBN4,ACE,MTOR,NPR1,DSC2,PDE4B,NOTCH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0060402	0.21	0.90	5	107	calcium ion transport into cytosol	BP	1	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0002262	0.21	0.90	6	134	myeloid cell homeostasis	BP	1	IREB2,ADGRF5,IL6,INPP5D,KLF1,PDE4B	turquoise	VSMC_M6
GO:0006909	0.21	0.89	7	163	phagocytosis	BP	1	MEGF10,SYK,ARHGAP25,P2RY6,CD36,PECAM1,IRF8	turquoise	VSMC_M6
GO:0001101	0.21	0.90	5	107	response to acid chemical	BP	1	BCL11A,MAPK10,COL18A1,MTOR,COL4A6	turquoise	VSMC_M6
GO:0051606	0.21	0.89	6	135	detection of stimulus	BP	1	CXCR4,CTNNB1,ATP8A2,ANO3,GNGT2,OR6N2	turquoise	VSMC_M6
GO:0043067	0.22	0.83	38	1119	regulation of programmed cell death	BP	1	FLT4,KDR,SYK,IL6,PIK3CG,DLL1,CTSC,NOS3,PPARG,CXCR4,EDNRB,CTNNB1,TMC8,SFRP1,CXCL10,COL2A1,SNCA,HYAL2,LAPTM5,INPP5D,BMP7,IGFBP3,FANK1,PRAME,LTF,TBX1,RGN,PRKCH,MTOR,SARM1,TNFRSF18,NOTCH1,ENDOG,CDH5,ALOX12,PMAIP1,VSTM2L,CCR7	turquoise	VSMC_M6
GO:0050680	0.22	0.90	5	108	negative regulation of epithelial cell proliferation	BP	1	PPARG,TGFB1,SFRP1,EAF2,RGN	turquoise	VSMC_M6
GO:0043279	0.22	0.91	4	81	response to alkaloid	BP	1	CXCR4,SNCA,PPP1R1B,MTOR	turquoise	VSMC_M6
GO:0030004	0.22	0.91	4	81	cellular monovalent inorganic cation homeostasis	BP	1	RAB38,SLC4A5,ATP6V0D2,ATP1A4	turquoise	VSMC_M6
GO:0048588	0.22	0.87	8	195	developmental cell growth	BP	1	SYT17,BCL11A,CXCR4,CTNNB1,MTOR,ISLR2,SEMA6B,LHX2	turquoise	VSMC_M6
GO:0099173	0.22	0.89	6	137	postsynapse organization	BP	1	LRRC4B,CTNND2,CNKSR2,ABI3,RELN,SHANK3	turquoise	VSMC_M6
GO:0071675	0.22	0.91	4	81	regulation of mononuclear cell migration	BP	1	RARRES2,CXCL10,C3AR1,CCR7	turquoise	VSMC_M6
GO:0009615	0.22	0.87	10	253	response to virus	BP	1	IL23A,IL6,CXCR4,CXCL10,HYAL2,ISG20,TLR7,GBP1,MMP12,PMAIP1	turquoise	VSMC_M6
GO:0009790	0.22	0.83	29	841	embryo development	BP	1	CELSR1,PDGFB,ADGRF5,KDR,C5,DLL1,RARRES2,ITGB4,TGFB1,CTNNB1,TIE1,SFRP1,PCDH12,ATP8A2,SOX7,CYP26B1,COL2A1,BMP7,PROX1,HOXD10,TBX1,LFNG,NRARP,NOTCH1,ENDOG,LHX2,SOX17,SOX18,LPAR6	turquoise	VSMC_M6
GO:0097435	0.22	0.84	22	622	supramolecular fiber organization	BP	1	ARHGAP25,SPTBN4,SFRP1,CD36,COL2A1,BMP1,SNCA,NRAP,ESAM,PROX1,CCDC88B,BAIAP2L1,PPM1F,MTOR,ARHGEF15,THSD4,S1PR1,CDH5,PDLIM1,KANK3,SHANK3,CCR7	turquoise	VSMC_M6
GO:0007610	0.22	0.85	15	406	behavior	BP	1	ATP8A1,SPTBN4,SNAP25,ATP8A2,THBS4,SNCA,SHANK2,HCRTR1,HOXD10,TBX1,SNCG,PPP1R1B,MTOR,RELN,SHANK3	turquoise	VSMC_M6
GO:0045944	0.22	0.83	31	904	positive regulation of transcription by RNA polymerase II	BP	1	NOTCH4,PDGFB,IL6,MAML3,DLL1,PPARG,TGFB1,CTNNB1,HHEX,CXCL10,TOX2,IRX6,NKX2-3,HYAL2,ESRRG,NFATC2,EAF2,TLR7,BMP7,PROX1,HOXD10,PAX9,TBX1,NOTCH1,IRF8,S1PR1,LHX2,MMP12,SOX17,SOX18,FLI1	turquoise	VSMC_M6
GO:0051494	0.23	0.88	6	138	negative regulation of cytoskeleton organization	BP	1	SPTBN4,SNCA,S1PR1,CDH5,KANK3,SHANK3	turquoise	VSMC_M6
GO:0007369	0.23	0.88	6	138	gastrulation	BP	1	ITGB4,CTNNB1,SFRP1,SOX7,BMP7,SOX17	turquoise	VSMC_M6
GO:1901652	0.23	0.85	14	375	response to peptide	BP	1	RARRES2,PPARG,EDNRB,CD36,HHEX,SOGA1,GOT1,BMP7,PTPRE,BAIAP2L1,MTOR,KLF1,NOTCH1,MMP12	turquoise	VSMC_M6
GO:1901890	0.23	0.90	4	82	positive regulation of cell junction assembly	BP	1	KDR,LRRC4B,SFRP1,PPM1F	turquoise	VSMC_M6
GO:0001843	0.23	0.90	4	82	neural tube closure	BP	1	CELSR1,TGFB1,SFRP1,LHX2	turquoise	VSMC_M6
GO:0046488	0.23	0.88	6	138	phosphatidylinositol metabolic process	BP	1	IP6K3,PDGFB,PIK3CG,PLCB2,INPP5D,PITPNM3	turquoise	VSMC_M6
GO:0051302	0.23	0.88	6	138	regulation of cell division	BP	1	PDGFB,DLL1,TGFB1,THBS4,SSTR5,SOX17	turquoise	VSMC_M6
GO:0003006	0.23	0.83	24	685	developmental process involved in reproduction	BP	1	PDGFB,SLC22A16,PPARG,CTNNB1,SFRP1,PCDH12,CFAP54,ANGPT2,CYP26B1,SPATA25,EAF2,BMP7,MGST1,OAZ3,ACE,RGN,C19orf57,MTOR,BCKDK,GREB1L,NOTCH1,GGN,ATP1A4,SOX17	turquoise	VSMC_M6
GO:0007269	0.23	0.89	5	110	neurotransmitter secretion	BP	1	SYN2,SNAP25,SNCA,MCTP2,SNCG	turquoise	VSMC_M6
GO:0099643	0.23	0.89	5	110	signal release from synapse	BP	1	SYN2,SNAP25,SNCA,MCTP2,SNCG	turquoise	VSMC_M6
GO:1902904	0.23	0.88	6	139	negative regulation of supramolecular fiber organization	BP	1	SPTBN4,SNCA,S1PR1,CDH5,KANK3,SHANK3	turquoise	VSMC_M6
GO:0051048	0.23	0.89	5	110	negative regulation of secretion	BP	1	SFRP1,SNCA,FGF23,NOTCH1,NMB	turquoise	VSMC_M6
GO:0048839	0.23	0.88	6	139	inner ear development	BP	1	DLL1,ATP8A2,COL2A1,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0060606	0.23	0.90	4	83	tube closure	BP	1	CELSR1,TGFB1,SFRP1,LHX2	turquoise	VSMC_M6
GO:0006836	0.23	0.88	6	139	neurotransmitter transport	BP	1	SLC6A6,SYN2,SNAP25,SNCA,MCTP2,SNCG	turquoise	VSMC_M6
GO:0031098	0.23	0.87	8	197	stress-activated protein kinase signaling cascade	BP	1	FLT4,ANKRD6,SFRP1,MAPK10,TLR7,CRACR2A,SH2D3C,CCR7	turquoise	VSMC_M6
GO:0045089	0.23	0.90	4	83	positive regulation of innate immune response	BP	1	IL18RAP,SYK,MMP12,TRIM62	turquoise	VSMC_M6
GO:0048609	0.23	0.83	20	563	multicellular organismal reproductive process	BP	1	SLC22A16,EDNRB,CTNNB1,CFAP54,ANGPT2,CYP26B1,SPATA25,OAZ3,ACE,RGN,PPP1R1B,C19orf57,MTOR,BCKDK,KLF1,NOTCH1,GGN,ATP1A4,SOX17,TRPM2	turquoise	VSMC_M6
GO:0046486	0.24	0.85	12	317	glycerolipid metabolic process	BP	1	ENPP2,IP6K3,PDGFB,PIK3CG,RAB38,PLCB2,NKX2-3,MTTP,INPP5D,RGN,PITPNM3,HRASLS	turquoise	VSMC_M6
GO:0002819	0.24	0.89	5	111	regulation of adaptive immune response	BP	1	IL23A,IL6,TGFB1,NFKBID,HFE	turquoise	VSMC_M6
GO:0001738	0.24	0.90	4	84	morphogenesis of a polarized epithelium	BP	1	CELSR1,ANKRD6,GPC6,SFRP1	turquoise	VSMC_M6

GO:0010976	0.24	0.88	6	140	positive regulation of neuron projection development	BP	1	ATP8A2,BMP7,MTOR,RELN,ALKAL1,SCARF1	turquoise	VSMC_M6
GO:0007268	0.24	0.84	17	471	chemical synaptic transmission	BP	1	SYBU,SLC6A6,SYN2,HTR5A,CTNNB1,SNAP25,CNTN4,SNCA,SHANK2,MCTP2,HCRTR1,GRID2IP,SNCG,MTOR,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0098916	0.24	0.84	17	471	anterograde trans-synaptic signaling	BP	1	SYBU,SLC6A6,SYN2,HTR5A,CTNNB1,SNAP25,CNTN4,SNCA,SHANK2,MCTP2,HCRTR1,GRID2IP,SNCG,MTOR,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0036293	0.24	0.85	10	258	response to decreased oxygen levels	BP	1	CXCR4,SFRP1,ANGPT2,CD34,BMP7,MTOR,NOTCH1,ENDOG,PMAIP1,PDLIM1	turquoise	VSMC_M6
GO:0006813	0.24	0.88	6	140	potassium ion transport	BP	1	KCNN2,KCNA7,SNAP25,HCN1,ATP1A4,KCNU1	turquoise	VSMC_M6
GO:0019953	0.24	0.83	20	565	sexual reproduction	BP	1	SLC22A16,EDNRB,CTNNB1,SPTBN4,CFAP54,ANGPT2,CYP26B1,SPATA25,OAZ3,ACE,HOXD10,RGN,PPP1R1B,C19orf57,MTOR,BCKDK,NOTCH1,GGN,ATP1A4,SOX17	turquoise	VSMC_M6
GO:1901565	0.24	0.81	36	1069	organonitrogen compound catabolic process	BP	1	ENPP2,DENND3,CTSC,NOS3,TGFB1,CTNNB1,SLCO2B1,PDE2A,NOTUM,ADAMTS9,LYVE1,GOT1,SNCA,HYAL2,NKD2,HFE,LAPTM5,ASCC2,GPC1,OAZ3,ACE,PRAME,RGN,CDA,MTOR,BCKDK,PDE4B,SARM1,NOTCH1,CDH1,MMP12,PMAIP1,SOX17,GNA12,MGAT3,NUDT4B	turquoise	VSMC_M6
GO:0071248	0.24	0.87	6	141	cellular response to metal ion	BP	1	SYT17,SNCA,HFE,ENDOG,CDH1,TRPM2	turquoise	VSMC_M6
GO:0032271	0.24	0.86	8	199	regulation of protein polymerization	BP	1	SPTBN4,SNCA,ESAM,BAIAP2L1,MTOR,CDH5,KANK3,CCR7	turquoise	VSMC_M6
GO:0030324	0.24	0.87	6	141	lung development	BP	1	FLT4,CELSR1,CTNNB1,PROX1,NOTCH1,MMP12	turquoise	VSMC_M6
GO:0043065	0.24	0.84	15	410	positive regulation of apoptotic process	BP	1	IL6,CTSC,PPARG,CTNNB1,SFRP1,SNCA,HYAL2,INPP5D,BMP7,IGFBP3,FANK1,NOTCH1,ENDOG,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0050708	0.25	0.86	8	200	regulation of protein secretion	BP	1	SYBU,EPHA5,IL6,TGFB1,SNAP25,SFRP1,SSTR5,TRPM2	turquoise	VSMC_M6
GO:0001501	0.25	0.83	15	413	skeletal system development	BP	1	FREM1,TGFB1,CTNNB1,SFRP1,NOTUM,CYP26B1,COL2A1,BMP1,HYAL2,BMP7,HOXD10,LTF,TBX1,RGN,FLI1	turquoise	VSMC_M6
GO:0051223	0.25	0.83	15	412	regulation of protein transport	BP	1	SYBU,EPHA5,IL6,TGFB1,SNAP25,SFRP1,CD36,PRR5L,HYAL2,OAZ3,PPM1F,SSTR5,CDH1,NUCB1,TRPM2	turquoise	VSMC_M6
GO:0008219	0.25	0.80	52	1587	cell death	BP	1	FLT4,MEGF10,KDR,SYK,IL6,PIK3CG,DLL1,CTSC,SLC6A6,NOS3,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TMC8,SFRP1,CD36,CXCL10,CYP26B1,COL2A1,SNCA,HYAL2,DPYSL4,LAPTM5,INPP5D,EAF2,CD34,ERN1,BMP7,IGFBP3,FANK1,PRAME,LTF,TBX1,RGN,LGALS12,PPM1F,PRKCH,SNCG,MTOR,SARM1,TNFRSF18,NOTCH1,ENDOG,CDH5,ALOX12,PMAIP1,VSTM2L,TRPM2,CCR7,PDE1B	turquoise	VSMC_M6
GO:0051668	0.25	0.82	19	537	localization within membrane	BP	1	RAB38,GRIP2,TGFB1,SPTBN4,GPC6,SNAP25,REEP1,MAPK10,NKD2,GPC1,TSPAN15,ATP13A1,PRKCH,TSPAN14,ABI3,GBP1,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0060348	0.25	0.86	7	172	bone development	BP	1	FREM1,NOTUM,CYP26B1,COL2A1,LTF,RGN,FLI1	turquoise	VSMC_M6
GO:1901615	0.25	0.83	14	382	organic hydroxy compound metabolic process	BP	1	IP6K3,OSBPL3,P2RY6,CYP26B1,GOT1,SNCA,PROX1,FGF23,NPR1,DEGS2,CDH3,ALOX12,NUDT4B,SCARF1	turquoise	VSMC_M6
GO:0001578	0.25	0.89	4	86	microtubule bundle formation	BP	1	DNAH8,CFAP100,DNAJB13,TTLL6	turquoise	VSMC_M6
GO:0007613	0.25	0.89	4	86	memory	BP	1	PPP1R1B,MTOR,RELN,SHANK3	turquoise	VSMC_M6
GO:0099537	0.25	0.82	17	477	trans-synaptic signaling	BP	1	SYBU,SLC6A6,SYN2,HTR5A,CTNNB1,SNAP25,CNTN4,SNCA,SHANK2,MCTP2,HCRTR1,GRID2IP,SNCG,MTOR,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0010927	0.25	0.89	4	87	cellular component assembly involved in morphogenesis	BP	1	ITGB4,NRAP,PROX1,GPC1	turquoise	VSMC_M6
GO:0046887	0.25	0.89	4	86	positive regulation of hormone secretion	BP	1	SYBU,HFE,TRPM2,NMB	turquoise	VSMC_M6
GO:0010557	0.25	0.79	47	1433	positive regulation of macromolecule biosynthetic process	BP	1	NOTCH4,PDGFB,KDR,IL6,MAML3,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,ZIC2,HHEX,SOX7,CXCL10,TOX2,IRX6,NKX2-3,HYAL2,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,PROX1,FANK1,HOXD10,PAX9,TBX1,FGF23,MTOR,KLF1,LYL1,NOTCH1,IRF8,S1PR1,LHX2,CDH1,MMP12,SOX17,PDLIM1,SOX18,PKIB,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0031333	0.26	0.87	5	115	negative regulation of protein-containing complex assembly	BP	1	TMC8,SPTBN4,SNCA,CDH5,KANK3	turquoise	VSMC_M6
GO:0006661	0.26	0.87	5	115	phosphatidylinositol biosynthetic process	BP	1	IP6K3,PDGFB,PIK3CG,INPP5D,PITPNM3	turquoise	VSMC_M6
GO:0097191	0.26	0.86	7	173	extrinsic apoptotic signaling pathway	BP	1	NOS3,TGFB1,TMC8,SFRP1,COL2A1,HYAL2,PMAIP1	turquoise	VSMC_M6
GO:0050773	0.26	0.88	4	87	regulation of dendrite development	BP	1	BCL11A,BMP7,SARM1,RELN	turquoise	VSMC_M6
GO:0035270	0.26	0.88	4	87	endocrine system development	BP	1	IL6,DLL1,TBX1,CDH1	turquoise	VSMC_M6
GO:1902600	0.26	0.87	5	115	proton transmembrane transport	BP	1	NDUFA4,SLC4A11,ATP6V0D2,SLC25A18,ATP1A4	turquoise	VSMC_M6
GO:0072330	0.26	0.86	6	144	monocarboxylic acid biosynthetic process	BP	1	OSBPL3,PROX1,RGN,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:0046777	0.26	0.85	8	204	protein autophosphorylation	BP	1	FLT4,PDGFB,KDR,SYK,ERN1,SRMS,ACE,MTOR	turquoise	VSMC_M6
GO:1903038	0.26	0.88	4	87	negative regulation of leukocyte cell-cell adhesion	BP	1	HFE,LAPTM5,CD86,NRARP	turquoise	VSMC_M6
GO:0030100	0.26	0.85	7	174	regulation of endocytosis	BP	1	SYK,DLL1,CD177,CD36,SNCA,HFE,SELE	turquoise	VSMC_M6
GO:0030323	0.26	0.86	6	145	respiratory tube development	BP	1	FLT4,CELSR1,CTNNB1,PROX1,NOTCH1,MMP12	turquoise	VSMC_M6
GO:0052547	0.26	0.83	11	294	regulation of peptidase activity	BP	1	SYK,C5,PPARG,SOX7,SNCA,LAPTM5,LTF,PPM1F,ALOX12,PRSS22,PMAIP1	turquoise	VSMC_M6
GO:0001889	0.26	0.87	5	116	liver development	BP	1	IL6,HFE,PROX1,RGN,NOTCH1	turquoise	VSMC_M6
GO:0007266	0.26	0.87	5	116	Rho protein signal transduction	BP	1	CELSR1,RASIP1,PRAG1,GNA12,LPAR6	turquoise	VSMC_M6
GO:0009636	0.26	0.85	7	174	response to toxic substance	BP	1	NOS3,CD36,BMP7,MGST1,PTGS1,CDH1,GPX3	turquoise	VSMC_M6
GO:0017038	0.26	0.85	7	174	protein import	BP	1	SYK,TGFB1,CD36,HYAL2,NOTCH1,CDH1,MMP12	turquoise	VSMC_M6
GO:0090066	0.26	0.82	15	418	regulation of anatomical structure size	BP	1	GRIP2,NOS3,EDNRB,SPTBN4,P2RY2,ESAM,ACE,BAIAP2L1,MTOR,NPR1,ISLR2,SEMA6B,KANK3,SHANK3,CCR7	turquoise	VSMC_M6
GO:0030833	0.26	0.86	6	145	regulation of actin filament polymerization	BP	1	SPTBN4,ESAM,BAIAP2L1,MTOR,KANK3,CCR7	turquoise	VSMC_M6
GO:2001257	0.26	0.87	5	116	regulation of cation channel activity	BP	1	P2RY6,CRACR2A,PDE4B,RELN,SHANK3	turquoise	VSMC_M6
GO:0055088	0.26	0.87	5	116	lipid homeostasis	BP	1	PPARG,MALL,GOT1,MTTP,RBP1	turquoise	VSMC_M6
GO:0009628	0.26	0.80	30	891	response to abiotic stimulus	BP	1	TNFRSF11A,KDM4D,NOS3,CXCR4,CTNNB1,PDE2A,SFRP1,SLC4A11,ATP8A2,TSC22D2,CXCL10,ANGPT2,MAPK10,GOT1,ANO3,HYAL2,TLR7,CD34,COL18A1,BMP7,RCSD1,PPP1R1B,MTOR,GNGT2,NOTCH1,ENDOG,PMAIP1,PDLIM1,SHANK3,TRPM2	turquoise	VSMC_M6
GO:0051897	0.26	0.88	4	88	positive regulation of protein kinase B signaling	BP	1	PIK3CG,TGFB1,MTOR,CCR7	turquoise	VSMC_M6
GO:0007283	0.27	0.82	13	357	spermatogenesis	BP	1	SLC22A16,CFAP54,CYP26B1,SPATA25,OAZ3,ACE,RGN,C19orf57,BCKDK,NOTCH1,GGN,ATP1A4,SOX17	turquoise	VSMC_M6

GO:0007265	0.27	0.83	11	296	Ras protein signal transduction	BP	1	CELSR1,DENND3,RASIP1,PIK3CG,RASGRP3,PRAG1,ERAS,NOTCH1,GRAP,GNA12,LPAR6	turquoise	VSMC_M6
GO:0046700	0.27	0.82	13	357	heterocycle catabolic process	BP	1	IL6,SLCO2B1,PDE2A,PRR5L,ISG20,ERN1,RGN,CDA,MTOR,PDE4B,SARM1,ENDOG,NUDT4B	turquoise	VSMC_M6
GO:0010629	0.27	0.80	26	766	negative regulation of gene expression	BP	1	IL23A,PDGFB,IREB2,KDR,IL6,DLL1,PPARG,TGFB1,CTNNB1,SFRP1,CD36,PRR5L,HFE,LAPTM5,INPP5D,CD34,ERN1,ACE,LTF,MTOR,NOTCH1,GBP1,LHX2,CDH3,MIR1307,CCR7	turquoise	VSMC_M6
GO:0007044	0.27	0.88	4	89	cell-substrate junction assembly	BP	1	KDR,ITGB4,SFRP1,PPM1F	turquoise	VSMC_M6
GO:0009306	0.27	0.83	10	266	protein secretion	BP	1	SYBU,EPHA5,IL6,TGFB1,SNAP25,SFRP1,MTTP,SNCG,SSTR5,TRPM2	turquoise	VSMC_M6
GO:0035592	0.27	0.83	10	266	establishment of protein localization to extracellular region	BP	1	SYBU,EPHA5,IL6,TGFB1,SNAP25,SFRP1,MTTP,SNCG,SSTR5,TRPM2	turquoise	VSMC_M6
GO:1901605	0.27	0.85	6	146	alpha-amino acid metabolic process	BP	1	NOS3,GOT1,SLC39A8,ART4,AGMAT,BCKDK	turquoise	VSMC_M6
GO:0051054	0.27	0.85	7	176	positive regulation of DNA metabolic process	BP	1	PDGFB,IL6,KDM4D,TGFB1,CTNNB1,ENDOG,PKIB	turquoise	VSMC_M6
GO:0042752	0.27	0.88	4	89	regulation of circadian rhythm	BP	1	PPARG,MAPK10,PROX1,MTOR	turquoise	VSMC_M6
GO:0043491	0.27	0.85	6	147	protein kinase B signaling	BP	1	KDR,PIK3CG,TGFB1,HYAL2,MTOR,CCR7	turquoise	VSMC_M6
GO:0042471	0.27	0.87	4	89	ear morphogenesis	BP	1	ATP8A2,COL2A1,PROX1,TBX1	turquoise	VSMC_M6
GO:0015918	0.27	0.87	4	89	sterol transport	BP	1	OSBPL3,PPARG,CD36,MTTP	turquoise	VSMC_M6
GO:0042542	0.28	0.86	5	118	response to hydrogen peroxide	BP	1	IL18RAP,IL6,ERN1,ENDOG,TRPM2	turquoise	VSMC_M6
GO:0044270	0.28	0.81	13	361	cellular nitrogen compound catabolic process	BP	1	IL6,SLCO2B1,PDE2A,PRR5L,ISG20,ERN1,RGN,CDA,MTOR,PDE4B,SARM1,ENDOG,NUDT4B	turquoise	VSMC_M6
GO:0022414	0.28	0.78	34	1029	reproductive process	BP	1	PDGFB,SLC22A16,ITGB4,PPARG,EDNRB,CTNNB1,SPTBN4,SFRP1,PCDH12,CFAP54,STK35,ANGPT2,CYP26B1,SPATA25,HFE,EAF2,BMP7,MGST1,OAZ3,ACE,HOXD10,RGN,PPP1R1B,C19orf57,MTOR,BCKDK,KLF1,GREB1L,NOTCH1,GGN,ATP1A4,SOX17,KCNU1,TRPM2	turquoise	VSMC_M6
GO:0051704	0.28	0.79	24	709	multi-organism process	BP	1	SLC22A16,ITGB4,EDNRB,CTNNB1,SPTBN4,CFAP54,ANGPT2,CYP26B1,SPATA25,HYAL2,HFE,OAZ3,ACE,HOXD10,RGN,PPP1R1B,C19orf57,MTOR,BCKDK,KLF1,NOTCH1,GGN,ATP1A4,SOX17	turquoise	VSMC_M6
GO:1902905	0.28	0.84	7	179	positive regulation of supramolecular fiber organization	BP	1	SFRP1,PROX1,BAIAP2L1,PPM1F,MTOR,ARHGEF15,CCR7	turquoise	VSMC_M6
GO:0055001	0.28	0.84	6	150	muscle cell development	BP	1	MEGF10,NRAP,NFATC2,PROX1,MTOR,NOTCH1	turquoise	VSMC_M6
GO:0052548	0.29	0.82	10	270	regulation of endopeptidase activity	BP	1	SYK,C5,PPARG,SOX7,SNCA,LAPTM5,LTF,PPM1F,ALOX12,PMAIP1	turquoise	VSMC_M6
GO:0051101	0.29	0.87	4	91	regulation of DNA binding	BP	1	PPARG,TGFB1,CTNNB1,LHX2	turquoise	VSMC_M6
GO:0000003	0.29	0.77	34	1031	reproduction	BP	1	PDGFB,SLC22A16,ITGB4,PPARG,EDNRB,CTNNB1,SPTBN4,SFRP1,PCDH12,CFAP54,STK35,ANGPT2,CYP26B1,SPATA25,HFE,EAF2,BMP7,MGST1,OAZ3,ACE,HOXD10,RGN,PPP1R1B,C19orf57,MTOR,BCKDK,KLF1,GREB1L,NOTCH1,GGN,ATP1A4,SOX17,KCNU1,TRPM2	turquoise	VSMC_M6
GO:0007178	0.29	0.82	10	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	PPARG,TGFB1,SFRP1,GOT1,HFE,BMP7,LRG1,NOTCH1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0071692	0.29	0.81	10	271	protein localization to extracellular region	BP	1	SYBU,EPHA5,IL6,TGFB1,SNAP25,SFRP1,MTTP,SNCG,SSTR5,TRPM2	turquoise	VSMC_M6
GO:0042180	0.29	0.84	6	150	cellular ketone metabolic process	BP	1	PPARG,SNCA,PROX1,RGN,MTOR,BCKDK	turquoise	VSMC_M6
GO:0006639	0.29	0.86	4	92	acylglycerol metabolic process	BP	1	PIK3CG,NKX2-3,MTTP,RGN	turquoise	VSMC_M6
GO:0002224	0.29	0.86	4	92	toll-like receptor signaling pathway	BP	1	CD36,TLR7,LTF,SARM1	turquoise	VSMC_M6
GO:0034655	0.30	0.80	12	335	nucleobase-containing compound catabolic process	BP	1	IL6,PDE2A,PRR5L,ISG20,ERN1,RGN,CDA,MTOR,PDE4B,SARM1,ENDOG,NUDT4B	turquoise	VSMC_M6
GO:0008286	0.30	0.86	4	93	insulin receptor signaling pathway	BP	1	RARRES2,SOGA1,PTPRE,BAIAP2L1	turquoise	VSMC_M6
GO:0007611	0.30	0.82	7	183	learning or memory	BP	1	ATP8A1,SNAP25,SHANK2,PPP1R1B,MTOR,RELN,SHANK3	turquoise	VSMC_M6
GO:0030203	0.30	0.86	4	93	glycosaminoglycan metabolic process	BP	1	PDGFB,TGFB1,LYVE1,HYAL2	turquoise	VSMC_M6
GO:0099536	0.30	0.78	17	494	synaptic signaling	BP	1	SYBU,SLC6A6,SYN2,HTR5A,CTNNB1,SNAP25,CNTN4,SNCA,SHANK2,MCTP2,HCRTR1,GRID2IP,SNCG,MTOR,CDH1,RELN,SHANK3	turquoise	VSMC_M6
GO:0050890	0.30	0.82	8	214	cognition	BP	1	ATP8A1,SNAP25,SHANK2,PPP1R1B,MTOR,RELN,SHANK3,MGAT3	turquoise	VSMC_M6
GO:0007601	0.30	0.84	5	123	visual perception	BP	1	ZIC2,ATP8A2,COL2A1,COL18A1,CDH3	turquoise	VSMC_M6
GO:0034504	0.30	0.81	9	244	protein localization to nucleus	BP	1	SYK,TGFB1,CD36,HHEX,HYAL2,BMP7,NOTCH1,CDH1,MMP12	turquoise	VSMC_M6
GO:0046394	0.30	0.81	8	213	carboxylic acid biosynthetic process	BP	1	SYK,OSBPL3,GOT1,PROX1,RGN,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:0009749	0.30	0.83	6	153	response to glucose	BP	1	SYBU,EPHA5,ANGPT2,ERN1,SARM1,ENDOG	turquoise	VSMC_M6
GO:0007009	0.31	0.85	4	94	plasma membrane organization	BP	1	CXCR4,TIE1,ANO3,BAIAP2L1	turquoise	VSMC_M6
GO:0046822	0.31	0.85	4	94	regulation of nucleocytoplasmic transport	BP	1	TGFB1,CD36,HYAL2,CDH1	turquoise	VSMC_M6
GO:0051648	0.31	0.83	6	154	vesicle localization	BP	1	SYBU,PIK3CG,SYN2,CTNNB1,SNCA,CDH3	turquoise	VSMC_M6
GO:0150115	0.31	0.85	4	95	cell-substrate junction organization	BP	1	KDR,ITGB4,SFRP1,PPM1F	turquoise	VSMC_M6
GO:0051216	0.31	0.83	6	154	cartilage development	BP	1	TGFB1,CTNNB1,COL2A1,BMP1,HYAL2,BMP7	turquoise	VSMC_M6
GO:0044703	0.31	0.76	23	688	multi-organism reproductive process	BP	1	SLC22A16,ITGB4,EDNRB,CTNNB1,SPTBN4,CFAP54,ANGPT2,CYP26B1,SPATA25,HFE,OAZ3,ACE,HOXD10,RGN,PPP1R1B,C19orf57,MTOR,BCKDK,KLF1,NOTCH1,GGN,ATP1A4,SOX17	turquoise	VSMC_M6
GO:0048232	0.31	0.78	13	371	male gamete generation	BP	1	SLC22A16,CFAP54,CYP26B1,SPATA25,OAZ3,ACE,RGN,C19orf57,BCKDK,NOTCH1,GGN,ATP1A4,SOX17	turquoise	VSMC_M6
GO:1902679	0.31	0.75	31	946	negative regulation of RNA biosynthetic process	BP	1	NOTCH4,PDGFB,ETV7,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,MAPK10,SNCA,NFATC2,BMP7,PROX1,PRAME,PAX9,RGN,PPM1F,BCL6B,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0016053	0.31	0.81	8	215	organic acid biosynthetic process	BP	1	SYK,OSBPL3,GOT1,PROX1,RGN,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:2000278	0.31	0.85	4	95	regulation of DNA biosynthetic process	BP	1	PDGFB,CTNNB1,RGN,PKIB	turquoise	VSMC_M6
GO:1903305	0.31	0.85	4	95	regulation of regulated secretory pathway	BP	1	SYT17,SYK,CD177,NOTCH1	turquoise	VSMC_M6
GO:0006006	0.31	0.82	6	155	glucose metabolic process	BP	1	SOGA1,RGN,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0051896	0.31	0.83	5	125	regulation of protein kinase B signaling	BP	1	PIK3CG,TGFB1,HYAL2,MTOR,CCR7	turquoise	VSMC_M6
GO:0034341	0.31	0.85	4	95	response to interferon-gamma	BP	1	PPARG,SNCA,IRF8,GBP1	turquoise	VSMC_M6
GO:0007179	0.31	0.82	6	156	transforming growth factor beta receptor signaling pathway	BP	1	PPARG,TGFB1,GOT1,LRG1,CDH5,BAMBI	turquoise	VSMC_M6
GO:0060401	0.32	0.83	5	126	cytosolic calcium ion transport	BP	1	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0061025	0.32	0.83	5	125	membrane fusion	BP	1	TIE1,SNAP25,SNCA,HYAL2,NKD2	turquoise	VSMC_M6
GO:0009743	0.32	0.81	7	186	response to carbohydrate	BP	1	SYBU,EPHA5,ANGPT2,GOT1,ERN1,SARM1,ENDOG	turquoise	VSMC_M6
GO:0001654	0.32	0.79	10	280	eye development	BP	1	DLL1,CTNNB1,ATP8A2,SLC4A5,BMP7,PROX1,ARHGEF15,HCN1,LHX2,HRASLS	turquoise	VSMC_M6

GO:0070201	0.32	0.77	15	436	regulation of establishment of protein localization	BP	1	SYBU,EPHA5,IL6,TGFB1,SNAP25,SFRP1,CD36,PRR5L,HYAL2,OAZ3,PPM1F,SSTR5,CDH1,NUCB1,TRPM2	turquoise	VSMC_M6
GO:0050953	0.32	0.83	5	126	sensory perception of light stimulus	BP	1	ZIC2,ATP8A2,COL2A1,COL18A1,CDH3	turquoise	VSMC_M6
GO:0070482	0.32	0.79	10	280	response to oxygen levels	BP	1	CXCR4,SFRP1,ANGPT2,CD34,BMP7,MTOR,NOTCH1,ENDOG,PMAIP1,PDLIM1	turquoise	VSMC_M6
GO:0007276	0.32	0.77	16	469	gamete generation	BP	1	SLC22A16,CTNNB1,CFAP54,ANGPT2,CYP26B1,SPATA25,OAZ3,ACE,RGN,C19orf57,MTOR,BCKDK,NOTCH1,GGN,ATP1A4,SOX17	turquoise	VSMC_M6
GO:0046434	0.32	0.83	5	126	organophosphate catabolic process	BP	1	ENPP2,PDE2A,PDE4B,SARM1,NUDT4B	turquoise	VSMC_M6
GO:0019439	0.32	0.77	13	375	aromatic compound catabolic process	BP	1	IL6,SLCO2B1,PDE2A,PRR5L,ISG20,ERN1,RGN,CDA,MTOR,PDE4B,SARM1,ENDOG,NUDT4B	turquoise	VSMC_M6
GO:0150063	0.33	0.78	10	282	visual system development	BP	1	DLL1,CTNNB1,ATP8A2,SLC4A5,BMP7,PROX1,ARHGEF15,HCN1,LHX2,HRASLS	turquoise	VSMC_M6
GO:0032874	0.33	0.84	4	97	positive regulation of stress-activated MAPK cascade	BP	1	FLT4,ANKRD6,CRACR2A,CCR7	turquoise	VSMC_M6
GO:0007163	0.33	0.80	7	189	establishment or maintenance of cell polarity	BP	1	PARD6G,CYP26B1,KIF26B,LHX2,CDH5,PDLIM1,CCR7	turquoise	VSMC_M6
GO:0032269	0.33	0.75	25	760	negative regulation of cellular protein metabolic process	BP	1	IREB2,C5,RASIP1,KDM4D,PPARG,TGFB1,EDNRB,CTNNB1,SFRP1,KIRREL2,PRR5L,HHEX,PPP1R16B,SNCA,HYAL2,HFE,BMP7,IGFBP3,LTF,RGN,PPM1F,PPP1R1B,MTOR,PKIB,MGAT3	turquoise	VSMC_M6
GO:0016241	0.33	0.82	5	128	regulation of macroautophagy	BP	1	KDR,ATP6V0D2,ERN1,MTOR,RUFY4	turquoise	VSMC_M6
GO:0001701	0.33	0.78	11	314	in utero embryonic development	BP	1	PDGFB,C5,CTNNB1,TIE1,PCDH12,BMP7,NOTCH1,ENDOG,SOX17,SOX18,LPAR6	turquoise	VSMC_M6
GO:0044089	0.33	0.76	15	441	positive regulation of cellular component biogenesis	BP	1	KDR,SYK,LRRC4B,RASIP1,TGFB1,SFRP1,CD36,SNCA,BMP7,BAIAP2L1,PPM1F,MTOR,ARHGEF15,CDH5,CCR7	turquoise	VSMC_M6
GO:0051260	0.33	0.82	5	128	protein homooligomerization	BP	1	STEAP4,KCNA7,KCTD12,HCN1,TRPM2	turquoise	VSMC_M6
GO:0051129	0.33	0.75	19	569	negative regulation of cellular component organization	BP	1	BCL11A,PPARG,TGFB1,TMC8,SPTBN4,PRAG1,CXCL10,SNCA,BMP7,ACE,ABI3,ARHGEF15,SEMA6B,NOTCH1,S1PR1,CDH5,KANK3,SHANK3,RTN4RL2	turquoise	VSMC_M6
GO:0006022	0.33	0.83	4	98	aminoglycan metabolic process	BP	1	PDGFB,TGFB1,LYVE1,HYAL2	turquoise	VSMC_M6
GO:0007259	0.33	0.83	4	98	receptor signaling pathway via JAK-STAT	BP	1	IL23A,IL6,TNFRSF18,NOTCH1	turquoise	VSMC_M6
GO:0050777	0.33	0.82	5	128	negative regulation of immune response	BP	1	SYK,PPARG,HFE,INPP5D,MMP12	turquoise	VSMC_M6
GO:0006644	0.33	0.77	11	314	phospholipid metabolic process	BP	1	ENPP2,IP6K3,PDGFB,ADGRF5,PIK3CG,RAB38,PLCB2,SNCA,INPP5D,PITPNM3,HRASLS	turquoise	VSMC_M6
GO:0008064	0.33	0.81	6	159	regulation of actin polymerization or depolymerization	BP	1	SPTBN4,ESAM,BAIAP2L1,MTOR,KANK3,CCR7	turquoise	VSMC_M6
GO:2001235	0.34	0.83	4	98	positive regulation of apoptotic signaling pathway	BP	1	CTSC,SFRP1,HYAL2,PMAIP1	turquoise	VSMC_M6
GO:0009746	0.34	0.80	6	159	response to hexose	BP	1	SYBU,EPHA5,ANGPT2,ERN1,SARM1,ENDOG	turquoise	VSMC_M6
GO:0007623	0.34	0.80	6	160	circadian rhythm	BP	1	TNFRSF11A,PPARG,MAPK10,MTTP,PROX1,MTOR	turquoise	VSMC_M6
GO:0051100	0.34	0.81	5	129	negative regulation of binding	BP	1	PDGFB,TMC8,HFE,ACE,LHX2	turquoise	VSMC_M6
GO:0030832	0.34	0.80	6	160	regulation of actin filament length	BP	1	SPTBN4,ESAM,BAIAP2L1,MTOR,KANK3,CCR7	turquoise	VSMC_M6
GO:0070304	0.34	0.83	4	99	positive regulation of stress-activated protein kinase signaling cascade	BP	1	FLT4,ANKRD6,CRACR2A,CCR7	turquoise	VSMC_M6
GO:0030041	0.34	0.80	6	160	actin filament polymerization	BP	1	SPTBN4,ESAM,BAIAP2L1,MTOR,KANK3,CCR7	turquoise	VSMC_M6
GO:0019079	0.34	0.83	4	99	viral genome replication	BP	1	ISG20,PROX1,LTF,NOTCH1	turquoise	VSMC_M6
GO:1903828	0.34	0.83	4	99	negative regulation of cellular protein localization	BP	1	TGFB1,CD36,ABI3,GBP1	turquoise	VSMC_M6
GO:0048880	0.34	0.77	10	286	sensory system development	BP	1	DLL1,CTNNB1,ATP8A2,SLC4A5,BMP7,PROX1,ARHGEF15,HCN1,LHX2,HRASLS	turquoise	VSMC_M6
GO:0046578	0.34	0.80	6	161	regulation of Ras protein signal transduction	BP	1	DENND3,RASIP1,PIK3CG,PRAG1,NOTCH1,LPAR6	turquoise	VSMC_M6
GO:0032869	0.34	0.80	6	161	cellular response to insulin stimulus	BP	1	RARRES2,PPARG,SOGA1,GOT1,PTPRE,BAIAP2L1	turquoise	VSMC_M6
GO:0042981	0.35	0.72	35	1092	regulation of apoptotic process	BP	1	FLT4,KDR,IL6,PIK3CG,DLL1,CTSC,NOS3,PPARG,EDNRB,CTNNB1,TMC8,SFRP1,CXCL10,COL2A1,SNCA,HYAL2,INPP5D,BMP7,IGFBP3,FANK1,PRAME,LTF,TBX1,RGN,PRKCH,MTOR,SARM1,TNFRSF18,NOTCH1,ENDOG,CDH5,ALOX12,PMAIP1,VSTM2L,CCR7	turquoise	VSMC_M6
GO:0046718	0.35	0.82	4	100	viral entry into host cell	BP	1	CXCR4,HYAL2,CD86,TRIM62	turquoise	VSMC_M6
GO:0090101	0.35	0.82	4	101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	PPARG,SFRP1,NOTCH1,BAMBI	turquoise	VSMC_M6
GO:0007423	0.35	0.75	14	415	sensory organ development	BP	1	DLL1,CTNNB1,ATP8A2,SLC4A5,CYP26B1,COL2A1,BMP7,PROX1,TBX1,ARHGEF15,HCN1,NOTCH1,LHX2,HRASLS	turquoise	VSMC_M6
GO:0043409	0.35	0.81	5	131	negative regulation of MAPK cascade	BP	1	PPARG,SFRP1,HYAL2,BMP7,GBP1	turquoise	VSMC_M6
GO:0043583	0.35	0.79	6	162	ear development	BP	1	DLL1,ATP8A2,COL2A1,PROX1,TBX1,NOTCH1	turquoise	VSMC_M6
GO:0002831	0.35	0.78	8	224	regulation of response to biotic stimulus	BP	1	IL23A,IL18RAP,SYK,PPARG,CD36,LTF,MMP12,TRIM62	turquoise	VSMC_M6
GO:0070997	0.35	0.76	10	288	neuron death	BP	1	CTNNB1,SNCA,DPYSL4,CD34,SNCG,MTOR,SARM1,ENDOG,VSTM2L,TRPM2	turquoise	VSMC_M6
GO:0060541	0.35	0.79	6	163	respiratory system development	BP	1	FLT4,CELSR1,CTNNB1,PROX1,NOTCH1,MMP12	turquoise	VSMC_M6
GO:0051495	0.35	0.78	7	194	positive regulation of cytoskeleton organization	BP	1	SFRP1,PROX1,BAIAP2L1,PPM1F,MTOR,ARHGEF15,CCR7	turquoise	VSMC_M6
GO:0002833	0.35	0.82	4	101	positive regulation of response to biotic stimulus	BP	1	IL18RAP,SYK,MMP12,TRIM62	turquoise	VSMC_M6
GO:0051253	0.36	0.71	33	1032	negative regulation of RNA metabolic process	BP	1	NOTCH4,PDGFB,ETV7,IL6,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,MAPK10,SNCA,NFATC2,BMP7,PROX1,PRAME,PAX9,RGN,PPM1F,BCL6B,MTOR,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0006650	0.36	0.76	9	257	glycerophospholipid metabolic process	BP	1	ENPP2,IP6K3,PDGFB,PIK3CG,RAB38,PLCB2,INPP5D,PITPNM3,HRASLS	turquoise	VSMC_M6
GO:0034284	0.36	0.78	6	164	response to monosaccharide	BP	1	SYBU,EPHA5,ANGPT2,ERN1,SARM1,ENDOG	turquoise	VSMC_M6
GO:0050905	0.36	0.81	4	103	neuromuscular process	BP	1	ATP8A2,HOXD10,RCSD1,MTOR	turquoise	VSMC_M6
GO:0071241	0.36	0.78	6	165	cellular response to inorganic substance	BP	1	SYT17,SNCA,HFE,ENDOG,CDH1,TRPM2	turquoise	VSMC_M6
GO:0008360	0.37	0.79	5	134	regulation of cell shape	BP	1	KDR,FGD5,PRAG1,PALMD,BAMBI	turquoise	VSMC_M6
GO:0033157	0.37	0.77	7	196	regulation of intracellular protein transport	BP	1	TGFB1,CD36,PRR5L,HYAL2,OAZ3,CDH1,NUCB1	turquoise	VSMC_M6
GO:0030307	0.37	0.79	5	134	positive regulation of cell growth	BP	1	SYT17,CXCR4,SFRP1,MTOR,ISLR2	turquoise	VSMC_M6
GO:0035265	0.37	0.79	5	134	organ growth	BP	1	DLL1,PROX1,MTOR,NOTCH1,S1PR1	turquoise	VSMC_M6
GO:0044255	0.37	0.71	24	743	cellular lipid metabolic process	BP	1	ENPP2,IP6K3,PDGFB,ADGRF5,PIK3CG,RAB38,RARRES2,PPARG,CD36,CYP26B1,PLCB2,NKX2-3,SNCA,MTTP,INPP5D,RGN,PITPNM3,MTOR,DEGS2,B4GALT6,PTGS1,ALOX12,HRASLS,RBP1	turquoise	VSMC_M6
GO:0043467	0.37	0.80	4	104	regulation of generation of precursor metabolites and energy	BP	1	NDUFA4,SNCA,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0045892	0.38	0.70	30	943	negative regulation of transcription, DNA-templated	BP	1	NOTCH4,PDGFB,ETV7,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,MAPK10,SNCA,NFATC2,BMP7,PROX1,PRAME,PAX9,PPM1F,BCL6B,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6

GO:0010468	0.38	0.67	105	3428	regulation of gene expression	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,PDGFB,ETV7,IREB2,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,C5,MAML3,PIK3CG,DLL1,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,NFKBID,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,SLC4A5,ADGRG3,PRDM8,CYP26B1,COL2A1,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,NFATC2,INPP5D,EAF2,TLR7,CD34,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,ACE,HOXD10,PRAME,PAX9,LTF,CCDC88B,TBX1,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,PDE4B,NRARP,HES3,NOTCH1,IRF8,S1PR1,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,TRIM43,SOX17,RELN,ACKR1,C3AR1,MIR1307,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0031929	0.38	0.80	4	105	TOR signaling	BP	1	PRR5L,MTOR,RELN,GNA12	turquoise	VSMC_M6
GO:0090316	0.38	0.78	5	136	positive regulation of intracellular protein transport	BP	1	TGFB1,PRR5L,HYAL2,OAZ3,CDH1	turquoise	VSMC_M6
GO:1903507	0.38	0.69	30	945	negative regulation of nucleic acid-templated transcription	BP	1	NOTCH4,PDGFB,ETV7,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,MAPK10,SNCA,NFATC2,BMP7,PROX1,PRAME,PAX9,PPM1F,BCL6B,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:1905039	0.38	0.80	4	105	carboxylic acid transmembrane transport	BP	1	SLC16A8,SLC6A6,CD36,SLC25A18	turquoise	VSMC_M6
GO:0032147	0.38	0.80	4	105	activation of protein kinase activity	BP	1	IL23A,PDGFB,CD86,MTOR	turquoise	VSMC_M6
GO:0051098	0.39	0.73	10	296	regulation of binding	BP	1	PDGFB,KDM4D,PPARG,TGFB1,CTNNB1,TMC8,HFE,ACE,LHX2,BAMBI	turquoise	VSMC_M6
GO:0044409	0.39	0.79	4	106	entry into host	BP	1	CXCR4,HYAL2,CD86,TRIM62	turquoise	VSMC_M6
GO:0012501	0.39	0.67	46	1474	programmed cell death	BP	1	FLT4,MEGF10,KDR,SYK,IL6,PIK3CG,DLL1,CTSC,NOS3,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TMC8,SFRP1,CXCL10,CYP26B1,COL2A1,SNCA,HYAL2,LAPTM5,INPP5D,EAF2,ERN1,BMP7,IGFBP3,FANK1,PRAME,LTF,TBX1,RGN,LGALS12,PPM1F,PRKCH,MTOR,SARM1,TNFRSF18,NOTCH1,ENDOG,CDH5,ALOX12,PMAIP1,VSTM2L,CCR7,PDE1B	turquoise	VSMC_M6
GO:1903825	0.39	0.79	4	106	organic acid transmembrane transport	BP	1	SLC16A8,SLC6A6,CD36,SLC25A18	turquoise	VSMC_M6
GO:0099504	0.39	0.77	5	138	synaptic vesicle cycle	BP	1	SYN2,CTNNB1,SNAP25,SNCA,SNCG	turquoise	VSMC_M6
GO:0043547	0.39	0.75	7	202	positive regulation of GTPase activity	BP	1	ARHGAP25,SFRP1,ARHGAP27,RGN,ARHGEF15,S1PR1,CCR7	turquoise	VSMC_M6
GO:0006629	0.39	0.68	31	982	lipid metabolic process	BP	1	ENPP2,IP6K3,PDGFB,ADGRF5,OSBPL3,PIK3CG,RAB38,RARRES2,PPARG,TGFB1,CD36,CYP26B1,PLCB2,NKX2-3,SNCA,MTTP,INPP5D,PROX1,RGN,LGALS12,FGF23,PITPNM3,MTOR,DEGS2,B4GALT6,PTGS1,ALOX12,CCR7,HRASLS,SCARF1,RBP1	turquoise	VSMC_M6
GO:0035195	0.39	0.79	4	107	gene silencing by miRNA	BP	1	IL6,PPARG,TGFB1,MIR1307	turquoise	VSMC_M6
GO:0007565	0.40	0.77	5	139	female pregnancy	BP	1	ITGB4,ANGPT2,HFE,MTOR,KLF1	turquoise	VSMC_M6
GO:0016043	0.40	0.64	141	4652	cellular component organization	BP	1	PARD6G,MEGF10,SYBU,CELSR1,ENPP2,SYT17,PDGFB,FRMD3,MDGA1,DNAH8,ATP8A1,STEAP4,KDR,SYK,THSD7A,EPHA5,IL6,BCL11A,LRRC4B,ARHGAP25,GJA4,CFAP100,KCNA7,RASIP1,DLL1,KDM4D,NOVA2,RAB38,FGD5,NOS3,CD177,ITGB4,PPARG,TGFB1,KCTD12,CXCR4,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,MAP6,DNAJB13,SNAP25,PDE2A,SFRP1,CNTN4,CD36,CFAP54,PRAG1,ADAMTS9,ATP8A2,HHEX,REEP1,CXCL10,SLC4A5,CYP26B1,PPP1R16B,COL2A1,BMP1,SNCA,CTNND2,ANO3,SHANK2,MTTP,HYAL2,SLC39A8,NKD2,HFE,DPYSL4,ROBO4,NRAP,ESAM,LAPTM5,NFATC2,EAF2,CD34,PECAM1,COL18A1,BMP7,PROX1,GPC1,ACE,CNKSR2,LAMC2,CLDN16,SUN3,CCDC88B,CDA,SELE,SELP,BAIAP2L1,PPM1F,PITPNM3,PRKCH,SNCG,C19orf57,MTOR,TTLL6,ABI3,ARHGEF15,MAST1,NPR1,THSD4,ISLR2,CCDC69,COL4A6,COL4A5,B4GALT6,KIF26A,HCN1,SARM1,SEMA6B,NOTCH1,S1PR1,ENDOG,LHX2,COL24A1,CDH1,ADGRL4,CDH5,MMP12,TSPYL1,PMAIP1,RUFY4,SOX17,RELN,ALKAL1,PDLIM1,VSTM2L,HIST1H4G,KANK3,SHANK3,TRPM2,PKIB,CCR7,HRASLS,NSG2,RTN4RL2,GNG4,SCARF1	turquoise	VSMC_M6
GO:0071496	0.40	0.73	9	267	cellular response to external stimulus	BP	1	PDE2A,SFRP1,GOT1,HFE,TLR7,FGF23,MTOR,KIF26A,PMAIP1	turquoise	VSMC_M6
GO:0009100	0.40	0.72	10	299	glycoprotein metabolic process	BP	1	CTNNB1,ADAMTS9,COL2A1,SLC39A8,GPC1,ST6GAL1,B4GALT6,MMP12,CCR7,MGAT3	turquoise	VSMC_M6
GO:0071214	0.40	0.73	9	267	cellular response to abiotic stimulus	BP	1	KDM4D,PDE2A,SFRP1,SLC4A11,MAPK10,GOT1,HYAL2,TLR7,RCSD1	turquoise	VSMC_M6
GO:0104004	0.40	0.73	9	267	cellular response to environmental stimulus	BP	1	KDM4D,PDE2A,SFRP1,SLC4A11,MAPK10,GOT1,HYAL2,TLR7,RCSD1	turquoise	VSMC_M6
GO:0046165	0.40	0.78	4	108	alcohol biosynthetic process	BP	1	IP6K3,P2RY6,GOT1,SNCA	turquoise	VSMC_M6
GO:0031346	0.41	0.72	10	302	positive regulation of cell projection organization	BP	1	ENPP2,MAP6,ATP8A2,BMP7,MTOR,ISLR2,RELN,ALKAL1,CCR7,SCARF1	turquoise	VSMC_M6
GO:0000122	0.41	0.68	22	694	negative regulation of transcription by RNA polymerase II	BP	1	NOTCH4,PDGFB,ETV7,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,CD36,HHEX,MAPK10,SNCA,NFATC2,PROX1,BCL6B,NRARP,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0032868	0.41	0.73	7	206	response to insulin	BP	1	RARRES2,PPARG,SOGA1,GOT1,PTPRE,BAIAP2L1,MTOR	turquoise	VSMC_M6
GO:0009755	0.41	0.75	5	142	hormone-mediated signaling pathway	BP	1	PPARG,SFRP1,ESRRG,BMP7,SSTR5	turquoise	VSMC_M6
GO:0097305	0.41	0.74	6	174	response to alcohol	BP	1	TGFB1,CTNNB1,P2RY6,SFRP1,CDH1,CCR7	turquoise	VSMC_M6
GO:0051259	0.41	0.74	6	174	protein complex oligomerization	BP	1	STEAP4,KCNA7,KCTD12,SNCA,HCN1,TRPM2	turquoise	VSMC_M6
GO:0071333	0.41	0.77	4	110	cellular response to glucose stimulus	BP	1	SYBU,EPHA5,ERN1,ENDOG	turquoise	VSMC_M6
GO:0016192	0.41	0.65	37	1192	vesicle-mediated transport	BP	1	MEGF10,ENPP2,SYT17,DENND3,SYK,ARHGAP25,PIK3CG,DLL1,RAB38,GRIP2,EXOC3L2,CD177,SYN2,CTNNB1,SPTBN4,P2RY6,SNAP25,CD36,ADAMTS9,STAB1,MAPK10,SNCA,NKD2,HFE,LAPTM5,PECAM1,SSC4D,ARHGAP27,SYTL5,SELE,SNCG,NOTCH1,IRF8,EXOC3L1,NSG2,TMEM50B,SCARF1	turquoise	VSMC_M6
GO:0048589	0.42	0.68	16	501	developmental growth	BP	1	SYT17,BCL11A,DLL1,CXCR4,CTNNB1,SPTBN4,SFRP1,ATP8A2,PROX1,KIF26B,MTOR,ISLR2,SEMA6B,NOTCH1,S1PR1,LHX2	turquoise	VSMC_M6
GO:0031330	0.42	0.73	7	207	negative regulation of cellular catabolic process	BP	1	RASIP1,PIK3CG,SNCA,HFE,RGN,MTOR,MGAT3	turquoise	VSMC_M6
GO:0061351	0.42	0.77	4	111	neural precursor cell proliferation	BP	1	CTNNB1,PROX1,NOTCH1,LHX2	turquoise	VSMC_M6

GO:0019058	0.42	0.72	8	239	viral life cycle	BP	1	CXCR4,HYAL2,ISG20,CD86,PROX1,LTF,NOTCH1,TRIM62	turquoise	VSMC_M6
GO:0034101	0.42	0.77	4	111	erythrocyte homeostasis	BP	1	IREB2,ADGRF5,INPP5D,KLF1	turquoise	VSMC_M6
GO:0008016	0.43	0.74	5	144	regulation of heart contraction	BP	1	KCNN2,PIK3CG,SPTBN4,DSC2,PDE4B	turquoise	VSMC_M6
GO:0035194	0.43	0.76	4	112	post-transcriptional gene silencing by RNA	BP	1	IL6,PPARG,TGFB1,MIR1307	turquoise	VSMC_M6
GO:0010469	0.43	0.76	4	112	regulation of signaling receptor activity	BP	1	PPARG,HFE,RELN,SHANK3	turquoise	VSMC_M6
GO:0071331	0.43	0.76	4	112	cellular response to hexose stimulus	BP	1	SYBU,EPHA5,ERN1,ENDOG	turquoise	VSMC_M6
GO:0043434	0.43	0.69	10	308	response to peptide hormone	BP	1	RARRES2,PPARG,EDNRB,HHEX,SOGA1,GOT1,BMP7,PTPRE,BAIAP2L1,MTOR	turquoise	VSMC_M6
GO:0071326	0.43	0.75	4	113	cellular response to monosaccharide stimulus	BP	1	SYBU,EPHA5,ERN1,ENDOG	turquoise	VSMC_M6
GO:0035637	0.43	0.75	4	114	multicellular organismal signaling	BP	1	KCNN2,SPTBN4,DSC2,S1PR1	turquoise	VSMC_M6
GO:0009566	0.43	0.75	4	113	fertilization	BP	1	SLC22A16,SPTBN4,HOXD10,ATP1A4	turquoise	VSMC_M6
GO:0030162	0.44	0.66	17	538	regulation of proteolysis	BP	1	SYK,C5,CTSC,PPARG,KLKB1,SOX7,SNCA,NKD2,HFE,LAPTM5,LTF,RGN,PPM1F,ALOX12,PRSS22,PMAIP1,GNA12	turquoise	VSMC_M6
GO:0051592	0.44	0.75	4	114	response to calcium ion	BP	1	SYT17,MTTP,ENDOG,TRPM2	turquoise	VSMC_M6
GO:0042176	0.44	0.68	11	342	regulation of protein catabolic process	BP	1	CTSC,SNCA,NKD2,HFE,LAPTM5,OAZ3,RGN,CDH1,SOX17,GNA12,MGAT3	turquoise	VSMC_M6
GO:0016311	0.44	0.68	11	342	dephosphorylation	BP	1	TGFB1,PPP1R16B,INPP5D,PTPRE,PALD1,RGN,PPM1F,PPP1R1B,MTOR,CDH5,PPP1R3C	turquoise	VSMC_M6
GO:1903522	0.44	0.72	6	179	regulation of blood circulation	BP	1	KCNN2,PIK3CG,SPTBN4,ACE,DSC2,PDE4B	turquoise	VSMC_M6
GO:0090257	0.44	0.72	6	179	regulation of muscle system process	BP	1	PIK3CG,NOS3,MTOR,DSC2,PDE4B,NOTCH1	turquoise	VSMC_M6
GO:0017157	0.45	0.73	5	147	regulation of exocytosis	BP	1	SYT17,SYK,CD177,SNCA,NOTCH1	turquoise	VSMC_M6
GO:0001505	0.45	0.73	5	147	regulation of neurotransmitter levels	BP	1	SYN2,SNAP25,SNCA,MCTP2,SNCG	turquoise	VSMC_M6
GO:0016441	0.45	0.74	4	115	posttranscriptional gene silencing	BP	1	IL6,PPARG,TGFB1,MIR1307	turquoise	VSMC_M6
GO:0010038	0.45	0.68	9	279	response to metal ion	BP	1	SYT17,GOT1,SNCA,MTTP,HFE,FGF23,ENDOG,CDH1,TRPM2	turquoise	VSMC_M6
GO:0051235	0.45	0.69	8	248	maintenance of location	BP	1	IL6,PPARG,P2RY6,CD36,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0032872	0.45	0.72	5	148	regulation of stress-activated MAPK cascade	BP	1	FLT4,ANKRD6,SFRP1,CRACR2A,CCR7	turquoise	VSMC_M6
GO:0030902	0.45	0.74	4	116	hindbrain development	BP	1	DLL1,CTNNB1,BMP7,PROX1	turquoise	VSMC_M6
GO:0045088	0.45	0.72	5	148	regulation of innate immune response	BP	1	IL18RAP,SYK,PPARG,MMP12,TRIM62	turquoise	VSMC_M6
GO:0019222	0.45	0.59	146	4858	regulation of metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,ETV7,MOB3B,IREB2,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,NDUFA4,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,RARRES2,NOS3,CD177,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,NFKBID,KIRREL2,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,SLC4A5,ADGRG3,ATP6V0D2,PRDM8,THBS4,CYP26B1,PPP1R16B,COL2A1,TOX2,MAPK10,IRX6,GOT1,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,OAZ3,FANK1,ACE,HOXD10,PRAME,PAX9,LTF,LPAR2,CCDC88B,TBX1,RGN,CDA,LGALS12,SELE,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,BCKDK,KLF1,LYL1,PDE4B,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,RUFY4,TRIM43,SOX17,RELN,ACKR1,ALKAL1,C3AR1,MIR1307,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:0045017	0.45	0.69	7	214	glycerolipid biosynthetic process	BP	1	IP6K3,PDGFB,PIK3CG,RAB38,INPP5D,RGN,PITPNM3	turquoise	VSMC_M6
GO:0010977	0.45	0.74	4	116	negative regulation of neuron projection development	BP	1	BCL11A,PRAG1,SEMA6B,RTN4RL2	turquoise	VSMC_M6
GO:1900180	0.46	0.74	4	116	regulation of protein localization to nucleus	BP	1	TGFB1,CD36,HYAL2,CDH1	turquoise	VSMC_M6
GO:2001141	0.46	0.59	73	2416	regulation of RNA biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0006164	0.46	0.71	5	149	purine nucleotide biosynthetic process	BP	1	NOS3,TGFB1,SNCA,GUCY1A2,NPR1	turquoise	VSMC_M6
GO:0001890	0.46	0.73	4	117	placenta development	BP	1	PDGFB,PPARG,PCDH12,BMP7	turquoise	VSMC_M6
GO:0051248	0.46	0.62	25	813	negative regulation of protein metabolic process	BP	1	IREB2,C5,RASIP1,KDM4D,PPARG,TGFB1,EDNRB,CTNNB1,SFRP1,KIRREL2,PRR5L,HHEX,PPP1R16B,SNCA,HYAL2,HFE,BMP7,IGFBP3,LTF,RGN,PPM1F,PPP1R1B,MTOR,PKIB,MGAT3	turquoise	VSMC_M6
GO:0031960	0.46	0.73	4	117	response to corticosteroid	BP	1	IL6,GOT1,SSTR5,NOTCH1	turquoise	VSMC_M6
GO:0008154	0.46	0.70	6	183	actin polymerization or depolymerization	BP	1	SPTBN4,ESAM,BAIAP2L1,MTOR,KANK3,CCR7	turquoise	VSMC_M6
GO:0031345	0.46	0.71	5	150	negative regulation of cell projection organization	BP	1	BCL11A,PRAG1,ABI3,SEMA6B,RTN4RL2	turquoise	VSMC_M6
GO:0045934	0.46	0.61	34	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	NOTCH4,PDGFB,ETV7,IL6,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,MAPK10,SNCA,NFATC2,BMP7,PROX1,PRAME,PAX9,RGN,CDA,PPM1F,BCL6B,MTOR,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0051258	0.47	0.67	8	250	protein polymerization	BP	1	SPTBN4,SNCA,ESAM,BAIAP2L1,MTOR,CDH5,KANK3,CCR7	turquoise	VSMC_M6
GO:0070302	0.47	0.71	5	151	regulation of stress-activated protein kinase signaling cascade	BP	1	FLT4,ANKRD6,SFRP1,CRACR2A,CCR7	turquoise	VSMC_M6
GO:1903052	0.47	0.72	4	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	CTSC,NKD2,LAPTM5,RGN	turquoise	VSMC_M6
GO:1901214	0.47	0.67	8	251	regulation of neuron death	BP	1	CTNNB1,SNCA,CD34,SNCG,MTOR,SARM1,VSTM2L,TRPM2	turquoise	VSMC_M6
GO:0019318	0.47	0.69	6	185	hexose metabolic process	BP	1	SOGA1,RGN,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0046474	0.47	0.69	6	185	glycerophospholipid biosynthetic process	BP	1	IP6K3,PDGFB,PIK3CG,RAB38,INPP5D,PITPNM3	turquoise	VSMC_M6
GO:0009725	0.47	0.62	20	652	response to hormone	BP	1	IL6,RARRES2,NOS3,PPARG,TGFB1,EDNRB,P2RY6,SFRP1,HHEX,SOGA1,GOT1,ESRRG,BMP7,PTPRE,BAIAP2L1,FGF23,MTOR,SSTR5,NOTCH1,CCR7	turquoise	VSMC_M6
GO:0009991	0.48	0.64	12	385	response to extracellular stimulus	BP	1	RARRES2,PPARG,SFRP1,CXCL10,CYP26B1,HFE,BMP7,PROX1,FGF23,MTOR,KIF26A,PMAIP1	turquoise	VSMC_M6

GO:0080135	0.48	0.62	17	553	regulation of cellular response to stress	BP	1	FLT4,ANKRD6,KDM4D,CTNNB1,SFRP1,CD36,CD34,ERN1,BMP7,CRACR2A,MTOR,ABI3,ENDOG,PMAIP1,TRPM2,CCR7,SCARF1	turquoise	VSMC_M6
GO:0043123	0.48	0.69	5	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	CTNNB1,CD36,LTF,TRIM62,CCR7	turquoise	VSMC_M6
GO:0071322	0.49	0.71	4	121	cellular response to carbohydrate stimulus	BP	1	SYBU,EPHA5,ERN1,ENDOG	turquoise	VSMC_M6
GO:1901575	0.49	0.57	49	1628	organic substance catabolic process	BP	1	ENPP2,DENND3,IL6,PIK3CG,CTSC,RARRES2,NOS3,TGFB1,CTNNB1,SLCO2B1,PDE2A,NOTUM,ADAMTS9,PRR5L,LYVE1,CYP26B1,PLCB2,GOT1,SNCA,HYAL2,NKD2,HFE,LAPTM5,ISG20,ERN1,ASCC2,GPC1,OAZ3,ACE,PRAME,RGN,CDA,LGALS12,FGF23,MTOR,BCKDK,PDE4B,SARM1,NOTCH1,ENDOG,CDH1,MMP12,PMAIP1,SOX17,GNA12,HRASLS,MGAT3,NUDT4B,SCARF1	turquoise	VSMC_M6
GO:1903362	0.49	0.66	7	222	regulation of cellular protein catabolic process	BP	1	CTSC,NKD2,HFE,LAPTM5,RGN,GNA12,MGAT3	turquoise	VSMC_M6
GO:0008654	0.49	0.66	7	222	phospholipid biosynthetic process	BP	1	IP6K3,PDGFB,ADGRF5,PIK3CG,RAB38,INPP5D,PITPNM3	turquoise	VSMC_M6
GO:0048511	0.49	0.66	7	223	rhythmic process	BP	1	TNFRSF11A,PPARG,MAPK10,MTTP,PROX1,MTOR,TRPM2	turquoise	VSMC_M6
GO:0030010	0.49	0.70	4	123	establishment of cell polarity	BP	1	CYP26B1,KIF26B,CDH5,CCR7	turquoise	VSMC_M6
GO:0006913	0.50	0.64	8	257	nucleocytoplasmic transport	BP	1	SYK,TGFB1,CD36,HHEX,HYAL2,NOTCH1,CDH1,MMP12	turquoise	VSMC_M6
GO:0051169	0.50	0.64	8	257	nuclear transport	BP	1	SYK,TGFB1,CD36,HHEX,HYAL2,NOTCH1,CDH1,MMP12	turquoise	VSMC_M6
GO:0005975	0.50	0.61	14	458	carbohydrate metabolic process	BP	1	PDGFB,TGFB1,P2RY6,PCDH12,SOGA1,GOT1,SNCA,HYAL2,RGN,MTOR,BCKDK,B4GALT6,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0019752	0.50	0.59	20	659	carboxylic acid metabolic process	BP	1	IREB2,SYK,OSBPL3,NOS3,PPARG,CD36,CYP26B1,GOT1,SNCA,SLC39A8,PROX1,ART4,ST6GAL1,RGN,AGMAT,MTOR,BCKDK,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:0048545	0.50	0.64	8	258	response to steroid hormone	BP	1	IL6,TGFB1,SFRP1,GOT1,ESRRG,BMP7,SSTR5,NOTCH1	turquoise	VSMC_M6
GO:0006355	0.50	0.55	72	2411	regulation of transcription, DNA-templated	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0009314	0.50	0.62	11	359	response to radiation	BP	1	TNFRSF11A,KDM4D,SFRP1,ATP8A2,CXCL10,ANGPT2,MAPK10,HYAL2,PPP1R1B,MTOR,GNGT2	turquoise	VSMC_M6
GO:0072522	0.50	0.67	5	157	purine-containing compound biosynthetic process	BP	1	NOS3,TGFB1,SNCA,GUCY1A2,NPR1	turquoise	VSMC_M6
GO:1903506	0.50	0.55	72	2412	regulation of nucleic acid-templated transcription	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0010821	0.51	0.69	4	124	regulation of mitochondrion organization	BP	1	KDR,PPARG,PDE2A,PMAIP1	turquoise	VSMC_M6
GO:0001678	0.51	0.69	4	124	cellular glucose homeostasis	BP	1	SYBU,EPHA5,ERN1,ENDOG	turquoise	VSMC_M6
GO:0120032	0.51	0.67	5	158	regulation of plasma membrane bounded cell projection assembly	BP	1	PPP1R16B,MTOR,ABI3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0006915	0.51	0.56	43	1436	apoptotic process	BP	1	FLT4,MEGF10,KDR,IL6,PIK3CG,DLL1,CTSC,NOS3,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,TMC8,SFRP1,CXCL10,COL2A1,SNCA,HYAL2,INPP5D,EAF2,ERN1,BMP7,IGFBP3,FANK1,PRAME,LTF,TBX1,RGN,LGALS12,PPM1F,PRKCH,MTOR,SARM1,TNFRSF18,NOTCH1,ENDOG,CDH5,ALOX12,PMAIP1,VSTM2L,CCR7,PDE1B	turquoise	VSMC_M6
GO:0010638	0.51	0.61	13	428	positive regulation of organelle organization	BP	1	PDGFB,KDR,CTNNB1,SFRP1,SNCA,PROX1,BAIAP2L1,PPM1F,MTOR,ARHGEF15,PMAIP1,PKIB,CCR7	turquoise	VSMC_M6
GO:0015980	0.51	0.63	8	259	energy derivation by oxidation of organic compounds	BP	1	IREB2,ADGRF5,NDUFA4,PCDH12,SNCA,SLC25A18,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:1903050	0.51	0.65	6	192	regulation of proteolysis involved in cellular protein catabolic process	BP	1	CTSC,NKD2,HFE,LAPTM5,RGN,GNA12	turquoise	VSMC_M6
GO:0060491	0.51	0.67	5	159	regulation of cell projection assembly	BP	1	PPP1R16B,MTOR,ABI3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0044706	0.51	0.66	5	159	multi-multicellular organism process	BP	1	ITGB4,ANGPT2,HFE,MTOR,KLF1	turquoise	VSMC_M6
GO:0031667	0.51	0.61	11	362	response to nutrient levels	BP	1	RARRES2,PPARG,SFRP1,CXCL10,CYP26B1,HFE,BMP7,PROX1,FGF23,MTOR,PMAIP1	turquoise	VSMC_M6
GO:0048608	0.52	0.61	10	330	reproductive structure development	BP	1	PDGFB,PPARG,CTNNB1,SFRP1,PCDH12,EAF2,BMP7,MGST1,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0007010	0.52	0.55	35	1177	cytoskeleton organization	BP	1	PARD6G,CELSR1,FRMD3,DNAH8,THSD7A,EPHA5,ARHGAP25,CFAP100,FGD5,CTNNB1,SPTBN4,MAP6,DNAJB13,SFRP1,ATP8A2,SNCA,NRAP,ESAM,PROX1,CCDC88B,BAIAP2L1,PPM1F,MTOR,TTLL6,ABI3,ARHGEF15,MAST1,CCDC69,S1PR1,CDH5,PDLIM1,KANK3,SHANK3,TRPM2,CCR7	turquoise	VSMC_M6
GO:0052126	0.53	0.67	4	127	movement in host environment	BP	1	CXCR4,HYAL2,CD86,TRIM62	turquoise	VSMC_M6
GO:0009894	0.53	0.56	24	806	regulation of catabolic process	BP	1	KDR,IL6,RASIP1,PIK3CG,CTSC,RARRES2,PRR5L,SOGA1,ATP6V0D2,SNCA,NKD2,HFE,LAPTM5,ERN1,OAZ3,RGN,LGALS12,MTOR,ENDOG,CDH1,RUFY4,SOX17,GNA12,MGAT3	turquoise	VSMC_M6
GO:0051651	0.53	0.65	5	163	maintenance of location in cell	BP	1	P2RY6,CXCL10,SNCA,TRPM2,CCR7	turquoise	VSMC_M6
GO:0043393	0.53	0.65	5	162	regulation of protein binding	BP	1	PDGFB,TMC8,HFE,ACE,BAMBI	turquoise	VSMC_M6
GO:0120031	0.53	0.58	13	435	plasma membrane bounded cell projection assembly	BP	1	DNAH8,CFAP100,FGD5,ITGB4,DNAJB13,CFAP54,PPP1R16B,MTOR,ABI3,NOTCH1,S1PR1,TRPM2,CCR7	turquoise	VSMC_M6
GO:0061458	0.53	0.60	10	333	reproductive system development	BP	1	PDGFB,PPARG,CTNNB1,SFRP1,PCDH12,EAF2,BMP7,MGST1,GREB1L,NOTCH1	turquoise	VSMC_M6
GO:0046661	0.53	0.67	4	128	male sex differentiation	BP	1	CTNNB1,SFRP1,MGST1,GREB1L	turquoise	VSMC_M6

GO:0071840	0.53	0.51	143	4827	cellular component organization or biogenesis	BP	1	PARD6G,MEGF10,SYBU,CELSR1,ENPP2,SYT17,PDGFB,FRMD3,MDGA1,DNAH8,ATP8A1,STEAP4,KDR,SYK,THSD7A,EPHA5,IL6,BCL11A,LRRC4B,ARHGAP25,GJA4,CFAP100,KCNA7,RASIP1,DLL1,KDM4D,NSUN4,NOVA2,RAB38,FGD5,NOS3,CD177,ITGB4,PPARG,TGFB1,KCTD12,CXCR4,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,MAP6,DNAJB13,SNAP25,PDE2A,SFRP1,CNTN4,CD36,CFAP54,PRAG1,ADAMTS9,ATP8A2,HHEX,REEP1,CXCL10,SLC4A5,CYP26B1,PPP1R16B,COL2A1,BMP1,SNCA,CTNND2,ANO3,SHANK2,MTTP,HYAL2,SLC39A8,NKD2,HFE,DPYSL4,ROBO4,NRAP,ESAM,LAPTM5,ISG20,NFATC2,EAF2,CD34,PECAM1,COL18A1,BMP7,PROX1,GPC1,ACE,CNKSR2,LAMC2,CLDN16,SUN3,CCDC88B,CDA,SELE,SELP,BAIAP2L1,PPM1F,PITPNM3,PRKCH,SNCG,C19orf57,MTOR,TTLL6,ABI3,ARHGEF15,MAST1,NPR1,THSD4,ISLR2,CCDC69,COL4A6,COL4A5,B4GALT6,KIF26A,HCN1,SARM1,SEMA6B,NOTCH1,S1PR1,ENDOG,LHX2,COL24A1,CDH1,ADGRL4,CDH5,MMP12,TSPYL1,PMAIP1,RUFY4,SOX17,RELN,ALKAL1,PDLIM1,VSTM2L,HIST1H4G,KANK3,SHANK3,TRPM2,PKIB,CCR7,HRASLS,NSG2,RTN4RL2,GNG4,SCARF1	turquoise	VSMC_M6
GO:0031047	0.54	0.66	4	129	gene silencing by RNA	BP	1	IL6,PPARG,TGFB1,MIR1307	turquoise	VSMC_M6
GO:0010506	0.54	0.60	8	268	regulation of autophagy	BP	1	KDR,RASIP1,SOGA1,ATP6V0D2,SNCA,ERN1,MTOR,RUFY4	turquoise	VSMC_M6
GO:0009267	0.54	0.66	4	130	cellular response to starvation	BP	1	SFRP1,HFE,MTOR,PMAIP1	turquoise	VSMC_M6
GO:0033043	0.54	0.53	28	950	regulation of organelle organization	BP	1	CELSR1,PDGFB,KDR,EPHA5,LRRC4B,PPARG,CTNNB1,SPTBN4,MAP6,PDE2A,SFRP1,SNCA,ESAM,BMP7,PROX1,BAIAP2L1,PPM1F,MTOR,ABI3,ARHGEF15,S1PR1,CDH5,PMAIP1,KANK3,SHANK3,TRPM2,PKIB,CCR7	turquoise	VSMC_M6
GO:0005996	0.54	0.62	6	199	monosaccharide metabolic process	BP	1	SOGA1,RGN,MTOR,BCKDK,PMAIP1,PPP1R3C	turquoise	VSMC_M6
GO:0009890	0.55	0.52	36	1222	negative regulation of biosynthetic process	BP	1	NOTCH4,PDGFB,ETV7,IREB2,IL6,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,SOGA1,MAPK10,GOT1,SNCA,NFATC2,CD34,BMP7,PROX1,PRAME,PAX9,RGN,PPM1F,BCL6B,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0043436	0.55	0.54	20	677	oxoacid metabolic process	BP	1	IREB2,SYK,OSBPL3,NOS3,PPARG,CD36,CYP26B1,GOT1,SNCA,SLC39A8,PROX1,ART4,ST6GAL1,RGN,AGMAT,MTOR,BCKDK,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:1901653	0.55	0.59	8	270	cellular response to peptide	BP	1	RARRES2,PPARG,CD36,SOGA1,GOT1,PTPRE,BAIAP2L1,KLF1	turquoise	VSMC_M6
GO:0030031	0.56	0.56	13	443	cell projection assembly	BP	1	DNAH8,CFAP100,FGD5,ITGB4,DNAJB13,CFAP54,PPP1R16B,MTOR,ABI3,NOTCH1,S1PR1,TRPM2,CCR7	turquoise	VSMC_M6
GO:0008610	0.56	0.55	16	544	lipid biosynthetic process	BP	1	IP6K3,PDGFB,ADGRF5,OSBPL3,PIK3CG,RAB38,INPP5D,PROX1,RGN,PITPNM3,MTOR,DEGS2,B4GALT6,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:0042445	0.56	0.64	4	133	hormone metabolic process	BP	1	CYP26B1,HFE,ACE,RBP1	turquoise	VSMC_M6
GO:0045732	0.56	0.60	6	203	positive regulation of protein catabolic process	BP	1	CTSC,NKD2,LAPTM5,OAZ3,RGN,SOX17	turquoise	VSMC_M6
GO:0002221	0.57	0.63	4	134	pattern recognition receptor signaling pathway	BP	1	CD36,TLR7,LTF,SARM1	turquoise	VSMC_M6
GO:0031668	0.57	0.59	6	205	cellular response to extracellular stimulus	BP	1	SFRP1,HFE,FGF23,MTOR,KIF26A,PMAIP1	turquoise	VSMC_M6
GO:0009892	0.58	0.48	66	2254	negative regulation of metabolic process	BP	1	IL23A,NOTCH4,PDGFB,ETV7,IREB2,KDR,IL6,BCL11A,C5,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,KIRREL2,PRR5L,HHEX,SOX7,SOGA1,PPP1R16B,MAPK10,GOT1,SNCA,HYAL2,HFE,LAPTM5,NFATC2,INPP5D,CD34,ERN1,BMP7,IGFBP3,PROX1,ACE,PRAME,PAX9,LTF,RGN,CDA,PPM1F,BCL6B,PPP1R1B,MTOR,BCKDK,NRARP,HES3,NOTCH1,IRF8,GBP1,LHX2,CDH3,MMP12,MIR1307,OLIG2,SOX18,PKIB,CCR7,MGAT3	turquoise	VSMC_M6
GO:0051222	0.58	0.57	7	241	positive regulation of protein transport	BP	1	SYBU,TGFB1,PRR5L,HYAL2,OAZ3,CDH1,TRPM2	turquoise	VSMC_M6
GO:0032870	0.58	0.53	13	450	cellular response to hormone stimulus	BP	1	RARRES2,PPARG,P2RY6,SFRP1,SOGA1,GOT1,ESRRG,BMP7,PTPRE,BAIAP2L1,FGF23,SSTR5,NOTCH1	turquoise	VSMC_M6
GO:0007034	0.58	0.62	4	137	vacuolar transport	BP	1	DENND3,ATP6V0D2,LAPTM5,TMEM50B	turquoise	VSMC_M6
GO:0044283	0.58	0.54	12	414	small molecule biosynthetic process	BP	1	IP6K3,SYK,OSBPL3,P2RY6,SOGA1,GOT1,SNCA,PROX1,RGN,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:0006082	0.58	0.51	20	689	organic acid metabolic process	BP	1	IREB2,SYK,OSBPL3,NOS3,PPARG,CD36,CYP26B1,GOT1,SNCA,SLC39A8,PROX1,ART4,ST6GAL1,RGN,AGMAT,MTOR,BCKDK,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:1903364	0.59	0.61	4	137	positive regulation of cellular protein catabolic process	BP	1	CTSC,NKD2,LAPTM5,RGN	turquoise	VSMC_M6
GO:0009152	0.59	0.61	4	137	purine ribonucleotide biosynthetic process	BP	1	TGFB1,SNCA,GUCY1A2,NPR1	turquoise	VSMC_M6
GO:0032388	0.59	0.59	5	173	positive regulation of intracellular transport	BP	1	TGFB1,PRR5L,HYAL2,OAZ3,CDH1	turquoise	VSMC_M6
GO:0043086	0.59	0.51	16	555	negative regulation of catalytic activity	BP	1	C5,RASIP1,PPARG,EDNRB,SFRP1,HHEX,SNCA,HYAL2,BMP7,OAZ3,LTF,RGN,PPM1F,PPP1R1B,NOTCH1,PKIB	turquoise	VSMC_M6
GO:0032774	0.59	0.46	74	2534	RNA biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0090407	0.59	0.52	13	452	organophosphate biosynthetic process	BP	1	IP6K3,PDGFB,ADGRF5,PIK3CG,RAB38,NOS3,TGFB1,P2RY6,SNCA,INPP5D,GUCY1A2,PITPNM3,NPR1	turquoise	VSMC_M6
GO:0051051	0.59	0.54	9	314	negative regulation of transport	BP	1	SFRP1,CD36,SNCA,OAZ3,FGF23,PPM1F,MTOR,NOTCH1,NMB	turquoise	VSMC_M6
GO:0009896	0.60	0.52	12	420	positive regulation of catabolic process	BP	1	KDR,IL6,CTSC,PRR5L,SNCA,NKD2,LAPTM5,OAZ3,RGN,ENDOG,RUFY4,SOX17	turquoise	VSMC_M6

GO:0060255	0.60	0.45	131	4468	regulation of macromolecule metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,ETV7,MOB3B,IREB2,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,PDE2A,SFRP1,ZIC2,CD36,NFKBID,KIRREL2,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,SLC4A5,ADGRG3,PRDM8,THBS4,CYP26B1,PPP1R16B,COL2A1,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,OAZ3,FANK1,ACE,HOXD10,PRAME,PAX9,LTF,CCDC88B,TBX1,RGN,SELE,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,PDE4B,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,TRIM43,SOX17,RELN,ACKR1,ALKAL1,C3AR1,MIR1307,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:0007018	0.60	0.54	8	283	microtubule-based movement	BP	1	SYBU,DNAH8,CFAP100,SLC22A16,CFAP54,RGN,TTLL6,ATP1A4	turquoise	VSMC_M6
GO:0009056	0.61	0.45	58	2000	catabolic process	BP	1	ENPP2,DENND3,KDR,IL6,RASIP1,PIK3CG,CTSC,RARRES2,NOS3,ITGB4,TGFB1,CTNNB1,SLCO2B1,PDE2A,NOTUM,CD36,ADAMTS9,PRR5L,LYVE1,SOGA1,ATP6V0D2,CYP26B1,PLCB2,GOT1,SNCA,HYAL2,NKD2,HFE,LAPTM5,ISG20,ERN1,ASCC2,GPC1,OAZ3,ACE,PRAME,RGN,CDA,LGALS12,FGF23,MTOR,BCKDK,PDE4B,SARM1,NOTCH1,IRF8,ENDOG,CDH1,MMP12,PMAIP1,RUFY4,SOX17,GNA12,HRASLS,MGAT3,NUDT4B,SCARF1,GPX3	turquoise	VSMC_M6
GO:0044092	0.61	0.47	23	806	negative regulation of molecular function	BP	1	PDGFB,C5,RASIP1,PPARG,EDNRB,TMC8,SFRP1,HHEX,ADGRG3,SNCA,HYAL2,HFE,BMP7,PROX1,OAZ3,ACE,LTF,RGN,PPM1F,PPP1R1B,NOTCH1,LHX2,PKIB	turquoise	VSMC_M6
GO:0044282	0.62	0.53	8	284	small molecule catabolic process	BP	1	NOS3,CYP26B1,GOT1,CDA,FGF23,MTOR,BCKDK,SCARF1	turquoise	VSMC_M6
GO:0051650	0.62	0.58	4	143	establishment of vesicle localization	BP	1	SYBU,CTNNB1,SNCA,CDH3	turquoise	VSMC_M6
GO:2000058	0.62	0.58	4	143	regulation of ubiquitin-dependent protein catabolic process	BP	1	NKD2,HFE,LAPTM5,GNA12	turquoise	VSMC_M6
GO:0006351	0.62	0.43	73	2521	transcription, DNA-templated	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0097659	0.62	0.43	73	2522	nucleic acid-templated transcription	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0030522	0.63	0.53	6	217	intracellular receptor signaling pathway	BP	1	PPARG,SFRP1,CYP26B1,ESRRG,PRAME,TBX1	turquoise	VSMC_M6
GO:0031323	0.63	0.41	128	4391	regulation of cellular metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,ETV7,MOB3B,IREB2,ADGRF5,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,NDUFA4,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,RARRES2,NOS3,CD177,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,KIRREL2,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,ATP6V0D2,PRDM8,THBS4,PPP1R16B,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,NFATC2,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,FANK1,ACE,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,CDA,SELE,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,BCKDK,KLF1,LYL1,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,LHX6,CDH3,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,RUFY4,SOX17,RELN,ALKAL1,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:0019637	0.63	0.46	21	743	organophosphate metabolic process	BP	1	ENPP2,IP6K3,PDGFB,ADGRF5,PIK3CG,RAB38,NOS3,TGFB1,P2RY6,PDE2A,PLCB2,SNCA,INPP5D,GUCY1A2,CDA,PITPNM3,NPR1,PDE4B,SARM1,HRASLS,NUDT4B	turquoise	VSMC_M6
GO:0032535	0.63	0.50	9	325	regulation of cellular component size	BP	1	SPTBN4,ESAM,BAIAP2L1,MTOR,ISLR2,SEMA6B,KANK3,SHANK3,CCR7	turquoise	VSMC_M6
GO:0009895	0.63	0.52	7	254	negative regulation of catabolic process	BP	1	RASIP1,PIK3CG,SNCA,HFE,RGN,MTOR,MGAT3	turquoise	VSMC_M6
GO:0031669	0.63	0.54	5	182	cellular response to nutrient levels	BP	1	SFRP1,HFE,FGF23,MTOR,PMAIP1	turquoise	VSMC_M6
GO:0016032	0.63	0.50	9	325	viral process	BP	1	CXCR4,HYAL2,ISG20,CD86,PROX1,ST6GAL1,LTF,NOTCH1,TRIM62	turquoise	VSMC_M6
GO:0071375	0.64	0.52	6	219	cellular response to peptide hormone stimulus	BP	1	RARRES2,PPARG,SOGA1,GOT1,PTPRE,BAIAP2L1	turquoise	VSMC_M6
GO:0046395	0.64	0.54	5	182	carboxylic acid catabolic process	BP	1	NOS3,CYP26B1,GOT1,MTOR,BCKDK	turquoise	VSMC_M6

GO:0010605	0.64	0.42	60	2090	negative regulation of macromolecule metabolic process	BP	1	IL23A,NOTCH4,PDGFB,ETV7,IREB2,KDR,IL6,BCL11A,C5,RASIP1,DLL1,KDM4D,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,KIRREL2,PRR5L,HHEX,SOX7,PPP1R16B,MAPK10,SNCA,HYAL2,HFE,LAPTM5,NFATC2,INPP5D,CD34,ERN1,BMP7,IGFBP3,PROX1,ACE,PRAME,PAX9,LTF,RGN,PPM1F,BCL6B,PPP1R1B,MTOR,NRARP,HES3,NOTCH1,IRF8,GBP1,LHX2,CDH3,MMP12,MIR1307,OLIG2,SOX18,PKIB,CCR7,MGAT3	turquoise	VSMC_M6
GO:0031327	0.64	0.43	34	1198	negative regulation of cellular biosynthetic process	BP	1	NOTCH4,PDGFB,ETV7,IREB2,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,SOGA1,MAPK10,SNCA,NFATC2,CD34,BMP7,PROX1,PRAME,PAX9,RGN,PPM1F,BCL6B,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0022607	0.64	0.41	64	2230	cellular component assembly	BP	1	MDGA1,DNAH8,STEAP4,KDR,SYK,LRRC4B,GJA4,CFAP100,KCNA7,RASIP1,RAB38,FGD5,ITGB4,TGFB1,KCTD12,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,DNAJB13,SNAP25,SFRP1,CD36,CFAP54,PPP1R16B,SNCA,CTNND2,SHANK2,MTTP,HFE,NRAP,ESAM,CD34,PECAM1,BMP7,PROX1,GPC1,ACE,CLDN16,SELP,BAIAP2L1,PPM1F,PRKCH,MTOR,ABI3,ARHGEF15,THSD4,CCDC69,HCN1,NOTCH1,S1PR1,CDH1,ADGRL4,CDH5,TSPYL1,RUFY4,PDLIM1,HIST1H4G,KANK3,SHANK3,TRPM2,CCR7,NSG2	turquoise	VSMC_M6
GO:0006357	0.64	0.42	51	1784	regulation of transcription by RNA polymerase II	BP	1	NOTCH4,PDGFB,ETV7,BARX1,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NFATC2,EAF2,TLR7,BMP7,PROX1,HOXD10,PAX9,TBX1,BCL6B,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,MMP12,SOX17,OLIG2,PDLIM1,SOX18,ZNF775,FLI1	turquoise	VSMC_M6
GO:2001233	0.65	0.49	8	292	regulation of apoptotic signaling pathway	BP	1	CTSC,NOS3,CTNNB1,TMC8,SFRP1,COL2A1,HYAL2,PMAIP1	turquoise	VSMC_M6
GO:1904951	0.65	0.50	7	257	positive regulation of establishment of protein localization	BP	1	SYBU,TGFB1,PRR5L,HYAL2,OAZ3,CDH1,TRPM2	turquoise	VSMC_M6
GO:0080090	0.65	0.39	122	4206	regulation of primary metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,ETV7,MOB3B,IREB2,ADGRF5,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,P2RY6,PDE2A,SFRP1,ZIC2,CD36,KIRREL2,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,PRDM8,THBS4,PPP1R16B,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,NFATC2,EAF2,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,OAZ3,FANK1,ACE,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,CDA,LGALS12,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,BCKDK,KLF1,LYL1,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,LHX6,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,SOX17,RELN,ALKAL1,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:0071702	0.65	0.40	54	1891	organic substance transport	BP	1	TNFRSF11A,SYBU,SYT17,SLC16A8,ATP8A1,SYK,EPHA5,IL6,OSBPL3,SLC22A16,RAB38,SLC6A6,GRIP2,PPARG,TGFB1,SLCO2B1,SNAP25,SFRP1,SLC4A11,CD36,SLCO2A1,ADAMTS9,PRR5L,ATP8A2,HHEX,SLCO5A1,SLC4A5,MAPK10,SNCA,MFSD4A,ANO3,MTTP,HYAL2,SLC39A8,HFE,LAPTM5,MGST1,SLCO4A1,OAZ3,ACE,SYTL5,ATP13A1,PPM1F,PITPNM3,SNCG,SLC25A18,SSTR5,NOTCH1,CDH1,EXOC3L1,MMP12,NUCB1,TRPM2,NMB	turquoise	VSMC_M6
GO:0031348	0.65	0.54	4	149	negative regulation of defense response	BP	1	SYK,PPARG,CDH5,MMP12	turquoise	VSMC_M6
GO:0007249	0.65	0.51	6	222	I-kappaB kinase/NF-kappaB signaling	BP	1	CTNNB1,CD36,TLR7,LTF,TRIM62,CCR7	turquoise	VSMC_M6
GO:0031331	0.65	0.47	10	366	positive regulation of cellular catabolic process	BP	1	KDR,IL6,CTSC,PRR5L,SNCA,NKD2,LAPTM5,RGN,ENDOG,RUFY4	turquoise	VSMC_M6
GO:0006066	0.65	0.50	7	258	alcohol metabolic process	BP	1	IP6K3,P2RY6,GOT1,SNCA,DEGS2,NUDT4B,SCARF1	turquoise	VSMC_M6
GO:0009260	0.65	0.54	4	149	ribonucleotide biosynthetic process	BP	1	TGFB1,SNCA,GUCY1A2,NPR1	turquoise	VSMC_M6
GO:0022900	0.65	0.54	4	149	electron transport chain	BP	1	STEAP4,NDUFA4,SNCA,SLC25A18	turquoise	VSMC_M6
GO:0016054	0.66	0.52	5	186	organic acid catabolic process	BP	1	NOS3,CYP26B1,GOT1,MTOR,BCKDK	turquoise	VSMC_M6
GO:0071897	0.66	0.54	4	150	DNA biosynthetic process	BP	1	PDGFB,CTNNB1,RGN,PKIB	turquoise	VSMC_M6
GO:0051701	0.66	0.54	4	150	biological process involved in interaction with host	BP	1	CXCR4,HYAL2,CD86,TRIM62	turquoise	VSMC_M6
GO:0010639	0.66	0.48	8	297	negative regulation of organelle organization	BP	1	PPARG,SPTBN4,SNCA,BMP7,S1PR1,CDH5,KANK3,SHANK3	turquoise	VSMC_M6
GO:1901654	0.66	0.53	4	151	response to ketone	BP	1	TGFB1,P2RY6,SFRP1,CCR7	turquoise	VSMC_M6
GO:0051052	0.66	0.48	8	297	regulation of DNA metabolic process	BP	1	PDGFB,IL6,KDM4D,TGFB1,CTNNB1,RGN,ENDOG,PKIB	turquoise	VSMC_M6
GO:0006520	0.66	0.50	6	224	cellular amino acid metabolic process	BP	1	NOS3,GOT1,SLC39A8,ART4,AGMAT,BCKDK	turquoise	VSMC_M6
GO:0051171	0.66	0.38	118	4082	regulation of nitrogen compound metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,PDGFB,ETV7,MOB3B,IREB2,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NOVA2,CTSC,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,PDE2A,SFRP1,ZIC2,CD36,KIRREL2,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,THBS4,PPP1R16B,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,NFATC2,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,OAZ3,FANK1,ACE,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,BCKDK,KLF1,LYL1,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,LHX6,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,SOX17,RELN,ALKAL1,OLIG2,PDLIM1,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6

GO:0051252	0.66	0.38	76	2654	regulation of RNA metabolic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,NOVA2,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0032787	0.66	0.45	11	404	monocarboxylic acid metabolic process	BP	1	OSBPL3,PPARG,CD36,CYP26B1,SNCA,PROX1,RGN,MTOR,PTGS1,ALOX12,RBP1	turquoise	VSMC_M6
GO:0031329	0.66	0.42	19	689	regulation of cellular catabolic process	BP	1	KDR,IL6,RASIP1,PIK3CG,CTSC,PRR5L,SOGA1,ATP6V0D2,SNCA,NKD2,HFE,LAPTM5,ERN1,RGN,MTOR,ENDOG,RUFY4,GNA12,MGAT3	turquoise	VSMC_M6
GO:1902532	0.67	0.45	11	407	negative regulation of intracellular signal transduction	BP	1	ARHGAP25,RASIP1,PPARG,PDE2A,SFRP1,ADGRG3,SHANK2,HYAL2,BMP7,MTOR,GBP1	turquoise	VSMC_M6
GO:2000113	0.67	0.40	32	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	NOTCH4,PDGFB,ETV7,IREB2,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,MAPK10,SNCA,NFATC2,BMP7,PROX1,PRAME,PAX9,RGN,PPM1F,BCL6B,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0051172	0.68	0.38	50	1770	negative regulation of nitrogen compound metabolic process	BP	1	NOTCH4,PDGFB,ETV7,IREB2,IL6,BCL11A,C5,RASIP1,KDM4D,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,KIRREL2,PRR5L,HHEX,SOX7,PPP1R16B,MAPK10,SNCA,HYAL2,HFE,NFATC2,CD34,BMP7,IGFBP3,PROX1,PRAME,PAX9,LTF,RGN,CDA,PPM1F,BCL6B,PPP1R1B,MTOR,BCKDK,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18,PKIB,MGAT3	turquoise	VSMC_M6
GO:0010558	0.68	0.39	32	1150	negative regulation of macromolecule biosynthetic process	BP	1	NOTCH4,PDGFB,ETV7,IREB2,BCL11A,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,MAPK10,SNCA,NFATC2,BMP7,PROX1,PRAME,PAX9,RGN,PPM1F,BCL6B,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18	turquoise	VSMC_M6
GO:0006163	0.68	0.45	8	302	purine nucleotide metabolic process	BP	1	NOS3,TGFB1,PDE2A,SNCA,GUCY1A2,NPR1,PDE4B,NUDT4B	turquoise	VSMC_M6
GO:0009889	0.68	0.36	86	3010	regulation of biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,ADGRF5,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,RAB38,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,GOT1,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD34,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH3,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0051604	0.69	0.47	6	230	protein maturation	BP	1	F11,KLKB1,NKD2,ACE,TSPAN15,TSPAN14	turquoise	VSMC_M6
GO:0046390	0.69	0.50	4	156	ribose phosphate biosynthetic process	BP	1	TGFB1,SNCA,GUCY1A2,NPR1	turquoise	VSMC_M6
GO:0008361	0.69	0.50	4	157	regulation of cell size	BP	1	MTOR,ISLR2,SEMA6B,SHANK3	turquoise	VSMC_M6
GO:0042594	0.70	0.49	4	158	response to starvation	BP	1	SFRP1,HFE,MTOR,PMAIP1	turquoise	VSMC_M6
GO:0019219	0.70	0.35	81	2852	regulation of nucleobase-containing compound metabolic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,KDM4D,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0031326	0.70	0.34	84	2955	regulation of cellular biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,ADGRF5,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,RAB38,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD34,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH3,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0043122	0.70	0.46	5	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	CTNNB1,CD36,LTF,TRIM62,CCR7	turquoise	VSMC_M6
GO:0006631	0.70	0.44	7	271	fatty acid metabolic process	BP	1	PPARG,CD36,SNCA,RGN,MTOR,PTGS1,ALOX12	turquoise	VSMC_M6
GO:0009117	0.70	0.41	10	381	nucleotide metabolic process	BP	1	NOS3,TGFB1,PDE2A,SNCA,GUCY1A2,CDA,NPR1,PDE4B,SARM1,NUDT4B	turquoise	VSMC_M6
GO:0009165	0.71	0.46	5	198	nucleotide biosynthetic process	BP	1	NOS3,TGFB1,SNCA,GUCY1A2,NPR1	turquoise	VSMC_M6
GO:0044281	0.71	0.35	36	1301	small molecule metabolic process	BP	1	IP6K3,IREB2,SYK,OSBPL3,NOS3,PPARG,TGFB1,P2RY6,PDE2A,CD36,SOGA1,CYP26B1,GOT1,SNCA,SLC39A8,PROX1,ART4,ST6GAL1,GUCY1A2,RGN,CDA,FGF23,AGMAT,MTOR,BCKDK,NPR1,DEGS2,PDE4B,SARM1,PTGS1,ALOX12,PMAIP1,PPP1R3C,NUDT4B,SCARF1,RBP1	turquoise	VSMC_M6
GO:1901215	0.71	0.48	4	161	negative regulation of neuron death	BP	1	CTNNB1,SNCA,CD34,VSTM2L	turquoise	VSMC_M6
GO:1901293	0.71	0.45	5	199	nucleoside phosphate biosynthetic process	BP	1	NOS3,TGFB1,SNCA,GUCY1A2,NPR1	turquoise	VSMC_M6
GO:0030163	0.71	0.37	22	815	protein catabolic process	BP	1	DENND3,CTSC,CTNNB1,NOTUM,ADAMTS9,SNCA,NKD2,HFE,LAPTM5,ASCC2,GPC1,OAZ3,PRAME,RGN,MTOR,NOTCH1,CDH1,MMP12,PMAIP1,SOX17,GNA12,MGAT3	turquoise	VSMC_M6
GO:0071383	0.72	0.47	4	163	cellular response to steroid hormone stimulus	BP	1	SFRP1,ESRRG,BMP7,SSTR5	turquoise	VSMC_M6
GO:0032886	0.72	0.45	5	202	regulation of microtubule-based process	BP	1	MAP6,SNCA,RGN,TTLL6,CDH5	turquoise	VSMC_M6

GO:0034613	0.72	0.34	40	1451	cellular protein localization	BP	1	CELSR1,SYK,RAB38,GRIP2,EXOC3L2,CD177,TGFB1,CTNNB1,SPTBN4,GPC6,SNAP25,CD36,PRR5L,HHEX,REEP1,MAPK10,HYAL2,NKD2,HFE,ESAM,LAPTM5,BMP7,GPC1,OAZ3,TSPAN15,SYTL5,ATP13A1,PPM1F,PRKCH,TSPAN14,ABI3,NOTCH1,GBP1,CDH1,EXOC3L1,MMP12,RELN,NUCB1,SHANK3,MGAT3	turquoise	VSMC_M6
GO:0009416	0.72	0.43	6	239	response to light stimulus	BP	1	ATP8A2,MAPK10,HYAL2,PPP1R1B,MTOR,GNGT2	turquoise	VSMC_M6
GO:0006753	0.72	0.39	10	387	nucleoside phosphate metabolic process	BP	1	NOS3,TGFB1,PDE2A,SNCA,GUCY1A2,CDA,NPR1,PDE4B,SARM1,NUDT4B	turquoise	VSMC_M6
GO:0009057	0.72	0.34	30	1102	macromolecule catabolic process	BP	1	DENND3,IL6,CTSC,TGFB1,CTNNB1,NOTUM,ADAMTS9,PRR5L,LYVE1,SNCA,HYAL2,NKD2,HFE,LAPTM5,ISG20,ERN1,ASCC2,GPC1,OAZ3,PRAME,RGN,MTOR,NOTCH1,ENDOG,CDH1,MMP12,PMAIP1,SOX17,GNA12,MGAT3	turquoise	VSMC_M6
GO:0044242	0.72	0.46	4	164	cellular lipid catabolic process	BP	1	ENPP2,PIK3CG,CYP26B1,MTOR	turquoise	VSMC_M6
GO:1903829	0.73	0.42	6	241	positive regulation of cellular protein localization	BP	1	TGFB1,HYAL2,NKD2,PRKCH,CDH1,MGAT3	turquoise	VSMC_M6
GO:0070727	0.74	0.32	40	1462	cellular macromolecule localization	BP	1	CELSR1,SYK,RAB38,GRIP2,EXOC3L2,CD177,TGFB1,CTNNB1,SPTBN4,GPC6,SNAP25,CD36,PRR5L,HHEX,REEP1,MAPK10,HYAL2,NKD2,HFE,ESAM,LAPTM5,BMP7,GPC1,OAZ3,TSPAN15,SYTL5,ATP13A1,PPM1F,PRKCH,TSPAN14,ABI3,NOTCH1,GBP1,CDH1,EXOC3L1,MMP12,RELN,NUCB1,SHANK3,MGAT3	turquoise	VSMC_M6
GO:0044403	0.74	0.42	5	206	biological process involved in symbiotic interaction	BP	1	CXCR4,HYAL2,CD86,LTF,TRIM62	turquoise	VSMC_M6
GO:0072521	0.74	0.39	8	319	purine-containing compound metabolic process	BP	1	NOS3,TGFB1,PDE2A,SNCA,GUCY1A2,NPR1,PDE4B,NUDT4B	turquoise	VSMC_M6
GO:1901135	0.74	0.34	21	791	carbohydrate derivative metabolic process	BP	1	PDGFB,TGFB1,CTNNB1,PDE2A,ADAMTS9,LYVE1,COL2A1,SNCA,HYAL2,SLC39A8,GPC1,ST6GAL1,GUCY1A2,CDA,NPR1,B4GALT6,PDE4B,MMP12,CCR7,MGAT3,NUDT4B	turquoise	VSMC_M6
GO:0009101	0.74	0.40	6	245	glycoprotein biosynthetic process	BP	1	CTNNB1,SLC39A8,ST6GAL1,B4GALT6,CCR7,MGAT3	turquoise	VSMC_M6
GO:0016458	0.74	0.43	4	169	gene silencing	BP	1	IL6,PPARG,TGFB1,MIR1307	turquoise	VSMC_M6
GO:0022412	0.75	0.40	6	247	cellular process involved in reproduction in multicellular organism	BP	1	CTNNB1,SFRP1,ANGPT2,CYP26B1,C19orf57,MTOR	turquoise	VSMC_M6
GO:0016485	0.75	0.43	4	170	protein processing	BP	1	F11,KLKB1,NKD2,ACE	turquoise	VSMC_M6
GO:0097190	0.75	0.35	12	471	apoptotic signaling pathway	BP	1	CTSC,NOS3,TGFB1,CTNNB1,TMC8,SFRP1,COL2A1,HYAL2,ERN1,LGALS12,PPM1F,PMAIP1	turquoise	VSMC_M6
GO:0006464	0.75	0.29	80	2859	cellular protein modification process	BP	1	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,BCL11A,RASIP1,PIK3CG,KDM4D,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SFRP1,NOTUM,CD36,NEURL3,KIRREL2,STK35,PRAG1,PRR5L,HHEX,HUNK,THBS4,PPP1R16B,MAPK10,SNCA,MTTP,HYAL2,SLC39A8,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,SRMS,ART4,ACE,PTPRE,PRAME,ST6GAL1,LTF,PALD1,TBX1,RGN,FGF23,PPM1F,PRKCH,PPP1R1B,MTOR,BCKDK,TTLL6,MAST1,NPR1,B4GALT6,MATK,TNFRSF18,SH2D3C,CDH5,TRIM43,RELN,ALKAL1,PPP1R3C,PKIB,TRIM62,CCR7,MGAT3	turquoise	VSMC_M6
GO:0036211	0.75	0.29	80	2859	protein modification process	BP	1	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,BCL11A,RASIP1,PIK3CG,KDM4D,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SFRP1,NOTUM,CD36,NEURL3,KIRREL2,STK35,PRAG1,PRR5L,HHEX,HUNK,THBS4,PPP1R16B,MAPK10,SNCA,MTTP,HYAL2,SLC39A8,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,SRMS,ART4,ACE,PTPRE,PRAME,ST6GAL1,LTF,PALD1,TBX1,RGN,FGF23,PPM1F,PRKCH,PPP1R1B,MTOR,BCKDK,TTLL6,MAST1,NPR1,B4GALT6,MATK,TNFRSF18,SH2D3C,CDH5,TRIM43,RELN,ALKAL1,PPP1R3C,PKIB,TRIM62,CCR7,MGAT3	turquoise	VSMC_M6
GO:0009150	0.75	0.38	7	286	purine ribonucleotide metabolic process	BP	1	TGFB1,PDE2A,SNCA,GUCY1A2,NPR1,PDE4B,NUDT4B	turquoise	VSMC_M6
GO:0090150	0.75	0.40	5	210	establishment of protein localization to membrane	BP	1	GRIP2,SNAP25,REEP1,MAPK10,ATP13A1	turquoise	VSMC_M6
GO:0031324	0.76	0.29	52	1896	negative regulation of cellular metabolic process	BP	1	NOTCH4,PDGFB,ETV7,IREB2,IL6,BCL11A,C5,RASIP1,PIK3CG,KDM4D,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,KIRREL2,PRR5L,HHEX,SOX7,SOGA1,PPP1R16B,MAPK10,SNCA,HYAL2,HFE,NFATC2,CD34,BMP7,IGFBP3,PROX1,PRAME,PAX9,LTF,RGN,CDA,PPM1F,BCL6B,PPP1R1B,MTOR,BCKDK,NRARP,HES3,NOTCH1,IRF8,MMP12,OLIG2,SOX18,PKIB,MGAT3	turquoise	VSMC_M6
GO:0006366	0.76	0.29	51	1862	transcription by RNA polymerase II	BP	1	NOTCH4,PDGFB,ETV7,BARX1,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,ESRRG,NFATC2,EAF2,TLR7,BMP7,PROX1,HOXD10,PAX9,TBX1,BCL6B,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,MMP12,SOX17,OLIG2,PDLIM1,SOX18,ZNF775,FLI1	turquoise	VSMC_M6
GO:0019438	0.76	0.28	81	2902	aromatic compound biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,NPR1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH3,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0055086	0.76	0.34	11	439	nucleobase-containing small molecule metabolic process	BP	1	NOS3,TGFB1,PDE2A,SNCA,GUCY1A2,CDA,MTOR,NPR1,PDE4B,SARM1,NUDT4B	turquoise	VSMC_M6
GO:0032386	0.76	0.36	7	290	regulation of intracellular transport	BP	1	TGFB1,CD36,PRR5L,HYAL2,OAZ3,CDH1,NUCB1	turquoise	VSMC_M6
GO:0090305	0.76	0.39	5	213	nucleic acid phosphodiester bond hydrolysis	BP	1	ENPP2,IL6,ISG20,ERN1,ENDOG	turquoise	VSMC_M6

GO:0034654	0.77	0.27	79	2841	nucleobase-containing compound biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,NPR1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0051641	0.78	0.27	63	2295	cellular localization	BP	1	PARD6G,KCNN2,SYBU,CELSR1,DENND3,STEAP4,SYK,EPHA5,PIK3CG,RAB38,GRIP2,EXOC3L2,CD177,SYN2,TGFB1,CTNNB1,SPTBN4,GPC6,MAP6,P2RY6,SNAP25,CD36,PRR5L,HHEX,REEP1,CXCL10,SLC4A5,MAPK10,SNCA,HYAL2,SLC39A8,NKD2,HFE,MCTP2,ESAM,LAPTM5,BMP7,GPC1,OAZ3,TSPAN15,SYTL5,ATP13A1,CCDC88B,PPM1F,PRKCH,TSPAN14,SNCG,MTOR,ABI3,NOTCH1,GBP1,CDH3,CDH1,EXOC3L1,MMP12,RELN,NUCB1,SHANK3,TRPM2,CCR7,NSG2,MGAT3,TMEM50B	turquoise	VSMC_M6
GO:0008202	0.78	0.37	5	217	steroid metabolic process	BP	1	OSBPL3,CYP26B1,PROX1,FGF23,SCARF1	turquoise	VSMC_M6
GO:0051640	0.78	0.32	11	447	organelle localization	BP	1	SYBU,SYK,PIK3CG,SYN2,CTNNB1,MAP6,SNAP25,SLC4A5,SNCA,MTOR,CDH3	turquoise	VSMC_M6
GO:0006486	0.80	0.36	4	182	protein glycosylation	BP	1	SLC39A8,ST6GAL1,B4GALT6,MGAT3	turquoise	VSMC_M6
GO:0043413	0.80	0.36	4	182	macromolecule glycosylation	BP	1	SLC39A8,ST6GAL1,B4GALT6,MGAT3	turquoise	VSMC_M6
GO:0018130	0.80	0.24	80	2900	heterocycle biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,NPR1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0009259	0.80	0.32	7	302	ribonucleotide metabolic process	BP	1	TGFB1,PDE2A,SNCA,GUCY1A2,NPR1,PDE4B,NUDT4B	turquoise	VSMC_M6
GO:0010556	0.81	0.22	78	2846	regulation of macromolecule biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:2000112	0.82	0.21	77	2822	regulation of cellular macromolecule biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0019693	0.83	0.28	7	312	ribose phosphate metabolic process	BP	1	TGFB1,PDE2A,SNCA,GUCY1A2,NPR1,PDE4B,NUDT4B	turquoise	VSMC_M6
GO:0045333	0.83	0.32	4	191	cellular respiration	BP	1	IREB2,NDUFA4,SNCA,SLC25A18	turquoise	VSMC_M6
GO:0006091	0.83	0.26	9	392	generation of precursor metabolites and energy	BP	1	IREB2,STEAP4,ADGRF5,NDUFA4,PCDH12,SNCA,SLC25A18,MTOR,PPP1R3C	turquoise	VSMC_M6
GO:0072594	0.83	0.27	8	355	establishment of protein localization to organelle	BP	1	SYK,TGFB1,CD36,HYAL2,LAPTM5,NOTCH1,CDH1,MMP12	turquoise	VSMC_M6
GO:0070085	0.83	0.31	4	194	glycosylation	BP	1	SLC39A8,ST6GAL1,B4GALT6,MGAT3	turquoise	VSMC_M6
GO:0044085	0.84	0.20	66	2454	cellular component biogenesis	BP	1	MDGA1,DNAH8,STEAP4,KDR,SYK,LRRC4B,GJA4,CFAP100,KCNA7,RASIP1,NSUN4,RAB38,FGD5,ITGB4,TGFB1,KCTD12,CTNNB1,TMC8,SPTBN4,TIE1,GPC6,DNAJB13,SNAP25,SFRP1,CD36,CFAP54,PPP1R16B,SNCA,CTND2,SHANK2,MTTP,HFE,NRAP,ESAM,ISG20,CD34,PECAM1,BMP7,PROX1,GPC1,ACE,CLDN16,SELP,BAIAP2L1,PPM1F,PRKCH,MTOR,ABI3,ARHGEF15,THSD4,CCDC69,HCN1,NOTCH1,S1PR1,CDH1,ADGRL4,CDH5,TSPYL1,RUFY4,PDLIM1,HIST1H4G,KANK3,SHANK3,TRPM2,CCR7,NSG2	turquoise	VSMC_M6

GO:0008150	0.84	0.22	358	12183	biological_process	BP	1	PARD6G,TNFRSF11A,IL23A,KCNN2,NMBR,LYZ,FLT4,MYCT1,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,IP6K3,DENND3,PDGFB,ETV7,SLC16A8,FRMD3,MDGA1,DNAH8,CSF2RB,FREM1,MOB3B,IREB2,ATP8A1,STEAP4,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,TMPRSS11F,OSBPL3,BCL11A,LRRC4B,ANKRD6,NDUFA4,ARHGAP25,C5,GJA4,MAML3,CFAP100,KCNA7,KIAA1147,SLC22A16,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RAB38,SLC6A6,GRIP2,FGD5,EXOC3L2,RARRES2,NOS3,LYPD3,CD177,ITGB4,PPARG,SYN2,TGFB1,KCTD12,HTR5A,CXCR4,EDNRB,CTNNB1,TMC6,TMC8,SPTBN4,TIE1,GPC6,MAP6,SLCO2B1,DNAJB13,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,ZIC2,RASGRP3,NOTUM,CNTN4,PCDH12,SLC4A11,CD36,CFAP54,NEURL3,SLCO2A1,NFKBID,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,ATP8A2,MALL,CCM2L,F11,BPIFB3,KLKB1,HHEX,REEP1,LYVE1,SLCO5A1,PROCR,SOX7,CP,TSC22D2,P2RY14,CXCL10,ANGPT2,SOGA1,SLC4A5,ADGRG3,ATP6V0D2,TMEM116,HUNK,PRDM8,THBS4,EVA1C,CYP26B1,PPP1R16B,PLCB2,COL2A1,GSTA4,STAB1,TOX2,MAPK10,IRX6,GOT1,NKX2-3,CLIC6,BMP1,SPATA25,IGSF3,SNCA,MMRN1,CTNND2,MFSD4A,ANO3,SHANK2,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,LSAMP,UPK1B,HFE,MCTP2,DPYSL4,HCRTR1,ROBO4,NRAP,ESAM,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,COL18A1,SLAMF9,BMP7,IGFBP3,ASCC2,PROX1,MGST1,GPC1,SLCO4A1,JAML,OAZ3,SRM5,FANK1,ART4,ACE,PTPRE,CNKSR2,LAMC2,HOXD10,PRAME,SSC4D,PAX9,ST6GAL1,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,SYTL5,CLDN16,GSTT2B,PALD1,SUN3,ATP13A1,LPAR2,AGFG	turquoise	VSMC_M6
GO:1901362	0.84	0.19	82	3012	organic cyclic compound biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,OSBPL3,BCL11A,MAML3,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,NPR1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH3,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0033036	0.84	0.19	63	2356	macromolecule localization	BP	1	TNFRSF11A,SYBU,CELSR1,ATP8A1,SYK,EPHA5,IL6,OSBPL3,RAB38,GRIP2,EXOC3L2,CD177,PPARG,TGFB1,CTNNB1,SPTBN4,GPC6,SLCO2B1,SNAP25,SFRP1,CD36,SLCO2A1,ADAMTS9,PRR5L,ATP8A2,HHEX,REEP1,MAPK10,ANO3,MTTP,HYAL2,NKD2,HFE,ESAM,LAPTM5,PECAM1,BMP7,GPC1,OAZ3,ACE,TSPAN15,SYTL5,ATP13A1,PPM1F,PITPNM3,PRKCH,TSPAN14,SNCG,ABI3,HCN1,SSTR5,NOTCH1,GBP1,CDH1,EXOC3L1,CDH5,MMP12,RELN,NUCB1,SHANK3,TRPM2,MGAT3,NMB	turquoise	VSMC_M6
GO:0044248	0.84	0.20	46	1755	cellular catabolic process	BP	1	ENPP2,DENND3,KDR,IL6,RASIP1,PIK3CG,CTSC,NOS3,ITGB4,TGFB1,CTNNB1,SLCO2B1,PDE2A,CD36,ADAMTS9,PRR5L,SOGA1,ATP6V0D2,CYP26B1,GOT1,SNCA,NKD2,HFE,LAPTM5,ISG20,ERN1,ASCC2,GPC1,ACE,PRAME,RGN,CDA,FGF23,MTOR,BCKDK,PDE4B,SARM1,IRF8,ENDOG,MMP12,PMAIP1,RUFY4,GNA12,MGAT3,NUDT4B,GPX3	turquoise	VSMC_M6
GO:0051346	0.85	0.27	5	242	negative regulation of hydrolase activity	BP	1	C5,SNCA,LTF,RGN,PPP1R1B	turquoise	VSMC_M6
GO:0060627	0.85	0.24	9	403	regulation of vesicle-mediated transport	BP	1	SYT17,SYK,DLL1,CD177,CD36,SNCA,HFE,SELE,NOTCH1	turquoise	VSMC_M6
GO:0007548	0.86	0.26	4	206	sex differentiation	BP	1	CTNNB1,SFRP1,MGST1,GREB1L	turquoise	VSMC_M6
GO:0006914	0.86	0.21	10	450	autophagy	BP	1	KDR,RASIP1,ITGB4,SOGA1,ATP6V0D2,SNCA,ERN1,MTOR,IRF8,RUFY4	turquoise	VSMC_M6
GO:0061919	0.86	0.21	10	450	process utilizing autophagic mechanism	BP	1	KDR,RASIP1,ITGB4,SOGA1,ATP6V0D2,SNCA,ERN1,MTOR,IRF8,RUFY4	turquoise	VSMC_M6
GO:0008104	0.87	0.17	53	2028	protein localization	BP	1	SYBU,CELSR1,SYK,EPHA5,IL6,RAB38,GRIP2,EXOC3L2,CD177,PPARG,TGFB1,CTNNB1,SPTBN4,GPC6,SNAP25,SFRP1,CD36,ADAMTS9,PRR5L,HHEX,REEP1,MAPK10,MTTP,HYAL2,NKD2,HFE,ESAM,LAPTM5,PECAM1,BMP7,GPC1,OAZ3,TSPAN15,SYTL5,ATP13A1,PPM1F,PRKCH,TSPAN14,SNCG,ABI3,HCN1,SSTR5,NOTCH1,GBP1,CDH1,EXOC3L1,CDH5,MMP12,RELN,NUCB1,SHANK3,TRPM2,MGAT3	turquoise	VSMC_M6
GO:1901137	0.88	0.20	11	494	carbohydrate derivative biosynthetic process	BP	1	PDGFB,TGFB1,CTNNB1,SNCA,SLC39A8,ST6GAL1,GUCY1A2,NPR1,B4GALT6,CCR7,MGAT3	turquoise	VSMC_M6
GO:0043412	0.88	0.15	81	3029	macromolecule modification	BP	1	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,PDGFB,MOB3B,KDR,SYK,EPHA5,IL6,BCL11A,RASIP1,PIK3CG,KDM4D,NSUN4,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SFRP1,NOTUM,CD36,NEURL3,KIRREL2,STK35,PRAG1,PRR5L,HHEX,HUNK,THBS4,PPP1R16B,MAPK10,SNCA,MTTP,HYAL2,SLC39A8,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,PROX1,SRM5,ART4,ACE,PTPRE,PRAME,ST6GAL1,LTF,PALD1,TBX1,RGN,FGF23,PPM1F,PRKCH,PPP1R1B,MTOR,BCKDK,TTLL6,MAST1,NPR1,B4GALT6,MATK,TNFRSF18,SH2D3C,CDH5,TRIM43,RELN,ALKAL1,PPP1R3C,PKIB,TRIM62,CCR7,MGAT3	turquoise	VSMC_M6
GO:0016050	0.88	0.23	5	255	vesicle organization	BP	1	RAB38,SNAP25,SNCA,NKD2,CD34	turquoise	VSMC_M6
GO:0045861	0.88	0.24	4	213	negative regulation of proteolysis	BP	1	C5,SNCA,HFE,LTF	turquoise	VSMC_M6
GO:0016236	0.90	0.20	5	265	macroautophagy	BP	1	KDR,ATP6V0D2,ERN1,MTOR,RUFY4	turquoise	VSMC_M6
GO:0060271	0.90	0.19	5	266	cilium assembly	BP	1	DNAH8,CFAP100,DNAJB13,CFAP54,NOTCH1	turquoise	VSMC_M6
GO:0007017	0.91	0.14	16	715	microtubule-based process	BP	1	PARD6G,SYBU,DNAH8,CFAP100,SLC22A16,CTNNB1,MAP6,DNAJB13,CFAP54,SNCA,CCDC88B,RGN,TTLL6,CCDC69,CDH5,ATP1A4	turquoise	VSMC_M6
GO:0000226	0.91	0.15	11	522	microtubule cytoskeleton organization	BP	1	PARD6G,DNAH8,CFAP100,CTNNB1,MAP6,DNAJB13,SNCA,CCDC88B,TTLL6,CCDC69,CDH5	turquoise	VSMC_M6
GO:0033554	0.92	0.10	38	1561	cellular response to stress	BP	1	FLT4,IL18RAP,IL6,ANKRD6,KDM4D,NOS3,CTNNB1,SFRP1,SLC4A11,CD36,PRR5L,CXCL10,THBS4,MAPK10,SNCA,HFE,NFATC2,TLR7,CD34,ERN1,BMP7,ASCC2,MGST1,CRACR2A,RCSD1,C19orf57,MTOR,ABI3,NOTCH1,ENDOG,SH2D3C,PMAIP1,GGN,TRPM2,CCR7,MGAT3,RTN4RL2,SCARF1	turquoise	VSMC_M6
GO:0006401	0.93	0.16	4	237	RNA catabolic process	BP	1	PRR5L,ISG20,ERN1,MTOR	turquoise	VSMC_M6

GO:0071705	0.93	0.09	39	1609	nitrogen compound transport	BP	1	SYBU,SYT17,ATP8A1,SYK,EPHA5,IL6,SLC22A16,RAB38,SLC6A6,GRIP2,PPARG,TGFB1,SNAP25,SFRP1,CD36,ADAMTS9,PRR5L,ATP8A2,HHEX,MAPK10,SNCA,MTTP,HYAL2,HFE,LAPTM5,MGST1,OAZ3,SYTL5,ATP13A1,PPM1F,SNCG,SLC25A18,SSTR5,NOTCH1,CDH1,EXOC3L1,MMP12,NUCB1,TRPM2	turquoise	VSMC_M6
GO:0044782	0.93	0.14	5	288	cilium organization	BP	1	DNAH8,CFAP100,DNAJB13,CFAP54,NOTCH1	turquoise	VSMC_M6
GO:0097193	0.93	0.15	4	242	intrinsic apoptotic signaling pathway	BP	1	ERN1,LGALS12,PPM1F,PMAIP1	turquoise	VSMC_M6
GO:0051656	0.93	0.13	6	334	establishment of organelle localization	BP	1	SYBU,SYK,PIK3CG,CTNNB1,SNCA,CDH3	turquoise	VSMC_M6
GO:0006310	0.94	0.14	4	245	DNA recombination	BP	1	KDM4D,TGFB1,C19orf57,ENDOG	turquoise	VSMC_M6
GO:0010256	0.94	0.12	8	422	endomembrane system organization	BP	1	RAB38,CXCR4,TIE1,SNAP25,REEP1,ANO3,SUN3,BAIAP2L1	turquoise	VSMC_M6
GO:0065003	0.94	0.09	28	1210	protein-containing complex assembly	BP	1	DNAH8,STEAP4,SYK,CFAP100,KCNA7,RASIP1,TGFB1,KCTD12,TMC8,SPTBN4,SNAP25,CD36,SNCA,MTTP,HFE,ESAM,SELP,BAIAP2L1,MTOR,HCN1,ADGRL4,CDH5,TSPYL1,HIST1H4G,KANK3,TRPM2,CCR7,NSG2	turquoise	VSMC_M6
GO:0044265	0.94	0.09	21	947	cellular macromolecule catabolic process	BP	1	DENND3,IL6,CTSC,CTNNB1,ADAMTS9,PRR5L,NKD2,HFE,LAPTM5,ISG20,ERN1,ASCC2,GPC1,PRAME,RGN,MTOR,ENDOG,MMP12,PMAIP1,GNA12,MGAT3	turquoise	VSMC_M6
GO:0009987	0.94	0.08	338	11676	cellular process	BP	1	PARD6G,TNFRSF11A,IL23A,KCNN2,NMBR,LYZ,FLT4,MEGF10,SYBU,CELSR1,NOTCH4,ENPP2,SYT17,IP6K3,DENND3,PDGFB,ETV7,SLC16A8,FRMD3,MDGA1,DNAH8,CSF2RB,FREM1,MOB3B,IREB2,ATP8A1,STEAP4,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,THSD7A,EPHA5,IL6,OSBPL3,BCL11A,LRRC4B,ANKRD6,NDUFA4,ARHGAP25,C5,GJA4,MAML3,CFAP100,KCNA7,SLC22A16,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RAB38,SLC6A6,GRIP2,FGD5,EXOC3L2,RARRES2,NOS3,LYPD3,CD177,ITGB4,PPARG,SYN2,TGFB1,KCTD12,HTR5A,CXCR4,EDNRB,CTNNB1,TMC6,TMC8,SPTBN4,TIE1,GPC6,MAP6,SLCO2B1,DNAJB13,P2RY6,P2RY2,SNAP25,PDE2A,SFRP1,ZIC2,RASGRP3,NOTUM,CNTN4,PCDH12,SLC4A11,CD36,CFAP54,NEURL3,SLCO2A1,NFKBID,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,ATP8A2,MALL,KLKB1,HHEX,REEP1,LYVE1,SLCO5A1,SOX7,CP,TSC22D2,P2RY14,CXCL10,ANGPT2,SOGA1,SLC4A5,ADGRG3,ATP6V0D2,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,GSTA4,STAB1,TOX2,MAPK10,IRX6,GOT1,NKX2-3,CLIC6,BMP1,SPATA25,SNCA,MMRN1,CTNND2,MFSD4A,ANO3,SHANK2,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,LSAMP,UPK1B,HFE,MCTP2,DPYSL4,HCRTR1,ROBO4,NRAP,ESAM,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,GPR146,ERN1,COL18A1,SLAMF9,BMP7,IGFBP3,ASCC2,PROX1,MGST1,GPC1,SLCO4A1,JAML,OAZ3,SRM5,FANK1,ART4,ACE,PTPRE,CNKSR2,LAMC2,HOXD10,PRAME,SSC4D,PAX9,ST6GAL1,ADGRA1,LTF,ARHGAP27,CCRL2,TSPAN15,SYTL5,CLDN16,GSTT2B,PALD1,SUN3,ATP13A1,LPAR2,CCDC88B,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,SELP,VWF,PLVA	turquoise	VSMC_M6
GO:0006508	0.94	0.08	30	1295	proteolysis	BP	1	SYK,TMPRSS11F,C5,CTSC,PPARG,TGFB1,CTNNB1,SFRP1,ADAMTS9,F11,KLKB1,SOX7,BMP1,SNCA,NKD2,HFE,LAPTM5,ASCC2,ACE,PRAME,LTF,RGN,PPM1F,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,RELN,GNA12	turquoise	VSMC_M6
GO:0010467	0.95	0.06	118	4455	gene expression	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,PDGFB,ETV7,IREB2,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,BCL11A,C5,MAML3,PIK3CG,DLL1,NSUN4,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,NFKBID,PRR5L,F11,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,ANGPT2,SLC4A5,ADGRG3,PRDM8,CYP26B1,COL2A1,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,CD86,ERN1,SLAMF9,BMP7,ASCC2,PROX1,FANK1,ACE,HOXD10,PRAME,PAX9,LTF,TSPAN15,CCDC88B,TBX1,FGF23,PPM1F,PRKCH,TSPAN14,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,PDE4B,NRARP,HES3,NOTCH1,IRF8,S1PR1,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,SNORD1A,SNORA69,ALOX12,MMP12,TRIM43,SOX17,RELN,ACKR1,C3AR1,SNORD8,SNORD70,MIR1307,SNORD124,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,CCR7,FLI1	turquoise	VSMC_M6
GO:0007005	0.95	0.09	8	436	mitochondrion organization	BP	1	KDR,RAB38,NOS3,PPARG,PDE2A,SLC4A5,SNCA,PMAIP1	turquoise	VSMC_M6
GO:0045786	0.95	0.10	5	306	negative regulation of cell cycle	BP	1	TGFB1,CTNNB1,HHEX,BMP7,PROX1	turquoise	VSMC_M6
GO:0070925	0.96	0.07	14	705	organelle assembly	BP	1	DNAH8,LRRC4B,CFAP100,RAB38,DNAJB13,CFAP54,NRAP,CD34,PROX1,ABI3,CCDC69,NOTCH1,RUFY4,SHANK3	turquoise	VSMC_M6
GO:0051649	0.96	0.05	39	1679	establishment of localization in cell	BP	1	KCNN2,SYBU,DENND3,STEAP4,SYK,EPHA5,PIK3CG,RAB38,GRIP2,CD177,SYN2,TGFB1,CTNNB1,MAP6,P2RY6,SNAP25,CD36,PRR5L,HHEX,CXCL10,SNCA,HYAL2,SLC39A8,HFE,MCTP2,LAPTM5,OAZ3,SYTL5,CCDC88B,SNCG,NOTCH1,CDH3,CDH1,MMP12,NUCB1,TRPM2,CCR7,NSG2,TMEM50B	turquoise	VSMC_M6
GO:0043161	0.97	0.07	6	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	CTNNB1,NKD2,HFE,ASCC2,PRAME,GNA12	turquoise	VSMC_M6
GO:0022411	0.97	0.07	6	375	cellular component disassembly	BP	1	IL6,TGFB1,SPTBN4,ENDOG,MMP12,HRASLS	turquoise	VSMC_M6

GO:0019538	0.97	0.04	106	4113	protein metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,DENND3,PDGFB,MOB3B,IREB2,KDR,SYK,EPHA5,IL6,TMPRSS11F,BCL11A,C5,RASIP1,PIK3CG,KDM4D,CTSC,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SFRP1,NOTUM,CD36,NEURL3,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,F11,KLKB1,HHEX,SOX7,HUNK,THBS4,PPP1R16B,COL2A1,MAPK10,BMP1,SNCA,MTTP,HYAL2,SLC39A8,NKD2,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,ART4,ACE,PTPRE,PRAME,ST6GAL1,LTF,TSPAN15,PALD1,TBX1,RGN,FGF23,PPM1F,PRKCH,TSPAN14,PPP1R1B,MTOR,BCKDK,TTLL6,MAST1,NPR1,B4GALT6,MATK,TNFRSF18,NOTCH1,SH2D3C,CDH1,CDH5,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,TRIM43,SOX17,RELN,ALKAL1,PPP1R3C,GNA12,PKIB,TRIM62,CCR7,MGAT3	turquoise	VSMC_M6
GO:0032259	0.97	0.06	4	290	methylation	BP	1	KDM4D,NSUN4,CTNNB1,PRDM8	turquoise	VSMC_M6
GO:0010498	0.98	0.05	7	434	proteasomal protein catabolic process	BP	1	CTNNB1,NKD2,HFE,ASCC2,PRAME,PMAIP1,GNA12	turquoise	VSMC_M6
GO:0010608	0.98	0.05	8	480	posttranscriptional regulation of gene expression	BP	1	IREB2,IL6,PPARG,TGFB1,ASCC2,ACE,MTOR,MIR1307	turquoise	VSMC_M6
GO:0006886	0.98	0.04	14	739	intracellular protein transport	BP	1	SYK,RAB38,GRIP2,TGFB1,CD36,PRR5L,HYAL2,LAPTM5,OAZ3,SYTL5,NOTCH1,CDH1,MMP12,NUCB1	turquoise	VSMC_M6
GO:0015031	0.98	0.04	28	1301	protein transport	BP	1	SYBU,SYK,EPHA5,IL6,RAB38,GRIP2,PPARG,TGFB1,SNAP25,SFRP1,CD36,ADAMTS9,PRR5L,MAPK10,MTTP,HYAL2,LAPTM5,OAZ3,SYTL5,ATP13A1,PPM1F,SNCG,SSTR5,NOTCH1,CDH1,MMP12,NUCB1,TRPM2	turquoise	VSMC_M6
GO:0034622	0.98	0.04	16	830	cellular protein-containing complex assembly	BP	1	DNAH8,CFAP100,TGFB1,SPTBN4,SNAP25,CD36,SNCA,ESAM,BAIAP2L1,MTOR,CDH5,TSPYL1,HIST1H4G,KANK3,CCR7,NSG2	turquoise	VSMC_M6
GO:0048285	0.98	0.04	6	401	organelle fission	BP	1	PDGFB,KDR,PPARG,CYP26B1,BMP7,C19orf57	turquoise	VSMC_M6
GO:0044271	0.98	0.02	85	3436	cellular nitrogen compound biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD34,CD86,BMP7,ASCC2,PROX1,OAZ3,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,AGMAT,PPP1R1B,MTOR,KLF1,NPR1,DEGS2,LYL1,B4GALT6,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0018205	0.98	0.04	4	313	peptidyl-lysine modification	BP	1	BCL11A,KDM4D,CTNNB1,SNCA	turquoise	VSMC_M6
GO:0044257	0.99	0.03	12	685	cellular protein catabolic process	BP	1	DENND3,CTSC,CTNNB1,NKD2,HFE,LAPTM5,ASCC2,PRAME,RGN,PMAIP1,GNA12,MGAT3	turquoise	VSMC_M6
GO:0033365	0.99	0.02	13	737	protein localization to organelle	BP	1	SYK,TGFB1,GPC6,CD36,HHEX,HYAL2,LAPTM5,BMP7,NOTCH1,GBP1,CDH1,MMP12,MGAT3	turquoise	VSMC_M6
GO:0044267	0.99	0.02	92	3725	cellular protein metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,DENND3,PDGFB,MOB3B,IREB2,KDR,SYK,EPHA5,IL6,BCL11A,C5,RASIP1,PIK3CG,KDM4D,CTSC,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SFRP1,NOTUM,CD36,NEURL3,KIRREL2,STK35,PRAG1,PRR5L,KLKB1,HHEX,SOX7,HUNK,THBS4,PPP1R16B,MAPK10,SNCA,MTTP,HYAL2,SLC39A8,NKD2,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,SRMS,ART4,ACE,PTPRE,PRAME,ST6GAL1,LTF,PALD1,TBX1,RGN,FGF23,PPM1F,PRKCH,PPP1R1B,MTOR,BCKDK,TTLL6,MAST1,NPR1,B4GALT6,MATK,TNFRSF18,SH2D3C,CDH5,ALOX12,PRSS22,PMAIP1,TRIM43,RELN,ALKAL1,PPP1R3C,GNA12,PKIB,TRIM62,CCR7,MGAT3	turquoise	VSMC_M6
GO:0016070	0.99	0.02	85	3480	RNA metabolic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,NSUN4,NOVA2,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,ISG20,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH1,SNORD1A,SNORA69,MMP12,SOX17,RELN,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,SOX18,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0045184	0.99	0.02	29	1395	establishment of protein localization	BP	1	SYBU,SYK,EPHA5,IL6,RAB38,GRIP2,PPARG,TGFB1,SNAP25,SFRP1,CD36,ADAMTS9,PRR5L,REEP1,MAPK10,MTTP,HYAL2,LAPTM5,OAZ3,SYTL5,ATP13A1,PPM1F,SNCG,SSTR5,NOTCH1,CDH1,MMP12,NUCB1,TRPM2	turquoise	VSMC_M6
GO:1901564	0.99	0.02	122	4789	organonitrogen compound metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,ENPP2,IP6K3,DENND3,PDGFB,MOB3B,IREB2,KDR,SYK,EPHA5,IL6,TMPRSS11F,BCL11A,C5,RASIP1,PIK3CG,KDM4D,CTSC,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SLCO2B1,PDE2A,SFRP1,NOTUM,CD36,NEURL3,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,F11,KLKB1,HHEX,LYVE1,SOX7,HUNK,THBS4,PPP1R16B,COL2A1,GSTA4,MAPK10,GOT1,BMP1,SNCA,MTTP,HYAL2,SLC39A8,NKD2,HFE,LAPTM5,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,ART4,ACE,PTPRE,PRAME,ST6GAL1,LTF,TSPAN15,GSTT2B,PALD1,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,TSPAN14,AGMAT,PPP1R1B,MTOR,BCKDK,TTLL6,MAST1,NPR1,DEGS2,B4GALT6,PDE4B,SARM1,MATK,TNFRSF18,NOTCH1,SH2D3C,CDH1,CDH5,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,TRIM43,SOX17,RELN,ALKAL1,PPP1R3C,GNA12,PKIB,TRIM62,CCR7,HRASLS,MGAT3,NUDT4B	turquoise	VSMC_M6
GO:0051301	0.99	0.02	8	525	cell division	BP	1	PARD6G,PDGFB,DLL1,TGFB1,THBS4,SSTR5,NOTCH1,SOX17	turquoise	VSMC_M6

GO:0043933	0.99	0.02	28	1370	protein-containing complex subunit organization	BP	1	DNAH8,STEAP4,SYK,CFAP100,KCNA7,RASIP1,TGFB1,KCTD12,TMC8,SPTBN4,SNAP25,CD36,SNCA,MTTP,HFE,ESAM,SELP,BAIAP2L1,MTOR,HCN1,ADGRL4,CDH5,TSPYL1,HIST1H4G,KANK3,TRPM2,CCR7,NSG2	turquoise	VSMC_M6
GO:0006417	0.99	0.02	4	341	regulation of translation	BP	1	IREB2,IL6,ASCC2,MTOR	turquoise	VSMC_M6
GO:0034248	0.99	0.02	5	395	regulation of cellular amide metabolic process	BP	1	IREB2,IL6,SNCA,ASCC2,MTOR	turquoise	VSMC_M6
GO:0051603	0.99	0.02	10	639	proteolysis involved in cellular protein catabolic process	BP	1	CTSC,CTNNB1,NKD2,HFE,LAPTM5,ASCC2,PRAME,RGN,PMAIP1,GNA12	turquoise	VSMC_M6
GO:0000280	0.99	0.02	4	355	nuclear division	BP	1	PDGFB,CYP26B1,BMP7,C19orf57	turquoise	VSMC_M6
GO:0006259	0.99	0.01	12	741	DNA metabolic process	BP	1	PDGFB,IL6,KDM4D,TGFB1,CTNNB1,ISG20,ASCC2,RGN,C19orf57,ENDOG,GGN,PKIB	turquoise	VSMC_M6
GO:0007346	0.99	0.02	4	360	regulation of mitotic cell cycle	BP	1	PDGFB,TGFB1,CTNNB1,BMP7	turquoise	VSMC_M6
GO:0044249	1.00	0.01	104	4271	cellular biosynthetic process	BP	1	TNFRSF11A,NOTCH4,IP6K3,PDGFB,ETV7,IREB2,ADGRF5,IL18RAP,SYK,BARX1,EPHA5,IL6,OSBPL3,BCL11A,MAML3,PIK3CG,DLL1,RAB38,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,GOT1,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NFATC2,INPP5D,EAF2,TLR7,CD34,CD86,BMP7,ASCC2,PROX1,OAZ3,FANK1,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PITPNM3,PRKCH,BCL6B,AGMAT,PPP1R1B,MTOR,KLF1,NPR1,DEGS2,LYL1,B4GALT6,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,PTGS1,LHX6,CDH3,CDH1,ALOX12,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1,RBP1	turquoise	VSMC_M6
GO:0006511	1.00	0.01	7	542	ubiquitin-dependent protein catabolic process	BP	1	CTNNB1,NKD2,HFE,LAPTM5,ASCC2,PRAME,GNA12	turquoise	VSMC_M6
GO:0009058	1.00	0.00	106	4393	biosynthetic process	BP	1	TNFRSF11A,NOTCH4,IP6K3,PDGFB,ETV7,IREB2,ADGRF5,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,OSBPL3,BCL11A,MAML3,PIK3CG,DLL1,RAB38,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,GOT1,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,HFE,NFATC2,INPP5D,EAF2,TLR7,CD34,CD86,BMP7,ASCC2,PROX1,OAZ3,FANK1,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PITPNM3,PRKCH,BCL6B,AGMAT,PPP1R1B,MTOR,KLF1,NPR1,DEGS2,LYL1,B4GALT6,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,PTGS1,LHX6,CDH3,CDH1,ALOX12,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1,RBP1	turquoise	VSMC_M6
GO:0009059	1.00	0.00	83	3569	macromolecule biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,B4GALT6,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:1901576	1.00	0.00	104	4324	organic substance biosynthetic process	BP	1	TNFRSF11A,NOTCH4,IP6K3,PDGFB,ETV7,IREB2,ADGRF5,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,OSBPL3,BCL11A,MAML3,PIK3CG,DLL1,RAB38,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,P2RY6,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,GOT1,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NFATC2,INPP5D,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,OAZ3,FANK1,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PITPNM3,PRKCH,BCL6B,AGMAT,PPP1R1B,MTOR,KLF1,NPR1,DEGS2,LYL1,B4GALT6,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,PTGS1,LHX6,CDH3,CDH1,ALOX12,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1,RBP1	turquoise	VSMC_M6
GO:0034645	1.00	0.00	82	3533	cellular macromolecule biosynthetic process	BP	1	TNFRSF11A,NOTCH4,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NFATC2,EAF2,TLR7,CD86,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,MTOR,KLF1,LYL1,B4GALT6,NRARP,HES3,NOTCH1,IRF8,S1PR1,LHX2,LHX6,CDH1,MMP12,SOX17,RELN,OLIG2,PDLIM1,PPP1R3C,SOX18,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:0019941	1.00	0.01	7	550	modification-dependent protein catabolic process	BP	1	CTNNB1,NKD2,HFE,LAPTM5,ASCC2,PRAME,GNA12	turquoise	VSMC_M6
GO:0016570	1.00	0.01	4	399	histone modification	BP	1	KDM4D,CTNNB1,SNCA,PPM1F	turquoise	VSMC_M6
GO:0043632	1.00	0.01	7	561	modification-dependent macromolecule catabolic process	BP	1	CTNNB1,NKD2,HFE,LAPTM5,ASCC2,PRAME,GNA12	turquoise	VSMC_M6
GO:0010564	1.00	0.01	6	515	regulation of cell cycle process	BP	1	PDGFB,CTNNB1,SFRP1,BMP7,PROX1,SSTR5	turquoise	VSMC_M6

GO:0090304	1.00	0.00	90	3916	nucleic acid metabolic process	BP	1	TNFRSF11A,NOTCH4,ENPP2,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,KDM4D,NSUN4,NOVA2,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,ISG20,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,RGN,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,C19orf57,MTOR,KLF1,LYL1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH1,SNORD1A,SNORA69,MMP12,GGN,SOX17,RELN,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,FLI1	turquoise	VSMC_M6
GO:0043603	1.00	0.00	13	897	cellular amide metabolic process	BP	1	IREB2,IL6,GSTA4,SNCA,ASCC2,ACE,ST6GAL1,GSTT2B,MTOR,DEGS2,B4GALT6,HRASLS,MGAT3	turquoise	VSMC_M6
GO:0006996	1.00	0.00	63	2943	organelle organization	BP	1	PARD6G,CELSR1,PDGFB,FRMD3,DNAH8,KDR,THSD7A,EPHA5,LRRC4B,ARHGAP25,CFAP100,KDM4D,RAB38,FGD5,NOS3,PPARG,CTNNB1,SPTBN4,MAP6,DNAJB13,SNAP25,PDE2A,SFRP1,CFAP54,ATP8A2,HHEX,REEP1,SLC4A5,CYP26B1,SNCA,NKD2,NRAP,ESAM,LAPTM5,CD34,BMP7,PROX1,SUN3,CCDC88B,BAIAP2L1,PPM1F,C19orf57,MTOR,TTLL6,ABI3,ARHGEF15,MAST1,CCDC69,NOTCH1,S1PR1,CDH5,TSPYL1,PMAIP1,RUFY4,RELN,PDLIM1,HIST1H4G,KANK3,SHANK3,TRPM2,PKIB,CCR7,HRASLS	turquoise	VSMC_M6
GO:0046907	1.00	0.00	21	1261	intracellular transport	BP	1	SYBU,DENND3,SYK,RAB38,GRIP2,TGFB1,MAP6,CD36,PRR5L,HHEX,HYAL2,LAPTM5,OAZ3,SYTL5,CCDC88B,NOTCH1,CDH1,MMP12,NUCB1,NSG2,TMEM50B	turquoise	VSMC_M6
GO:1901566	1.00	0.00	22	1317	organonitrogen compound biosynthetic process	BP	1	PDGFB,IREB2,IL6,RAB38,NOS3,TGFB1,CTNNB1,GOT1,SNCA,MTTP,SLC39A8,ASCC2,OAZ3,ST6GAL1,GUCY1A2,AGMAT,MTOR,NPR1,DEGS2,B4GALT6,CCR7,MGAT3	turquoise	VSMC_M6
GO:0006281	1.00	0.00	4	455	DNA repair	BP	1	KDM4D,ASCC2,C19orf57,GGN	turquoise	VSMC_M6
GO:0006518	1.00	0.00	8	688	peptide metabolic process	BP	1	IREB2,IL6,GSTA4,ASCC2,ACE,GSTT2B,MTOR,MGAT3	turquoise	VSMC_M6
GO:0046483	1.00	0.00	100	4376	heterocycle metabolic process	BP	1	TNFRSF11A,NOTCH4,ENPP2,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,KDM4D,NSUN4,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SLCO2B1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,ISG20,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,C19orf57,MTOR,KLF1,NPR1,LYL1,PDE4B,SARM1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH1,SNORD1A,SNORA69,ALOX12,MMP12,GGN,SOX17,RELN,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,NUDT4B,FLI1	turquoise	VSMC_M6
GO:0006139	1.00	0.00	97	4274	nucleobase-containing compound metabolic process	BP	1	TNFRSF11A,NOTCH4,ENPP2,PDGFB,ETV7,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,KDM4D,NSUN4,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,ISG20,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,C19orf57,MTOR,KLF1,NPR1,LYL1,PDE4B,SARM1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH1,SNORD1A,SNORA69,MMP12,GGN,SOX17,RELN,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,NUDT4B,FLI1	turquoise	VSMC_M6
GO:0032446	1.00	0.00	8	703	protein modification by small protein conjugation	BP	1	BCL11A,CTNNB1,NEURL3,LAPTM5,PRAME,MTOR,TRIM43,TRIM62	turquoise	VSMC_M6
GO:0044260	1.00	0.00	143	5916	cellular macromolecule metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,IP6K3,DENND3,PDGFB,ETV7,MOB3B,IREB2,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,CTSC,RARRES2,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,PCDH12,CD36,NEURL3,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,HUNK,PRDM8,THBS4,PPP1R16B,COL2A1,TOX2,MAPK10,IRX6,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,EAF2,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,SRMS,FANK1,ART4,ACE,PTPRE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,PALD1,TBX1,RGN,SELE,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,C19orf57,MTOR,BCKDK,TTLL6,KLF1,MAST1,NPR1,LYL1,B4GALT6,MATK,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,LHX6,CDH1,CDH5,ALOX12,MMP12,PRSS22,PMAIP1,GGN,TRIM43,SOX17,RELN,ALKAL1,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:0016567	1.00	0.00	7	656	protein ubiquitination	BP	1	CTNNB1,NEURL3,LAPTM5,PRAME,MTOR,TRIM43,TRIM62	turquoise	VSMC_M6

GO:0006725	1.00	0.00	100	4410	cellular aromatic compound metabolic process	BP	1	TNFRSF11A,NOTCH4,ENPP2,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,KDM4D,NSUN4,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SLCO2B1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,ISG20,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,C19orf57,MTOR,KLF1,NPR1,LYL1,PDE4B,SARM1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH3,CDH1,SNORD1A,SNORA69,MMP12,GGN,SOX17,RELN,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,NUDT4B,FLI1	turquoise	VSMC_M6
GO:0051726	1.00	0.00	10	827	regulation of cell cycle	BP	1	PDGFB,TGFB1,CTNNB1,SFRP1,HHEX,ERN1,BMP7,PROX1,SSTR5,NOTCH1	turquoise	VSMC_M6
GO:1901360	1.00	0.00	104	4575	organic cyclic compound metabolic process	BP	1	TNFRSF11A,NOTCH4,ENPP2,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,OSBPL3,BCL11A,MAML3,DLL1,KDM4D,NSUN4,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SLCO2B1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,CYP26B1,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,ISG20,NFATC2,EAF2,TLR7,CD86,ERN1,BMP7,ASCC2,PROX1,FANK1,HOXD10,PRAME,PAX9,LTF,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,PPP1R1B,C19orf57,MTOR,KLF1,NPR1,LYL1,PDE4B,SARM1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH3,CDH1,SNORD1A,SNORA69,ALOX12,MMP12,GGN,SOX17,RELN,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,NUDT4B,SCARF1,FLI1	turquoise	VSMC_M6
GO:0043604	1.00	0.00	7	672	amide biosynthetic process	BP	1	IREB2,IL6,SNCA,ASCC2,MTOR,DEGS2,B4GALT6	turquoise	VSMC_M6
GO:0034641	1.00	0.00	111	4878	cellular nitrogen compound metabolic process	BP	1	TNFRSF11A,NOTCH4,ENPP2,PDGFB,ETV7,IREB2,IL18RAP,SYK,BARX1,EPHA5,IL6,BCL11A,MAML3,DLL1,KDM4D,NSUN4,NOVA2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SLCO2B1,PDE2A,SFRP1,ZIC2,CD36,PRR5L,HHEX,SOX7,TSC22D2,CXCL10,ADGRG3,PRDM8,GSTA4,TOX2,MAPK10,IRX6,NKX2-3,SNCA,HYAL2,SLC39A8,ESRRG,ISG20,NFATC2,EAF2,TLR7,CD34,CD86,ERN1,BMP7,ASCC2,PROX1,OAZ3,FANK1,ACE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,GSTT2B,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,BCL6B,AGMAT,PPP1R1B,C19orf57,MTOR,BCKDK,KLF1,NPR1,DEGS2,LYL1,B4GALT6,PDE4B,SARM1,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,LHX2,LHX6,CDH1,SNORD1A,SNORA69,MMP12,GGN,SOX17,RELN,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,SOX18,PKIB,ZNF775,TRIM62,BAMBI,HRASLS,MGAT3,NUDT4B,FLI1	turquoise	VSMC_M6
GO:0043170	1.00	0.00	173	7034	macromolecule metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,IP6K3,DENND3,PDGFB,ETV7,MOB3B,IREB2,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,TMPRSS11F,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,PCDH12,CD36,NEURL3,NFKBID,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,F11,KLKB1,HHEX,LYVE1,SOX7,TSC22D2,CXCL10,ANGPT2,SLC4A5,ADGRG3,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,COL2A1,TOX2,MAPK10,IRX6,NKX2-3,BMP1,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,SLAMF9,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,FANK1,ART4,ACE,PTPRE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TSPAN15,PALD1,CCDC88B,TBX1,RGN,SELE,FGF23,PPM1F,PRKCH,TSPAN14,BCL6B,PPP1R1B,C19orf57,MTOR,BCKDK,TTLL6,KLF1,MAST1,NPR1,LYL1,B4GALT6,PDE4B,MATK,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,LHX6,CDH3,CDH1,CDH5,SNORD1A,SNORA69,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,GGN,TRIM43,SOX17,RELN,ACKR1,ALKAL1,C3AR1,SNORD8,SNORD70,MIR1307,SNORD124,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,MGAT3,FLI1	turquoise	VSMC_M6
GO:0006412	1.00	0.00	4	548	translation	BP	1	IREB2,IL6,ASCC2,MTOR	turquoise	VSMC_M6
GO:0006396	1.00	0.00	11	950	RNA processing	BP	1	IL6,NSUN4,NOVA2,TGFB1,ISG20,ERN1,SNORD1A,SNORA69,SNORD8,SNORD70,SNORD124	turquoise	VSMC_M6
GO:0051276	1.00	0.00	6	682	chromosome organization	BP	1	KDM4D,CTNNB1,HHEX,TSPYL1,HIST1H4G,PKIB	turquoise	VSMC_M6
GO:0043043	1.00	0.00	4	566	peptide biosynthetic process	BP	1	IREB2,IL6,ASCC2,MTOR	turquoise	VSMC_M6
GO:0070647	1.00	0.00	8	806	protein modification by small protein conjugation or removal	BP	1	BCL11A,CTNNB1,NEURL3,LAPTM5,PRAME,MTOR,TRIM43,TRIM62	turquoise	VSMC_M6
GO:0006974	1.00	0.00	6	699	cellular response to DNA damage stimulus	BP	1	KDM4D,NFATC2,ASCC2,C19orf57,PMAIP1,GGN	turquoise	VSMC_M6
GO:0016071	1.00	0.00	4	586	mRNA metabolic process	BP	1	NOVA2,PRR5L,ERN1,MTOR	turquoise	VSMC_M6
GO:0022402	1.00	0.00	10	951	cell cycle process	BP	1	PARD6G,PDGFB,CTNNB1,SFRP1,CYP26B1,BMP7,PROX1,C19orf57,CCDC69,SSTR5	turquoise	VSMC_M6

GO:0071704	1.00	0.00	195	8083	organic substance metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,IP6K3,DENND3,PDGFB,ETV7,MOB3B,IREB2,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,TMPRSS11F,OSBPL3,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SLCO2B1,P2RY6,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,PCDH12,CD36,NEURL3,NFKBID,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,F11,KLKB1,HHEX,LYVE1,SOX7,TSC22D2,CXCL10,ANGPT2,SOGA1,SLC4A5,ADGRG3,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,GSTA4,TOX2,MAPK10,IRX6,GOT1,NKX2-3,BMP1,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,SLAMF9,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,FANK1,ART4,ACE,PTPRE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TSPAN15,GSTT2B,PALD1,CCDC88B,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,FGF23,PPM1F,PITPNM3,PRKCH,TSPAN14,BCL6B,AGMAT,PPP1R1B,C19orf57,MTOR,BCKDK,TTLL6,KLF1,MAST1,NPR1,DEGS2,LYL1,B4GALT6,PDE4B,SARM1,MATK,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,PTGS1,LHX6,CDH3,CDH1,CDH5,SNORD1A,SNORA69,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,GGN,TRIM43,SOX17,RELN,ACKR1,ALKAL1,C3AR1,SNORD8,SNORD70,MIR1307,SNORD124,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,HRASLS,MGAT3,NUDT4B,SCARF1,FLI1,RBP1	turquoise	VSMC_M6
GO:0008152	1.00	0.00	206	8467	metabolic process	BP	1	TNFRSF11A,IL23A,LYZ,FLT4,NOTCH4,ENPP2,IP6K3,DENND3,PDGFB,ETV7,MOB3B,IREB2,STEAP4,ADGRF5,KDR,IL18RAP,IL1RL2,SYK,BARX1,EPHA5,IL6,TMPRSS11F,OSBPL3,BCL11A,NDUFA4,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RAB38,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,CXCR4,EDNRB,CTNNB1,SPTBN4,TIE1,SLCO2B1,P2RY6,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,PCDH12,CD36,NEURL3,NFKBID,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,F11,KLKB1,HHEX,LYVE1,SOX7,TSC22D2,CXCL10,ANGPT2,SOGA1,SLC4A5,ADGRG3,ATP6V0D2,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,GSTA4,TOX2,MAPK10,IRX6,GOT1,NKX2-3,BMP1,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,SLAMF9,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,FANK1,ART4,ACE,PTPRE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TSPAN15,GSTT2B,PALD1,LPAR2,CCDC88B,TBX1,GUCY1A2,RGN,CDA,LGALS12,SELE,FGF23,PPM1F,PITPNM3,PRKCH,TSPAN14,BCL6B,SLC25A18,AGMAT,PPP1R1B,C19orf57,MTOR,BCKDK,TTLL6,KLF1,MAST1,NPR1,DEGS2,LYL1,B4GALT6,PDE4B,SARM1,MATK,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,GBP1,LHX2,PTGS1,LHX6,CDH3,CDH1,CDH5,SNORD1A,SNORA69,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,GGN,RUFY4,TRIM43,SOX17,RELN,ACKR1,ALKAL1,C3AR1,SNORD8,SNORD70,MIR1307,SNORD124,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,HRASLS,MGAT3,NUDT4B,SCARF1,GPX3,FLI1,RBP1	turquoise	VSMC_M6
GO:0000278	1.00	0.00	4	729	mitotic cell cycle	BP	1	PDGFB,TGFB1,CTNNB1,BMP7	turquoise	VSMC_M6
GO:0006807	1.00	0.00	169	7284	nitrogen compound metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,IP6K3,DENND3,PDGFB,ETV7,MOB3B,IREB2,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,TMPRSS11F,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SLCO2B1,PDE2A,SFRP1,ZIC2,NOTUM,CD36,NEURL3,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,F11,KLKB1,HHEX,LYVE1,SOX7,TSC22D2,CXCL10,ADGRG3,HUNK,PRDM8,THBS4,PPP1R16B,COL2A1,GSTA4,TOX2,MAPK10,IRX6,GOT1,NKX2-3,BMP1,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,FANK1,ART4,ACE,PTPRE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TSPAN15,GSTT2B,PALD1,TBX1,GUCY1A2,RGN,CDA,FGF23,PPM1F,PRKCH,TSPAN14,BCL6B,AGMAT,PPP1R1B,C19orf57,MTOR,BCKDK,TTLL6,KLF1,MAST1,NPR1,DEGS2,LYL1,B4GALT6,PDE4B,SARM1,MATK,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,LHX6,CDH1,CDH5,SNORD1A,SNORA69,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,GGN,TRIM43,SOX17,RELN,ALKAL1,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,HRASLS,MGAT3,NUDT4B,FLI1	turquoise	VSMC_M6
GO:0007049	1.00	0.00	15	1405	cell cycle	BP	1	PARD6G,PDGFB,TGFB1,CTNNB1,SFRP1,STK35,HHEX,CYP26B1,ERN1,BMP7,PROX1,C19orf57,CCDC69,SSTR5,NOTCH1	turquoise	VSMC_M6

GO:0044238	1.00	0.00	177	7641	primary metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,IP6K3,DENND3,PDGFB,ETV7,MOB3B,IREB2,ADGRF5,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,TMPRSS11F,OSBPL3,BCL11A,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RAB38,RARRES2,NOS3,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,P2RY6,PDE2A,SFRP1,ZIC2,NOTUM,PCDH12,CD36,NEURL3,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,F11,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,TOX2,MAPK10,IRX6,GOT1,NKX2-3,BMP1,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,FANK1,ART4,ACE,PTPRE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,TSPAN15,PALD1,TBX1,GUCY1A2,RGN,CDA,LGALS12,FGF23,PPM1F,PITPNM3,PRKCH,TSPAN14,BCL6B,AGMAT,PPP1R1B,C19orf57,MTOR,BCKDK,TTLL6,KLF1,MAST1,NPR1,DEGS2,LYL1,B4GALT6,PDE4B,SARM1,MATK,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,PTGS1,LHX6,CDH1,CDH5,SNORD1A,SNORA69,ALOX12,PRSS50,MMP12,PRSS22,PMAIP1,GGN,TRIM43,SOX17,RELN,ALKAL1,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,HRASLS,MGAT3,NUDT4B,SCARF1,FLI1,RBP1	turquoise	VSMC_M6
GO:0044237	1.00	0.00	184	7918	cellular metabolic process	BP	1	TNFRSF11A,IL23A,FLT4,NOTCH4,ENPP2,IP6K3,DENND3,PDGFB,ETV7,MOB3B,IREB2,STEAP4,ADGRF5,KDR,IL18RAP,SYK,BARX1,EPHA5,IL6,OSBPL3,BCL11A,NDUFA4,C5,MAML3,RASIP1,PIK3CG,DLL1,KDM4D,NSUN4,NOVA2,CTSC,RAB38,RARRES2,NOS3,CD177,ITGB4,PPARG,TGFB1,EDNRB,CTNNB1,SPTBN4,TIE1,SLCO2B1,P2RY6,SNAP25,PDE2A,SFRP1,ZIC2,NOTUM,PCDH12,CD36,NEURL3,KIRREL2,STK35,PRAG1,ADAMTS9,PRR5L,KLKB1,HHEX,SOX7,TSC22D2,CXCL10,SOGA1,ADGRG3,ATP6V0D2,HUNK,PRDM8,THBS4,CYP26B1,PPP1R16B,PLCB2,COL2A1,GSTA4,TOX2,MAPK10,IRX6,GOT1,NKX2-3,SNCA,MTTP,HYAL2,SLC39A8,ESRRG,NKD2,HFE,LAPTM5,ISG20,NFATC2,INPP5D,EAF2,TLR7,CD34,PECAM1,CD86,ERN1,BMP7,IGFBP3,ASCC2,PROX1,GPC1,OAZ3,SRMS,FANK1,ART4,ACE,PTPRE,HOXD10,PRAME,PAX9,ST6GAL1,LTF,GSTT2B,PALD1,TBX1,GUCY1A2,RGN,CDA,SELE,FGF23,PPM1F,PITPNM3,PRKCH,BCL6B,SLC25A18,AGMAT,PPP1R1B,C19orf57,MTOR,BCKDK,TTLL6,KLF1,MAST1,NPR1,DEGS2,LYL1,B4GALT6,PDE4B,SARM1,MATK,TNFRSF18,NRARP,HES3,NOTCH1,IRF8,S1PR1,ENDOG,SH2D3C,LHX2,PTGS1,LHX6,CDH3,CDH1,CDH5,SNORD1A,SNORA69,ALOX12,MMP12,PRSS22,PMAIP1,GGN,RUFY4,TRIM43,SOX17,RELN,ALKAL1,SNORD8,SNORD70,SNORD124,OLIG2,PDLIM1,PPP1R3C,SOX18,GNA12,PKIB,ZNF775,TRIM62,BAMBI,CCR7,HRASLS,MGAT3,NUDT4B,GPX3,FLI1,RBP1	turquoise	VSMC_M6
GO:0051276	0.00	1.00	186	682	chromosome organization	BP	1.4E-53	NUP107,CCT2,FBXO5,TCP1,RAD21,DSCC1,KIFC1,ATAD2,SRPK1,RECQL4,MCM5,HSP90AB1,MCM3,TRIM28,ANP32B,SMC2,TTK,HNRNPA2B1,CCT4,CDCA8,EZH2,NUP62,PHF19,SMC6,GEN1,RUVBL2,GRWD1,MCM2,CENPO,RUVBL1,DNAJC2,RAD54L,CENPA,NASP,KIF2C,MCM6,FANCD2,NCAPG2,CDC20,SUPT16H,NAP1L1,CHMP6,SGO1,PCNA,CHFR,RFC3,RRP8,CDC16,NCAPH,CCNB1,MCM4,ESPL1,BUB1,ANAPC1,STAG1,CENPK,CCNE1,CENPH,KNTC1,HMGB2,SSRP1,TERF1,HELLS,RACGAP1,ESCO2,DSN1,CCT8,RBL1,MSH3,BUB1B,MIS18A,CCT7,GNL3,KNSTRN,RAD51,DCLRE1B,CCNE2,OIP5,NUSAP1,CHAF1B,UBE2C,NAV2,NCAPD3,RFC5,HMGN1,CCT5,CCT6A,NUCKS1,DEK,KIF18A,TENT4A,NAA50,SMC3,CENPE,TRIP13,CHD1L,SGO2,KIF14,POLQ,ANP32E,HJURP,RFC2,RPA2,MCM3AP,IPO4,NEK2,PRC1,NUP133,H2AFX,BLM,CENPF,BUB3,HAT1,CDK1,SMARCC1,DHX9,MKI67,NUF2,RFC4,DNA2,ZW10,KIF18B,CDCA5,FANCM,SMC4,SMARCAL1,DNAJC9,MCM7,PSMC3IP,TACC3,DLGAP5,NCAPD2,ZWINT,SUV39H1,MNAT1,EXO1,HNRNPU,INCENP,SMARCE1,RFC1,TOP2A,CDC6,SMC1A,ASF1B,NCAPG,EXOSC10,CCT3,KIF4A,KIF22,SPDL1,AURKB,HIRIP3,PTTG1,ZWILCH,KIF23,CENPI,PLK1,BRIP1,DNMT1,TADA2A,TOP3A,NDC80,AIFM1,CHAF1A,NDC1,RPA1,SMG6,NOC2L,HASPIN,CHTF18,DKC1,CDT1,CENPN,NEK6,ACD,ERCC6L,HIST1H1A,CENPP,HNRNPD,MAD2L1,HMGB3,CENPW,POLE3,FEN1,HIST1H2BB,MBD2	darkgrey	VSMC_M8

GO:0007049	0.00	1.00	279	1405	cell cycle	BP	1.5E-52	TXNL4A,RTTN,CDK2,NUP43,TUBB,DDX39B,FBXO5,EZR,GTSE1,RAD21,DSCC1,MTBP,KIFC1,KIF20A,CDC25C,DBF4,VCP,HSP90AB1,CDC5L,CENPQ,CEP135,CKS2,MCM3,MELK,SMC2,MSH6,TTK,ANLN,CDCA8,EZH2,NUP62,CLSPN,CASP2,ORC1,GEN1,PLK4,STIL,LIG1,MCM2,RUVBL1,CCNA2,RAD54L,CHORDC1,RNASEH2B,PPP5C,MASTL,CENPA,NASP,KIF2C,BORA,SPHK1,MCM6,SRSF2,FANCD2,NCAPG2,CDC20,BIRC5,GTPBP4,IPO5,CHMP6,E2F7,SGO1,CKAP2,RRM1,PCNA,CHFR,CDC25B,POLE,ZNF703,HGF,TOPBP1,PSMD13,RRP8,CDC16,NCAPH,CCNB1,MCM4,WDR62,HAUS5,AAAS,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,SKA3,KIF2A,STAG1,CENPJ,CENPK,WEE1,E2F1,KIF11,CCNE1,CENPH,KNTC1,CEP55,TERF1,HELLS,MND1,RACGAP1,PBK,ESCO2,DSN1,TUBA1B,TUBA4B,RBL1,TRIM35,MSH3,BUB1B,MIS18A,CCNL1,CDCA2,FAM83D,CKAP5,KNSTRN,KNL1,TBX3,RAD51,MYBL2,CCNE2,E2F8,BAP1,OIP5,NUSAP1,REEP4,MDM4,CHAF1B,UBE2C,NCAPD3,NOLC1,CIT,KIF18A,TENT4A,NSUN2,GMNN,CHEK1,RASSF1,NAA50,SMC3,KHDRBS1,CENPE,TRIP13,CEP72,SGO2,KIF14,PRMT5,ASPM,BCAT1,RAD9A,FANCI,RCC1,PHACTR4,SPC25,HJURP,TICRR,RPA2,NEK2,PRC1,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,RBM14,CEP85,CENPF,EIF4G1,BUB3,AUNIP,CDK1,CDC25A,FOSL1,MKI67,NUF2,WDR76,POLA1,DNA2,ZW10,KIF18B,CDCA5,FANCM,MIS18BP1,KIF15,RANBP1,BARD1,SMC4,CDC45,BRCA1,CDCA3,HAUS3,CDKN3,PSMC3IP,WDHD1,TACC3,CDK16,DLGAP5,NCAPD2,MYBBP1A,RAD51AP1,ECT2,PIMREG,ZWINT,SUV39H1,HAUS8,MNAT1,MAPK6,FOXM1,MSX1,EXO1,HNRNPU,INCENP,CCNB3,TOP2A,CDC6,LIN9,BID,SMC1A,SRSF5,CCNB2,IQGAP3,NCAPG,NES,KIF4A,PMF1,LMNA,	darkgrey	VSMC_M8
GO:0022402	0.00	1.00	219	951	cell cycle process	BP	8.8E-51	RTTN,CDK2,TUBB,DDX39B,FBXO5,EZR,GTSE1,RAD21,DSCC1,MTBP,KIFC1,KIF20A,CDC25C,DBF4,VCP,CDC5L,CENPQ,CEP135,CKS2,MCM3,MELK,SMC2,MSH6,TTK,ANLN,CDCA8,EZH2,NUP62,CLSPN,CASP2,ORC1,GEN1,PLK4,STIL,LIG1,MCM2,CCNA2,RAD54L,CHORDC1,RNASEH2B,MASTL,CENPA,NASP,KIF2C,BORA,SPHK1,MCM6,FANCD2,NCAPG2,CDC20,CHMP6,E2F7,SGO1,CKAP2,PCNA,CHFR,CDC25B,POLE,TOPBP1,PSMD13,CDC16,NCAPH,CCNB1,MCM4,WDR62,HAUS5,AAAS,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,KIF2A,STAG1,CENPJ,CENPK,WEE1,E2F1,KIF11,CCNE1,CENPH,KNTC1,CEP55,TERF1,MND1,RACGAP1,ESCO2,DSN1,RBL1,MSH3,BUB1B,CDCA2,FAM83D,CKAP5,KNSTRN,KNL1,RAD51,MYBL2,CCNE2,E2F8,NUSAP1,REEP4,UBE2C,NCAPD3,CIT,KIF18A,TENT4A,NSUN2,GMNN,CHEK1,NAA50,SMC3,KHDRBS1,CENPE,TRIP13,CEP72,SGO2,KIF14,PRMT5,ASPM,BCAT1,RAD9A,RCC1,SPC25,TICRR,RPA2,NEK2,PRC1,INTS7,HINFP,DTL,H2AFX,BLM,PDE3A,RBM14,CEP85,CENPF,EIF4G1,BUB3,AUNIP,CDK1,CDC25A,MKI67,NUF2,WDR76,POLA1,DNA2,ZW10,KIF18B,CDCA5,FANCM,KIF15,RANBP1,SMC4,CDC45,BRCA1,HAUS3,CDKN3,PSMC3IP,TACC3,CDK16,DLGAP5,NCAPD2,RAD51AP1,ECT2,ZWINT,HAUS8,MNAT1,FOXM1,MSX1,HNRNPU,INCENP,CCNB3,TOP2A,CDC6,BID,SMC1A,CCNB2,IQGAP3,NCAPG,NES,KIF4A,LMNA,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,HAUS1,PLK1,BRIP1,VRK1,TOP3A,NDC80,SEPT6,ATAD5,POLDIP2,NDE1,CEP76,NDC1,HAUS7,TFAP4,PKMYT1,HASPIN,CCNF,FANCA,CDT1,SASS6,ODF2,NEK6,TMOD3,MAD2L1,CDKN2C,STMN1,AURKA,GINS1,UBE2S,FEN1	darkgrey	VSMC_M8
GO:0000278	0.00	1.00	188	729	mitotic cell cycle	BP	1.1E-50	CDK2,TUBB,FBXO5,GTSE1,RAD21,DSCC1,MTBP,KIFC1,KIF20A,CDC25C,DBF4,VCP,CDC5L,CKS2,MCM3,MELK,SMC2,TTK,ANLN,CDCA8,EZH2,NUP62,CLSPN,CASP2,ORC1,GEN1,PLK4,STIL,LIG1,MCM2,CCNA2,RNASEH2B,PPP5C,MASTL,CENPA,NASP,KIF2C,BORA,SPHK1,MCM6,SRSF2,FANCD2,NCAPG2,CDC20,CHMP6,E2F7,SGO1,CKAP2,RRM1,PCNA,CHFR,CDC25B,POLE,HGF,TOPBP1,CDC16,NCAPH,CCNB1,MCM4,WDR62,AAAS,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,SKA3,KIF2A,STAG1,CENPK,WEE1,E2F1,KIF11,CCNE1,CENPH,KNTC1,CEP55,RACGAP1,PBK,DSN1,TUBA1B,TUBA4B,RBL1,TRIM35,BUB1B,CDCA2,CKAP5,KNSTRN,RAD51,MYBL2,CCNE2,E2F8,NUSAP1,REEP4,UBE2C,NCAPD3,NOLC1,CIT,KIF18A,TENT4A,CHEK1,NAA50,SMC3,KHDRBS1,CENPE,TRIP13,SGO2,KIF14,PRMT5,BCAT1,RAD9A,RCC1,SPC25,TICRR,RPA2,NEK2,PRC1,HINFP,DTL,BLM,CEP85,CENPF,EIF4G1,BUB3,CDK1,CDC25A,MKI67,NUF2,POLA1,DNA2,ZW10,KIF18B,CDCA5,KIF15,RANBP1,SMC4,CDC45,BRCA1,CDKN3,WDHD1,TACC3,CDK16,DLGAP5,NCAPD2,ECT2,ZWINT,MNAT1,FOXM1,HNRNPU,INCENP,CCNB3,CDC6,BID,SMC1A,CCNB2,IQGAP3,NCAPG,NES,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,VRK1,NDC80,SEPT6,POLDIP2,NDE1,TUBB6,TFAP4,PKMYT1,HASPIN,CCNF,TUBB4B,TP73,CDT1,NEK6,TMOD3,MAD2L1,CDKN2C,STMN1,AURKA,GINS1,UBE2S,CENPW	darkgrey	VSMC_M8

GO:1903047	0.00	1.00	169	608	mitotic cell cycle process	BP	4.1E-50	CDK2,FBXO5,GTSE1,RAD21,DSCC1,MTBP,KIFC1,KIF20A,CDC25C,DBF4,VCP,CKS2,MCM3,MELK,SMC2,TTK,ANLN,CDCA8,EZH2,NUP62,CLSPN,CASP2,ORC1,GEN1,STIL,LIG1,MCM2,CCNA2,RNASEH2B,MASTL,CENPA,NASP,KIF2C,BORA,SPHK1,MCM6,FANCD2,NCAPG2,CDC20,CHMP6,E2F7,SGO1,CKAP2,PCNA,CHFR,CDC25B,POLE,TOPBP1,CDC16,NCAPH,CCNB1,MCM4,WDR62,AAAS,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,KIF2A,STAG1,CENPK,WEE1,E2F1,KIF11,CCNE1,CENPH,KNTC1,CEP55,RACGAP1,DSN1,RBL1,BUB1B,CDCA2,CKAP5,KNSTRN,RAD51,MYBL2,CCNE2,NUSAP1,REEP4,UBE2C,NCAPD3,CIT,KIF18A,TENT4A,CHEK1,NAA50,SMC3,KHDRBS1,CENPE,TRIP13,SGO2,KIF14,PRMT5,BCAT1,RAD9A,RCC1,SPC25,TICRR,RPA2,NEK2,PRC1,HINFP,DTL,BLM,CEP85,CENPF,EIF4G1,BUB3,CDK1,CDC25A,MKI67,NUF2,POLA1,DNA2,ZW10,KIF18B,CDCA5,KIF15,RANBP1,SMC4,CDC45,BRCA1,CDKN3,TACC3,CDK16,DLGAP5,NCAPD2,ECT2,ZWINT,MNAT1,FOXM1,HNRNPU,INCENP,CCNB3,CDC6,BID,SMC1A,CCNB2,IQGAP3,NCAPG,NES,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,VRK1,NDC80,SEPT6,POLDIP2,NDE1,TFAP4,PKMYT1,HASPIN,CCNF,CDT1,NEK6,TMOD3,MAD2L1,CDKN2C,STMN1,AURKA,GINS1,UBE2S	darkgrey	VSMC_M8
GO:0007059	0.00	1.00	109	288	chromosome segregation	BP	2.9E-45	NUP43,FBXO5,RAD21,DSCC1,KIFC1,SRPK1,CENPQ,SMC2,TTK,CDCA8,NUP62,SMC6,GEN1,KIF2C,FANCD2,NCAPG2,CDC20,BIRC5,RAD18,CHMP6,SGO1,CHFR,CDC16,NCAPH,CCNB1,ESPL1,BUB1,ANAPC1,SKA3,STAG1,CENPK,CCNE1,CENPH,KNTC1,TERF1,RACGAP1,ESCO2,DSN1,BUB1B,MIS18A,CDCA2,FAM83D,KNSTRN,KNL1,CCNE2,OIP5,NUSAP1,UBE2C,NCAPD3,KIF18A,TENT4A,NAA50,SMC3,CENPE,TRIP13,SGO2,KIF14,RCC1,SPC25,HJURP,NEK2,PRC1,CEP85,CENPF,BUB3,MKI67,NUF2,ZW10,KIF18B,CDCA5,FANCM,SMC4,BRCA1,PSMC3IP,TACC3,DLGAP5,NCAPD2,ECT2,ZWINT,HNRNPU,INCENP,TOP2A,CDC6,SMC1A,NCAPG,KIF4A,PMF1,KIF22,SPDL1,AURKB,CIAO2A,PTTG1,ZWILCH,KIF23,SPC24,PLK1,BRIP1,TOP3A,SLC25A5,NDC80,NDE1,NDC1,HASPIN,CDT1,CENPN,NEK6,MAD2L1,CENPW,FEN1	darkgrey	VSMC_M8
GO:0000280	0.00	1.00	117	355	nuclear division	BP	9.9E-42	FBXO5,RAD21,DSCC1,MTBP,KIFC1,CDC25C,CKS2,SMC2,TTK,ANLN,CDCA8,NUP62,GEN1,RAD54L,KIF2C,BORA,SPHK1,FANCD2,NCAPG2,CDC20,CHMP6,SGO1,CHFR,CDC25B,PSMD13,CDC16,NCAPH,CCNB1,AAAS,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,KIF2A,STAG1,CENPK,KIF11,CCNE1,KNTC1,TERF1,MND1,RACGAP1,DSN1,MSH3,BUB1B,CDCA2,KNSTRN,RAD51,MYBL2,CCNE2,NUSAP1,REEP4,UBE2C,NCAPD3,KIF18A,TENT4A,CHEK1,NAA50,SMC3,CENPE,TRIP13,SGO2,KIF14,PRMT5,ASPM,RCC1,NEK2,PRC1,PDE3A,CEP85,CENPF,BUB3,MKI67,NUF2,ZW10,KIF18B,CDCA5,FANCM,KIF15,RANBP1,SMC4,PSMC3IP,TACC3,DLGAP5,NCAPD2,RAD51AP1,ZWINT,MSX1,HNRNPU,INCENP,TOP2A,CDC6,SMC1A,CCNB2,NCAPG,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,BRIP1,NDC80,POLDIP2,NDE1,NDC1,PKMYT1,HASPIN,FANCA,CDT1,NEK6,MAD2L1,AURKA,UBE2S	darkgrey	VSMC_M8
GO:0006259	0.00	1.00	175	741	DNA metabolic process	BP	1.9E-41	CDK2,PRIM1,CCT2,DDX39B,TCP1,RAD21,DSCC1,RECQL4,TONSL,MCM5,APTX,POLH,VCP,HSP90AB1,CDC5L,MCM3,TRIM28,MSH6,HNRNPA2B1,POLD1,CCT4,EZH2,MMS22L,CLSPN,ORC6,SMC6,ORC1,GEN1,RUVBL2,LIG1,MCM2,RUVBL1,DNAJC2,RAD54L,PPP5C,WDR33,MCM10,SPHK1,MCM6,FANCD2,XRN2,TK1,PARP2,POLD3,RAD18,SUPT16H,GINS4,ALYREF,PCNA,POLE,RFC3,HGF,TOPBP1,MCM4,PARPBP,CCNE1,HMGB2,SSRP1,TERF1,HELLS,MND1,ESCO2,NEIL3,CCT8,MSH3,MIS18A,CCT7,GNL3,RAD51,DCLRE1B,CCNE2,CHAF1B,RFC5,PSMD14,HMGN1,CCT5,CCT6A,NUCKS1,DEK,TENT4A,UBE2T,CHEK1,SMC3,TRIP13,CHD1L,TRAIP,UNG,PRMT5,POLQ,RAD9A,FANCI,FANCB,TICRR,RFC2,RPA2,NEK2,HINFP,DTL,H2AFX,BLM,NSMCE4A,CENPF,AUNIP,CDK1,TFRC,DHX9,POLA1,AP000944.2,RFC4,DNA2,DDX21,CDCA5,FANCM,BARD1,C17orf53,SMARCAL1,CDC45,BRCA1,MCM7,PSMC3IP,NSD2,WDHD1,RAD51AP1,ANKLE1,MNAT1,FOXM1,FH,EXO1,HNRNPU,RFC1,TOP2A,CDC6,LIN9,SMC1A,NUDT1,DCTPP1,EXOSC10,CCT3,FUS,KIF22,AURKB,RAD23A,PTTG1,BRIP1,MORF4L2,DNMT1,ZSWIM7,TOP3A,TYMS,POLDIP2,WDR70,AIFM1,USP1,UHRF1,CHAF1A,RPA1,SMG6,TP73,CHTF18,DKC1,REXO4,FANCA,CDT1,FAM129B,ACD,PRIM2,HIST1H1A,HNRNPD,DDX23,HMGB3,GINS1,POLE3,FEN1,PALB2,MBD2	darkgrey	VSMC_M8
GO:0140014	0.00	1.00	94	244	mitotic nuclear division	BP	2.1E-39	FBXO5,RAD21,DSCC1,MTBP,KIFC1,CDC25C,SMC2,TTK,ANLN,CDCA8,NUP62,GEN1,KIF2C,BORA,SPHK1,NCAPG2,CDC20,CHMP6,SGO1,CDC16,NCAPH,CCNB1,AAAS,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,KIF2A,STAG1,CENPK,KIF11,KNTC1,RACGAP1,DSN1,BUB1B,CDCA2,KNSTRN,MYBL2,NUSAP1,REEP4,UBE2C,NCAPD3,KIF18A,TENT4A,CHEK1,NAA50,SMC3,CENPE,TRIP13,SGO2,KIF14,PRMT5,RCC1,NEK2,PRC1,CEP85,CENPF,BUB3,MKI67,NUF2,ZW10,KIF18B,CDCA5,KIF15,RANBP1,SMC4,TACC3,DLGAP5,NCAPD2,ZWINT,HNRNPU,INCENP,CDC6,SMC1A,NCAPG,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,NDC80,POLDIP2,NDE1,PKMYT1,HASPIN,CDT1,NEK6,MAD2L1,AURKA,UBE2S	darkgrey	VSMC_M8

GO:0048285	0.00	1.00	120	401	organelle fission	BP	3.8E-38	MTFR2,FBXO5,RAD21,DSCC1,MTBP,KIFC1,FAM49B,CDC25C,CKS2,SMC2,TTK,ANLN,CDCA8,NUP62,GEN1,RAD54L,KIF2C,BORA,SPHK1,FANCD2,NCAPG2,CDC20,CHMP6,SGO1,CHFR,PGAM5,CDC25B,PSMD13,CDC16,NCAPH,CCNB1,AAAS,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,KIF2A,STAG1,CENPK,KIF11,CCNE1,KNTC1,TERF1,MND1,RACGAP1,DSN1,MSH3,BUB1B,CDCA2,KNSTRN,RAD51,MYBL2,CCNE2,NUSAP1,REEP4,UBE2C,NCAPD3,KIF18A,TENT4A,CHEK1,NAA50,SMC3,CENPE,TRIP13,SGO2,KIF14,PRMT5,ASPM,RCC1,NEK2,PRC1,PDE3A,CEP85,CENPF,BUB3,MKI67,NUF2,ZW10,KIF18B,CDCA5,FANCM,KIF15,RANBP1,SMC4,PSMC3IP,TACC3,DLGAP5,NCAPD2,RAD51AP1,ZWINT,MSX1,HNRNPU,INCENP,TOP2A,CDC6,SMC1A,CCNB2,NCAPG,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,BRIP1,NDC80,POLDIP2,NDE1,NDC1,PKMYT1,HASPIN,FANCA,CDT1,NEK6,MAD2L1,AURKA,UBE2S	darkgrey	VSMC_M8
GO:0051301	0.00	1.00	137	525	cell division	BP	8.6E-37	TXNL4A,CDK2,NUP43,TUBB,FBXO5,RAD21,KIFC1,KIF20A,CDC25C,CKS2,SMC2,ANLN,CDCA8,NUP62,ORC6,PLK4,LIG1,RUVBL1,CCNA2,MASTL,CENPA,KIF2C,BORA,NCAPG2,CDC20,BIRC5,CHMP6,E2F7,SGO1,CKAP2,CHFR,CDC25B,CDC16,NCAPH,CCNB1,HAUS5,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,SKA3,KIF2A,STAG1,CENPJ,WEE1,KIF11,CCNE1,KNTC1,CEP55,TERF1,HELLS,RACGAP1,DSN1,TUBA1B,RBL1,BUB1B,MIS18A,CDCA2,GNL3,FAM83D,CKAP5,KNSTRN,KNL1,CCNE2,E2F8,OIP5,NUSAP1,REEP4,UBE2C,NCAPD3,CIT,NSUN2,SMC3,CENPE,SGO2,KIF14,ASPM,RCC1,SPC25,NEK2,PRC1,BLM,CENPF,BUB3,CDK1,CDC25A,NUF2,ZW10,KIF18B,CDCA5,MIS18BP1,SMC4,CDCA3,HAUS3,TACC3,NCAPD2,ECT2,PIMREG,ZWINT,HAUS8,HNRNPU,INCENP,CCNB3,TOP2A,CDC6,SMC1A,CCNB2,NCAPG,KIF4A,PMF1,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,SPC24,HAUS1,PLK1,BRIP1,VRK1,NDC80,SEPT6,POLDIP2,NDE1,HAUS7,CCNF,CDT1,BCAR1,NEK6,ERCC6L,ARF6,MAD2L1,STMN1,AURKA,UBE2S,CENPW	darkgrey	VSMC_M8
GO:0000070	0.00	1.00	68	143	mitotic sister chromatid segregation	BP	8.9E-35	FBXO5,RAD21,DSCC1,KIFC1,SMC2,TTK,CDCA8,NUP62,GEN1,KIF2C,NCAPG2,CDC20,CHMP6,SGO1,CDC16,NCAPH,CCNB1,ESPL1,BUB1,ANAPC1,CENPK,KNTC1,RACGAP1,DSN1,BUB1B,KNSTRN,NUSAP1,UBE2C,NCAPD3,KIF18A,TENT4A,NAA50,SMC3,CENPE,TRIP13,SGO2,KIF14,NEK2,PRC1,CENPF,BUB3,NUF2,ZW10,KIF18B,CDCA5,SMC4,TACC3,DLGAP5,NCAPD2,ZWINT,HNRNPU,INCENP,CDC6,SMC1A,NCAPG,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,NDC80,HASPIN,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0006260	0.00	1.00	86	230	DNA replication	BP	1.6E-34	CDK2,PRIM1,FBXO5,DSCC1,RECQL4,TONSL,MCM5,DBF4,POLH,MCM3,POLD1,MMS22L,ORC6,ORC1,GEN1,GRWD1,LIG1,MCM2,CCNA2,DNAJC2,NASP,MCM10,MCM6,POLD3,GTPBP4,SUPT16H,NAP1L1,E2F7,GINS4,ALYREF,RRM1,PCNA,POLE,RFC3,TOPBP1,MCM4,CCNE1,ATF1,SSRP1,TERF1,ESCO2,RAD51,CCNE2,E2F8,CHAF1B,RFC5,RBMS1,NUCKS1,GMNN,CHEK1,SMC3,TRAIP,POLQ,TICRR,RFC2,RPA2,DTL,BLM,CDK1,S100A11,DHX9,POLA1,AP000944.2,RFC4,DNA2,DDX21,FANCM,DUT,SMARCAL1,CDC45,MCM7,WDHD1,RAC1,RFC1,CDC6,ATAD5,CHAF1A,RPA1,CHTF18,CDT1,PRIM2,FAM111B,DDX23,GINS1,POLE3,FEN1	darkgrey	VSMC_M8
GO:0000819	0.00	1.00	73	168	sister chromatid segregation	BP	3E-34	FBXO5,RAD21,DSCC1,KIFC1,SMC2,TTK,CDCA8,NUP62,GEN1,KIF2C,NCAPG2,CDC20,CHMP6,SGO1,CHFR,CDC16,NCAPH,CCNB1,ESPL1,BUB1,ANAPC1,STAG1,CENPK,KNTC1,RACGAP1,ESCO2,DSN1,BUB1B,KNSTRN,NUSAP1,UBE2C,NCAPD3,KIF18A,TENT4A,NAA50,SMC3,CENPE,TRIP13,SGO2,KIF14,NEK2,PRC1,CENPF,BUB3,NUF2,ZW10,KIF18B,CDCA5,SMC4,TACC3,DLGAP5,NCAPD2,ZWINT,HNRNPU,INCENP,TOP2A,CDC6,SMC1A,NCAPG,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,NDC80,HASPIN,CDT1,NEK6,MAD2L1,FEN1	darkgrey	VSMC_M8
GO:0098813	0.00	1.00	85	230	nuclear chromosome segregation	BP	5.6E-34	FBXO5,RAD21,DSCC1,KIFC1,CENPQ,SMC2,TTK,CDCA8,NUP62,GEN1,KIF2C,FANCD2,NCAPG2,CDC20,CHMP6,SGO1,CHFR,CDC16,NCAPH,CCNB1,ESPL1,BUB1,ANAPC1,STAG1,CENPK,CCNE1,KNTC1,TERF1,RACGAP1,ESCO2,DSN1,BUB1B,FAM83D,KNSTRN,KNL1,CCNE2,NUSAP1,UBE2C,NCAPD3,KIF18A,TENT4A,NAA50,SMC3,CENPE,TRIP13,SGO2,KIF14,NEK2,PRC1,CENPF,BUB3,NUF2,ZW10,KIF18B,CDCA5,FANCM,SMC4,PSMC3IP,TACC3,DLGAP5,NCAPD2,ECT2,ZWINT,HNRNPU,INCENP,TOP2A,CDC6,SMC1A,NCAPG,KIF4A,KIF22,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,BRIP1,NDC80,NDC1,HASPIN,CDT1,NEK6,MAD2L1,FEN1	darkgrey	VSMC_M8
GO:0006281	0.00	1.00	113	455	DNA repair	BP	9.3E-28	CDK2,RAD21,RECQL4,TONSL,MCM5,APTX,POLH,VCP,CDC5L,MCM3,TRIM28,MSH6,POLD1,MMS22L,CLSPN,SMC6,GEN1,RUVBL2,LIG1,MCM2,RUVBL1,RAD54L,PPP5C,WDR33,MCM6,FANCD2,PARP2,POLD3,RAD18,SUPT16H,GINS4,PCNA,POLE,RFC3,TOPBP1,MCM4,PARPBP,HMGB2,SSRP1,ESCO2,NEIL3,MSH3,RAD51,DCLRE1B,CHAF1B,RFC5,PSMD14,HMGN1,NUCKS1,DEK,TENT4A,UBE2T,CHEK1,SMC3,TRIP13,CHD1L,TRAIP,UNG,POLQ,RAD9A,FANCI,FANCB,TICRR,RFC2,RPA2,HINFP,DTL,H2AFX,BLM,NSMCE4A,AUNIP,CDK1,DHX9,POLA1,RFC4,DNA2,CDCA5,FANCM,BARD1,C17orf53,SMARCAL1,CDC45,BRCA1,MCM7,NSD2,WDHD1,RAD51AP1,ANKLE1,MNAT1,FOXM1,FH,EXO1,RFC1,SMC1A,NUDT1,FUS,KIF22,RAD23A,PTTG1,BRIP1,MORF4L2,ZSWIM7,POLDIP2,WDR70,USP1,UHRF1,CHAF1A,RPA1,TP73,REXO4,FANCA,FEN1,PALB2	darkgrey	VSMC_M8

GO:0006261	0.00	1.00	59	137	DNA-dependent DNA replication	BP	4.5E-27	PRIM1,FBXO5,DSCC1,RECQL4,TONSL,MCM5,DBF4,MCM3,POLD1,MMS22L,ORC6,ORC1,GEN1,LIG1,MCM2,MCM10,MCM6,POLD3,E2F7,GINS4,ALYREF,PCNA,POLE,RFC3,TOPBP1,MCM4,CCNE1,TERF1,RAD51,CCNE2,E2F8,RFC5,NUCKS1,GMNN,TRAIP,POLQ,TICRR,RFC2,BLM,POLA1,AP000944.2,RFC4,DNA2,DDX21,FANCM,SMARCAL1,CDC45,MCM7,WDHD1,RFC1,CDC6,RPA1,CHTF18,CDT1,PRIM2,DDX23,GINS1,POLE3,FEN1	darkgrey	VSMC_M8
GO:0071103	0.00	1.00	71	200	DNA conformation change	BP	7.4E-27	DSCC1,SRPK1,RECQL4,MCM5,MCM3,ANP32B,SMC2,HNRNPA2B1,RUVBL2,GRWD1,MCM2,RUVBL1,RAD54L,NASP,MCM6,NCAPG2,NAP1L1,RFC3,RRP8,NCAPH,CCNB1,MCM4,HMGB2,HELLS,MIS18A,RAD51,OIP5,NUSAP1,CHAF1B,NAV2,NCAPD3,RFC5,TENT4A,CHD1L,POLQ,HJURP,RFC2,IPO4,H2AFX,BLM,HAT1,CDK1,DHX9,RFC4,DNA2,CDCA5,FANCM,SMC4,DNAJC9,MCM7,NCAPD2,SUV39H1,MNAT1,INCENP,TOP2A,ASF1B,NCAPG,PLK1,BRIP1,TOP3A,AIFM1,CHAF1A,RPA1,NOC2L,CHTF18,ERCC6L,HIST1H1A,CENPP,HMGB3,CENPW,HIST1H2BB	darkgrey	VSMC_M8
GO:0006974	0.00	1.00	143	699	cellular response to DNA damage stimulus	BP	3.4E-26	CDK2,BCLAF1,DDX39B,FBXO5,GTSE1,RAD21,RECQL4,TONSL,MCM5,APTX,POLH,VCP,CDC5L,MCM3,TRIM28,MSH6,POLD1,MMS22L,CLSPN,CASP2,SMC6,GEN1,RUVBL2,LIG1,MCM2,RUVBL1,RAD54L,RNASEH2B,PPP5C,WDR33,MASTL,MCM10,MCM6,FANCD2,PARP2,POLD3,RAD18,SUPT16H,E2F7,GINS4,PCNA,POLE,RFC3,TOPBP1,CBX5,MCM4,SNAI2,CD44,PARPBP,E2F1,HMGB2,SSRP1,ESCO2,NEIL3,MSH3,RAD51,DCLRE1B,EEF1E1,MDM4,CHAF1B,RFC5,PSMD14,HMGN1,NUCKS1,DEK,TENT4A,UBE2T,CHEK1,SMC3,TRIP13,CHD1L,TRAIP,UNG,POLQ,RAD9A,FANCI,MNDA,DDX5,FANCB,TICRR,RFC2,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,NSMCE4A,AUNIP,CDK1,DHX9,WDR76,POLA1,RFC4,DNA2,CDCA5,FANCM,BARD1,C17orf53,SMARCAL1,CDC45,BRCA1,MCM7,NSD2,WDHD1,DCUN1D5,RAD51AP1,ANKLE1,SUV39H1,MNAT1,FOXM1,FH,MSX1,EXO1,NEDD4,RFC1,TOP2A,BID,SMC1A,NUDT1,FUS,KIF22,RAD23A,PTTG1,PLK1,BRIP1,MORF4L2,ZSWIM7,ATAD5,POLDIP2,WDR70,USP1,UHRF1,CHAF1A,TFAP4,RPA1,TP73,REXO4,FANCA,ACD,POLE3,FEN1,PALB2	darkgrey	VSMC_M8
GO:0010564	0.00	1.00	118	515	regulation of cell cycle process	BP	1.1E-25	CDK2,DDX39B,FBXO5,GTSE1,RAD21,MTBP,KIF20A,CDC25C,DBF4,CDC5L,TTK,ANLN,EZH2,NUP62,CLSPN,CASP2,ORC1,GEN1,PLK4,STIL,CHORDC1,RNASEH2B,BORA,SPHK1,FANCD2,CDC20,E2F7,CHFR,CDC25B,TOPBP1,CDC16,CCNB1,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,CENPJ,WEE1,E2F1,KIF11,KNTC1,TERF1,RACGAP1,RBL1,BUB1B,CDCA2,FAM83D,KNSTRN,E2F8,NUSAP1,UBE2C,CIT,NSUN2,CHEK1,CENPE,TRIP13,KIF14,PRMT5,RAD9A,RCC1,TICRR,RPA2,NEK2,PRC1,INTS7,HINFP,DTL,H2AFX,BLM,PDE3A,RBM14,CEP85,CENPF,EIF4G1,BUB3,CDK1,CDC25A,MKI67,WDR76,DNA2,ZW10,CDCA5,KIF15,RANBP1,CDC45,BRCA1,TACC3,DLGAP5,RAD51AP1,ECT2,ZWINT,MSX1,HNRNPU,INCENP,CCNB3,CDC6,BID,SPDL1,AURKB,PTTG1,ZWILCH,KIF23,PLK1,BRIP1,NDC80,ATAD5,POLDIP2,CEP76,TFAP4,PKMYT1,CCNF,CDT1,NEK6,TMOD3,MAD2L1,AURKA,FEN1	darkgrey	VSMC_M8
GO:0006996	0.00	1.00	368	2943	organelle organization	BP	3.1E-24	RTTN,CDK2,TMED9,MTFR2,NUP107,CCT2,TUBB,FBXO5,EZR,TCP1,RAD21,DSCC1,TTLL1,ARFGAP3,MTBP,KIFC1,ATAD2,FAM49B,KIF20A,CDC25C,HSPA9,CHCHD3,SRPK1,KIF27,RECQL4,CEP78,MCM5,KIF24,VCP,HSP90AB1,CEP135,CKS2,MCM3,TRIM28,ANP32B,SMC2,TTK,HNRNPA2B1,CCT4,NUP205,ANLN,CDCA8,EZH2,NUP62,PHF19,SMC6,GEN1,SDC1,RUVBL2,PLK4,GRWD1,STIL,MCM2,CENPO,SEC61A1,RUVBL1,AMOTL1,SAE1,DNAJC2,RAD54L,CHORDC1,MAST2,CHCHD4,CENPA,CDC42EP4,NASP,COG3,TOMM40,PREB,PLAUR,MRPS7,KIF2C,DIAPH3,BORA,SPHK1,MCM6,FANCD2,ULK4,NCAPG2,CDC20,SEC23B,SUPT16H,NAP1L1,CHMP6,SGO1,ARHGDIA,CKAP2,SIPA1L3,PCNA,CHFR,PGAM5,CDC25B,RFC3,HGF,PSMD13,RRP8,CDC16,NCAPH,USPL1,CCNB1,MCM4,WDR62,GAS2L3,HAUS5,AAAS,ESPL1,BUB1,TPX2,ANAPC1,POLR1B,KIF20B,SKA3,KIF2A,ATG101,STAG1,CENPJ,CENPK,WEE1,HSP90B1,CEP89,KIF11,CCNE1,VAMP8,CENPH,KNTC1,HMGB2,TRAM1,SSRP1,TERF1,HELLS,FHDC1,MND1,RACGAP1,ESCO2,FMNL3,DSN1,TUBA1B,TUBA4B,CCT8,PPID,RBL1,MSH3,BUB1B,MIS18A,CCT7,CDCA2,CFAP298,GNL3,CKAP5,NUP93,KNSTRN,KNL1,RAD51,DCLRE1B,TOMM70,MYBL2,CCNE2,BAP1,OIP5,NUSAP1,NDUFAF1,REEP4,CHAF1B,UBE2C,NAV2,NCAPD3,RFC5,HMGN1,NOLC1,CCT5,CIT,FASTKD3,NUP153,CCT6A,NUCKS1,DEK,KIF18A,ETS1,TENT4A,CHEK1,RASSF1,FP565260.1,NAA50,NAV1,SMC3,CENPE,TRIP13,CEP72,CHD1L,SGO2,KIF14,PRMT5,ASPM,POLQ,EFS,IQCB1,ANP32E,RCC1,PHACTR4,PITPNB,SPC25,HJURP,RFC2,RPA2,MCM3AP,IPO4,NEK2,PRC1,NUP133,NF2,H2AFX,SEC24D,BLM,PDE3A,RBM14,CEP85,CENPF,BUB3,AUNIP,HAT1,CDK1,TFRC,PAK2,SM	darkgrey	VSMC_M8

GO:0051726	0.00	1.00	154	827	regulation of cell cycle	BP	8.5E-24	CDK2,DDX39B,FBXO5,GTSE1,RAD21,MTBP,KIF20A,CDC25C,DBF4,HSP90AB1,CDC5L,CKS2,TTK,ANLN,EZH2,NUP62,CLSPN,CASP2,ORC1,GEN1,PLK4,STIL,CCNA2,CHORDC1,RNASEH2B,MASTL,BORA,SPHK1,FANCD2,CDC20,BIRC5,GTPBP4,IPO5,E2F7,CHFR,CDC25B,ZNF703,TOPBP1,RRP8,CDC16,CCNB1,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,CENPJ,WEE1,E2F1,KIF11,CCNE1,KNTC1,TERF1,RACGAP1,RBL1,TRIM35,BUB1B,CCNL1,CDCA2,FAM83D,KNSTRN,TBX3,CCNE2,E2F8,BAP1,NUSAP1,MDM4,UBE2C,CIT,NSUN2,GMNN,CHEK1,RASSF1,CENPE,TRIP13,KIF14,PRMT5,ASPM,RAD9A,RCC1,PHACTR4,TICRR,RPA2,NEK2,PRC1,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,RBM14,CEP85,CENPF,EIF4G1,BUB3,CDK1,CDC25A,FOSL1,MKI67,WDR76,DNA2,ZW10,CDCA5,KIF15,RANBP1,BARD1,CDC45,BRCA1,CDKN3,TACC3,CDK16,DLGAP5,MYBBP1A,RAD51AP1,ECT2,ZWINT,MNAT1,FOXM1,MSX1,HNRNPU,INCENP,CCNB3,CDC6,LIN9,BID,SRSF5,CCNB2,ALOX15B,SPDL1,AURKB,RAD23A,PTTG1,ZWILCH,KIF23,PRR11,PLK1,BRIP1,NDC80,ATAD5,POLDIP2,CEP76,TFAP4,PKMYT1,CCNF,TP73,CDT1,NEK6,TMOD3,MAD2L1,CDKN2C,AURKA,FEN1	darkgrey	VSMC_M8
GO:0044770	0.00	1.00	99	426	cell cycle phase transition	BP	1E-21	CDK2,DDX39B,FBXO5,GTSE1,RAD21,MTBP,CDC25C,DBF4,CDC5L,CKS2,MELK,TTK,ANLN,EZH2,CLSPN,CASP2,ORC1,GEN1,CCNA2,RNASEH2B,MASTL,NASP,FANCD2,E2F7,CHFR,CDC25B,POLE,TOPBP1,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,WEE1,E2F1,CCNE1,KNTC1,RBL1,BUB1B,FAM83D,CCNE2,UBE2C,NSUN2,CHEK1,KHDRBS1,CENPE,TRIP13,KIF14,BCAT1,RAD9A,RCC1,TICRR,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,CENPF,EIF4G1,BUB3,CDK1,CDC25A,WDR76,DNA2,ZW10,CDCA5,CDC45,BRCA1,CDKN3,TACC3,CDK16,DLGAP5,ZWINT,MNAT1,FOXM1,CCNB3,CDC6,BID,CCNB2,IQGAP3,NES,SPDL1,AURKB,ZWILCH,PLK1,BRIP1,NDC80,ATAD5,TFAP4,PKMYT1,CCNF,CDT1,NEK6,TMOD3,MAD2L1,CDKN2C,AURKA,UBE2S	darkgrey	VSMC_M8
GO:0071840	0.00	1.00	520	4827	cellular component organization or biogenesis	BP	1E-21	TXNL4A,RTTN,CDK2,TMED9,MTFR2,NUP107,CCT2,TUBB,DDX39B,SRFBP1,FBXO5,EZR,TCP1,RAD21,DSCC1,TTLL1,ARFGAP3,MTBP,KIFC1,ATAD2,FAM49B,KIF20A,CDC25C,HSPA9,CHCHD3,SRPK1,KIF27,PSIP1,RECQL4,CEP78,BYSL,MCM5,PWP1,TJP2,KIF24,VCP,HSP90AB1,COL1A2,CEP135,CKS2,MCM3,NOL8,TRIM28,POLR1E,NCBP1,ANP32B,PPIH,SMC2,TTK,HNRNPA2B1,COL9A2,MFSD2A,CCT4,B3GNT2,NUP205,ANLN,CDCA8,GNL2,EZH2,NUP62,NOL10,PHF19,PRMT1,SMC6,GEN1,SDC1,RUVBL2,PLK4,GRWD1,STIL,MCM2,CENPO,SEC61A1,RUVBL1,AMOTL1,SAE1,SLC1A5,DNAJC2,RAD54L,CHORDC1,MAST2,CHCHD4,CENPA,CDC42EP4,NASP,COG3,NUFIP1,TOMM40,PREB,MRPL58,NIFK,KCNN4,NUP85,PLAUR,MRPS7,KIF2C,DIAPH3,DDX18,BORA,DIS3,AXL,RNF157,SPHK1,MCM6,FANCD2,XRN2,ULK4,NCAPG2,NET1,WDR43,CDC20,TK1,SERPINH1,PARP2,SEC23B,FBL,GTPBP4,SUPT16H,EIF4A3,NAP1L1,CHMP6,SGO1,ARHGDIA,CKAP2,STRN,RRM1,SIPA1L3,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,ZNF703,RFC3,NOC4L,DDX51,MAK16,HGF,SNRPF,PSMD13,RRP8,CDC16,NCAPH,USPL1,CCNB1,MCM4,WDR62,SFSWAP,SNAI2,NOP56,SNRPB,GAS2L3,CD44,HAUS5,AAAS,UTP20,ESPL1,BUB1,TPX2,ANAPC1,POLR1B,KIF20B,SKA3,KIF2A,ATG101,ADAMTS6,SGK3,EIF3M,STAG1,WDR36,CENPJ,CENPK,WEE1,HSP90B1,CEP89,KIF11,ABCE1,CCNE1,VAMP8,CENPH,KNTC1,HMGB2,TRAM1,CEP55,ATF1,SSRP1,TERF1,HELLS,FHDC1,UTP15,MND1,RACGAP1,LOXL3,ESCO2,FMNL3,DSN1,TUBA1B,TUBA4B,CCT8,PPID,RBL1,MSH3,BUB1B,MIS18A,CCT7,CDCA2,CFAP298,GNL3,CKAP5,EXOSC1,NUP93,KNSTRN,KNL1,RAD51,DCLRE1B,CREB3L1,TOMM70,MYBL2,CCNE2,MTDH,BAP1,OIP5,	darkgrey	VSMC_M8
GO:0000375	0.00	1.00	73	259	RNA splicing, via transesterification reactions	BP	3.6E-21	TXNL4A,HNRNPH1,DDX39B,PHF5A,SRPK1,SRSF3,PSIP1,CDC5L,NCBP1,PPIH,U2AF2,HNRNPA2B1,SYNCRIP,PPIE,THRAP3,SNRPA,SRSF2,RBM17,SNRPB2,EIF4A3,ALYREF,SNRPF,SFSWAP,SNRPB,HNRNPF,CWC27,SNRNP35,DBR1,RSRC1,RBM19,CWF19L1,MPHOSPH10,SNRPA1,U2AF1,KHDRBS1,SF3B1,NCL,SNRNP40,RBM23,PRMT5,SF3B4,DDX5,PRPF3,RBM14,STRAP,SF3B2,DHX9,HNRNPR,TRA2B,HNRNPA3,HNRNPH3,DDX20,PNN,EFTUD2,SF1,RBM3,HNRNPU,DDX39A,SRSF5,GEMIN5,SNRPD1,HNRNPM,RBMX,RNPS1,SF3A2,DAZAP1,PTBP1,SF3B3,DHX38,USP4,GEMIN4,DDX23,SRSF7	darkgrey	VSMC_M8
GO:0000377	0.00	1.00	72	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	6.2E-21	TXNL4A,HNRNPH1,DDX39B,PHF5A,SRPK1,SRSF3,PSIP1,CDC5L,NCBP1,PPIH,U2AF2,HNRNPA2B1,SYNCRIP,PPIE,THRAP3,SNRPA,SRSF2,RBM17,SNRPB2,EIF4A3,ALYREF,SNRPF,SFSWAP,SNRPB,HNRNPF,CWC27,SNRNP35,DBR1,RSRC1,RBM19,CWF19L1,SNRPA1,U2AF1,KHDRBS1,SF3B1,NCL,SNRNP40,RBM23,PRMT5,SF3B4,DDX5,PRPF3,RBM14,STRAP,SF3B2,DHX9,HNRNPR,TRA2B,HNRNPA3,HNRNPH3,DDX20,PNN,EFTUD2,SF1,RBM3,HNRNPU,DDX39A,SRSF5,GEMIN5,SNRPD1,HNRNPM,RBMX,RNPS1,SF3A2,DAZAP1,PTBP1,SF3B3,DHX38,USP4,GEMIN4,DDX23,SRSF7	darkgrey	VSMC_M8
GO:0000398	0.00	1.00	72	255	mRNA splicing, via spliceosome	BP	6.2E-21	TXNL4A,HNRNPH1,DDX39B,PHF5A,SRPK1,SRSF3,PSIP1,CDC5L,NCBP1,PPIH,U2AF2,HNRNPA2B1,SYNCRIP,PPIE,THRAP3,SNRPA,SRSF2,RBM17,SNRPB2,EIF4A3,ALYREF,SNRPF,SFSWAP,SNRPB,HNRNPF,CWC27,SNRNP35,DBR1,RSRC1,RBM19,CWF19L1,SNRPA1,U2AF1,KHDRBS1,SF3B1,NCL,SNRNP40,RBM23,PRMT5,SF3B4,DDX5,PRPF3,RBM14,STRAP,SF3B2,DHX9,HNRNPR,TRA2B,HNRNPA3,HNRNPH3,DDX20,PNN,EFTUD2,SF1,RBM3,HNRNPU,DDX39A,SRSF5,GEMIN5,SNRPD1,HNRNPM,RBMX,RNPS1,SF3A2,DAZAP1,PTBP1,SF3B3,DHX38,USP4,GEMIN4,DDX23,SRSF7	darkgrey	VSMC_M8

GO:0044772	0.00	1.00	86	350	mitotic cell cycle phase transition	BP	1.5E-20	CDK2,FBXO5,GTSE1,RAD21,MTBP,CDC25C,DBF4,CKS2,MELK,TTK,ANLN,EZH2,CLSPN,CASP2,ORC1,GEN1,CCNA2,RNASEH2B,MASTL,NASP,E2F7,CHFR,CDC25B,POLE,TOPBP1,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,WEE1,E2F1,CCNE1,KNTC1,RBL1,BUB1B,CCNE2,UBE2C,CHEK1,KHDRBS1,CENPE,TRIP13,KIF14,BCAT1,RCC1,TICRR,RPA2,HINFP,DTL,BLM,CENPF,EIF4G1,BUB3,CDK1,CDC25A,ZW10,CDCA5,BRCA1,CDKN3,TACC3,CDK16,DLGAP5,ZWINT,MNAT1,FOXM1,CCNB3,CDC6,BID,CCNB2,IQGAP3,NES,SPDL1,AURKB,ZWILCH,PLK1,NDC80,TFAP4,PKMYT1,CCNF,CDT1,NEK6,TMOD3,MAD2L1,CDKN2C,AURKA,UBE2S	darkgrey	VSMC_M8
GO:0006396	0.00	1.00	154	950	RNA processing	BP	1.6E-20	TXNL4A,METTL1,HNRNPH1,POP1,DDX39B,SRFBP1,PHF5A,SRPK1,SRSF3,PSIP1,BYSL,PWP1,CDC5L,NOL8,NCBP1,THADA,PPIH,U2AF2,HNRNPA2B1,GRSF1,SYNCRIP,PPIE,PABPC4,THRAP3,NOL10,PRMT1,PUS7,WDR33,NUFIP1,NIFK,DDX18,TSEN2,DIS3,HNRNPUL1,SNRPA,SRSF2,XRN2,RBM17,WDR43,FBL,SNRPB2,GTPBP4,EIF4A3,ALYREF,DUS1L,EXOSC8,NOC4L,DDX51,MAK16,SNRPF,RRP8,TCERG1,CCNB1,SFSWAP,NOP56,SNRPB,UTP20,HNRNPF,CWC27,WDR36,SNRNP35,DBR1,UTP15,RBM12,CTNNBL1,CCNL1,RSRC1,EXOSC1,RBM19,CWF19L1,WDR3,RBMS1,RRP9,NOLC1,FASTKD3,METTL15,TENT4A,NSUN2,MPHOSPH10,SNRPA1,U2AF1,RRP1,FP565260.1,KHDRBS1,SF3B1,NCL,SNRNP40,RBM23,PRMT5,DDX27,NOL11,TARBP1,SF3B4,DDX5,PRPF3,UTP25,INTS7,RBM14,SSB,NOP58,STRAP,SF3B2,DHX9,HNRNPR,TRA2B,HNRNPA3,HNRNPH3,DDX20,DDX21,PNN,EFTUD2,DGCR8,SF1,BARD1,SLBP,RBM3,SUV39H1,LYAR,HNRNPU,CPSF7,DDX39A,DHX15,SRSF5,EXOSC10,FUS,GEMIN5,ELAC2,SNRPD1,HNRNPM,BRIX1,RSL1D1,RBMX,THOC6,RNPS1,SF3A2,DAZAP1,DKC1,PTBP1,REXO4,EXOSC2,TRMT13,TRUB2,SF3B3,DHX38,NOB1,SRRT,USP4,GEMIN4,HNRNPD,DDX23,SNORD36B,ABT1,SRSF7,IMP4	darkgrey	VSMC_M8
GO:0022613	0.00	1.00	88	376	ribonucleoprotein complex biogenesis	BP	1.8E-20	TXNL4A,DDX39B,SRFBP1,SRPK1,PSIP1,BYSL,PWP1,HSP90AB1,NOL8,NCBP1,GNL2,NOL10,RUVBL2,RUVBL1,NUFIP1,NIFK,MRPS7,DDX18,DIS3,XRN2,WDR43,FBL,GTPBP4,EIF4A3,EXOSC8,NOC4L,DDX51,MAK16,SNRPF,RRP8,SFSWAP,NOP56,SNRPB,UTP20,EIF3M,WDR36,ABCE1,UTP15,EXOSC1,PAK1IP1,WDR3,HEATR3,RRP9,NOLC1,METTL15,MPHOSPH10,RRP1,FP565260.1,SF3B1,PRMT5,DDX27,NOL11,PRPF3,UTP25,EIF4H,NOP58,STRAP,DHX9,LSG1,DDX20,DDX21,SF1,NMD3,MYBBP1A,SUV39H1,LYAR,CPSF7,EIF3B,SRSF5,EXOSC10,GEMIN5,EIF5,SNRPD1,BRIX1,RSL1D1,NOC2L,SF3A2,DKC1,REXO4,EXOSC2,NOB1,DDX28,USP4,GEMIN4,DDX23,ABT1,NIP7,IMP4	darkgrey	VSMC_M8
GO:0006139	0.00	1.00	465	4274	nucleobase-containing compound metabolic process	BP	4.4E-20	TXNL4A,CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,VARS,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,RECQL4,BYSL,TONSL,MCM5,PWP1,APTX,POLR3B,POLR1C,TJP2,POLH,VCP,HSP90AB1,CDC5L,CKS2,MCM3,PAICS,NOL8,TRIM28,POLR1E,NCBP1,THADA,NANS,TWISTNB,PPIH,U2AF2,MSH6,CDCA7L,CTPS1,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,THRAP3,EZH2,NUP62,NOL10,MMS22L,CLSPN,PHF19,PRMT1,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,DNAJC2,RAD54L,RNASEH2B,PPP5C,WDR33,FOSB,CD3EAP,NUFIP1,NIFK,SMG9,NUP85,MCM10,CAD,DDX18,TSEN2,DIS3,HNRNPUL1,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,NCAPG2,WDR43,TK1,AFMID,BIRC5,PARP2,FBL,POLR3F,POLD3,SNRPB2,GTPBP4,RAD18,SUPT16H,EIF4A3,E2F7,GINS4,ALYREF,CKAP2,RRM1,DUS1L,PCNA,EXOSC8,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,HGF,SNRPF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,HNRNPF,POLR1B,PARPBP,CWC27,PDHB,SGK3,WDR36,CENPJ,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,AADAT,ZNF827,HMGB2,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,UTP15,RBM12,MND1,LOXL3,ESCO2,HEY1,NEIL3,ZBTB10,CCT8,PPID,RBL1,MSH3,CTNNBL1,MIS18A,CCT7,CCNL1,RSRC1,GNL3,EXOSC1,RBM19,TBX3,RAD51,DCLRE1B,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,ENTPD7,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,CWF19L1,HR,MDM4,CHAF1B,RFC5,WDR3,RBMS1,PSMD14,NCOA5,PPRC1,HMGN1,RRP9,NOLC1,C	darkgrey	VSMC_M8

GO:0090304	0.00	1.00	434	3916	nucleic acid metabolic process	BP	1E-19	TXNL4A,CDK2,NARS,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,VARS,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,RECQL4,BYSL,TONSL,MCM5,PWP1,APTX,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,CKS2,MCM3,NOL8,TRIM28,POLR1E,NCBP1,THADA,TWISTNB,PPIH,U2AF2,MSH6,CDCA7L,HNRNPA2B1,GRSF1,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,THRAP3,EZH2,NUP62,NOL10,MMS22L,CLSPN,PHF19,PRMT1,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,RUVBL2,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,DNAJC2,RAD54L,RNASEH2B,PPP5C,WDR33,FOSB,CD3EAP,NUFIP1,NIFK,SMG9,NUP85,MCM10,DDX18,TSEN2,DIS3,HNRNPUL1,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,NCAPG2,WDR43,TK1,BIRC5,PARP2,FBL,POLR3F,POLD3,SNRPB2,GTPBP4,RAD18,SUPT16H,EIF4A3,E2F7,GINS4,ALYREF,CKAP2,DUS1L,PCNA,EXOSC8,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,HGF,SNRPF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,HNRNPF,POLR1B,PARPBP,CWC27,SGK3,WDR36,CENPJ,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,ZNF827,HMGB2,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,UTP15,RBM12,MND1,LOXL3,ESCO2,HEY1,NEIL3,ZBTB10,CCT8,PPID,RBL1,MSH3,CTNNBL1,MIS18A,CCT7,CCNL1,RSRC1,GNL3,EXOSC1,RBM19,TBX3,RAD51,DCLRE1B,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,CWF19L1,HR,MDM4,CHAF1B,RFC5,WDR3,RBMS1,PSMD14,NCOA5,PPRC1,HMGN1,RRP9,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,METTL15,ETS1,TENT4A,NSUN2,PHC2,ICE1,MPHOSPH1	darkgrey	VSMC_M8
GO:0046483	0.00	1.00	472	4376	heterocycle metabolic process	BP	1E-19	TXNL4A,CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,VARS,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,RECQL4,BYSL,TONSL,MCM5,PWP1,APTX,POLR3B,POLR1C,TJP2,POLH,ALDH1L2,VCP,HSP90AB1,CDC5L,CKS2,MCM3,PAICS,NOL8,TRIM28,POLR1E,NCBP1,THADA,NANS,TWISTNB,PPIH,U2AF2,MSH6,CDCA7L,CTPS1,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,THRAP3,EZH2,NUP62,NOL10,MMS22L,CLSPN,PHF19,PRMT1,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,DNAJC2,RAD54L,RNASEH2B,PPP5C,WDR33,FOSB,CD3EAP,NUFIP1,NIFK,SMG9,NUP85,MCM10,SLC25A19,CAD,DDX18,TSEN2,DIS3,HNRNPUL1,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,NCAPG2,WDR43,TK1,AFMID,BIRC5,PARP2,FBL,POLR3F,POLD3,SNRPB2,GTPBP4,RAD18,SUPT16H,EIF4A3,E2F7,GINS4,ALYREF,CKAP2,RRM1,DUS1L,PCNA,EXOSC8,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,HGF,SNRPF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,HNRNPF,POLR1B,GGH,PARPBP,CWC27,PDHB,SGK3,WDR36,CENPJ,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,AADAT,ZNF827,HMGB2,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,UTP15,RBM12,MND1,LOXL3,ESCO2,HEY1,NEIL3,ZBTB10,CCT8,PPID,RBL1,MSH3,CTNNBL1,MIS18A,CCT7,CCNL1,RSRC1,GNL3,EXOSC1,RBM19,TBX3,RAD51,DCLRE1B,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,ENTPD7,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,CWF19L1,HR,MDM4,CHAF1B,RFC5,WDR3,RBMS1,PSMD14,NCOA5,PPRC	darkgrey	VSMC_M8
GO:0033044	0.00	1.00	56	168	regulation of chromosome organization	BP	1.4E-19	CCT2,FBXO5,TCP1,RAD21,TRIM28,TTK,HNRNPA2B1,CCT4,GEN1,MCM2,CHFR,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,TERF1,CCT8,BUB1B,CCT7,GNL3,UBE2C,CCT5,CCT6A,CENPE,TRIP13,NEK2,CENPF,BUB3,ZW10,CDCA5,TACC3,DLGAP5,ZWINT,MNAT1,HNRNPU,TOP2A,CDC6,EXOSC10,CCT3,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,DNMT1,NDC80,SMG6,DKC1,CDT1,NEK6,ACD,HNRNPD,MAD2L1,FEN1	darkgrey	VSMC_M8
GO:0007051	0.00	1.00	55	165	spindle organization	BP	3.6E-19	TUBB,FBXO5,EZR,KIFC1,VCP,TTK,NUP62,STIL,BORA,CDC20,CCNB1,WDR62,HAUS5,AAAS,ESPL1,TPX2,KIF2A,STAG1,CENPJ,KIF11,CENPH,RACGAP1,CKAP5,KNSTRN,MYBL2,SMC3,CENPE,CEP72,ASPM,RCC1,SPC25,NEK2,PRC1,AUNIP,NUF2,KIF15,HAUS3,TACC3,DLGAP5,HAUS8,HNRNPU,INCENP,SMC1A,CCNB2,KIF4A,AURKB,KIF23,HAUS1,PLK1,NDC80,POLDIP2,HAUS7,NEK6,STMN1,AURKA	darkgrey	VSMC_M8

GO:0006725	0.00	1.00	472	4410	cellular aromatic compound metabolic process	BP	5.8E-19	TXNL4A,CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,VARS,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,RECQL4,BYSL,TONSL,MCM5,PWP1,APTX,POLR3B,POLR1C,TJP2,POLH,ALDH1L2,VCP,HSP90AB1,CDC5L,CKS2,MCM3,PAICS,NOL8,TRIM28,POLR1E,NCBP1,THADA,NANS,TWISTNB,PPIH,U2AF2,MSH6,CDCA7L,CTPS1,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,THRAP3,EZH2,NUP62,NOL10,MMS22L,CLSPN,PHF19,PRMT1,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,DNAJC2,RAD54L,RNASEH2B,PPP5C,WDR33,FOSB,CD3EAP,NUFIP1,NIFK,SMG9,NUP85,MCM10,SLC25A19,CAD,DDX18,TSEN2,DIS3,HNRNPUL1,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,NCAPG2,WDR43,TK1,AFMID,BIRC5,PARP2,FBL,POLR3F,POLD3,SNRPB2,GTPBP4,RAD18,SUPT16H,EIF4A3,E2F7,GINS4,ALYREF,CKAP2,RRM1,DUS1L,PCNA,EXOSC8,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,HGF,SNRPF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,HNRNPF,POLR1B,GGH,PARPBP,CWC27,PDHB,SGK3,WDR36,CENPJ,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,AADAT,ZNF827,HMGB2,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,UTP15,RBM12,MND1,LOXL3,ESCO2,HEY1,NEIL3,ZBTB10,CCT8,PPID,RBL1,MSH3,CTNNBL1,MIS18A,CCT7,CCNL1,RSRC1,GNL3,EXOSC1,RBM19,TBX3,RAD51,DCLRE1B,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,ENTPD7,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,CWF19L1,HR,MDM4,CHAF1B,RFC5,WDR3,RBMS1,PSMD14,NCOA5,PPRC	darkgrey	VSMC_M8
GO:0034641	0.00	1.00	508	4878	cellular nitrogen compound metabolic process	BP	7.7E-19	TXNL4A,CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,VARS,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,RECQL4,BYSL,TONSL,MCM5,PWP1,MRPL2,APTX,POLR3B,POLR1C,TJP2,POLH,ALDH1L2,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,NOL8,TRIM28,POLR1E,NCBP1,THADA,NANS,TWISTNB,PPIH,U2AF2,MSH6,CDCA7L,CTPS1,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,DNAJC2,RAD54L,RNASEH2B,PPP5C,WDR33,FOSB,CD3EAP,NUFIP1,MRPL58,NIFK,SMG9,NUP85,MRPS7,MCM10,SLC25A19,CAD,DDX18,TSEN2,DIS3,HNRNPUL1,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,NCAPG2,WDR43,TK1,AFMID,BIRC5,PARP2,FBL,POLR3F,RRBP1,POLD3,SNRPB2,GTPBP4,RAD18,SUPT16H,EIF4A3,E2F7,GINS4,ALYREF,CKAP2,RRM1,DUS1L,PCNA,EXOSC8,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,HGF,SNRPF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,MRPS5,HNRNPF,POLR1B,PARPBP,CWC27,PDHB,SGK3,EIF3M,WDR36,CENPJ,EIF2B1,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,AADAT,ZNF827,HMGB2,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,UTP15,RBM12,MND1,LOXL3,ESCO2,HEY1,NEIL3,ZBTB10,SELENOT,CCT8,PPID,RBL1,MSH3,CTNNBL1,MIS18A,CCT7,CCNL1,RSRC1,GNL3,EXOSC1,RBM19,TBX3,RAD51,DCLRE1B,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,ENTPD7,MTDH,YWHAB,HMGCR,BAP1	darkgrey	VSMC_M8
GO:0051321	0.00	1.00	59	192	meiotic cell cycle	BP	9E-19	CDK2,FBXO5,RAD21,CDC25C,CKS2,SMC2,MSH6,TTK,RAD54L,FANCD2,CDC20,SGO1,CHFR,CDC25B,PSMD13,ESPL1,BUB1,CCNE1,TERF1,MND1,MSH3,BUB1B,RAD51,CCNE2,NCAPD3,KIF18A,NSUN2,SMC3,TRIP13,SGO2,ASPM,NEK2,H2AFX,PDE3A,BUB3,CDC25A,NUF2,ZW10,FANCM,SMC4,PSMC3IP,NCAPD2,RAD51AP1,MSX1,EXO1,INCENP,CCNB3,TOP2A,SMC1A,CCNB2,PTTG1,PLK1,BRIP1,TOP3A,NDC1,RPA1,PKMYT1,FANCA,AURKA	darkgrey	VSMC_M8
GO:0051983	0.00	1.00	37	78	regulation of chromosome segregation	BP	9.4E-19	FBXO5,RAD21,TTK,SMC6,GEN1,KIF2C,RAD18,CHFR,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,CDCA2,UBE2C,CENPE,TRIP13,CENPF,BUB3,MKI67,ZW10,TACC3,DLGAP5,ZWINT,HNRNPU,CDC6,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0008380	0.00	1.00	82	356	RNA splicing	BP	5.9E-18	TXNL4A,HNRNPH1,DDX39B,PHF5A,SRPK1,SRSF3,PSIP1,CDC5L,NCBP1,PPIH,U2AF2,HNRNPA2B1,GRSF1,SYNCRIP,PPIE,THRAP3,PRMT1,TSEN2,SNRPA,SRSF2,RBM17,SNRPB2,EIF4A3,ALYREF,SNRPF,TCERG1,SFSWAP,SNRPB,HNRNPF,CWC27,SNRNP35,DBR1,RBM12,CTNNBL1,RSRC1,RBM19,CWF19L1,MPHOSPH10,SNRPA1,U2AF1,KHDRBS1,SF3B1,NCL,SNRNP40,RBM23,PRMT5,SF3B4,DDX5,PRPF3,RBM14,STRAP,SF3B2,DHX9,HNRNPR,TRA2B,HNRNPA3,HNRNPH3,DDX20,PNN,EFTUD2,SF1,RBM3,HNRNPU,DDX39A,DHX15,SRSF5,FUS,GEMIN5,SNRPD1,HNRNPM,RBMX,THOC6,RNPS1,SF3A2,DAZAP1,PTBP1,SF3B3,DHX38,USP4,GEMIN4,DDX23,SRSF7	darkgrey	VSMC_M8
GO:1901987	0.00	1.00	75	311	regulation of cell cycle phase transition	BP	2.9E-17	CDK2,DDX39B,FBXO5,GTSE1,RAD21,MTBP,CDC25C,DBF4,CDC5L,TTK,ANLN,EZH2,CLSPN,CASP2,ORC1,GEN1,RNASEH2B,FANCD2,E2F7,CHFR,CDC25B,TOPBP1,CDC16,CCNB1,ESPL1,BUB1,WEE1,E2F1,KNTC1,RBL1,BUB1B,FAM83D,UBE2C,NSUN2,CHEK1,CENPE,TRIP13,KIF14,RAD9A,TICRR,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,CENPF,EIF4G1,BUB3,CDK1,CDC25A,WDR76,DNA2,ZW10,CDCA5,CDC45,BRCA1,DLGAP5,ZWINT,CCNB3,CDC6,BID,SPDL1,AURKB,ZWILCH,PLK1,BRIP1,NDC80,ATAD5,TFAP4,CDT1,NEK6,TMOD3,MAD2L1,AURKA	darkgrey	VSMC_M8

GO:0000226	0.00	1.00	103	522	microtubule cytoskeleton organization	BP	4.3E-17	RTTN,CDK2,TUBB,FBXO5,EZR,TTLL1,KIFC1,KIF20A,KIF24,VCP,CEP135,TTK,NUP62,GEN1,PLK4,STIL,CHORDC1,CENPA,KIF2C,BORA,ULK4,CDC20,SGO1,CKAP2,CCNB1,WDR62,GAS2L3,HAUS5,AAAS,ESPL1,TPX2,SKA3,KIF2A,STAG1,CENPJ,WEE1,KIF11,CENPH,RACGAP1,TUBA1B,TUBA4B,CKAP5,KNSTRN,MYBL2,NUSAP1,KIF18A,CHEK1,RASSF1,NAV1,SMC3,CENPE,CEP72,ASPM,RCC1,SPC25,NEK2,PRC1,RBM14,CEP85,AUNIP,CDK1,NUF2,ZW10,KIF18B,KIF15,RANBP1,BRCA1,HAUS3,TACC3,DLGAP5,HAUS8,FKBP4,RAC1,HNRNPU,INCENP,SMC1A,CCNB2,KIF4A,LMNA,SPDL1,AURKB,KIF23,LRRC49,HAUS1,PLK1,NDC80,POLDIP2,MTCL1,NDE1,TUBB6,CEP76,HOOK1,MAP7D3,HAUS7,CCNF,TUBB4B,SASS6,ODF2,NEK6,TPPP3,MAD2L1,STMN1,AURKA	darkgrey	VSMC_M8
GO:0033045	0.00	1.00	32	64	regulation of sister chromatid segregation	BP	5.9E-17	FBXO5,RAD21,TTK,GEN1,CHFR,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,TACC3,DLGAP5,ZWINT,HNRNPU,CDC6,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0006397	0.00	1.00	87	407	mRNA processing	BP	8.9E-17	TXNL4A,HNRNPH1,DDX39B,PHF5A,SRPK1,SRSF3,PSIP1,CDC5L,NCBP1,PPIH,U2AF2,HNRNPA2B1,GRSF1,SYNCRIP,PPIE,THRAP3,WDR33,TSEN2,SNRPA,SRSF2,XRN2,RBM17,SNRPB2,EIF4A3,ALYREF,SNRPF,TCERG1,CCNB1,SFSWAP,SNRPB,HNRNPF,CWC27,SNRNP35,DBR1,CTNNBL1,RSRC1,RBM19,CWF19L1,TENT4A,SNRPA1,U2AF1,KHDRBS1,SF3B1,NCL,SNRNP40,RBM23,PRMT5,SF3B4,DDX5,PRPF3,RBM14,STRAP,SF3B2,DHX9,HNRNPR,TRA2B,HNRNPA3,HNRNPH3,DDX20,PNN,EFTUD2,SF1,BARD1,SLBP,RBM3,HNRNPU,CPSF7,DDX39A,DHX15,SRSF5,GEMIN5,SNRPD1,HNRNPM,RBMX,THOC6,RNPS1,SF3A2,DAZAP1,PTBP1,TRUB2,SF3B3,DHX38,SRRT,USP4,GEMIN4,DDX23,SRSF7	darkgrey	VSMC_M8
GO:0034502	0.00	1.00	37	86	protein localization to chromosome	BP	9.8E-17	CCT2,TCP1,RAD21,MTBP,VCP,CENPQ,TTK,CCT4,EZH2,RUVBL2,CENPA,KNTC1,TERF1,ESCO2,CCT8,BUB1B,CCT7,GNL3,KNL1,CCT5,CCT6A,RPA2,BUB3,CDK1,ZW10,CDCA5,CCT3,SPDL1,AURKB,ZWILCH,PLK1,NDC80,RPA1,HASPIN,DKC1,CDT1,ACD	darkgrey	VSMC_M8
GO:1902850	0.00	1.00	46	133	microtubule cytoskeleton organization involved in mitosis	BP	1.3E-16	KIFC1,VCP,TTK,NUP62,STIL,CENPA,BORA,CDC20,CCNB1,WDR62,AAAS,ESPL1,TPX2,KIF2A,STAG1,KIF11,CENPH,RACGAP1,CKAP5,MYBL2,NUSAP1,SMC3,CENPE,RCC1,SPC25,NEK2,PRC1,NUF2,ZW10,KIF15,TACC3,DLGAP5,HNRNPU,SMC1A,KIF4A,SPDL1,AURKB,KIF23,PLK1,NDC80,POLDIP2,NDE1,NEK6,MAD2L1,STMN1,AURKA	darkgrey	VSMC_M8
GO:1901360	0.00	1.00	476	4575	organic cyclic compound metabolic process	BP	1.4E-16	TXNL4A,CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,VARS,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,RECQL4,BYSL,TONSL,MCM5,PWP1,APTX,POLR3B,POLR1C,TJP2,POLH,ALDH1L2,CYP51A1,VCP,HSP90AB1,CDC5L,CKS2,MCM3,PAICS,NOL8,TRIM28,POLR1E,NCBP1,THADA,NANS,TWISTNB,PPIH,U2AF2,MSH6,CDCA7L,CTPS1,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,THRAP3,EZH2,NUP62,NOL10,MMS22L,CLSPN,PHF19,PRMT1,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,DNAJC2,RAD54L,RNASEH2B,PPP5C,WDR33,FOSB,CD3EAP,NUFIP1,NIFK,SMG9,NUP85,MCM10,SLC25A19,CAD,DDX18,TSEN2,DIS3,HNRNPUL1,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,NCAPG2,WDR43,TK1,AFMID,BIRC5,PARP2,FBL,POLR3F,POLD3,SNRPB2,GTPBP4,RAD18,SUPT16H,EIF4A3,E2F7,GINS4,ALYREF,CKAP2,RRM1,DUS1L,PCNA,EXOSC8,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,HGF,SNRPF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,HNRNPF,POLR1B,GGH,PARPBP,CWC27,PDHB,SGK3,WDR36,CENPJ,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,AADAT,ZNF827,HMGB2,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,UTP15,RBM12,MND1,LOXL3,ESCO2,HEY1,NEIL3,ZBTB10,CCT8,PPID,RBL1,MSH3,CTNNBL1,MIS18A,CCT7,CCNL1,RSRC1,GNL3,EXOSC1,RBM19,TBX3,RAD51,DCLRE1B,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,ENTPD7,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,CWF19L1,HR,MDM4,CHAF1B,RFC5,WDR3,RBMS1,PSMD14,NCOA	darkgrey	VSMC_M8
GO:0071897	0.00	1.00	49	150	DNA biosynthetic process	BP	1.4E-16	CCT2,DDX39B,TCP1,DSCC1,POLH,VCP,HSP90AB1,HNRNPA2B1,POLD1,CCT4,LIG1,DNAJC2,SPHK1,TK1,POLD3,PCNA,POLE,RFC3,HGF,TERF1,CCT8,CCT7,RFC5,CCT5,CCT6A,POLQ,RFC2,NEK2,DTL,CENPF,POLA1,RFC4,C17orf53,HNRNPU,RFC1,LIN9,EXOSC10,CCT3,AURKB,TYMS,POLDIP2,RPA1,SMG6,CHTF18,DKC1,FAM129B,ACD,HNRNPD,POLE3	darkgrey	VSMC_M8
GO:0051783	0.00	1.00	42	114	regulation of nuclear division	BP	1.9E-16	FBXO5,RAD21,MTBP,CDC25C,TTK,NUP62,GEN1,BORA,SPHK1,CDC20,CDC16,CCNB1,ESPL1,BUB1,KIF20B,KNTC1,BUB1B,CDCA2,NUSAP1,CHEK1,TRIP13,PRMT5,RCC1,NEK2,PDE3A,CENPF,BUB3,MKI67,ZW10,DLGAP5,RAD51AP1,ZWINT,MSX1,SPDL1,AURKB,ZWILCH,PLK1,NDC80,PKMYT1,CDT1,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:0010965	0.00	1.00	30	58	regulation of mitotic sister chromatid separation	BP	2E-16	FBXO5,RAD21,TTK,GEN1,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,TACC3,DLGAP5,ZWINT,CDC6,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0006403	0.00	1.00	52	171	RNA localization	BP	2E-16	XPOT,NUP43,NUP107,CCT2,DDX39B,TCP1,NUP50,SRSF3,NCBP1,HNRNPA2B1,CCT4,NUP205,NUP62,RUVBL2,RUVBL1,NUP85,FBL,EIF4A3,ALYREF,AAAS,TERF1,NUP160,CCT8,CCT7,CKAP5,NUP93,CCT5,NUP153,CCT6A,NSUN2,KHDRBS1,MCM3AP,NUP133,SSB,NOP58,DHX9,HNRNPA3,SLBP,HNRNPU,EIF5A,DDX39A,EXOSC10,CCT3,NUP62CL,NDC1,SMG6,THOC6,DKC1,EXOSC2,NUP188,GLE1,SRSF7	darkgrey	VSMC_M8

GO:0007088	0.00	1.00	38	96	regulation of mitotic nuclear division	BP	5.4E-16	FBXO5,RAD21,MTBP,CDC25C,TTK,NUP62,GEN1,BORA,SPHK1,CDC16,CCNB1,ESPL1,BUB1,KIF20B,KNTC1,BUB1B,CDCA2,NUSAP1,CHEK1,TRIP13,PRMT5,RCC1,NEK2,CENPF,BUB3,MKI67,ZW10,DLGAP5,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,PKMYT1,CDT1,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:0051306	0.00	1.00	30	60	mitotic sister chromatid separation	BP	6.6E-16	FBXO5,RAD21,TTK,GEN1,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,TACC3,DLGAP5,ZWINT,CDC6,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0044784	0.00	1.00	30	60	metaphase/anaphase transition of cell cycle	BP	6.7E-16	FBXO5,RAD21,TTK,GEN1,CHFR,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,TACC3,DLGAP5,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:1905818	0.00	1.00	31	65	regulation of chromosome separation	BP	1E-15	FBXO5,RAD21,TTK,GEN1,CHFR,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,TACC3,DLGAP5,ZWINT,CDC6,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0016071	0.00	1.00	107	586	mRNA metabolic process	BP	1.3E-15	TXNL4A,HNRNPH1,DDX39B,PHF5A,SRPK1,SRSF3,PSIP1,CDC5L,NCBP1,PPIH,U2AF2,HNRNPA2B1,GRSF1,SYNCRIP,PPIE,PABPC4,THRAP3,NBAS,PUS7,WDR33,SMG9,TSEN2,DIS3,SNRPA,SRSF2,XRN2,RBM17,SNRPB2,EIF4A3,ALYREF,EXOSC8,SNRPF,TCERG1,CCNB1,SFSWAP,SNRPB,HNRNPF,CWC27,E2F1,SNRNP35,DBR1,CTNNBL1,RSRC1,RBM19,CWF19L1,FASTKD3,TENT4A,NSUN2,SNRPA1,U2AF1,KHDRBS1,SF3B1,NCL,SNRNP40,RBM23,PRMT5,SF3B4,DDX5,PRPF3,RBM14,SSB,STRAP,SF3B2,DHX9,HNRNPR,TRA2B,HNRNPA3,HNRNPH3,DDX20,PNN,EFTUD2,SF1,BARD1,CNOT9,SLBP,RBM3,HNRNPU,CPSF7,DDX39A,DHX15,SRSF5,EXOSC10,FUS,GEMIN5,EDC3,TAF15,SNRPD1,HNRNPM,SERBP1,RBMX,SMG6,THOC6,RNPS1,SF3A2,DAZAP1,DKC1,PTBP1,EXOSC2,TRUB2,SF3B3,DHX38,SRRT,USP4,GEMIN4,HNRNPD,DDX23,SRSF7	darkgrey	VSMC_M8
GO:0007091	0.00	1.00	29	57	metaphase/anaphase transition of mitotic cell cycle	BP	1.3E-15	FBXO5,RAD21,TTK,GEN1,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,TACC3,DLGAP5,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0044085	0.00	1.00	293	2454	cellular component biogenesis	BP	1.8E-15	TXNL4A,RTTN,CDK2,NUP107,CCT2,TUBB,DDX39B,SRFBP1,FBXO5,EZR,TCP1,RAD21,TTLL1,KIFC1,FAM49B,HSPA9,SRPK1,KIF27,PSIP1,BYSL,PWP1,KIF24,VCP,HSP90AB1,COL1A2,CEP135,NOL8,TRIM28,POLR1E,NCBP1,ANP32B,PPIH,MFSD2A,NUP205,ANLN,GNL2,NUP62,NOL10,PRMT1,SDC1,RUVBL2,PLK4,GRWD1,STIL,MCM2,CENPO,RUVBL1,SLC1A5,CHCHD4,CENPA,CDC42EP4,NASP,NUFIP1,PREB,NIFK,NUP85,MRPS7,DIAPH3,DDX18,DIS3,SPHK1,XRN2,WDR43,CDC20,TK1,FBL,GTPBP4,EIF4A3,NAP1L1,CHMP6,STRN,RRM1,EXOSC8,ZNF703,NOC4L,DDX51,MAK16,SNRPF,RRP8,CCNB1,WDR62,SFSWAP,SNAI2,NOP56,SNRPB,HAUS5,AAAS,UTP20,TPX2,POLR1B,KIF2A,ATG101,EIF3M,STAG1,WDR36,CENPJ,CENPK,HSP90B1,CEP89,KIF11,ABCE1,VAMP8,CENPH,KNTC1,HMGB2,ATF1,TERF1,HELLS,FHDC1,UTP15,RACGAP1,CCT8,PPID,MIS18A,CFAP298,CKAP5,EXOSC1,NUP93,KNL1,RAD51,MYBL2,MTDH,OIP5,NDUFAF1,REEP4,MDM4,CHAF1B,PAK1IP1,UBE2C,WDR3,HEATR3,RRP9,NOLC1,FASTKD3,NUP153,METTL15,ICE1,MPHOSPH10,GMNN,RRP1,FP565260.1,SMC3,SF3B1,CENPE,TRIP13,CEP72,KIF14,PRMT5,DDX27,ASPM,POLQ,NOL11,IQCB1,RCC1,PRPF3,HJURP,UTP25,EIF4H,IPO4,NEK2,PRC1,NF2,H2AFX,BLM,RBM14,NOP58,CENPF,STRAP,EIF4G1,PSMC5,HAT1,CDK1,TFRC,PAK2,DHX9,NDUFS1,LSG1,DDX20,DNA2,ZW10,DDX21,KIF15,IFT80,SF1,EPHB2,NMD3,SMARCAL1,CDC45,BRCA1,DNAJC9,HAUS3,DLGAP5,MYBBP1A,ECT2,DHX33,SUV39H1,HAUS8,FKBP4,SIX4,MNAT1,LYAR,RAC1,EXO1,HNRNPU,INCENP,RAB27A,UBE2K,UGDH,FSCN1,CPSF7,BID,SMC1A,EIF2S1,EIF3B,PSMG3,ASF1B,SRSF5,CCNB2,EXOSC10,SH3PXD2B,CCT3,KIF4A,FUS,AURKB,CIAO2A,KIF23,C	darkgrey	VSMC_M8
GO:0007346	0.00	1.00	78	360	regulation of mitotic cell cycle	BP	2.5E-15	CDK2,FBXO5,GTSE1,RAD21,MTBP,CDC25C,CKS2,TTK,ANLN,EZH2,NUP62,CLSPN,CASP2,ORC1,GEN1,RNASEH2B,BORA,SPHK1,FANCD2,E2F7,CHFR,CDC25B,TOPBP1,CDC16,CCNB1,ESPL1,BUB1,KIF20B,WEE1,E2F1,KNTC1,RBL1,TRIM35,BUB1B,CDCA2,NUSAP1,UBE2C,CHEK1,CENPE,TRIP13,KIF14,PRMT5,RAD9A,RCC1,TICRR,RPA2,NEK2,DTL,BLM,CENPF,EIF4G1,BUB3,CDK1,CDC25A,MKI67,ZW10,CDCA5,BRCA1,DLGAP5,ZWINT,HNRNPU,CCNB3,CDC6,BID,SPDL1,AURKB,ZWILCH,PLK1,NDC80,POLDIP2,TFAP4,PKMYT1,TP73,CDT1,NEK6,TMOD3,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:0010948	0.00	1.00	61	237	negative regulation of cell cycle process	BP	2.6E-15	CDK2,DDX39B,FBXO5,GTSE1,RAD21,MTBP,CDC5L,TTK,EZH2,CLSPN,CASP2,ORC1,GEN1,RNASEH2B,FANCD2,E2F7,CHFR,TOPBP1,CCNB1,ESPL1,BUB1,WEE1,E2F1,KNTC1,TERF1,RBL1,BUB1B,E2F8,NSUN2,CHEK1,TRIP13,RAD9A,TICRR,RPA2,NEK2,INTS7,HINFP,DTL,H2AFX,BLM,RBM14,CENPF,BUB3,CDK1,WDR76,DNA2,ZW10,CDC45,BRCA1,ZWINT,CDC6,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,BRIP1,NDC80,CCNF,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:1903046	0.00	1.00	47	153	meiotic cell cycle process	BP	5.4E-15	FBXO5,RAD21,CDC25C,CKS2,SMC2,MSH6,TTK,RAD54L,FANCD2,CDC20,SGO1,CHFR,CDC25B,PSMD13,ESPL1,BUB1,CCNE1,TERF1,MND1,MSH3,BUB1B,RAD51,CCNE2,NCAPD3,KIF18A,NSUN2,TRIP13,SGO2,ASPM,PDE3A,CDC25A,NUF2,FANCM,SMC4,PSMC3IP,NCAPD2,RAD51AP1,MSX1,INCENP,TOP2A,CCNB2,PTTG1,PLK1,BRIP1,NDC1,FANCA,AURKA	darkgrey	VSMC_M8

GO:0006323	0.00	1.00	41	119	DNA packaging	BP	6.3E-15	SRPK1,ANP32B,SMC2,GRWD1,MCM2,NASP,NCAPG2,NAP1L1,RRP8,NCAPH,CCNB1,HMGB2,HELLS,MIS18A,OIP5,NUSAP1,CHAF1B,NCAPD3,TENT4A,HJURP,IPO4,H2AFX,HAT1,CDK1,CDCA5,SMC4,DNAJC9,NCAPD2,SUV39H1,INCENP,TOP2A,ASF1B,NCAPG,PLK1,AIFM1,CHAF1A,NOC2L,HIST1H1A,CENPP,CENPW,HIST1H2BB	darkgrey	VSMC_M8
GO:1901990	0.00	1.00	60	237	regulation of mitotic cell cycle phase transition	BP	6.3E-15	CDK2,FBXO5,GTSE1,RAD21,MTBP,CDC25C,TTK,ANLN,EZH2,CLSPN,CASP2,ORC1,GEN1,RNASEH2B,E2F7,CHFR,CDC25B,TOPBP1,CDC16,CCNB1,ESPL1,BUB1,WEE1,E2F1,KNTC1,RBL1,BUB1B,UBE2C,CHEK1,CENPE,TRIP13,KIF14,TICRR,RPA2,DTL,BLM,CENPF,EIF4G1,BUB3,CDK1,CDC25A,ZW10,CDCA5,BRCA1,DLGAP5,ZWINT,CCNB3,CDC6,BID,SPDL1,AURKB,ZWILCH,PLK1,NDC80,TFAP4,CDT1,NEK6,TMOD3,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:0007052	0.00	1.00	39	109	mitotic spindle organization	BP	1.2E-14	KIFC1,VCP,TTK,NUP62,STIL,BORA,CDC20,CCNB1,WDR62,AAAS,TPX2,KIF2A,STAG1,KIF11,CENPH,RACGAP1,CKAP5,MYBL2,SMC3,CENPE,RCC1,SPC25,NEK2,PRC1,NUF2,KIF15,TACC3,DLGAP5,HNRNPU,SMC1A,KIF4A,AURKB,KIF23,PLK1,NDC80,POLDIP2,NEK6,STMN1,AURKA	darkgrey	VSMC_M8
GO:0000075	0.00	1.00	47	155	cell cycle checkpoint signaling	BP	1.3E-14	CDK2,DDX39B,GTSE1,CDC5L,TTK,CLSPN,CASP2,ORC1,GEN1,RNASEH2B,FANCD2,CHFR,TOPBP1,CCNB1,BUB1,E2F1,KNTC1,BUB1B,NSUN2,CHEK1,TRIP13,RAD9A,TICRR,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,CENPF,BUB3,CDK1,WDR76,DNA2,ZW10,CDC45,BRCA1,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,BRIP1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0051304	0.00	1.00	34	85	chromosome separation	BP	1.8E-14	FBXO5,RAD21,TTK,GEN1,CHFR,CDC16,CCNB1,ESPL1,BUB1,ANAPC1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,FANCM,TACC3,DLGAP5,ZWINT,TOP2A,CDC6,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,TOP3A,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0140694	0.00	1.00	69	305	non-membrane-bounded organelle assembly	BP	1.9E-14	RTTN,CDK2,TUBB,FBXO5,EZR,KIFC1,CEP135,ANLN,NUP62,PLK4,STIL,CENPA,MRPS7,CDC20,WDR62,HAUS5,AAAS,TPX2,KIF2A,STAG1,CENPJ,CENPK,KIF11,CENPH,KNTC1,RACGAP1,MYBL2,FP565260.1,SMC3,CENPE,CEP72,ASPM,RCC1,NEK2,PRC1,RBM14,CENPF,KIF15,BRCA1,HAUS3,DLGAP5,HAUS8,SIX4,HNRNPU,INCENP,FSCN1,SMC1A,EIF2S1,CCNB2,SH3PXD2B,KIF4A,AURKB,KIF23,HAUS1,PLK1,EDC3,POLDIP2,BRIX1,CEP76,HAUS7,CENPN,SASS6,NEK6,DDX28,TMOD3,ABT1,AURKA,NIP7,CENPW	darkgrey	VSMC_M8
GO:0016043	0.00	1.00	477	4652	cellular component organization	BP	2E-14	TXNL4A,RTTN,CDK2,TMED9,MTFR2,NUP107,CCT2,TUBB,DDX39B,FBXO5,EZR,TCP1,RAD21,DSCC1,TTLL1,ARFGAP3,MTBP,KIFC1,ATAD2,FAM49B,KIF20A,CDC25C,HSPA9,CHCHD3,SRPK1,KIF27,PSIP1,RECQL4,CEP78,MCM5,TJP2,KIF24,VCP,HSP90AB1,COL1A2,CEP135,CKS2,MCM3,TRIM28,POLR1E,NCBP1,ANP32B,PPIH,SMC2,TTK,HNRNPA2B1,COL9A2,MFSD2A,CCT4,B3GNT2,NUP205,ANLN,CDCA8,EZH2,NUP62,PHF19,PRMT1,SMC6,GEN1,SDC1,RUVBL2,PLK4,GRWD1,STIL,MCM2,CENPO,SEC61A1,RUVBL1,AMOTL1,SAE1,SLC1A5,DNAJC2,RAD54L,CHORDC1,MAST2,CHCHD4,CENPA,CDC42EP4,NASP,COG3,NUFIP1,TOMM40,PREB,MRPL58,NIFK,KCNN4,NUP85,PLAUR,MRPS7,KIF2C,DIAPH3,BORA,AXL,RNF157,SPHK1,MCM6,FANCD2,ULK4,NCAPG2,NET1,CDC20,TK1,SERPINH1,PARP2,SEC23B,SUPT16H,NAP1L1,CHMP6,SGO1,ARHGDIA,CKAP2,STRN,RRM1,SIPA1L3,PCNA,CHFR,PGAM5,CDC25B,ZNF703,RFC3,HGF,SNRPF,PSMD13,RRP8,CDC16,NCAPH,USPL1,CCNB1,MCM4,WDR62,SFSWAP,SNAI2,SNRPB,GAS2L3,CD44,HAUS5,AAAS,ESPL1,BUB1,TPX2,ANAPC1,POLR1B,KIF20B,SKA3,KIF2A,ATG101,ADAMTS6,SGK3,EIF3M,STAG1,CENPJ,CENPK,WEE1,HSP90B1,CEP89,KIF11,ABCE1,CCNE1,VAMP8,CENPH,KNTC1,HMGB2,TRAM1,CEP55,ATF1,SSRP1,TERF1,HELLS,FHDC1,MND1,RACGAP1,LOXL3,ESCO2,FMNL3,DSN1,TUBA1B,TUBA4B,CCT8,PPID,RBL1,MSH3,BUB1B,MIS18A,CCT7,CDCA2,CFAP298,GNL3,CKAP5,NUP93,KNSTRN,KNL1,RAD51,DCLRE1B,CREB3L1,TOMM70,MYBL2,CCNE2,MTDH,BAP1,OIP5,NUSAP1,NDUFAF1,RUNX1,REEP4,MDM4,CHAF1B,UBE2C,NAV2,NCAPD3,RFC5,HMGN1,NOLC1,CCT5,CIT,FASTKD3,NUP153,CCT6A,NUCKS1,DEK,KIF18A,MANF,	darkgrey	VSMC_M8
GO:1902099	0.00	1.00	28	58	regulation of metaphase/anaphase transition of cell cycle	BP	2.2E-14	FBXO5,RAD21,TTK,GEN1,CHFR,CDC16,CCNB1,ESPL1,BUB1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,DLGAP5,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:0030071	0.00	1.00	27	55	regulation of mitotic metaphase/anaphase transition	BP	4.7E-14	FBXO5,RAD21,TTK,GEN1,CDC16,CCNB1,ESPL1,BUB1,KNTC1,BUB1B,UBE2C,CENPE,TRIP13,CENPF,BUB3,ZW10,DLGAP5,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,NEK6,MAD2L1	darkgrey	VSMC_M8
GO:1901988	0.00	1.00	53	201	negative regulation of cell cycle phase transition	BP	1.1E-13	CDK2,DDX39B,FBXO5,GTSE1,RAD21,CDC5L,TTK,EZH2,CLSPN,CASP2,ORC1,GEN1,RNASEH2B,FANCD2,E2F7,CHFR,TOPBP1,CCNB1,BUB1,WEE1,E2F1,KNTC1,RBL1,BUB1B,NSUN2,CHEK1,TRIP13,RAD9A,TICRR,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,CENPF,BUB3,CDK1,WDR76,DNA2,ZW10,CDC45,BRCA1,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,BRIP1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8

GO:0043170	0.00	1.00	652	7034	macromolecule metabolic process	BP	1.3E-13	TXNL4A,CDK2,ALPK2,NARS,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,CCT2,VARS2,POP1,TCF19,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,PANX2,TCP1,RAD21,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,ATAD2,DESI1,PHF5A,FAM49B,ZNF367,SLC35D2,CDC25C,FKBP5,MATR3,SRPK1,SRSF3,PSIP1,RECQL4,BYSL,TONSL,MCM5,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,POLR1C,UBAP2,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,TWISTNB,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,NRDC,RUVBL2,PLK4,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,SAE1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,NAALAD2,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,NASP,COG3,NUFIP1,GRIN2C,PRCP,MRPL58,NIFK,SMG9,NUP85,PLAUR,MRPS7,MCM10,CAD,ALG8,DBI,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,AXL,RNF157,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,ULK4,NCAPG2,WDR43,CDC20,TK1,BIRC5,SERPINH1,PARP2,FBL,POLR3F,RRBP1,POLD3,SNRPB2,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,GINS4,ALYREF,CKAP2,RRM1,DUS1L,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,METAP2,DCUN1D2,HGF,SNRPF,TOPBP1,ELK3,PSMD13,RRP8,CDC16,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,CD44,UTP20,TCEA1,ESPL1,MRPS5,HNRNPF,BUB1,TPX2,ANAPC1,	darkgrey	VSMC_M8
GO:0032392	0.00	1.00	32	80	DNA geometric change	BP	2.1E-13	DSCC1,RECQL4,MCM5,MCM3,HNRNPA2B1,RUVBL2,MCM2,RUVBL1,RAD54L,MCM6,RFC3,MCM4,HMGB2,RAD51,NAV2,RFC5,CHD1L,POLQ,RFC2,BLM,DHX9,RFC4,DNA2,FANCM,MCM7,MNAT1,TOP2A,BRIP1,RPA1,CHTF18,ERCC6L,HMGB3	darkgrey	VSMC_M8
GO:0045786	0.00	1.00	67	306	negative regulation of cell cycle	BP	3.7E-13	CDK2,DDX39B,FBXO5,GTSE1,RAD21,MTBP,CDC5L,TTK,EZH2,CLSPN,CASP2,ORC1,GEN1,RNASEH2B,FANCD2,IPO5,E2F7,CHFR,TOPBP1,CCNB1,ESPL1,BUB1,WEE1,E2F1,KNTC1,TERF1,RBL1,TRIM35,BUB1B,E2F8,NSUN2,GMNN,CHEK1,TRIP13,RAD9A,TICRR,RPA2,NEK2,INTS7,HINFP,DTL,H2AFX,BLM,RBM14,CENPF,BUB3,CDK1,WDR76,DNA2,ZW10,CDC45,BRCA1,ZWINT,CDC6,ALOX15B,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,BRIP1,NDC80,TFAP4,CCNF,CDT1,MAD2L1,CDKN2C	darkgrey	VSMC_M8
GO:0051052	0.00	1.00	65	297	regulation of DNA metabolic process	BP	8.7E-13	CCT2,DDX39B,TCP1,DSCC1,POLH,HSP90AB1,TRIM28,MSH6,HNRNPA2B1,CCT4,DNAJC2,ALYREF,PCNA,RFC3,HGF,PARPBP,TERF1,CCT8,MSH3,MIS18A,CCT7,GNL3,RAD51,RFC5,CCT5,CCT6A,NUCKS1,DEK,CHEK1,PRMT5,POLQ,FANCB,TICRR,RFC2,RPA2,NEK2,H2AFX,BLM,AUNIP,TFRC,DHX9,RFC4,BRCA1,NSD2,RAD51AP1,ANKLE1,FOXM1,HNRNPU,EXOSC10,CCT3,FUS,AURKB,WDR70,AIFM1,USP1,SMG6,CHTF18,DKC1,CDT1,FAM129B,ACD,PRIM2,HIST1H1A,HNRNPD,MBD2	darkgrey	VSMC_M8
GO:0042254	0.00	1.00	58	256	ribosome biogenesis	BP	9.5E-13	SRFBP1,BYSL,PWP1,NOL8,GNL2,NOL10,NIFK,MRPS7,DDX18,DIS3,XRN2,WDR43,FBL,GTPBP4,EIF4A3,EXOSC8,NOC4L,DDX51,MAK16,RRP8,NOP56,UTP20,WDR36,ABCE1,UTP15,EXOSC1,PAK1IP1,WDR3,HEATR3,RRP9,NOLC1,METTL15,MPHOSPH10,RRP1,FP565260.1,DDX27,NOL11,UTP25,NOP58,LSG1,DDX21,NMD3,MYBBP1A,SUV39H1,LYAR,EXOSC10,BRIX1,RSL1D1,NOC2L,DKC1,REXO4,EXOSC2,NOB1,DDX28,GEMIN4,ABT1,NIP7,IMP4	darkgrey	VSMC_M8
GO:0051985	0.00	1.00	22	41	negative regulation of chromosome segregation	BP	2.1E-12	FBXO5,RAD21,TTK,GEN1,CHFR,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:1905819	0.00	1.00	22	41	negative regulation of chromosome separation	BP	2.1E-12	FBXO5,RAD21,TTK,GEN1,CHFR,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0140013	0.00	1.00	41	139	meiotic nuclear division	BP	2.1E-12	FBXO5,RAD21,CKS2,SMC2,TTK,RAD54L,FANCD2,CDC20,SGO1,CHFR,CDC25B,PSMD13,ESPL1,BUB1,CCNE1,TERF1,MND1,MSH3,BUB1B,RAD51,CCNE2,KIF18A,TRIP13,SGO2,ASPM,PDE3A,NUF2,FANCM,SMC4,PSMC3IP,RAD51AP1,MSX1,INCENP,TOP2A,CCNB2,PTTG1,PLK1,BRIP1,NDC1,FANCA,AURKA	darkgrey	VSMC_M8
GO:0033047	0.00	1.00	22	41	regulation of mitotic sister chromatid segregation	BP	2.2E-12	FBXO5,RAD21,TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,HNRNPU,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:2001251	0.00	1.00	30	77	negative regulation of chromosome organization	BP	2.2E-12	FBXO5,RAD21,TTK,GEN1,MCM2,CCNB1,ESPL1,BUB1,KNTC1,TERF1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,MNAT1,HNRNPU,TOP2A,EXOSC10,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,SMG6,CDT1,ACD,MAD2L1	darkgrey	VSMC_M8

GO:0006807	0.00	1.00	664	7284	nitrogen compound metabolic process	BP	3.2E-12	TXNL4A,CDK2,ALPK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,TCP1,RAD21,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,ATAD2,DESI1,PHF5A,ZNF367,SLC35D2,CDC25C,FKBP5,SRPK1,SRSF3,GCAT,PSIP1,RECQL4,BYSL,TONSL,MCM5,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,POLR1C,TJP2,POLH,ALDH1L2,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,NANS,TWISTNB,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,CTPS1,TTK,CYCS,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,NRDC,RUVBL2,PLK4,AMD1,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,SAE1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,NAALAD2,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,COG3,NUFIP1,GRIN2C,PRCP,MRPL58,NIFK,SMG9,NUP85,PLAUR,MRPS7,MCM10,SLC25A19,CAD,ALG8,DBI,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,AXL,RNF157,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,ULK4,NCAPG2,WDR43,CDC20,TK1,AFMID,BIRC5,SERPINH1,PARP2,FBL,POLR3F,RRBP1,POLD3,SNRPB2,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,GINS4,ALYREF,CKAP2,RRM1,DUS1L,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,METAP2,DCUN1D2,HGF,SNRPF,TOPBP1,ELK3,PSMD13,RRP8,CDC16,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,CD44,UTP20,TCEA1,ESPL1,MRPS5,HN	darkgrey	VSMC_M8
GO:0090068	0.00	1.00	47	180	positive regulation of cell cycle process	BP	4.3E-12	DDX39B,FBXO5,RAD21,MTBP,CDC25C,DBF4,EZH2,NUP62,GEN1,PLK4,SPHK1,E2F7,CDC25B,CDC16,CCNB1,ESPL1,KIF20B,CENPJ,RACGAP1,FAM83D,E2F8,NUSAP1,UBE2C,CIT,KIF14,DTL,EIF4G1,CDK1,CDC25A,CDCA5,RANBP1,DLGAP5,RAD51AP1,ECT2,MSX1,HNRNPU,CDC6,AURKB,KIF23,NDC80,ATAD5,POLDIP2,CDT1,TMOD3,MAD2L1,AURKA,FEN1	darkgrey	VSMC_M8
GO:0033046	0.00	1.00	21	39	negative regulation of sister chromatid segregation	BP	7.2E-12	FBXO5,RAD21,TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0033048	0.00	1.00	21	39	negative regulation of mitotic sister chromatid segregation	BP	7.2E-12	FBXO5,RAD21,TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:2000816	0.00	1.00	21	39	negative regulation of mitotic sister chromatid separation	BP	7.2E-12	FBXO5,RAD21,TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0006271	0.00	1.00	13	14	DNA strand elongation involved in DNA replication	BP	7.7E-12	MCM3,LIG1,POLD3,PCNA,POLE,RFC3,MCM4,POLA1,RFC4,DNA2,MCM7,GINS1,POLE3	darkgrey	VSMC_M8
GO:0033554	0.00	1.00	197	1561	cellular response to stress	BP	1.2E-11	CDK2,BCLAF1,DDX39B,FBXO5,EZR,GTSE1,RAD21,MAN1A1,HSPA9,RECQL4,TONSL,MCM5,APTX,POLH,VCP,HSP90AB1,CDC5L,MCM3,MIOS,MELK,TRIM28,MSH6,POLD1,MFSD2A,EZH2,MMS22L,CLSPN,PRMT1,CASP2,SMC6,GEN1,RUVBL2,NAMPT,LIG1,MCM2,RUVBL1,CCNA2,DNAJC2,RAD54L,CHORDC1,RNASEH2B,PPP5C,WDR33,MASTL,MCM10,AXL,SPHK1,MCM6,FANCD2,ULK4,NET1,PARP2,POLD3,RAD18,SUPT16H,E2F7,GINS4,PCNA,POLE,RFC3,HGF,TOPBP1,RRP8,CBX5,CCNB1,MCM4,SNAI2,CD44,PARPBP,HSP90B1,E2F1,HMGB2,SSRP1,PBK,ESCO2,NEIL3,RBL1,MSH3,TBX3,RAD51,DCLRE1B,CREB3L1,HMGCR,EEF1E1,CHUK,PPP1R15B,MDM4,CHAF1B,RFC5,PSMD14,HMGN1,NUCKS1,DEK,GCN1,MANF,ETS1,TENT4A,UBE2T,CHEK1,SMC3,TRIP13,CHD1L,TRAIP,UNG,POLQ,RAD9A,FANCI,MNDA,DDX5,FANCB,XBP1,TICRR,RFC2,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,NSMCE4A,EIF4G1,AUNIP,CDK1,DHX9,WDR76,POLA1,RFC4,DNA2,CDCA5,FANCM,BARD1,C17orf53,SMARCAL1,CDC45,UFD1,BRCA1,MCM7,NSD2,WDHD1,DCUN1D5,MYBBP1A,RAD51AP1,ANKLE1,ECT2,SUV39H1,MNAT1,FOXM1,EIF2AK1,FH,MSX1,DNAJC7,EXO1,UBE2K,NEDD4,RFC1,TOP2A,BID,SMC1A,EIF2S1,ARG2,NUDT1,DCTPP1,FUS,LMNA,KIF22,RAD23A,PTTG1,PLK1,BRIP1,MORF4L2,ZSWIM7,ATAD5,HNRNPM,POLDIP2,WDR70,AIFM1,USP1,RSL1D1,UHRF1,CHAF1A,TFAP4,RPA1,TP73,G6PD,REXO4,FANCA,TOR1A,NEK6,ACD,CTH,HAS2,SIGMAR1,ERP29,POLE3,FEN1,PALB2,UBE2J2	darkgrey	VSMC_M8
GO:0006302	0.00	1.00	53	225	double-strand break repair	BP	1.2E-11	RAD21,RECQL4,TONSL,MCM5,APTX,VCP,MCM3,MMS22L,SMC6,GEN1,MCM2,RAD54L,PPP5C,MCM6,FANCD2,PARP2,GINS4,MCM4,PARPBP,HMGB2,ESCO2,RAD51,DCLRE1B,PSMD14,NUCKS1,DEK,TENT4A,CHEK1,TRIP13,POLQ,FANCB,RPA2,H2AFX,BLM,AUNIP,POLA1,DNA2,CDCA5,FANCM,SMARCAL1,CDC45,BRCA1,MCM7,NSD2,RAD51AP1,FOXM1,FUS,BRIP1,ZSWIM7,WDR70,RPA1,FEN1,PALB2	darkgrey	VSMC_M8
GO:0007017	0.00	1.00	112	715	microtubule-based process	BP	1.2E-11	RTTN,CDK2,TUBB,FBXO5,EZR,GTSE1,TTLL1,KIFC1,KIF20A,KIF27,KIF24,VCP,CEP135,TTK,NUP62,GEN1,PLK4,STIL,CHORDC1,CENPA,KIF2C,BORA,ULK4,CDC20,SGO1,CKAP2,CCNB1,WDR62,GAS2L3,HAUS5,AAAS,ESPL1,TPX2,KIF20B,SKA3,KIF2A,STAG1,CENPJ,WEE1,KIF11,CENPH,RACGAP1,TUBA1B,TUBA4B,CFAP298,CKAP5,KNSTRN,MYBL2,NUSAP1,KIF18A,CHEK1,RASSF1,NAV1,SMC3,CENPE,CEP72,KIF14,ASPM,RCC1,SPC25,NEK2,PRC1,RBM14,CEP85,AUNIP,CDK1,NUF2,ZW10,KIF18B,KIF15,CABYR,RANBP1,BRCA1,HAUS3,TACC3,DLGAP5,HAUS8,FKBP4,RAC1,HNRNPU,UCHL1,INCENP,SMC1A,CCNB2,KIF4A,LMNA,KIF22,SPDL1,AURKB,KIF23,LRRC49,HAUS1,PLK1,NDC80,POLDIP2,MTCL1,NDE1,TUBB6,CEP76,HOOK1,MAP7D3,HAUS7,CCNF,TUBB4B,SASS6,ODF2,NEK6,TPPP3,MAD2L1,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8

GO:0032508	0.00	1.00	29	75	DNA duplex unwinding	BP	1.2E-11	DSCC1,RECQL4,MCM5,MCM3,RUVBL2,MCM2,RUVBL1,RAD54L,MCM6,RFC3,MCM4,RAD51,NAV2,RFC5,CHD1L,POLQ,RFC2,BLM,DHX9,RFC4,DNA2,FANCM,MCM7,MNAT1,TOP2A,BRIP1,RPA1,CHTF18,ERCC6L	darkgrey	VSMC_M8
GO:1902100	0.00	1.00	21	40	negative regulation of metaphase/anaphase transition of cell cycle	BP	1.4E-11	FBXO5,RAD21,TTK,GEN1,CHFR,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0071824	0.00	1.00	43	163	protein-DNA complex subunit organization	BP	2.7E-11	POLR1E,ANP32B,GRWD1,MCM2,CENPO,CENPA,NASP,SUPT16H,NAP1L1,CENPK,CENPH,KNTC1,HMGB2,TERF1,HELLS,MIS18A,RAD51,OIP5,CHAF1B,GMNN,CENPE,ANP32E,HJURP,MCM3AP,IPO4,H2AFX,CENPF,HAT1,SMARCC1,CDC45,DNAJC9,DLGAP5,SMARCE1,ASF1B,CENPI,CHAF1A,CDT1,CENPN,HIST1H1A,CENPP,CENPW,POLE3,HIST1H2BB	darkgrey	VSMC_M8
GO:0006310	0.00	1.00	55	245	DNA recombination	BP	2.8E-11	RAD21,RECQL4,TONSL,MCM5,MCM3,MSH6,MMS22L,SMC6,GEN1,RUVBL2,MCM2,RUVBL1,RAD54L,MCM6,FANCD2,GINS4,ALYREF,MCM4,PARPBP,HMGB2,MND1,MSH3,RAD51,PSMD14,NUCKS1,CHEK1,TRIP13,UNG,POLQ,FANCB,RPA2,H2AFX,BLM,NSMCE4A,AUNIP,TFRC,FANCM,C17orf53,CDC45,BRCA1,MCM7,PSMC3IP,NSD2,RAD51AP1,ANKLE1,EXO1,TOP2A,FUS,BRIP1,ZSWIM7,RPA1,HIST1H1A,HMGB3,FEN1,PALB2	darkgrey	VSMC_M8
GO:0022616	0.00	1.00	15	20	DNA strand elongation	BP	3.4E-11	MCM3,LIG1,POLD3,PCNA,POLE,RFC3,MCM4,DCLRE1B,NUCKS1,POLA1,RFC4,DNA2,MCM7,GINS1,POLE3	darkgrey	VSMC_M8
GO:0071459	0.00	1.00	16	23	protein localization to chromosome, centromeric region	BP	3.5E-11	MTBP,CENPQ,TTK,CENPA,KNTC1,BUB1B,KNL1,BUB3,CDK1,ZW10,SPDL1,AURKB,ZWILCH,NDC80,HASPIN,CDT1	darkgrey	VSMC_M8
GO:0045839	0.00	1.00	22	46	negative regulation of mitotic nuclear division	BP	3.9E-11	FBXO5,RAD21,MTBP,TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,CHEK1,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0051225	0.00	1.00	33	101	spindle assembly	BP	4E-11	TUBB,FBXO5,KIFC1,CDC20,HAUS5,AAAS,TPX2,KIF2A,STAG1,KIF11,RACGAP1,MYBL2,SMC3,ASPM,RCC1,NEK2,PRC1,KIF15,HAUS3,HAUS8,HNRNPU,INCENP,SMC1A,CCNB2,KIF4A,AURKB,KIF23,HAUS1,PLK1,POLDIP2,HAUS7,NEK6,AURKA	darkgrey	VSMC_M8
GO:0006364	0.00	1.00	47	198	rRNA processing	BP	4.2E-11	SRFBP1,BYSL,PWP1,NOL8,NOL10,NIFK,DDX18,DIS3,XRN2,WDR43,FBL,GTPBP4,EIF4A3,EXOSC8,NOC4L,DDX51,MAK16,RRP8,NOP56,UTP20,WDR36,UTP15,EXOSC1,WDR3,RRP9,NOLC1,METTL15,MPHOSPH10,RRP1,FP565260.1,DDX27,NOL11,UTP25,NOP58,DDX21,SUV39H1,LYAR,EXOSC10,BRIX1,RSL1D1,DKC1,REXO4,EXOSC2,NOB1,GEMIN4,ABT1,IMP4	darkgrey	VSMC_M8
GO:0045841	0.00	1.00	20	38	negative regulation of mitotic metaphase/anaphase transition	BP	4.8E-11	FBXO5,RAD21,TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0034508	0.00	1.00	17	28	centromere complex assembly	BP	8.3E-11	CENPO,CENPA,NASP,CENPK,CENPH,KNTC1,HELLS,MIS18A,OIP5,CENPE,HJURP,CENPF,DLGAP5,CENPI,CENPN,CENPP,CENPW	darkgrey	VSMC_M8
GO:0007093	0.00	1.00	35	117	mitotic cell cycle checkpoint signaling	BP	1E-10	CDK2,GTSE1,TTK,CLSPN,CASP2,ORC1,GEN1,FANCD2,CHFR,TOPBP1,CCNB1,BUB1,KNTC1,BUB1B,CHEK1,TRIP13,RAD9A,TICRR,RPA2,DTL,BLM,CENPF,BUB3,CDK1,ZW10,BRCA1,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:1901991	0.00	1.00	39	142	negative regulation of mitotic cell cycle phase transition	BP	1.1E-10	CDK2,FBXO5,GTSE1,RAD21,TTK,EZH2,CLSPN,CASP2,ORC1,GEN1,E2F7,CHFR,TOPBP1,CCNB1,BUB1,WEE1,KNTC1,RBL1,BUB1B,CHEK1,TRIP13,TICRR,RPA2,DTL,BLM,CENPF,BUB3,CDK1,ZW10,BRCA1,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0000723	0.00	1.00	35	118	telomere maintenance	BP	1.3E-10	CCT2,TCP1,RECQL4,HSP90AB1,HNRNPA2B1,CCT4,SMC6,PCNA,CCNE1,TERF1,CCT8,CCT7,GNL3,RAD51,DCLRE1B,CCNE2,CCT5,CCT6A,RPA2,NEK2,BLM,DNA2,SMARCAL1,EXO1,HNRNPU,RFC1,EXOSC10,CCT3,AURKB,RPA1,SMG6,DKC1,ACD,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0065004	0.00	1.00	37	132	protein-DNA complex assembly	BP	1.4E-10	POLR1E,ANP32B,GRWD1,MCM2,CENPO,CENPA,NASP,NAP1L1,CENPK,CENPH,KNTC1,HMGB2,TERF1,HELLS,MIS18A,RAD51,OIP5,CHAF1B,GMNN,CENPE,HJURP,IPO4,H2AFX,CENPF,HAT1,CDC45,DNAJC9,DLGAP5,ASF1B,CENPI,CHAF1A,CDT1,CENPN,HIST1H1A,CENPP,CENPW,HIST1H2BB	darkgrey	VSMC_M8
GO:0016072	0.00	1.00	47	206	rRNA metabolic process	BP	1.9E-10	SRFBP1,BYSL,PWP1,NOL8,NOL10,NIFK,DDX18,DIS3,XRN2,WDR43,FBL,GTPBP4,EIF4A3,EXOSC8,NOC4L,DDX51,MAK16,RRP8,NOP56,UTP20,WDR36,UTP15,EXOSC1,WDR3,RRP9,NOLC1,METTL15,MPHOSPH10,RRP1,FP565260.1,DDX27,NOL11,UTP25,NOP58,DDX21,SUV39H1,LYAR,EXOSC10,BRIX1,RSL1D1,DKC1,REXO4,EXOSC2,NOB1,GEMIN4,ABT1,IMP4	darkgrey	VSMC_M8
GO:0045787	0.00	1.00	53	243	positive regulation of cell cycle	BP	1.9E-10	DDX39B,FBXO5,RAD21,MTBP,CDC25C,DBF4,CKS2,EZH2,NUP62,GEN1,PLK4,SPHK1,E2F7,CDC25B,CDC16,CCNB1,ESPL1,KIF20B,CENPJ,RACGAP1,FAM83D,TBX3,E2F8,NUSAP1,UBE2C,CIT,CHEK1,KIF14,DTL,EIF4G1,CDK1,CDC25A,FOSL1,CDCA5,RANBP1,DLGAP5,RAD51AP1,ECT2,MNAT1,MSX1,HNRNPU,CDC6,AURKB,RAD23A,KIF23,NDC80,ATAD5,POLDIP2,CDT1,TMOD3,MAD2L1,AURKA,FEN1	darkgrey	VSMC_M8
GO:0044786	0.00	1.00	20	40	cell cycle DNA replication	BP	2.7E-10	FBXO5,DBF4,MCM3,LIG1,MCM2,MCM6,E2F7,PCNA,MCM4,TERF1,RAD51,E2F8,GMNN,BLM,POLA1,DNA2,CDC45,CDT1,GINS1,FEN1	darkgrey	VSMC_M8
GO:0034501	0.00	1.00	14	19	protein localization to kinetochore	BP	2.8E-10	MTBP,CENPQ,TTK,KNTC1,KNL1,BUB3,CDK1,ZW10,SPDL1,AURKB,ZWILCH,NDC80,HASPIN,CDT1	darkgrey	VSMC_M8
GO:1903083	0.00	1.00	14	19	protein localization to condensed chromosome	BP	2.8E-10	MTBP,CENPQ,TTK,KNTC1,KNL1,BUB3,CDK1,ZW10,SPDL1,AURKB,ZWILCH,NDC80,HASPIN,CDT1	darkgrey	VSMC_M8
GO:0031577	0.00	1.00	19	37	spindle checkpoint signaling	BP	2.9E-10	TTK,GEN1,CHFR,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8

GO:0050000	0.00	1.00	26	70	chromosome localization	BP	4.3E-10	KIFC1,CENPQ,CDCA8,NUP62,KIF2C,CHMP6,CCNB1,TERF1,FAM83D,KIF18A,CENPE,KIF14,CENPF,NUF2,ZW10,CDCA5,DLGAP5,HNRNPU,INCENP,LMNA,KIF22,SPDL1,AURKB,NDC80,NDE1,CDT1	darkgrey	VSMC_M8
GO:0006270	0.00	1.00	18	33	DNA replication initiation	BP	4.3E-10	MCM5,MCM3,ORC6,ORC1,MCM2,MCM10,MCM6,TOPBP1,MCM4,CCNE1,CCNE2,TICRR,POLA1,AP000944.2,CDC45,MCM7,CDC6,CDT1	darkgrey	VSMC_M8
GO:0007098	0.00	1.00	34	115	centrosome cycle	BP	4.5E-10	RTTN,CDK2,CEP135,NUP62,GEN1,PLK4,STIL,CHORDC1,SGO1,WDR62,HAUS5,CENPJ,KIF11,CKAP5,CHEK1,CEP72,NEK2,RBM14,CEP85,CDK1,RANBP1,BRCA1,HAUS3,HAUS8,HAUS1,PLK1,NDC80,NDE1,CEP76,HAUS7,CCNF,SASS6,ODF2,AURKA	darkgrey	VSMC_M8
GO:0051784	0.00	1.00	22	51	negative regulation of nuclear division	BP	4.8E-10	FBXO5,RAD21,MTBP,TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,CHEK1,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0006275	0.00	1.00	30	92	regulation of DNA replication	BP	4.8E-10	FBXO5,DSCC1,DBF4,CCNA2,GTPBP4,E2F7,PCNA,RFC3,ATF1,TERF1,ESCO2,E2F8,RFC5,NUCKS1,GMNN,SMC3,TICRR,RFC2,BLM,CDK1,S100A11,DHX9,RFC4,DNA2,SMARCAL1,RAC1,CDC6,ATAD5,CHTF18,CDT1	darkgrey	VSMC_M8
GO:0043933	0.00	1.00	171	1370	protein-containing complex subunit organization	BP	5.8E-10	TXNL4A,NUP107,CCT2,DDX39B,FBXO5,TCP1,FAM49B,SRPK1,PSIP1,KIF24,VCP,HSP90AB1,COL1A2,POLR1E,NCBP1,ANP32B,PPIH,MFSD2A,NUP205,ANLN,PRMT1,RUVBL2,GRWD1,MCM2,CENPO,RUVBL1,SLC1A5,CHCHD4,CENPA,CDC42EP4,NASP,NUFIP1,PREB,MRPL58,NIFK,MRPS7,KIF2C,DIAPH3,TK1,SUPT16H,NAP1L1,CHMP6,CKAP2,RRM1,SNRPF,CCNB1,SFSWAP,SNRPB,TPX2,KIF2A,EIF3M,CENPJ,CENPK,ABCE1,VAMP8,CENPH,KNTC1,HMGB2,ATF1,TERF1,HELLS,CCT8,PPID,MIS18A,CKAP5,NUP93,RAD51,OIP5,NDUFAF1,MDM4,CHAF1B,UBE2C,FASTKD3,NUP153,KIF18A,ICE1,GMNN,FP565260.1,SF3B1,CENPE,KIF14,PRMT5,POLQ,ANP32E,PRPF3,HJURP,MCM3AP,EIF4H,IPO4,NUP133,H2AFX,BLM,CENPF,STRAP,EIF4G1,HAT1,CDK1,TFRC,SMARCC1,DHX9,NDUFS1,DDX20,ZW10,KIF18B,SF1,CDC45,DNAJC9,DLGAP5,ECT2,DHX33,FKBP4,MNAT1,RAC1,UBE2K,UGDH,FSCN1,SMARCE1,EIF5A,CPSF7,BID,EIF3B,PSMG3,ASF1B,SRSF5,NES,SH3PXD2B,CCT3,FUS,CENPI,GEMIN5,LRRC49,EIF5,SNRPD1,PSMD11,NDE1,AIFM1,BRIX1,MAP7D3,RBMX,LIPG,CHAF1A,NDC1,TFAP4,SF3A2,TP73,FANCA,CDT1,CENPN,GLE1,DDX28,TPPP3,CTH,ARPC4,ARF6,USP4,HIST1H1A,CENPP,GEMIN4,GBP5,TMOD3,DDX23,ACSL3,STMN1,ABT1,UBE2S,STXBP6,CENPW,SIGMAR1,POLE3,HIST1H2BB,MBD2	darkgrey	VSMC_M8
GO:2000278	0.00	1.00	30	95	regulation of DNA biosynthetic process	BP	1.1E-09	CCT2,DDX39B,TCP1,DSCC1,HSP90AB1,HNRNPA2B1,CCT4,DNAJC2,PCNA,RFC3,HGF,TERF1,CCT8,CCT7,RFC5,CCT5,CCT6A,RFC2,NEK2,RFC4,HNRNPU,EXOSC10,CCT3,AURKB,SMG6,CHTF18,DKC1,FAM129B,ACD,HNRNPD	darkgrey	VSMC_M8
GO:0030261	0.00	1.00	17	31	chromosome condensation	BP	1.1E-09	SMC2,NCAPG2,NCAPH,CCNB1,NUSAP1,NCAPD3,TENT4A,CDK1,CDCA5,SMC4,NCAPD2,INCENP,TOP2A,NCAPG,PLK1,AIFM1,HIST1H1A	darkgrey	VSMC_M8
GO:0000725	0.00	1.00	35	126	recombinational repair	BP	1.2E-09	RAD21,RECQL4,TONSL,MCM5,MCM3,MMS22L,SMC6,GEN1,MCM2,RAD54L,MCM6,GINS4,MCM4,PARPBP,RAD51,PSMD14,NUCKS1,CHEK1,POLQ,FANCB,RPA2,H2AFX,BLM,AUNIP,FANCM,C17orf53,CDC45,BRCA1,MCM7,RAD51AP1,FUS,ZSWIM7,RPA1,FEN1,PALB2	darkgrey	VSMC_M8
GO:0051303	0.00	1.00	25	68	establishment of chromosome localization	BP	1.3E-09	KIFC1,CENPQ,CDCA8,NUP62,KIF2C,CHMP6,CCNB1,TERF1,FAM83D,KIF18A,CENPE,KIF14,CENPF,NUF2,ZW10,CDCA5,DLGAP5,HNRNPU,INCENP,KIF22,SPDL1,AURKB,NDC80,NDE1,CDT1	darkgrey	VSMC_M8
GO:0051383	0.00	1.00	14	21	kinetochore organization	BP	1.6E-09	SMC2,CENPA,CENPK,CENPH,KNTC1,CENPE,CENPF,NUF2,SMC4,DLGAP5,NDC80,CDT1,CENPN,CENPW	darkgrey	VSMC_M8
GO:0007094	0.00	1.00	18	36	mitotic spindle assembly checkpoint signaling	BP	1.8E-09	TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0071173	0.00	1.00	18	36	spindle assembly checkpoint signaling	BP	1.8E-09	TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0071174	0.00	1.00	18	36	mitotic spindle checkpoint signaling	BP	1.8E-09	TTK,GEN1,CCNB1,BUB1,KNTC1,BUB1B,TRIP13,CENPF,BUB3,ZW10,ZWINT,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0034470	0.00	1.00	63	345	ncRNA processing	BP	1.9E-09	METTL1,POP1,SRFBP1,BYSL,PWP1,NOL8,THADA,HNRNPA2B1,GRSF1,NOL10,PUS7,NIFK,DDX18,TSEN2,DIS3,XRN2,WDR43,FBL,GTPBP4,EIF4A3,DUS1L,EXOSC8,NOC4L,DDX51,MAK16,RRP8,NOP56,UTP20,WDR36,UTP15,EXOSC1,WDR3,RRP9,NOLC1,METTL15,NSUN2,MPHOSPH10,RRP1,FP565260.1,DDX27,NOL11,TARBP1,UTP25,INTS7,SSB,NOP58,DDX21,DGCR8,SUV39H1,LYAR,EXOSC10,ELAC2,BRIX1,RSL1D1,DKC1,REXO4,EXOSC2,TRMT13,NOB1,SRRT,GEMIN4,ABT1,IMP4	darkgrey	VSMC_M8
GO:0061982	0.00	1.00	30	99	meiosis I cell cycle process	BP	2.1E-09	FBXO5,RAD21,CDC25C,CKS2,MSH6,RAD54L,FANCD2,SGO1,CDC25B,PSMD13,ESPL1,CCNE1,TERF1,MND1,MSH3,RAD51,CCNE2,TRIP13,SGO2,CDC25A,FANCM,PSMC3IP,RAD51AP1,TOP2A,CCNB2,PTTG1,PLK1,BRIP1,NDC1,AURKA	darkgrey	VSMC_M8
GO:0032200	0.00	1.00	35	130	telomere organization	BP	2.1E-09	CCT2,TCP1,RECQL4,HSP90AB1,HNRNPA2B1,CCT4,SMC6,PCNA,CCNE1,TERF1,CCT8,CCT7,GNL3,RAD51,DCLRE1B,CCNE2,CCT5,CCT6A,RPA2,NEK2,BLM,DNA2,SMARCAL1,EXO1,HNRNPU,RFC1,EXOSC10,CCT3,AURKB,RPA1,SMG6,DKC1,ACD,HNRNPD,FEN1	darkgrey	VSMC_M8

GO:0034622	0.00	1.00	115	830	cellular protein-containing complex assembly	BP	2.6E-09	TXNL4A,NUP107,CCT2,DDX39B,FBXO5,TCP1,FAM49B,SRPK1,PSIP1,HSP90AB1,POLR1E,NCBP1,ANP32B,NUP205,ANLN,RUVBL2,GRWD1,MCM2,CENPO,RUVBL1,CHCHD4,CENPA,CDC42EP4,NASP,NUFIP1,MRPS7,DIAPH3,NAP1L1,SNRPF,SFSWAP,SNRPB,TPX2,EIF3M,CENPJ,CENPK,VAMP8,CENPH,KNTC1,HMGB2,ATF1,TERF1,HELLS,MIS18A,CKAP5,NUP93,RAD51,OIP5,NDUFAF1,CHAF1B,UBE2C,FASTKD3,NUP153,GMNN,FP565260.1,SF3B1,CENPE,PRMT5,PRPF3,HJURP,EIF4H,IPO4,H2AFX,CENPF,STRAP,EIF4G1,HAT1,DHX9,NDUFS1,DDX20,SF1,CDC45,DNAJC9,DLGAP5,DHX33,FKBP4,RAC1,UBE2K,CPSF7,EIF3B,PSMG3,ASF1B,SRSF5,CENPI,GEMIN5,LRRC49,EIF5,SNRPD1,PSMD11,NDE1,AIFM1,BRIX1,MAP7D3,CHAF1A,NDC1,SF3A2,CDT1,CENPN,DDX28,TPPP3,ARPC4,ARF6,USP4,HIST1H1A,CENPP,GEMIN4,GBP5,TMOD3,DDX23,STMN1,ABT1,UBE2S,STXBP6,CENPW,HIST1H2BB,MBD2	darkgrey	VSMC_M8
GO:0051236	0.00	1.00	36	138	establishment of RNA localization	BP	2.8E-09	XPOT,NUP43,NUP107,DDX39B,NUP50,SRSF3,NCBP1,HNRNPA2B1,NUP205,NUP62,NUP85,EIF4A3,ALYREF,AAAS,TERF1,NUP160,CKAP5,NUP93,NUP153,NSUN2,KHDRBS1,MCM3AP,NUP133,SSB,DHX9,HNRNPA3,SLBP,EIF5A,DDX39A,NUP62CL,NDC1,SMG6,THOC6,NUP188,GLE1,SRSF7	darkgrey	VSMC_M8
GO:0000724	0.00	1.00	34	124	double-strand break repair via homologous recombination	BP	3.2E-09	RAD21,RECQL4,TONSL,MCM5,MCM3,MMS22L,SMC6,GEN1,MCM2,RAD54L,MCM6,GINS4,MCM4,PARPBP,RAD51,PSMD14,NUCKS1,CHEK1,POLQ,FANCB,RPA2,H2AFX,BLM,AUNIP,FANCM,CDC45,BRCA1,MCM7,RAD51AP1,FUS,ZSWIM7,RPA1,FEN1,PALB2	darkgrey	VSMC_M8
GO:0051310	0.00	1.00	22	55	metaphase plate congression	BP	3.2E-09	KIFC1,CENPQ,CDCA8,NUP62,KIF2C,CHMP6,CCNB1,FAM83D,KIF18A,CENPE,KIF14,CENPF,NUF2,ZW10,CDCA5,HNRNPU,INCENP,KIF22,SPDL1,AURKB,NDC80,CDT1	darkgrey	VSMC_M8
GO:0045930	0.00	1.00	43	186	negative regulation of mitotic cell cycle	BP	3.4E-09	CDK2,FBXO5,GTSE1,RAD21,MTBP,TTK,EZH2,CLSPN,CASP2,ORC1,GEN1,FANCD2,E2F7,CHFR,TOPBP1,CCNB1,BUB1,WEE1,KNTC1,RBL1,TRIM35,BUB1B,CHEK1,TRIP13,RAD9A,TICRR,RPA2,DTL,BLM,CENPF,BUB3,CDK1,ZW10,BRCA1,ZWINT,CDC6,SPDL1,AURKB,ZWILCH,PLK1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0044238	0.00	1.00	674	7641	primary metabolic process	BP	4.3E-09	TXNL4A,CDK2,ALPK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,TCP1,RAD21,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,ATAD2,DESI1,PHF5A,ZNF367,CDC25C,FKBP5,SRPK1,SRSF3,GCAT,PSIP1,RECQL4,BYSL,TONSL,MCM5,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,POLR1C,TJP2,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,NANS,TWISTNB,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,CTPS1,TTK,CYCS,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,NRDC,RUVBL2,PLK4,AMD1,PGR,NAMPT,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,SAE1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,NAALAD2,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,COG3,NUFIP1,GRIN2C,PRCP,MRPL58,NIFK,SMG9,NUP85,PLAUR,MRPS7,MCM10,CAD,ALG8,DBI,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,AXL,RNF157,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,ULK4,NCAPG2,WDR43,CDC20,TK1,AFMID,BIRC5,PGS1,SERPINH1,PARP2,FBL,POLR3F,RRBP1,POLD3,SNRPB2,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,GINS4,PCCA,ALYREF,CKAP2,RRM1,DUS1L,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,METAP2,DCUN1D2,HGF,SNRPF,TOPBP1,ELK3,PSMD13,RRP8,CDC16,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,CD44,UTP20,TCEA1,ESPL1,MRPS5,HNRNPF,BUB1,TPX2,A	darkgrey	VSMC_M8
GO:0044839	0.00	1.00	35	132	cell cycle G2/M phase transition	BP	4.3E-09	CDK2,FBXO5,RAD21,CDC25C,MELK,CLSPN,ORC1,CCNA2,RNASEH2B,MASTL,CHFR,CDC25B,TOPBP1,CCNB1,WEE1,CHEK1,KHDRBS1,KIF14,TICRR,DTL,BLM,CENPF,CDK1,CDC25A,BRCA1,FOXM1,CCNB3,CDC6,CCNB2,NES,AURKB,PLK1,ATAD5,PKMYT1,AURKA	darkgrey	VSMC_M8
GO:0065003	0.00	1.00	152	1210	protein-containing complex assembly	BP	4.4E-09	TXNL4A,NUP107,CCT2,DDX39B,FBXO5,TCP1,FAM49B,SRPK1,PSIP1,VCP,HSP90AB1,COL1A2,POLR1E,NCBP1,ANP32B,PPIH,MFSD2A,NUP205,ANLN,PRMT1,RUVBL2,GRWD1,MCM2,CENPO,RUVBL1,SLC1A5,CHCHD4,CENPA,CDC42EP4,NASP,NUFIP1,PREB,NIFK,MRPS7,DIAPH3,TK1,NAP1L1,CHMP6,RRM1,SNRPF,CCNB1,SFSWAP,SNRPB,TPX2,EIF3M,CENPJ,CENPK,VAMP8,CENPH,KNTC1,HMGB2,ATF1,TERF1,HELLS,CCT8,PPID,MIS18A,CKAP5,NUP93,RAD51,OIP5,NDUFAF1,MDM4,CHAF1B,UBE2C,FASTKD3,NUP153,ICE1,GMNN,FP565260.1,SF3B1,CENPE,KIF14,PRMT5,POLQ,PRPF3,HJURP,EIF4H,IPO4,H2AFX,BLM,CENPF,STRAP,EIF4G1,HAT1,CDK1,TFRC,DHX9,NDUFS1,DDX20,ZW10,SF1,CDC45,DNAJC9,DLGAP5,ECT2,DHX33,FKBP4,MNAT1,RAC1,UBE2K,UGDH,FSCN1,CPSF7,BID,EIF3B,PSMG3,ASF1B,SRSF5,SH3PXD2B,CCT3,FUS,CENPI,GEMIN5,LRRC49,EIF5,SNRPD1,PSMD11,NDE1,AIFM1,BRIX1,MAP7D3,RBMX,CHAF1A,NDC1,TFAP4,SF3A2,TP73,FANCA,CDT1,CENPN,DDX28,TPPP3,CTH,ARPC4,ARF6,USP4,HIST1H1A,CENPP,GEMIN4,GBP5,TMOD3,DDX23,ACSL3,STMN1,ABT1,UBE2S,STXBP6,CENPW,SIGMAR1,HIST1H2BB,MBD2	darkgrey	VSMC_M8

GO:0000003	0.00	1.00	136	1031	reproduction	BP	5.2E-09	CDK2,NUP107,CCT2,FBXO5,TCP1,RAD21,TTLL1,KIFC1,CDC25C,SRPK1,HSP90AB1,CKS2,TRIM28,SMC2,MSH6,TTK,CCT4,NUP62,GJB3,CASP2,SDC1,PLK4,PGR,NAMPT,RUVBL1,RAD54L,WDR33,MAST2,FOSB,NASP,CAD,AXL,FANCD2,XRN2,CDC20,E2F7,SGO1,RRM1,PCNA,CHFR,CDC25B,PSMD13,CCNB1,AAAS,ESPL1,BUB1,POLR1B,E2F1,CCNE1,HMGB2,RBP4,TERF1,NRIP1,MND1,RACGAP1,HEY1,CCT8,MSH3,BUB1B,CCT7,KNL1,TBX3,RAD51,CCNE2,E2F8,NCAPD3,CCT5,KIF18A,ETS1,NSUN2,SNRPA1,SMC3,KHDRBS1,TRIP13,SGO2,ASPM,EIF4H,NEK2,H2AFX,PDE3A,UMPS,BUB3,CDK1,CDC25A,FOSL1,SMARCC1,NUF2,DDX20,ZW10,FANCM,CABYR,SF1,C17orf53,SMC4,CNOT9,PSMC3IP,CDK16,NCAPD2,RAD51AP1,SIX4,USP42,MSX1,EXO1,INCENP,ADIPOR2,CCNB3,TOP2A,LIN9,SMC1A,NUDT1,ASF1B,CCNB2,CCT3,ALOX15B,PTTG1,CENPI,PLK1,BRIP1,ACSL4,TOP3A,SEPT6,RAI14,HOOK1,EMP2,NDC1,RPA1,PKMYT1,CCNF,DAZAP1,FANCA,ODF2,TPPP3,HIST1H1A,AURKA,HAS2,MBD2	darkgrey	VSMC_M8
GO:0050657	0.00	1.00	35	135	nucleic acid transport	BP	5.8E-09	XPOT,NUP43,NUP107,DDX39B,NUP50,SRSF3,NCBP1,HNRNPA2B1,NUP205,NUP62,NUP85,EIF4A3,ALYREF,AAAS,NUP160,CKAP5,NUP93,NUP153,NSUN2,KHDRBS1,MCM3AP,NUP133,SSB,DHX9,HNRNPA3,SLBP,EIF5A,DDX39A,NUP62CL,NDC1,SMG6,THOC6,NUP188,GLE1,SRSF7	darkgrey	VSMC_M8
GO:0050658	0.00	1.00	35	135	RNA transport	BP	5.8E-09	XPOT,NUP43,NUP107,DDX39B,NUP50,SRSF3,NCBP1,HNRNPA2B1,NUP205,NUP62,NUP85,EIF4A3,ALYREF,AAAS,NUP160,CKAP5,NUP93,NUP153,NSUN2,KHDRBS1,MCM3AP,NUP133,SSB,DHX9,HNRNPA3,SLBP,EIF5A,DDX39A,NUP62CL,NDC1,SMG6,THOC6,NUP188,GLE1,SRSF7	darkgrey	VSMC_M8
GO:0070203	0.00	1.00	10	11	regulation of establishment of protein localization to telomere	BP	7.6E-09	CCT2,TCP1,CCT4,TERF1,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0031023	0.00	1.00	34	127	microtubule organizing center organization	BP	7.7E-09	RTTN,CDK2,CEP135,NUP62,GEN1,PLK4,STIL,CHORDC1,SGO1,WDR62,HAUS5,CENPJ,KIF11,CKAP5,CHEK1,CEP72,NEK2,RBM14,CEP85,CDK1,RANBP1,BRCA1,HAUS3,HAUS8,HAUS1,PLK1,NDC80,NDE1,CEP76,HAUS7,CCNF,SASS6,ODF2,AURKA	darkgrey	VSMC_M8
GO:0022414	0.00	1.00	135	1029	reproductive process	BP	8.6E-09	CDK2,NUP107,CCT2,FBXO5,TCP1,RAD21,TTLL1,KIFC1,CDC25C,SRPK1,HSP90AB1,CKS2,TRIM28,SMC2,MSH6,TTK,CCT4,NUP62,GJB3,CASP2,SDC1,PLK4,PGR,NAMPT,RUVBL1,RAD54L,WDR33,MAST2,FOSB,NASP,CAD,AXL,FANCD2,XRN2,CDC20,E2F7,SGO1,RRM1,PCNA,CHFR,CDC25B,PSMD13,CCNB1,AAAS,ESPL1,BUB1,POLR1B,E2F1,CCNE1,HMGB2,RBP4,TERF1,NRIP1,MND1,RACGAP1,HEY1,CCT8,MSH3,BUB1B,CCT7,KNL1,TBX3,RAD51,CCNE2,E2F8,NCAPD3,CCT5,KIF18A,ETS1,NSUN2,SNRPA1,SMC3,KHDRBS1,TRIP13,SGO2,ASPM,EIF4H,NEK2,H2AFX,PDE3A,UMPS,BUB3,CDK1,CDC25A,FOSL1,SMARCC1,NUF2,DDX20,ZW10,FANCM,CABYR,SF1,C17orf53,SMC4,CNOT9,PSMC3IP,CDK16,NCAPD2,RAD51AP1,SIX4,USP42,MSX1,EXO1,INCENP,ADIPOR2,CCNB3,TOP2A,SMC1A,NUDT1,ASF1B,CCNB2,CCT3,ALOX15B,PTTG1,CENPI,PLK1,BRIP1,ACSL4,TOP3A,SEPT6,RAI14,HOOK1,EMP2,NDC1,RPA1,PKMYT1,CCNF,DAZAP1,FANCA,ODF2,TPPP3,HIST1H1A,AURKA,HAS2,MBD2	darkgrey	VSMC_M8
GO:0006405	0.00	1.00	24	69	RNA export from nucleus	BP	1.2E-08	XPOT,NUP107,DDX39B,SRSF3,NCBP1,HNRNPA2B1,NUP62,NUP85,ALYREF,NUP160,NUP93,NUP153,NSUN2,KHDRBS1,MCM3AP,NUP133,SSB,DHX9,DDX39A,NUP62CL,SMG6,THOC6,NUP188,GLE1	darkgrey	VSMC_M8
GO:0044260	0.00	1.00	546	5916	cellular macromolecule metabolic process	BP	1.4E-08	CDK2,ALPK2,NARS,PRIM1,HNRNPAB,BCLAF1,METTL1,MRPS18B,NUP107,CCT2,VARS2,POP1,DDX39B,FBXO5,PRRC1,VARS,EZR,TCP1,RAD21,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,ATAD2,DESI1,PHF5A,ZNF367,CDC25C,FKBP5,SRPK1,PSIP1,RECQL4,TONSL,MCM5,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,TWISTNB,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,NUP62,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,NRDC,RUVBL2,PLK4,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,SAE1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,NASP,COG3,NUFIP1,MRPL58,NIFK,SMG9,NUP85,PLAUR,MRPS7,MCM10,CAD,ALG8,DBI,TRIM47,BORA,DIS3,AXL,RNF157,SPHK1,MCM6,SRSF2,FANCD2,XRN2,ULK4,NCAPG2,WDR43,CDC20,TK1,BIRC5,SERPINH1,PARP2,FBL,POLR3F,RRBP1,POLD3,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,GINS4,ALYREF,CKAP2,RRM1,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,POLE,ZNF703,RFC3,METAP2,DCUN1D2,HGF,TOPBP1,ELK3,PSMD13,RRP8,CDC16,TCERG1,USPL1,CBX5,CCNB1,MCM4,SNAI2,SNRPB,CD44,TCEA1,MRPS5,BUB1,TPX2,ANAPC1,POLR1B,GGH,UBA2,PARPBP,CWC27,SGK3,EIF3M,CENPJ,WEE1,HSP90B1,NECAB3,EIF2B1,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,GALNT6,HMGB2,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,UTP15,MND1,LOXL3,PBK,ESCO2,HEY1,NEIL3,ZBTB10,SELENOT,FAM98B,CCT8,PPID,RBL1,TRI	darkgrey	VSMC_M8
GO:0000086	0.00	1.00	33	124	G2/M transition of mitotic cell cycle	BP	1.5E-08	CDK2,FBXO5,RAD21,CDC25C,MELK,CLSPN,ORC1,CCNA2,RNASEH2B,MASTL,CHFR,CDC25B,TOPBP1,CCNB1,WEE1,CHEK1,KHDRBS1,KIF14,TICRR,DTL,BLM,CENPF,CDK1,CDC25A,BRCA1,FOXM1,CCNB3,CDC6,NES,AURKB,PLK1,PKMYT1,AURKA	darkgrey	VSMC_M8
GO:0051168	0.00	1.00	34	131	nuclear export	BP	1.5E-08	XPOT,NUP107,DDX39B,DESI1,RANGAP1,HSPA9,SRSF3,NCBP1,ANP32B,HNRNPA2B1,NUP62,NUP85,ALYREF,ABCE1,NUP160,NUP93,NUP153,NSUN2,KHDRBS1,CSE1L,MCM3AP,NUP133,SSB,DHX9,LSG1,BARD1,NMD3,ANKLE1,DDX39A,NUP62CL,SMG6,THOC6,NUP188,GLE1	darkgrey	VSMC_M8

GO:1904814	0.00	1.00	11	14	regulation of protein localization to chromosome, telomeric region	BP	1.7E-08	CCT2,TCP1,CCT4,TERF1,CCT8,CCT7,GNL3,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:2000573	0.00	1.00	22	60	positive regulation of DNA biosynthetic process	BP	1.8E-08	CCT2,DDX39B,TCP1,DSCC1,HSP90AB1,CCT4,PCNA,RFC3,HGF,CCT8,CCT7,RFC5,CCT5,CCT6A,RFC2,NEK2,RFC4,CCT3,AURKB,CHTF18,DKC1,ACD	darkgrey	VSMC_M8
GO:0033260	0.00	1.00	17	36	nuclear DNA replication	BP	3.1E-08	DBF4,MCM3,LIG1,MCM2,MCM6,PCNA,MCM4,TERF1,RAD51,GMNN,BLM,POLA1,DNA2,CDC45,CDT1,GINS1,FEN1	darkgrey	VSMC_M8
GO:0034660	0.00	1.00	68	412	ncRNA metabolic process	BP	3.2E-08	NARS,METTL1,VARS2,POP1,SRFBP1,VARS,BYSL,PWP1,NOL8,THADA,HNRNPA2B1,GRSF1,GARS,NOL10,PUS7,NIFK,DDX18,TSEN2,DIS3,XRN2,WDR43,FBL,GTPBP4,EIF4A3,DUS1L,EXOSC8,NOC4L,DDX51,MAK16,RRP8,NOP56,UTP20,WDR36,UTP15,EXOSC1,WDR3,RRP9,NOLC1,METTL15,NSUN2,MPHOSPH10,RRP1,FP565260.1,DDX27,NOL11,TARBP1,UTP25,INTS7,SSB,NOP58,DDX21,DGCR8,SUV39H1,LYAR,EXOSC10,RARS,ELAC2,BRIX1,RSL1D1,DKC1,REXO4,EXOSC2,TRMT13,NOB1,SRRT,GEMIN4,ABT1,IMP4	darkgrey	VSMC_M8
GO:0051028	0.00	1.00	30	109	mRNA transport	BP	3.6E-08	NUP43,NUP107,DDX39B,NUP50,SRSF3,NCBP1,HNRNPA2B1,NUP205,NUP62,NUP85,EIF4A3,ALYREF,AAAS,NUP160,NUP93,NUP153,NSUN2,MCM3AP,NUP133,DHX9,HNRNPA3,SLBP,EIF5A,DDX39A,NDC1,SMG6,THOC6,NUP188,GLE1,SRSF7	darkgrey	VSMC_M8
GO:1904872	0.00	1.00	12	18	regulation of telomerase RNA localization to Cajal body	BP	3.6E-08	CCT2,TCP1,CCT4,RUVBL2,RUVBL1,CCT8,CCT7,CCT5,CCT6A,EXOSC10,CCT3,DKC1	darkgrey	VSMC_M8
GO:1904874	0.00	1.00	11	15	positive regulation of telomerase RNA localization to Cajal body	BP	3.6E-08	CCT2,TCP1,CCT4,RUVBL2,RUVBL1,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0006913	0.00	1.00	50	257	nucleocytoplasmic transport	BP	3.9E-08	XPOT,NUP107,DDX39B,NUP50,DESI1,RANGAP1,HSPA9,SRSF3,TNPO3,HSP90AB1,TRIM28,NCBP1,ANP32B,HNRNPA2B1,NUP205,NUP62,NUP85,IPO5,ALYREF,AAAS,ABCE1,NUP160,RSRC1,NUP93,HEATR3,NOLC1,NUP153,NSUN2,KHDRBS1,CSE1L,MCM3AP,IPO4,NUP133,SSB,CDK1,DHX9,LSG1,BARD1,NMD3,ANKLE1,ECT2,NEDD4,DDX39A,LMNA,NUP62CL,NDC1,SMG6,THOC6,NUP188,GLE1	darkgrey	VSMC_M8
GO:0051169	0.00	1.00	50	257	nuclear transport	BP	3.9E-08	XPOT,NUP107,DDX39B,NUP50,DESI1,RANGAP1,HSPA9,SRSF3,TNPO3,HSP90AB1,TRIM28,NCBP1,ANP32B,HNRNPA2B1,NUP205,NUP62,NUP85,IPO5,ALYREF,AAAS,ABCE1,NUP160,RSRC1,NUP93,HEATR3,NOLC1,NUP153,NSUN2,KHDRBS1,CSE1L,MCM3AP,IPO4,NUP133,SSB,CDK1,DHX9,LSG1,BARD1,NMD3,ANKLE1,ECT2,NEDD4,DDX39A,LMNA,NUP62CL,NDC1,SMG6,THOC6,NUP188,GLE1	darkgrey	VSMC_M8
GO:1904816	0.00	1.00	10	12	positive regulation of protein localization to chromosome, telomeric region	BP	3.9E-08	CCT2,TCP1,CCT4,CCT8,CCT7,GNL3,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0070202	0.00	1.00	10	12	regulation of establishment of protein localization to chromosome	BP	3.9E-08	CCT2,TCP1,CCT4,TERF1,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0071704	0.00	1.00	700	8083	organic substance metabolic process	BP	3.9E-08	TXNL4A,CDK2,ALPK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,CCT2,VARS2,POP1,TCF19,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,PANX2,TCP1,RAD21,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,ATAD2,DESI1,PHF5A,FAM49B,ZNF367,SLC35D2,CDC25C,FKBP5,MATR3,SRPK1,SRSF3,GCAT,PSIP1,RECQL4,BYSL,TONSL,MCM5,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,POLR1C,UBAP2,TJP2,POLH,ALDH1L2,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,NANS,TWISTNB,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,CTPS1,TTK,CYCS,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,NRDC,RUVBL2,PLK4,AMD1,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,SAE1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,NAALAD2,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,NASP,COG3,NUFIP1,GRIN2C,PRCP,MRPL58,NIFK,SMG9,NUP85,PLAUR,MRPS7,MCM10,SLC25A19,CAD,ALG8,DBI,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,AXL,RNF157,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,ULK4,NCAPG2,WDR43,CDC20,TK1,AFMID,BIRC5,PGS1,SERPINH1,PARP2,FBL,POLR3F,RRBP1,POLD3,SNRPB2,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,GINS4,PCCA,ALYREF,CKAP2,RRM1,DUS1L,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,METAP2,DCUN1D2,HGF,SNRPF,TOPBP1,ELK3,PSMD13,RRP8,CDC16,TCERG1,USPL1,CBX5,CCNB1,	darkgrey	VSMC_M8
GO:0007062	0.00	1.00	19	47	sister chromatid cohesion	BP	5.5E-08	RAD21,DSCC1,CDC20,SGO1,ESPL1,BUB1,STAG1,ESCO2,BUB1B,TENT4A,NAA50,SMC3,SGO2,CDCA5,SMC1A,KIF22,PLK1,HASPIN,FEN1	darkgrey	VSMC_M8

GO:0044237	0.00	1.00	686	7918	cellular metabolic process	BP	7.3E-08	TXNL4A,CDK2,ALPK2,NARS,ATP5F1B,PRIM1,HNRNPAB,MTFR2,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,CCT2,VARS2,POP1,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,TCP1,RAD21,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,ATAD2,DESI1,PHF5A,ZNF367,SLC35D2,CDC25C,HSPA9,FKBP5,SRPK1,SRSF3,GCAT,CYC1,PSIP1,RECQL4,BYSL,TONSL,MCM5,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,POLR1C,TJP2,POLH,ALDH1L2,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,NANS,TWISTNB,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,CTPS1,TTK,CYCS,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,NRDC,RUVBL2,PLK4,AMD1,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,SAE1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,NASP,COG3,NUFIP1,PRCP,MRPL58,NIFK,SMG9,NUP85,PLAUR,MRPS7,MCM10,SLC25A19,CAD,ALG8,DBI,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,AXL,RNF157,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,ULK4,NCAPG2,WDR43,CDC20,TK1,AFMID,BIRC5,PGS1,SERPINH1,PARP2,FBL,POLR3F,RRBP1,POLD3,SNRPB2,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,GINS4,PCCA,ALYREF,CKAP2,RRM1,DUS1L,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,METAP2,DCUN1D2,HGF,SNRPF,TOPBP1,ELK3,PSMD13,RRP8,CDC16,TCERG1,USPL1,CBX5,CCNB1,MCM4,SFSWAP,SNAI2,NOP56,SNRPB,CD44,UTP20,T	darkgrey	VSMC_M8
GO:1904851	0.00	1.00	9	10	positive regulation of establishment of protein localization to telomere	BP	7.7E-08	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0007127	0.00	1.00	27	94	meiosis I	BP	7.9E-08	FBXO5,RAD21,CKS2,RAD54L,FANCD2,SGO1,CDC25B,PSMD13,ESPL1,CCNE1,TERF1,MND1,MSH3,RAD51,CCNE2,TRIP13,SGO2,FANCM,PSMC3IP,RAD51AP1,TOP2A,CCNB2,PTTG1,PLK1,BRIP1,NDC1,AURKA	darkgrey	VSMC_M8
GO:0008608	0.00	1.00	15	30	attachment of spindle microtubules to kinetochore	BP	8.2E-08	KIF2C,SGO1,CCNB1,RACGAP1,KNSTRN,KNL1,CENPE,NEK2,BUB3,NUF2,ECT2,HNRNPU,AURKB,NDC80,CDT1	darkgrey	VSMC_M8
GO:0007080	0.00	1.00	18	43	mitotic metaphase plate congression	BP	8.2E-08	KIFC1,CDCA8,NUP62,KIF2C,CHMP6,CCNB1,KIF18A,CENPE,KIF14,NUF2,ZW10,CDCA5,HNRNPU,KIF22,SPDL1,AURKB,NDC80,CDT1	darkgrey	VSMC_M8
GO:0090670	0.00	1.00	12	19	RNA localization to Cajal body	BP	8.4E-08	CCT2,TCP1,CCT4,RUVBL2,RUVBL1,CCT8,CCT7,CCT5,CCT6A,EXOSC10,CCT3,DKC1	darkgrey	VSMC_M8
GO:0090671	0.00	1.00	12	19	telomerase RNA localization to Cajal body	BP	8.4E-08	CCT2,TCP1,CCT4,RUVBL2,RUVBL1,CCT8,CCT7,CCT5,CCT6A,EXOSC10,CCT3,DKC1	darkgrey	VSMC_M8
GO:0090672	0.00	1.00	12	19	telomerase RNA localization	BP	8.4E-08	CCT2,TCP1,CCT4,RUVBL2,RUVBL1,CCT8,CCT7,CCT5,CCT6A,EXOSC10,CCT3,DKC1	darkgrey	VSMC_M8
GO:0090685	0.00	1.00	12	19	RNA localization to nucleus	BP	8.4E-08	CCT2,TCP1,CCT4,RUVBL2,RUVBL1,CCT8,CCT7,CCT5,CCT6A,EXOSC10,CCT3,DKC1	darkgrey	VSMC_M8
GO:1902749	0.00	1.00	26	87	regulation of cell cycle G2/M phase transition	BP	8.6E-08	CDK2,FBXO5,RAD21,CDC25C,CLSPN,ORC1,RNASEH2B,CHFR,CDC25B,TOPBP1,CCNB1,CHEK1,KIF14,TICRR,DTL,BLM,CENPF,CDK1,CDC25A,BRCA1,CCNB3,CDC6,AURKB,PLK1,ATAD5,AURKA	darkgrey	VSMC_M8
GO:0022607	0.00	1.00	240	2230	cellular component assembly	BP	1E-07	TXNL4A,RTTN,CDK2,NUP107,CCT2,TUBB,DDX39B,FBXO5,EZR,TCP1,RAD21,TTLL1,KIFC1,FAM49B,HSPA9,SRPK1,KIF27,PSIP1,KIF24,VCP,HSP90AB1,COL1A2,CEP135,POLR1E,NCBP1,ANP32B,PPIH,MFSD2A,NUP205,ANLN,NUP62,PRMT1,SDC1,RUVBL2,PLK4,GRWD1,STIL,MCM2,CENPO,RUVBL1,SLC1A5,CHCHD4,CENPA,CDC42EP4,NASP,NUFIP1,PREB,NIFK,NUP85,MRPS7,DIAPH3,CDC20,TK1,NAP1L1,CHMP6,STRN,RRM1,ZNF703,SNRPF,RRP8,CCNB1,WDR62,SFSWAP,SNAI2,SNRPB,HAUS5,AAAS,TPX2,KIF2A,ATG101,EIF3M,STAG1,CENPJ,CENPK,HSP90B1,CEP89,KIF11,VAMP8,CENPH,KNTC1,HMGB2,ATF1,TERF1,HELLS,FHDC1,RACGAP1,CCT8,PPID,MIS18A,CFAP298,CKAP5,NUP93,KNL1,RAD51,MYBL2,MTDH,OIP5,NDUFAF1,REEP4,MDM4,CHAF1B,UBE2C,FASTKD3,NUP153,ICE1,GMNN,FP565260.1,SMC3,SF3B1,CENPE,TRIP13,CEP72,KIF14,PRMT5,ASPM,POLQ,IQCB1,RCC1,PRPF3,HJURP,EIF4H,IPO4,NEK2,PRC1,NF2,H2AFX,BLM,RBM14,CENPF,STRAP,EIF4G1,PSMC5,HAT1,CDK1,TFRC,PAK2,DHX9,NDUFS1,DDX20,DNA2,ZW10,KIF15,IFT80,SF1,EPHB2,SMARCAL1,CDC45,BRCA1,DNAJC9,HAUS3,DLGAP5,ECT2,DHX33,SUV39H1,HAUS8,FKBP4,SIX4,MNAT1,RAC1,EXO1,HNRNPU,INCENP,UBE2K,UGDH,FSCN1,CPSF7,BID,SMC1A,EIF2S1,EIF3B,PSMG3,ASF1B,SRSF5,CCNB2,SH3PXD2B,CCT3,KIF4A,FUS,AURKB,CIAO2A,KIF23,CENPI,GEMIN5,LRRC49,HAUS1,PLK1,BRIP1,EDC3,EIF5,SNRPD1,PSMD11,SEPT6,POLDIP2,NDE1,AIFM1,BRIX1,CEP76,HOOK1,MAP7D3,EMP2,RBMX,CHAF1A,NDC1,HAUS7,TFAP4,NOC2L,SF3A2,TP73,FANCA,CDT1,CENPN,SASS6,NEK6,DDX28,ACD,TPPP3,CTH,ARPC4,ARF6,RAPGEF6,USP4,HIST1H1A,CENPP,GEMIN4,GBP5,TMOD3,DDX23,ACSL3,ST	darkgrey	VSMC_M8
GO:0010389	0.00	1.00	25	82	regulation of G2/M transition of mitotic cell cycle	BP	1.1E-07	CDK2,FBXO5,RAD21,CDC25C,CLSPN,ORC1,RNASEH2B,CHFR,CDC25B,TOPBP1,CCNB1,CHEK1,KIF14,TICRR,DTL,BLM,CENPF,CDK1,CDC25A,BRCA1,CCNB3,CDC6,AURKB,PLK1,AURKA	darkgrey	VSMC_M8
GO:0070200	0.00	1.00	11	16	establishment of protein localization to telomere	BP	1.5E-07	CCT2,TCP1,CCT4,TERF1,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1,ACD	darkgrey	VSMC_M8
GO:0071826	0.00	1.00	37	170	ribonucleoprotein complex subunit organization	BP	1.5E-07	TXNL4A,DDX39B,SRPK1,PSIP1,VCP,HSP90AB1,NCBP1,RUVBL2,RUVBL1,NUFIP1,MRPS7,SNRPF,SFSWAP,SNRPB,EIF3M,FP565260.1,SF3B1,PRMT5,PRPF3,EIF4H,STRAP,DHX9,DDX20,SF1,CPSF7,EIF3B,SRSF5,GEMIN5,EIF5,SNRPD1,BRIX1,SF3A2,DDX28,USP4,GEMIN4,DDX23,ABT1	darkgrey	VSMC_M8
GO:0022618	0.00	1.00	36	163	ribonucleoprotein complex assembly	BP	1.6E-07	TXNL4A,DDX39B,SRPK1,PSIP1,HSP90AB1,NCBP1,RUVBL2,RUVBL1,NUFIP1,MRPS7,SNRPF,SFSWAP,SNRPB,EIF3M,FP565260.1,SF3B1,PRMT5,PRPF3,EIF4H,STRAP,DHX9,DDX20,SF1,CPSF7,EIF3B,SRSF5,GEMIN5,EIF5,SNRPD1,BRIX1,SF3A2,DDX28,USP4,GEMIN4,DDX23,ABT1	darkgrey	VSMC_M8

GO:0045132	0.00	1.00	23	73	meiotic chromosome segregation	BP	1.7E-07	RAD21,SMC2,TTK,FANCD2,SGO1,CHFR,ESPL1,BUB1,CCNE1,TERF1,BUB1B,CCNE2,TRIP13,SGO2,NUF2,FANCM,SMC4,PSMC3IP,TOP2A,PTTG1,PLK1,BRIP1,NDC1	darkgrey	VSMC_M8
GO:0015931	0.00	1.00	39	181	nucleobase-containing compound transport	BP	2E-07	XPOT,NUP43,NUP107,DDX39B,NUP50,SLC35D2,SRSF3,NCBP1,HNRNPA2B1,NUP205,NUP62,NUP85,SLC25A19,EIF4A3,ALYREF,AAAS,NUP160,CKAP5,NUP93,NUP153,NSUN2,KHDRBS1,MCM3AP,NUP133,SSB,SLC17A9,DHX9,HNRNPA3,SLBP,EIF5A,DDX39A,NUP62CL,SLC25A5,NDC1,SMG6,THOC6,NUP188,GLE1,SRSF7	darkgrey	VSMC_M8
GO:0031570	0.00	1.00	29	111	DNA integrity checkpoint signaling	BP	2.8E-07	CDK2,DDX39B,GTSE1,CDC5L,CLSPN,CASP2,ORC1,RNASEH2B,FANCD2,TOPBP1,E2F1,CHEK1,RAD9A,TICRR,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,CDK1,WDR76,DNA2,CDC45,BRCA1,CDC6,PLK1,BRIP1,CDT1	darkgrey	VSMC_M8
GO:0006333	0.00	1.00	28	106	chromatin assembly or disassembly	BP	2.9E-07	ANP32B,GRWD1,MCM2,NASP,SUPT16H,NAP1L1,RRP8,HMGB2,HELLS,MIS18A,OIP5,CHAF1B,HJURP,IPO4,H2AFX,HAT1,SMARCC1,DNAJC9,SUV39H1,SMARCE1,ASF1B,HIRIP3,CHAF1A,NOC2L,HIST1H1A,CENPP,CENPW,HIST1H2BB	darkgrey	VSMC_M8
GO:0034645	0.00	1.00	348	3533	cellular macromolecule biosynthetic process	BP	3.2E-07	CDK2,NARS,PRIM1,HNRNPAB,BCLAF1,MRPS18B,NUP107,CCT2,VARS2,DDX39B,FBXO5,VARS,EZR,TCP1,RAD21,DSCC1,NUS1,MAN1A1,ATAD2,PHF5A,ZNF367,PSIP1,RECQL4,TONSL,MCM5,PWP1,MRPL2,DBF4,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,TRIM28,POLR1E,NCBP1,TWISTNB,CDCA7L,HNRNPA2B1,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,NUP62,MMS22L,MRPL32,PHF19,PRMT1,ORC6,NAA15,ORC1,GEN1,RUVBL2,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,DNAJC2,PPP5C,FOSB,CD3EAP,NASP,COG3,NUFIP1,MRPL58,NIFK,NUP85,MRPS7,MCM10,ALG8,DBI,DIS3,SPHK1,MCM6,SRSF2,XRN2,NCAPG2,WDR43,TK1,BIRC5,POLR3F,RRBP1,POLD3,GTPBP4,SUPT16H,EIF4A3,NAP1L1,E2F7,GINS4,ALYREF,CKAP2,RRM1,PCNA,EXOSC8,POLE,ZNF703,RFC3,HGF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,MCM4,SNAI2,TCEA1,MRPS5,POLR1B,SGK3,EIF3M,CENPJ,NECAB3,EIF2B1,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,GALNT6,HMGB2,MSC,ATF1,SSRP1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,BAP1,EEF1E1,CHUK,RUNX1,PPP1R15B,HR,MDM4,CHAF1B,RFC5,RBMS1,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,STT3A,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,DDX5,XBP1,TICRR,RFC2,RPA2,EIF4H,NEK2,EWSR1,HINFP,DTL,BLM,RBM14,CENPF,STRAP,EIF4G1,MRPL11,PSMC5,CDK1,S100A11,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,PSMA6,POLA1,DDX2	darkgrey	VSMC_M8
GO:0009059	0.00	1.00	351	3569	macromolecule biosynthetic process	BP	3.2E-07	CDK2,NARS,PRIM1,HNRNPAB,BCLAF1,MRPS18B,NUP107,CCT2,VARS2,DDX39B,FBXO5,VARS,EZR,TCP1,RAD21,DSCC1,NUS1,MAN1A1,ATAD2,PHF5A,ZNF367,SLC35D2,PSIP1,RECQL4,TONSL,MCM5,PWP1,MRPL2,DBF4,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,TRIM28,POLR1E,NCBP1,TWISTNB,CDCA7L,HNRNPA2B1,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,NUP62,MMS22L,MRPL32,PHF19,PRMT1,ORC6,NAA15,ORC1,GEN1,RUVBL2,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,DNAJC2,PPP5C,FOSB,CD3EAP,NASP,COG3,NUFIP1,MRPL58,NIFK,NUP85,MRPS7,MCM10,ALG8,DBI,DIS3,SPHK1,MCM6,SRSF2,XRN2,NCAPG2,WDR43,TK1,BIRC5,POLR3F,RRBP1,POLD3,GTPBP4,SUPT16H,EIF4A3,NAP1L1,E2F7,GINS4,ALYREF,CKAP2,RRM1,PCNA,EXOSC8,POLE,ZNF703,RFC3,HGF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,MCM4,SNAI2,TCEA1,MRPS5,POLR1B,SGK3,EIF3M,CENPJ,NECAB3,EIF2B1,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,SLC10A7,GALNT6,HMGB2,MSC,ATF1,SSRP1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,BAP1,EEF1E1,CHUK,RUNX1,PPP1R15B,HR,MDM4,CHAF1B,RFC5,RBMS1,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,STT3A,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,DDX5,XBP1,TICRR,RFC2,RPA2,EIF4H,NEK2,EWSR1,HINFP,DTL,BLM,RBM14,CENPF,STRAP,EIF4G1,MRPL11,PSMC5,CDK1,S100A11,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,PSMA	darkgrey	VSMC_M8
GO:0090307	0.00	1.00	20	57	mitotic spindle assembly	BP	3.4E-07	KIFC1,CDC20,AAAS,TPX2,KIF2A,STAG1,KIF11,RACGAP1,MYBL2,SMC3,NEK2,PRC1,KIF15,HNRNPU,SMC1A,KIF4A,AURKB,KIF23,PLK1,POLDIP2	darkgrey	VSMC_M8
GO:1904869	0.00	1.00	9	11	regulation of protein localization to Cajal body	BP	3.6E-07	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:1904871	0.00	1.00	9	11	positive regulation of protein localization to Cajal body	BP	3.6E-07	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0031497	0.00	1.00	24	84	chromatin assembly	BP	5.7E-07	ANP32B,GRWD1,MCM2,NASP,NAP1L1,RRP8,HMGB2,HELLS,MIS18A,OIP5,CHAF1B,HJURP,IPO4,H2AFX,HAT1,DNAJC9,SUV39H1,ASF1B,CHAF1A,NOC2L,HIST1H1A,CENPP,CENPW,HIST1H2BB	darkgrey	VSMC_M8
GO:0070192	0.00	1.00	19	54	chromosome organization involved in meiotic cell cycle	BP	5.8E-07	RAD21,SMC2,FANCD2,SGO1,BUB1,CCNE1,TERF1,BUB1B,RAD51,CCNE2,NCAPD3,TRIP13,SGO2,SMC4,PSMC3IP,NCAPD2,INCENP,BRIP1,NDC1	darkgrey	VSMC_M8

GO:0033365	0.00	1.00	99	737	protein localization to organelle	BP	6.1E-07	NUP107,CCT2,EZR,TCP1,RAD21,NUP50,MAN1A1,MTBP,RANGAP1,TNPO3,BYSL,VCP,HSP90AB1,CENPQ,NOL8,TRIM28,TTK,CCT4,EZH2,NUP62,RUVBL2,STIL,SEC61A1,SAE1,CHCHD4,CENPA,COG3,TOMM40,NUP85,SRP68,IPO5,KIF20B,KNTC1,TRAM1,TERF1,ESCO2,CCT8,BUB1B,CCT7,GNL3,FAM83D,NUP93,KNL1,TOMM70,BAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,CEP72,CSE1L,RPA2,UTP25,IPO4,NUP133,NF2,SSB,BUB3,CDK1,TFRC,DHX9,ZW10,CDCA5,IFT80,BARD1,NMD3,ECT2,SIX4,MSX1,KDELR2,HNRNPU,NEDD4,BID,CCT3,LMNA,SPDL1,AURKB,COL1A1,ZWILCH,TIMM8A,PLK1,NUP62CL,TIMM44,NDC80,AIFM1,RPA1,HASPIN,DKC1,CDT1,EMC8,TOR1A,NUP188,ACD,ARF6,GBP5,SPCS3,AURKA,UBE2J2	darkgrey	VSMC_M8
GO:0071426	0.00	1.00	21	66	ribonucleoprotein complex export from nucleus	BP	6.9E-07	XPOT,NUP107,DDX39B,SRSF3,NCBP1,HNRNPA2B1,NUP85,ALYREF,ABCE1,NUP160,NUP93,NSUN2,MCM3AP,NUP133,SSB,LSG1,NMD3,DDX39A,SMG6,THOC6,GLE1	darkgrey	VSMC_M8
GO:0034728	0.00	1.00	26	97	nucleosome organization	BP	7E-07	ANP32B,GRWD1,MCM2,NASP,SUPT16H,NAP1L1,HMGB2,MIS18A,OIP5,CHAF1B,ANP32E,HJURP,MCM3AP,IPO4,H2AFX,HAT1,SMARCC1,DNAJC9,SMARCE1,ASF1B,CHAF1A,HIST1H1A,CENPP,CENPW,POLE3,HIST1H2BB	darkgrey	VSMC_M8
GO:0071166	0.00	1.00	21	67	ribonucleoprotein complex localization	BP	9.1E-07	XPOT,NUP107,DDX39B,SRSF3,NCBP1,HNRNPA2B1,NUP85,ALYREF,ABCE1,NUP160,NUP93,NSUN2,MCM3AP,NUP133,SSB,LSG1,NMD3,DDX39A,SMG6,THOC6,GLE1	darkgrey	VSMC_M8
GO:0051054	0.00	1.00	37	176	positive regulation of DNA metabolic process	BP	9.7E-07	CCT2,DDX39B,TCP1,DSCC1,HSP90AB1,TRIM28,HNRNPA2B1,CCT4,PCNA,RFC3,HGF,CCT8,CCT7,GNL3,RAD51,RFC5,CCT5,CCT6A,FANCB,RFC2,NEK2,H2AFX,TFRC,DHX9,RFC4,BRCA1,NSD2,RAD51AP1,FOXM1,CCT3,FUS,AURKB,CHTF18,DKC1,ACD,PRIM2,HNRNPD	darkgrey	VSMC_M8
GO:0010833	0.00	1.00	22	73	telomere maintenance via telomere lengthening	BP	1.1E-06	CCT2,TCP1,HSP90AB1,HNRNPA2B1,CCT4,TERF1,CCT8,CCT7,RAD51,DCLRE1B,CCT5,CCT6A,NEK2,HNRNPU,RFC1,EXOSC10,CCT3,AURKB,RPA1,SMG6,DKC1,ACD	darkgrey	VSMC_M8
GO:1903405	0.00	1.00	9	12	protein localization to nuclear body	BP	1.3E-06	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:1904867	0.00	1.00	9	12	protein localization to Cajal body	BP	1.3E-06	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0042770	0.00	1.00	34	155	signal transduction in response to DNA damage	BP	1.4E-06	CDK2,DDX39B,GTSE1,CDC5L,CLSPN,CASP2,RNASEH2B,FANCD2,E2F7,TOPBP1,SNAI2,CD44,E2F1,EEF1E1,MDM4,CHEK1,RAD9A,DDX5,TICRR,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,CDK1,WDR76,BRCA1,FOXM1,MSX1,BID,PLK1,BRIP1,TFAP4	darkgrey	VSMC_M8
GO:0090329	0.00	1.00	16	41	regulation of DNA-dependent DNA replication	BP	1.6E-06	FBXO5,DSCC1,DBF4,E2F7,PCNA,RFC3,E2F8,RFC5,GMNN,TICRR,RFC2,BLM,RFC4,SMARCAL1,CHTF18,CDT1	darkgrey	VSMC_M8
GO:0000281	0.00	1.00	20	63	mitotic cytokinesis	BP	1.8E-06	KIF20A,ANLN,NUP62,CENPA,CHMP6,CKAP2,ESPL1,KIF20B,CEP55,RACGAP1,NUSAP1,CIT,ECT2,INCENP,KIF4A,KIF23,PLK1,SEPT6,POLDIP2,STMN1	darkgrey	VSMC_M8
GO:0008152	0.00	1.00	716	8467	metabolic process	BP	2.3E-06	TXNL4A,CDK2,ALPK2,NARS,ATP5F1B,PRIM1,HNRNPAB,MTFR2,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,CCT2,VARS2,POP1,TCF19,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,PANX2,TCP1,RAD21,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,ATAD2,DESI1,PHF5A,FAM49B,ZNF367,SLC35D2,CDC25C,HSPA9,FKBP5,MATR3,SRPK1,SRSF3,GCAT,CYC1,PSIP1,RECQL4,BYSL,TONSL,MCM5,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,POLR1C,UBAP2,TJP2,POLH,ALDH1L2,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,COL1A2,CKS2,MCM3,PAICS,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,NANS,TWISTNB,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,CTPS1,TTK,CYCS,HNRNPA2B1,GRSF1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,SMC6,ORC1,GEN1,NRDC,RUVBL2,PLK4,AMD1,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,SAE1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,NAALAD2,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,NASP,COG3,NUFIP1,GRIN2C,PRCP,MRPL58,NIFK,SMG9,NUP85,PLAUR,MRPS7,MCM10,SLC25A19,CAD,ALG8,DBI,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,AXL,RNF157,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM17,ULK4,NCAPG2,WDR43,CDC20,TK1,AFMID,BIRC5,PGS1,SERPINH1,PARP2,FBL,POLR3F,RRBP1,POLD3,SNRPB2,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,GINS4,PCCA,ALYREF,CKAP2,RRM1,DUS1L,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,POLE,ZNF703,RFC3,NOC4L,DDX51,MAK16,METAP2,DCUN1D2,HGF,SNRPF,TOPBP1,ELK3,PSMD13,RRP8,CDC16,TCE	darkgrey	VSMC_M8
GO:0033043	0.00	1.00	118	950	regulation of organelle organization	BP	2.4E-06	TMED9,CCT2,FBXO5,EZR,TCP1,RAD21,MTBP,FAM49B,CDC25C,CEP135,TRIM28,TTK,HNRNPA2B1,CCT4,NUP62,GEN1,SDC1,PLK4,STIL,MCM2,CDC42EP4,PREB,PLAUR,BORA,SPHK1,CDC20,ARHGDIA,CKAP2,CHFR,PGAM5,HGF,CDC16,CCNB1,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,SKA3,CENPJ,KNTC1,TERF1,CCT8,BUB1B,CCT7,CDCA2,GNL3,CKAP5,NUSAP1,UBE2C,CCT5,CCT6A,KIF18A,CHEK1,RASSF1,CENPE,TRIP13,PRMT5,RCC1,NEK2,NF2,PDE3A,RBM14,CENPF,BUB3,TFRC,PAK2,MKI67,ZW10,CDCA5,KIF15,BRCA1,TACC3,DLGAP5,RAD51AP1,ECT2,ZWINT,FKBP4,MNAT1,MSX1,RAC1,HNRNPU,FSCN1,TOP2A,CDC6,BID,PRELID1,IQGAP3,EXOSC10,NES,CCT3,LMNA,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,SYT4,DNMT1,SLC25A5,NDC80,CEP76,SMG6,PKMYT1,CCNF,DKC1,CDT1,NEK6,ACD,ARPC4,ARF6,TMOD3,HNRNPD,MAD2L1,STMN1,AURKA,FEN1,PID1	darkgrey	VSMC_M8
GO:0070199	0.00	1.00	12	24	establishment of protein localization to chromosome	BP	3.4E-06	CCT2,TCP1,CCT4,RUVBL2,TERF1,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1,ACD	darkgrey	VSMC_M8
GO:0007076	0.00	1.00	10	16	mitotic chromosome condensation	BP	3.7E-06	SMC2,NCAPH,NUSAP1,NCAPD3,TENT4A,CDCA5,SMC4,NCAPD2,NCAPG,PLK1	darkgrey	VSMC_M8

GO:0009987	0.00	1.00	934	11676	cellular process	BP	4.9E-06	TXNL4A,RTTN,CDK2,ALPK2,NARS,ATP5F1B,PRIM1,TMED9,HNRNPAB,MTFR2,BCLAF1,ABRACL,METTL1,HNRNPH1,XPOT,NUP43,MRPS18B,NUP107,CCT2,TUBB,VARS2,POP1,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,FBN2,PANX2,TCP1,GTSE1,RAD21,NUP50,DSCC1,TTLL1,NUS1,ARFGAP3,MAN1A1,MTBP,KIFC1,ATAD2,DESI1,PHF5A,FAM49B,RANGAP1,KIF20A,ZNF367,SLC35D2,CDC25C,HSPA9,CHCHD3,FKBP5,SRPK1,SRSF3,KIF27,GCAT,CYC1,TNPO3,PSIP1,RECQL4,CEP78,BYSL,TONSL,MCM5,HMGXB4,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,STEAP1,POLR1C,TJP2,KIF24,POLH,ALDH1L2,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,COL1A2,ARHGEF39,CENPQ,CEP135,CKS2,MCM3,PAICS,MIOS,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,NANS,TWISTNB,PPIH,U2AF2,PPP6R1,SMC2,MSH6,CDCA7L,CTPS1,TTK,CYCS,HNRNPA2B1,GRSF1,CLEC11A,DCK,POLD1,HOXA5,COL9A2,DNAJC25,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,SLC31A1,NUP205,ANLN,CDCA8,GNL2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,GJB3,CASP2,NBAS,ORC6,SHCBP1,NAA15,SMC6,ORC1,GEN1,NRDC,SDC1,RUVBL2,PLK4,AMD1,PGR,NAMPT,GRWD1,STIL,PUS7,LIG1,MCM2,CENPO,SEC61A1,RUVBL1,CCNA2,AMOTL1,RPN1,SAE1,SLC1A5,DNAJC2,RAD54L,CHORDC1,RNASEH2B,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,CENPA,CDC42EP4,NASP,COG3,NUFIP1,GRIN2C,TOMM40,PRCP,TMEM214,PREB,MRPL58,NIFK,KCNN4,SMG9,NUP85,PLAUR,MRPS7,MCM10,SLC25A19,CAD,KIF2C,SLC5A6,ALG8,DBI,DIAPH3,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,SRP68,AXL,RNF157,SPHK1,SNRPA,MCM6,SRSF2,FANCD2,XRN2,RBM	darkgrey	VSMC_M8
GO:0006334	0.00	1.00	20	68	nucleosome assembly	BP	5.4E-06	ANP32B,GRWD1,MCM2,NASP,NAP1L1,HMGB2,MIS18A,OIP5,CHAF1B,HJURP,IPO4,H2AFX,HAT1,DNAJC9,ASF1B,CHAF1A,HIST1H1A,CENPP,CENPW,HIST1H2BB	darkgrey	VSMC_M8
GO:0006997	0.00	1.00	27	112	nucleus organization	BP	5.7E-06	NUP107,SRPK1,NUP205,CHMP6,RRP8,USPL1,POLR1B,HMGB2,NUP93,REEP4,NOLC1,NUP153,ETS1,CHEK1,RCC1,PITPNB,NUP133,CDK1,SF1,SUV39H1,LMNA,PLK1,VRK1,SERBP1,NDC1,TOR1A,NEK6	darkgrey	VSMC_M8
GO:0006325	0.00	1.00	50	301	chromatin organization	BP	6.4E-06	ATAD2,SRPK1,TRIM28,ANP32B,EZH2,PHF19,RUVBL2,GRWD1,MCM2,RUVBL1,DNAJC2,NASP,SUPT16H,NAP1L1,RRP8,HMGB2,SSRP1,HELLS,RBL1,MIS18A,OIP5,CHAF1B,HMGN1,NUCKS1,DEK,CHD1L,ANP32E,HJURP,MCM3AP,IPO4,H2AFX,HAT1,SMARCC1,MKI67,DNAJC9,SUV39H1,HNRNPU,SMARCE1,ASF1B,HIRIP3,DNMT1,TADA2A,CHAF1A,NOC2L,HIST1H1A,CENPP,CENPW,POLE3,HIST1H2BB,MBD2	darkgrey	VSMC_M8
GO:1900262	0.00	1.00	7	8	regulation of DNA-directed DNA polymerase activity	BP	7.8E-06	DSCC1,PCNA,RFC3,RFC5,RFC2,RFC4,CHTF18	darkgrey	VSMC_M8
GO:1900264	0.00	1.00	7	8	positive regulation of DNA-directed DNA polymerase activity	BP	7.8E-06	DSCC1,PCNA,RFC3,RFC5,RFC2,RFC4,CHTF18	darkgrey	VSMC_M8
GO:1990173	0.00	1.00	9	14	protein localization to nucleoplasm	BP	8.2E-06	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT6A,CCT3,DKC1	darkgrey	VSMC_M8
GO:0007004	0.00	1.00	19	63	telomere maintenance via telomerase	BP	1E-05	CCT2,TCP1,HSP90AB1,CCT4,TERF1,CCT8,CCT7,CCT5,CCT6A,NEK2,HNRNPU,RFC1,EXOSC10,CCT3,AURKB,RPA1,SMG6,DKC1,ACD	darkgrey	VSMC_M8
GO:1904029	0.00	1.00	22	83	regulation of cyclin-dependent protein kinase activity	BP	1.2E-05	CDC25C,HSP90AB1,CKS2,CCNA2,GTPBP4,IPO5,CCNB1,CCNE1,CCNL1,CCNE2,BLM,CDC25A,CDKN3,MNAT1,CCNB3,CDC6,CCNB2,PLK1,TFAP4,PKMYT1,CCNF,CDKN2C	darkgrey	VSMC_M8
GO:1902969	0.00	1.00	9	14	mitotic DNA replication	BP	1.2E-05	MCM3,LIG1,MCM2,MCM6,MCM4,RAD51,POLA1,CDC45,GINS1	darkgrey	VSMC_M8
GO:0034504	0.00	1.00	43	244	protein localization to nucleus	BP	1.3E-05	NUP107,CCT2,TCP1,NUP50,RANGAP1,TNPO3,BYSL,HSP90AB1,NOL8,TRIM28,CCT4,NUP62,NUP85,IPO5,CCT8,CCT7,NUP93,HEATR3,NOLC1,CCT5,NUP153,CCT6A,CSE1L,UTP25,IPO4,NUP133,NF2,CDK1,TFRC,BARD1,NMD3,ECT2,SIX4,MSX1,HNRNPU,CCT3,LMNA,COL1A1,PLK1,NUP62CL,DKC1,TOR1A,NUP188	darkgrey	VSMC_M8
GO:0000727	0.00	1.00	8	11	double-strand break repair via break-induced replication	BP	1.3E-05	MCM5,MCM3,MCM2,MCM6,GINS4,MCM4,CDC45,MCM7	darkgrey	VSMC_M8
GO:0006278	0.00	1.00	19	64	RNA-dependent DNA biosynthetic process	BP	1.3E-05	CCT2,TCP1,HSP90AB1,CCT4,TERF1,CCT8,CCT7,CCT5,CCT6A,NEK2,HNRNPU,RFC1,EXOSC10,CCT3,AURKB,RPA1,SMG6,DKC1,ACD	darkgrey	VSMC_M8
GO:0051298	0.00	1.00	19	64	centrosome duplication	BP	1.6E-05	RTTN,CDK2,CEP135,NUP62,GEN1,PLK4,STIL,CHORDC1,WDR62,CENPJ,CKAP5,CEP72,RBM14,BRCA1,NDC80,NDE1,CEP76,CCNF,SASS6	darkgrey	VSMC_M8
GO:0043484	0.00	1.00	28	126	regulation of RNA splicing	BP	2E-05	HNRNPH1,SRPK1,SRSF3,NCBP1,U2AF2,GRSF1,THRAP3,SRSF2,SFSWAP,HNRNPF,RBM12,KHDRBS1,NCL,RBM23,SF3B4,DDX5,TRA2B,HNRNPH3,SF1,RBM3,HNRNPU,SRSF5,FUS,RBMX,RNPS1,DAZAP1,PTBP1,SRSF7	darkgrey	VSMC_M8
GO:2001252	0.00	1.00	20	72	positive regulation of chromosome organization	BP	2.2E-05	CCT2,TCP1,RAD21,TRIM28,HNRNPA2B1,CCT4,CCT8,CCT7,GNL3,CCT5,CCT6A,NEK2,CCT3,AURKB,DNMT1,DKC1,CDT1,ACD,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0000076	0.00	1.00	9	15	DNA replication checkpoint signaling	BP	2.3E-05	CLSPN,ORC1,TOPBP1,RAD9A,TICRR,DNA2,CDC45,CDC6,CDT1	darkgrey	VSMC_M8
GO:0000079	0.00	1.00	21	80	regulation of cyclin-dependent protein serine/threonine kinase activity	BP	2.5E-05	CDC25C,CKS2,CCNA2,GTPBP4,IPO5,CCNB1,CCNE1,CCNL1,CCNE2,BLM,CDC25A,CDKN3,MNAT1,CCNB3,CDC6,CCNB2,PLK1,TFAP4,PKMYT1,CCNF,CDKN2C	darkgrey	VSMC_M8

GO:0016070	0.00	1.00	327	3480	RNA metabolic process	BP	3.1E-05	TXNL4A,NARS,PRIM1,HNRNPAB,BCLAF1,METTL1,HNRNPH1,NUP107,VARS2,POP1,DDX39B,SRFBP1,VARS,EZR,RAD21,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,BYSL,PWP1,POLR3B,POLR1C,CDC5L,CKS2,NOL8,TRIM28,POLR1E,NCBP1,THADA,TWISTNB,PPIH,U2AF2,CDCA7L,HNRNPA2B1,GRSF1,HOXA5,SYNCRIP,PPIE,PABPC4,GARS,THRAP3,EZH2,NUP62,NOL10,PHF19,PRMT1,NBAS,NAA15,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,DNAJC2,RNASEH2B,PPP5C,WDR33,FOSB,CD3EAP,NUFIP1,NIFK,SMG9,NUP85,DDX18,TSEN2,DIS3,HNRNPUL1,SPHK1,SNRPA,SRSF2,XRN2,RBM17,NCAPG2,WDR43,BIRC5,FBL,POLR3F,SNRPB2,GTPBP4,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,DUS1L,PCNA,EXOSC8,ZNF703,NOC4L,DDX51,MAK16,HGF,SNRPF,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,HNRNPF,POLR1B,CWC27,SGK3,WDR36,CENPJ,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,RBM12,LOXL3,HEY1,ZBTB10,PPID,RBL1,CTNNBL1,CCNL1,RSRC1,GNL3,EXOSC1,RBM19,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,CWF19L1,HR,MDM4,WDR3,RBMS1,NCOA5,PPRC1,HMGN1,RRP9,NOLC1,FASTKD3,NUCKS1,DEK,GCN1,METTL15,ETS1,TENT4A,NSUN2,PHC2,ICE1,MPHOSPH10,GMNN,CHEK1,SNRPA1,U2AF1,H2AFZ,RRP1,FP565260.1,KHDRBS1,SF3B1,TRIP13,NCL,TRAIP,SNRNP40,RBM23,PRMT5,DDX27,NOL11,TARBP1,SF3B4,DDX5,PRPF3,XBP1,UTP25,EWSR1,INTS7,HINFP,BLM,RBM14,SSB,NOP58,CENPF,STRAP,PSMC5,TFRC,SF3B2,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,PSMA6,HNRNPA3,POLA1,HNRNPH3,DDX20,AP000944.2,DNA2,DDX21,PNN,EFTUD2,DGCR	darkgrey	VSMC_M8
GO:0051382	0.00	1.00	9	16	kinetochore assembly	BP	3.4E-05	CENPA,CENPK,CENPH,KNTC1,CENPE,CENPF,DLGAP5,CENPN,CENPW	darkgrey	VSMC_M8
GO:0010639	0.00	1.00	48	297	negative regulation of organelle organization	BP	3.6E-05	FBXO5,RAD21,MTBP,FAM49B,TTK,GEN1,MCM2,CKAP2,HGF,CCNB1,ESPL1,BUB1,TPX2,KNTC1,TERF1,BUB1B,CHEK1,TRIP13,RBM14,CENPF,BUB3,TFRC,PAK2,ZW10,BRCA1,ZWINT,FKBP4,MNAT1,HNRNPU,TOP2A,PRELID1,EXOSC10,LMNA,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,SYT4,SLC25A5,NDC80,SMG6,CCNF,CDT1,ACD,TMOD3,MAD2L1,STMN1	darkgrey	VSMC_M8
GO:0032210	0.00	1.00	16	50	regulation of telomere maintenance via telomerase	BP	4E-05	CCT2,TCP1,CCT4,TERF1,CCT8,CCT7,CCT5,CCT6A,NEK2,HNRNPU,EXOSC10,CCT3,AURKB,SMG6,DKC1,ACD	darkgrey	VSMC_M8
GO:0070198	0.00	1.00	12	29	protein localization to chromosome, telomeric region	BP	4.5E-05	CCT2,TCP1,CCT4,TERF1,CCT8,CCT7,GNL3,CCT5,CCT6A,CCT3,DKC1,ACD	darkgrey	VSMC_M8
GO:1904356	0.00	1.00	17	57	regulation of telomere maintenance via telomere lengthening	BP	5.1E-05	CCT2,TCP1,HNRNPA2B1,CCT4,TERF1,CCT8,CCT7,CCT5,CCT6A,NEK2,HNRNPU,EXOSC10,CCT3,AURKB,SMG6,DKC1,ACD	darkgrey	VSMC_M8
GO:0000910	0.00	1.00	29	141	cytokinesis	BP	5.2E-05	KIF20A,ANLN,NUP62,PLK4,CENPA,CHMP6,E2F7,CKAP2,CDC25B,ESPL1,KIF20B,CEP55,RACGAP1,E2F8,NUSAP1,CIT,KIF14,PRC1,ECT2,INCENP,CDC6,KIF4A,AURKB,KIF23,PLK1,SEPT6,POLDIP2,STMN1,AURKA	darkgrey	VSMC_M8
GO:0031055	0.00	1.00	7	10	chromatin remodeling at centromere	BP	5.8E-05	NASP,HELLS,MIS18A,OIP5,HJURP,CENPP,CENPW	darkgrey	VSMC_M8
GO:1904358	0.00	1.00	13	35	positive regulation of telomere maintenance via telomere lengthening	BP	5.9E-05	CCT2,TCP1,HNRNPA2B1,CCT4,CCT8,CCT7,CCT5,CCT6A,NEK2,CCT3,AURKB,DKC1,ACD	darkgrey	VSMC_M8
GO:0034080	0.00	1.00	6	7	CENP-A containing nucleosome assembly	BP	6.2E-05	NASP,MIS18A,OIP5,HJURP,CENPP,CENPW	darkgrey	VSMC_M8
GO:0061641	0.00	1.00	6	7	CENP-A containing chromatin organization	BP	6.2E-05	NASP,MIS18A,OIP5,HJURP,CENPP,CENPW	darkgrey	VSMC_M8
GO:0060255	0.00	1.00	410	4468	regulation of macromolecule metabolic process	BP	6.6E-05	CDK2,ALPK2,HNRNPAB,BCLAF1,HNRNPH1,NUP107,CCT2,TCF19,DDX39B,FBXO5,PRRC1,EZR,PANX2,TCP1,RAD21,DSCC1,MTBP,ATAD2,DESI1,PHF5A,FAM49B,ZNF367,CDC25C,MATR3,SRPK1,SRSF3,PSIP1,PPP2R5D,PWP1,DBF4,POLR3B,UBAP2,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,THRAP3,EZH2,ODC1,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,NRDC,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,SAE1,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,MAST2,FOSB,NUFIP1,GRIN2C,SMG9,NUP85,PLAUR,DBI,BORA,DIS3,AXL,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,CDC20,BIRC5,SERPINH1,POLR3F,GTPBP4,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,TCEA1,HNRNPF,TPX2,UBA2,PARPBP,SGK3,CENPJ,HSP90B1,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,RBP4,MSC,ATF1,TERF1,HELLS,NRIP1,UTP15,RBM12,LOXL3,PBK,ESCO2,HEY1,ZBTB10,SELENOT,FAM98B,CCT8,PPID,RBL1,MSH3,MIS18A,CCT7,CCNL1,HNRNPDL,CDCA2,GNL3,FAM83D,TBX3,RAD51,CREB3L1,TOMM70,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,SETD4,PPP1R15B,HR,MDM4,UBE2C,RFC5,PSMD14,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,CENPE,TRIP13,NCL,TRAIP,KIF14,RBM23,PRMT5,POLQ,NOL11,TARBP1,SF3B4,FANCI,MNDA,DDX5,FANCB,XBP1,TICRR,RFC2,RPA2,SPP2,EI	darkgrey	VSMC_M8
GO:0000077	0.00	1.00	24	105	DNA damage checkpoint signaling	BP	6.8E-05	CDK2,DDX39B,GTSE1,CDC5L,CLSPN,CASP2,RNASEH2B,FANCD2,TOPBP1,E2F1,CHEK1,RAD9A,TICRR,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,CDK1,WDR76,BRCA1,PLK1,BRIP1	darkgrey	VSMC_M8
GO:0045005	0.00	1.00	14	41	DNA-dependent DNA replication maintenance of fidelity	BP	7.6E-05	TONSL,POLD1,MMS22L,GEN1,ALYREF,PCNA,POLE,RAD51,NUCKS1,TRAIP,BLM,DNA2,FANCM,SMARCAL1	darkgrey	VSMC_M8
GO:0007100	0.00	1.00	8	13	mitotic centrosome separation	BP	7.7E-05	NUP62,KIF11,CHEK1,NEK2,CEP85,RANBP1,NDE1,AURKA	darkgrey	VSMC_M8
GO:0006406	0.00	1.00	16	53	mRNA export from nucleus	BP	7.8E-05	NUP107,DDX39B,SRSF3,NCBP1,HNRNPA2B1,NUP85,ALYREF,NUP160,NUP93,NSUN2,MCM3AP,NUP133,DDX39A,SMG6,THOC6,GLE1	darkgrey	VSMC_M8
GO:0071427	0.00	1.00	16	53	mRNA-containing ribonucleoprotein complex export from nucleus	BP	7.8E-05	NUP107,DDX39B,SRSF3,NCBP1,HNRNPA2B1,NUP85,ALYREF,NUP160,NUP93,NSUN2,MCM3AP,NUP133,DDX39A,SMG6,THOC6,GLE1	darkgrey	VSMC_M8

GO:0007010	0.00	1.00	134	1177	cytoskeleton organization	BP	7.8E-05	RTTN,CDK2,TUBB,FBXO5,EZR,TTLL1,KIFC1,FAM49B,KIF20A,KIF24,VCP,CEP135,TTK,ANLN,NUP62,GEN1,PLK4,STIL,AMOTL1,CHORDC1,MAST2,CENPA,CDC42EP4,KIF2C,DIAPH3,BORA,ULK4,CDC20,SGO1,ARHGDIA,CKAP2,SIPA1L3,CCNB1,WDR62,GAS2L3,HAUS5,AAAS,ESPL1,TPX2,SKA3,KIF2A,STAG1,CENPJ,WEE1,HSP90B1,KIF11,CENPH,FHDC1,RACGAP1,FMNL3,TUBA1B,TUBA4B,CKAP5,KNSTRN,MYBL2,NUSAP1,CIT,KIF18A,CHEK1,RASSF1,NAV1,SMC3,CENPE,CEP72,ASPM,EFS,RCC1,PHACTR4,SPC25,NEK2,PRC1,NF2,RBM14,CEP85,AUNIP,CDK1,PAK2,NUF2,ZW10,KIF18B,KIF15,RANBP1,BRCA1,FRMD6,HAUS3,TACC3,DLGAP5,ECT2,HAUS8,FKBP4,SIX4,RAC1,MYO5A,HNRNPU,INCENP,FSCN1,SMC1A,CCNB2,IQGAP3,NES,KIF4A,LMNA,SPDL1,AURKB,TPM3,KIF23,LRRC49,HAUS1,PLK1,NDC80,POLDIP2,MTCL1,NDE1,TUBB6,CEP76,HOOK1,MAP7D3,EMP2,HAUS7,CCNF,TUBB4B,TOR1A,SASS6,ODF2,BCAR1,NEK6,RANBP10,TPPP3,ARPC4,ARF6,TMOD3,MAD2L1,STMN1,AURKA	darkgrey	VSMC_M8
GO:0051988	0.00	1.00	7	10	regulation of attachment of spindle microtubules to kinetochore	BP	8.5E-05	CCNB1,RACGAP1,KNSTRN,NEK2,ECT2,HNRNPU,AURKB	darkgrey	VSMC_M8
GO:0032465	0.00	1.00	19	72	regulation of cytokinesis	BP	8.9E-05	KIF20A,NUP62,PLK4,E2F7,CDC25B,KIF20B,RACGAP1,E2F8,CIT,KIF14,PRC1,ECT2,INCENP,CDC6,AURKB,KIF23,PLK1,POLDIP2,AURKA	darkgrey	VSMC_M8
GO:0048024	0.00	1.00	21	85	regulation of mRNA splicing, via spliceosome	BP	8.9E-05	SRPK1,SRSF3,NCBP1,U2AF2,THRAP3,SRSF2,SFSWAP,KHDRBS1,NCL,RBM23,SF3B4,DDX5,TRA2B,SF1,RBM3,HNRNPU,RBMX,RNPS1,DAZAP1,PTBP1,SRSF7	darkgrey	VSMC_M8
GO:0061640	0.00	1.00	21	87	cytoskeleton-dependent cytokinesis	BP	0.0001	KIF20A,ANLN,NUP62,CENPA,CHMP6,CKAP2,ESPL1,KIF20B,CEP55,RACGAP1,NUSAP1,CIT,ECT2,INCENP,KIF4A,AURKB,KIF23,PLK1,SEPT6,POLDIP2,STMN1	darkgrey	VSMC_M8
GO:0000731	0.00	1.00	11	26	DNA synthesis involved in DNA repair	BP	0.0001	POLH,VCP,POLD1,POLD3,PCNA,POLE,RFC3,DTL,POLA1,C17orf53,POLDIP2	darkgrey	VSMC_M8
GO:0032206	0.00	1.00	15	48	positive regulation of telomere maintenance	BP	0.00011	CCT2,TCP1,HNRNPA2B1,CCT4,CCT8,CCT7,GNL3,CCT5,CCT6A,NEK2,CCT3,AURKB,DKC1,ACD,HNRNPD	darkgrey	VSMC_M8
GO:0032467	0.00	1.00	11	27	positive regulation of cytokinesis	BP	0.00012	NUP62,CDC25B,KIF20B,RACGAP1,CIT,KIF14,ECT2,CDC6,AURKB,KIF23,POLDIP2	darkgrey	VSMC_M8
GO:0032212	0.00	1.00	12	32	positive regulation of telomere maintenance via telomerase	BP	0.00012	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT6A,NEK2,CCT3,AURKB,DKC1,ACD	darkgrey	VSMC_M8
GO:0032204	0.00	1.00	19	74	regulation of telomere maintenance	BP	0.00014	CCT2,TCP1,HNRNPA2B1,CCT4,TERF1,CCT8,CCT7,GNL3,CCT5,CCT6A,NEK2,HNRNPU,EXOSC10,CCT3,AURKB,SMG6,DKC1,ACD,HNRNPD	darkgrey	VSMC_M8
GO:0051299	0.00	1.00	8	14	centrosome separation	BP	0.00016	NUP62,KIF11,CHEK1,NEK2,CEP85,RANBP1,NDE1,AURKA	darkgrey	VSMC_M8
GO:0007099	0.00	1.00	13	37	centriole replication	BP	0.00016	RTTN,CDK2,CEP135,NUP62,PLK4,STIL,WDR62,CENPJ,CEP72,RBM14,BRCA1,CEP76,SASS6	darkgrey	VSMC_M8
GO:0006338	0.00	1.00	32	175	chromatin remodeling	BP	0.00017	ANP32B,RUVBL2,GRWD1,MCM2,RUVBL1,NASP,SUPT16H,NAP1L1,HMGB2,HELLS,MIS18A,OIP5,CHAF1B,CHD1L,ANP32E,HJURP,MCM3AP,IPO4,H2AFX,HAT1,SMARCC1,DNAJC9,SMARCE1,ASF1B,TADA2A,CHAF1A,HIST1H1A,CENPP,CENPW,POLE3,HIST1H2BB,MBD2	darkgrey	VSMC_M8
GO:0010467	0.00	1.00	401	4455	gene expression	BP	0.0002	TXNL4A,CDK2,ALPK2,NARS,HNRNPAB,BCLAF1,METTL1,HNRNPH1,MRPS18B,NUP107,VARS2,POP1,TCF19,DDX39B,SRFBP1,VARS,EZR,PANX2,RAD21,ATAD2,PHF5A,FAM49B,ZNF367,MATR3,SRPK1,SRSF3,PSIP1,BYSL,PWP1,MRPL2,POLR3B,POLR1C,UBAP2,HSP90AB1,CDC5L,PUM3,CKS2,NOL8,TRIM28,POLR1E,NCBP1,THADA,TWISTNB,PPIH,U2AF2,MSH6,CDCA7L,HNRNPA2B1,GRSF1,HOXA5,SYNCRIP,PPIE,PABPC4,GARS,THRAP3,EZH2,NUP62,NOL10,MRPL32,PHF19,PRMT1,CASP2,NBAS,NAA15,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,DNAJC2,RNASEH2B,PPP5C,WDR33,MAST2,CHCHD4,FOSB,CD3EAP,NUFIP1,MRPL58,NIFK,SMG9,NUP85,MRPS7,DDX18,TSEN2,DIS3,HNRNPUL1,AXL,SPHK1,SNRPA,SRSF2,XRN2,RBM17,NCAPG2,WDR43,BIRC5,SERPINH1,FBL,POLR3F,RRBP1,SNRPB2,GTPBP4,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,DUS1L,PCNA,EXOSC8,ZNF703,NOC4L,DDX51,MAK16,METAP2,HGF,SNRPF,ELK3,RRP8,TCERG1,USPL1,CBX5,CCNB1,SFSWAP,SNAI2,NOP56,SNRPB,UTP20,TCEA1,MRPS5,HNRNPF,POLR1B,CWC27,SGK3,EIF3M,WDR36,CENPJ,EIF2B1,E2F1,SNRNP35,DBR1,ABCE1,CCNE1,ZNF827,HMGB2,RBP4,MSC,ATF1,HELLS,NRIP1,UTP15,RBM12,NUP160,LOXL3,HEY1,ZBTB10,SELENOT,FAM98B,PPID,RBL1,MSH3,CTNBL1,CCNL1,RSRC1,HNRNPDL,GNL3,EXOSC1,NUP93,RBM19,TBX3,CREB3L1,TOMM70,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,EEF1E1,CHUK,RUNX1,SETD4,CWF19L1,PPP1R15B,HR,MDM4,WDR3,RBMS1,NCOA5,PPRC1,HMGN1,RRP9,NOLC1,FASTKD3,NUCKS1,DEK,GCN1,METTL15,ETS1,METAP1,TENT4A,NSUN2,PHC2,ICE1,MPHOSPH10,GMNN,CHEK1,SNRPA1,U2AF1,H2AFZ,RRP1,FP565260.1,NAA50,KHDRBS1,SF3B1,TRIP12,NCL,TRNP,UNC,5NPNP49,PPM32,PPMT5,PPY7,P	darkgrey	VSMC_M8
GO:0051984	0.00	1.00	7	11	positive regulation of chromosome segregation	BP	0.0002	SMC6,RAD18,CCNB1,HNRNPU,CDC6,AURKB,CDT1	darkgrey	VSMC_M8
GO:0050684	0.00	1.00	25	118	regulation of mRNA processing	BP	0.0002	SRPK1,SRSF3,NCBP1,U2AF2,THRAP3,SRSF2,CCNB1,SFSWAP,KHDRBS1,NCL,RBM23,SF3B4,DDX5,DHX9,TRA2B,SF1,BARD1,RBM3,HNRNPU,CPSF7,RBMX,RNPS1,DAZAP1,PTBP1,SRSF7	darkgrey	VSMC_M8
GO:1901989	0.00	1.00	21	91	positive regulation of cell cycle phase transition	BP	0.00021	DDX39B,FBXO5,MTBP,CDC25C,EZH2,CDC25B,CDC16,CCNB1,ESPL1,FAM83D,UBE2C,DTL,EIF4G1,CDK1,CDC25A,CDCA5,DLGAP5,CDC6,ATAD5,CDT1,TMOD3	darkgrey	VSMC_M8

GO:1901576	0.00	1.00	395	4324	organic substance biosynthetic process	BP	0.00023	CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,MRPS18B,NUP107,CCT2,VARS2,DDX39B,FBXO5,VARS,EZR,TCP1,RAD21,DSCC1,NUS1,MAN1A1,ATAD2,PHF5A,ZNF367,SLC35D2,PSIP1,RECQL4,TONSL,MCM5,PWP1,MRPL2,DBF4,POLR3B,POLR1C,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,TRIM28,POLR1E,NCBP1,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,MMS22L,MRPL32,PHF19,PRMT1,ORC6,NAA15,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,DNAJC2,PPP5C,FOSB,CD3EAP,NASP,COG3,NUFIP1,MRPL58,NIFK,NUP85,MRPS7,MCM10,CAD,ALG8,DBI,DIS3,SPHK1,MCM6,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,PGS1,POLR3F,RRBP1,POLD3,GTPBP4,SUPT16H,EIF4A3,NAP1L1,E2F7,GINS4,ALYREF,CKAP2,RRM1,PCNA,EXOSC8,POLE,ZNF703,RFC3,HGF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,MCM4,SNAI2,TCEA1,MRPS5,POLR1B,PDHB,SGK3,EIF3M,CENPJ,NECAB3,EIF2B1,E2F1,PPIP5K2,ABCE1,CCNE1,PXYLP1,ZNF827,SLC10A7,GALNT6,HMGB2,RBP4,MSC,ATF1,SSRP1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,AGPAT5,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,EEF1E1,CHUK,RUNX1,PPP1R15B,HR,MDM4,CHAF1B,RFC5,RBMS1,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,STT3A,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,BCAT1,NOL11,TARBP1,ELOVL6,DDX5,XBP1,TICRR,RFC2,RPA2,EI	darkgrey	VSMC_M8
GO:0009058	0.00	1.00	400	4393	biosynthetic process	BP	0.00029	CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,MRPS18B,NUP107,CCT2,VARS2,DDX39B,FBXO5,VARS,EZR,TCP1,RAD21,DSCC1,NUS1,MAN1A1,ATAD2,PHF5A,ZNF367,SLC35D2,GCAT,PSIP1,RECQL4,TONSL,MCM5,PWP1,MRPL2,DBF4,POLR3B,POLR1C,POLH,ALDH1L2,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,TRIM28,POLR1E,NCBP1,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,MMS22L,MRPL32,PHF19,PRMT1,ORC6,NAA15,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,DNAJC2,PPP5C,FOSB,CD3EAP,NASP,COG3,NUFIP1,MRPL58,NIFK,NUP85,MRPS7,MCM10,CAD,ALG8,DBI,DIS3,SPHK1,MCM6,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,PGS1,SERPINH1,POLR3F,RRBP1,POLD3,GTPBP4,SUPT16H,EIF4A3,NAP1L1,E2F7,GINS4,ALYREF,CKAP2,RRM1,PCNA,EXOSC8,POLE,ZNF703,RFC3,HGF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,MCM4,SNAI2,TCEA1,MRPS5,POLR1B,PDHB,SGK3,EIF3M,CENPJ,NECAB3,EIF2B1,E2F1,PPIP5K2,ABCE1,CCNE1,PXYLP1,AADAT,ZNF827,SLC10A7,GALNT6,HMGB2,RBP4,MSC,ATF1,SSRP1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,AGPAT5,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,EEF1E1,CHUK,RUNX1,PPP1R15B,HR,MDM4,CHAF1B,RFC5,RBMS1,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,STT3A,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,BCAT1,NOL11,TARBP1,ELO	darkgrey	VSMC_M8
GO:0044249	0.00	1.00	390	4271	cellular biosynthetic process	BP	0.00031	CDK2,NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,MRPS18B,NUP107,CCT2,VARS2,DDX39B,FBXO5,VARS,EZR,TCP1,RAD21,DSCC1,NUS1,MAN1A1,ATAD2,PHF5A,ZNF367,SLC35D2,PSIP1,RECQL4,TONSL,MCM5,PWP1,MRPL2,DBF4,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,PUM3,CKS2,MCM3,PAICS,TRIM28,POLR1E,NCBP1,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,THRAP3,EZH2,ODC1,NUP62,MMS22L,MRPL32,PHF19,PRMT1,ORC6,NAA15,ORC1,GEN1,RUVBL2,AMD1,PGR,NAMPT,GRWD1,PUS7,LIG1,MCM2,RUVBL1,CCNA2,RPN1,DNAJC2,PPP5C,FOSB,CD3EAP,NASP,COG3,NUFIP1,MRPL58,NIFK,NUP85,MRPS7,MCM10,CAD,ALG8,DBI,DIS3,SPHK1,MCM6,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,PGS1,POLR3F,RRBP1,POLD3,GTPBP4,SUPT16H,EIF4A3,NAP1L1,E2F7,GINS4,ALYREF,CKAP2,RRM1,PCNA,EXOSC8,POLE,ZNF703,RFC3,HGF,TOPBP1,ELK3,RRP8,TCERG1,USPL1,CBX5,MCM4,SNAI2,TCEA1,MRPS5,POLR1B,PDHB,SGK3,EIF3M,CENPJ,NECAB3,EIF2B1,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,SLC10A7,GALNT6,HMGB2,MSC,ATF1,SSRP1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,AGPAT5,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,EEF1E1,CHUK,RUNX1,PPP1R15B,HR,MDM4,CHAF1B,RFC5,RBMS1,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,STT3A,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,BCAT1,NOL11,TARBP1,ELOVL6,DDX5,XBP1,TICRR,RFC2,RPA2,EIF4H,NEK2,EWSR1,HI	darkgrey	VSMC_M8
GO:0006268	0.00	1.00	8	15	DNA unwinding involved in DNA replication	BP	0.00031	RECQL4,MCM2,MCM6,MCM4,RAD51,BLM,MCM7,RPA1	darkgrey	VSMC_M8
GO:1903311	0.00	1.00	40	247	regulation of mRNA metabolic process	BP	0.00036	SRPK1,SRSF3,NCBP1,U2AF2,SYNCRIP,PABPC4,THRAP3,NBAS,DIS3,SRSF2,EXOSC8,CCNB1,SFSWAP,E2F1,FASTKD3,TENT4A,KHDRBS1,NCL,RBM23,SF3B4,DDX5,DHX9,HNRNPR,TRA2B,SF1,BARD1,RBM3,HNRNPU,CPSF7,FUS,TAF15,HNRNPM,SERBP1,RBMX,RNPS1,DAZAP1,PTBP1,EXOSC2,HNRNPD,SRSF7	darkgrey	VSMC_M8
GO:0051445	0.00	1.00	12	35	regulation of meiotic cell cycle	BP	0.00037	FBXO5,CDC25C,TTK,CDC20,CHFR,CDC25B,TRIP13,ASPM,PDE3A,CDC25A,RAD51AP1,MSX1	darkgrey	VSMC_M8
GO:0031297	0.00	1.00	12	35	replication fork processing	BP	0.00037	TONSL,MMS22L,GEN1,ALYREF,PCNA,RAD51,NUCKS1,TRAIP,BLM,DNA2,FANCM,SMARCAL1	darkgrey	VSMC_M8
GO:0045143	0.00	1.00	14	47	homologous chromosome segregation	BP	0.00038	RAD21,FANCD2,SGO1,ESPL1,CCNE1,TERF1,CCNE2,TRIP13,SGO2,PSMC3IP,PTTG1,PLK1,BRIP1,NDC1	darkgrey	VSMC_M8

GO:0098534	0.00	1.00	13	40	centriole assembly	BP	0.00041	RTTN,CDK2,CEP135,NUP62,PLK4,STIL,WDR62,CENPJ,CEP72,RBM14,BRCA1,CEP76,SASS6	darkgrey	VSMC_M8
GO:0051315	0.00	1.00	7	12	attachment of mitotic spindle microtubules to kinetochore	BP	0.00053	KIF2C,CENPE,NUF2,HNRNPU,AURKB,NDC80,CDT1	darkgrey	VSMC_M8
GO:0000082	0.00	1.00	29	160	G1/S transition of mitotic cell cycle	BP	0.00056	CDK2,GTSE1,MTBP,DBF4,EZH2,CASP2,NASP,E2F7,POLE,WEE1,E2F1,CCNE1,RBL1,CCNE2,KHDRBS1,KIF14,BCAT1,RCC1,RPA2,HINFP,EIF4G1,CDC25A,CDKN3,CDK16,MNAT1,CDC6,BID,IQGAP3,CDKN2C	darkgrey	VSMC_M8
GO:0034724	0.00	1.00	10	26	DNA replication-independent nucleosome organization	BP	0.00062	NASP,SUPT16H,MIS18A,OIP5,HJURP,IPO4,HAT1,ASF1B,CENPP,CENPW	darkgrey	VSMC_M8
GO:0006401	0.00	1.00	38	237	RNA catabolic process	BP	0.00067	POP1,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,NBAS,RNASEH2B,SMG9,DIS3,XRN2,EIF4A3,EXOSC8,E2F1,FASTKD3,TENT4A,NSUN2,DDX5,SSB,DHX9,HNRNPR,DNA2,CNOT9,HNRNPU,EXOSC10,FUS,ELAC2,EDC3,TAF15,HNRNPM,SERBP1,SMG6,RNPS1,DKC1,ZC3H18,EXOSC2,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0072527	0.00	1.00	16	63	pyrimidine-containing compound metabolic process	BP	0.0007	CTPS1,DCK,SLC25A19,CAD,TK1,RRM1,ENTPD7,UNG,UMPS,UCK2,DUT,SLC19A2,DCTPP1,PRPS1,TYMS,ERH	darkgrey	VSMC_M8
GO:0036297	0.00	1.00	12	37	interstrand cross-link repair	BP	0.00071	VCP,MSH6,FANCD2,NEIL3,RAD51,DCLRE1B,NUCKS1,FANCB,FANCM,C17orf53,RAD51AP1,FANCA	darkgrey	VSMC_M8
GO:0006457	0.00	1.00	29	166	protein folding	BP	0.00074	CCT2,TCP1,HSPA9,FKBP5,HSP90AB1,PPIH,DNAJC25,PPIE,CCT4,RUVBL2,DNAJC2,CHORDC1,CHCHD4,CWC27,HSP90B1,CCT8,PPID,CCT7,CCT5,CCT6A,FKBP4,DNAJC7,CCT3,PPIB,AHSA1,DNAJC21,QSOX2,TOR1A,ERP29	darkgrey	VSMC_M8
GO:0048026	0.00	1.00	8	17	positive regulation of mRNA splicing, via spliceosome	BP	0.00076	NCBP1,THRAP3,NCL,SF3B4,TRA2B,RBM3,RBMX,DAZAP1	darkgrey	VSMC_M8
GO:0051171	0.00	1.00	373	4082	regulation of nitrogen compound metabolic process	BP	0.00083	CDK2,HNRNPAB,BCLAF1,HNRNPH1,NUP107,CCT2,DDX39B,FBXO5,PRRC1,EZR,TCP1,RAD21,DSCC1,MTBP,ATAD2,DESI1,PHF5A,ZNF367,CDC25C,SRPK1,SRSF3,PSIP1,PPP2R5D,PWP1,DBF4,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,THRAP3,EZH2,ODC1,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,NRDC,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,SAE1,DNAJC2,CHORDC1,PPP5C,MASTL,FOSB,NUFIP1,GRIN2C,NUP85,PLAUR,DBI,BORA,DIS3,SPHK1,SRSF2,NCAPG2,WDR43,CDC20,BIRC5,SERPINH1,POLR3F,GTPBP4,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,TCEA1,HNRNPF,TPX2,UBA2,PARPBP,SGK3,CENPJ,HSP90B1,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,RBM12,LOXL3,PBK,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,MSH3,MIS18A,CCT7,CCNL1,CDCA2,GNL3,FAM83D,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,PPP1R15B,HR,MDM4,UBE2C,RFC5,PSMD14,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,CENPE,TRIP13,NCL,TRAIP,KIF14,RBM23,PRMT5,POLQ,NOL11,TARBP1,SF3B4,FANCI,DDX5,FANCB,XBP1,TICRR,RFC2,RPA2,SPP2,EIF4H,PRKAR2A,NEK2,EWSR1,HINFP,DTL,NF2,H2AFX,BLM,RBM14,CEP85,CENPF,STRAP,EIF4G1,PSMC5,AUNIP,CDC25A,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HN	darkgrey	VSMC_M8
GO:0044843	0.00	1.00	31	180	cell cycle G1/S phase transition	BP	0.00083	CDK2,GTSE1,MTBP,DBF4,EZH2,CASP2,CCNA2,NASP,E2F7,POLE,WEE1,E2F1,CCNE1,RBL1,FAM83D,CCNE2,KHDRBS1,KIF14,BCAT1,RCC1,RPA2,HINFP,EIF4G1,CDC25A,CDKN3,CDK16,MNAT1,CDC6,BID,IQGAP3,CDKN2C	darkgrey	VSMC_M8
GO:0051256	0.00	1.00	5	6	mitotic spindle midzone assembly	BP	0.00083	RACGAP1,PRC1,KIF4A,AURKB,KIF23	darkgrey	VSMC_M8
GO:0010032	0.00	1.00	5	6	meiotic chromosome condensation	BP	0.00098	SMC2,NCAPD3,SMC4,NCAPD2,INCENP	darkgrey	VSMC_M8
GO:0007064	0.00	1.00	9	22	mitotic sister chromatid cohesion	BP	0.00113	RAD21,DSCC1,CDC20,SGO1,NAA50,SMC3,CDCA5,SMC1A,HASPIN	darkgrey	VSMC_M8
GO:0010972	0.00	1.00	14	51	negative regulation of G2/M transition of mitotic cell cycle	BP	0.00116	RAD21,CLSPN,ORC1,CHFR,TOPBP1,CHEK1,TICRR,DTL,BLM,CDK1,BRCA1,CDC6,AURKB,PLK1	darkgrey	VSMC_M8
GO:0006284	0.00	1.00	12	39	base-excision repair	BP	0.00121	POLD1,LIG1,PARP2,PCNA,POLE,NEIL3,UNG,POLQ,RPA2,DNA2,RPA1,FEN1	darkgrey	VSMC_M8
GO:1901992	0.00	1.00	17	73	positive regulation of mitotic cell cycle phase transition	BP	0.00131	FBXO5,MTBP,CDC25C,CDC25B,CDC16,CCNB1,ESPL1,UBE2C,DTL,EIF4G1,CDK1,CDC25A,CDCA5,DLGAP5,CDC6,CDT1,TMOD3	darkgrey	VSMC_M8
GO:1902750	0.00	1.00	14	52	negative regulation of cell cycle G2/M phase transition	BP	0.00147	RAD21,CLSPN,ORC1,CHFR,TOPBP1,CHEK1,TICRR,DTL,BLM,CDK1,BRCA1,CDC6,AURKB,PLK1	darkgrey	VSMC_M8
GO:0035825	0.00	1.00	13	46	homologous recombination	BP	0.00147	RAD21,RAD54L,FANCD2,MND1,MSH3,RAD51,NUCKS1,TRIP13,FANCM,PSMC3IP,RAD51AP1,TOP2A,BRIP1	darkgrey	VSMC_M8
GO:0051255	0.00	1.00	6	10	spindle midzone assembly	BP	0.00153	RACGAP1,PRC1,INCENP,KIF4A,AURKB,KIF23	darkgrey	VSMC_M8
GO:0044774	0.00	1.00	17	74	mitotic DNA integrity checkpoint signaling	BP	0.00173	CDK2,GTSE1,CLSPN,CASP2,ORC1,FANCD2,TOPBP1,CHEK1,RAD9A,TICRR,RPA2,DTL,BLM,CDK1,BRCA1,CDC6,PLK1	darkgrey	VSMC_M8

GO:0044271	0.00	1.00	317	3436	cellular nitrogen compound biosynthetic process	BP	0.00178	NARS,ATP5F1B,PRIM1,HNRNPAB,BCLAF1,MRPS18B,NUP107,CCT2,VARS2,DDX39B,VARS,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,MRPL2,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,PUM3,CKS2,PAICS,TRIM28,POLR1E,NCBP1,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,GARS,THRAP3,EZH2,ODC1,NUP62,MRPL32,PHF19,NAA15,RUVBL2,AMD1,PGR,NAMPT,PUS7,LIG1,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,MRPL58,NIFK,NUP85,MRPS7,CAD,DIS3,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,POLR3F,RRBP1,POLD3,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,RRM1,PCNA,EXOSC8,POLE,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,MRPS5,POLR1B,PDHB,SGK3,EIF3M,CENPJ,EIF2B1,E2F1,ABCE1,CCNE1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,EEF1E1,CHUK,RUNX1,PPP1R15B,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,ELOVL6,DDX5,XBP1,RFC2,EIF4H,NEK2,EWSR1,HINFP,DTL,HMBS,FLVCR1,BLM,UMPS,RBM14,CENPF,STRAP,EIF4G1,MRPL11,PSMC5,TFRC,PDHA1,UAP1,FOSL1,SMARCC1,DHX9,HNRNPR,PSMA6,UCK2,POLA1,DDX20,AP000944.2,RFC4,DDX21,DLAT,SF1,DUT,C17orf53,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,RPL22L1,CDK16,GABPB1,MYBBP1A,CREG1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,EIF2AK	darkgrey	VSMC_M8
GO:0044771	0.00	1.00	6	10	meiotic cell cycle phase transition	BP	0.00185	CDC25C,TTK,CHFR,CDC25B,CDC25A,CCNB2	darkgrey	VSMC_M8
GO:0006272	0.00	1.00	4	4	leading strand elongation	BP	0.00199	PCNA,POLE,POLA1,POLE3	darkgrey	VSMC_M8
GO:0008315	0.00	1.00	4	4	G2/MI transition of meiotic cell cycle	BP	0.00203	CDC25C,CDC25B,CDC25A,CCNB2	darkgrey	VSMC_M8
GO:1903312	0.00	1.00	17	74	negative regulation of mRNA metabolic process	BP	0.00204	U2AF2,SYNCRIP,THRAP3,NBAS,SFSWAP,E2F1,TENT4A,DHX9,BARD1,HNRNPU,FUS,TAF15,RBMX,RNPS1,PTBP1,HNRNPD,SRSF7	darkgrey	VSMC_M8
GO:0033120	0.00	1.00	10	30	positive regulation of RNA splicing	BP	0.00243	NCBP1,U2AF2,THRAP3,NCL,SF3B4,TRA2B,RBM3,SRSF5,RBMX,DAZAP1	darkgrey	VSMC_M8
GO:0000022	0.00	1.00	5	7	mitotic spindle elongation	BP	0.00262	RACGAP1,PRC1,KIF4A,AURKB,KIF23	darkgrey	VSMC_M8
GO:0051231	0.00	1.00	5	7	spindle elongation	BP	0.00262	RACGAP1,PRC1,KIF4A,AURKB,KIF23	darkgrey	VSMC_M8
GO:0070925	0.00	1.00	83	705	organelle assembly	BP	0.00268	RTTN,CDK2,TUBB,FBXO5,EZR,TTLL1,KIFC1,KIF27,KIF24,CEP135,ANLN,NUP62,SDC1,PLK4,STIL,CENPA,MRPS7,CDC20,CHMP6,WDR62,HAUS5,AAAS,TPX2,KIF2A,ATG101,STAG1,CENPJ,CENPK,CEP89,KIF11,CENPH,KNTC1,FHDC1,RACGAP1,CFAP298,KNL1,MYBL2,FP565260.1,SMC3,CENPE,CEP72,ASPM,IQCB1,RCC1,NEK2,PRC1,RBM14,CENPF,KIF15,IFT80,BRCA1,HAUS3,DLGAP5,HAUS8,SIX4,HNRNPU,INCENP,FSCN1,SMC1A,EIF2S1,CCNB2,SH3PXD2B,KIF4A,AURKB,KIF23,LRRC49,HAUS1,PLK1,EDC3,SEPT6,POLDIP2,BRIX1,CEP76,HAUS7,CENPN,SASS6,NEK6,DDX28,TMOD3,ABT1,AURKA,NIP7,CENPW	darkgrey	VSMC_M8
GO:1900182	0.00	1.00	17	76	positive regulation of protein localization to nucleus	BP	0.00274	CCT2,TCP1,HSP90AB1,TRIM28,CCT4,IPO5,CCT8,CCT7,CCT5,CCT6A,CDK1,TFRC,NMD3,ECT2,CCT3,PLK1,DKC1	darkgrey	VSMC_M8
GO:0051972	0.00	1.00	12	42	regulation of telomerase activity	BP	0.00278	CCT2,TCP1,HSP90AB1,HNRNPA2B1,CCT4,TERF1,NEK2,AURKB,SMG6,DKC1,ACD,HNRNPD	darkgrey	VSMC_M8
GO:0072594	0.00	1.00	48	355	establishment of protein localization to organelle	BP	0.00281	NUP107,CCT2,TCP1,NUP50,MAN1A1,TNPO3,HSP90AB1,TRIM28,CCT4,NUP62,RUVBL2,SEC61A1,SAE1,CHCHD4,TOMM40,NUP85,SRP68,IPO5,TRAM1,TERF1,CCT8,CCT7,NUP93,TOMM70,BAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,CSE1L,IPO4,NUP133,CDK1,ECT2,NEDD4,BID,CCT3,LMNA,TIMM8A,NUP62CL,TIMM44,AIFM1,DKC1,NUP188,ACD,SPCS3,UBE2J2	darkgrey	VSMC_M8
GO:0006336	0.00	1.00	9	25	DNA replication-independent nucleosome assembly	BP	0.00281	NASP,MIS18A,OIP5,HJURP,IPO4,HAT1,ASF1B,CENPP,CENPW	darkgrey	VSMC_M8
GO:0016078	0.00	1.00	6	11	tRNA catabolic process	BP	0.00289	POP1,EXOSC8,NSUN2,EXOSC10,ELAC2,EXOSC2	darkgrey	VSMC_M8
GO:2001020	0.00	1.00	32	200	regulation of response to DNA damage stimulus	BP	0.00291	BCLAF1,DDX39B,FBXO5,POLH,TRIM28,RNASEH2B,PCNA,SNAI2,CD44,PARPBP,RAD51,EEF1E1,DEK,CHEK1,POLQ,DDX5,FANCB,RPA2,H2AFX,NSMCE4A,AUNIP,DHX9,WDR76,BRCA1,NSD2,RAD51AP1,ANKLE1,FOXM1,MSX1,BID,FUS,USP1	darkgrey	VSMC_M8
GO:0045740	0.00	1.00	11	36	positive regulation of DNA replication	BP	0.00302	DBF4,E2F7,PCNA,ATF1,E2F8,CDK1,DHX9,DNA2,RAC1,ATAD5,CDT1	darkgrey	VSMC_M8
GO:0050685	0.00	1.00	9	25	positive regulation of mRNA processing	BP	0.00302	NCBP1,THRAP3,CCNB1,NCL,SF3B4,TRA2B,RBM3,RBMX,DAZAP1	darkgrey	VSMC_M8
GO:0009124	0.00	1.00	11	37	nucleoside monophosphate biosynthetic process	BP	0.0031	PAICS,DCK,CAD,TK1,UMPS,UCK2,DUT,PFAS,PRPS1,TYMS,GART	darkgrey	VSMC_M8
GO:1900180	0.00	1.00	22	116	regulation of protein localization to nucleus	BP	0.00325	CCT2,TCP1,BYSL,HSP90AB1,TRIM28,CCT4,NUP62,IPO5,CCT8,CCT7,NOLC1,CCT5,CCT6A,NF2,CDK1,TFRC,NMD3,ECT2,CCT3,LMNA,PLK1,DKC1	darkgrey	VSMC_M8
GO:0044818	0.00	1.00	12	43	mitotic G2/M transition checkpoint	BP	0.00335	CLSPN,ORC1,CHFR,TOPBP1,CHEK1,TICRR,DTL,BLM,CDK1,BRCA1,CDC6,PLK1	darkgrey	VSMC_M8
GO:0034655	0.00	1.00	46	335	nucleobase-containing compound catabolic process	BP	0.00356	POP1,VCP,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,NBAS,RNASEH2B,SMG9,DIS3,XRN2,EIF4A3,EXOSC8,E2F1,ENTPD7,FASTKD3,TENT4A,NSUN2,UNG,DDX5,SSB,DHX9,HNRNPR,DNA2,DUT,CNOT9,HNRNPU,NUDT1,DCTPP1,EXOSC10,FUS,ELAC2,EDC3,TAF15,HNRNPM,SERBP1,AIFM1,SMG6,RNPS1,DKC1,REXO4,ZC3H18,EXOSC2,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0046700	0.00	1.00	48	357	heterocycle catabolic process	BP	0.00404	POP1,ALDH1L2,VCP,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,NBAS,RNASEH2B,SMG9,DIS3,XRN2,AFMID,EIF4A3,EXOSC8,E2F1,ENTPD7,FASTKD3,TENT4A,NSUN2,UNG,DDX5,SSB,DHX9,HNRNPR,DNA2,DUT,CNOT9,HNRNPU,NUDT1,DCTPP1,EXOSC10,FUS,ELAC2,EDC3,TAF15,HNRNPM,SERBP1,AIFM1,SMG6,RNPS1,DKC1,REXO4,ZC3H18,EXOSC2,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0007131	0.00	1.00	12	44	reciprocal meiotic recombination	BP	0.00404	RAD21,RAD54L,FANCD2,MND1,MSH3,RAD51,TRIP13,FANCM,PSMC3IP,RAD51AP1,TOP2A,BRIP1	darkgrey	VSMC_M8
GO:0140527	0.00	1.00	12	44	reciprocal homologous recombination	BP	0.00404	RAD21,RAD54L,FANCD2,MND1,MSH3,RAD51,TRIP13,FANCM,PSMC3IP,RAD51AP1,TOP2A,BRIP1	darkgrey	VSMC_M8

GO:0044270	0.00	1.00	48	361	cellular nitrogen compound catabolic process	BP	0.00521	POP1,ALDH1L2,VCP,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,NBAS,RNASEH2B,SMG9,DIS3,XRN2,AFMID,EIF4A3,EXOSC8,E2F1,ENTPD7,FASTKD3,TENT4A,NSUN2,UNG,DDX5,SSB,DHX9,HNRNPR,DNA2,DUT,CNOT9,HNRNPU,NUDT1,DCTPP1,EXOSC10,FUS,ELAC2,EDC3,TAF15,HNRNPM,SERBP1,AIFM1,SMG6,RNPS1,DKC1,REXO4,ZC3H18,EXOSC2,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0006298	0.00	1.00	9	27	mismatch repair	BP	0.0053	MSH6,LIG1,POLD3,PCNA,MSH3,RPA2,EXO1,RPA1,TP73	darkgrey	VSMC_M8
GO:0051302	0.00	1.00	24	138	regulation of cell division	BP	0.0056	KIF20A,NUP62,ORC6,PLK4,E2F7,CDC25B,KIF20B,RACGAP1,RBL1,E2F8,CIT,KIF14,ASPM,PRC1,BLM,KIF18B,ECT2,INCENP,CDC6,AURKB,KIF23,PLK1,POLDIP2,AURKA	darkgrey	VSMC_M8
GO:0045931	0.00	1.00	19	97	positive regulation of mitotic cell cycle	BP	0.0056	FBXO5,MTBP,CDC25C,SPHK1,CDC25B,CDC16,CCNB1,ESPL1,UBE2C,DTL,EIF4G1,CDK1,CDC25A,CDCA5,DLGAP5,CDC6,POLDIP2,CDT1,TMOD3	darkgrey	VSMC_M8
GO:0006301	0.00	1.00	9	27	postreplication repair	BP	0.00578	POLH,VCP,POLD1,WDR33,RAD18,PCNA,DTL,BRCA1,POLDIP2	darkgrey	VSMC_M8
GO:0046602	0.00	1.00	5	8	regulation of mitotic centrosome separation	BP	0.00588	KIF11,CHEK1,NEK2,CEP85,RANBP1	darkgrey	VSMC_M8
GO:0008150	0.00	1.00	953	12183	biological_process	BP	0.00604	TXNL4A,RTTN,CDK2,ALPK2,NARS,ATP5F1B,PRIM1,TMED9,HNRNPAB,MTFR2,BCLAF1,ABRACL,METTL1,HNRNPH1,XPOT,NUP43,MRPS18B,NUP107,CCT2,TUBB,VARS2,POP1,TCF19,DDX39B,SRFBP1,FBXO5,PRRC1,VARS,EZR,FBN2,PANX2,ISOC1,TCP1,GTSE1,RAD21,NUP50,DSCC1,TTLL1,NUS1,ARFGAP3,MAN1A1,MTBP,KIFC1,ATAD2,DESI1,PHF5A,FAM49B,RANGAP1,KIF20A,ZNF367,SLC35D2,CDC25C,HSPA9,CHCHD3,FKBP5,MATR3,SRPK1,SRSF3,KIF27,GCAT,CYC1,TNPO3,PSIP1,RECQL4,CEP78,BYSL,TONSL,MCM5,HMGXB4,PPP2R5D,PWP1,MRPL2,APTX,DBF4,POLR3B,STEAP1,POLR1C,UBAP2,TJP2,KIF24,POLH,ALDH1L2,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,COL1A2,ARHGEF39,CENPQ,CEP135,CKS2,MCM3,PAICS,MIOS,NOL8,MELK,TRIM28,POLR1E,NCBP1,THADA,ANP32B,NANS,TWISTNB,PPIH,U2AF2,PPP6R1,SMC2,MSH6,CDCA7L,CTPS1,TTK,CYCS,HNRNPA2B1,GRSF1,CLEC11A,DCK,POLD1,HOXA5,COL9A2,DNAJC25,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,GARS,B3GNT2,SLC31A1,NUP205,ANLN,YRDC,CDCA8,GNL2,THRAP3,EZH2,ODC1,NUP62,NOL10,MMS22L,MRPL32,CLSPN,PHF19,PRMT1,GJB3,CASP2,NBAS,ORC6,SHCBP1,CRYBG1,NAA15,SMC6,ORC1,GEN1,NRDC,SDC1,RUVBL2,PLK4,AMD1,PGR,NAMPT,GRWD1,STIL,PUS7,LIG1,MCM2,CENPO,SEC61A1,RUVBL1,CCNA2,AMOTL1,RPN1,SAE1,SLC1A5,DNAJC2,RAD54L,CHORDC1,RNASEH2B,NAALAD2,PPP5C,WDR33,MASTL,MAST2,CHCHD4,FOSB,CD3EAP,CENPA,CDC42EP4,NASP,COG3,NUFIP1,GRIN2C,TOMM40,PRCP,TMEM214,PREB,MRPL58,NIFK,KCNN4,SMG9,NUP85,PLAUR,MRPS7,MCM10,SLC25A19,CAD,KIF2C,SLC5A6,ALG8,DBI,DIAPH3,DDX18,TRIM47,BORA,TSEN2,DIS3,HNRNPUL1,SRP68,AXL,RNF1	darkgrey	VSMC_M8
GO:0043486	0.00	1.00	7	17	histone exchange	BP	0.00607	NASP,MIS18A,OIP5,ANP32E,HJURP,CENPP,CENPW	darkgrey	VSMC_M8
GO:0000380	0.00	1.00	15	66	alternative mRNA splicing, via spliceosome	BP	0.00614	THRAP3,SRSF2,RBM17,SFSWAP,RSRC1,KHDRBS1,DDX5,STRAP,DHX9,TRA2B,HNRNPU,HNRNPM,RBMX,RNPS1,PTBP1	darkgrey	VSMC_M8
GO:0006999	0.00	1.00	6	12	nuclear pore organization	BP	0.00647	NUP107,NUP205,NUP93,NUP153,NUP133,NDC1	darkgrey	VSMC_M8
GO:0051292	0.00	1.00	5	8	nuclear pore complex assembly	BP	0.00682	NUP107,NUP205,NUP93,NUP153,NDC1	darkgrey	VSMC_M8
GO:0071478	0.00	1.00	25	150	cellular response to radiation	BP	0.00716	POLH,POLD1,RUVBL2,NAMPT,NET1,POLD3,PCNA,PBK,PPID,RAD51,NUCKS1,CHEK1,RGS9,RAD9A,INTS7,H2AFX,BLM,CDC25A,RAD51AP1,ECT2,AIPL1,NEDD4,EIF2S1,AURKB,NOC2L	darkgrey	VSMC_M8
GO:0051338	0.00	1.00	81	706	regulation of transferase activity	BP	0.00728	CCT2,FBXO5,PRRC1,TCP1,DSCC1,CDC25C,DBF4,HSP90AB1,CKS2,HNRNPA2B1,CCT4,EZH2,NUP62,CLSPN,CCNA2,CHORDC1,DBI,BORA,AXL,NCAPG2,CDC20,GTPBP4,IPO5,CHMP6,PCNA,CDC25B,RFC3,DCUN1D2,HGF,CCNB1,TPX2,CCNE1,TERF1,RBL1,CCNL1,CCNE2,HMGCR,UBE2C,RFC5,HMGN1,GCN1,CENPE,KIF14,RFC2,PRKAR2A,NEK2,NF2,BLM,CEP85,CDC25A,PAK2,RFC4,EPHB2,CDKN3,DCUN1D5,ECT2,MNAT1,HNRNPU,UCHL1,INCENP,CCNB3,CDC6,CCNB2,AURKB,PLK1,RAP2C,EMP2,TFAP4,SMG6,PKMYT1,CCNF,CHTF18,DKC1,ACD,PRIM2,HNRNPD,MAD2L1,CDKN2C,UBE2S,ERP29,DUSP7	darkgrey	VSMC_M8
GO:0090666	0.00	1.00	4	5	scaRNA localization to Cajal body	BP	0.00735	CCT2,TCP1,CCT4,DKC1	darkgrey	VSMC_M8
GO:0051656	0.00	1.00	45	334	establishment of organelle localization	BP	0.00761	TMED9,EZR,ARFGAP3,KIFC1,CENPQ,CDCA8,NUP62,CENPA,PREB,KIF2C,CHMP6,CCNB1,ESPL1,ABCE1,VAMP8,TERF1,FAM83D,NUSAP1,KIF18A,CENPE,KIF14,CENPF,NUF2,LSG1,ZW10,CDCA5,NMD3,DLGAP5,MYO5A,HNRNPU,UCHL1,INCENP,RAB27A,KIF22,SPDL1,AURKB,PLK1,SYT4,NDC80,NDE1,PIK3CD,CDT1,TOR1A,MAD2L1,BLOC1S2	darkgrey	VSMC_M8
GO:0071392	0.00	1.00	9	28	cellular response to estradiol stimulus	BP	0.00765	RUVBL2,CCNA2,DDX18,ZNF703,NRIP1,KIF18A,H2AFZ,AIFM1,HNRNPD	darkgrey	VSMC_M8

GO:0006950	0.00	1.00	253	2715	response to stress	BP	0.00868	CDK2,BCLAF1,TUBB,DDX39B,FBXO5,EZR,PANX2,GTSE1,RAD21,MAN1A1,RANGAP1,HSPA9,MATR3,SRPK1,PSIP1,RECQL4,TONSL,MCM5,APTX,POLR3B,POLH,VCP,HSP90AB1,CDC5L,MCM3,MIOS,MELK,TRIM28,MSH6,POLD1,MFSD2A,SYNCRIP,PABPC4,EZH2,MMS22L,CLSPN,PRMT1,CASP2,SMC6,GEN1,SDC1,RUVBL2,NAMPT,LIG1,MCM2,SEC61A1,RUVBL1,CCNA2,DNAJC2,RAD54L,CHORDC1,RNASEH2B,PPP5C,WDR33,MASTL,CDC42EP4,GRIN2C,PRCP,KCNN4,PLAUR,MCM10,CAD,AXL,SPHK1,MCM6,FANCD2,ULK4,NET1,SERPINH1,PARP2,POLR3F,POLD3,RAD18,SUPT16H,E2F7,GINS4,PCNA,POLE,RFC3,HGF,TOPBP1,ELK3,RRP8,CBX5,CCNB1,MCM4,SNAI2,CD44,PARPBP,HSP90B1,EIF2B1,E2F1,VAMP8,HMGB2,TRAM1,SSRP1,LOXL3,PBK,ESCO2,NEIL3,RBL1,TRIM35,MSH3,TBX3,RAD51,DCLRE1B,CREB3L1,TOMM70,HMGCR,BAP1,EEF1E1,CHUK,SETD4,PPP1R15B,MDM4,CHAF1B,RFC5,PSMD14,HMGN1,NOLC1,NUCKS1,DEK,GCN1,MANF,ETS1,METAP1,TENT4A,UBE2T,CHEK1,SMC3,TRIP13,CHD1L,TRAIP,UNG,POLQ,RAD9A,FANCI,MNDA,DDX5,FANCB,XBP1,TICRR,RFC2,RPA2,INTS7,HINFP,DTL,H2AFX,BLM,RBM14,NSMCE4A,EIF4G1,AUNIP,CDK1,PAK2,FOSL1,DHX9,TRA2B,PSMA6,WDR76,POLA1,RFC4,DNA2,DDX21,CDCA5,FANCM,BARD1,C17orf53,EPHB2,SMARCAL1,CDC45,UFD1,BRCA1,MCM7,TFPI,NSD2,WDHD1,DCUN1D5,MYBBP1A,RAD51AP1,ANKLE1,ECT2,SUV39H1,MNAT1,FOXM1,EIF2AK1,LYAR,FH,MSX1,RAC1,DNAJC7,EXO1,UCHL1,RAB27A,ADIPOR2,UBE2K,NEDD4,RFC1,TOP2A,BID,SMC1A,PDPN,EIF2S1,ARG2,NUDT1,DCTPP1,FUS,LMNA,KIF22,COL1A1,RAD23A,PTTG1,PLK1,ILF3,BRIP1,MORF4L2,ZSWIM7,ATAD5,HNRNPM,POLDIP2,WDR70,ELF4,AIFM	darkgrey	VSMC_M8
GO:1902292	0.00	1.00	4	5	cell cycle DNA replication initiation	BP	0.00868	MCM3,MCM2,MCM4,POLA1	darkgrey	VSMC_M8
GO:1902315	0.00	1.00	4	5	nuclear cell cycle DNA replication initiation	BP	0.00868	MCM3,MCM2,MCM4,POLA1	darkgrey	VSMC_M8
GO:1902975	0.00	1.00	4	5	mitotic DNA replication initiation	BP	0.00868	MCM3,MCM2,MCM4,POLA1	darkgrey	VSMC_M8
GO:0045935	0.00	1.00	151	1489	positive regulation of nucleobase-containing compound metabolic process	BP	0.00877	HNRNPAB,BCLAF1,CCT2,DDX39B,TCP1,DSCC1,ATAD2,PHF5A,PWP1,VCP,HSP90AB1,CDC5L,TRIM28,NCBP1,U2AF2,HNRNPA2B1,GRSF1,HOXA5,CCT4,THRAP3,NUP62,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DIS3,WDR43,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,RFC3,HGF,ELK3,TCERG1,CCNB1,TCEA1,CENPJ,E2F1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,CCT8,CCT7,GNL3,TBX3,RAD51,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,RFC5,PPRC1,HMGN1,NOLC1,CCT5,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,NCL,RBM23,NOL11,SF3B4,DDX5,FANCB,XBP1,RFC2,NEK2,HINFP,H2AFX,BLM,RBM14,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,RFC4,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,GABPB1,RAD51AP1,RBM3,DHX33,SIX4,FOXM1,LYAR,MSX1,HNRNPU,SMARCE1,RFC1,TOP2A,EIF5A,SRSF5,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,DAZAP1,CHTF18,DKC1,ZC3H18,EXOSC2,FAM129B,ACD,CBFB,PRIM2,HNRNPD,DRAP1,ABT1,PID1	darkgrey	VSMC_M8
GO:0031503	0.00	1.00	29	186	protein-containing complex localization	BP	0.00929	XPOT,NUP107,DDX39B,EZR,SRSF3,MIOS,NCBP1,HNRNPA2B1,NUP85,BIRC5,ALYREF,ABCE1,TERF1,NUP160,NUP93,NSUN2,CEP72,MCM3AP,NUP133,SSB,LSG1,NMD3,HNRNPU,DDX39A,NDC1,SMG6,THOC6,HASPIN,GLE1	darkgrey	VSMC_M8
GO:0031145	0.00	1.00	7	18	anaphase-promoting complex-dependent catabolic process	BP	0.00929	CDK2,CDC20,CDC16,ANAPC1,UBE2C,PLK1,UBE2S	darkgrey	VSMC_M8
GO:0016572	0.00	1.00	10	34	histone phosphorylation	BP	0.00935	CDK2,CCNA2,CCNB1,CHEK1,CDK1,INCENP,AURKB,VRK1,HASPIN,AURKA	darkgrey	VSMC_M8
GO:0006220	0.00	1.00	11	42	pyrimidine nucleotide metabolic process	BP	0.00936	CTPS1,DCK,CAD,ENTPD7,UNG,UMPS,UCK2,DUT,DCTPP1,PRPS1,TYMS	darkgrey	VSMC_M8
GO:0070601	0.00	1.00	5	9	centromeric sister chromatid cohesion	BP	0.00958	SGO1,BUB1,BUB1B,NAA50,SGO2	darkgrey	VSMC_M8
GO:0044773	0.00	1.00	15	71	mitotic DNA damage checkpoint signaling	BP	0.01121	CDK2,GTSE1,CLSPN,CASP2,FANCD2,TOPBP1,CHEK1,RAD9A,TICRR,RPA2,DTL,BLM,CDK1,BRCA1,PLK1	darkgrey	VSMC_M8
GO:0000387	0.00	1.00	10	38	spliceosomal snRNP assembly	BP	0.01126	SNRPF,SNRPB,PRMT5,PRPF3,STRAP,DDX20,GEMIN5,SNRPD1,USP4,GEMIN4	darkgrey	VSMC_M8
GO:0046605	0.00	1.00	11	42	regulation of centrosome cycle	BP	0.01167	NUP62,GEN1,PLK4,STIL,CHORDC1,CENPJ,RBM14,BRCA1,CEP76,CCNF,AURKA	darkgrey	VSMC_M8
GO:0080090	0.00	1.00	373	4206	regulation of primary metabolic process	BP	0.01167	CDK2,HNRNPAB,BCLAF1,HNRNPH1,NUP107,CCT2,DDX39B,FBXO5,PRRC1,EZR,TCP1,RAD21,DSCC1,MTBP,ATAD2,DESI1,PHF5A,ZNF367,CDC25C,SRPK1,SRSF3,PSIP1,PPP2R5D,PWP1,DBF4,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,THRAP3,EZH2,ODC1,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,NRDC,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,SAE1,DNAJC2,CHORDC1,PPP5C,MASTL,FOSB,NUFIP1,GRIN2C,NUP85,PLAUR,DBI,BORA,DIS3,SPHK1,SRSF2,NCAPG2,WDR43,CDC20,BIRC5,SERPINH1,POLR3F,GTPBP4,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,TCEA1,HNRNPF,TPX2,UBA2,PARPBP,SGK3,CENPJ,HSP90B1,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,RBM12,LOXL3,PBK,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,MSH3,MIS18A,CCT7,CCNL1,CDCA2,GNL3,FAM83D,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,PPP1R15B,HR,MDM4,UBE2C,RFC5,PSMD14,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,CENPE,TRIP13,NCL,TRAIP,KIF14,RBM23,PRMT5,POLQ,NOL11,TARBP1,SF3B4,FANCI,DDX5,FANCB,XBP1,TICRR,RFC2,RPA2,SPP2,EIF4H,PRKAR2A,NEK2,EWSR1,HINFP,DTL,NF2,H2AFX,BLM,RBM14,CEP85,CENPF,STRAP,EIF4G1,PSMC5,AUNIP,CDC25A,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,PSMA6,HNRNPU2,DDX20,PSC1,FANCM	darkgrey	VSMC_M8

GO:0008156	0.00	1.00	8	24	negative regulation of DNA replication	BP	0.01185	FBXO5,GTPBP4,TERF1,GMNN,BLM,S100A11,SMARCAL1,CDC6	darkgrey	VSMC_M8
GO:0019439	0.00	1.00	48	375	aromatic compound catabolic process	BP	0.01192	POP1,ALDH1L2,VCP,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,NBAS,RNASEH2B,SMG9,DIS3,XRN2,AFMID,EIF4A3,EXOSC8,E2F1,ENTPD7,FASTKD3,TENT4A,NSUN2,UNG,DDX5,SSB,DHX9,HNRNPR,DNA2,DUT,CNOT9,HNRNPU,NUDT1,DCTPP1,EXOSC10,FUS,ELAC2,EDC3,TAF15,HNRNPM,SERBP1,AIFM1,SMG6,RNPS1,DKC1,REXO4,ZC3H18,EXOSC2,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0009147	0.00	1.00	7	19	pyrimidine nucleoside triphosphate metabolic process	BP	0.01199	CTPS1,CAD,ENTPD7,UCK2,DUT,DCTPP1,TYMS	darkgrey	VSMC_M8
GO:1901993	0.00	1.00	5	9	regulation of meiotic cell cycle phase transition	BP	0.01211	CDC25C,TTK,CHFR,CDC25B,CDC25A	darkgrey	VSMC_M8
GO:0033314	0.00	1.00	5	9	mitotic DNA replication checkpoint signaling	BP	0.01211	CLSPN,ORC1,TOPBP1,TICRR,CDC6	darkgrey	VSMC_M8
GO:0032201	0.00	1.00	5	9	telomere maintenance via semi-conservative replication	BP	0.01299	PCNA,TERF1,BLM,DNA2,FEN1	darkgrey	VSMC_M8
GO:0000245	0.00	1.00	12	51	spliceosomal complex assembly	BP	0.01345	TXNL4A,DDX39B,SRPK1,PSIP1,NCBP1,SFSWAP,SF3B1,SF1,SRSF5,SNRPD1,SF3A2,DDX23	darkgrey	VSMC_M8
GO:0046931	0.00	1.00	7	19	pore complex assembly	BP	0.01644	NUP107,NUP205,CCT8,NUP93,NUP153,CCT3,NDC1	darkgrey	VSMC_M8
GO:0007143	0.00	1.00	8	25	female meiotic nuclear division	BP	0.01663	FBXO5,TTK,CDC25B,TRIP13,TOP2A,CCNB2,PLK1,AURKA	darkgrey	VSMC_M8
GO:1901976	0.00	1.00	9	31	regulation of cell cycle checkpoint	BP	0.01785	DDX39B,GEN1,RNASEH2B,CCNB1,RPA2,WDR76,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0040001	0.00	1.00	9	31	establishment of mitotic spindle localization	BP	0.01802	CENPA,ESPL1,NUSAP1,ZW10,SPDL1,PLK1,NDC80,NDE1,MAD2L1	darkgrey	VSMC_M8
GO:0033313	0.00	1.00	4	6	meiotic cell cycle checkpoint signaling	BP	0.01961	TTK,CHFR,NSUN2,TRIP13	darkgrey	VSMC_M8
GO:0006269	0.00	1.00	4	6	DNA replication, synthesis of RNA primer	BP	0.02025	PRIM1,POLA1,AP000944.2,PRIM2	darkgrey	VSMC_M8
GO:0034654	0.00	1.00	261	2841	nucleobase-containing compound biosynthetic process	BP	0.0205	ATP5F1B,PRIM1,HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,CKS2,PAICS,TRIM28,POLR1E,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,PPIE,CCT4,GARS,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,AMD1,PGR,NAMPT,LIG1,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,NIFK,NUP85,CAD,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,POLR3F,POLD3,SUPT16H,E2F7,ALYREF,CKAP2,RRM1,PCNA,POLE,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,POLR1B,PDHB,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,CCT6A,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,ELOVL6,DDX5,XBP1,RFC2,NEK2,EWSR1,HINFP,DTL,BLM,UMPS,RBM14,CENPF,STRAP,PSMC5,TFRC,PDHA1,UAP1,FOSL1,SMARCC1,DHX9,PSMA6,UCK2,POLA1,DDX20,AP000944.2,RFC4,DDX21,DLAT,SF1,DUT,C17orf53,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,MTHFD1,NEDD4,UGDH,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,PFAS,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,PRPS1,ACSL4,TADA2A,TAF15,TYMS,CDCA4,POLDIP2,ELF4,RAP2C,UHRF1,RBMX,TFAP	darkgrey	VSMC_M8
GO:0006412	0.00	1.00	62	548	translation	BP	0.0205	NARS,MRPS18B,VARS2,DDX39B,VARS,MRPL2,PUM3,NCBP1,SYNCRIP,PABPC4,GARS,MRPL32,PUS7,MRPL58,MRPS7,DIS3,RRBP1,EIF4A3,EXOSC8,MRPS5,EIF3M,EIF2B1,ABCE1,SELENOT,EEF1E1,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,NCL,EIF4H,EIF4G1,MRPL11,DHX9,HNRNPR,CNOT9,RPL22L1,RBM3,DHX33,EIF2AK1,EIF5A,EIF2S1,EIF3B,EIF4A1,MRPL24,RARS,MRPS23,GEMIN5,ILF3,EIF5,TYMS,DRG2,MRPL37,ZNF598,EXOSC2,GLE1,TRUB2,HNRNPD,MRPS15	darkgrey	VSMC_M8
GO:0007339	0.00	1.00	7	20	binding of sperm to zona pellucida	BP	0.02088	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT3	darkgrey	VSMC_M8
GO:0007144	0.00	1.00	5	10	female meiosis I	BP	0.02088	FBXO5,CDC25B,TRIP13,CCNB2,AURKA	darkgrey	VSMC_M8
GO:0090306	0.00	1.00	4	6	meiotic spindle assembly	BP	0.02094	FBXO5,ASPM,CCNB2,AURKA	darkgrey	VSMC_M8
GO:1902412	0.00	1.00	4	6	regulation of mitotic cytokinesis	BP	0.02094	NUP62,KIF20B,INCENP,POLDIP2	darkgrey	VSMC_M8
GO:0007095	0.00	1.00	9	32	mitotic G2 DNA damage checkpoint signaling	BP	0.02119	CLSPN,TOPBP1,CHEK1,TICRR,DTL,BLM,CDK1,BRCA1,PLK1	darkgrey	VSMC_M8
GO:0000018	0.00	1.00	16	83	regulation of DNA recombination	BP	0.02141	MSH6,ALYREF,PARPBP,MSH3,RAD51,CHEK1,POLQ,FANCB,RPA2,BLM,TFRC,NSD2,RAD51AP1,ANKLE1,FUS,HIST1H1A	darkgrey	VSMC_M8
GO:0010557	0.00	1.00	143	1433	positive regulation of macromolecule biosynthetic process	BP	0.02375	HNRNPAB,BCLAF1,CCT2,DDX39B,TCP1,DSCC1,ATAD2,PHF5A,PWP1,DBF4,HSP90AB1,CDC5L,TRIM28,HOXA5,CCT4,THRAP3,NUP62,PRMT1,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,WDR43,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,RFC3,HGF,ELK3,TCERG1,TCEA1,CENPJ,E2F1,PXYLP1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,CCT8,CCT7,GNL3,TBX3,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,RFC5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,NCL,RBM23,NOL11,XBP1,RFC2,NEK2,HINFP,BLM,RBM14,EIF4G1,PSMC5,CDK1,FOSL1,SMARCC1,DHX9,RFC4,DNA2,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,GABPB1,RBM3,DHX33,SIX4,FOXM1,LYAR,MSX1,RAC1,HNRNPU,SMARCE1,RFC1,TOP2A,EIF5A,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ATAD5,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,CHTF18,DKC1,CDT1,TRUB2,FAM129B,ACD,CBFB,PRIM2,HNRNPD,DRAP1,ABT1,HAS2,PID1	darkgrey	VSMC_M8
GO:0010824	0.00	1.00	10	39	regulation of centrosome duplication	BP	0.02378	NUP62,GEN1,PLK4,STIL,CHORDC1,CENPJ,RBM14,BRCA1,CEP76,CCNF	darkgrey	VSMC_M8

GO:0010604	0.00	1.00	239	2586	positive regulation of macromolecule metabolic process	BP	0.02468	HNRNPAB,BCLAF1,CCT2,DDX39B,PRRC1,EZR,PANX2,TCP1,DSCC1,ATAD2,PHF5A,FAM49B,PPP2R5D,PWP1,DBF4,POLR3B,VCP,HSP90AB1,CDC5L,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,SYNCRIP,CCT4,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,NRDC,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,SAE1,DNAJC2,FOSB,NUFIP1,NUP85,PLAUR,BORA,DIS3,SPHK1,WDR43,CDC20,POLR3F,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,RFC3,DCUN1D2,HGF,ELK3,TCERG1,CCNB1,CD44,TCEA1,TPX2,UBA2,CENPJ,E2F1,PXYLP1,ZNF827,HMGB2,RBP4,ATF1,NRIP1,UTP15,HEY1,FAM98B,CCT8,CCT7,CDCA2,GNL3,TBX3,RAD51,CREB3L1,TOMM70,MYBL2,E2F8,MTDH,CHUK,RUNX1,SETD4,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,CENPE,NCL,KIF14,RBM23,NOL11,SF3B4,FANCI,MNDA,DDX5,FANCB,XBP1,RFC2,NEK2,HINFP,DTL,H2AFX,BLM,RBM14,EIF4G1,PSMC5,CDK1,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,RFC4,DNA2,DDX21,FANCM,BARD1,EPHB2,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,DCUN1D5,GABPB1,RAD51AP1,ECT2,RBM3,DHX33,SIX4,MNAT1,FOXM1,LYAR,MSX1,RAC1,HNRNPU,INCENP,RAB27A,ADIPOR2,UBE2K,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,EIF5A,BID,PRELID1,SRSF5,IQGAP3,CCT3,PMF1,HOXB7,FUS,LMNA,ALOX15B,MAZ,AURKB,COL1A1,RAD23A,NFATC2IP,ILF2,PLK1,ILF3,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ATAD5,ELF4,AIFM1,RAP2C,UHRF1,EMP2,RBMX,TFAP4,TP73,DAZAP1,CHTF18,DKC1,PTBP1,PIK3CD,CDT1,ZC3H18,EXOSC2,TRUB2,FAM129B,ACD,FU	darkgrey	VSMC_M8
GO:0046599	0.00	1.00	7	20	regulation of centriole replication	BP	0.02488	NUP62,PLK4,STIL,CENPJ,RBM14,BRCA1,CEP76	darkgrey	VSMC_M8
GO:0051173	0.00	1.00	218	2331	positive regulation of nitrogen compound metabolic process	BP	0.02535	HNRNPAB,BCLAF1,CCT2,DDX39B,PRRC1,EZR,TCP1,DSCC1,ATAD2,PHF5A,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,CDC5L,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,CCT4,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NAA15,NRDC,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,SAE1,DNAJC2,FOSB,NUFIP1,NUP85,PLAUR,BORA,DIS3,SPHK1,WDR43,CDC20,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,RFC3,DCUN1D2,HGF,ELK3,TCERG1,CCNB1,CD44,TCEA1,TPX2,UBA2,CENPJ,E2F1,PXYLP1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,CCT8,CCT7,CDCA2,GNL3,TBX3,RAD51,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,CENPE,NCL,KIF14,RBM23,NOL11,SF3B4,FANCI,DDX5,FANCB,XBP1,RFC2,NEK2,HINFP,DTL,H2AFX,BLM,RBM14,EIF4G1,PSMC5,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,RFC4,FANCM,BARD1,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,DCUN1D5,GABPB1,RAD51AP1,ECT2,RBM3,DHX33,SIX4,MNAT1,FOXM1,LYAR,MSX1,RAC1,HNRNPU,INCENP,ADIPOR2,UBE2K,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,EIF5A,BID,PRELID1,SRSF5,IQGAP3,CCT3,PMF1,HOXB7,FUS,LMNA,MAZ,AURKB,COL1A1,RAD23A,NFATC2IP,ILF2,PLK1,ILF3,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ELF4,AIFM1,RAP2C,UHRF1,EMP2,RBMX,TFAP4,TP73,DAZAP1,CHTF18,DKC1,PTBP1,ZC3H18,EXOSC2,TRUB2,FAM129B,ACD,CBFB,PRIM2,HNRNPD,DRAP1,ACSL3,ABT1,AURKA,UBE2S,HAS2,ERP29,PDCD2,PID1	darkgrey	VSMC_M8
GO:0051782	0.00	1.00	6	15	negative regulation of cell division	BP	0.02542	ORC6,E2F7,E2F8,ASPM,BLM,AURKB	darkgrey	VSMC_M8
GO:0019222	0.00	1.00	420	4858	regulation of metabolic process	BP	0.02725	CDK2,ALPK2,HNRNPAB,BCLAF1,HNRNPH1,NUP107,CCT2,TCF19,DDX39B,FBXO5,PRRC1,EZR,PANX2,TCP1,RAD21,DSCC1,MTBP,ATAD2,DESI1,PHF5A,FAM49B,ZNF367,CDC25C,MATR3,SRPK1,SRSF3,PSIP1,PPP2R5D,PWP1,DBF4,POLR3B,UBAP2,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,THRAP3,EZH2,ODC1,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,NRDC,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,SAE1,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,MAST2,FOSB,NUFIP1,GRIN2C,PRCP,SMG9,NUP85,PLAUR,DBI,BORA,DIS3,AXL,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,CDC20,BIRC5,SERPINH1,POLR3F,GTPBP4,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,TCEA1,HNRNPF,TPX2,UBA2,PARPBP,SGK3,CENPJ,HSP90B1,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,RBP4,MSC,ATF1,TERF1,HELLS,NRIP1,UTP15,RBM12,LOXL3,PBK,ESCO2,HEY1,ZBTB10,SELENOT,FAM98B,CCT8,PPID,RBL1,MSH3,MIS18A,CCT7,CCNL1,HNRNPDL,CDCA2,GNL3,FAM83D,TBX3,RAD51,CREB3L1,TOMM70,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,SETD4,PPP1R15B,HR,MDM4,UBE2C,RFC5,PSMD14,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,CENPE,TRIP13,NCL,TRAIP,KIF14,RBM23,PRMT5,POLQ,NOL11,TARBP1,ELOVL6,SF3B4,FANCI,MNDA,DDX5,FANCB,XB	darkgrey	VSMC_M8
GO:0043043	0.00	1.00	63	566	peptide biosynthetic process	BP	0.02789	NARS,MRPS18B,VARS2,DDX39B,VARS,MRPL2,PUM3,NCBP1,SYNCRIP,PABPC4,GARS,MRPL32,PUS7,MRPL58,MRPS7,DIS3,RRBP1,EIF4A3,EXOSC8,MRPS5,EIF3M,EIF2B1,ABCE1,SELENOT,EEF1E1,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,NCL,EIF4H,EIF4G1,MRPL11,DHX9,HNRNPR,CNOT9,RPL22L1,RBM3,DHX33,EIF2AK1,EIF5A,EIF2S1,EIF3B,EIF4A1,MRPL24,RARS,MRPS23,GEMIN5,ILF3,EIF5,TYMS,DRG2,MRPL37,ZNF598,EXOSC2,GLE1,TRUB2,GCLM,HNRNPD,MRPS15	darkgrey	VSMC_M8
GO:0051053	0.00	1.00	17	94	negative regulation of DNA metabolic process	BP	0.02812	TRIM28,MSH6,DNAJC2,PARPBP,TERF1,MSH3,POLQ,FANCB,BLM,AUNIP,ANKLE1,HNRNPU,EXOSC10,SMG6,FAM129B,ACD,HIST1H1A	darkgrey	VSMC_M8

GO:1902751	0.00	1.00	8	27	positive regulation of cell cycle G2/M phase transition	BP	0.02863	FBXO5,CDC25C,CDC25B,CCNB1,DTL,CDK1,CDC25A,ATAD5	darkgrey	VSMC_M8
GO:0051785	0.00	1.00	10	41	positive regulation of nuclear division	BP	0.03028	NUP62,SPHK1,CDC16,ESPL1,NUSAP1,DLGAP5,RAD51AP1,MSX1,CDT1,AURKA	darkgrey	VSMC_M8
GO:0016446	0.00	1.00	5	11	somatic hypermutation of immunoglobulin genes	BP	0.03028	MSH6,UNG,POLQ,MCM3AP,EXO1	darkgrey	VSMC_M8
GO:0007135	0.00	1.00	4	7	meiosis II	BP	0.03028	SGO1,BUB1,BUB1B,SGO2	darkgrey	VSMC_M8
GO:0045144	0.00	1.00	4	7	meiotic sister chromatid segregation	BP	0.03028	SGO1,BUB1,BUB1B,SGO2	darkgrey	VSMC_M8
GO:0051177	0.00	1.00	4	7	meiotic sister chromatid cohesion	BP	0.03028	SGO1,BUB1,BUB1B,SGO2	darkgrey	VSMC_M8
GO:0061983	0.00	1.00	4	7	meiosis II cell cycle process	BP	0.03028	SGO1,BUB1,BUB1B,SGO2	darkgrey	VSMC_M8
GO:0048025	0.00	1.00	6	16	negative regulation of mRNA splicing, via spliceosome	BP	0.03063	U2AF2,SFSWAP,RBMX,RNPS1,PTBP1,SRSF7	darkgrey	VSMC_M8
GO:0006402	0.00	1.00	29	201	mRNA catabolic process	BP	0.03063	NCBP1,SYNCRIP,PABPC4,THRAP3,NBAS,SMG9,DIS3,XRN2,EIF4A3,EXOSC8,E2F1,FASTKD3,TENT4A,DDX5,SSB,DHX9,HNRNPR,CNOT9,HNRNPU,EXOSC10,FUS,EDC3,TAF15,HNRNPM,SERBP1,SMG6,RNPS1,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0090305	0.00	1.00	30	213	nucleic acid phosphodiester bond hydrolysis	BP	0.03084	POP1,APTX,NCBP1,POLD1,GEN1,TSEN2,DIS3,XRN2,EXOSC8,POLE,UTP20,DBR1,DCLRE1B,RAD9A,DNA2,FANCM,ANKLE1,EXO1,CPSF7,EXOSC10,ELAC2,REXO5,EDC3,AIFM1,SMG6,REXO4,EXOSC2,NOB1,ABT1,FEN1	darkgrey	VSMC_M8
GO:1901361	0.00	1.00	48	395	organic cyclic compound catabolic process	BP	0.0334	POP1,ALDH1L2,VCP,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,NBAS,RNASEH2B,SMG9,DIS3,XRN2,AFMID,EIF4A3,EXOSC8,E2F1,ENTPD7,FASTKD3,TENT4A,NSUN2,UNG,DDX5,SSB,DHX9,HNRNPR,DNA2,DUT,CNOT9,HNRNPU,NUDT1,DCTPP1,EXOSC10,FUS,ELAC2,EDC3,TAF15,HNRNPM,SERBP1,AIFM1,SMG6,RNPS1,DKC1,REXO4,ZC3H18,EXOSC2,HNRNPD,FEN1	darkgrey	VSMC_M8
GO:0000212	0.00	1.00	5	11	meiotic spindle organization	BP	0.03445	FBXO5,ESPL1,ASPM,CCNB2,AURKA	darkgrey	VSMC_M8
GO:0006335	0.00	1.00	6	16	DNA replication-dependent nucleosome assembly	BP	0.03526	NASP,CHAF1B,IPO4,HAT1,ASF1B,CHAF1A	darkgrey	VSMC_M8
GO:0034723	0.00	1.00	6	16	DNA replication-dependent nucleosome organization	BP	0.03526	NASP,CHAF1B,IPO4,HAT1,ASF1B,CHAF1A	darkgrey	VSMC_M8
GO:0001833	0.00	1.00	5	11	inner cell mass cell proliferation	BP	0.03572	NCAPG2,GINS4,CHEK1,GINS1,PALB2	darkgrey	VSMC_M8
GO:0045943	0.00	1.00	7	22	positive regulation of transcription by RNA polymerase I	BP	0.03606	PWP1,WDR43,UTP15,NCL,NOL11,DHX33,LYAR	darkgrey	VSMC_M8
GO:1904668	0.00	1.00	4	7	positive regulation of ubiquitin protein ligase activity	BP	0.03637	CDC20,UBE2C,PLK1,UBE2S	darkgrey	VSMC_M8
GO:0032506	0.00	1.00	9	35	cytokinetic process	BP	0.03745	KIF20A,ANLN,NUP62,CHMP6,KIF20B,CEP55,RACGAP1,ECT2,AURKB	darkgrey	VSMC_M8
GO:0009157	0.00	1.00	4	7	deoxyribonucleoside monophosphate biosynthetic process	BP	0.03751	DCK,TK1,DUT,TYMS	darkgrey	VSMC_M8
GO:0018130	0.00	1.00	263	2900	heterocycle biosynthetic process	BP	0.03845	ATP5F1B,PRIM1,HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,CKS2,PAICS,TRIM28,POLR1E,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,PPIE,CCT4,GARS,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,AMD1,PGR,NAMPT,LIG1,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,NIFK,NUP85,CAD,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,POLR3F,POLD3,SUPT16H,E2F7,ALYREF,CKAP2,RRM1,PCNA,POLE,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,POLR1B,PDHB,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,CCT6A,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,ELOVL6,DDX5,XBP1,RFC2,NEK2,EWSR1,HINFP,DTL,HMBS,FLVCR1,BLM,UMPS,RBM14,CENPF,STRAP,PSMC5,TFRC,PDHA1,UAP1,FOSL1,SMARCC1,DHX9,PSMA6,UCK2,POLA1,DDX20,AP000944.2,RFC4,DDX21,DLAT,SF1,DUT,C17orf53,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,MTHFD1,NEDD4,UGDH,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,PFAS,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,PRPS1,ACSL4,TADA2A,TAF15,TYMS,CDCA4,POLDIP2,ELF4,RAP2C,U	darkgrey	VSMC_M8
GO:0019438	0.00	1.00	263	2902	aromatic compound biosynthetic process	BP	0.04028	ATP5F1B,PRIM1,HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,POLR3B,POLR1C,POLH,VCP,HSP90AB1,CDC5L,CKS2,PAICS,TRIM28,POLR1E,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,PPIE,CCT4,GARS,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,AMD1,PGR,NAMPT,LIG1,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,NIFK,NUP85,CAD,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,POLR3F,POLD3,SUPT16H,E2F7,ALYREF,CKAP2,RRM1,PCNA,POLE,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,POLR1B,PDHB,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,CCT6A,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,ELOVL6,DDX5,XBP1,RFC2,NEK2,EWSR1,HINFP,DTL,HMBS,FLVCR1,BLM,UMPS,RBM14,CENPF,STRAP,PSMC5,TFRC,PDHA1,UAP1,FOSL1,SMARCC1,DHX9,PSMA6,UCK2,POLA1,DDX20,AP000944.2,RFC4,DDX21,DLAT,SF1,DUT,C17orf53,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,MTHFD1,NEDD4,UGDH,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,PFAS,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,PRPS1,ACSL4,TADA2A,TAF15,TYMS,CDCA4,POLDIP2,ELF4,RAP2C,U	darkgrey	VSMC_M8

GO:0010605	0.00	1.00	195	2090	negative regulation of macromolecule metabolic process	BP	0.04327	CDK2,BCLAF1,FBXO5,EZR,PPP2R5D,PWP1,CYP51A1,HSP90AB1,TRIM28,NCBP1,U2AF2,MSH6,HNRNPA2B1,SYNCRIP,PABPC4,THRAP3,EZH2,NUP62,PHF19,NBAS,RUVBL2,PGR,PUS7,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,FOSB,GRIN2C,SMG9,PLAUR,DBI,DIS3,AXL,SRSF2,XRN2,NCAPG2,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,E2F7,PCNA,EXOSC8,ZNF703,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,PARPBP,E2F1,ABCE1,CCNE1,HMGB2,MSC,TERF1,HELLS,NRIP1,LOXL3,PBK,HEY1,PPID,RBL1,MSH3,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,RUNX1,PPP1R15B,MDM4,NCOA5,FASTKD3,TENT4A,NSUN2,PHC2,GMNN,KHDRBS1,NCL,TRAIP,PRMT5,POLQ,DDX5,FANCB,SPP2,PRKAR2A,HINFP,NF2,BLM,SSB,CEP85,CENPF,STRAP,EIF4G1,PSMC5,AUNIP,CDK1,S100A11,PAK2,SMARCC1,DHX9,HNRNPR,DDX20,DGCR8,SF1,BARD1,EPHB2,SMARCAL1,UFD1,BRCA1,TFPI,CNOT9,NSD2,MYBBP1A,CREG1,ANKLE1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,UCHL1,ADIPOR2,NEDD4,SMARCE1,RFC1,CDC6,EIF2S1,ARG2,IQGAP3,EXOSC10,HDGF,FUS,MAZ,AURKB,PTTG1,SPAG9,PLK1,PTRH2,ILF3,BRIP1,DNMT1,EDC3,TAF15,TYMS,HNRNPM,SERBP1,NNT,UHRF1,RBMX,NXN,TFAP4,SMG6,NOC2L,RNPS1,G6PD,DKC1,PTBP1,PIK3CD,EXOSC2,FAM129B,SF3B3,ACD,CBFB,DEPDC1,SRRT,USP4,HIST1H1A,HNRNPD,MAD2L1,DRAP1,CDKN2C,AURKA,SRSF7,ERP29,POLE3,PID1,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0044806	0.00	1.00	4	7	G-quadruplex DNA unwinding	BP	0.04357	HNRNPA2B1,BLM,DHX9,DNA2	darkgrey	VSMC_M8
GO:0002566	0.00	1.00	5	12	somatic diversification of immune receptors via somatic mutation	BP	0.04747	MSH6,UNG,POLQ,MCM3AP,EXO1	darkgrey	VSMC_M8
GO:0009130	0.00	1.00	5	12	pyrimidine nucleoside monophosphate biosynthetic process	BP	0.04767	CAD,UMPS,UCK2,DUT,TYMS	darkgrey	VSMC_M8
GO:0019985	0.00	1.00	6	17	translesion synthesis	BP	0.05027	POLH,VCP,POLD1,PCNA,DTL,POLDIP2	darkgrey	VSMC_M8
GO:1904666	0.00	1.00	6	19	regulation of ubiquitin protein ligase activity	BP	0.05027	FBXO5,CDC20,UBE2C,PLK1,MAD2L1,UBE2S	darkgrey	VSMC_M8
GO:0006221	0.00	1.00	7	24	pyrimidine nucleotide biosynthetic process	BP	0.05328	CTPS1,CAD,UMPS,UCK2,DUT,PRPS1,TYMS	darkgrey	VSMC_M8
GO:0051973	0.00	1.00	8	30	positive regulation of telomerase activity	BP	0.05437	CCT2,TCP1,HSP90AB1,CCT4,NEK2,AURKB,DKC1,ACD	darkgrey	VSMC_M8
GO:0017038	0.00	1.00	25	174	protein import	BP	0.05673	NUP107,NUP50,TNPO3,HSP90AB1,TRIM28,NUP62,CHCHD4,TOMM40,NUP85,IPO5,NUP93,TOMM70,HEATR3,NOLC1,NUP153,CSE1L,IPO4,NUP133,CDK1,ECT2,LMNA,NUP62CL,TIMM44,AIFM1,NUP188	darkgrey	VSMC_M8
GO:0043604	0.00	1.00	71	672	amide biosynthetic process	BP	0.05881	NARS,MRPS18B,VARS2,DDX39B,VARS,MRPL2,PUM3,NCBP1,SYNCRIP,PABPC4,GARS,MRPL32,PUS7,MRPL58,MRPS7,DIS3,SPHK1,RRBP1,EIF4A3,EXOSC8,MRPS5,PDHB,EIF3M,EIF2B1,ABCE1,SELENOT,EEF1E1,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,NCL,ELOVL6,EIF4H,EIF4G1,MRPL11,PDHA1,DHX9,HNRNPR,DLAT,CNOT9,RPL22L1,RBM3,DHX33,EIF2AK1,EIF5A,EIF2S1,EIF3B,ARG2,EIF4A1,MRPL24,RARS,MRPS23,GEMIN5,ILF3,ACSL4,EIF5,TYMS,DRG2,MRPL37,ZNF598,EXOSC2,GLE1,TRUB2,GCLM,HNRNPD,ACSL3,MRPS15	darkgrey	VSMC_M8
GO:0035036	0.00	1.00	7	24	sperm-egg recognition	BP	0.0599	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT3	darkgrey	VSMC_M8
GO:0000413	0.00	1.00	8	32	protein peptidyl-prolyl isomerization	BP	0.0599	FKBP5,PPIH,PPIE,CWC27,PPID,AIPL1,FKBP4,PPIB	darkgrey	VSMC_M8
GO:0046112	0.00	1.00	6	18	nucleobase biosynthetic process	BP	0.06048	PAICS,CTPS1,CAD,UMPS,PRPS1,GART	darkgrey	VSMC_M8
GO:0006282	0.00	1.00	19	118	regulation of DNA repair	BP	0.06119	POLH,TRIM28,PCNA,PARPBP,RAD51,DEK,CHEK1,POLQ,FANCB,RPA2,H2AFX,AUNIP,DHX9,BRCA1,NSD2,RAD51AP1,FOXM1,FUS,USP1	darkgrey	VSMC_M8
GO:0043489	0.00	1.00	11	52	RNA stabilization	BP	0.06542	SYNCRIP,THRAP3,E2F1,TENT4A,NSUN2,DHX9,HNRNPU,FUS,TAF15,DKC1,HNRNPD	darkgrey	VSMC_M8
GO:0030490	0.00	1.00	10	46	maturation of SSU-rRNA	BP	0.06542	SRFBP1,BYSL,NOL10,UTP20,WDR3,FP565260.1,NOL11,UTP25,NOB1,ABT1	darkgrey	VSMC_M8
GO:0016074	0.00	1.00	5	13	sno(s)RNA metabolic process	BP	0.06542	FBL,NOLC1,EXOSC10,DKC1,EXOSC2	darkgrey	VSMC_M8
GO:0072331	0.00	1.00	21	139	signal transduction by p53 class mediator	BP	0.06602	GTSE1,CASP2,E2F7,RRP8,SNAI2,CD44,E2F1,EEF1E1,MDM4,PAK1IP1,CHEK1,PRMT5,DDX5,MYBBP1A,FOXM1,MSX1,EIF5A,AURKB,TFAP4,TP73,AURKA	darkgrey	VSMC_M8
GO:0085020	0.00	1.00	4	8	protein K6-linked ubiquitination	BP	0.06631	UBE2T,BARD1,BRCA1,UBE2S	darkgrey	VSMC_M8
GO:1902369	0.00	1.00	12	60	negative regulation of RNA catabolic process	BP	0.06644	SYNCRIP,THRAP3,NBAS,E2F1,TENT4A,NSUN2,DHX9,HNRNPU,FUS,TAF15,DKC1,HNRNPD	darkgrey	VSMC_M8
GO:0046822	0.00	1.00	16	94	regulation of nucleocytoplasmic transport	BP	0.06644	RANGAP1,HSP90AB1,TRIM28,ANP32B,NUP62,IPO5,AAAS,NOLC1,NUP153,NSUN2,KHDRBS1,CDK1,DHX9,BARD1,ECT2,NEDD4	darkgrey	VSMC_M8
GO:0006606	0.00	1.00	20	129	protein import into nucleus	BP	0.06696	NUP107,NUP50,TNPO3,HSP90AB1,TRIM28,NUP62,NUP85,IPO5,NUP93,HEATR3,NOLC1,NUP153,CSE1L,IPO4,NUP133,CDK1,ECT2,LMNA,NUP62CL,NUP188	darkgrey	VSMC_M8
GO:0009112	0.00	1.00	8	31	nucleobase metabolic process	BP	0.06766	PAICS,CTPS1,CAD,RRM1,UMPS,PRPS1,TYMS,GART	darkgrey	VSMC_M8
GO:1901293	0.00	1.00	27	199	nucleoside phosphate biosynthetic process	BP	0.06766	ATP5F1B,VCP,PAICS,CTPS1,DCK,GARS,NAMPT,CAD,TK1,AFMID,RRM1,PDHB,ELOVL6,UMPS,PDHA1,UCK2,DLAT,DUT,MTHFD1,PFAS,PRPS1,ACSL4,TYMS,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0031123	0.00	1.00	16	94	RNA 3'-end processing	BP	0.06849	NCBP1,GRSF1,WDR33,FBL,EXOSC8,CCNB1,TENT4A,INTS7,SSB,BARD1,SLBP,CPSF7,EXOSC10,ELAC2,DKC1,EXOSC2	darkgrey	VSMC_M8

GO:0019219	0.00	1.00	257	2852	regulation of nucleobase-containing compound metabolic process	BP	0.06912	HNRNPAB,BCLAF1,HNRNPH1,NUP107,CCT2,DDX39B,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,PWP1,POLH,VCP,HSP90AB1,CDC5L,CKS2,TRIM28,NCBP1,U2AF2,MSH6,CDCA7L,HNRNPA2B1,GRSF1,HOXA5,SYNCRIP,PPIE,PABPC4,CCT4,THRAP3,EZH2,NUP62,PHF19,NBAS,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DIS3,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,TCEA1,HNRNPF,PARPBP,SGK3,CENPJ,E2F1,ABCE1,CCNE1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,RBM12,LOXL3,HEY1,ZBTB10,CCT8,PPID,RBL1,MSH3,MIS18A,CCT7,CCNL1,GNL3,TBX3,RAD51,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,SF3B4,DDX5,FANCB,XBP1,TICRR,RFC2,RPA2,NEK2,EWSR1,HINFP,H2AFX,BLM,RBM14,CENPF,STRAP,PSMC5,AUNIP,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,PSMA6,HNRNPH3,DDX20,RFC4,SF1,BARD1,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,RAD51AP1,CREG1,ANKLE1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,CPSF7,SRSF5,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,HNRNPM,SERBP1,WDR70,ELF4,AIFM1,USP1,RAP2C,UHRF1,R	darkgrey	VSMC_M8
GO:0031323	0.00	1.00	379	4391	regulation of cellular metabolic process	BP	0.06957	CDK2,HNRNPAB,BCLAF1,HNRNPH1,NUP107,CCT2,DDX39B,FBXO5,PRRC1,EZR,TCP1,RAD21,DSCC1,MTBP,ATAD2,DESI1,PHF5A,ZNF367,CDC25C,SRPK1,SRSF3,PSIP1,PPP2R5D,PWP1,DBF4,POLH,VCP,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,NRDC,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,SAE1,DNAJC2,CHORDC1,PPP5C,MASTL,FOSB,NUFIP1,PRCP,NUP85,PLAUR,DBI,BORA,DIS3,AXL,SPHK1,SRSF2,NCAPG2,WDR43,CDC20,BIRC5,SERPINH1,POLR3F,GTPBP4,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,TCEA1,HNRNPF,TPX2,UBA2,PARPBP,SGK3,CENPJ,HSP90B1,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,RBM12,LOXL3,PBK,ESCO2,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,MSH3,MIS18A,CCT7,CCNL1,CDCA2,GNL3,TBX3,RAD51,CREB3L1,MYBL2,CCNE2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,PPP1R15B,HR,MDM4,UBE2C,RFC5,PSMD14,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,CENPE,TRIP13,NCL,TRAIP,KIF14,RBM23,PRMT5,POLQ,NOL11,TARBP1,SF3B4,FANCI,DDX5,FANCB,XBP1,TICRR,RFC2,RPA2,SPP2,EIF4H,PRKAR2A,NEK2,EWSR1,HINFP,NF2,H2AFX,BLM,RBM14,CEP85,CENPF,STRAP,EIF4G1,PSMC5,AUNIP,CDK1,S100A11,CDC25A,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRN	darkgrey	VSMC_M8
GO:0031328	0.00	1.00	145	1503	positive regulation of cellular biosynthetic process	BP	0.07106	HNRNPAB,BCLAF1,CCT2,DDX39B,TCP1,DSCC1,ATAD2,PHF5A,PWP1,DBF4,VCP,HSP90AB1,CDC5L,TRIM28,HOXA5,MFSD2A,CCT4,THRAP3,NUP62,PRMT1,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,WDR43,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,RFC3,HGF,ELK3,TCERG1,TCEA1,CENPJ,E2F1,PXYLP1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,CCT8,CCT7,GNL3,TBX3,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,RFC5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,NCL,RBM23,NOL11,XBP1,RFC2,NEK2,HINFP,BLM,RBM14,EIF4G1,PSMC5,CDK1,FOSL1,SMARCC1,DHX9,RFC4,DNA2,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,GABPB1,RBM3,DHX33,SIX4,FOXM1,LYAR,MSX1,RAC1,HNRNPU,SMARCE1,RFC1,TOP2A,EIF5A,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ATAD5,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,CHTF18,DKC1,CDT1,TRUB2,FAM129B,ACD,CBFB,PRIM2,HNRNPD,DRAP1,ACSL3,ABT1,PID1	darkgrey	VSMC_M8
GO:0010971	0.00	1.00	7	25	positive regulation of G2/M transition of mitotic cell cycle	BP	0.07536	FBXO5,CDC25C,CDC25B,CCNB1,DTL,CDK1,CDC25A	darkgrey	VSMC_M8
GO:0042273	0.00	1.00	11	56	ribosomal large subunit biogenesis	BP	0.07536	NIFK,DDX18,GTPBP4,MAK16,PAK1IP1,HEATR3,BRIX1,RSL1D1,NOC2L,DDX28,NIP7	darkgrey	VSMC_M8
GO:0050686	0.00	1.00	7	25	negative regulation of mRNA processing	BP	0.07541	U2AF2,SFSWAP,BARD1,RBMX,RNPS1,PTBP1,SRSF7	darkgrey	VSMC_M8
GO:0006287	0.00	1.00	5	13	base-excision repair, gap-filling	BP	0.07596	POLD1,LIG1,PCNA,POLE,FEN1	darkgrey	VSMC_M8
GO:0033119	0.00	1.00	6	19	negative regulation of RNA splicing	BP	0.07722	U2AF2,SFSWAP,RBMX,RNPS1,PTBP1,SRSF7	darkgrey	VSMC_M8
GO:0045840	0.00	1.00	8	32	positive regulation of mitotic nuclear division	BP	0.07952	NUP62,SPHK1,CDC16,ESPL1,NUSAP1,DLGAP5,CDT1,AURKA	darkgrey	VSMC_M8

GO:0009891	0.00	1.00	147	1533	positive regulation of biosynthetic process	BP	0.08191	HNRNPAB,BCLAF1,CCT2,DDX39B,TCP1,DSCC1,ATAD2,PHF5A,PWP1,DBF4,VCP,HSP90AB1,CDC5L,TRIM28,HOXA5,MFSD2A,CCT4,THRAP3,NUP62,PRMT1,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,WDR43,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,RFC3,HGF,ELK3,TCERG1,TCEA1,CENPJ,E2F1,PXYLP1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,CCT8,CCT7,GNL3,TBX3,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,RFC5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,NCL,RBM23,NOL11,XBP1,RFC2,NEK2,HINFP,BLM,RBM14,EIF4G1,PSMC5,CDK1,FOSL1,SMARCC1,DHX9,RFC4,DNA2,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,GABPB1,RBM3,DHX33,SIX4,FOXM1,LYAR,MSX1,RAC1,HNRNPU,RAB27A,SMARCE1,RFC1,TOP2A,EIF5A,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ATAD5,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,CHTF18,DKC1,CDT1,TRUB2,FAM129B,ACD,CBFB,PRIM2,HNRNPD,DRAP1,ACSL3,ABT1,HAS2,PID1	darkgrey	VSMC_M8
GO:0032355	0.00	1.00	17	105	response to estradiol	BP	0.08341	EZH2,RUVBL2,CCNA2,DDX18,PCNA,ZNF703,NRIP1,KIF18A,ETS1,H2AFZ,RGS9,TFPI,BID,COL1A1,AIFM1,HNRNPD,MBD2	darkgrey	VSMC_M8
GO:0001556	0.00	1.00	6	19	oocyte maturation	BP	0.08499	FBXO5,CDC25B,CCNB1,TRIP13,PDE3A,AURKA	darkgrey	VSMC_M8
GO:0051170	0.00	1.00	20	132	import into nucleus	BP	0.08572	NUP107,NUP50,TNPO3,HSP90AB1,TRIM28,NUP62,NUP85,IPO5,NUP93,HEATR3,NOLC1,NUP153,CSE1L,IPO4,NUP133,CDK1,ECT2,LMNA,NUP62CL,NUP188	darkgrey	VSMC_M8
GO:0001325	0.00	1.00	5	14	formation of extrachromosomal circular DNA	BP	0.08835	TERF1,BLM,DNA2,SMARCAL1,EXO1	darkgrey	VSMC_M8
GO:0090656	0.00	1.00	5	14	t-circle formation	BP	0.08835	TERF1,BLM,DNA2,SMARCAL1,EXO1	darkgrey	VSMC_M8
GO:0090737	0.00	1.00	5	14	telomere maintenance via telomere trimming	BP	0.08835	TERF1,BLM,DNA2,SMARCAL1,EXO1	darkgrey	VSMC_M8
GO:0010608	0.00	1.00	53	480	posttranscriptional regulation of gene expression	BP	0.09028	DDX39B,MATR3,PUM3,NCBP1,HNRNPA2B1,SYNCRIP,PABPC4,THRAP3,PUS7,DIS3,EIF4A3,EXOSC8,E2F1,ABCE1,SELENOT,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,NSUN2,KHDRBS1,NCL,DDX5,EIF4H,EIF4G1,DHX9,HNRNPR,DGCR8,CNOT9,RBM3,EIF2AK1,HNRNPU,EIF5A,EIF2S1,EIF3B,FUS,GEMIN5,ILF3,TAF15,EIF5,TYMS,HNRNPM,SERBP1,ZNF598,DKC1,ZC3H18,EXOSC2,GLE1,TRUB2,SRRT,HNRNPD	darkgrey	VSMC_M8
GO:0044417	0.00	1.00	4	9	translocation of molecules into host	BP	0.09418	DDX39B,TCP1,ALYREF,THOC6	darkgrey	VSMC_M8
GO:0000132	0.00	1.00	7	26	establishment of mitotic spindle orientation	BP	0.09571	CENPA,ZW10,SPDL1,PLK1,NDC80,NDE1,MAD2L1	darkgrey	VSMC_M8
GO:0007019	0.00	1.00	9	40	microtubule depolymerization	BP	0.10097	KIF24,KIF2C,CKAP2,TPX2,KIF2A,CKAP5,KIF18A,KIF18B,STMN1	darkgrey	VSMC_M8
GO:0009123	0.00	1.00	12	65	nucleoside monophosphate metabolic process	BP	0.10177	TJP2,PAICS,DCK,CAD,TK1,UMPS,UCK2,DUT,PFAS,PRPS1,TYMS,GART	darkgrey	VSMC_M8
GO:0007569	0.00	1.00	16	98	cell aging	BP	0.10601	CDK2,FBXO5,NUP62,SMC6,NAMPT,RBL1,TBX3,EEF1E1,CHEK1,H2AFX,CDK1,FOXM1,ARG2,LMNA,RSL1D1,NEK6	darkgrey	VSMC_M8
GO:0007096	0.00	1.00	5	15	regulation of exit from mitosis	BP	0.10678	ANLN,KNTC1,UBE2C,ZW10,CDCA5	darkgrey	VSMC_M8
GO:0010457	0.00	1.00	5	14	centriole-centriole cohesion	BP	0.11026	RTTN,CEP135,SGO1,NEK2,ODF2	darkgrey	VSMC_M8
GO:0045910	0.00	1.00	8	34	negative regulation of DNA recombination	BP	0.11026	MSH6,PARPBP,MSH3,POLQ,FANCB,BLM,ANKLE1,HIST1H1A	darkgrey	VSMC_M8
GO:1901362	0.00	1.00	267	3012	organic cyclic compound biosynthetic process	BP	0.11254	ATP5F1B,PRIM1,HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,POLR3B,POLR1C,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,CKS2,PAICS,TRIM28,POLR1E,NANS,TWISTNB,CDCA7L,CTPS1,HNRNPA2B1,DCK,POLD1,HOXA5,PPIE,CCT4,GARS,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,AMD1,PGR,NAMPT,LIG1,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,NIFK,NUP85,CAD,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,TK1,AFMID,BIRC5,POLR3F,POLD3,SUPT16H,E2F7,ALYREF,CKAP2,RRM1,PCNA,POLE,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,POLR1B,PDHB,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,CHUK,RUNX1,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,CCT6A,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,POLQ,NOL11,TARBP1,ELOVL6,DDX5,XBP1,RFC2,NEK2,EWSR1,HINFP,DTL,HMBS,FLVCR1,BLM,UMPS,RBM14,CENPF,STRAP,PSMC5,TFRC,PDHA1,UAP1,FOSL1,SMARCC1,DHX9,PSMA6,UCK2,POLA1,DDX20,AP000944.2,RFC4,DDX21,DLAT,SF1,DUT,C17orf53,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,MTHFD1,NEDD4,UGDH,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,LBR,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,PFAS,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,PRPS1,ACSL4,TADA2A,TAF15,TYMS,CDCA4,	darkgrey	VSMC_M8

GO:0031325	0.00	1.00	224	2483	positive regulation of cellular metabolic process	BP	0.11554	HNRNPAB,BCLAF1,CCT2,DDX39B,PRRC1,EZR,TCP1,DSCC1,ATAD2,PHF5A,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,CDC5L,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,MFSD2A,CCT4,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NAA15,NRDC,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,SAE1,DNAJC2,FOSB,NUFIP1,NUP85,PLAUR,BORA,DIS3,AXL,SPHK1,WDR43,CDC20,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,RFC3,DCUN1D2,HGF,ELK3,TCERG1,CCNB1,CD44,TCEA1,TPX2,UBA2,CENPJ,E2F1,PXYLP1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,CCT8,CCT7,CDCA2,GNL3,TBX3,RAD51,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,CENPE,NCL,KIF14,RBM23,NOL11,SF3B4,FANCI,DDX5,FANCB,XBP1,RFC2,NEK2,HINFP,H2AFX,BLM,RBM14,EIF4G1,PSMC5,CDK1,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,RFC4,DNA2,FANCM,EPHB2,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,DCUN1D5,GABPB1,RAD51AP1,ECT2,RBM3,DHX33,SIX4,MNAT1,FOXM1,LYAR,MSX1,RAC1,HNRNPU,INCENP,RAB27A,ADIPOR2,UBE2K,SMARCE1,RFC1,TOP2A,CDC6,EIF5A,BID,PRELID1,SRSF5,IQGAP3,CCT3,PMF1,HOXB7,FUS,LMNA,MAZ,AURKB,COL1A1,RAD23A,NFATC2IP,ILF2,PLK1,ILF3,MORF4L2,DNMT1,TADA2A,TAF15,SLC25A5,CDCA4,ATAD5,NNT,ELF4,AIFM1,RAP2C,UHRF1,EMP2,RBMX,TFAP4,TP73,DAZAP1,CHTF18,DKC1,PTBP1,CDT1,ZC3H18,EXOSC2,TRUB2,FAM129B,ACD,CBFB,PRIM2,HNRNPD,DRAP1,ACSL3,ABT1,AURKA,UBE2S,ERP29,PDCD2,PID1	darkgrey	VSMC_M8
GO:0071168	0.00	1.00	7	27	protein localization to chromatin	BP	0.11882	RAD21,VCP,EZH2,RUVBL2,ESCO2,CDCA5,PLK1	darkgrey	VSMC_M8
GO:0051653	0.00	1.00	10	49	spindle localization	BP	0.11882	CENPA,ESPL1,NUSAP1,ASPM,ZW10,SPDL1,PLK1,NDC80,NDE1,MAD2L1	darkgrey	VSMC_M8
GO:0009165	0.00	1.00	26	198	nucleotide biosynthetic process	BP	0.11882	ATP5F1B,VCP,PAICS,CTPS1,DCK,GARS,NAMPT,CAD,AFMID,RRM1,PDHB,ELOVL6,UMPS,PDHA1,UCK2,DLAT,DUT,MTHFD1,PFAS,PRPS1,ACSL4,TYMS,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0031100	0.00	1.00	11	58	animal organ regeneration	BP	0.12077	EZH2,CCNA2,CAD,AXL,PCNA,HGF,PRMT5,CDK1,SRSF5,TYMS,AURKA	darkgrey	VSMC_M8
GO:0040020	0.00	1.00	6	21	regulation of meiotic nuclear division	BP	0.12134	FBXO5,CDC20,TRIP13,PDE3A,RAD51AP1,MSX1	darkgrey	VSMC_M8
GO:0090342	0.00	1.00	9	42	regulation of cell aging	BP	0.12507	FBXO5,NAMPT,RBL1,EEF1E1,FOXM1,ARG2,LMNA,RSL1D1,NEK6	darkgrey	VSMC_M8
GO:1902373	0.00	1.00	10	49	negative regulation of mRNA catabolic process	BP	0.12662	SYNCRIP,THRAP3,NBAS,E2F1,TENT4A,DHX9,HNRNPU,FUS,TAF15,HNRNPD	darkgrey	VSMC_M8
GO:0072528	0.00	1.00	7	28	pyrimidine-containing compound biosynthetic process	BP	0.12662	CTPS1,CAD,UMPS,UCK2,DUT,PRPS1,TYMS	darkgrey	VSMC_M8
GO:0007292	0.00	1.00	16	101	female gamete generation	BP	0.1287	FBXO5,TTK,PGR,CDC25B,CCNB1,NRIP1,TRIP13,ASPM,PDE3A,FOSL1,DDX20,C17orf53,TOP2A,CCNB2,PLK1,AURKA	darkgrey	VSMC_M8
GO:0031109	0.00	1.00	17	109	microtubule polymerization or depolymerization	BP	0.12999	FBXO5,KIF24,KIF2C,CKAP2,TPX2,SKA3,KIF2A,CENPJ,CKAP5,KIF18A,KIF18B,FKBP4,RAC1,NDE1,MAP7D3,TPPP3,STMN1	darkgrey	VSMC_M8
GO:0090231	0.00	1.00	5	15	regulation of spindle checkpoint	BP	0.13295	GEN1,CCNB1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0090266	0.00	1.00	5	15	regulation of mitotic cell cycle spindle assembly checkpoint	BP	0.13295	GEN1,CCNB1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:1903504	0.00	1.00	5	15	regulation of mitotic spindle checkpoint	BP	0.13295	GEN1,CCNB1,NDC80,CDT1,MAD2L1	darkgrey	VSMC_M8
GO:0006360	0.00	1.00	10	50	transcription by RNA polymerase I	BP	0.13295	PWP1,POLR1C,POLR1E,CD3EAP,WDR43,UTP15,NCL,NOL11,DHX33,LYAR	darkgrey	VSMC_M8
GO:0006206	0.00	1.00	5	15	pyrimidine nucleobase metabolic process	BP	0.13478	CTPS1,CAD,RRM1,UMPS,TYMS	darkgrey	VSMC_M8
GO:0031126	0.00	1.00	4	10	sno(s)RNA 3'-end processing	BP	0.1369	FBL,EXOSC10,DKC1,EXOSC2	darkgrey	VSMC_M8
GO:0043628	0.00	1.00	8	36	ncRNA 3'-end processing	BP	0.13735	FBL,EXOSC8,INTS7,SSB,EXOSC10,ELAC2,DKC1,EXOSC2	darkgrey	VSMC_M8
GO:0051095	0.00	1.00	4	10	regulation of helicase activity	BP	0.14029	MSH6,MCM2,MSH3,MNAT1	darkgrey	VSMC_M8
GO:0071482	0.00	1.00	15	94	cellular response to light stimulus	BP	0.14433	POLH,POLD1,RUVBL2,POLD3,PCNA,PBK,PPID,CHEK1,RGS9,CDC25A,AIPL1,NEDD4,EIF2S1,AURKB,NOC2L	darkgrey	VSMC_M8
GO:0000956	0.00	1.00	16	102	nuclear-transcribed mRNA catabolic process	BP	0.15035	NCBP1,THRAP3,NBAS,SMG9,DIS3,XRN2,EIF4A3,EXOSC8,TENT4A,DDX5,SSB,EXOSC10,EDC3,SMG6,RNPS1,EXOSC2	darkgrey	VSMC_M8
GO:0034644	0.00	1.00	13	77	cellular response to UV	BP	0.15368	POLH,POLD1,RUVBL2,POLD3,PCNA,PBK,PPID,CHEK1,CDC25A,NEDD4,EIF2S1,AURKB,NOC2L	darkgrey	VSMC_M8
GO:0051446	0.01	1.00	5	16	positive regulation of meiotic cell cycle	BP	0.16026	CDC25C,CDC25B,CDC25A,RAD51AP1,MSX1	darkgrey	VSMC_M8
GO:0048255	0.01	1.00	9	43	mRNA stabilization	BP	0.16112	SYNCRIP,THRAP3,E2F1,TENT4A,DHX9,HNRNPU,FUS,TAF15,HNRNPD	darkgrey	VSMC_M8
GO:0035404	0.01	1.00	4	10	histone-serine phosphorylation	BP	0.16112	CCNB1,AURKB,VRK1,AURKA	darkgrey	VSMC_M8
GO:2001022	0.01	1.00	15	95	positive regulation of response to DNA damage stimulus	BP	0.16329	BCLAF1,TRIM28,PCNA,EEF1E1,DDX5,FANCB,H2AFX,NSMCE4A,DHX9,BRCA1,RAD51AP1,ANKLE1,FOXM1,MSX1,FUS	darkgrey	VSMC_M8
GO:0044703	0.01	1.00	71	688	multi-organism reproductive process	BP	0.1676	CCT2,FBXO5,TCP1,TTLL1,KIFC1,CDC25C,SRPK1,TRIM28,TTK,CCT4,NUP62,GJB3,PGR,NAMPT,RUVBL1,WDR33,MAST2,FOSB,CAD,AXL,XRN2,CDC25B,CCNB1,AAAS,POLR1B,E2F1,HMGB2,NRIP1,RACGAP1,CCT8,CCT7,KNL1,CCT5,KIF18A,ETS1,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,EIF4H,H2AFX,PDE3A,UMPS,CDK1,FOSL1,DDX20,CABYR,C17orf53,CDK16,USP42,ADIPOR2,TOP2A,ASF1B,CCNB2,CCT3,PTTG1,PLK1,BRIP1,ACSL4,SEPT6,RAI14,HOOK1,EMP2,NDC1,DAZAP1,FANCA,ODF2,TPPP3,HIST1H1A,AURKA	darkgrey	VSMC_M8
GO:0090501	0.01	1.00	18	124	RNA phosphodiester bond hydrolysis	BP	0.16966	POP1,NCBP1,TSEN2,DIS3,XRN2,EXOSC8,UTP20,DBR1,EXO1,CPSF7,EXOSC10,ELAC2,EDC3,SMG6,EXOSC2,NOB1,ABT1,FEN1	darkgrey	VSMC_M8
GO:1990830	0.01	1.00	13	77	cellular response to leukemia inhibitory factor	BP	0.16988	SRSF3,B3GNT2,MSC,HELLS,MYBL2,NCL,TFRC,HNRNPU,SLC25A5,GCLM,CTH,SRSF7,SRM	darkgrey	VSMC_M8
GO:0019953	0.01	1.00	60	565	sexual reproduction	BP	0.16988	CCT2,FBXO5,TCP1,TTLL1,KIFC1,CDC25C,SRPK1,TTK,CCT4,NUP62,GJB3,PGR,RUVBL1,WDR33,MAST2,AXL,XRN2,CDC25B,CCNB1,AAAS,E2F1,HMGB2,NRIP1,RACGAP1,CCT8,CCT7,KNL1,CCT5,KIF18A,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,EIF4H,H2AFX,PDE3A,CDK1,FOSL1,DDX20,CABYR,C17orf53,CDK16,USP42,TOP2A,ASF1B,CCNB2,CCT3,PTTG1,PLK1,BRIP1,SEPT6,RAI14,HOOK1,NDC1,DAZAP1,FANCA,ODF2,HIST1H1A,AURKA	darkgrey	VSMC_M8

GO:0042274	0.01	1.00	11	64	ribosomal small subunit biogenesis	BP	0.17212	SRFBP1,BYSL,NOL10,MRPS7,UTP20,WDR3,FP565260.1,NOL11,UTP25,NOB1,ABT1	darkgrey	VSMC_M8
GO:0051293	0.01	1.00	9	44	establishment of spindle localization	BP	0.17212	CENPA,ESPL1,NUSAP1,ZW10,SPDL1,PLK1,NDC80,NDE1,MAD2L1	darkgrey	VSMC_M8
GO:0051443	0.01	1.00	6	23	positive regulation of ubiquitin-protein transferase activity	BP	0.17484	CDC20,DCUN1D2,UBE2C,DCUN1D5,PLK1,UBE2S	darkgrey	VSMC_M8
GO:1903829	0.01	1.00	30	241	positive regulation of cellular protein localization	BP	0.17484	CCT2,EZR,TCP1,HSP90AB1,CENPQ,TRIM28,CCT4,NUP62,SAE1,IPO5,CCT8,CCT7,GNL3,BAP1,CCT5,CCT6A,CDK1,TFRC,EPHB2,NMD3,ECT2,CCT3,PLK1,NDC80,MTCL1,DKC1,CDT1,ARF6,ACSL3,UBE2J2	darkgrey	VSMC_M8
GO:0009156	0.01	1.00	7	30	ribonucleoside monophosphate biosynthetic process	BP	0.18022	PAICS,CAD,UMPS,UCK2,PFAS,PRPS1,GART	darkgrey	VSMC_M8
GO:0090502	0.01	1.00	11	62	RNA phosphodiester bond hydrolysis, endonucleolytic	BP	0.18161	POP1,TSEN2,UTP20,DBR1,EXO1,ELAC2,EDC3,SMG6,NOB1,ABT1,FEN1	darkgrey	VSMC_M8
GO:1990823	0.01	1.00	13	78	response to leukemia inhibitory factor	BP	0.1817	SRSF3,B3GNT2,MSC,HELLS,MYBL2,NCL,TFRC,HNRNPU,SLC25A5,GCLM,CTH,SRSF7,SRM	darkgrey	VSMC_M8
GO:0010629	0.01	1.00	77	766	negative regulation of gene expression	BP	0.18402	CDK2,EZR,HSP90AB1,TRIM28,NCBP1,U2AF2,HNRNPA2B1,SYNCRIP,PABPC4,THRAP3,EZH2,NBAS,PGR,PUS7,RNASEH2B,SMG9,DIS3,AXL,XRN2,EIF4A3,EXOSC8,HGF,RRP8,CCNB1,SFSWAP,E2F1,HMGB2,HELLS,RBL1,CREB3L1,FASTKD3,TENT4A,NCL,TRAIP,DDX5,HINFP,SSB,EIF4G1,CDK1,DHX9,HNRNPR,DGCR8,UFD1,CNOT9,SUV39H1,EIF2AK1,RAC1,HNRNPU,ADIPOR2,EIF2S1,ARG2,IQGAP3,EXOSC10,FUS,PTRH2,ILF3,BRIP1,DNMT1,EDC3,TAF15,TYMS,HNRNPM,SERBP1,RBMX,TFAP4,SMG6,RNPS1,PTBP1,PIK3CD,EXOSC2,SRRT,HNRNPD,AURKA,SRSF7,ERP29,POLE3,MBD2	darkgrey	VSMC_M8
GO:0043144	0.01	1.00	4	11	sno(s)RNA processing	BP	0.18465	FBL,EXOSC10,DKC1,EXOSC2	darkgrey	VSMC_M8
GO:0032886	0.01	1.00	26	202	regulation of microtubule-based process	BP	0.19559	NUP62,GEN1,PLK4,STIL,CHORDC1,BORA,CKAP2,TPX2,SKA3,CENPJ,CFAP298,CKAP5,KIF18A,RASSF1,RBM14,KIF15,BRCA1,TACC3,FKBP4,RAC1,HNRNPU,PLK1,CEP76,CCNF,STMN1,AURKA	darkgrey	VSMC_M8
GO:0042542	0.01	1.00	17	118	response to hydrogen peroxide	BP	0.19559	APTX,EZH2,SDC1,PPP5C,AXL,SPHK1,NET1,PCNA,HGF,PPP1R15B,ETS1,CDK1,FOSL1,ECT2,COL1A1,AIFM1,SIGMAR1	darkgrey	VSMC_M8
GO:0006413	0.01	1.00	15	99	translational initiation	BP	0.19612	NCBP1,EIF3M,EIF2B1,ABCE1,PPP1R15B,KHDRBS1,EIF4H,EIF4G1,DHX33,EIF2AK1,EIF2S1,EIF3B,EIF4A1,EIF5,GLE1	darkgrey	VSMC_M8
GO:0051781	0.01	1.00	11	63	positive regulation of cell division	BP	0.19873	NUP62,CDC25B,KIF20B,RACGAP1,CIT,KIF14,ECT2,CDC6,AURKB,KIF23,POLDIP2	darkgrey	VSMC_M8
GO:0009129	0.01	1.00	5	17	pyrimidine nucleoside monophosphate metabolic process	BP	0.20103	CAD,UMPS,UCK2,DUT,TYMS	darkgrey	VSMC_M8
GO:0051172	0.01	0.99	162	1770	negative regulation of nitrogen compound metabolic process	BP	0.20307	BCLAF1,FBXO5,EZR,PPP2R5D,PWP1,CYP51A1,HSP90AB1,TRIM28,U2AF2,MSH6,SYNCRIP,THRAP3,EZH2,NUP62,PHF19,NBAS,RUVBL2,PUS7,DNAJC2,CHORDC1,PPP5C,MASTL,FOSB,GRIN2C,PLAUR,DBI,DIS3,SPHK1,SRSF2,NCAPG2,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,E2F7,PCNA,EXOSC8,ZNF703,HGF,ELK3,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,PARPBP,E2F1,ABCE1,CCNE1,HMGB2,MSC,TERF1,NRIP1,LOXL3,PBK,HEY1,PPID,RBL1,MSH3,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,RUNX1,PPP1R15B,MDM4,NCOA5,TENT4A,NSUN2,PHC2,GMNN,KHDRBS1,NCL,PRMT5,POLQ,DDX5,FANCB,SPP2,PRKAR2A,HINFP,NF2,BLM,CEP85,CENPF,STRAP,EIF4G1,PSMC5,AUNIP,PAK2,SMARCC1,DHX9,HNRNPR,DDX20,SF1,BARD1,EPHB2,BRCA1,TFPI,CNOT9,NSD2,MYBBP1A,CREG1,ANKLE1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM22OA,HNRNPU,UCHL1,NEDD4,SMARCE1,RFC1,EIF2S1,EXOSC10,HDGF,FUS,MAZ,AURKB,PTTG1,SPAG9,PLK1,ILF3,DNMT1,TAF15,TYMS,NNT,UHRF1,RBMX,NXN,TFAP4,SMG6,NOC2L,RNPS1,G6PD,DKC1,PTBP1,EXOSC2,FAM129B,SF3B3,ACD,CBFB,DEPDC1,USP4,HIST1H1A,HNRNPD,MAD2L1,DRAP1,CDKN2C,SRSF7,PID1,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0034770	0.01	1.00	4	11	histone H4-K20 methylation	BP	0.20635	PWP1,SETD4,BRCA1,NSD2	darkgrey	VSMC_M8
GO:0051704	0.01	0.99	72	709	multi-organism process	BP	0.20994	CCT2,FBXO5,TCP1,TTLL1,KIFC1,CDC25C,SRPK1,TRIM28,TTK,CCT4,NUP62,GJB3,PGR,NAMPT,RUVBL1,WDR33,MAST2,FOSB,CAD,AXL,XRN2,CDC25B,CCNB1,AAAS,POLR1B,E2F1,HMGB2,NRIP1,RACGAP1,CCT8,CCT7,KNL1,CCT5,NUP153,KIF18A,ETS1,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,EIF4H,H2AFX,PDE3A,UMPS,CDK1,FOSL1,DDX20,CABYR,C17orf53,CDK16,USP42,ADIPOR2,TOP2A,ASF1B,CCNB2,CCT3,PTTG1,PLK1,BRIP1,ACSL4,SEPT6,RAI14,HOOK1,EMP2,NDC1,DAZAP1,FANCA,ODF2,TPPP3,HIST1H1A,AURKA	darkgrey	VSMC_M8
GO:2000105	0.01	1.00	4	11	positive regulation of DNA-dependent DNA replication	BP	0.21187	DBF4,E2F7,E2F8,CDT1	darkgrey	VSMC_M8
GO:0006356	0.01	1.00	7	31	regulation of transcription by RNA polymerase I	BP	0.2127	PWP1,WDR43,UTP15,NCL,NOL11,DHX33,LYAR	darkgrey	VSMC_M8
GO:0030330	0.01	1.00	11	63	DNA damage response, signal transduction by p53 class mediator	BP	0.21528	GTSE1,CASP2,E2F7,SNAI2,CD44,EEF1E1,MDM4,DDX5,FOXM1,MSX1,TFAP4	darkgrey	VSMC_M8

GO:0009892	0.01	0.99	201	2254	negative regulation of metabolic process	BP	0.21548	CDK2,BCLAF1,FBXO5,EZR,PPP2R5D,PWP1,CYP51A1,HSP90AB1,TRIM28,NCBP1,U2AF2,MSH6,HNRNPA2B1,MFSD2A,SYNCRIP,PABPC4,THRAP3,EZH2,NUP62,PHF19,NBAS,NRDC,RUVBL2,PGR,NAMPT,PUS7,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,FOSB,GRIN2C,SMG9,PLAUR,DBI,DIS3,AXL,SPHK1,SRSF2,XRN2,NCAPG2,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,E2F7,PCNA,EXOSC8,PGAM5,ZNF703,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,PARPBP,E2F1,ABCE1,CCNE1,HMGB2,MSC,TERF1,HELLS,NRIP1,LOXL3,PBK,HEY1,PPID,RBL1,MSH3,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,RUNX1,PPP1R15B,MDM4,NCOA5,FASTKD3,TENT4A,NSUN2,PHC2,GMNN,KHDRBS1,NCL,TRAIP,PRMT5,POLQ,DDX5,FANCB,SPP2,PRKAR2A,HINFP,NF2,BLM,SSB,CEP85,CENPF,STRAP,EIF4G1,PSMC5,AUNIP,CDK1,S100A11,PAK2,SMARCC1,DHX9,HNRNPR,DDX20,DGCR8,SF1,BARD1,EPHB2,SMARCAL1,UFD1,BRCA1,TFPI,CNOT9,NSD2,MYBBP1A,CREG1,ANKLE1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,UCHL1,ADIPOR2,NEDD4,SMARCE1,RFC1,CDC6,EIF2S1,ARG2,IQGAP3,EXOSC10,HDGF,FUS,MAZ,AURKB,PTTG1,SPAG9,PLK1,PTRH2,ILF3,BRIP1,DNMT1,EDC3,TAF15,TYMS,HNRNPM,SERBP1,NNT,POLDIP2,UHRF1,RBMX,NXN,TFAP4,SMG6,NOC2L,RNPS1,G6PD,DKC1,PTBP1,PIK3CD,EXOSC2,FAM129B,SF3B3,ACD,CBFB,DEPDC1,SRRT,USP4,HIST1H1A,HNRNPD,MAD2L1,DRAP1,CDKN2C,AURKA,SRSF7,ERP29,POLE3,PID1,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0009411	0.01	1.00	18	127	response to UV	BP	0.21567	POLH,MSH6,POLD1,RUVBL2,POLD3,PCNA,PBK,PPID,HMGN1,CHEK1,DTL,CDC25A,NEDD4,EIF2S1,AURKB,USP1,NOC2L,FEN1	darkgrey	VSMC_M8
GO:0060236	0.01	1.00	7	31	regulation of mitotic spindle organization	BP	0.21567	NUP62,BORA,TPX2,KIF15,TACC3,HNRNPU,PLK1	darkgrey	VSMC_M8
GO:0032069	0.01	1.00	5	17	regulation of nuclease activity	BP	0.21581	PCNA,TCEA1,ABCE1,HMGB2,TERF1	darkgrey	VSMC_M8
GO:0051640	0.01	1.00	49	447	organelle localization	BP	0.216	TMED9,EZR,ARFGAP3,KIFC1,CENPQ,CDCA8,NUP62,CENPA,PREB,KIF2C,CHMP6,CCNB1,ESPL1,ABCE1,VAMP8,TERF1,FAM83D,NUSAP1,KIF18A,CENPE,KIF14,ASPM,ARCN1,CENPF,NUF2,LSG1,ZW10,CDCA5,NMD3,DLGAP5,MYO5A,HNRNPU,UCHL1,INCENP,RAB27A,LMNA,KIF22,SPDL1,AURKB,SPAG9,PLK1,SYT4,NDC80,NDE1,PIK3CD,CDT1,TOR1A,MAD2L1,BLOC1S2	darkgrey	VSMC_M8
GO:1904951	0.01	1.00	31	257	positive regulation of establishment of protein localization	BP	0.21762	CCT2,EZR,TCP1,HSP90AB1,CEP135,TRIM28,ANP32B,CCT4,SAE1,KCNN4,IPO5,KIF20B,CENPJ,RBP4,CCT8,PPID,CCT7,BAP1,CCT5,CCT6A,ICE1,CDK1,ECT2,RAC1,CCT3,ACSL4,MTCL1,DKC1,ARF6,ACSL3,UBE2J2	darkgrey	VSMC_M8
GO:0070727	0.01	0.99	136	1462	cellular macromolecule localization	BP	0.22063	TMED9,XPOT,NUP107,CCT2,EZR,TCP1,RAD21,NUP50,ARFGAP3,MAN1A1,MTBP,DESI1,RANGAP1,HSPA9,TNPO3,BYSL,VCP,HSP90AB1,CENPQ,MIOS,NOL8,TRIM28,ANP32B,TTK,CCT4,EZH2,NUP62,RUVBL2,STIL,SEC61A1,SAE1,CHCHD4,CENPA,COG3,GRIN2C,TOMM40,PREB,NUP85,SRP68,SEC23B,IPO5,KIF20B,HSP90B1,CCNE1,VAMP8,ATP1B3,KNTC1,TRAM1,TERF1,ESCO2,CCT8,BUB1B,CCT7,GNL3,FAM83D,NUP93,KNL1,TOMM70,CCNE2,YWHAB,BAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,ICE1,CEP72,CSE1L,RPA2,UTP25,IPO4,NUP133,NF2,SEC24D,SSB,ARCN1,BUB3,CDK1,TFRC,DHX9,ZW10,CDCA5,IFT80,BARD1,EPHB2,NMD3,UFD1,ANKLE1,ECT2,SIX4,MSX1,KDELR2,MYO5A,HNRNPU,RAB27A,NEDD4,BID,EXOSC10,SH3PXD2B,CCT3,LMNA,LTBP2,SPDL1,AURKB,COL1A1,ZWILCH,TIMM8A,PLK1,NUP62CL,TIMM44,NDC80,SEPT6,MTCL1,AIFM1,EMP2,NDC1,RPA1,HASPIN,DKC1,CDT1,EMC8,EXOSC2,TOR1A,NUP188,ACD,ARF6,RAPGEF6,USP4,GBP5,SPCS3,ACSL3,AURKA,ERP29,PID1,UBE2J2	darkgrey	VSMC_M8
GO:1901998	0.01	1.00	7	31	toxin transport	BP	0.2209	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT3	darkgrey	VSMC_M8
GO:0051294	0.01	1.00	7	31	establishment of spindle orientation	BP	0.22206	CENPA,ZW10,SPDL1,PLK1,NDC80,NDE1,MAD2L1	darkgrey	VSMC_M8
GO:0007129	0.01	1.00	8	39	homologous chromosome pairing at meiosis	BP	0.22617	RAD21,FANCD2,CCNE1,CCNE2,TRIP13,PSMC3IP,BRIP1,NDC1	darkgrey	VSMC_M8
GO:0033036	0.01	0.99	209	2356	macromolecule localization	BP	0.24055	TMED9,XPOT,NUP43,NUP107,CCT2,DDX39B,EZR,FBN2,TCP1,RAD21,NUP50,NUS1,ARFGAP3,MAN1A1,MTBP,DESI1,RANGAP1,KIF20A,HSPA9,SRSF3,TNPO3,BYSL,TJP2,CYP51A1,VCP,HSP90AB1,CENPQ,CEP135,MIOS,NOL8,TRIM28,NCBP1,ANP32B,TTK,HNRNPA2B1,MFSD2A,CCT4,NUP205,EZH2,NUP62,NBAS,RUVBL2,STIL,SEC61A1,RUVBL1,SAE1,CHCHD4,CENPA,NASP,COG3,GRIN2C,TOMM40,PREB,KCNN4,NUP85,DBI,BORA,SRP68,GDI2,SEC23B,FBL,RRBP1,IPO5,EIF4A3,CHMP6,ARHGDIA,ALYREF,AAAS,KIF20B,CENPJ,HSP90B1,NECAB3,CCNE1,VAMP8,ATP1B3,SLC10A7,KNTC1,TRAM1,CEP55,RBP4,TERF1,NRIP1,NUP160,ESCO2,SELENOT,CCT8,PPID,BUB1B,CCT7,GNL3,FAM83D,CKAP5,NUP93,KNL1,TOMM70,CCNE2,YWHAB,HMGCR,BAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,KIF18A,NSUN2,ICE1,KHDRBS1,CEP72,KIF14,CSE1L,PITPNB,XBP1,RPA2,UTP25,MCM3AP,IPO4,NUP133,HINFP,NF2,SEC24D,SSB,NOP58,ARCN1,CENPF,BUB3,ARFGAP1,CDK1,HDLBP,TFRC,PAK2,DHX9,LSG1,HNRNPA3,ZW10,CDCA5,IFT80,BARD1,EPHB2,NMD3,UFD1,NSD2,CDK16,SLBP,ANKLE1,ECT2,SIX4,MSX1,RAC1,KDELR2,MYO5A,HNRNPU,RAB27A,NEDD4,EIF5A,BID,DDX39A,PRELID1,EXOSC10,SH3PXD2B,CCT3,LMNA,LTBP2,SPDL1,AURKB,COL1A1,CEP128,ZWILCH,TIMM8A,PLK1,NUP62CL,ACSL4,TIMM44,NDC80,SEPT6,MTCL1,AIFM1,RSL1D1,HOOK1,EMP2,LIPG,NDC1,RPA1,SMG6,THOC6,HASPIN,DKC1,CDT1,EMC8,EXOSC2,TOR1A,NUP188,GLE1,ODF2,ACD,ARF6,RAPGEF6,USP4,GBP5,SPCS3,ACSL3,AURKA,SRSF7,SIGMAR1,ERP29,XKR5,PID1,CLSTN3,UBE2J2	darkgrey	VSMC_M8

GO:0043487	0.01	1.00	20	148	regulation of RNA stability	BP	0.25752	SYNCRIP,PABPC4,THRAP3,DIS3,EXOSC8,E2F1,FASTKD3,TENT4A,NSUN2,DHX9,HNRNPR,HNRNPU,FUS,TAF15,HNRNPM,SERBP1,DKC1,ZC3H18,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0045934	0.01	0.99	107	1115	negative regulation of nucleobase-containing compound metabolic process	BP	0.26091	BCLAF1,EZR,TRIM28,U2AF2,MSH6,SYNCRIP,THRAP3,EZH2,PHF19,NBAS,RUVBL2,DNAJC2,FOSB,SRSF2,BIRC5,E2F7,PCNA,ZNF703,ELK3,TCERG1,CBX5,SFSWAP,SNAI2,PARPBP,E2F1,ABCE1,CCNE1,HMGB2,MSC,TERF1,NRIP1,LOXL3,HEY1,PPID,RBL1,MSH3,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,TENT4A,NSUN2,PHC2,GMNN,KHDRBS1,PRMT5,POLQ,DDX5,FANCB,HINFP,BLM,CENPF,STRAP,PSMC5,AUNIP,DHX9,DDX20,SF1,BARD1,BRCA1,NSD2,MYBBP1A,CREG1,ANKLE1,SUV39H1,SIX4,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,EXOSC10,HDGF,FUS,MAZ,AURKB,PLK1,ILF3,DNMT1,TAF15,UHRF1,RBMX,TFAP4,SMG6,NOC2L,RNPS1,DKC1,PTBP1,FAM129B,ACD,CBFB,DEPDC1,HIST1H1A,HNRNPD,DRAP1,SRSF7,PID1,MBD2	darkgrey	VSMC_M8
GO:0044030	0.01	1.00	5	18	regulation of DNA methylation	BP	0.26267	MIS18A,PRMT5,BRCA1,FAM129B,MBD2	darkgrey	VSMC_M8
GO:0007063	0.01	1.00	5	18	regulation of sister chromatid cohesion	BP	0.26295	RAD21,ESPL1,BUB1,CDCA5,FEN1	darkgrey	VSMC_M8
GO:0051246	0.01	0.99	175	1953	regulation of protein metabolic process	BP	0.26295	CDK2,DDX39B,FBXO5,PRRC1,EZR,MTBP,DESI1,CDC25C,PPP2R5D,PWP1,DBF4,CYP51A1,VCP,HSP90AB1,PUM3,CKS2,NCBP1,ANP32B,U2AF2,PPP6R1,TTK,CYCS,SYNCRIP,EZH2,ODC1,NUP62,CLSPN,PHF19,PRMT1,CASP2,NRDC,RUVBL2,PUS7,CCNA2,SAE1,CHORDC1,PPP5C,MASTL,GRIN2C,PLAUR,DBI,BORA,DIS3,SPHK1,NCAPG2,CDC20,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,CHFR,EXOSC8,CDC25B,DCUN1D2,HGF,CCNB1,CD44,TPX2,UBA2,HSP90B1,NECAB3,ABCE1,CCNE1,PXYLP1,PBK,SELENOT,CCNL1,CDCA2,GNL3,FAM83D,RAD51,CCNE2,YWHAB,HMGCR,RUNX1,PPP1R15B,MDM4,UBE2C,PSMD14,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,CHEK1,KHDRBS1,CENPE,NCL,KIF14,FANCI,SPP2,EIF4H,PRKAR2A,DTL,NF2,BLM,CEP85,EIF4G1,PSMC5,CDC25A,TFRC,PAK2,SMARCC1,DHX9,HNRNPR,FANCM,BARD1,EPHB2,BRCA1,TFPI,CNOT9,CDKN3,DCUN1D5,ECT2,RBM3,MNAT1,EIF2AK1,RAC1,UCHL1,INCENP,ADIPOR2,UBE2K,NEDD4,CCNB3,CDC6,EIF5A,BID,PSMD3,EIF2S1,EIF3B,PRELID1,CCNB2,IQGAP3,LMNA,RAD23A,PTTG1,SPAG9,GEMIN5,PLK1,ILF3,DNMT1,TADA2A,EIF5,TYMS,NNT,WDR70,AIFM1,RAP2C,UHRF1,EMP2,LIPG,NXN,TFAP4,PKMYT1,NOC2L,CCNF,ZNF598,G6PD,PTBP1,EXOSC2,GLE1,TRUB2,SF3B3,USP4,HNRNPD,MAD2L1,CDKN2C,AURKA,UBE2S,ERP29,PDCD2,PID1,DUSP7	darkgrey	VSMC_M8
GO:0009893	0.01	0.99	246	2815	positive regulation of metabolic process	BP	0.26295	HNRNPAB,BCLAF1,CCT2,DDX39B,PRRC1,EZR,PANX2,TCP1,DSCC1,ATAD2,PHF5A,FAM49B,PPP2R5D,PWP1,DBF4,POLR3B,VCP,HSP90AB1,CDC5L,CKS2,TRIM28,NCBP1,ANP32B,U2AF2,TTK,CYCS,HNRNPA2B1,GRSF1,HOXA5,MFSD2A,SYNCRIP,CCT4,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,NRDC,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,SAE1,DNAJC2,FOSB,NUFIP1,NUP85,PLAUR,BORA,DIS3,AXL,SPHK1,WDR43,CDC20,POLR3F,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,CDC25B,RFC3,DCUN1D2,HGF,ELK3,TCERG1,CCNB1,CD44,TCEA1,TPX2,UBA2,CENPJ,E2F1,PXYLP1,ZNF827,HMGB2,RBP4,ATF1,NRIP1,UTP15,HEY1,FAM98B,CCT8,CCT7,CDCA2,GNL3,TBX3,RAD51,CREB3L1,TOMM70,MYBL2,E2F8,MTDH,CHUK,RUNX1,SETD4,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,CENPE,NCL,KIF14,RBM23,NOL11,ELOVL6,SF3B4,FANCI,MNDA,DDX5,FANCB,XBP1,RFC2,NEK2,HINFP,DTL,H2AFX,BLM,RBM14,EIF4G1,PSMC5,CDK1,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,RFC4,DNA2,DDX21,FANCM,BARD1,EPHB2,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,DCUN1D5,GABPB1,RAD51AP1,ECT2,RBM3,DHX33,SIX4,MNAT1,FOXM1,LYAR,FH,MSX1,RAC1,HNRNPU,INCENP,RAB27A,ADIPOR2,UBE2K,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,EIF5A,BID,PRELID1,SRSF5,IQGAP3,CCT3,PMF1,HOXB7,FUS,LMNA,ALOX15B,MAZ,AURKB,COL1A1,RAD23A,NFATC2IP,ILF2,PLK1,ILF3,MORF4L2,DNMT1,TADA2A,TAF15,SLC25A5,CDCA4,ATAD5,NNT,ELF4,AIFM1,RAP2C,UHRF1,EMP2,RBMX,TFAP4,TP73,DAZAP1,CHTF18,DKC1,PTBP1,PIK3CD,CDT1,ZC	darkgrey	VSMC_M8
GO:0007276	0.01	0.99	50	469	gamete generation	BP	0.26386	FBXO5,TTLL1,KIFC1,CDC25C,SRPK1,TTK,NUP62,GJB3,PGR,RUVBL1,WDR33,MAST2,AXL,XRN2,CDC25B,CCNB1,E2F1,HMGB2,NRIP1,RACGAP1,KNL1,KIF18A,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,H2AFX,PDE3A,FOSL1,DDX20,CABYR,C17orf53,CDK16,USP42,TOP2A,ASF1B,CCNB2,PTTG1,PLK1,BRIP1,SEPT6,RAI14,HOOK1,NDC1,DAZAP1,FANCA,ODF2,HIST1H1A,AURKA	darkgrey	VSMC_M8
GO:0009303	0.01	1.00	7	33	rRNA transcription	BP	0.26578	PWP1,POLR1E,CD3EAP,NIFK,POLR1B,NCL,NOL11	darkgrey	VSMC_M8
GO:1905214	0.01	1.00	4	12	regulation of RNA binding	BP	0.2667	NCBP1,EIF4A3,NUCKS1,EIF4G1	darkgrey	VSMC_M8
GO:0001832	0.01	1.00	5	18	blastocyst growth	BP	0.26882	NCAPG2,GINS4,CHEK1,GINS1,PALB2	darkgrey	VSMC_M8
GO:0010458	0.01	1.00	6	26	exit from mitosis	BP	0.28089	ANLN,KNTC1,UBE2C,ZW10,CDCA5,UBE2S	darkgrey	VSMC_M8

GO:0034613	0.01	0.99	134	1451	cellular protein localization	BP	0.28233	TMED9,XPOT,NUP107,CCT2,EZR,TCP1,RAD21,NUP50,ARFGAP3,MAN1A1,MTBP,DESI1,RANGAP1,HSPA9,TNPO3,BYSL,VCP,HSP90AB1,CENPQ,MIOS,NOL8,TRIM28,ANP32B,TTK,CCT4,EZH2,NUP62,RUVBL2,STIL,SEC61A1,SAE1,CHCHD4,CENPA,COG3,GRIN2C,TOMM40,PREB,NUP85,SRP68,SEC23B,IPO5,KIF20B,HSP90B1,CCNE1,VAMP8,ATP1B3,KNTC1,TRAM1,TERF1,ESCO2,CCT8,BUB1B,CCT7,GNL3,FAM83D,NUP93,KNL1,TOMM70,CCNE2,YWHAB,BAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,ICE1,CEP72,CSE1L,RPA2,UTP25,IPO4,NUP133,NF2,SEC24D,SSB,ARCN1,BUB3,CDK1,TFRC,DHX9,ZW10,CDCA5,IFT80,BARD1,EPHB2,NMD3,UFD1,ANKLE1,ECT2,SIX4,MSX1,KDELR2,MYO5A,HNRNPU,RAB27A,NEDD4,BID,SH3PXD2B,CCT3,LMNA,LTBP2,SPDL1,AURKB,COL1A1,ZWILCH,TIMM8A,PLK1,NUP62CL,TIMM44,NDC80,SEPT6,MTCL1,AIFM1,EMP2,NDC1,RPA1,HASPIN,DKC1,CDT1,EMC8,TOR1A,NUP188,ACD,ARF6,RAPGEF6,USP4,GBP5,SPCS3,ACSL3,AURKA,ERP29,PID1,UBE2J2	darkgrey	VSMC_M8
GO:0000469	0.01	1.00	6	26	cleavage involved in rRNA processing	BP	0.29089	EXOSC8,UTP20,EXOSC10,EXOSC2,NOB1,ABT1	darkgrey	VSMC_M8
GO:0051438	0.01	1.00	8	43	regulation of ubiquitin-protein transferase activity	BP	0.29865	FBXO5,CDC20,DCUN1D2,UBE2C,DCUN1D5,PLK1,MAD2L1,UBE2S	darkgrey	VSMC_M8
GO:0045842	0.01	1.00	4	12	positive regulation of mitotic metaphase/anaphase transition	BP	0.29865	CDC16,ESPL1,DLGAP5,CDT1	darkgrey	VSMC_M8
GO:1901970	0.01	1.00	4	12	positive regulation of mitotic sister chromatid separation	BP	0.29865	CDC16,ESPL1,DLGAP5,CDT1	darkgrey	VSMC_M8
GO:0046831	0.01	1.00	4	12	regulation of RNA export from nucleus	BP	0.30554	NUP153,NSUN2,KHDRBS1,DHX9	darkgrey	VSMC_M8
GO:1902410	0.01	1.00	5	19	mitotic cytokinetic process	BP	0.30969	KIF20A,NUP62,CHMP6,KIF20B,CEP55	darkgrey	VSMC_M8
GO:0010638	0.01	0.99	46	428	positive regulation of organelle organization	BP	0.30969	TMED9,CCT2,TCP1,RAD21,CEP135,TRIM28,HNRNPA2B1,CCT4,NUP62,SDC1,PLK4,CDC42EP4,PLAUR,SPHK1,PGAM5,CDC16,ESPL1,CENPJ,CCT8,CCT7,GNL3,CKAP5,NUSAP1,CCT5,CCT6A,NEK2,NF2,DLGAP5,RAD51AP1,MSX1,RAC1,FSCN1,BID,NES,CCT3,AURKB,DNMT1,SLC25A5,DKC1,CDT1,ACD,ARPC4,ARF6,HNRNPD,AURKA,FEN1	darkgrey	VSMC_M8
GO:0031507	0.01	1.00	7	33	heterochromatin assembly	BP	0.31419	TRIM28,RRP8,HELLS,SUV39H1,DNMT1,POLE3,MBD2	darkgrey	VSMC_M8
GO:0048012	0.01	1.00	4	13	hepatocyte growth factor receptor signaling pathway	BP	0.31873	HGF,RAC1,BCAR1,STMN1	darkgrey	VSMC_M8
GO:0006289	0.01	1.00	9	50	nucleotide-excision repair	BP	0.32032	POLD1,POLD3,POLE,HMGN1,RPA2,MNAT1,RAD23A,BRIP1,RPA1	darkgrey	VSMC_M8
GO:0009208	0.01	1.00	4	13	pyrimidine ribonucleoside triphosphate metabolic process	BP	0.32574	CTPS1,CAD,ENTPD7,UCK2	darkgrey	VSMC_M8
GO:0009263	0.01	1.00	4	13	deoxyribonucleotide biosynthetic process	BP	0.32899	DCK,RRM1,DUT,TYMS	darkgrey	VSMC_M8
GO:2000104	0.01	1.00	4	13	negative regulation of DNA-dependent DNA replication	BP	0.32899	FBXO5,GMNN,BLM,SMARCAL1	darkgrey	VSMC_M8
GO:0006099	0.01	1.00	6	27	tricarboxylic acid cycle	BP	0.3322	PDHB,SUCLG1,PDHA1,DLAT,FH,NNT	darkgrey	VSMC_M8
GO:0090224	0.01	1.00	7	34	regulation of spindle organization	BP	0.33533	NUP62,BORA,TPX2,KIF15,TACC3,HNRNPU,PLK1	darkgrey	VSMC_M8
GO:2000779	0.01	0.99	12	76	regulation of double-strand break repair	BP	0.33622	PARPBP,RAD51,DEK,CHEK1,POLQ,FANCB,RPA2,AUNIP,NSD2,RAD51AP1,FOXM1,FUS	darkgrey	VSMC_M8
GO:0051347	0.01	0.99	47	441	positive regulation of transferase activity	BP	0.34077	CCT2,PRRC1,TCP1,DSCC1,DBF4,HSP90AB1,CKS2,HNRNPA2B1,CCT4,EZH2,CLSPN,DBI,BORA,AXL,CDC20,PCNA,CDC25B,RFC3,DCUN1D2,CCNB1,TPX2,UBE2C,RFC5,HMGN1,GCN1,CENPE,KIF14,RFC2,NEK2,PAK2,RFC4,EPHB2,DCUN1D5,ECT2,MNAT1,INCENP,CDC6,AURKB,PLK1,EMP2,CHTF18,DKC1,ACD,PRIM2,HNRNPD,UBE2S,ERP29	darkgrey	VSMC_M8
GO:1903827	0.01	0.99	48	454	regulation of cellular protein localization	BP	0.34512	CCT2,EZR,TCP1,RANGAP1,BYSL,VCP,HSP90AB1,CENPQ,TRIM28,ANP32B,CCT4,NUP62,SAE1,IPO5,KIF20B,CCNE1,VAMP8,TERF1,CCT8,CCT7,GNL3,CCNE2,BAP1,NOLC1,CCT5,CCT6A,ICE1,CEP72,NF2,CDK1,TFRC,CDCA5,BARD1,EPHB2,NMD3,ECT2,CCT3,LMNA,PLK1,NDC80,MTCL1,DKC1,CDT1,TOR1A,ARF6,ACSL3,PID1,UBE2J2	darkgrey	VSMC_M8
GO:0090398	0.01	0.99	11	68	cellular senescence	BP	0.3477	CDK2,FBXO5,SMC6,NAMPT,RBL1,TBX3,EEF1E1,H2AFX,ARG2,RSL1D1,NEK6	darkgrey	VSMC_M8
GO:1903313	0.01	0.99	15	105	positive regulation of mRNA metabolic process	BP	0.34891	NCBP1,THRAP3,DIS3,EXOSC8,CCNB1,TENT4A,NCL,SF3B4,HNRNPR,TRA2B,RBM3,RBMX,DAZAP1,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0040029	0.01	0.99	13	86	regulation of gene expression, epigenetic	BP	0.34891	TRIM28,EZH2,RRP8,HELLS,CHEK1,BRCA1,SUV39H1,HNRNPU,EXOSC10,DNMT1,CDCA4,POLE3,MBD2	darkgrey	VSMC_M8
GO:2000045	0.01	0.99	14	97	regulation of G1/S transition of mitotic cell cycle	BP	0.35941	CDK2,GTSE1,MTBP,EZH2,CASP2,E2F7,WEE1,E2F1,RBL1,KIF14,RPA2,EIF4G1,CDC6,BID	darkgrey	VSMC_M8
GO:0070301	0.01	0.99	12	79	cellular response to hydrogen peroxide	BP	0.35946	EZH2,PPP5C,AXL,SPHK1,NET1,PCNA,HGF,ETS1,CDK1,ECT2,AIFM1,SIGMAR1	darkgrey	VSMC_M8
GO:0000184	0.01	1.00	7	34	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	0.36395	NCBP1,NBAS,SMG9,EIF4A3,EXOSC10,SMG6,RNPS1	darkgrey	VSMC_M8

GO:0010556	0.01	0.99	247	2846	regulation of macromolecule biosynthetic process	BP	0.36577	HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,FBXO5,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,DBF4,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,CDCA7L,HNRNPA2B1,HOXA5,SYNCRIP,PPIE,CCT4,THRAP3,EZH2,NUP62,PHF19,PRMT1,NAA15,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DBI,DIS3,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,GTPBP4,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,CBX5,SNAI2,TCEA1,SGK3,CENPJ,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,PPP1R15B,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,TICRR,RFC2,EIF4H,NEK2,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,EIF4G1,PSMC5,CDK1,S100A11,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,PSMA6,DDX20,RFC4,DNA2,SF1,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,LIN9,EIF5A,EIF2S1,EIF3B,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,GEMIN5,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,EIF5,TYMS,CDCA4,ATAD5,ELF4,RAP2C,UHRF1,RBMX,TFAP4,SMG6,NOC2L,ZNF598,TP73,CHTF18,DKC1,REXO4,FANCA,C	darkgrey	VSMC_M8
GO:0050790	0.02	0.99	163	1823	regulation of catalytic activity	BP	0.36904	CCT2,FBXO5,PRRC1,TCP1,DSCC1,NUS1,ARFGAP3,RANGAP1,CDC25C,PPP2R5D,DBF4,VCP,HSP90AB1,ARHGEF39,CKS2,ANP32B,PPP6R1,MSH6,CYCS,HNRNPA2B1,CCT4,EZH2,NUP62,CLSPN,CASP2,NRDC,MCM2,CCNA2,SAE1,DNAJC2,CHORDC1,MASTL,PREB,PLAUR,DBI,BORA,DIS3,AXL,NCAPG2,GDI2,NET1,CDC20,BIRC5,SERPINH1,SEC23B,GTPBP4,IPO5,CHMP6,DOCK9,ARHGDIA,SIPA1L3,PCNA,PGAM5,CDC25B,RFC3,DCUN1D2,HGF,CCNB1,CD44,TCEA1,TPX2,DEPDC1B,PSD4,HSP90B1,EIF2B1,ABCE1,CCNE1,ATP1B3,HMGB2,TERF1,ARHGAP11A,RACGAP1,RBL1,MSH3,CCNL1,CCNE2,YWHAB,HMGCR,CWF19L1,PPP1R15B,UBE2C,RFC5,PSMD14,HMGN1,CIT,GCN1,CENPE,KIF14,RGS9,ANP32E,RCC1,PHACTR4,RFC2,SPP2,PRKAR2A,NEK2,NF2,BLM,CDC42SE1,CEP85,ARFGAP1,CDC25A,PAK2,DHX9,HNRNPR,RFC4,RANBP1,PPP2R1B,EPHB2,DNAJC9,TFPI,CDKN3,DCUN1D5,ECT2,MNAT1,DNAJC7,HNRNPU,UCHL1,INCENP,CCNB3,RFC1,CDC6,BID,PSMD3,EIF2S1,PRELID1,CCNB2,IQGAP3,NES,SH3PXD2B,AURKB,AHSA1,PTTG1,PLK1,EIF5,POLDIP2,AIFM1,RAP2C,FAM122B,UHRF1,EMP2,TFAP4,SMG6,PKMYT1,CCNF,CHTF18,DKC1,GCLM,ACD,PLEKHG4,PDP2,DEPDC1,PRIM2,RAPGEF6,HNRNPD,MAD2L1,CDKN2C,STMN1,UBE2S,ERP29,PDCD2,PRPSAP1,DUSP7	darkgrey	VSMC_M8
GO:0006337	0.02	1.00	4	13	nucleosome disassembly	BP	0.36918	GRWD1,SUPT16H,SMARCC1,SMARCE1	darkgrey	VSMC_M8
GO:0071732	0.02	1.00	4	13	cellular response to nitric oxide	BP	0.37287	CDK2,CCNA2,AIFM1,HNRNPD	darkgrey	VSMC_M8
GO:1902101	0.02	1.00	4	13	positive regulation of metaphase/anaphase transition of cell cycle	BP	0.37287	CDC16,ESPL1,DLGAP5,CDT1	darkgrey	VSMC_M8
GO:0034661	0.02	1.00	7	35	ncRNA catabolic process	BP	0.37287	POP1,DIS3,EXOSC8,NSUN2,EXOSC10,ELAC2,EXOSC2	darkgrey	VSMC_M8
GO:0010569	0.02	1.00	8	43	regulation of double-strand break repair via homologous recombination	BP	0.37575	PARPBP,RAD51,CHEK1,POLQ,FANCB,RPA2,RAD51AP1,FUS	darkgrey	VSMC_M8
GO:0097421	0.02	1.00	6	28	liver regeneration	BP	0.37896	EZH2,PCNA,PRMT5,SRSF5,TYMS,AURKA	darkgrey	VSMC_M8
GO:0006998	0.02	1.00	8	43	nuclear envelope organization	BP	0.37994	NUP93,REEP4,RCC1,LMNA,PLK1,VRK1,TOR1A,NEK6	darkgrey	VSMC_M8
GO:0045814	0.02	1.00	8	43	negative regulation of gene expression, epigenetic	BP	0.38433	TRIM28,EZH2,RRP8,HELLS,SUV39H1,DNMT1,POLE3,MBD2	darkgrey	VSMC_M8
GO:0009988	0.02	1.00	7	35	cell-cell recognition	BP	0.38433	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CCT3	darkgrey	VSMC_M8
GO:0009314	0.02	0.99	39	359	response to radiation	BP	0.40324	POLH,MSH6,POLD1,RUVBL2,NAMPT,RAD54L,FANCD2,NET1,POLD3,RRM1,PCNA,TOPBP1,PBK,PPID,RAD51,HMGCR,HMGN1,NUCKS1,CHEK1,RGS9,RAD9A,TICRR,INTS7,DTL,H2AFX,BLM,CDC25A,BRCA1,RAD51AP1,ECT2,AIPL1,NEDD4,SMC1A,EIF2S1,AURKB,COPS3,USP1,NOC2L,FEN1	darkgrey	VSMC_M8
GO:0098781	0.02	0.99	9	53	ncRNA transcription	BP	0.40663	PWP1,POLR1E,CD3EAP,NIFK,USPL1,POLR1B,ICE1,NCL,NOL11	darkgrey	VSMC_M8
GO:0006417	0.02	0.99	37	341	regulation of translation	BP	0.41353	DDX39B,PUM3,NCBP1,SYNCRIP,PUS7,DIS3,EIF4A3,EXOSC8,ABCE1,SELENOT,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,NCL,EIF4H,EIF4G1,DHX9,HNRNPR,CNOT9,RBM3,EIF2AK1,EIF5A,EIF2S1,EIF3B,GEMIN5,ILF3,EIF5,TYMS,ZNF598,EXOSC2,GLE1,TRUB2,HNRNPD	darkgrey	VSMC_M8
GO:0048609	0.02	0.99	57	563	multicellular organismal reproductive process	BP	0.41353	FBXO5,TTLL1,KIFC1,CDC25C,SRPK1,TTK,NUP62,GJB3,CASP2,PGR,RUVBL1,WDR33,MAST2,AXL,XRN2,PCNA,CDC25B,CCNB1,E2F1,HMGB2,NRIP1,RACGAP1,KNL1,KIF18A,ETS1,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,H2AFX,PDE3A,FOSL1,DDX20,CABYR,C17orf53,CDK16,USP42,TOP2A,ASF1B,CCNB2,PTTG1,PLK1,BRIP1,ACSL4,SEPT6,RAI14,HOOK1,NDC1,DAZAP1,FANCA,ODF2,TPPP3,HIST1H1A,AURKA,HAS2,MBD2	darkgrey	VSMC_M8
GO:0006518	0.02	0.99	66	688	peptide metabolic process	BP	0.4148	NARS,MRPS18B,VARS2,DDX39B,VARS,MRPL2,PUM3,NCBP1,SYNCRIP,PABPC4,GARS,MRPL32,PUS7,MRPL58,MRPS7,DIS3,RRBP1,EIF4A3,EXOSC8,MRPS5,EIF3M,EIF2B1,ABCE1,SELENOT,EEF1E1,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,NCL,EIF4H,EIF4G1,MRPL11,DHX9,HNRNPR,CNOT9,RPL22L1,RBM3,DHX33,EIF2AK1,EIF5A,EIF2S1,EIF3B,EIF4A1,MRPL24,RARS,MRPS23,GEMIN5,ILF3,EIF5,TYMS,DRG2,MRPL37,THOP1,ZNF598,G6PD,EXOSC2,GLE1,TRUB2,GCLM,HNRNPD,SPCS3,MRPS15	darkgrey	VSMC_M8

GO:0002200	0.02	0.99	10	61	somatic diversification of immune receptors	BP	0.41583	MSH6,HMGB2,MSH3,CTNNBL1,UNG,POLQ,MCM3AP,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0007000	0.02	1.00	4	14	nucleolus organization	BP	0.41583	RRP8,POLR1B,NOLC1,SUV39H1	darkgrey	VSMC_M8
GO:0006312	0.02	1.00	5	21	mitotic recombination	BP	0.41599	SMC6,GEN1,MSH3,RAD51,ANKLE1	darkgrey	VSMC_M8
GO:0045070	0.02	1.00	6	28	positive regulation of viral genome replication	BP	0.42033	SRPK1,PPIH,PPIE,PPID,TOP2A,RAD23A	darkgrey	VSMC_M8
GO:2000112	0.02	0.98	244	2822	regulation of cellular macromolecule biosynthetic process	BP	0.42033	HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,FBXO5,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,DBF4,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,CDCA7L,HNRNPA2B1,HOXA5,SYNCRIP,PPIE,CCT4,THRAP3,EZH2,NUP62,PHF19,PRMT1,NAA15,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DBI,DIS3,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,GTPBP4,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,CBX5,SNAI2,TCEA1,SGK3,CENPJ,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,PPP1R15B,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,TICRR,RFC2,EIF4H,NEK2,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,EIF4G1,PSMC5,CDK1,S100A11,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,PSMA6,DDX20,RFC4,DNA2,SF1,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,LIN9,EIF5A,EIF2S1,EIF3B,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,GEMIN5,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,EIF5,TYMS,CDCA4,ATAD5,ELF4,RAP2C,UHRF1,RBMX,TFAP4,SMG6,NOC2L,ZNF598,TP73,CHTF18,DKC1,REXO4,FANCA,CDT1,EXOS	darkgrey	VSMC_M8
GO:0000381	0.02	0.99	9	52	regulation of alternative mRNA splicing, via spliceosome	BP	0.42082	THRAP3,SRSF2,KHDRBS1,DDX5,TRA2B,HNRNPU,RBMX,RNPS1,PTBP1	darkgrey	VSMC_M8
GO:0051307	0.02	1.00	5	21	meiotic chromosome separation	BP	0.42909	TTK,CHFR,ESPL1,FANCM,TOP2A	darkgrey	VSMC_M8
GO:0008104	0.02	0.98	179	2028	protein localization	BP	0.43117	TMED9,XPOT,NUP43,NUP107,CCT2,EZR,FBN2,TCP1,RAD21,NUP50,ARFGAP3,MAN1A1,MTBP,DESI1,RANGAP1,KIF20A,HSPA9,TNPO3,BYSL,TJP2,CYP51A1,VCP,HSP90AB1,CENPQ,CEP135,MIOS,NOL8,TRIM28,ANP32B,TTK,CCT4,NUP205,EZH2,NUP62,NBAS,RUVBL2,STIL,SEC61A1,SAE1,CHCHD4,CENPA,NASP,COG3,GRIN2C,TOMM40,PREB,KCNN4,NUP85,BORA,SRP68,GDI2,SEC23B,RRBP1,IPO5,CHMP6,ARHGDIA,AAAS,KIF20B,CENPJ,HSP90B1,NECAB3,CCNE1,VAMP8,ATP1B3,SLC10A7,KNTC1,TRAM1,CEP55,RBP4,TERF1,NUP160,ESCO2,SELENOT,CCT8,PPID,BUB1B,CCT7,GNL3,FAM83D,NUP93,KNL1,TOMM70,CCNE2,YWHAB,HMGCR,BAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,KIF18A,ICE1,CEP72,KIF14,CSE1L,XBP1,RPA2,UTP25,MCM3AP,IPO4,NUP133,HINFP,NF2,SEC24D,SSB,ARCN1,CENPF,BUB3,ARFGAP1,CDK1,TFRC,PAK2,DHX9,LSG1,ZW10,CDCA5,IFT80,BARD1,EPHB2,NMD3,UFD1,NSD2,CDK16,ANKLE1,ECT2,SIX4,MSX1,RAC1,KDELR2,MYO5A,HNRNPU,RAB27A,NEDD4,EIF5A,BID,SH3PXD2B,CCT3,LMNA,LTBP2,SPDL1,AURKB,COL1A1,CEP128,ZWILCH,TIMM8A,PLK1,NUP62CL,ACSL4,TIMM44,NDC80,SEPT6,MTCL1,AIFM1,RSL1D1,HOOK1,EMP2,NDC1,RPA1,HASPIN,DKC1,CDT1,EMC8,TOR1A,NUP188,GLE1,ODF2,ACD,ARF6,RAPGEF6,USP4,GBP5,SPCS3,ACSL3,AURKA,ERP29,PID1,CLSTN3,UBE2J2	darkgrey	VSMC_M8
GO:0002377	0.02	0.99	12	81	immunoglobulin production	BP	0.43117	MSH6,RBP4,MSH3,CTNNBL1,UNG,POLQ,XBP1,MCM3AP,TFRC,EPHB2,NSD2,EXO1	darkgrey	VSMC_M8
GO:1902570	0.02	1.00	4	14	protein localization to nucleolus	BP	0.43117	BYSL,NOL8,UTP25,NMD3	darkgrey	VSMC_M8
GO:0061077	0.02	0.99	9	55	chaperone-mediated protein folding	BP	0.43166	CCT2,HSPA9,FKBP5,CHORDC1,PPID,FKBP4,DNAJC7,PPIB,TOR1A	darkgrey	VSMC_M8
GO:0006305	0.02	0.99	9	53	DNA alkylation	BP	0.44255	TRIM28,EZH2,HELLS,MIS18A,PRMT5,BRCA1,DNMT1,FAM129B,MBD2	darkgrey	VSMC_M8
GO:0006306	0.02	0.99	9	53	DNA methylation	BP	0.44255	TRIM28,EZH2,HELLS,MIS18A,PRMT5,BRCA1,DNMT1,FAM129B,MBD2	darkgrey	VSMC_M8
GO:0051128	0.02	0.98	167	1877	regulation of cellular component organization	BP	0.44427	TMED9,CCT2,TUBB,DDX39B,FBXO5,EZR,TCP1,RAD21,MTBP,FAM49B,CDC25C,VCP,CEP135,TRIM28,NCBP1,TTK,HNRNPA2B1,MFSD2A,CCT4,ANLN,EZH2,NUP62,GEN1,SDC1,PLK4,STIL,MCM2,CHORDC1,CDC42EP4,PREB,PLAUR,BORA,AXL,RNF157,SPHK1,ULK4,NET1,CDC20,PARP2,ARHGDIA,CKAP2,CHFR,PGAM5,HGF,CDC16,CCNB1,SNAI2,CD44,ESPL1,BUB1,TPX2,ANAPC1,KIF20B,SKA3,SGK3,CENPJ,KNTC1,ATF1,SSRP1,TERF1,CCT8,BUB1B,CCT7,CDCA2,GNL3,CKAP5,BAP1,NUSAP1,RUNX1,UBE2C,CCT5,CCT6A,KIF18A,ETS1,ICE1,CHEK1,RASSF1,CENPE,TRIP13,KIF14,PRMT5,RCC1,HJURP,NEK2,NF2,PDE3A,RBM14,CENPF,EIF4G1,BUB3,PSMC5,ARFGAP1,TFRC,PAK2,MKI67,ZW10,CDCA5,KIF15,EPHB2,BRCA1,TACC3,DLGAP5,DCUN1D5,RAD51AP1,ECT2,ZWINT,DHX33,FKBP4,SIX4,MNAT1,MSX1,RAC1,HNRNPU,ADIPOR2,NEDD4,FSCN1,TOP2A,CDC6,EIF5A,BID,PDPN,PRELID1,IQGAP3,EXOSC10,NES,CCT3,LMNA,SPDL1,AURKB,PTTG1,SPAG9,ZWILCH,PLK1,SYT4,DNMT1,SLC25A5,NDC80,POLDIP2,CEP76,SMG6,PKMYT1,CCNF,SF3A2,G6PD,DKC1,CDT1,EXOSC2,TOR1A,GLE1,BCAR1,NEK6,ACD,TPPP3,ARPC4,ARF6,GBP5,TMOD3,HNRNPD,MAD2L1,CDKN2C,STMN1,AURKA,HAS2,STXBP6,FEN1,PID1,CLSTN3	darkgrey	VSMC_M8
GO:0051447	0.02	1.00	4	14	negative regulation of meiotic cell cycle	BP	0.44712	FBXO5,TTK,CHFR,TRIP13	darkgrey	VSMC_M8
GO:2000772	0.02	0.99	7	37	regulation of cellular senescence	BP	0.449	FBXO5,NAMPT,RBL1,EEF1E1,ARG2,RSL1D1,NEK6	darkgrey	VSMC_M8
GO:0009148	0.02	1.00	4	15	pyrimidine nucleoside triphosphate biosynthetic process	BP	0.4523	CTPS1,CAD,UCK2,TYMS	darkgrey	VSMC_M8
GO:0034629	0.02	1.00	5	21	cellular protein-containing complex localization	BP	0.45442	EZR,MIOS,CEP72,NDC1,HASPIN	darkgrey	VSMC_M8
GO:0030575	0.02	1.00	4	14	nuclear body organization	BP	0.45714	USPL1,ETS1,SF1,SERBP1	darkgrey	VSMC_M8

GO:0006399	0.02	0.99	20	162	tRNA metabolic process	BP	0.46498	NARS,METTL1,VARS2,POP1,VARS,THADA,GRSF1,GARS,PUS7,TSEN2,DUS1L,EXOSC8,NSUN2,TARBP1,SSB,EXOSC10,RARS,ELAC2,EXOSC2,TRMT13	darkgrey	VSMC_M8
GO:0032239	0.02	1.00	4	14	regulation of nucleobase-containing compound transport	BP	0.46527	NUP153,NSUN2,KHDRBS1,DHX9	darkgrey	VSMC_M8
GO:0016445	0.02	0.99	9	54	somatic diversification of immunoglobulins	BP	0.47465	MSH6,MSH3,CTNNBL1,UNG,POLQ,MCM3AP,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0046824	0.02	0.99	9	54	positive regulation of nucleocytoplasmic transport	BP	0.47494	HSP90AB1,TRIM28,ANP32B,IPO5,KHDRBS1,CDK1,DHX9,ECT2,NEDD4	darkgrey	VSMC_M8
GO:0071479	0.02	0.99	10	64	cellular response to ionizing radiation	BP	0.4754	NAMPT,NET1,RAD51,NUCKS1,RAD9A,INTS7,H2AFX,BLM,RAD51AP1,ECT2	darkgrey	VSMC_M8
GO:0006760	0.02	1.00	5	22	folic acid-containing compound metabolic process	BP	0.47911	ALDH1L2,GGH,MTHFD1,TYMS,GART	darkgrey	VSMC_M8
GO:0003006	0.02	0.98	67	685	developmental process involved in reproduction	BP	0.48591	NUP107,FBXO5,TTLL1,KIFC1,CDC25C,SRPK1,HSP90AB1,TRIM28,NUP62,GJB3,CASP2,SDC1,PLK4,PGR,RUVBL1,WDR33,MAST2,NASP,AXL,XRN2,E2F7,RRM1,CDC25B,CCNB1,E2F1,HMGB2,RBP4,NRIP1,RACGAP1,HEY1,KNL1,TBX3,E2F8,KIF18A,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,H2AFX,PDE3A,FOSL1,SMARCC1,DDX20,CABYR,SF1,CNOT9,CDK16,SIX4,USP42,NUDT1,ASF1B,ALOX15B,PTTG1,CENPI,BRIP1,SEPT6,RAI14,HOOK1,NDC1,CCNF,DAZAP1,FANCA,ODF2,TPPP3,HIST1H1A,AURKA	darkgrey	VSMC_M8
GO:0032504	0.02	0.98	57	571	multicellular organism reproduction	BP	0.49688	FBXO5,TTLL1,KIFC1,CDC25C,SRPK1,TTK,NUP62,GJB3,CASP2,PGR,RUVBL1,WDR33,MAST2,AXL,XRN2,PCNA,CDC25B,CCNB1,E2F1,HMGB2,NRIP1,RACGAP1,KNL1,KIF18A,ETS1,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,H2AFX,PDE3A,FOSL1,DDX20,CABYR,C17orf53,CDK16,USP42,TOP2A,ASF1B,CCNB2,PTTG1,PLK1,BRIP1,ACSL4,SEPT6,RAI14,HOOK1,NDC1,DAZAP1,FANCA,ODF2,TPPP3,HIST1H1A,AURKA,HAS2,MBD2	darkgrey	VSMC_M8
GO:0002183	0.02	0.99	6	30	cytoplasmic translational initiation	BP	0.49986	EIF3M,EIF4H,EIF4G1,EIF3B,EIF4A1,EIF5	darkgrey	VSMC_M8
GO:0018208	0.02	0.99	8	48	peptidyl-proline modification	BP	0.50383	FKBP5,PPIH,PPIE,CWC27,PPID,AIPL1,FKBP4,PPIB	darkgrey	VSMC_M8
GO:0032986	0.02	1.00	4	15	protein-DNA complex disassembly	BP	0.5149	GRWD1,SUPT16H,SMARCC1,SMARCE1	darkgrey	VSMC_M8
GO:0001837	0.02	0.99	17	131	epithelial to mesenchymal transition	BP	0.52214	HNRNPAB,TRIM28,EZH2,ZNF703,HGF,SNAI2,POLR1B,LOXL3,HEY1,FAM83D,TBX3,NOLC1,DDX5,MSX1,PDPN,COL1A1,HAS2	darkgrey	VSMC_M8
GO:0046390	0.02	0.99	19	156	ribose phosphate biosynthetic process	BP	0.53316	ATP5F1B,VCP,PAICS,CTPS1,CAD,PDHB,ELOVL6,UMPS,PDHA1,UCK2,DLAT,PFAS,PRPS1,ACSL4,G6PD,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:2000001	0.02	1.00	4	15	regulation of DNA damage checkpoint	BP	0.54561	DDX39B,RNASEH2B,RPA2,WDR76	darkgrey	VSMC_M8
GO:0000470	0.03	0.99	5	23	maturation of LSU-rRNA	BP	0.54711	NIFK,DDX18,GTPBP4,MAK16,RSL1D1	darkgrey	VSMC_M8
GO:0006266	0.03	1.00	4	15	DNA ligation	BP	0.55149	APTX,LIG1,RAD51,TOP2A	darkgrey	VSMC_M8
GO:0032268	0.03	0.98	160	1819	regulation of cellular protein metabolic process	BP	0.55257	CDK2,DDX39B,FBXO5,PRRC1,EZR,MTBP,DESI1,CDC25C,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,PUM3,CKS2,NCBP1,ANP32B,U2AF2,PPP6R1,TTK,CYCS,SYNCRIP,EZH2,NUP62,CLSPN,PHF19,CASP2,NRDC,RUVBL2,PUS7,CCNA2,SAE1,CHORDC1,PPP5C,MASTL,PLAUR,DBI,BORA,DIS3,SPHK1,NCAPG2,CDC20,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,CHFR,EXOSC8,CDC25B,DCUN1D2,HGF,CCNB1,CD44,TPX2,UBA2,HSP90B1,ABCE1,CCNE1,PBK,SELENOT,CCNL1,CDCA2,GNL3,RAD51,CCNE2,YWHAB,HMGCR,PPP1R15B,UBE2C,PSMD14,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,CHEK1,KHDRBS1,CENPE,NCL,KIF14,FANCI,SPP2,EIF4H,PRKAR2A,NF2,BLM,CEP85,EIF4G1,PSMC5,CDC25A,TFRC,PAK2,SMARCC1,DHX9,HNRNPR,FANCM,EPHB2,BRCA1,TFPI,CNOT9,CDKN3,DCUN1D5,ECT2,RBM3,MNAT1,EIF2AK1,RAC1,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,EIF5A,BID,EIF2S1,EIF3B,PRELID1,CCNB2,IQGAP3,LMNA,RAD23A,PTTG1,SPAG9,GEMIN5,PLK1,ILF3,DNMT1,TADA2A,EIF5,TYMS,NNT,WDR70,AIFM1,RAP2C,UHRF1,EMP2,NXN,TFAP4,PKMYT1,NOC2L,CCNF,ZNF598,G6PD,PTBP1,EXOSC2,GLE1,TRUB2,USP4,HNRNPD,MAD2L1,CDKN2C,AURKA,UBE2S,ERP29,PDCD2,PID1,DUSP7	darkgrey	VSMC_M8
GO:0031498	0.03	1.00	4	15	chromatin disassembly	BP	0.55364	GRWD1,SUPT16H,SMARCC1,SMARCE1	darkgrey	VSMC_M8
GO:0006304	0.03	0.99	12	84	DNA modification	BP	0.55554	TRIM28,EZH2,PARP2,HELLS,NEIL3,MIS18A,UNG,PRMT5,BRCA1,DNMT1,FAM129B,MBD2	darkgrey	VSMC_M8
GO:1905820	0.03	1.00	4	15	positive regulation of chromosome separation	BP	0.55554	CDC16,ESPL1,DLGAP5,CDT1	darkgrey	VSMC_M8
GO:0051642	0.03	0.99	6	30	centrosome localization	BP	0.55554	EZR,ASPM,DLGAP5,NDE1,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:1902170	0.03	1.00	4	15	cellular response to reactive nitrogen species	BP	0.55554	CDK2,CCNA2,AIFM1,HNRNPD	darkgrey	VSMC_M8
GO:0009218	0.03	0.99	5	23	pyrimidine ribonucleotide metabolic process	BP	0.55937	CTPS1,CAD,ENTPD7,UMPS,UCK2	darkgrey	VSMC_M8
GO:0046653	0.03	1.00	4	16	tetrahydrofolate metabolic process	BP	0.56982	ALDH1L2,MTHFD1,TYMS,GART	darkgrey	VSMC_M8
GO:0051131	0.03	1.00	4	16	chaperone-mediated protein complex assembly	BP	0.57682	CCT2,HSP90AB1,NDUFAF1,PSMG3	darkgrey	VSMC_M8
GO:0006446	0.03	0.99	10	66	regulation of translational initiation	BP	0.58571	NCBP1,PPP1R15B,KHDRBS1,EIF4H,EIF4G1,EIF2AK1,EIF2S1,EIF3B,EIF5,GLE1	darkgrey	VSMC_M8
GO:1902806	0.03	0.99	15	115	regulation of cell cycle G1/S phase transition	BP	0.59649	CDK2,GTSE1,MTBP,EZH2,CASP2,E2F7,WEE1,E2F1,RBL1,FAM83D,KIF14,RPA2,EIF4G1,CDC6,BID	darkgrey	VSMC_M8
GO:1903320	0.03	0.98	24	211	regulation of protein modification by small protein conjugation or removal	BP	0.59799	FBXO5,MTBP,VCP,HSP90AB1,U2AF2,SAE1,SPHK1,CDC20,GTPBP4,CHFR,DCUN1D2,UBA2,GNL3,UBE2C,FANCI,FANCM,BRCA1,DCUN1D5,PLK1,WDR70,NXN,USP4,MAD2L1,UBE2S	darkgrey	VSMC_M8
GO:0061013	0.03	0.99	18	144	regulation of mRNA catabolic process	BP	0.60248	SYNCRIP,PABPC4,THRAP3,NBAS,DIS3,EXOSC8,E2F1,FASTKD3,TENT4A,DHX9,HNRNPR,HNRNPU,FUS,TAF15,HNRNPM,SERBP1,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0019081	0.03	0.99	4	16	viral translation	BP	0.62594	SSB,DHX9,EIF3B,PTBP1	darkgrey	VSMC_M8
GO:0030010	0.03	0.99	16	123	establishment of cell polarity	BP	0.62735	ALPK2,FAM49B,HSP90AB1,AMOTL1,CENPA,SIPA1L3,KIF20B,WEE1,ZW10,FSCN1,SPDL1,PLK1,NDC80,NDE1,ARF6,MAD2L1	darkgrey	VSMC_M8
GO:0061842	0.03	0.99	6	31	microtubule organizing center localization	BP	0.62883	EZR,ASPM,DLGAP5,NDE1,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:0006415	0.03	0.99	4	16	translational termination	BP	0.63313	MRPL58,ABCE1,EIF5A,GLE1	darkgrey	VSMC_M8
GO:0071731	0.03	0.99	4	16	response to nitric oxide	BP	0.63336	CDK2,CCNA2,AIFM1,HNRNPD	darkgrey	VSMC_M8

GO:0051254	0.03	0.98	123	1357	positive regulation of RNA metabolic process	BP	0.63483	HNRNPAB,BCLAF1,DDX39B,ATAD2,PHF5A,PWP1,CDC5L,TRIM28,NCBP1,U2AF2,GRSF1,HOXA5,THRAP3,NUP62,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DIS3,WDR43,SUPT16H,E2F7,ALYREF,CKAP2,EXOSC8,HGF,ELK3,TCERG1,CCNB1,TCEA1,CENPJ,E2F1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,PPRC1,HMGN1,NOLC1,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,NCL,RBM23,NOL11,SF3B4,DDX5,XBP1,HINFP,BLM,RBM14,PSMC5,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,GABPB1,RBM3,DHX33,SIX4,FOXM1,LYAR,MSX1,HNRNPU,SMARCE1,RFC1,TOP2A,EIF5A,SRSF5,PMF1,HOXB7,FUS,MAZ,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,DAZAP1,ZC3H18,EXOSC2,FAM129B,CBFB,PRIM2,HNRNPD,DRAP1,ABT1,PID1	darkgrey	VSMC_M8
GO:0032784	0.03	0.99	8	49	regulation of DNA-templated transcription, elongation	BP	0.63483	DDX39B,EZH2,WDR43,SUPT16H,ALYREF,TCERG1,HMGN1,HNRNPU	darkgrey	VSMC_M8
GO:0000466	0.03	0.99	5	24	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	0.63974	EXOSC8,UTP20,EXOSC10,EXOSC2,ABT1	darkgrey	VSMC_M8
GO:0048146	0.03	0.99	7	41	positive regulation of fibroblast proliferation	BP	0.64216	CCNA2,RNASEH2B,SPHK1,CCNB1,E2F1,DHX9,CDC6	darkgrey	VSMC_M8
GO:0045292	0.03	0.99	5	24	mRNA cis splicing, via spliceosome	BP	0.65393	PSIP1,NCBP1,RBM17,SFSWAP,DDX23	darkgrey	VSMC_M8
GO:0000729	0.03	0.99	4	16	DNA double-strand break processing	BP	0.65646	BLM,DNA2,BRIP1,WDR70	darkgrey	VSMC_M8
GO:0070828	0.03	0.99	7	40	heterochromatin organization	BP	0.65823	TRIM28,RRP8,HELLS,SUV39H1,DNMT1,POLE3,MBD2	darkgrey	VSMC_M8
GO:0006346	0.03	0.99	4	16	DNA methylation-dependent heterochromatin assembly	BP	0.66301	TRIM28,HELLS,DNMT1,MBD2	darkgrey	VSMC_M8
GO:0048599	0.03	0.99	6	32	oocyte development	BP	0.66945	FBXO5,CDC25B,CCNB1,TRIP13,PDE3A,AURKA	darkgrey	VSMC_M8
GO:0071763	0.03	0.99	6	32	nuclear membrane organization	BP	0.66945	REEP4,RCC1,PLK1,VRK1,TOR1A,NEK6	darkgrey	VSMC_M8
GO:0048469	0.03	0.98	15	116	cell maturation	BP	0.66945	FBXO5,HOXA5,PGR,AXL,CDC25B,CCNB1,TRIP13,KIF14,FLVCR1,PDE3A,CABYR,TYMS,G6PD,CBFB,AURKA	darkgrey	VSMC_M8
GO:0070979	0.03	0.99	5	25	protein K11-linked ubiquitination	BP	0.6706	CDC16,ANAPC1,UBE2C,UBE2T,UBE2S	darkgrey	VSMC_M8
GO:0009220	0.03	0.99	4	17	pyrimidine ribonucleotide biosynthetic process	BP	0.67961	CTPS1,CAD,UMPS,UCK2	darkgrey	VSMC_M8
GO:0006303	0.03	0.99	9	59	double-strand break repair via nonhomologous end joining	BP	0.68184	HMGB2,DCLRE1B,PSMD14,DEK,POLQ,AUNIP,POLA1,SMARCAL1,NSD2	darkgrey	VSMC_M8
GO:0016075	0.03	0.99	4	17	rRNA catabolic process	BP	0.68567	DIS3,EXOSC8,EXOSC10,EXOSC2	darkgrey	VSMC_M8
GO:0043488	0.03	0.98	17	137	regulation of mRNA stability	BP	0.68567	SYNCRIP,PABPC4,THRAP3,DIS3,EXOSC8,E2F1,FASTKD3,TENT4A,DHX9,HNRNPR,HNRNPU,FUS,TAF15,HNRNPM,SERBP1,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0006450	0.03	0.99	4	17	regulation of translational fidelity	BP	0.69289	VARS2,VARS,YRDC,DNAJC2	darkgrey	VSMC_M8
GO:0000083	0.03	0.99	4	17	regulation of transcription involved in G1/S transition of mitotic cell cycle	BP	0.693	E2F7,E2F1,HINFP,CDK16	darkgrey	VSMC_M8
GO:0009161	0.04	0.99	8	51	ribonucleoside monophosphate metabolic process	BP	0.70554	TJP2,PAICS,CAD,UMPS,UCK2,PFAS,PRPS1,GART	darkgrey	VSMC_M8
GO:0016973	0.04	0.99	4	17	poly(A)+ mRNA export from nucleus	BP	0.70554	NUP93,MCM3AP,NUP133,GLE1	darkgrey	VSMC_M8
GO:0071214	0.04	0.98	29	267	cellular response to abiotic stimulus	BP	0.70987	POLH,POLD1,CASP2,RUVBL2,NAMPT,NET1,POLD3,ARHGDIA,PCNA,PBK,PPID,RAD51,NUCKS1,CHEK1,RGS9,RAD9A,INTS7,H2AFX,BLM,CDC25A,RAD51AP1,ECT2,AIPL1,RAC1,NEDD4,EIF2S1,AURKB,COL1A1,NOC2L	darkgrey	VSMC_M8
GO:0104004	0.04	0.98	29	267	cellular response to environmental stimulus	BP	0.70987	POLH,POLD1,CASP2,RUVBL2,NAMPT,NET1,POLD3,ARHGDIA,PCNA,PBK,PPID,RAD51,NUCKS1,CHEK1,RGS9,RAD9A,INTS7,H2AFX,BLM,CDC25A,RAD51AP1,ECT2,AIPL1,RAC1,NEDD4,EIF2S1,AURKB,COL1A1,NOC2L	darkgrey	VSMC_M8
GO:0006458	0.04	0.99	6	33	'de novo' protein folding	BP	0.71321	CCT2,HSPA9,DNAJC2,CHCHD4,DNAJC7,TOR1A	darkgrey	VSMC_M8
GO:0000462	0.04	0.99	6	34	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	0.71985	BYSL,NOL10,UTP20,FP565260.1,UTP25,ABT1	darkgrey	VSMC_M8
GO:0048232	0.04	0.98	38	371	male gamete generation	BP	0.71985	TTLL1,KIFC1,CDC25C,SRPK1,NUP62,GJB3,RUVBL1,WDR33,MAST2,AXL,XRN2,CCNB1,E2F1,HMGB2,RACGAP1,KNL1,KIF18A,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,H2AFX,CABYR,C17orf53,CDK16,USP42,ASF1B,PTTG1,BRIP1,SEPT6,RAI14,HOOK1,NDC1,DAZAP1,FANCA,ODF2,HIST1H1A	darkgrey	VSMC_M8
GO:0019079	0.04	0.98	13	99	viral genome replication	BP	0.72847	SRPK1,VCP,TRIM28,PPIH,PPIE,PPID,NUCKS1,DEK,DDX5,TOP2A,PPIB,RAD23A,ILF3	darkgrey	VSMC_M8
GO:0072091	0.04	0.99	6	33	regulation of stem cell proliferation	BP	0.72854	CCNE1,HMGB2,TBX3,NF2,HNRNPU,PDCD2	darkgrey	VSMC_M8
GO:0080135	0.04	0.97	54	553	regulation of cellular response to stress	BP	0.73217	BCLAF1,DDX39B,FBXO5,EZR,POLH,TRIM28,PRMT1,NAMPT,DNAJC2,CHORDC1,RNASEH2B,SPHK1,ULK4,PCNA,HGF,SNAI2,CD44,PARPBP,PBK,RBL1,RAD51,CREB3L1,HMGCR,EEF1E1,PPP1R15B,DEK,MANF,CHEK1,POLQ,DDX5,FANCB,XBP1,RPA2,H2AFX,NSMCE4A,EIF4G1,AUNIP,DHX9,WDR76,BRCA1,NSD2,RAD51AP1,ANKLE1,FOXM1,EIF2AK1,MSX1,DNAJC7,BID,ARG2,FUS,USP1,RSL1D1,NEK6,ERP29	darkgrey	VSMC_M8
GO:2000279	0.04	0.99	6	32	negative regulation of DNA biosynthetic process	BP	0.73217	DNAJC2,TERF1,HNRNPU,EXOSC10,FAM129B,ACD	darkgrey	VSMC_M8
GO:2000648	0.04	0.99	4	17	positive regulation of stem cell proliferation	BP	0.7342	CCNE1,TBX3,HNRNPU,PDCD2	darkgrey	VSMC_M8
GO:0071900	0.04	0.98	32	300	regulation of protein serine/threonine kinase activity	BP	0.7342	CDC25C,DBF4,HSP90AB1,CKS2,EZH2,NUP62,CCNA2,CHORDC1,GTPBP4,IPO5,CCNB1,CCNE1,CCNL1,CCNE2,HMGCR,PRKAR2A,BLM,CDC25A,CDKN3,MNAT1,UCHL1,INCENP,CCNB3,CDC6,CCNB2,PLK1,TFAP4,PKMYT1,CCNF,CDKN2C,ERP29,DUSP7	darkgrey	VSMC_M8

GO:0031324	0.04	0.97	165	1896	negative regulation of cellular metabolic process	BP	0.74287	BCLAF1,FBXO5,EZR,PPP2R5D,PWP1,HSP90AB1,TRIM28,U2AF2,MSH6,MFSD2A,SYNCRIP,THRAP3,EZH2,NUP62,PHF19,NBAS,RUVBL2,NAMPT,PUS7,DNAJC2,CHORDC1,PPP5C,MASTL,FOSB,PLAUR,DBI,DIS3,SPHK1,SRSF2,NCAPG2,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,E2F7,PCNA,EXOSC8,ZNF703,HGF,ELK3,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,CD44,PARPBP,E2F1,ABCE1,CCNE1,HMGB2,MSC,TERF1,NRIP1,LOXL3,PBK,HEY1,PPID,RBL1,MSH3,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,RUNX1,PPP1R15B,MDM4,NCOA5,TENT4A,NSUN2,PHC2,GMNN,KHDRBS1,NCL,PRMT5,POLQ,DDX5,FANCB,SPP2,PRKAR2A,HINFP,NF2,BLM,CEP85,CENPF,STRAP,EIF4G1,PSMC5,AUNIP,S100A11,PAK2,SMARCC1,DHX9,HNRNPR,DDX20,SF1,BARD1,EPHB2,SMARCAL1,BRCA1,TFPI,CNOT9,NSD2,MYBBP1A,CREG1,ANKLE1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,HNRNPU,UCHL1,NEDD4,SMARCE1,RFC1,CDC6,EIF2S1,EXOSC10,HDGF,FUS,MAZ,AURKB,PTTG1,SPAG9,PLK1,ILF3,DNMT1,TAF15,TYMS,NNT,POLDIP2,UHRF1,RBMX,NXN,TFAP4,SMG6,NOC2L,RNPS1,G6PD,DKC1,PTBP1,EXOSC2,FAM129B,ACD,CBFB,DEPDC1,USP4,HIST1H1A,HNRNPD,MAD2L1,DRAP1,CDKN2C,SRSF7,PID1,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0000460	0.04	0.99	6	34	maturation of 5.8S rRNA	BP	0.75931	EXOSC8,MAK16,UTP20,EXOSC10,EXOSC2,ABT1	darkgrey	VSMC_M8
GO:0006354	0.04	0.98	11	80	DNA-templated transcription, elongation	BP	0.76328	DDX39B,POLR1E,EZH2,WDR43,SUPT16H,ALYREF,TCERG1,HMGN1,CHEK1,HNRNPU,CDCA4	darkgrey	VSMC_M8
GO:0032786	0.04	0.99	5	25	positive regulation of DNA-templated transcription, elongation	BP	0.77304	DDX39B,SUPT16H,ALYREF,TCERG1,HMGN1	darkgrey	VSMC_M8
GO:0043085	0.04	0.97	81	875	positive regulation of catalytic activity	BP	0.77865	CCT2,PRRC1,TCP1,DSCC1,NUS1,RANGAP1,DBF4,VCP,HSP90AB1,CKS2,ANP32B,MSH6,CYCS,HNRNPA2B1,CCT4,EZH2,CLSPN,CASP2,DBI,BORA,AXL,NET1,CDC20,DOCK9,SIPA1L3,PCNA,CDC25B,RFC3,DCUN1D2,CCNB1,TCEA1,TPX2,ATP1B3,HMGB2,ARHGAP11A,MSH3,YWHAB,PPP1R15B,UBE2C,RFC5,PSMD14,HMGN1,GCN1,CENPE,KIF14,PHACTR4,RFC2,NEK2,PAK2,DHX9,RFC4,EPHB2,DNAJC9,DCUN1D5,ECT2,MNAT1,HNRNPU,INCENP,CDC6,BID,PRELID1,AURKB,AHSA1,PLK1,EIF5,POLDIP2,AIFM1,UHRF1,EMP2,TFAP4,CHTF18,DKC1,GCLM,ACD,PDP2,PRIM2,RAPGEF6,HNRNPD,UBE2S,ERP29,PDCD2	darkgrey	VSMC_M8
GO:0051101	0.04	0.98	12	91	regulation of DNA binding	BP	0.78143	TRIM28,PLAUR,E2F1,HMGB2,HEY1,HJURP,NEK2,MSX1,TFAP4,CDT1,FAM129B,ACD	darkgrey	VSMC_M8
GO:0009069	0.04	0.99	5	26	serine family amino acid metabolic process	BP	0.78387	GCAT,MTHFD1,GCLM,CTH,GART	darkgrey	VSMC_M8
GO:0009994	0.04	0.99	6	34	oocyte differentiation	BP	0.79837	FBXO5,CDC25B,CCNB1,TRIP13,PDE3A,AURKA	darkgrey	VSMC_M8
GO:0006244	0.04	0.99	4	18	pyrimidine nucleotide catabolic process	BP	0.80726	ENTPD7,UNG,DUT,DCTPP1	darkgrey	VSMC_M8
GO:1903322	0.04	0.98	15	121	positive regulation of protein modification by small protein conjugation or removal	BP	0.81201	VCP,SAE1,SPHK1,CDC20,CHFR,DCUN1D2,UBA2,GNL3,UBE2C,FANCI,FANCM,BRCA1,DCUN1D5,PLK1,UBE2S	darkgrey	VSMC_M8
GO:0055021	0.04	0.98	8	53	regulation of cardiac muscle tissue growth	BP	0.8186	DDX39B,PARP2,CCNB1,RBP4,RUNX1,CDK1,TP73,G6PD	darkgrey	VSMC_M8
GO:0042790	0.04	0.99	4	18	nucleolar large rRNA transcription by RNA polymerase I	BP	0.82133	PWP1,POLR1E,NCL,NOL11	darkgrey	VSMC_M8
GO:0009226	0.04	0.99	4	18	nucleotide-sugar biosynthetic process	BP	0.82889	NANS,UAP1,UGDH,GMPPB	darkgrey	VSMC_M8
GO:0043624	0.04	0.98	15	119	cellular protein complex disassembly	BP	0.83677	KIF24,MRPL58,KIF2C,CKAP2,TPX2,KIF2A,ABCE1,CKAP5,KIF18A,KIF18B,EIF5A,NES,GLE1,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0045069	0.05	0.98	9	62	regulation of viral genome replication	BP	0.855	SRPK1,TRIM28,PPIH,PPIE,PPID,DDX5,TOP2A,RAD23A,ILF3	darkgrey	VSMC_M8
GO:0071695	0.05	0.97	19	163	anatomical structure maturation	BP	0.85785	FBXO5,HOXA5,PGR,AXL,CDC25B,CCNB1,NSUN2,TRIP13,KIF14,FLVCR1,PDE3A,ARCN1,CABYR,IFT80,XYLT1,TYMS,G6PD,CBFB,AURKA	darkgrey	VSMC_M8
GO:0031399	0.05	0.96	106	1182	regulation of protein modification process	BP	0.85785	FBXO5,PRRC1,MTBP,CDC25C,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,PUM3,CKS2,U2AF2,PPP6R1,TTK,EZH2,NUP62,CLSPN,PHF19,RUVBL2,CCNA2,SAE1,CHORDC1,PPP5C,MASTL,PLAUR,DBI,BORA,SPHK1,NCAPG2,CDC20,GTPBP4,IPO5,CHMP6,CHFR,CDC25B,DCUN1D2,HGF,CCNB1,CD44,TPX2,UBA2,HSP90B1,CCNE1,PBK,CCNL1,CDCA2,GNL3,RAD51,CCNE2,YWHAB,HMGCR,PPP1R15B,UBE2C,CHEK1,CENPE,KIF14,FANCI,PRKAR2A,NF2,BLM,CEP85,EIF4G1,CDC25A,TFRC,PAK2,FANCM,EPHB2,BRCA1,CNOT9,CDKN3,DCUN1D5,ECT2,MNAT1,EIF2AK1,RAC1,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,CCNB2,IQGAP3,LMNA,SPAG9,PLK1,DNMT1,TADA2A,NNT,WDR70,RAP2C,EMP2,NXN,TFAP4,PKMYT1,NOC2L,CCNF,G6PD,PTBP1,USP4,MAD2L1,CDKN2C,UBE2S,ERP29,PID1,DUSP7	darkgrey	VSMC_M8
GO:0090344	0.05	0.99	4	18	negative regulation of cell aging	BP	0.86229	FBXO5,NAMPT,RBL1,FOXM1	darkgrey	VSMC_M8
GO:1901566	0.05	0.96	115	1317	organonitrogen compound biosynthetic process	BP	0.86233	NARS,ATP5F1B,MRPS18B,VARS2,DDX39B,VARS,NUS1,MAN1A1,SLC35D2,MRPL2,VCP,PUM3,PAICS,NCBP1,CTPS1,DCK,MFSD2A,SYNCRIP,PABPC4,GARS,B3GNT2,ODC1,MRPL32,PRMT1,AMD1,NAMPT,PUS7,RPN1,COG3,MRPL58,MRPS7,CAD,ALG8,DBI,DIS3,SPHK1,AFMID,RRBP1,EIF4A3,EXOSC8,MRPS5,PDHB,EIF3M,NECAB3,EIF2B1,ABCE1,PXYLP1,SLC10A7,GALNT6,SELENOT,EEF1E1,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,STT3A,NCL,BCAT1,ELOVL6,EIF4H,HMBS,FLVCR1,UMPS,EIF4G1,MRPL11,PDHA1,DHX9,HNRNPR,UCK2,DLAT,DUT,CNOT9,RPL22L1,RBM3,DHX33,EIF2AK1,MTHFD1,UGDH,EIF5A,EIF2S1,EIF3B,ARG2,EIF4A1,MRPL24,PFAS,RARS,MRPS23,GEMIN5,ILF3,PRPS1,ACSL4,XYLT1,EIF5,TYMS,DRG2,MRPL37,ZNF598,EXOSC2,DOLPP1,GLE1,TRUB2,GCLM,CTH,GMPPB,HNRNPD,ACSL3,HAS2,MRPS15,PID1,GART,PRPSAP1,SRM	darkgrey	VSMC_M8
GO:0043555	0.05	0.99	4	18	regulation of translation in response to stress	BP	0.87293	PPP1R15B,EIF4G1,EIF2AK1,EIF2S1	darkgrey	VSMC_M8
GO:1901796	0.05	0.98	11	83	regulation of signal transduction by p53 class mediator	BP	0.87293	SNAI2,CD44,EEF1E1,PAK1IP1,CHEK1,PRMT5,DDX5,MSX1,EIF5A,AURKB,AURKA	darkgrey	VSMC_M8

GO:0031326	0.05	0.96	249	2955	regulation of cellular biosynthetic process	BP	0.8756	HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,FBXO5,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,DBF4,VCP,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,CDCA7L,HNRNPA2B1,HOXA5,MFSD2A,SYNCRIP,PPIE,CCT4,THRAP3,EZH2,NUP62,PHF19,PRMT1,NAA15,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DBI,DIS3,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,GTPBP4,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,CBX5,SNAI2,TCEA1,SGK3,CENPJ,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,PPP1R15B,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,X8P1,TICRR,RFC2,EIF4H,NEK2,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,EIF4G1,PSMC5,CDK1,S100A11,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,PSMA6,DDX20,RFC4,DNA2,SF1,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,LIN9,EIF5A,EIF2S1,EIF3B,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,GEMIN5,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,EIF5,TYMS,CDCA4,ATAD5,ELF4,RAP2C,UHRF1,RBMX,TFAP4,SMG6,NOC2L,ZNF598,TP73,CHTF18,DKC1,REX	darkgrey	VSMC_M8
GO:0008283	0.05	0.96	127	1442	cell population proliferation	BP	0.88488	CDK2,DDX39B,FBXO5,MTBP,CDC25C,BYSL,CKS2,MELK,CDCA7L,CTPS1,TTK,CLEC11A,HOXA5,EZH2,NUP62,PRMT1,SHCBP1,PGR,NAMPT,CCNA2,RNASEH2B,MCM10,SPHK1,NCAPG2,CDC20,BIRC5,GTPBP4,NAP1L1,E2F7,GINS4,STRN,RRM1,CDC25B,ZNF703,HGF,USPL1,CCNB1,SNAI2,UTP20,BUB1,KIF20B,SGK3,E2F1,CCNE1,HMGB2,RBP4,HELLS,RACGAP1,FAM98B,GNL3,FAM83D,TBX3,E2F8,HMGCR,BAP1,NRAS,EEF1E1,RUNX1,SETD4,MDM4,PAK1IP1,HMGN1,NOLC1,ETS1,CHEK1,KIF14,ASPM,MNDA,XBP1,PRC1,NF2,CDK1,S100A11,CDC25A,TFRC,FOSL1,DHX9,DDX20,IFT80,SF1,EPHB2,MCM7,CDKN3,TACC3,DPT,SIX4,MNAT1,FOXM1,EIF2AK1,MSX1,RAC1,HNRNPU,UCHL1,CDC6,BID,PDPN,ARG2,IQGAP3,EFNB1,NES,LMNA,ALOX15B,MAZ,AURKB,BRIP1,DNMT1,SLC25A5,POLDIP2,NDE1,ELF4,UHRF1,EMP2,LIPG,TFAP4,TP73,DAZAP1,PIK3CD,FANCA,FAM129B,CDKN2C,GINS1,HAS2,SAAL1,PDCD2,PID1,PALB2,MBD2	darkgrey	VSMC_M8
GO:0009162	0.05	0.99	4	19	deoxyribonucleoside monophosphate metabolic process	BP	0.88827	DCK,TK1,DUT,TYMS	darkgrey	VSMC_M8
GO:0072698	0.05	0.98	8	52	protein localization to microtubule cytoskeleton	BP	0.89163	TTK,NUP62,STIL,KIF20B,FAM83D,CEP72,HNRNPU,AURKA	darkgrey	VSMC_M8
GO:0032211	0.05	0.99	4	18	negative regulation of telomere maintenance via telomerase	BP	0.90223	TERF1,HNRNPU,EXOSC10,ACD	darkgrey	VSMC_M8
GO:0032880	0.05	0.96	65	693	regulation of protein localization	BP	0.90457	CCT2,EZR,TCP1,RANGAP1,BYSL,CYP51A1,VCP,HSP90AB1,CENPQ,CEP135,TRIM28,ANP32B,CCT4,NUP62,SAE1,KCNN4,BORA,IPO5,ARHGDIA,KIF20B,CENPJ,CCNE1,VAMP8,RBP4,TERF1,CCT8,PPID,CCT7,GNL3,CCNE2,HMGCR,BAP1,NOLC1,CCT5,CCT6A,ICE1,CEP72,NF2,CDK1,TFRC,CDCA5,BARD1,EPHB2,NMD3,NSD2,CDK16,ECT2,SIX4,RAC1,CCT3,LMNA,PLK1,ACSL4,NDC80,MTCL1,RSL1D1,DKC1,CDT1,TOR1A,ARF6,ACSL3,ERP29,PID1,CLSTN3,UBE2J2	darkgrey	VSMC_M8
GO:0030866	0.05	0.98	6	35	cortical actin cytoskeleton organization	BP	0.90457	EZR,ANLN,RACGAP1,FMNL3,ECT2,ARF6	darkgrey	VSMC_M8
GO:0006353	0.05	0.99	4	19	DNA-templated transcription, termination	BP	0.91085	XRN2,PRMT5,DHX9,MAZ	darkgrey	VSMC_M8
GO:0048522	0.05	0.96	347	4212	positive regulation of cellular process	BP	0.9253	CDK2,ATP5F1B,TMED9,HNRNPAB,BCLAF1,CCT2,DDX39B,FBXO5,PRRC1,EZR,FBN2,TCP1,RAD21,DSCC1,NUS1,MTBP,ATAD2,PHF5A,FAM49B,CDC25C,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,CDC5L,ARHGEF39,CENPQ,CEP135,CKS2,MIOS,MELK,TRIM28,NCBP1,ANP32B,U2AF2,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,CLEC11A,HOXA5,MFSD2A,CCT4,ANLN,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NAA15,SMC6,GEN1,NRDC,SDC1,RUVBL2,PLK4,PGR,NAMPT,RUVBL1,CCNA2,SAE1,DNAJC2,RNASEH2B,PPP5C,FOSB,CDC42EP4,NUFIP1,GRIN2C,KCNN4,NUP85,PLAUR,BORA,DIS3,AXL,RNF157,SPHK1,NET1,WDR43,CDC20,BIRC5,PARP2,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,ELK3,CDC16,TCERG1,MEDAG,CCNB1,SNAI2,CD44,TCEA1,ESPL1,TPX2,DEPDC1B,KIF20B,SLC20A1,UBA2,CENPJ,E2F1,CCNE1,PXYLP1,VAMP8,ZNF827,ATP1B3,HMGB2,RBP4,ATF1,TERF1,NRIP1,UTP15,RACGAP1,LOXL3,HEY1,SELENOT,FAM98B,CCT8,PPID,TRIM35,CTNNBL1,CCT7,CDCA2,GNL3,FAM83D,CKAP5,NUP93,TBX3,RAD51,CREB3L1,MYBL2,E2F8,MTDH,HMGCR,BAP1,NRAS,NUSAP1,EEF1E1,CHUK,RUNX1,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,NOLC1,CCT5,CIT,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,CENPE,NCL,KIF14,RGS9,RBM23,PRMT5,ASPM,NOL11,SF3B4,FANCI,MNDA,DDX5,FANCB,XBP1,RFC2,NEK2,PRC1,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,RBM14,NSMCE4A,EIF4G1,PSMC5,CDK1,S100A11,CDC25A,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,DDX20,RFC4,DNA2,DDX21,CDCA5,FANCM,RANBP1,PPP2R1B,BARD1,EPHB2,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,PLCABP,DCUN1D	darkgrey	VSMC_M8
GO:0031396	0.05	0.97	20	180	regulation of protein ubiquitination	BP	0.93126	FBXO5,MTBP,HSP90AB1,U2AF2,SPHK1,CDC20,GTPBP4,CHFR,DCUN1D2,UBE2C,FANCI,FANCM,BRCA1,DCUN1D5,PLK1,WDR70,NXN,USP4,MAD2L1,UBE2S	darkgrey	VSMC_M8
GO:0065002	0.05	0.98	7	47	intracellular protein transmembrane transport	BP	0.95414	SEC61A1,CHCHD4,TOMM40,TRAM1,TOMM70,TIMM44,AIFM1	darkgrey	VSMC_M8
GO:0072089	0.05	0.98	8	54	stem cell proliferation	BP	0.95798	CCNE1,HMGB2,TBX3,RUNX1,NF2,HNRNPU,NES,PDCD2	darkgrey	VSMC_M8

GO:0042558	0.05	0.98	5	28	pteridine-containing compound metabolic process	BP	0.95952	ALDH1L2,GGH,MTHFD1,TYMS,GART	darkgrey	VSMC_M8
GO:0045089	0.06	0.97	11	83	positive regulation of innate immune response	BP	0.96651	MATR3,POLR3B,POLR3F,HMGB2,TOMM70,MNDA,RBM14,PAK2,DHX9,UBE2K,GBP5	darkgrey	VSMC_M8
GO:2000241	0.06	0.97	13	105	regulation of reproductive process	BP	0.9765	FBXO5,CDC25C,TTK,CDC20,CHFR,CDC25B,TRIP13,ASPM,PDE3A,CDC25A,RAD51AP1,MSX1,AURKA	darkgrey	VSMC_M8
GO:0001649	0.06	0.97	21	190	osteoblast differentiation	BP	0.97719	ATP5F1B,FBXO5,FBN2,SYNCRIP,FBL,RRBP1,GTPBP4,ALYREF,HGF,SNAI2,CREB3L1,DDX5,DHX9,DDX21,IFT80,MYBBP1A,HNRNPU,COL1A1,RSL1D1,RBMX,CBFB	darkgrey	VSMC_M8
GO:0034471	0.06	0.99	4	20	ncRNA 5'-end processing	BP	0.98066	POP1,UTP20,SSB,ABT1	darkgrey	VSMC_M8
GO:0006376	0.06	0.98	5	28	mRNA splice site selection	BP	0.98984	PSIP1,SFSWAP,SF1,SRSF5,SF3A2	darkgrey	VSMC_M8
GO:0048524	0.06	0.98	8	55	positive regulation of viral process	BP	0.98984	SRPK1,PPIH,PPIE,AXL,PPID,DHX9,TOP2A,RAD23A	darkgrey	VSMC_M8
GO:0046785	0.06	0.97	10	74	microtubule polymerization	BP	0.99243	FBXO5,TPX2,CENPJ,CKAP5,FKBP4,RAC1,NDE1,MAP7D3,TPPP3,STMN1	darkgrey	VSMC_M8
GO:0055013	0.06	0.98	9	65	cardiac muscle cell development	BP	0.99358	ALPK2,DDX39B,PARP2,CCNB1,TBX3,CDK1,HNRNPU,LMNA,G6PD	darkgrey	VSMC_M8
GO:0010212	0.06	0.97	16	137	response to ionizing radiation	BP	1	NAMPT,RAD54L,FANCD2,NET1,RRM1,TOPBP1,RAD51,NUCKS1,RAD9A,TICRR,INTS7,H2AFX,BLM,BRCA1,RAD51AP1,ECT2	darkgrey	VSMC_M8
GO:0009889	0.06	0.95	252	3010	regulation of biosynthetic process	BP	1	HNRNPAB,BCLAF1,NUP107,CCT2,DDX39B,FBXO5,EZR,TCP1,RAD21,DSCC1,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,DBF4,VCP,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,CDCA7L,HNRNPA2B1,HOXA5,MFSD2A,SYNCRIP,PPIE,CCT4,THRAP3,EZH2,NUP62,PHF19,PRMT1,NAA15,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DBI,DIS3,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,GTPBP4,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,ZNF703,RFC3,HGF,ELK3,RRP8,TCERG1,CBX5,SNAI2,TCEA1,SGK3,CENPJ,NECAB3,E2F1,ABCE1,CCNE1,PXYLP1,ZNF827,HMGB2,MSC,ATF1,TERF1,NRIP1,UTP15,LOXL3,ESCO2,HEY1,ZBTB10,SELENOT,CCT8,PPID,RBL1,CCT7,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,PPP1R15B,HR,MDM4,RFC5,NCOA5,PPRC1,HMGN1,NOLC1,CCT5,FASTKD3,CCT6A,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,PHC2,ICE1,GMNN,CHEK1,H2AFZ,SMC3,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,TICRR,RFC2,EIF4H,NEK2,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,EIF4G1,PSMC5,CDK1,S100A11,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,PSMA6,DDX20,RFC4,DNA2,SF1,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,RAB27A,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,LIN9,EIF5A,EIF2S1,EIF3B,ARG2,EXOSC10,HDGF,CCT3,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,GEMIN5,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,EIF5,TYMS,CDCA4,ATAD5,ELF4,RAP2C,UHRF1,RBMX,TFAP4,SMG6,NOC2L,ZNF598,TP73,C	darkgrey	VSMC_M8
GO:0007163	0.06	0.97	21	189	establishment or maintenance of cell polarity	BP	1	ALPK2,FAM49B,HSP90AB1,AMOTL1,CENPA,KIF2C,SIPA1L3,KIF20B,WEE1,CKAP5,ZW10,RAC1,FSCN1,LMNA,SPDL1,PLK1,NDC80,MTCL1,NDE1,ARF6,MAD2L1	darkgrey	VSMC_M8
GO:0009127	0.06	0.99	4	20	purine nucleoside monophosphate biosynthetic process	BP	1	PAICS,DCK,PFAS,GART	darkgrey	VSMC_M8
GO:0001889	0.06	0.97	14	116	liver development	BP	1	DDX39B,EZH2,CAD,E2F7,PCNA,HGF,E2F8,PRMT5,XBP1,SRSF5,TYMS,ARF6,HNRNPD,AURKA	darkgrey	VSMC_M8
GO:0042981	0.06	0.95	97	1092	regulation of apoptotic process	BP	1	ALPK2,BCLAF1,TCP1,HSPA9,VCP,HSP90AB1,MELK,ANP32B,HOXA5,NUP62,CASP2,NAA15,STIL,PLAUR,AXL,RNF157,SPHK1,NET1,BIRC5,ARHGDIA,HGF,SNAI2,API5,CD44,HSP90B1,E2F1,HMGB2,HELLS,PPID,TRIM35,CTNNBL1,TBX3,CREB3L1,TOMM70,MYBL2,MTDH,HMGCR,EEF1E1,MDM4,KIF14,UNG,MNDA,ANP32E,XBP1,NF2,PDE3A,CDK1,TFRC,PAK2,FOSL1,DDX20,PPP2R1B,BARD1,BRCA1,MYBBP1A,ECT2,AIPL1,SIX4,MNAT1,USP42,MSX1,TOP2A,EIF5A,BID,PDPN,EIF2S1,ARG2,PRELID1,NES,LMNA,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,SERBP1,NNT,AIFM1,RSL1D1,TFAP4,THOC6,NOC2L,RNPS1,TP73,G6PD,PIK3CD,BCAR1,GCLM,FAM129B,CTH,MAD2L1,AURKA,SIGMAR1,ERP29,PDCD2,PALB2	darkgrey	VSMC_M8
GO:0045739	0.06	0.97	9	66	positive regulation of DNA repair	BP	1	TRIM28,PCNA,FANCB,H2AFX,DHX9,BRCA1,RAD51AP1,FOXM1,FUS	darkgrey	VSMC_M8
GO:0009057	0.06	0.95	98	1102	macromolecule catabolic process	BP	1	CDK2,POP1,EZR,MAN1A1,DESI1,CYP51A1,VCP,HSP90AB1,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,ODC1,NBAS,NRDC,RNASEH2B,GRIN2C,SMG9,DIS3,XRN2,CDC20,EIF4A3,CHMP6,CHFR,EXOSC8,PSMD13,CDC16,CD44,ANAPC1,HSP90B1,E2F1,PBK,FAM83D,HMGCR,BAP1,MDM4,UBE2C,PSMD14,FASTKD3,TENT4A,NSUN2,KIF14,DDX5,XBP1,UTP25,DTL,SSB,PSMD4,PSMC5,SMARCC1,DHX9,HNRNPR,PSMA6,DNA2,BARD1,UFD1,CNOT9,USP42,HNRNPU,UCHL1,UBE2K,NEDD4,PSMD3,EXOSC10,FUS,RAD23A,PLK1,ELAC2,EDC3,TAF15,PSMD11,COPS3,HNRNPM,SERBP1,AIFM1,USP1,UHRF1,SMG6,CCNF,RNPS1,ZNF598,DKC1,REXO4,PSMA5,ZC3H18,EXOSC2,TOR1A,SF3B3,USP4,HNRNPD,MAD2L1,AURKA,UBE2S,FEN1,PJA1,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:2000134	0.06	0.97	8	56	negative regulation of G1/S transition of mitotic cell cycle	BP	1	CDK2,GTSE1,EZH2,CASP2,E2F7,WEE1,RBL1,RPA2	darkgrey	VSMC_M8
GO:0009262	0.06	0.98	6	38	deoxyribonucleotide metabolic process	BP	1	DCK,RRM1,UNG,DUT,DCTPP1,TYMS	darkgrey	VSMC_M8
GO:0060343	0.06	0.98	4	20	trabecula formation	BP	1	FBN2,RBP4,HEY1,COL1A1	darkgrey	VSMC_M8
GO:0031647	0.06	0.96	26	249	regulation of protein stability	BP	1	CCT2,TCP1,APTX,HSP90AB1,CCT4,NAA15,COG3,GTPBP4,CHFR,ATP1B3,CCT8,CCT7,MDM4,CCT5,CCT6A,UTP25,NF2,MSX1,CCT3,LMNA,PPIB,RAD23A,PLK1,ZSWIM7,USP4,AURKA	darkgrey	VSMC_M8
GO:2000243	0.06	0.98	7	47	positive regulation of reproductive process	BP	1	CDC25C,CDC25B,PDE3A,CDC25A,RAD51AP1,MSX1,AURKA	darkgrey	VSMC_M8
GO:0042698	0.06	0.98	7	46	ovulation cycle	BP	1	CASP2,PGR,AXL,PCNA,NRIP1,ETS1,HAS2	darkgrey	VSMC_M8

GO:0044093	0.06	0.95	102	1151	positive regulation of molecular function	BP	1	CCT2,PRRC1,TCP1,DSCC1,NUS1,RANGAP1,DBF4,VCP,HSP90AB1,CKS2,TRIM28,NCBP1,ANP32B,MSH6,CYCS,HNRNPA2B1,CCT4,EZH2,CLSPN,CASP2,PLAUR,DBI,BORA,AXL,SPHK1,NET1,CDC20,DOCK9,SIPA1L3,PCNA,CDC25B,RFC3,DCUN1D2,CCNB1,TCEA1,TPX2,ATP1B3,HMGB2,ARHGAP11A,MSH3,MTDH,YWHAB,CHUK,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,GCN1,GMNN,CENPE,KIF14,RGS9,PHACTR4,RFC2,NEK2,EIF4G1,TFRC,PAK2,FOSL1,DHX9,PSMA6,RFC4,EPHB2,NMD3,DNAJC9,DCUN1D5,ECT2,DHX33,MNAT1,HNRNPU,INCENP,CDC6,BID,EIF2S1,PRELID1,AURKB,AHSA1,PLK1,EIF5,POLDIP2,AIFM1,UHRF1,EMP2,TFAP4,CHTF18,DKC1,CDT1,GCLM,FAM129B,ACD,PDP2,CTH,PRIM2,RAPGEF6,HNRNPD,STMN1,UBE2S,ERP29,PDCD2,MBD2	darkgrey	VSMC_M8
GO:0032479	0.06	0.97	10	75	regulation of type I interferon production	BP	1	POLR3B,POLR3F,HMGB2,TOMM70,CHUK,TRAIP,DHX9,POLA1,UFD1,DHX33	darkgrey	VSMC_M8
GO:0032606	0.06	0.97	10	75	type I interferon production	BP	1	POLR3B,POLR3F,HMGB2,TOMM70,CHUK,TRAIP,DHX9,POLA1,UFD1,DHX33	darkgrey	VSMC_M8
GO:0016233	0.06	0.98	6	37	telomere capping	BP	1	DCLRE1B,NEK2,AURKB,SMG6,ACD,HNRNPD	darkgrey	VSMC_M8
GO:0044272	0.06	0.96	15	127	sulfur compound biosynthetic process	BP	1	SLC35D2,B3GNT2,AMD1,PDHB,SLC10A7,ELOVL6,PDHA1,DLAT,MTHFD1,UGDH,ACSL4,XYLT1,GCLM,CTH,ACSL3	darkgrey	VSMC_M8
GO:0044380	0.06	0.97	8	55	protein localization to cytoskeleton	BP	1	TTK,NUP62,STIL,KIF20B,FAM83D,CEP72,HNRNPU,AURKA	darkgrey	VSMC_M8
GO:0060317	0.07	0.98	5	28	cardiac epithelial to mesenchymal transition	BP	1	SNAI2,HEY1,TBX3,MSX1,HAS2	darkgrey	VSMC_M8
GO:0034243	0.07	0.98	5	29	regulation of transcription elongation from RNA polymerase II promoter	BP	1	EZH2,WDR43,SUPT16H,TCERG1,HNRNPU	darkgrey	VSMC_M8
GO:0043516	0.07	0.98	5	29	regulation of DNA damage response, signal transduction by p53 class mediator	BP	1	SNAI2,CD44,EEF1E1,DDX5,MSX1	darkgrey	VSMC_M8
GO:0045859	0.07	0.95	49	513	regulation of protein kinase activity	BP	1	PRRC1,CDC25C,DBF4,HSP90AB1,CKS2,EZH2,NUP62,CLSPN,CCNA2,CHORDC1,BORA,NCAPG2,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,TPX2,CCNE1,CCNL1,CCNE2,HMGCR,CENPE,KIF14,PRKAR2A,NF2,BLM,CEP85,CDC25A,PAK2,EPHB2,CDKN3,ECT2,MNAT1,UCHL1,INCENP,CCNB3,CDC6,CCNB2,PLK1,RAP2C,EMP2,TFAP4,PKMYT1,CCNF,CDKN2C,ERP29,DUSP7	darkgrey	VSMC_M8
GO:0045047	0.07	0.98	5	30	protein targeting to ER	BP	1	MAN1A1,SEC61A1,SRP68,TRAM1,SPCS3	darkgrey	VSMC_M8
GO:0001701	0.07	0.96	32	314	in utero embryonic development	BP	1	TTLL1,BYSL,TRIM28,PRMT1,GJB3,PLK4,STIL,RNASEH2B,NASP,SMG9,NCAPG2,E2F7,GINS4,CCNB1,HEY1,TBX3,E2F8,NSUN2,CHEK1,NEK2,HINFP,SEC24D,FLVCR1,FOSL1,MSX1,ASF1B,CCNB2,COPS3,NXN,GINS1,PALB2,SLC30A1	darkgrey	VSMC_M8
GO:0009219	0.07	0.98	4	21	pyrimidine deoxyribonucleotide metabolic process	BP	1	UNG,DUT,DCTPP1,TYMS	darkgrey	VSMC_M8
GO:0000966	0.07	0.98	4	21	RNA 5'-end processing	BP	1	POP1,UTP20,SSB,ABT1	darkgrey	VSMC_M8
GO:0045184	0.07	0.94	121	1395	establishment of protein localization	BP	1	TMED9,XPOT,NUP43,NUP107,CCT2,EZR,TCP1,NUP50,ARFGAP3,MAN1A1,DESI1,RANGAP1,KIF20A,HSPA9,TNPO3,CYP51A1,VCP,HSP90AB1,CEP135,TRIM28,ANP32B,CCT4,NUP205,NUP62,NBAS,RUVBL2,SEC61A1,SAE1,CHCHD4,NASP,COG3,TOMM40,PREB,KCNN4,NUP85,SRP68,GDI2,SEC23B,RRBP1,IPO5,CHMP6,AAAS,KIF20B,CENPJ,HSP90B1,NECAB3,VAMP8,SLC10A7,TRAM1,CEP55,RBP4,TERF1,NUP160,SELENOT,CCT8,PPID,CCT7,NUP93,TOMM70,YWHAB,HMGCR,BAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,KIF18A,ICE1,KIF14,CSE1L,XBP1,MCM3AP,IPO4,NUP133,HINFP,SEC24D,ARCN1,CENPF,ARFGAP1,CDK1,TFRC,LSG1,ZW10,BARD1,NMD3,UFD1,NSD2,CDK16,ANKLE1,ECT2,RAC1,KDELR2,MYO5A,RAB27A,NEDD4,EIF5A,BID,CCT3,LMNA,LTBP2,COL1A1,TIMM8A,PLK1,NUP62CL,ACSL4,TIMM44,MTCL1,AIFM1,HOOK1,NDC1,DKC1,EMC8,NUP188,GLE1,ACD,ARF6,SPCS3,ACSL3,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:0060420	0.07	0.97	8	58	regulation of heart growth	BP	1	DDX39B,PARP2,CCNB1,RBP4,RUNX1,CDK1,TP73,G6PD	darkgrey	VSMC_M8
GO:0051099	0.07	0.96	16	141	positive regulation of binding	BP	1	HSP90AB1,TRIM28,NCBP1,PLAUR,HMGB2,GMNN,EIF4G1,DHX9,NMD3,EIF2S1,POLDIP2,CDT1,FAM129B,ACD,STMN1,MBD2	darkgrey	VSMC_M8
GO:0044728	0.07	0.97	9	67	DNA methylation or demethylation	BP	1	TRIM28,EZH2,HELLS,MIS18A,PRMT5,BRCA1,DNMT1,FAM129B,MBD2	darkgrey	VSMC_M8
GO:0071364	0.07	0.97	6	38	cellular response to epidermal growth factor stimulus	BP	1	CAD,SNAI2,KNSTRN,NCL,MCM7,COL1A1	darkgrey	VSMC_M8
GO:1902275	0.07	0.98	5	29	regulation of chromatin organization	BP	1	TRIM28,SSRP1,MKI67,HNRNPU,DNMT1	darkgrey	VSMC_M8
GO:0061008	0.07	0.96	14	119	hepaticobiliary system development	BP	1	DDX39B,EZH2,CAD,E2F7,PCNA,HGF,E2F8,PRMT5,XBP1,SRSF5,TYMS,ARF6,HNRNPD,AURKA	darkgrey	VSMC_M8
GO:0000302	0.07	0.96	19	177	response to reactive oxygen species	BP	1	APTX,EZH2,SDC1,PPP5C,AXL,SPHK1,NET1,PCNA,HGF,CHUK,PPP1R15B,ETS1,CDK1,FOSL1,TRA2B,ECT2,COL1A1,AIFM1,SIGMAR1	darkgrey	VSMC_M8
GO:0007283	0.07	0.95	35	357	spermatogenesis	BP	1	TTLL1,KIFC1,CDC25C,SRPK1,NUP62,GJB3,RUVBL1,WDR33,MAST2,AXL,XRN2,CCNB1,E2F1,HMGB2,RACGAP1,KNL1,NSUN2,SNRPA1,KHDRBS1,TRIP13,ASPM,H2AFX,CABYR,CDK16,USP42,ASF1B,PTTG1,BRIP1,SEPT6,RAI14,HOOK1,NDC1,DAZAP1,ODF2,HIST1H1A	darkgrey	VSMC_M8
GO:1904031	0.07	0.98	5	30	positive regulation of cyclin-dependent protein kinase activity	BP	1	HSP90AB1,CKS2,CCNB1,MNAT1,CDC6	darkgrey	VSMC_M8
GO:0050821	0.07	0.96	17	154	protein stabilization	BP	1	CCT2,TCP1,HSP90AB1,CCT4,NAA15,COG3,GTPBP4,ATP1B3,CCT8,CCT7,MDM4,CCT5,CCT6A,MSX1,CCT3,PPIB,ZSWIM7	darkgrey	VSMC_M8
GO:0009895	0.07	0.95	26	254	negative regulation of catabolic process	BP	1	CYP51A1,HSP90AB1,MFSD2A,SYNCRIP,THRAP3,NBAS,NAMPT,GRIN2C,HGF,E2F1,PBK,HMGCR,MDM4,TENT4A,NSUN2,EIF4G1,SMARCC1,DHX9,HNRNPU,FUS,TAF15,POLDIP2,DKC1,SF3B3,HNRNPD,MAD2L1	darkgrey	VSMC_M8
GO:0007568	0.08	0.95	26	252	aging	BP	1	CDK2,FBXO5,MSH6,NUP62,CASP2,SMC6,NAMPT,RAD54L,RBL1,TBX3,HMGCR,EEF1E1,CHEK1,H2AFX,CDK1,FOXM1,EIF2S1,ARG2,NUDT1,LMNA,AURKB,TYMS,RSL1D1,GCLM,NEK6,MBD2	darkgrey	VSMC_M8
GO:0051084	0.08	0.98	5	30	'de novo' posttranslational protein folding	BP	1	CCT2,HSPA9,CHCHD4,DNAJC7,TOR1A	darkgrey	VSMC_M8

GO:0051641	0.08	0.94	193	2295	cellular localization	BP	1	ATP5F1B,TMED9,XPOT,NUP107,CCT2,TUBB,DDX39B,EZR,TCP1,RAD21,NUP50,NUS1,ARFGAP3,MAN1A1,MTBP,KIFC1,DESI1,RANGAP1,HSPA9,SRSF3,TNPO3,BYSL,HMGXB4,VCP,HSP90AB1,CENPQ,MIOS,NOL8,TRIM28,NCBP1,ANP32B,TTK,HNRNPA2B1,CCT4,NUP205,CDCA8,EZH2,NUP62,RUVBL2,STIL,SEC61A1,SAE1,CHCHD4,CENPA,COG3,GRIN2C,TOMM40,PREB,NUP85,KIF2C,SRP68,RNF157,SEC23B,IPO5,CHMP6,ALYREF,CCNB1,AAAS,ESPL1,KIF20B,HSP90B1,ABCE1,CCNE1,VAMP8,ATP1B3,KNTC1,TRAM1,TERF1,NUP160,ESCO2,SELENOT,TUBA1B,CCT8,BUB1B,CCT7,RSRC1,GNL3,FAM83D,NUP93,KNL1,TOMM70,CCNE2,YWHAB,HMGCR,BAP1,NUSAP1,HEATR3,NOLC1,CCT5,NUP153,CCT6A,KIF18A,NSUN2,ICE1,KHDRBS1,CENPE,CEP72,KIF14,CSE1L,ASPM,RPA2,UTP25,MCM3AP,IPO4,NUP133,NF2,SEC24D,SSB,ARCN1,CENPF,BUB3,CDK1,TFRC,DHX9,NUF2,LSG1,ZW10,CDCA5,RANBP1,IFT80,BARD1,EPHB2,NMD3,UFD1,CDK16,DLGAP5,ANKLE1,ECT2,ZWINT,SIX4,MSX1,RAC1,KDELR2,MYO5A,HNRNPU,UCHL1,INCENP,RAB27A,NEDD4,BID,DDX39A,EXOSC10,SH3PXD2B,CCT3,KIF4A,LMNA,LTBP2,KIF22,SPDL1,AURKB,COL1A1,SPAG9,ZWILCH,TIMM8A,PLK1,SYT4,NUP62CL,TIMM44,NDC80,SEPT6,MTCL1,NDE1,AIFM1,HOOK1,EMP2,NDC1,RPA1,SMG6,THOC6,HASPIN,DKC1,PIK3CD,CDT1,EMC8,EXOSC2,TOR1A,NUP188,GLE1,ACD,ARF6,RAPGEF6,USP4,GBP5,SPCS3,MAD2L1,ACSL3,AURKA,BLOC1S2,STXBP6,ERP29,PID1,SLC30A1,UBE2J2	darkgrey	VSMC_M8
GO:0034248	0.08	0.95	38	395	regulation of cellular amide metabolic process	BP	1	DDX39B,PUM3,NCBP1,SYNCRIP,PUS7,DIS3,SPHK1,EIF4A3,EXOSC8,ABCE1,SELENOT,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,NCL,EIF4H,EIF4G1,DHX9,HNRNPR,CNOT9,RBM3,EIF2AK1,EIF5A,EIF2S1,EIF3B,GEMIN5,ILF3,EIF5,TYMS,ZNF598,EXOSC2,GLE1,TRUB2,HNRNPD	darkgrey	VSMC_M8
GO:0016570	0.08	0.95	39	399	histone modification	BP	1	CDK2,PWP1,EZH2,PHF19,PRMT1,RUVBL2,RUVBL1,CCNA2,PPP5C,NCAPG2,PARP2,FBL,CCNB1,BAP1,SETD4,HR,CHEK1,NAA50,PRMT5,MCM3AP,RBM14,HAT1,CDK1,BRCA1,NSD2,SUV39H1,INCENP,LMNA,AURKB,MORF4L2,VRK1,DNMT1,TADA2A,WDR70,UHRF1,NOC2L,HASPIN,AURKA,POLE3	darkgrey	VSMC_M8
GO:0032481	0.08	0.97	7	48	positive regulation of type I interferon production	BP	1	POLR3B,POLR3F,HMGB2,TOMM70,CHUK,DHX9,DHX33	darkgrey	VSMC_M8
GO:0043414	0.08	0.95	26	254	macromolecule methylation	BP	1	METTL1,PWP1,TRIM28,THADA,EZH2,PHF19,PRMT1,FBL,SNRPB,HELLS,FAM98B,MIS18A,SETD4,METTL15,NSUN2,PRMT5,TARBP1,BRCA1,NSD2,SUV39H1,LMNA,DNMT1,TRMT13,FAM129B,CSKMT,MBD2	darkgrey	VSMC_M8
GO:0018107	0.08	0.96	12	98	peptidyl-threonine phosphorylation	BP	1	PPP2R5D,TTK,CAD,SPHK1,CIT,CHEK1,EIF4G1,CDK1,UBE2K,PLK1,VRK1,HASPIN	darkgrey	VSMC_M8
GO:0051253	0.08	0.94	92	1032	negative regulation of RNA metabolic process	BP	1	BCLAF1,EZR,TRIM28,U2AF2,SYNCRIP,THRAP3,EZH2,PHF19,NBAS,RUVBL2,FOSB,SRSF2,BIRC5,E2F7,PCNA,ZNF703,ELK3,TCERG1,CBX5,SFSWAP,SNAI2,E2F1,ABCE1,CCNE1,HMGB2,MSC,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,TENT4A,NSUN2,PHC2,GMNN,KHDRBS1,PRMT5,DDX5,HINFP,CENPF,STRAP,PSMC5,DHX9,DDX20,SF1,BARD1,BRCA1,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,HDGF,FUS,MAZ,AURKB,PLK1,ILF3,DNMT1,TAF15,UHRF1,RBMX,TFAP4,NOC2L,RNPS1,DKC1,PTBP1,FAM129B,CBFB,DEPDC1,HNRNPD,DRAP1,SRSF7,MBD2	darkgrey	VSMC_M8
GO:0043067	0.08	0.94	98	1119	regulation of programmed cell death	BP	1	ALPK2,BCLAF1,TCP1,HSPA9,VCP,HSP90AB1,MELK,ANP32B,HOXA5,NUP62,CASP2,NAA15,STIL,PLAUR,AXL,RNF157,SPHK1,NET1,BIRC5,ARHGDIA,HGF,SNAI2,API5,CD44,HSP90B1,E2F1,HMGB2,HELLS,PPID,TRIM35,CTNNBL1,TBX3,CREB3L1,TOMM70,MYBL2,MTDH,HMGCR,EEF1E1,MDM4,KIF14,UNG,MNDA,ANP32E,XBP1,NF2,PDE3A,PSMC5,CDK1,TFRC,PAK2,FOSL1,DDX20,PPP2R1B,BARD1,BRCA1,MYBBP1A,ECT2,AIPL1,SIX4,MNAT1,USP42,MSX1,TOP2A,EIF5A,BID,PDPN,EIF2S1,ARG2,PRELID1,NES,LMNA,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,SERBP1,NNT,AIFM1,RSL1D1,TFAP4,THOC6,NOC2L,RNPS1,TP73,G6PD,PIK3CD,BCAR1,GCLM,FAM129B,CTH,MAD2L1,AURKA,SIGMAR1,ERP29,PDCD2,PALB2	darkgrey	VSMC_M8
GO:0006611	0.08	0.97	7	49	protein export from nucleus	BP	1	DESI1,RANGAP1,HSPA9,ANP32B,CSE1L,BARD1,ANKLE1	darkgrey	VSMC_M8
GO:0072522	0.08	0.95	17	157	purine-containing compound biosynthetic process	BP	1	ATP5F1B,VCP,PAICS,DCK,AMD1,PDHB,ELOVL6,PDHA1,DLAT,MTHFD1,PFAS,PRPS1,ACSL4,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0032984	0.08	0.95	21	195	protein-containing complex disassembly	BP	1	KIF24,VCP,GRWD1,MRPL58,KIF2C,SUPT16H,CKAP2,TPX2,KIF2A,ABCE1,VAMP8,CKAP5,KIF18A,SMARCC1,KIF18B,SMARCE1,EIF5A,NES,GLE1,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0044743	0.08	0.97	5	32	protein transmembrane import into intracellular organelle	BP	1	CHCHD4,TOMM40,TOMM70,TIMM44,AIFM1	darkgrey	VSMC_M8
GO:0044265	0.08	0.93	84	947	cellular macromolecule catabolic process	BP	1	CDK2,POP1,EZR,MAN1A1,DESI1,VCP,HSP90AB1,NCBP1,GRSF1,SYNCRIP,PABPC4,THRAP3,NBAS,RNASEH2B,SMG9,DIS3,XRN2,CDC20,EIF4A3,CHFR,EXOSC8,PSMD13,CDC16,ANAPC1,HSP90B1,E2F1,PBK,BAP1,UBE2C,PSMD14,FASTKD3,TENT4A,NSUN2,KIF14,DDX5,XBP1,DTL,SSB,PSMD4,PSMC5,SMARCC1,DHX9,HNRNPR,PSMA6,DNA2,UFD1,CNOT9,USP42,HNRNPU,UCHL1,UBE2K,NEDD4,PSMD3,EXOSC10,FUS,RAD23A,PLK1,ELAC2,EDC3,TAF15,PSMD11,COPS3,HNRNPM,SERBP1,AIFM1,USP1,UHRF1,SMG6,CCNF,RNPS1,ZNF598,DKC1,REXO4,PSMA5,ZC3H18,EXOSC2,TOR1A,USP4,HNRNPD,AURKA,UBE2S,FEN1,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:1901798	0.09	0.98	4	24	positive regulation of signal transduction by p53 class mediator	BP	1	EEF1E1,DDX5,MSX1,EIF5A	darkgrey	VSMC_M8

GO:0048518	0.09	0.92	368	4533	positive regulation of biological process	BP	1	CDK2,ATP5F1B,TMED9,HNRNPAB,BCLAF1,CCT2,DDX39B,FBXO5,PRRC1,EZR,FBN2,PANX2,TCP1,RAD21,DSCC1,NUS1,MTBP,ATAD2,PHF5A,FAM49B,CDC25C,MATR3,SRPK1,PPP2R5D,PWP1,DBF4,POLR3B,VCP,HSP90AB1,CDC5L,ARHGEF39,CENPQ,CEP135,CKS2,MIOS,MELK,TRIM28,NCBP1,ANP32B,PPIH,U2AF2,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,CLEC11A,HOXA5,MFSD2A,SYNCRIP,PPIE,CCT4,ANLN,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,NAA15,SMC6,GEN1,NRDC,SDC1,RUVBL2,PLK4,PGR,NAMPT,RUVBL1,CCNA2,SAE1,DNAJC2,RNASEH2B,PPP5C,FOSB,CDC42EP4,NUFIP1,GRIN2C,KCNN4,NUP85,PLAUR,DBI,BORA,DIS3,AXL,RNF157,SPHK1,NET1,WDR43,CDC20,BIRC5,PARP2,POLR3F,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,E2F7,ALYREF,CKAP2,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,ELK3,CDC16,TCERG1,MEDAG,CCNB1,SNAI2,CD44,TCEA1,ESPL1,TPX2,DEPDC1B,KIF20B,SLC20A1,UBA2,CENPJ,EIF2B1,E2F1,CCNE1,PXYLP1,VAMP8,ZNF827,ATP1B3,HMGB2,RBP4,ATF1,TERF1,NRIP1,UTP15,RACGAP1,LOXL3,HEY1,SELENOT,FAM98B,CCT8,PPID,TRIM35,CTNNBL1,CCT7,CDCA2,GNL3,FAM83D,CKAP5,NUP93,RBM19,TBX3,RAD51,CREB3L1,TOMM70,MYBL2,E2F8,MTDH,HMGCR,BAP1,NRAS,NUSAP1,EEF1E1,CHUK,RUNX1,SETD4,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,NOLC1,CCT5,CIT,FASTKD3,CCT6A,NUCKS1,GCN1,ETS1,TENT4A,ICE1,CHEK1,H2AFZ,KHDRBS1,CENPE,NCL,KIF14,RGS9,RBM23,PRMT5,ASPM,NOL11,ELOVL6,SF3B4,FANCI,MNDA,DDX5,FANCB,XBP1,RFC2,UTP25,NEK2,PRC1,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,RBM14,NSMCE4A,EIF4G1,PSMC5,CDK1,S100A11,CDC25A,TFRC,PAK2,FOSL1	darkgrey	VSMC_M8
GO:1902807	0.09	0.96	8	60	negative regulation of cell cycle G1/S phase transition	BP	1	CDK2,GTSE1,EZH2,CASP2,E2F7,WEE1,RBL1,RPA2	darkgrey	VSMC_M8
GO:2000515	0.09	0.97	4	22	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	LOXL3,RUNX1,ARG2,CBFB	darkgrey	VSMC_M8
GO:0032205	0.09	0.97	5	31	negative regulation of telomere maintenance	BP	1	TERF1,HNRNPU,EXOSC10,SMG6,ACD	darkgrey	VSMC_M8
GO:0009060	0.09	0.95	16	161	aerobic respiration	BP	1	ATP5F1B,MTFR2,CYC1,VCP,CYCS,CCNB1,PDHB,SUCLG1,NDUFAF1,CDK1,PDHA1,NDUFS1,DLAT,FH,BID,NNT	darkgrey	VSMC_M8
GO:0003203	0.09	0.97	5	31	endocardial cushion morphogenesis	BP	1	SNAI2,HEY1,TBX3,MDM4,MSX1	darkgrey	VSMC_M8
GO:0006164	0.09	0.95	16	149	purine nucleotide biosynthetic process	BP	1	ATP5F1B,VCP,PAICS,DCK,PDHB,ELOVL6,PDHA1,DLAT,MTHFD1,PFAS,PRPS1,ACSL4,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0055086	0.09	0.93	41	439	nucleobase-containing small molecule metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,NANS,CTPS1,DCK,GARS,AMD1,NAMPT,RNASEH2B,CAD,TK1,AFMID,RRM1,PDHB,AADAT,ENTPD7,HMGCR,UNG,ELOVL6,UMPS,PDHA1,UAP1,UCK2,DLAT,DUT,MTHFD1,UGDH,NUDT1,DCTPP1,PFAS,PRPS1,ACSL4,TYMS,GMPPB,ACSL3,PID1,GART,PRPSAP1,ERH	darkgrey	VSMC_M8
GO:0055006	0.09	0.96	9	71	cardiac cell development	BP	1	ALPK2,DDX39B,PARP2,CCNB1,TBX3,CDK1,HNRNPU,LMNA,G6PD	darkgrey	VSMC_M8
GO:0043279	0.09	0.95	10	81	response to alkaloid	BP	1	HSP90AB1,CCNA2,PPP5C,FOSB,CAD,RAD51,BLM,EFTUD2,DHX15,CASP6	darkgrey	VSMC_M8
GO:0009260	0.09	0.95	16	149	ribonucleotide biosynthetic process	BP	1	ATP5F1B,VCP,PAICS,CTPS1,CAD,PDHB,ELOVL6,UMPS,PDHA1,UCK2,DLAT,PFAS,ACSL4,ACSL3,PID1,GART	darkgrey	VSMC_M8
GO:0022412	0.09	0.94	25	247	cellular process involved in reproduction in multicellular organism	BP	1	FBXO5,TTLL1,SRPK1,TTK,MAST2,CDC25B,CCNB1,HMGB2,KNL1,KIF18A,NSUN2,TRIP13,ASPM,PDE3A,FOSL1,DDX20,CABYR,TOP2A,CCNB2,PLK1,BRIP1,HOOK1,FANCA,ODF2,AURKA	darkgrey	VSMC_M8
GO:2000113	0.09	0.92	100	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	BCLAF1,FBXO5,EZR,TRIM28,SYNCRIP,EZH2,PHF19,RUVBL2,PUS7,DNAJC2,FOSB,DBI,DIS3,SRSF2,BIRC5,GTPBP4,EIF4A3,E2F7,PCNA,EXOSC8,ZNF703,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,HMGB2,MSC,TERF1,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,TENT4A,PHC2,GMNN,KHDRBS1,NCL,PRMT5,DDX5,HINFP,BLM,CENPF,STRAP,EIF4G1,PSMC5,S100A11,HNRNPR,DDX20,SF1,SMARCAL1,BRCA1,CNOT9,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,CDC6,EIF2S1,EXOSC10,HDGF,MAZ,AURKB,PLK1,ILF3,DNMT1,TYMS,UHRF1,TFAP4,NOC2L,EXOSC2,FAM129B,ACD,CBFB,DEPDC1,HNRNPD,DRAP1,MBD2	darkgrey	VSMC_M8
GO:0070201	0.09	0.93	41	436	regulation of establishment of protein localization	BP	1	CCT2,EZR,TCP1,RANGAP1,CYP51A1,HSP90AB1,CEP135,TRIM28,ANP32B,CCT4,NUP62,SAE1,KCNN4,IPO5,KIF20B,CENPJ,RBP4,TERF1,CCT8,PPID,CCT7,HMGCR,BAP1,NOLC1,CCT5,CCT6A,ICE1,CDK1,BARD1,NSD2,CDK16,ECT2,RAC1,CCT3,ACSL4,MTCL1,DKC1,ARF6,ACSL3,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:0070849	0.09	0.96	6	41	response to epidermal growth factor	BP	1	CAD,SNAI2,KNSTRN,NCL,MCM7,COL1A1	darkgrey	VSMC_M8
GO:0006626	0.10	0.95	10	86	protein targeting to mitochondrion	BP	1	SAE1,CHCHD4,TOMM40,TOMM70,BAP1,BID,TIMM8A,TIMM44,AIFM1,UBE2J2	darkgrey	VSMC_M8
GO:0002639	0.10	0.97	5	33	positive regulation of immunoglobulin production	BP	1	RBP4,XBP1,TFRC,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0051098	0.10	0.93	29	296	regulation of binding	BP	1	HSP90AB1,TRIM28,NCBP1,PLAUR,GTPBP4,EIF4A3,E2F1,HMGB2,HEY1,NUCKS1,GMNN,HJURP,NEK2,EIF4G1,DHX9,NMD3,MSX1,EIF2S1,NES,AURKB,PLK1,POLDIP2,TFAP4,CDT1,FAM129B,ACD,STMN1,AURKA,MBD2	darkgrey	VSMC_M8
GO:0048477	0.10	0.96	8	62	oogenesis	BP	1	FBXO5,CDC25B,CCNB1,TRIP13,ASPM,PDE3A,DDX20,AURKA	darkgrey	VSMC_M8
GO:2001021	0.10	0.95	9	72	negative regulation of response to DNA damage stimulus	BP	1	DDX39B,FBXO5,SNAI2,CD44,PARPBP,POLQ,FANCB,AUNIP,BID	darkgrey	VSMC_M8
GO:0060341	0.10	0.93	61	675	regulation of cellular localization	BP	1	CCT2,EZR,TCP1,NUS1,RANGAP1,BYSL,VCP,HSP90AB1,CENPQ,TRIM28,ANP32B,CCT4,NUP62,SAE1,PREB,IPO5,AAAS,KIF20B,CCNE1,VAMP8,TERF1,CCT8,CCT7,GNL3,CCNE2,HMGCR,BAP1,NOLC1,CCT5,NUP153,CCT6A,NSUN2,ICE1,KHDRBS1,CEP72,NF2,CDK1,TFRC,DHX9,CDCA5,BARD1,EPHB2,NMD3,CDK16,ECT2,RAC1,HNRNPU,NEDD4,CCT3,LMNA,AURKB,PLK1,NDC80,MTCL1,DKC1,CDT1,TOR1A,ARF6,ACSL3,PID1,UBE2J2	darkgrey	VSMC_M8
GO:0035384	0.10	0.96	6	42	thioester biosynthetic process	BP	1	PDHB,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0071616	0.10	0.96	6	42	acyl-CoA biosynthetic process	BP	1	PDHB,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8

GO:0042306	0.10	0.96	7	52	regulation of protein import into nucleus	BP	1	HSP90AB1,TRIM28,NUP62,IPO5,NOLC1,CDK1,ECT2	darkgrey	VSMC_M8
GO:0065009	0.10	0.92	192	2307	regulation of molecular function	BP	1	CCT2,FBXO5,PRRC1,TCP1,DSCC1,NUS1,ARFGAP3,RANGAP1,CDC25C,PPP2R5D,DBF4,VCP,HSP90AB1,ARHGEF39,CKS2,TRIM28,NCBP1,THADA,ANP32B,PPP6R1,MSH6,CYCS,HNRNPA2B1,CCT4,EZH2,NUP62,CLSPN,CASP2,NRDC,MCM2,CCNA2,SAE1,DNAJC2,CHORDC1,MASTL,PREB,PLAUR,DBI,BORA,DIS3,AXL,SPHK1,NCAPG2,GDI2,NET1,CDC20,BIRC5,SERPINH1,SEC23B,GTPBP4,IPO5,EIF4A3,CHMP6,DOCK9,ARHGDIA,SIPA1L3,PCNA,PGAM5,CDC25B,RFC3,DCUN1D2,HGF,CCNB1,CD44,TCEA1,TPX2,DEPDC1B,PSD4,SGK3,HSP90B1,EIF2B1,E2F1,ABCE1,CCNE1,ATP1B3,HMGB2,TERF1,ARHGAP11A,RACGAP1,HEY1,RBL1,MSH3,CCNL1,CCNE2,MTDH,YWHAB,HMGCR,CHUK,CWF19L1,PPP1R15B,UBE2C,RFC5,PSMD14,PPRC1,HMGN1,CIT,NUCKS1,GCN1,GMNN,CENPE,TRAIP,KIF14,RGS9,ANP32E,RCC1,PHACTR4,HJURP,RFC2,SPP2,PRKAR2A,NEK2,NF2,BLM,CDC42SE1,CEP85,EIF4G1,ARFGAP1,CDC25A,TFRC,PAK2,FOSL1,DHX9,HNRNPR,PSMA6,RFC4,RANBP1,PPP2R1B,EPHB2,NMD3,DNAJC9,TFPI,CDKN3,DCUN1D5,ECT2,DHX33,MNAT1,MSX1,DNAJC7,HNRNPU,UCHL1,INCENP,NEDD4,CCNB3,RFC1,CDC6,BID,PSMD3,EIF2S1,PRELID1,CCNB2,IQGAP3,NES,SH3PXD2B,AURKB,AHSA1,PTTG1,PLK1,EIF5,POLDIP2,AIFM1,RAP2C,FAM122B,UHRF1,EMP2,TFAP4,SMG6,PKMYT1,CCNF,CHTF18,DKC1,FANCA,CDT1,GCLM,FAM129B,ACD,PLEKHG4,PDP2,CTH,DEPDC1,PRIM2,RAPGEF6,HNRNPD,MAD2L1,CDKN2C,STMN1,AURKA,UBE2S,ERP29,PDCD2,PRPSAP1,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0070507	0.10	0.94	15	135	regulation of microtubule cytoskeleton organization	BP	1	NUP62,BORA,CKAP2,TPX2,SKA3,CKAP5,KIF18A,RASSF1,KIF15,TACC3,FKBP4,RAC1,HNRNPU,PLK1,STMN1	darkgrey	VSMC_M8
GO:0009141	0.10	0.95	10	86	nucleoside triphosphate metabolic process	BP	1	ATP5F1B,VCP,CTPS1,CAD,ENTPD7,UCK2,DUT,DCTPP1,TYMS,PID1	darkgrey	VSMC_M8
GO:0060055	0.10	0.97	4	24	angiogenesis involved in wound healing	BP	1	PRCP,ETS1,XBP1,ADIPOR2	darkgrey	VSMC_M8
GO:0071806	0.10	0.96	7	54	protein transmembrane transport	BP	1	SEC61A1,CHCHD4,TOMM40,TRAM1,TOMM70,TIMM44,AIFM1	darkgrey	VSMC_M8
GO:0031400	0.10	0.93	40	426	negative regulation of protein modification process	BP	1	FBXO5,PPP2R5D,PWP1,U2AF2,NUP62,CHORDC1,PPP5C,MASTL,DBI,NCAPG2,GTPBP4,IPO5,CHMP6,HGF,CCNB1,PBK,YWHAB,HMGCR,PPP1R15B,PRKAR2A,NF2,CEP85,EIF4G1,PAK2,EPHB2,BRCA1,UCHL1,SPAG9,PLK1,DNMT1,NNT,NXN,TFAP4,NOC2L,G6PD,USP4,MAD2L1,CDKN2C,PID1,DUSP7	darkgrey	VSMC_M8
GO:0072332	0.10	0.95	8	63	intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	RRP8,CD44,E2F1,DDX5,MYBBP1A,MSX1,EIF5A,TP73	darkgrey	VSMC_M8
GO:0051129	0.10	0.92	52	569	negative regulation of cellular component organization	BP	1	FBXO5,RAD21,MTBP,FAM49B,TTK,GEN1,MCM2,CKAP2,HGF,CCNB1,ESPL1,BUB1,TPX2,KNTC1,TERF1,BUB1B,CHEK1,TRIP13,KIF14,RBM14,CENPF,BUB3,TFRC,PAK2,ZW10,EPHB2,BRCA1,ZWINT,FKBP4,MNAT1,RAC1,HNRNPU,TOP2A,PRELID1,EXOSC10,LMNA,SPDL1,AURKB,PTTG1,ZWILCH,PLK1,SYT4,SLC25A5,NDC80,SMG6,CCNF,CDT1,ACD,ARF6,TMOD3,MAD2L1,STMN1	darkgrey	VSMC_M8
GO:1903900	0.10	0.94	12	104	regulation of viral life cycle	BP	1	SRPK1,TRIM28,PPIH,PPIE,AXL,PPID,TRIM35,DDX5,TOP2A,RAD23A,ILF3,TRIM59	darkgrey	VSMC_M8
GO:0010558	0.10	0.92	100	1150	negative regulation of macromolecule biosynthetic process	BP	1	BCLAF1,FBXO5,EZR,TRIM28,SYNCRIP,EZH2,PHF19,RUVBL2,PUS7,DNAJC2,FOSB,DBI,DIS3,SRSF2,BIRC5,GTPBP4,EIF4A3,E2F7,PCNA,EXOSC8,ZNF703,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,HMGB2,MSC,TERF1,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,TENT4A,PHC2,GMNN,KHDRBS1,NCL,PRMT5,DDX5,HINFP,BLM,CENPF,STRAP,EIF4G1,PSMC5,S100A11,HNRNPR,DDX20,SF1,SMARCAL1,BRCA1,CNOT9,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,CDC6,EIF2S1,EXOSC10,HDGF,MAZ,AURKB,PLK1,ILF3,DNMT1,TYMS,UHRF1,TFAP4,NOC2L,EXOSC2,FAM129B,ACD,CBFB,DEPDC1,HNRNPD,DRAP1,MBD2	darkgrey	VSMC_M8
GO:0042255	0.10	0.96	6	45	ribosome assembly	BP	1	MRPS7,FP565260.1,BRIX1,DDX28,ABT1,NIP7	darkgrey	VSMC_M8
GO:0072599	0.11	0.96	5	34	establishment of protein localization to endoplasmic reticulum	BP	1	MAN1A1,SEC61A1,SRP68,TRAM1,SPCS3	darkgrey	VSMC_M8
GO:0021700	0.11	0.93	21	204	developmental maturation	BP	1	FBXO5,HOXA5,PGR,AXL,CDC20,CDC25B,CCNB1,NSUN2,TRIP13,KIF14,FLVCR1,PDE3A,ARCN1,CABYR,IFT80,SYT4,XYLT1,TYMS,G6PD,CBFB,AURKA	darkgrey	VSMC_M8
GO:0009116	0.11	0.96	6	45	nucleoside metabolic process	BP	1	AMD1,TK1,UMPS,NUDT1,PRPS1,ERH	darkgrey	VSMC_M8
GO:0006915	0.11	0.91	122	1436	apoptotic process	BP	1	ALPK2,BCLAF1,TCP1,RAD21,HSPA9,VCP,HSP90AB1,MELK,ANP32B,MSH6,CYCS,HOXA5,NUP62,CASP2,NAA15,STIL,MCM2,TMEM214,PLAUR,AXL,RNF157,SPHK1,NET1,BIRC5,PARP2,ARHGDIA,CKAP2,HGF,RRP8,SNAI2,API5,CD44,ESPL1,BUB1,TPX2,HSP90B1,E2F1,HMGB2,HELLS,PPID,TRIM35,CTNNBL1,BUB1B,TBX3,CREB3L1,TOMM70,MYBL2,MTDH,HMGCR,EEF1E1,MDM4,CIT,CHEK1,TRAIP,KIF14,UNG,MNDA,DDX5,ANP32E,XBP1,NF2,PDE3A,CDK1,TFRC,PAK2,FOSL1,NDUFS1,DDX20,PPP2R1B,BARD1,BRCA1,MYBBP1A,ECT2,AIPL1,SIX4,MNAT1,USP42,MSX1,UBE2K,TOP2A,EIF5A,BID,PDPN,EIF2S1,ARG2,PRELID1,NES,LMNA,ALOX15B,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,SERBP1,NNT,AIFM1,RSL1D1,TFAP4,THOC6,NOC2L,RNPS1,TP73,G6PD,PIK3CD,BCAR1,GCLM,FAM129B,NEK6,CTH,ARF6,MAD2L1,AURKA,BLOC1S2,SIGMAR1,ERP29,XKR5,PDCD2,PALB2,CASP6,EVA1A	darkgrey	VSMC_M8
GO:0002218	0.11	0.96	5	33	activation of innate immune response	BP	1	MATR3,TOMM70,MNDA,RBM14,PAK2	darkgrey	VSMC_M8
GO:0016556	0.11	0.97	4	24	mRNA modification	BP	1	PUS7,NSUN2,DKC1,TRUB2	darkgrey	VSMC_M8
GO:0019058	0.11	0.93	24	239	viral life cycle	BP	1	SRPK1,VCP,HSP90AB1,TRIM28,PPIH,PPIE,SLC1A5,AXL,CHMP6,VAMP8,PPID,TRIM35,NUP153,NUCKS1,DEK,DDX5,CDK1,TFRC,NEDD4,TOP2A,PPIB,RAD23A,ILF3,TRIM59	darkgrey	VSMC_M8

GO:0018210	0.11	0.94	12	104	peptidyl-threonine modification	BP	1	PPP2R5D,TTK,CAD,SPHK1,CIT,CHEK1,EIF4G1,CDK1,UBE2K,PLK1,VRK1,HASPIN	darkgrey	VSMC_M8
GO:0012501	0.11	0.91	125	1474	programmed cell death	BP	1	ALPK2,BCLAF1,TCP1,RAD21,HSPA9,VCP,HSP90AB1,MELK,ANP32B,MSH6,CYCS,HOXA5,NUP62,CASP2,NAA15,STIL,MCM2,TMEM214,PLAUR,AXL,RNF157,SPHK1,NET1,BIRC5,PARP2,ARHGDIA,CKAP2,PGAM5,HGF,RRP8,SNAI2,API5,CD44,ESPL1,BUB1,TPX2,HSP90B1,E2F1,HMGB2,HELLS,PPID,TRIM35,CTNNBL1,BUB1B,TBX3,CREB3L1,TOMM70,MYBL2,MTDH,HMGCR,EEF1E1,MDM4,CIT,CHEK1,TRAIP,KIF14,UNG,MNDA,DDX5,ANP32E,XBP1,NF2,PDE3A,PSMC5,CDK1,TFRC,PAK2,FOSL1,DHX9,NDUFS1,DDX20,PPP2R1B,BARD1,BRCA1,MYBBP1A,ECT2,AIPL1,SIX4,MNAT1,USP42,MSX1,UBE2K,TOP2A,EIF5A,BID,PDPN,EIF2S1,ARG2,PRELID1,NES,LMNA,ALOX15B,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,SERBP1,NNT,AIFM1,RSL1D1,TFAP4,THOC6,NOC2L,RNPS1,TP73,G6PD,PIK3CD,BCAR1,GCLM,FAM129B,NEK6,CTH,ARF6,MAD2L1,AURKA,BLOC1S2,SIGMAR1,ERP29,XKR5,PDCD2,PALB2,CASP6,EVA1A	darkgrey	VSMC_M8
GO:0045736	0.11	0.97	4	24	negative regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	IPO5,PLK1,TFAP4,CDKN2C	darkgrey	VSMC_M8
GO:1904030	0.11	0.97	4	24	negative regulation of cyclin-dependent protein kinase activity	BP	1	IPO5,PLK1,TFAP4,CDKN2C	darkgrey	VSMC_M8
GO:0032728	0.11	0.96	5	33	positive regulation of interferon-beta production	BP	1	POLR3B,POLR3F,HMGB2,TOMM70,DHX9	darkgrey	VSMC_M8
GO:1904353	0.11	0.97	4	24	regulation of telomere capping	BP	1	NEK2,AURKB,SMG6,HNRNPD	darkgrey	VSMC_M8
GO:0035304	0.11	0.94	9	74	regulation of protein dephosphorylation	BP	1	PPP2R5D,HSP90AB1,PPP6R1,MASTL,HSP90B1,CDCA2,YWHAB,PPP1R15B,PTBP1	darkgrey	VSMC_M8
GO:1904357	0.11	0.97	4	24	negative regulation of telomere maintenance via telomere lengthening	BP	1	TERF1,HNRNPU,EXOSC10,ACD	darkgrey	VSMC_M8
GO:0072529	0.11	0.96	4	25	pyrimidine-containing compound catabolic process	BP	1	ENTPD7,UNG,DUT,DCTPP1	darkgrey	VSMC_M8
GO:0031571	0.11	0.96	4	25	mitotic G1 DNA damage checkpoint signaling	BP	1	CDK2,GTSE1,CASP2,RPA2	darkgrey	VSMC_M8
GO:0051148	0.12	0.95	7	55	negative regulation of muscle cell differentiation	BP	1	EZH2,XBP1,MED28,MSX1,DNMT1,G6PD,PTBP1	darkgrey	VSMC_M8
GO:0031365	0.12	0.96	4	25	N-terminal protein amino acid modification	BP	1	NAA15,METAP2,METAP1,NAA50	darkgrey	VSMC_M8
GO:0032259	0.12	0.92	28	290	methylation	BP	1	METTL1,PWP1,TRIM28,THADA,EZH2,PHF19,PRMT1,FBL,RRP8,SNRPB,HELLS,FAM98B,MIS18A,SETD4,METTL15,NSUN2,PRMT5,TARBP1,BRCA1,NSD2,SUV39H1,LMNA,DNMT1,TYMS,TRMT13,FAM129B,CSKMT,MBD2	darkgrey	VSMC_M8
GO:0001824	0.12	0.94	10	86	blastocyst development	BP	1	TTLL1,BYSL,NASP,NCAPG2,GINS4,CHEK1,NEK2,ASF1B,GINS1,PALB2	darkgrey	VSMC_M8
GO:0009394	0.12	0.96	5	35	2'-deoxyribonucleotide metabolic process	BP	1	DCK,UNG,DUT,DCTPP1,TYMS	darkgrey	VSMC_M8
GO:0001933	0.12	0.92	27	276	negative regulation of protein phosphorylation	BP	1	PPP2R5D,PWP1,NUP62,CHORDC1,PPP5C,NCAPG2,IPO5,CHMP6,HGF,CCNB1,PBK,HMGCR,PPP1R15B,PRKAR2A,NF2,CEP85,EIF4G1,PAK2,EPHB2,UCHL1,SPAG9,PLK1,NNT,TFAP4,CDKN2C,PID1,DUSP7	darkgrey	VSMC_M8
GO:0002562	0.12	0.95	7	54	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	MSH6,HMGB2,MSH3,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0016444	0.12	0.95	7	54	somatic cell DNA recombination	BP	1	MSH6,HMGB2,MSH3,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:1904589	0.12	0.95	7	55	regulation of protein import	BP	1	HSP90AB1,TRIM28,NUP62,IPO5,NOLC1,CDK1,ECT2	darkgrey	VSMC_M8
GO:0032608	0.12	0.95	6	44	interferon-beta production	BP	1	POLR3B,POLR3F,HMGB2,TOMM70,TRAIP,DHX9	darkgrey	VSMC_M8
GO:0032648	0.12	0.95	6	44	regulation of interferon-beta production	BP	1	POLR3B,POLR3F,HMGB2,TOMM70,TRAIP,DHX9	darkgrey	VSMC_M8
GO:0016073	0.12	0.95	5	35	snRNA metabolic process	BP	1	EXOSC8,INTS7,EXOSC10,DKC1,EXOSC2	darkgrey	VSMC_M8
GO:1901532	0.12	0.96	4	25	regulation of hematopoietic progenitor cell differentiation	BP	1	HSPA9,PUS7,ANKLE1,PDCD2	darkgrey	VSMC_M8
GO:0050792	0.12	0.93	13	119	regulation of viral process	BP	1	SRPK1,TRIM28,PPIH,PPIE,AXL,PPID,TRIM35,DDX5,DHX9,TOP2A,RAD23A,ILF3,TRIM59	darkgrey	VSMC_M8
GO:0016032	0.12	0.91	31	325	viral process	BP	1	SRPK1,VCP,HSP90AB1,TRIM28,PPIH,PPIE,SLC1A5,AXL,CHMP6,VAMP8,PPID,TRIM35,NUP153,NUCKS1,DEK,DDX5,RCC1,SSB,CDK1,TFRC,DHX9,NEDD4,TOP2A,EIF3B,PPIB,RAD23A,ILF3,TFAP4,PTBP1,SPCS3,TRIM59	darkgrey	VSMC_M8
GO:0010799	0.13	0.95	5	35	regulation of peptidyl-threonine phosphorylation	BP	1	PPP2R5D,SPHK1,EIF4G1,UBE2K,PLK1	darkgrey	VSMC_M8
GO:0030865	0.13	0.94	7	55	cortical cytoskeleton organization	BP	1	EZR,ANLN,RACGAP1,FMNL3,ECT2,RAC1,ARF6	darkgrey	VSMC_M8
GO:0045333	0.13	0.92	18	191	cellular respiration	BP	1	ATP5F1B,MTFR2,CYC1,VCP,CYCS,CCNB1,PDHB,SUCLG1,NDUFAF1,CDK1,PDHA1,NDUFS1,DLAT,MYBBP1A,FH,BID,PRELID1,NNT	darkgrey	VSMC_M8
GO:0042307	0.13	0.95	5	35	positive regulation of protein import into nucleus	BP	1	HSP90AB1,TRIM28,IPO5,CDK1,ECT2	darkgrey	VSMC_M8
GO:1902680	0.13	0.89	107	1246	positive regulation of RNA biosynthetic process	BP	1	HNRNPAB,BCLAF1,DDX39B,ATAD2,PHF5A,PWP1,CDC5L,TRIM28,HOXA5,THRAP3,NUP62,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,WDR43,SUPT16H,E2F7,ALYREF,CKAP2,HGF,ELK3,TCERG1,TCEA1,CENPJ,E2F1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,PPRC1,HMGN1,NOLC1,NUCKS1,GCN1,ETS1,ICE1,CHEK1,H2AFZ,NCL,RBM23,NOL11,XBP1,HINFP,BLM,RBM14,PSMC5,FOSL1,SMARCC1,DHX9,NMD3,ETV4,BRCA1,CNOT9,PSMC3IP,GABPB1,DHX33,SIX4,FOXM1,LYAR,MSX1,HNRNPU,SMARCE1,RFC1,TOP2A,EIF5A,PMF1,HOXB7,FUS,MAZ,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,FAM129B,CBFB,PRIM2,HNRNPD,DRAP1,ABT1,PID1	darkgrey	VSMC_M8
GO:0061311	0.13	0.96	4	25	cell surface receptor signaling pathway involved in heart development	BP	1	ALPK2,SNAI2,HEY1,MSX1	darkgrey	VSMC_M8
GO:0044819	0.13	0.96	4	26	mitotic G1/S transition checkpoint signaling	BP	1	CDK2,GTSE1,CASP2,RPA2	darkgrey	VSMC_M8
GO:0045737	0.13	0.96	4	26	positive regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	CKS2,CCNB1,MNAT1,CDC6	darkgrey	VSMC_M8
GO:0035307	0.13	0.95	5	35	positive regulation of protein dephosphorylation	BP	1	PPP2R5D,HSP90AB1,CDCA2,PPP1R15B,PTBP1	darkgrey	VSMC_M8
GO:0046686	0.13	0.94	6	47	response to cadmium ion	BP	1	PPP5C,PCNA,CHUK,CDK1,NUDT1,SLC30A1	darkgrey	VSMC_M8
GO:0022411	0.13	0.90	35	375	cellular component disassembly	BP	1	KIF24,VCP,GRWD1,MRPL58,KIF2C,SUPT16H,CKAP2,SNAI2,TPX2,KIF2A,ABCE1,VAMP8,CKAP5,KIF18A,ETS1,ADAMTS4,CDK1,SMARCC1,KIF18B,FSCN1,SMARCE1,TOP2A,EIF5A,PDPN,NES,SH3PXD2B,PLK1,VRK1,SLC25A5,AIFM1,GLE1,NEK6,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8

GO:0046620	0.13	0.93	9	78	regulation of organ growth	BP	1	DDX39B,PARP2,CCNB1,RBP4,RUNX1,FLVCR1,CDK1,TP73,G6PD	darkgrey	VSMC_M8
GO:0006919	0.14	0.94	7	57	activation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	VCP,ANP32B,CYCS,CASP2,BID,AIFM1,PDCD2	darkgrey	VSMC_M8
GO:0045911	0.14	0.95	5	36	positive regulation of DNA recombination	BP	1	FANCB,TFRC,NSD2,RAD51AP1,FUS	darkgrey	VSMC_M8
GO:0034101	0.14	0.92	12	111	erythrocyte homeostasis	BP	1	HSPA9,HOXA5,PRMT1,AXL,NCAPG2,HMGB2,ETS1,FLVCR1,LYAR,SLC25A5,G6PD,TMOD3	darkgrey	VSMC_M8
GO:0071353	0.14	0.95	4	26	cellular response to interleukin-4	BP	1	HSP90AB1,MCM2,TUBA1B,XBP1	darkgrey	VSMC_M8
GO:0002262	0.14	0.92	14	134	myeloid cell homeostasis	BP	1	HSPA9,HOXA5,PRMT1,AXL,NCAPG2,HMGB2,BAP1,ETS1,FLVCR1,LYAR,SLC25A5,G6PD,PIK3CD,TMOD3	darkgrey	VSMC_M8
GO:0051649	0.14	0.88	140	1679	establishment of localization in cell	BP	1	ATP5F1B,TMED9,XPOT,NUP107,TUBB,DDX39B,EZR,NUP50,NUS1,ARFGAP3,MAN1A1,KIFC1,DESI1,RANGAP1,HSPA9,SRSF3,TNPO3,HMGXB4,VCP,HSP90AB1,CENPQ,TRIM28,NCBP1,ANP32B,HNRNPA2B1,NUP205,CDCA8,NUP62,SEC61A1,SAE1,CHCHD4,CENPA,COG3,GRIN2C,TOMM40,PREB,NUP85,KIF2C,SRP68,RNF157,SEC23B,IPO5,CHMP6,ALYREF,CCNB1,AAAS,ESPL1,KIF20B,HSP90B1,ABCE1,VAMP8,TRAM1,TERF1,NUP160,SELENOT,TUBA1B,RSRC1,FAM83D,NUP93,TOMM70,YWHAB,HMGCR,BAP1,NUSAP1,HEATR3,NOLC1,NUP153,KIF18A,NSUN2,ICE1,KHDRBS1,CENPE,KIF14,CSE1L,MCM3AP,IPO4,NUP133,SEC24D,SSB,ARCN1,CENPF,CDK1,DHX9,NUF2,LSG1,ZW10,CDCA5,RANBP1,BARD1,NMD3,UFD1,CDK16,DLGAP5,ANKLE1,ECT2,ZWINT,RAC1,KDELR2,MYO5A,HNRNPU,UCHL1,INCENP,RAB27A,NEDD4,BID,DDX39A,KIF4A,LMNA,LTBP2,KIF22,SPDL1,AURKB,SPAG9,TIMM8A,PLK1,SYT4,NUP62CL,TIMM44,NDC80,MTCL1,NDE1,AIFM1,HOOK1,EMP2,NDC1,SMG6,THOC6,PIK3CD,CDT1,TOR1A,NUP188,GLE1,ACD,ARF6,SPCS3,MAD2L1,BLOC1S2,ERP29,SLC30A1,UBE2J2	darkgrey	VSMC_M8
GO:0034614	0.14	0.92	13	124	cellular response to reactive oxygen species	BP	1	EZH2,PPP5C,AXL,SPHK1,NET1,PCNA,HGF,CHUK,ETS1,CDK1,ECT2,AIFM1,SIGMAR1	darkgrey	VSMC_M8
GO:0031124	0.14	0.93	7	56	mRNA 3'-end processing	BP	1	NCBP1,GRSF1,WDR33,CCNB1,BARD1,SLBP,CPSF7	darkgrey	VSMC_M8
GO:0019692	0.14	0.94	5	37	deoxyribose phosphate metabolic process	BP	1	DCK,UNG,DUT,DCTPP1,TYMS	darkgrey	VSMC_M8
GO:0048608	0.14	0.90	31	330	reproductive structure development	BP	1	NUP107,HSP90AB1,TRIM28,GJB3,CASP2,SDC1,PLK4,PGR,NASP,AXL,E2F7,RRM1,HMGB2,RBP4,NRIP1,HEY1,TBX3,E2F8,KIF18A,ASPM,FOSL1,SMARCC1,SF1,SIX4,NUDT1,ALOX15B,BRIP1,CCNF,DAZAP1,FANCA,TPPP3	darkgrey	VSMC_M8
GO:0060485	0.14	0.90	23	235	mesenchyme development	BP	1	HNRNPAB,TRIM28,HOXA5,EZH2,ZNF703,HGF,SNAI2,POLR1B,LOXL3,HEY1,FAM83D,TBX3,MDM4,NOLC1,DDX5,PHACTR4,NUP133,SIX4,MSX1,PDPN,EFNB1,COL1A1,HAS2	darkgrey	VSMC_M8
GO:0031327	0.14	0.88	102	1198	negative regulation of cellular biosynthetic process	BP	1	BCLAF1,FBXO5,EZR,TRIM28,SYNCRIP,EZH2,PHF19,RUVBL2,PUS7,DNAJC2,FOSB,DBI,DIS3,SPHK1,SRSF2,BIRC5,GTPBP4,EIF4A3,E2F7,PCNA,EXOSC8,ZNF703,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,HMGB2,MSC,TERF1,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,TENT4A,PHC2,GMNN,KHDRBS1,NCL,PRMT5,DDX5,HINFP,BLM,CENPF,STRAP,EIF4G1,PSMC5,S100A11,HNRNPR,DDX20,SF1,SMARCAL1,BRCA1,CNOT9,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,CDC6,EIF2S1,EXOSC10,HDGF,MAZ,AURKB,PLK1,ILF3,DNMT1,TYMS,UHRF1,TFAP4,NOC2L,EXOSC2,FAM129B,ACD,CBFB,DEPDC1,HNRNPD,DRAP1,PID1,MBD2	darkgrey	VSMC_M8
GO:0048511	0.14	0.90	22	223	rhythmic process	BP	1	THRAP3,EZH2,CASP2,PGR,NAMPT,AXL,PCNA,NRIP1,ETS1,PRMT5,DDX5,DTL,CDK1,DHX9,HNRNPR,MYBBP1A,SUV39H1,HNRNPU,TOP2A,TYMS,HNRNPD,HAS2	darkgrey	VSMC_M8
GO:0017148	0.14	0.91	16	158	negative regulation of translation	BP	1	SYNCRIP,PUS7,DIS3,EIF4A3,EXOSC8,TENT4A,NCL,EIF4G1,HNRNPR,CNOT9,EIF2AK1,EIF2S1,ILF3,TYMS,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0021591	0.14	0.95	4	27	ventricular system development	BP	1	KIF27,ANP32B,CENPF,MNAT1	darkgrey	VSMC_M8
GO:0031440	0.15	0.95	4	26	regulation of mRNA 3'-end processing	BP	1	NCBP1,CCNB1,BARD1,CPSF7	darkgrey	VSMC_M8
GO:1900744	0.15	0.94	5	37	regulation of p38MAPK cascade	BP	1	EZR,PRMT1,SPHK1,ULK4,HGF	darkgrey	VSMC_M8
GO:0060043	0.15	0.94	5	37	regulation of cardiac muscle cell proliferation	BP	1	CCNB1,RBP4,RUNX1,CDK1,TP73	darkgrey	VSMC_M8
GO:1904591	0.15	0.94	5	37	positive regulation of protein import	BP	1	HSP90AB1,TRIM28,IPO5,CDK1,ECT2	darkgrey	VSMC_M8
GO:0006368	0.15	0.93	7	58	transcription elongation from RNA polymerase II promoter	BP	1	EZH2,WDR43,SUPT16H,TCERG1,CHEK1,HNRNPU,CDCA4	darkgrey	VSMC_M8
GO:0051261	0.15	0.91	11	99	protein depolymerization	BP	1	KIF24,KIF2C,CKAP2,TPX2,KIF2A,CKAP5,KIF18A,KIF18B,NES,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0043066	0.15	0.88	58	662	negative regulation of apoptotic process	BP	1	HSPA9,HSP90AB1,NUP62,CASP2,NAA15,STIL,PLAUR,AXL,RNF157,SPHK1,BIRC5,ARHGDIA,HGF,SNAI2,API5,CD44,HSP90B1,HMGB2,HELLS,TBX3,CREB3L1,MTDH,HMGCR,MDM4,KIF14,UNG,XBP1,PDE3A,CDK1,TFRC,PAK2,BARD1,BRCA1,AIPL1,SIX4,MNAT1,MSX1,BID,PDPN,ARG2,PRELID1,NES,LMNA,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,NNT,THOC6,NOC2L,GCLM,FAM129B,CTH,MAD2L1,AURKA,PALB2	darkgrey	VSMC_M8
GO:0090199	0.15	0.94	5	39	regulation of release of cytochrome c from mitochondria	BP	1	PLAUR,HGF,BID,PRELID1,LMNA	darkgrey	VSMC_M8
GO:0002833	0.15	0.91	11	101	positive regulation of response to biotic stimulus	BP	1	MATR3,POLR3B,POLR3F,HMGB2,TOMM70,MNDA,RBM14,PAK2,DHX9,UBE2K,GBP5	darkgrey	VSMC_M8
GO:0097193	0.15	0.89	23	242	intrinsic apoptotic signaling pathway	BP	1	BCLAF1,MELK,MSH6,CASP2,PLAUR,RRP8,SNAI2,CD44,E2F1,HELLS,CREB3L1,DDX5,XBP1,BRCA1,MYBBP1A,MSX1,UBE2K,EIF5A,BID,AIFM1,NOC2L,TP73,ERP29	darkgrey	VSMC_M8
GO:0048821	0.15	0.95	4	27	erythrocyte development	BP	1	FLVCR1,LYAR,G6PD,TMOD3	darkgrey	VSMC_M8
GO:0006418	0.15	0.94	5	37	tRNA aminoacylation for protein translation	BP	1	NARS,VARS2,VARS,GARS,RARS	darkgrey	VSMC_M8
GO:0070646	0.15	0.91	13	125	protein modification by small protein removal	BP	1	DESI1,VCP,USPL1,BAP1,PSMD14,CDK1,USP42,DESI2,UCHL1,COPS3,USP1,TOR1A,USP4	darkgrey	VSMC_M8
GO:0061458	0.16	0.89	31	333	reproductive system development	BP	1	NUP107,HSP90AB1,TRIM28,GJB3,CASP2,SDC1,PLK4,PGR,NASP,AXL,E2F7,RRM1,HMGB2,RBP4,NRIP1,HEY1,TBX3,E2F8,KIF18A,ASPM,FOSL1,SMARCC1,SF1,SIX4,NUDT1,ALOX15B,BRIP1,CCNF,DAZAP1,FANCA,TPPP3	darkgrey	VSMC_M8

GO:1901137	0.16	0.88	44	494	carbohydrate derivative biosynthetic process	BP	1	ATP5F1B,NUS1,MAN1A1,SLC35D2,VCP,PAICS,NANS,CTPS1,DCK,B3GNT2,AMD1,RPN1,COG3,CAD,ALG8,RRM1,PDHB,NECAB3,PXYLP1,SLC10A7,GALNT6,STT3A,ELOVL6,UMPS,PDHA1,UAP1,UCK2,GK,DLAT,DUT,UGDH,PFAS,PRPS1,ACSL4,XYLT1,TYMS,G6PD,DOLPP1,GMPPB,ACSL3,HAS2,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0030218	0.16	0.91	11	102	erythrocyte differentiation	BP	1	HSPA9,HOXA5,PRMT1,NCAPG2,HMGB2,ETS1,FLVCR1,LYAR,SLC25A5,G6PD,TMOD3	darkgrey	VSMC_M8
GO:0018193	0.16	0.87	85	997	peptidyl-amino acid modification	BP	1	CDK2,TTLL1,DESI1,FKBP5,PPP2R5D,PWP1,HSP90AB1,MELK,TRIM28,PPIH,TTK,PPIE,EZH2,CLSPN,PHF19,PRMT1,NAA15,RUVBL2,RUVBL1,RPN1,SAE1,MASTL,MAST2,CHCHD4,CAD,ALG8,AXL,SPHK1,NCAPG2,PARP2,CHMP6,METAP2,HGF,USPL1,CCNB1,CD44,UBA2,CWC27,SGK3,WEE1,LOXL3,PBK,PPID,GNL3,CHUK,SETD4,CIT,METAP1,CHEK1,NAA50,STT3A,PRMT5,MCM3AP,NF2,HMBS,EIF4G1,HAT1,CDK1,TFRC,PAK2,EPHB2,BRCA1,CNOT9,NSD2,AIPL1,SUV39H1,FKBP4,UBE2K,LMNA,AURKB,PPIB,PLK1,MORF4L2,VRK1,DNMT1,TADA2A,RAP2C,NOC2L,HASPIN,PKN3,NEK6,CTH,AURKA,CSKMT,POLE3	darkgrey	VSMC_M8
GO:0032543	0.16	0.92	8	72	mitochondrial translation	BP	1	MRPS18B,MRPL2,GARS,MRPL58,MRPS7,FASTKD3,TRUB2,MRPS15	darkgrey	VSMC_M8
GO:0043009	0.16	0.88	47	522	chordate embryonic development	BP	1	TTLL1,BYSL,TRIM28,HOXA5,PRMT1,GJB3,PLK4,STIL,RNASEH2B,NASP,SMG9,NCAPG2,EIF4A3,E2F7,GINS4,CCNB1,POLR1B,KIF20B,CENPU,RBP4,HEY1,TBX3,E2F8,NOLC1,NSUN2,CHEK1,PHACTR4,NEK2,NUP133,HINFP,SEC24D,FLVCR1,FOSL1,BRCA1,SIX4,MSX1,MTHFD1,ASF1B,CCNB2,HOXB7,COL1A1,XYLT1,COPS3,NXN,GINS1,PALB2,SLC30A1	darkgrey	VSMC_M8
GO:0009142	0.16	0.92	7	62	nucleoside triphosphate biosynthetic process	BP	1	ATP5F1B,VCP,CTPS1,CAD,UCK2,TYMS,PID1	darkgrey	VSMC_M8
GO:0031398	0.16	0.91	11	102	positive regulation of protein ubiquitination	BP	1	SPHK1,CDC20,CHFR,DCUN1D2,UBE2C,FANCI,FANCM,BRCA1,DCUN1D5,PLK1,UBE2S	darkgrey	VSMC_M8
GO:0010035	0.16	0.88	39	435	response to inorganic substance	BP	1	CDK2,APTX,VCP,EZH2,SDC1,CCNA2,PPP5C,FOSB,AXL,SPHK1,NET1,EIF4A3,PCNA,HGF,CCNB1,GGH,ATF1,RAD51,BAP1,CHUK,PPP1R15B,ETS1,BLM,CDK1,FOSL1,ECT2,MNAT1,NEDD4,EIF2S1,NUDT1,FUS,COL1A1,SYT4,AIFM1,G6PD,HNRNPD,SIGMAR1,GART,SLC30A1	darkgrey	VSMC_M8
GO:0043603	0.16	0.87	75	897	cellular amide metabolic process	BP	1	NARS,MRPS18B,VARS2,DDX39B,VARS,MRPL2,PUM3,NCBP1,SYNCRIP,PABPC4,GARS,MRPL32,PUS7,MRPL58,MRPS7,DIS3,SPHK1,RRBP1,EIF4A3,EXOSC8,MRPS5,PDHB,EIF3M,EIF2B1,ABCE1,AADAT,SELENOT,EEF1E1,PPP1R15B,NOLC1,FASTKD3,GCN1,METAP1,TENT4A,KHDRBS1,NCL,ELOVL6,EIF4H,EIF4G1,MRPL11,PDHA1,DHX9,HNRNPR,DLAT,CNOT9,RPL22L1,RBM3,DHX33,EIF2AK1,EIF5A,EIF2S1,EIF3B,ARG2,EIF4A1,MRPL24,RARS,MRPS23,GEMIN5,ILF3,ACSL4,EIF5,TYMS,DRG2,MRPL37,THOP1,ZNF598,G6PD,EXOSC2,GLE1,TRUB2,GCLM,HNRNPD,SPCS3,ACSL3,MRPS15	darkgrey	VSMC_M8
GO:0031062	0.16	0.94	4	28	positive regulation of histone methylation	BP	1	PHF19,BRCA1,LMNA,DNMT1	darkgrey	VSMC_M8
GO:0006479	0.16	0.90	15	148	protein methylation	BP	1	PWP1,EZH2,PHF19,PRMT1,FBL,SNRPB,FAM98B,SETD4,PRMT5,BRCA1,NSD2,SUV39H1,LMNA,DNMT1,CSKMT	darkgrey	VSMC_M8
GO:0008213	0.16	0.90	15	148	protein alkylation	BP	1	PWP1,EZH2,PHF19,PRMT1,FBL,SNRPB,FAM98B,SETD4,PRMT5,BRCA1,NSD2,SUV39H1,LMNA,DNMT1,CSKMT	darkgrey	VSMC_M8
GO:0009126	0.16	0.93	5	39	purine nucleoside monophosphate metabolic process	BP	1	TJP2,PAICS,DCK,PFAS,GART	darkgrey	VSMC_M8
GO:0016447	0.16	0.93	6	48	somatic recombination of immunoglobulin gene segments	BP	1	MSH6,MSH3,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:1990542	0.16	0.91	9	84	mitochondrial transmembrane transport	BP	1	ATP5F1B,CHCHD4,TOMM40,TOMM70,SFXN3,SFXN4,TIMM44,SLC25A5,AIFM1	darkgrey	VSMC_M8
GO:0031330	0.16	0.89	20	207	negative regulation of cellular catabolic process	BP	1	HSP90AB1,MFSD2A,SYNCRIP,THRAP3,NBAS,NAMPT,HGF,E2F1,PBK,TENT4A,NSUN2,EIF4G1,SMARCC1,DHX9,HNRNPU,FUS,TAF15,POLDIP2,DKC1,HNRNPD	darkgrey	VSMC_M8
GO:0051147	0.16	0.90	12	115	regulation of muscle cell differentiation	BP	1	DDX39B,EZH2,PARP2,XBP1,MED28,MSX1,MORF4L2,DNMT1,G6PD,PTBP1,FAM129B,CTH	darkgrey	VSMC_M8
GO:0016458	0.16	0.90	16	169	gene silencing	BP	1	CDK2,TRIM28,NCBP1,HNRNPA2B1,RRP8,HELLS,DDX5,EIF4G1,DHX9,DGCR8,CNOT9,SUV39H1,DNMT1,SRRT,POLE3,MBD2	darkgrey	VSMC_M8
GO:0009410	0.16	0.88	29	314	response to xenobiotic stimulus	BP	1	HSP90AB1,CTPS1,RAD54L,FOSB,CAD,SRP68,PCNA,CCNB1,GGH,E2F1,TERF1,RAD51,CHUK,TENT4A,PDE3A,UMPS,CENPF,CDK1,TFRC,FOSL1,EFTUD2,MCM7,UCHL1,ADIPOR2,COL1A1,PFAS,TYMS,TP73,GCLM	darkgrey	VSMC_M8
GO:0070670	0.16	0.94	4	28	response to interleukin-4	BP	1	HSP90AB1,MCM2,TUBA1B,XBP1	darkgrey	VSMC_M8
GO:0007584	0.16	0.90	14	137	response to nutrient	BP	1	SRSF2,SNAI2,HMGCR,XBP1,HAT1,ADIPOR2,COL1A1,BRIP1,ACSL4,TYMS,NNT,LIPG,GCLM,ACSL3	darkgrey	VSMC_M8
GO:0007548	0.17	0.89	20	206	sex differentiation	BP	1	NUP107,CASP2,SDC1,PGR,NASP,AXL,RRM1,HMGB2,RBP4,NRIP1,TBX3,KIF18A,ASPM,SF1,CNOT9,SIX4,NUDT1,CENPI,BRIP1,FANCA	darkgrey	VSMC_M8
GO:0030488	0.17	0.93	5	39	tRNA methylation	BP	1	METTL1,THADA,NSUN2,TARBP1,TRMT13	darkgrey	VSMC_M8
GO:0060323	0.17	0.94	4	28	head morphogenesis	BP	1	FLVCR1,MSX1,COL1A1,CRISPLD2	darkgrey	VSMC_M8
GO:0009792	0.17	0.87	48	537	embryo development ending in birth or egg hatching	BP	1	TTLL1,BYSL,TRIM28,HOXA5,PRMT1,GJB3,PLK4,STIL,RNASEH2B,NASP,SMG9,NCAPG2,EIF4A3,E2F7,GINS4,CCNB1,POLR1B,KIF20B,CENPU,RBP4,HEY1,TBX3,E2F8,NOLC1,NSUN2,CHEK1,PHACTR4,NEK2,NUP133,HINFP,SEC24D,FLVCR1,FOSL1,BRCA1,SIX4,MSX1,MTHFD1,ASF1B,CCNB2,HOXB7,COL1A1,ACSL4,XYLT1,COPS3,NXN,GINS1,PALB2,SLC30A1	darkgrey	VSMC_M8
GO:2000106	0.17	0.92	7	59	regulation of leukocyte apoptotic process	BP	1	TCP1,AXL,ARG2,PRELID1,AURKB,NOC2L,PIK3CD	darkgrey	VSMC_M8
GO:0071230	0.17	0.92	7	59	cellular response to amino acid stimulus	BP	1	COL1A2,IPO5,XBP1,COL1A1,DNMT1,GCLM,HNRNPD	darkgrey	VSMC_M8
GO:0009201	0.17	0.92	6	52	ribonucleoside triphosphate biosynthetic process	BP	1	ATP5F1B,VCP,CTPS1,CAD,UCK2,PID1	darkgrey	VSMC_M8
GO:0008033	0.17	0.90	12	117	tRNA processing	BP	1	METTL1,POP1,THADA,GRSF1,PUS7,TSEN2,DUS1L,NSUN2,TARBP1,SSB,ELAC2,TRMT13	darkgrey	VSMC_M8

GO:0071705	0.17	0.85	133	1609	nitrogen compound transport	BP	1	TMED9,XPOT,NUP43,NUP107,DDX39B,EZR,TCP1,NUP50,ARFGAP3,MAN1A1,DESI1,RANGAP1,KIF20A,SLC35D2,HSPA9,SRSF3,TNPO3,CYP51A1,VCP,HSP90AB1,TRIM28,NCBP1,ANP32B,HNRNPA2B1,NUP205,NUP62,NBAS,SEC61A1,SAE1,SLC1A5,CHCHD4,NASP,COG3,TOMM40,PREB,KCNN4,NUP85,SLC25A19,SLC5A6,SRP68,GDI2,SEC23B,RRBP1,IPO5,EIF4A3,CHMP6,ALYREF,AAAS,KIF20B,HSP90B1,NECAB3,VAMP8,SLC10A7,TRAM1,RBP4,NUP160,SELENOT,PPID,CKAP5,NUP93,TOMM70,YWHAB,HMGCR,BAP1,SFXN3,HEATR3,NOLC1,NUP153,KIF18A,NSUN2,ICE1,KHDRBS1,CSE1L,XBP1,MCM3AP,IPO4,SFXN4,NUP133,SEC24D,FLVCR1,SSB,ARCN1,CENPF,SLC17A9,ARFGAP1,CDK1,TFRC,DHX9,LSG1,HNRNPA3,ZW10,BARD1,NMD3,UFD1,CDK16,SLBP,SLC19A2,ANKLE1,ECT2,RAC1,KDELR2,MYO5A,RAB27A,NEDD4,EIF5A,BID,DDX39A,LMNA,LTBP2,COL1A1,TIMM8A,SYT4,NUP62CL,ACSL4,TIMM44,SLC25A5,MTCL1,AIFM1,HOOK1,NDC1,SMG6,THOC6,SLC6A17,TOR1A,NUP188,GLE1,ACD,ARF6,SPCS3,ACSL3,SRSF7,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:0043069	0.17	0.86	59	681	negative regulation of programmed cell death	BP	1	HSPA9,HSP90AB1,NUP62,CASP2,NAA15,STIL,PLAUR,AXL,RNF157,SPHK1,BIRC5,ARHGDIA,HGF,SNAI2,API5,CD44,HSP90B1,HMGB2,HELLS,TBX3,CREB3L1,MTDH,HMGCR,MDM4,KIF14,UNG,XBP1,PDE3A,PSMC5,CDK1,TFRC,PAK2,BARD1,BRCA1,AIPL1,SIX4,MNAT1,MSX1,BID,PDPN,ARG2,PRELID1,NES,LMNA,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,NNT,THOC6,NOC2L,GCLM,FAM129B,CTH,MAD2L1,AURKA,PALB2	darkgrey	VSMC_M8
GO:0055017	0.17	0.91	8	72	cardiac muscle tissue growth	BP	1	DDX39B,PARP2,CCNB1,RBP4,RUNX1,CDK1,TP73,G6PD	darkgrey	VSMC_M8
GO:0043388	0.17	0.93	5	40	positive regulation of DNA binding	BP	1	TRIM28,PLAUR,HMGB2,FAM129B,ACD	darkgrey	VSMC_M8
GO:0061647	0.17	0.93	5	38	histone H3-K9 modification	BP	1	CHEK1,BRCA1,SUV39H1,LMNA,DNMT1	darkgrey	VSMC_M8
GO:0007565	0.17	0.89	14	139	female pregnancy	BP	1	TRIM28,PGR,NAMPT,FOSB,CAD,POLR1B,ETS1,UMPS,FOSL1,ADIPOR2,ACSL4,EMP2,DAZAP1,TPPP3	darkgrey	VSMC_M8
GO:0010468	0.17	0.84	276	3428	regulation of gene expression	BP	1	CDK2,ALPK2,HNRNPAB,BCLAF1,HNRNPH1,NUP107,TCF19,DDX39B,EZR,PANX2,RAD21,ATAD2,PHF5A,FAM49B,ZNF367,MATR3,SRPK1,SRSF3,PSIP1,PWP1,POLR3B,UBAP2,HSP90AB1,CDC5L,PUM3,CKS2,TRIM28,NCBP1,U2AF2,CDCA7L,HNRNPA2B1,GRSF1,HOXA5,SYNCRIP,PPIE,PABPC4,THRAP3,EZH2,NUP62,PHF19,NBAS,NAA15,RUVBL2,PGR,NAMPT,PUS7,RUVBL1,CCNA2,DNAJC2,RNASEH2B,MAST2,FOSB,NUFIP1,SMG9,NUP85,DIS3,AXL,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,BIRC5,POLR3F,SUPT16H,EIF4A3,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,ZNF703,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,TCEA1,HNRNPF,SGK3,CENPJ,E2F1,ABCE1,CCNE1,ZNF827,HMGB2,RBP4,MSC,ATF1,HELLS,NRIP1,UTP15,RBM12,LOXL3,HEY1,ZBTB10,SELENOT,FAM98B,PPID,RBL1,CCNL1,HNRNPDL,GNL3,TBX3,CREB3L1,TOMM70,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,SETD4,PPP1R15B,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,FASTKD3,NUCKS1,DEK,GCN1,ETS1,METAP1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,SF3B4,MNDA,DDX5,XBP1,EIF4H,EWSR1,HINFP,BLM,RBM14,SSB,CENPF,STRAP,EIF4G1,PSMC5,CDK1,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,PSMA6,POLA1,HNRNPH3,DDX20,DDX21,DGCR8,SF1,EPHB2,SMARCAL1,ETV4,UFD1,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,RAB27A,ADIPOR2,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,EIF2S1,EIF3B,ARG2,SRSF5,IQGAP3,EXOSC10,HDGF,PMF1,HOXB7,FUS,LMNA,ALOX15B,MAZ,AURKB,COL1A1,NFA	darkgrey	VSMC_M8
GO:0045893	0.18	0.85	105	1244	positive regulation of transcription, DNA-templated	BP	1	HNRNPAB,BCLAF1,DDX39B,ATAD2,PHF5A,PWP1,CDC5L,TRIM28,HOXA5,THRAP3,NUP62,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,WDR43,SUPT16H,E2F7,ALYREF,CKAP2,HGF,ELK3,TCERG1,TCEA1,CENPJ,E2F1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,PPRC1,HMGN1,NOLC1,NUCKS1,GCN1,ETS1,ICE1,CHEK1,H2AFZ,NCL,RBM23,NOL11,XBP1,HINFP,BLM,RBM14,PSMC5,FOSL1,SMARCC1,DHX9,ETV4,BRCA1,CNOT9,PSMC3IP,GABPB1,DHX33,SIX4,FOXM1,LYAR,MSX1,HNRNPU,SMARCE1,RFC1,TOP2A,EIF5A,PMF1,HOXB7,FUS,MAZ,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,FAM129B,CBFB,HNRNPD,DRAP1,ABT1,PID1	darkgrey	VSMC_M8
GO:1903508	0.18	0.85	105	1244	positive regulation of nucleic acid-templated transcription	BP	1	HNRNPAB,BCLAF1,DDX39B,ATAD2,PHF5A,PWP1,CDC5L,TRIM28,HOXA5,THRAP3,NUP62,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,WDR43,SUPT16H,E2F7,ALYREF,CKAP2,HGF,ELK3,TCERG1,TCEA1,CENPJ,E2F1,ZNF827,HMGB2,ATF1,NRIP1,UTP15,HEY1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,MTDH,CHUK,RUNX1,PPRC1,HMGN1,NOLC1,NUCKS1,GCN1,ETS1,ICE1,CHEK1,H2AFZ,NCL,RBM23,NOL11,XBP1,HINFP,BLM,RBM14,PSMC5,FOSL1,SMARCC1,DHX9,ETV4,BRCA1,CNOT9,PSMC3IP,GABPB1,DHX33,SIX4,FOXM1,LYAR,MSX1,HNRNPU,SMARCE1,RFC1,TOP2A,EIF5A,PMF1,HOXB7,FUS,MAZ,COL1A1,NFATC2IP,ILF2,ILF3,MORF4L2,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,TP73,FAM129B,CBFB,HNRNPD,DRAP1,ABT1,PID1	darkgrey	VSMC_M8
GO:0006084	0.18	0.93	4	29	acetyl-CoA metabolic process	BP	1	PDHB,AADAT,PDHA1,DLAT	darkgrey	VSMC_M8
GO:0018023	0.18	0.93	5	39	peptidyl-lysine trimethylation	BP	1	PWP1,SETD4,SUV39H1,LMNA,CSKMT	darkgrey	VSMC_M8

GO:0044267	0.18	0.84	297	3725	cellular protein metabolic process	BP	1	CDK2,ALPK2,NARS,MRPS18B,VARS2,DDX39B,FBXO5,PRRC1,VARS,EZR,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,DESI1,CDC25C,FKBP5,SRPK1,PPP2R5D,PWP1,MRPL2,DBF4,VCP,HSP90AB1,PUM3,CKS2,MELK,TRIM28,NCBP1,ANP32B,PPIH,U2AF2,PPP6R1,TTK,CYCS,SYNCRIP,PPIE,PABPC4,GARS,B3GNT2,EZH2,NUP62,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NAA15,NRDC,RUVBL2,PLK4,PUS7,RUVBL1,CCNA2,RPN1,SAE1,CHORDC1,PPP5C,MASTL,MAST2,CHCHD4,COG3,MRPL58,PLAUR,MRPS7,CAD,ALG8,DBI,TRIM47,BORA,DIS3,AXL,RNF157,SPHK1,ULK4,NCAPG2,CDC20,BIRC5,SERPINH1,PARP2,FBL,RRBP1,GTPBP4,RAD18,IPO5,EIF4A3,CHMP6,CHFR,EXOSC8,PGAM5,CDC25B,METAP2,DCUN1D2,HGF,PSMD13,CDC16,USPL1,CCNB1,SNRPB,CD44,MRPS5,BUB1,TPX2,ANAPC1,UBA2,CWC27,SGK3,EIF3M,WEE1,HSP90B1,EIF2B1,ABCE1,CCNE1,GALNT6,LOXL3,PBK,ESCO2,SELENOT,FAM98B,PPID,TRIM35,BUB1B,CCNL1,RSRC1,CDCA2,GNL3,RAD51,CCNE2,TRIM33,YWHAB,HMGCR,BAP1,EEF1E1,CHUK,SETD4,PPP1R15B,HR,UBE2C,PSMD14,NOLC1,CIT,FASTKD3,GCN1,METAP1,TENT4A,UBE2T,CHEK1,NAA50,KHDRBS1,STT3A,CENPE,NCL,TRAIP,KIF14,PRMT5,FANCI,XBP1,SPP2,MCM3AP,EIF4H,PRKAR2A,NEK2,DTL,NF2,HMBS,BLM,RBM14,PSMD4,CEP85,EIF4G1,MRPL11,PSMC5,HAT1,CDK1,CDC25A,TFRC,PAK2,SMARCC1,DHX9,HNRNPR,PSMA6,FANCM,LRR1,PPP2R1B,BARD1,EPHB2,UFD1,BRCA1,CDCA3,TFPI,CNOT9,CDKN3,NSD2,RPL22L1,CDK16,DCUN1D5,ECT2,AIPL1,RBM3,DHX33,SUV39H1,FKBP4,MNAT1,MAPK6,EIF2AK1,USP42,FAM220A,RAC1,DESI2,UCHL1,INCENP,ADIPOR2,UBE2K,NEDD4,CCNB3,CDC6,EIF5A,BID,PSMD3,EIF2S1,DCAF15,EIF3B,PRELID1,CCNB2,IQGAP	darkgrey	VSMC_M8
GO:0046907	0.18	0.85	105	1261	intracellular transport	BP	1	ATP5F1B,TMED9,XPOT,NUP107,TUBB,DDX39B,EZR,NUP50,NUS1,ARFGAP3,MAN1A1,DESI1,RANGAP1,HSPA9,SRSF3,TNPO3,HMGXB4,VCP,HSP90AB1,TRIM28,NCBP1,ANP32B,HNRNPA2B1,NUP205,NUP62,SEC61A1,SAE1,CHCHD4,COG3,TOMM40,PREB,NUP85,SRP68,RNF157,SEC23B,IPO5,CHMP6,ALYREF,AAAS,KIF20B,HSP90B1,ABCE1,TRAM1,NUP160,TUBA1B,RSRC1,NUP93,TOMM70,YWHAB,BAP1,HEATR3,NOLC1,NUP153,NSUN2,ICE1,KHDRBS1,CSE1L,MCM3AP,IPO4,NUP133,SEC24D,SSB,ARCN1,CDK1,DHX9,LSG1,ZW10,RANBP1,BARD1,NMD3,UFD1,ANKLE1,ECT2,KDELR2,MYO5A,HNRNPU,UCHL1,RAB27A,NEDD4,BID,DDX39A,KIF4A,LMNA,LTBP2,SPAG9,TIMM8A,SYT4,NUP62CL,TIMM44,MTCL1,NDE1,AIFM1,HOOK1,EMP2,NDC1,SMG6,THOC6,NUP188,GLE1,ACD,ARF6,SPCS3,BLOC1S2,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:0046636	0.18	0.93	4	29	negative regulation of alpha-beta T cell activation	BP	1	LOXL3,RUNX1,ARG2,CBFB	darkgrey	VSMC_M8
GO:0006468	0.18	0.85	103	1223	protein phosphorylation	BP	1	CDK2,ALPK2,PRRC1,CDC25C,SRPK1,PPP2R5D,PWP1,DBF4,HSP90AB1,CKS2,MELK,TRIM28,TTK,EZH2,NUP62,CLSPN,PLK4,CCNA2,CHORDC1,PPP5C,MASTL,MAST2,PLAUR,CAD,BORA,AXL,SPHK1,ULK4,NCAPG2,BIRC5,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,CD44,BUB1,TPX2,SGK3,WEE1,CCNE1,PBK,BUB1B,CCNL1,RSRC1,RAD51,CCNE2,HMGCR,CHUK,PPP1R15B,CIT,CHEK1,CENPE,KIF14,PRKAR2A,NEK2,NF2,BLM,CEP85,EIF4G1,CDK1,CDC25A,TFRC,PAK2,EPHB2,CNOT9,CDKN3,CDK16,ECT2,MNAT1,MAPK6,EIF2AK1,RAC1,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,EIF2S1,CCNB2,IQGAP3,AURKB,SPAG9,PLK1,ILF3,VRK1,NNT,RAP2C,EMP2,TFAP4,PKMYT1,HASPIN,CCNF,PIK3CD,PKN3,NEK6,CDKN2C,AURKA,ERP29,PID1,DUSP7	darkgrey	VSMC_M8
GO:0010941	0.18	0.85	102	1223	regulation of cell death	BP	1	ALPK2,BCLAF1,TCP1,HSPA9,VCP,HSP90AB1,MELK,ANP32B,HOXA5,NUP62,CASP2,NAA15,STIL,PPP5C,PLAUR,AXL,RNF157,SPHK1,NET1,BIRC5,PARP2,RAD18,ARHGDIA,HGF,SNAI2,API5,CD44,HSP90B1,E2F1,HMGB2,HELLS,PPID,TRIM35,CTNNBL1,TBX3,CREB3L1,TOMM70,MYBL2,MTDH,HMGCR,EEF1E1,MDM4,KIF14,UNG,MNDA,ANP32E,XBP1,NF2,PDE3A,EIF4G1,PSMC5,CDK1,TFRC,PAK2,FOSL1,DDX20,PPP2R1B,BARD1,BRCA1,MYBBP1A,ECT2,AIPL1,SIX4,MNAT1,USP42,MSX1,TOP2A,EIF5A,BID,PDPN,EIF2S1,ARG2,PRELID1,NES,LMNA,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,SERBP1,NNT,AIFM1,RSL1D1,TFAP4,THOC6,NOC2L,RNPS1,TP73,G6PD,PIK3CD,BCAR1,GCLM,FAM129B,CTH,MAD2L1,AURKA,SIGMAR1,ERP29,PDCD2,PALB2	darkgrey	VSMC_M8
GO:0043200	0.18	0.90	10	93	response to amino acid	BP	1	COL1A2,IPO5,PCNA,CHUK,XBP1,COL1A1,DNMT1,AIFM1,GCLM,HNRNPD	darkgrey	VSMC_M8
GO:2000780	0.18	0.93	4	29	negative regulation of double-strand break repair	BP	1	PARPBP,POLQ,FANCB,AUNIP	darkgrey	VSMC_M8
GO:0071312	0.18	0.93	4	29	cellular response to alkaloid	BP	1	CCNA2,RAD51,BLM,CASP6	darkgrey	VSMC_M8
GO:0051153	0.18	0.90	8	72	regulation of striated muscle cell differentiation	BP	1	DDX39B,EZH2,PARP2,XBP1,MSX1,MORF4L2,G6PD,FAM129B	darkgrey	VSMC_M8
GO:0071398	0.18	0.93	4	29	cellular response to fatty acid	BP	1	CCNB1,E2F1,ADIPOR2,PID1	darkgrey	VSMC_M8
GO:0048515	0.18	0.89	11	106	spermatid differentiation	BP	1	TTLL1,SRPK1,MAST2,HMGB2,KNL1,NSUN2,TRIP13,CABYR,BRIP1,HOOK1,ODF2	darkgrey	VSMC_M8
GO:0071901	0.18	0.90	10	93	negative regulation of protein serine/threonine kinase activity	BP	1	NUP62,CHORDC1,IPO5,HMGCR,PRKAR2A,UCHL1,PLK1,TFAP4,CDKN2C,DUSP7	darkgrey	VSMC_M8

GO:0051252	0.18	0.84	216	2654	regulation of RNA metabolic process	BP	1	HNRNPAB,BCLAF1,HNRNPH1,NUP107,DDX39B,EZR,RAD21,ATAD2,PHF5A,ZNF367,SRPK1,SRSF3,PSIP1,PWP1,CDC5L,CKS2,TRIM28,NCBP1,U2AF2,CDCA7L,GRSF1,HOXA5,SYNCRIP,PPIE,PABPC4,THRAP3,EZH2,NUP62,PHF19,NBAS,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,DIS3,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,EXOSC8,ZNF703,HGF,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,TCEA1,HNRNPF,SGK3,CENPJ,E2F1,ABCE1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,RBM12,LOXL3,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,FASTKD3,NUCKS1,DEK,GCN1,ETS1,TENT4A,NSUN2,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,SF3B4,DDX5,XBP1,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,HNRNPR,TRA2B,PSMA6,HNRNPH3,DDX20,SF1,BARD1,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,RBM3,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,CPSF7,SRSF5,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,HNRNPM,SERBP1,ELF4,RAP2C,UHRF1,RBMX,TFAP4,NOC2L,RNPS1,TP73,DAZAP1,DKC1,PTBP1,REXO4,FANCA,ZC3H18,EXOSC2,FAM129B,CBFB,CTH,DEPDC1,PRIM2,SRRT,HNRNPD,DRAP1,HMGB3,ABT1,SRSF7,PID1,HOXC8,MBD2	darkgrey	VSMC_M8
GO:1903510	0.18	0.90	8	71	mucopolysaccharide metabolic process	BP	1	SLC35D2,B3GNT2,HGF,CD44,SLC10A7,UGDH,XYLT1,HAS2	darkgrey	VSMC_M8
GO:0009199	0.18	0.91	7	64	ribonucleoside triphosphate metabolic process	BP	1	ATP5F1B,VCP,CTPS1,CAD,ENTPD7,UCK2,PID1	darkgrey	VSMC_M8
GO:0021543	0.18	0.89	13	127	pallium development	BP	1	NARS,MFSD2A,EZH2,XRN2,WDR62,KIF14,ASPM,NF2,H2AFX,TRA2B,TACC3,NDE1,GART	darkgrey	VSMC_M8
GO:0051567	0.19	0.93	4	29	histone H3-K9 methylation	BP	1	BRCA1,SUV39H1,LMNA,DNMT1	darkgrey	VSMC_M8
GO:0035966	0.19	0.88	14	143	response to topologically incorrect protein	BP	1	HSPA9,VCP,HSP90AB1,SERPINH1,TRAM1,CREB3L1,PPP1R15B,MANF,XBP1,UFD1,EIF2S1,TOR1A,CTH,UBE2J2	darkgrey	VSMC_M8
GO:0043392	0.19	0.92	5	40	negative regulation of DNA binding	BP	1	E2F1,HEY1,NEK2,MSX1,TFAP4	darkgrey	VSMC_M8
GO:0002204	0.19	0.92	5	40	somatic recombination of immunoglobulin genes involved in immune response	BP	1	MSH6,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0002208	0.19	0.92	5	40	somatic diversification of immunoglobulins involved in immune response	BP	1	MSH6,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0045190	0.19	0.92	5	40	isotype switching	BP	1	MSH6,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0048762	0.19	0.87	19	198	mesenchymal cell differentiation	BP	1	HNRNPAB,TRIM28,EZH2,ZNF703,HGF,SNAI2,POLR1B,LOXL3,HEY1,FAM83D,TBX3,NOLC1,DDX5,PHACTR4,MSX1,PDPN,EFNB1,COL1A1,HAS2	darkgrey	VSMC_M8
GO:1902808	0.19	0.92	5	41	positive regulation of cell cycle G1/S phase transition	BP	1	MTBP,EZH2,FAM83D,EIF4G1,CDC6	darkgrey	VSMC_M8
GO:0016571	0.19	0.88	12	118	histone methylation	BP	1	PWP1,EZH2,PHF19,PRMT1,FBL,SETD4,PRMT5,BRCA1,NSD2,SUV39H1,LMNA,DNMT1	darkgrey	VSMC_M8
GO:0043039	0.20	0.91	5	40	tRNA aminoacylation	BP	1	NARS,VARS2,VARS,GARS,RARS	darkgrey	VSMC_M8
GO:0007281	0.20	0.87	17	177	germ cell development	BP	1	FBXO5,TTLL1,SRPK1,CDC25B,CCNB1,HMGB2,KNL1,NSUN2,TRIP13,ASPM,PDE3A,DDX20,CABYR,BRIP1,HOOK1,ODF2,AURKA	darkgrey	VSMC_M8
GO:0009890	0.20	0.83	102	1222	negative regulation of biosynthetic process	BP	1	BCLAF1,FBXO5,EZR,TRIM28,SYNCRIP,EZH2,PHF19,RUVBL2,PUS7,DNAJC2,FOSB,DBI,DIS3,SPHK1,SRSF2,BIRC5,GTPBP4,EIF4A3,E2F7,PCNA,EXOSC8,ZNF703,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,HMGB2,MSC,TERF1,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,TENT4A,PHC2,GMNN,KHDRBS1,NCL,PRMT5,DDX5,HINFP,BLM,CENPF,STRAP,EIF4G1,PSMC5,S100A11,HNRNPR,DDX20,SF1,SMARCAL1,BRCA1,CNOT9,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,CDC6,EIF2S1,EXOSC10,HDGF,MAZ,AURKB,PLK1,ILF3,DNMT1,TYMS,UHRF1,TFAP4,NOC2L,EXOSC2,FAM129B,ACD,CBFB,DEPDC1,HNRNPD,DRAP1,PID1,MBD2	darkgrey	VSMC_M8
GO:0048523	0.20	0.82	292	3647	negative regulation of cellular process	BP	1	CDK2,ALPK2,BCLAF1,DDX39B,FBXO5,EZR,FBN2,GTSE1,RAD21,MTBP,FAM49B,RANGAP1,HSPA9,HMGXB4,PPP2R5D,PWP1,CYP51A1,VCP,HSP90AB1,CDC5L,TRIM28,THADA,ANP32B,U2AF2,MSH6,TTK,HOXA5,MFSD2A,SYNCRIP,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,ORC1,GEN1,RUVBL2,NAMPT,STIL,PUS7,MCM2,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,FOSB,PLAUR,DBI,DIS3,AXL,RNF157,SPHK1,SRSF2,FANCD2,NCAPG2,BIRC5,SERPINH1,PARP2,GTPBP4,RAD18,IPO5,EIF4A3,CHMP6,E2F7,ARHGDIA,CKAP2,STRN,PCNA,CHFR,EXOSC8,ZNF703,HGF,TOPBP1,ELK3,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,API5,CD44,UTP20,ESPL1,BUB1,TPX2,PARPBP,WEE1,HSP90B1,E2F1,ABCE1,CCNE1,VAMP8,KNTC1,HMGB2,RBP4,MSC,TERF1,HELLS,NRIP1,LOXL3,PBK,HEY1,PPID,RBL1,TRIM35,MSH3,BUB1B,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,EEF1E1,RUNX1,PPP1R15B,MDM4,PAK1IP1,NCOA5,CIT,NUP153,ETS1,TENT4A,NSUN2,PHC2,GMNN,CHEK1,KHDRBS1,TRIP13,NCL,TRAIP,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,RAD9A,IQCB1,MNDA,DDX5,PHACTR4,FANCB,XBP1,TICRR,RPA2,SPP2,PRKAR2A,NEK2,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,RBM14,CEP85,CENPF,STRAP,EIF4G1,BUB3,PSMC5,AUNIP,CDK1,S100A11,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,WDR76,DDX20,DNA2,ZW10,IFT80,SF1,BARD1,EPHB2,SMARCAL1,CDC45,UFD1,BRCA1,TFPI,CNOT9,CDKN3,NSD2,MED28,DPT,MYBBP1A,CREG1,ANKLE1,AIPL1,ZWINT,SUV39H1,FKBP4,SIX4,MNAT1,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1,HNRNPU,UCHL1,ADIPOR2,NEDD4,SMARCE1,RFC1,TOP2A,CDC6,BID,PDPN,EIF2S1,ARG2,PRELID1,EXOSC1	darkgrey	VSMC_M8
GO:0055023	0.20	0.92	4	31	positive regulation of cardiac muscle tissue growth	BP	1	DDX39B,PARP2,CCNB1,CDK1	darkgrey	VSMC_M8

GO:0006753	0.20	0.85	34	387	nucleoside phosphate metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,CTPS1,DCK,GARS,NAMPT,RNASEH2B,CAD,TK1,AFMID,RRM1,PDHB,AADAT,ENTPD7,HMGCR,UNG,ELOVL6,UMPS,PDHA1,UCK2,DLAT,DUT,MTHFD1,DCTPP1,PFAS,PRPS1,ACSL4,TYMS,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0008219	0.20	0.83	130	1587	cell death	BP	1	ALPK2,BCLAF1,TCP1,RAD21,HSPA9,VCP,HSP90AB1,MELK,ANP32B,MSH6,CYCS,HOXA5,NUP62,CASP2,NAA15,NAMPT,STIL,MCM2,PPP5C,TMEM214,PLAUR,AXL,RNF157,SPHK1,NET1,BIRC5,PARP2,RAD18,ARHGDIA,CKAP2,PGAM5,HGF,RRP8,SNAI2,API5,CD44,ESPL1,BUB1,TPX2,HSP90B1,E2F1,HMGB2,HELLS,PPID,TRIM35,CTNNBL1,BUB1B,TBX3,CREB3L1,TOMM70,MYBL2,MTDH,HMGCR,EEF1E1,MDM4,CIT,CHEK1,TRAIP,KIF14,UNG,MNDA,DDX5,ANP32E,XBP1,NF2,PDE3A,EIF4G1,PSMC5,CDK1,TFRC,PAK2,FOSL1,DHX9,NDUFS1,DDX20,PPP2R1B,BARD1,BRCA1,MYBBP1A,ECT2,AIPL1,SIX4,MNAT1,USP42,MSX1,UBE2K,TOP2A,EIF5A,BID,PDPN,EIF2S1,ARG2,PRELID1,NES,LMNA,ALOX15B,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,SERBP1,NNT,AIFM1,RSL1D1,EMP2,TFAP4,THOC6,NOC2L,RNPS1,TP73,G6PD,PIK3CD,BCAR1,GCLM,FAM129B,NEK6,CTH,ARF6,MAD2L1,AURKA,BLOC1S2,SIGMAR1,ERP29,XKR5,PDCD2,PALB2,CASP6,EVA1A	darkgrey	VSMC_M8
GO:0003197	0.20	0.91	5	40	endocardial cushion development	BP	1	SNAI2,HEY1,TBX3,MDM4,MSX1	darkgrey	VSMC_M8
GO:0010628	0.20	0.83	68	803	positive regulation of gene expression	BP	1	DDX39B,EZR,PANX2,FAM49B,POLR3B,NCBP1,U2AF2,HOXA5,SYNCRIP,THRAP3,NBAS,PGR,SPHK1,POLR3F,EIF4A3,HGF,E2F1,HMGB2,RBP4,HEY1,FAM98B,TOMM70,CHUK,RUNX1,SETD4,FASTKD3,ETS1,TENT4A,CHEK1,KHDRBS1,NCL,SF3B4,MNDA,DDX5,XBP1,HINFP,EIF4G1,CDK1,TFRC,DHX9,TRA2B,DDX21,EPHB2,BRCA1,NSD2,RBM3,DHX33,HNRNPU,RAB27A,EIF5A,SRSF5,IQGAP3,FUS,LMNA,ALOX15B,MAZ,DNMT1,TAF15,CDCA4,RBMX,DAZAP1,PIK3CD,TRUB2,FUBP1,GBP5,HNRNPD,ERP29,PID1	darkgrey	VSMC_M8
GO:0008637	0.20	0.89	9	87	apoptotic mitochondrial changes	BP	1	PLAUR,HGF,NDUFS1,BID,PRELID1,LMNA,SLC25A5,GCLM,BLOC1S2	darkgrey	VSMC_M8
GO:0045727	0.20	0.88	11	109	positive regulation of translation	BP	1	DDX39B,EIF4A3,FASTKD3,TENT4A,KHDRBS1,EIF4G1,DHX9,RBM3,EIF5A,TRUB2,HNRNPD	darkgrey	VSMC_M8
GO:0032434	0.20	0.87	12	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	CDK2,DESI1,VCP,HSP90AB1,CDC20,CHFR,PBK,SMARCC1,UBE2K,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0006730	0.20	0.92	4	31	one-carbon metabolic process	BP	1	ALDH1L2,SFXN3,MTHFD1,TYMS	darkgrey	VSMC_M8
GO:0043549	0.21	0.83	53	612	regulation of kinase activity	BP	1	PRRC1,CDC25C,DBF4,HSP90AB1,CKS2,EZH2,NUP62,CLSPN,CCNA2,CHORDC1,BORA,AXL,NCAPG2,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,TPX2,CCNE1,RBL1,CCNL1,CCNE2,HMGCR,GCN1,CENPE,KIF14,PRKAR2A,NF2,BLM,CEP85,CDC25A,PAK2,EPHB2,CDKN3,ECT2,MNAT1,HNRNPU,UCHL1,INCENP,CCNB3,CDC6,CCNB2,PLK1,RAP2C,EMP2,TFAP4,PKMYT1,CCNF,CDKN2C,ERP29,DUSP7	darkgrey	VSMC_M8
GO:0043276	0.21	0.92	4	30	anoikis	BP	1	SNAI2,E2F1,MYBBP1A,PTRH2	darkgrey	VSMC_M8
GO:0032269	0.21	0.83	64	760	negative regulation of cellular protein metabolic process	BP	1	FBXO5,PPP2R5D,PWP1,HSP90AB1,U2AF2,SYNCRIP,NUP62,PUS7,CHORDC1,PPP5C,MASTL,PLAUR,DBI,DIS3,NCAPG2,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,EXOSC8,HGF,CCNB1,CD44,PBK,YWHAB,HMGCR,PPP1R15B,TENT4A,NCL,SPP2,PRKAR2A,NF2,CEP85,EIF4G1,PAK2,SMARCC1,HNRNPR,EPHB2,BRCA1,TFPI,CNOT9,EIF2AK1,UCHL1,EIF2S1,PTTG1,SPAG9,PLK1,ILF3,DNMT1,TYMS,NNT,NXN,TFAP4,NOC2L,G6PD,EXOSC2,USP4,HNRNPD,MAD2L1,CDKN2C,PID1,DUSP7	darkgrey	VSMC_M8
GO:0007265	0.21	0.85	27	296	Ras protein signal transduction	BP	1	CDK2,COL1A2,TRIM28,NUP62,CCNA2,CDC42EP4,NET1,ARHGDIA,PSD4,NRAS,CHUK,RASSF1,KIF14,PHACTR4,CDC42SE1,ARFGAP1,EPHB2,FOXM1,RAC1,PDPN,IQGAP3,LRRC59,DNMT1,RAP2C,ARF6,RAPGEF6,STMN1	darkgrey	VSMC_M8
GO:0045738	0.21	0.92	4	31	negative regulation of DNA repair	BP	1	PARPBP,POLQ,FANCB,AUNIP	darkgrey	VSMC_M8
GO:0043038	0.21	0.91	5	41	amino acid activation	BP	1	NARS,VARS2,VARS,GARS,RARS	darkgrey	VSMC_M8
GO:0045646	0.21	0.90	5	42	regulation of erythrocyte differentiation	BP	1	HSPA9,HOXA5,PRMT1,HMGB2,ETS1	darkgrey	VSMC_M8
GO:0051248	0.21	0.82	68	813	negative regulation of protein metabolic process	BP	1	FBXO5,PPP2R5D,PWP1,CYP51A1,HSP90AB1,U2AF2,SYNCRIP,NUP62,PUS7,CHORDC1,PPP5C,MASTL,GRIN2C,PLAUR,DBI,DIS3,NCAPG2,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,EXOSC8,HGF,CCNB1,CD44,PBK,YWHAB,HMGCR,PPP1R15B,MDM4,TENT4A,NCL,SPP2,PRKAR2A,NF2,CEP85,EIF4G1,PAK2,SMARCC1,HNRNPR,EPHB2,BRCA1,TFPI,CNOT9,EIF2AK1,UCHL1,EIF2S1,PTTG1,SPAG9,PLK1,ILF3,DNMT1,TYMS,NNT,NXN,TFAP4,NOC2L,G6PD,EXOSC2,SF3B3,USP4,HNRNPD,MAD2L1,CDKN2C,PID1,DUSP7	darkgrey	VSMC_M8
GO:0051154	0.21	0.91	4	32	negative regulation of striated muscle cell differentiation	BP	1	EZH2,XBP1,MSX1,G6PD	darkgrey	VSMC_M8
GO:0009416	0.21	0.85	22	239	response to light stimulus	BP	1	POLH,MSH6,POLD1,RUVBL2,POLD3,PCNA,PBK,PPID,HMGCR,HMGN1,CHEK1,RGS9,DTL,CDC25A,AIPL1,NEDD4,EIF2S1,AURKB,COPS3,USP1,NOC2L,FEN1	darkgrey	VSMC_M8
GO:0018105	0.22	0.84	23	249	peptidyl-serine phosphorylation	BP	1	CDK2,PWP1,HSP90AB1,TTK,CLSPN,MASTL,MAST2,HGF,CCNB1,CD44,SGK3,CHUK,EIF4G1,CDK1,TFRC,PAK2,CNOT9,AURKB,PLK1,VRK1,PKN3,NEK6,AURKA	darkgrey	VSMC_M8
GO:0051881	0.22	0.89	7	66	regulation of mitochondrial membrane potential	BP	1	VCP,NDUFS1,BID,PRELID1,NNT,GCLM,PID1	darkgrey	VSMC_M8
GO:0090503	0.22	0.90	5	42	RNA phosphodiester bond hydrolysis, exonucleolytic	BP	1	DIS3,XRN2,EXOSC8,EXOSC10,EXOSC2	darkgrey	VSMC_M8
GO:0018205	0.22	0.84	28	313	peptidyl-lysine modification	BP	1	DESI1,PWP1,TRIM28,EZH2,PHF19,RUVBL2,RUVBL1,SAE1,USPL1,UBA2,LOXL3,GNL3,SETD4,CHEK1,NAA50,MCM3AP,HAT1,BRCA1,NSD2,SUV39H1,LMNA,MORF4L2,DNMT1,TADA2A,NOC2L,CTH,CSKMT,POLE3	darkgrey	VSMC_M8
GO:0034605	0.22	0.89	6	53	cellular response to heat	BP	1	VCP,HSP90AB1,DNAJC2,CHORDC1,DNAJC7,EIF2S1	darkgrey	VSMC_M8

GO:0042326	0.22	0.84	28	311	negative regulation of phosphorylation	BP	1	PPP2R5D,PWP1,NUP62,CHORDC1,PPP5C,NCAPG2,IPO5,CHMP6,HGF,CCNB1,PBK,HMGCR,PPP1R15B,PRKAR2A,NF2,CEP85,EIF4G1,PAK2,EPHB2,HNRNPU,UCHL1,SPAG9,PLK1,NNT,TFAP4,CDKN2C,PID1,DUSP7	darkgrey	VSMC_M8
GO:0048519	0.22	0.80	315	3961	negative regulation of biological process	BP	1	CDK2,ALPK2,BCLAF1,DDX39B,FBXO5,EZR,FBN2,GTSE1,RAD21,MTBP,FAM49B,RANGAP1,HSPA9,SRPK1,HMGXB4,PPP2R5D,PWP1,CYP51A1,VCP,HSP90AB1,CDC5L,TRIM28,NCBP1,THADA,ANP32B,U2AF2,MSH6,TTK,HNRNPA2B1,HOXA5,MFSD2A,SYNCRIP,PABPC4,YRDC,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,NAA15,ORC1,GEN1,NRDC,RUVBL2,PGR,NAMPT,STIL,PUS7,MCM2,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,FOSB,GRIN2C,SMG9,PLAUR,DBI,DIS3,AXL,RNF157,SPHK1,SRSF2,FANCD2,XRN2,NCAPG2,BIRC5,SERPINH1,PARP2,GTPBP4,RAD18,IPO5,EIF4A3,CHMP6,E2F7,ARHGDIA,CKAP2,STRN,PCNA,CHFR,EXOSC8,PGAM5,ZNF703,HGF,TOPBP1,ELK3,RRP8,TCERG1,CBX5,CCNB1,SFSWAP,SNAI2,API5,CD44,UTP20,ESPL1,BUB1,TPX2,PARPBP,WEE1,HSP90B1,E2F1,ABCE1,CCNE1,VAMP8,KNTC1,HMGB2,RBP4,MSC,TERF1,HELLS,NRIP1,LOXL3,PBK,HEY1,PPID,RBL1,TRIM35,MSH3,BUB1B,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,HMGCR,BAP1,EEF1E1,RUNX1,PPP1R15B,MDM4,PAK1IP1,NCOA5,CIT,FASTKD3,NUP153,ETS1,TENT4A,NSUN2,PHC2,GMNN,CHEK1,KHDRBS1,TRIP13,NCL,TRAIP,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,RAD9A,IQCB1,MNDA,DDX5,PHACTR4,FANCB,XBP1,TICRR,RPA2,SPP2,PRKAR2A,NEK2,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,RBM14,SSB,CEP85,CENPF,STRAP,EIF4G1,BUB3,PSMC5,AUNIP,CDK1,S100A11,TFRC,PAK2,FOSL1,SMARCC1,DHX9,HNRNPR,WDR76,DDX20,DNA2,ZW10,DGCR8,IFT80,SF1,BARD1,EPHB2,SMARCAL1,CDC45,UFD1,BRCA1,TFPI,CNOT9,CDKN3,NSD2,MED28,DPT,MYBBP1A,CREG1,ANKLE1,AIPL1,ZWINT,SUV39H1,FKBP4,SIX4,MNAT1,FOXM1,EIF2AK1,LYAR,MSX1,FAM220A,RAC1	darkgrey	VSMC_M8
GO:0072655	0.22	0.87	10	103	establishment of protein localization to mitochondrion	BP	1	SAE1,CHCHD4,TOMM40,TOMM70,BAP1,BID,TIMM8A,TIMM44,AIFM1,UBE2J2	darkgrey	VSMC_M8
GO:0034249	0.22	0.85	17	183	negative regulation of cellular amide metabolic process	BP	1	SYNCRIP,PUS7,DIS3,SPHK1,EIF4A3,EXOSC8,TENT4A,NCL,EIF4G1,HNRNPR,CNOT9,EIF2AK1,EIF2S1,ILF3,TYMS,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0003161	0.22	0.91	4	31	cardiac conduction system development	BP	1	MSC,HEY1,TBX3,MSX1	darkgrey	VSMC_M8
GO:0071539	0.22	0.91	4	31	protein localization to centrosome	BP	1	NUP62,STIL,CEP72,AURKA	darkgrey	VSMC_M8
GO:0060419	0.22	0.88	8	77	heart growth	BP	1	DDX39B,PARP2,CCNB1,RBP4,RUNX1,CDK1,TP73,G6PD	darkgrey	VSMC_M8
GO:0001578	0.22	0.87	9	86	microtubule bundle formation	BP	1	TTLL1,KIF20A,AAAS,NAV1,PRC1,LRRC49,PLK1,MTCL1,TPPP3	darkgrey	VSMC_M8
GO:0010823	0.22	0.90	5	43	negative regulation of mitochondrion organization	BP	1	HGF,TFRC,PRELID1,LMNA,SLC25A5	darkgrey	VSMC_M8
GO:0006986	0.22	0.86	12	124	response to unfolded protein	BP	1	HSPA9,VCP,HSP90AB1,SERPINH1,TRAM1,CREB3L1,PPP1R15B,MANF,XBP1,EIF2S1,CTH,UBE2J2	darkgrey	VSMC_M8
GO:0006886	0.23	0.81	62	739	intracellular protein transport	BP	1	TMED9,XPOT,NUP107,NUP50,ARFGAP3,MAN1A1,DESI1,RANGAP1,HSPA9,TNPO3,VCP,HSP90AB1,TRIM28,ANP32B,NUP62,SEC61A1,SAE1,CHCHD4,COG3,TOMM40,PREB,NUP85,SRP68,SEC23B,IPO5,KIF20B,HSP90B1,TRAM1,NUP93,TOMM70,YWHAB,BAP1,HEATR3,NOLC1,NUP153,ICE1,CSE1L,IPO4,NUP133,SEC24D,ARCN1,CDK1,BARD1,UFD1,ANKLE1,ECT2,RAB27A,NEDD4,BID,LMNA,LTBP2,TIMM8A,NUP62CL,TIMM44,MTCL1,AIFM1,NUP188,ACD,ARF6,SPCS3,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:1903053	0.23	0.89	5	43	regulation of extracellular matrix organization	BP	1	RUNX1,ETS1,FSCN1,PDPN,HAS2	darkgrey	VSMC_M8
GO:0021987	0.23	0.87	9	87	cerebral cortex development	BP	1	NARS,WDR62,KIF14,ASPM,H2AFX,TRA2B,TACC3,NDE1,GART	darkgrey	VSMC_M8
GO:0048144	0.23	0.88	7	66	fibroblast proliferation	BP	1	CCNA2,RNASEH2B,SPHK1,CCNB1,E2F1,DHX9,CDC6	darkgrey	VSMC_M8
GO:0048145	0.23	0.88	7	66	regulation of fibroblast proliferation	BP	1	CCNA2,RNASEH2B,SPHK1,CCNB1,E2F1,DHX9,CDC6	darkgrey	VSMC_M8
GO:0008584	0.23	0.86	11	111	male gonad development	BP	1	SDC1,NASP,RRM1,HMGB2,KIF18A,ASPM,SF1,SIX4,NUDT1,BRIP1,FANCA	darkgrey	VSMC_M8
GO:0009117	0.23	0.82	33	381	nucleotide metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,CTPS1,DCK,GARS,NAMPT,RNASEH2B,CAD,AFMID,RRM1,PDHB,AADAT,ENTPD7,HMGCR,UNG,ELOVL6,UMPS,PDHA1,UCK2,DLAT,DUT,MTHFD1,DCTPP1,PFAS,PRPS1,ACSL4,TYMS,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0007286	0.23	0.86	10	100	spermatid development	BP	1	TTLL1,SRPK1,HMGB2,KNL1,NSUN2,TRIP13,CABYR,BRIP1,HOOK1,ODF2	darkgrey	VSMC_M8
GO:0030101	0.23	0.89	5	43	natural killer cell activation	BP	1	AXL,RAB27A,DCAF15,ELF4,PIK3CD	darkgrey	VSMC_M8
GO:0071229	0.24	0.87	7	65	cellular response to acid chemical	BP	1	COL1A2,IPO5,XBP1,COL1A1,DNMT1,GCLM,HNRNPD	darkgrey	VSMC_M8
GO:0007020	0.24	0.90	4	32	microtubule nucleation	BP	1	TPX2,CENPJ,CKAP5,NDE1	darkgrey	VSMC_M8
GO:0046546	0.24	0.85	11	112	development of primary male sexual characteristics	BP	1	SDC1,NASP,RRM1,HMGB2,KIF18A,ASPM,SF1,SIX4,NUDT1,BRIP1,FANCA	darkgrey	VSMC_M8
GO:0070830	0.24	0.89	5	44	bicellular tight junction assembly	BP	1	STRN,SNAI2,MTDH,PAK2,ECT2	darkgrey	VSMC_M8
GO:0051348	0.24	0.83	20	219	negative regulation of transferase activity	BP	1	FBXO5,NUP62,CHORDC1,NCAPG2,IPO5,CHMP6,TERF1,HMGCR,PRKAR2A,NF2,CEP85,PAK2,EPHB2,HNRNPU,UCHL1,PLK1,TFAP4,MAD2L1,CDKN2C,DUSP7	darkgrey	VSMC_M8
GO:0009225	0.24	0.90	4	33	nucleotide-sugar metabolic process	BP	1	NANS,UAP1,UGDH,GMPPB	darkgrey	VSMC_M8
GO:0038066	0.25	0.88	5	44	p38MAPK cascade	BP	1	EZR,PRMT1,SPHK1,ULK4,HGF	darkgrey	VSMC_M8
GO:0060548	0.25	0.80	63	754	negative regulation of cell death	BP	1	HSPA9,HSP90AB1,NUP62,CASP2,NAA15,STIL,PPP5C,PLAUR,AXL,RNF157,SPHK1,BIRC5,PARP2,RAD18,ARHGDIA,HGF,SNAI2,API5,CD44,HSP90B1,HMGB2,HELLS,TBX3,CREB3L1,MTDH,HMGCR,MDM4,KIF14,UNG,XBP1,PDE3A,EIF4G1,PSMC5,CDK1,TFRC,PAK2,BARD1,BRCA1,AIPL1,SIX4,MNAT1,MSX1,BID,PDPN,ARG2,PRELID1,NES,LMNA,MAZ,AURKB,PLK1,PTRH2,DNMT1,SLC25A5,NNT,THOC6,NOC2L,GCLM,FAM129B,CTH,MAD2L1,AURKA,PALB2	darkgrey	VSMC_M8
GO:0018209	0.25	0.82	24	267	peptidyl-serine modification	BP	1	CDK2,PWP1,HSP90AB1,TTK,CLSPN,MASTL,MAST2,PARP2,HGF,CCNB1,CD44,SGK3,CHUK,EIF4G1,CDK1,TFRC,PAK2,CNOT9,AURKB,PLK1,VRK1,PKN3,NEK6,AURKA	darkgrey	VSMC_M8
GO:0007007	0.25	0.89	4	35	inner mitochondrial membrane organization	BP	1	HSPA9,CHCHD3,TOMM70,TIMM8A	darkgrey	VSMC_M8

GO:0006890	0.25	0.88	5	45	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	BP	1	NBAS,COG3,PITPNB,ARCN1,KDELR2	darkgrey	VSMC_M8
GO:2001234	0.25	0.83	17	187	negative regulation of apoptotic signaling pathway	BP	1	PLAUR,HGF,SNAI2,CD44,HMGB2,HELLS,CREB3L1,XBP1,BRCA1,BID,PRELID1,LMNA,MAZ,SLC25A5,NOC2L,GCLM,CTH	darkgrey	VSMC_M8
GO:0097305	0.25	0.83	16	174	response to alcohol	BP	1	FOSB,CAD,GGH,RBP4,RAD51,HMGCR,PSMD14,BLM,CDK1,FOSL1,BRCA1,ADIPOR2,TYMS,AIFM1,G6PD,HNRNPD	darkgrey	VSMC_M8
GO:0032388	0.25	0.83	16	173	positive regulation of intracellular transport	BP	1	EZR,HSP90AB1,TRIM28,ANP32B,SAE1,IPO5,KIF20B,BAP1,ICE1,KHDRBS1,CDK1,DHX9,ECT2,NEDD4,MTCL1,UBE2J2	darkgrey	VSMC_M8
GO:0070585	0.26	0.84	10	107	protein localization to mitochondrion	BP	1	SAE1,CHCHD4,TOMM40,TOMM70,BAP1,BID,TIMM8A,TIMM44,AIFM1,UBE2J2	darkgrey	VSMC_M8
GO:0006900	0.26	0.87	6	55	vesicle budding from membrane	BP	1	TMED9,ARFGAP3,PREB,SEC23B,CHMP6,SEC24D	darkgrey	VSMC_M8
GO:1905508	0.26	0.89	4	33	protein localization to microtubule organizing center	BP	1	NUP62,STIL,CEP72,AURKA	darkgrey	VSMC_M8
GO:0006469	0.26	0.82	16	172	negative regulation of protein kinase activity	BP	1	NUP62,CHORDC1,NCAPG2,IPO5,CHMP6,HMGCR,PRKAR2A,NF2,CEP85,PAK2,EPHB2,UCHL1,PLK1,TFAP4,CDKN2C,DUSP7	darkgrey	VSMC_M8
GO:0072132	0.26	0.87	5	44	mesenchyme morphogenesis	BP	1	SNAI2,HEY1,TBX3,MDM4,MSX1	darkgrey	VSMC_M8
GO:0006024	0.26	0.86	7	66	glycosaminoglycan biosynthetic process	BP	1	SLC35D2,B3GNT2,PXYLP1,SLC10A7,UGDH,XYLT1,HAS2	darkgrey	VSMC_M8
GO:0002440	0.26	0.83	13	138	production of molecular mediator of immune response	BP	1	MSH6,RBP4,MSH3,CTNNBL1,UNG,POLQ,XBP1,MCM3AP,TFRC,DDX21,EPHB2,NSD2,EXO1	darkgrey	VSMC_M8
GO:0060038	0.26	0.87	5	45	cardiac muscle cell proliferation	BP	1	CCNB1,RBP4,RUNX1,CDK1,TP73	darkgrey	VSMC_M8
GO:0055001	0.27	0.82	14	150	muscle cell development	BP	1	ALPK2,DDX39B,SDC1,PARP2,CCNB1,TBX3,CDK1,SIX4,HNRNPU,UCHL1,LMNA,G6PD,FAM129B,TMOD3	darkgrey	VSMC_M8
GO:0051701	0.27	0.82	14	150	biological process involved in interaction with host	BP	1	DDX39B,TCP1,TRIM28,SLC1A5,AXL,ALYREF,VAMP8,PPID,TRIM35,NUP153,CDK1,TFRC,THOC6,TRIM59	darkgrey	VSMC_M8
GO:0035065	0.27	0.87	5	45	regulation of histone acetylation	BP	1	RUVBL2,CHEK1,BRCA1,TADA2A,NOC2L	darkgrey	VSMC_M8
GO:0051259	0.27	0.81	16	174	protein complex oligomerization	BP	1	COL1A2,PRMT1,SLC1A5,TK1,RRM1,POLQ,BLM,ECT2,UGDH,CPSF7,FUS,RBMX,TP73,CTH,GBP5,SIGMAR1	darkgrey	VSMC_M8
GO:0001932	0.27	0.77	70	845	regulation of protein phosphorylation	BP	1	PRRC1,CDC25C,PPP2R5D,PWP1,DBF4,HSP90AB1,CKS2,TTK,EZH2,NUP62,CLSPN,CCNA2,CHORDC1,PPP5C,PLAUR,BORA,SPHK1,NCAPG2,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,CD44,TPX2,CCNE1,PBK,CCNL1,RAD51,CCNE2,HMGCR,PPP1R15B,CENPE,KIF14,PRKAR2A,NF2,BLM,CEP85,EIF4G1,CDC25A,TFRC,PAK2,EPHB2,CNOT9,CDKN3,ECT2,MNAT1,EIF2AK1,RAC1,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,CCNB2,IQGAP3,SPAG9,PLK1,NNT,RAP2C,EMP2,TFAP4,PKMYT1,CCNF,CDKN2C,ERP29,PID1,DUSP7	darkgrey	VSMC_M8
GO:0030199	0.27	0.86	6	56	collagen fibril organization	BP	1	COL1A2,SERPINH1,LOXL3,ADAMTS14,DPT,COL1A1	darkgrey	VSMC_M8
GO:0060421	0.27	0.88	4	35	positive regulation of heart growth	BP	1	DDX39B,PARP2,CCNB1,CDK1	darkgrey	VSMC_M8
GO:2000107	0.27	0.88	4	34	negative regulation of leukocyte apoptotic process	BP	1	AXL,ARG2,AURKB,NOC2L	darkgrey	VSMC_M8
GO:0001836	0.27	0.87	5	48	release of cytochrome c from mitochondria	BP	1	PLAUR,HGF,BID,PRELID1,LMNA	darkgrey	VSMC_M8
GO:0033866	0.27	0.85	6	57	nucleoside bisphosphate biosynthetic process	BP	1	PDHB,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0034030	0.27	0.85	6	57	ribonucleoside bisphosphate biosynthetic process	BP	1	PDHB,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0034033	0.27	0.85	6	57	purine nucleoside bisphosphate biosynthetic process	BP	1	PDHB,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0046661	0.27	0.82	12	128	male sex differentiation	BP	1	SDC1,NASP,RRM1,HMGB2,TBX3,KIF18A,ASPM,SF1,SIX4,NUDT1,BRIP1,FANCA	darkgrey	VSMC_M8
GO:0031960	0.28	0.82	11	117	response to corticosteroid	BP	1	SDC1,FOSB,CAD,PCNA,HEY1,FOSL1,HNRNPU,COL1A1,TYMS,AIFM1,TFAP4	darkgrey	VSMC_M8
GO:0014075	0.28	0.87	4	36	response to amine	BP	1	CAD,RGS9,CDK1,ADIPOR2	darkgrey	VSMC_M8
GO:0009167	0.28	0.87	4	36	purine ribonucleoside monophosphate metabolic process	BP	1	TJP2,PAICS,PFAS,GART	darkgrey	VSMC_M8
GO:0019538	0.28	0.74	322	4113	protein metabolic process	BP	1	CDK2,ALPK2,NARS,MRPS18B,VARS2,DDX39B,FBXO5,PRRC1,VARS,EZR,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,DESI1,CDC25C,FKBP5,SRPK1,PPP2R5D,PWP1,MRPL2,DBF4,CYP51A1,VCP,HSP90AB1,PUM3,CKS2,MELK,TRIM28,NCBP1,ANP32B,PPIH,U2AF2,PPP6R1,TTK,CYCS,SYNCRIP,PPIE,PABPC4,GARS,B3GNT2,EZH2,ODC1,NUP62,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NAA15,NRDC,RUVBL2,PLK4,PUS7,RUVBL1,CCNA2,RPN1,SAE1,CHORDC1,NAALAD2,PPP5C,MASTL,MAST2,CHCHD4,COG3,GRIN2C,PRCP,MRPL58,PLAUR,MRPS7,CAD,ALG8,DBI,TRIM47,BORA,DIS3,AXL,RNF157,SPHK1,ULK4,NCAPG2,CDC20,BIRC5,SERPINH1,PARP2,FBL,RRBP1,GTPBP4,RAD18,IPO5,EIF4A3,CHMP6,CHFR,EXOSC8,PGAM5,CDC25B,METAP2,DCUN1D2,HGF,PSMD13,CDC16,USPL1,CCNB1,SNRPB,CD44,ESPL1,MRPS5,BUB1,TPX2,ANAPC1,GGH,UBA2,CWC27,ADAMTS6,SGK3,EIF3M,WEE1,HSP90B1,NECAB3,EIF2B1,ABCE1,CCNE1,PXYLP1,GALNT6,LOXL3,PBK,ESCO2,SELENOT,FAM98B,PPID,TRIM35,BUB1B,CCNL1,RSRC1,CDCA2,GNL3,FAM83D,RAD51,CCNE2,TRIM33,YWHAB,HMGCR,BAP1,EEF1E1,CHUK,RUNX1,SETD4,PPP1R15B,HR,MDM4,UBE2C,PSMD14,NOLC1,CIT,FASTKD3,GCN1,METAP1,TENT4A,UBE2T,CHEK1,NAA50,KHDRBS1,STT3A,CENPE,NCL,TRAIP,KIF14,PRMT5,FANCI,XBP1,SPP2,UTP25,MCM3AP,EIF4H,PRKAR2A,NEK2,DTL,NF2,HMBS,BLM,RBM14,PSMD4,CEP85,EIF4G1,MRPL11,PSMC5,ADAMTS4,HAT1,CDK1,CDC25A,TFRC,PAK2,SMARCC1,DHX9,HNRNPR,PSMA6,FANCM,ADAMTS14,LRR1,PPP2R1B,BARD1,EPHB2,UFD1,BRCA1,CDCA3,TFPI,CNOT9,CDKN3,NSD2,RPL22L1,CDK16,DCUN1D5,ECT2,AIPL1,RBM3,DHX33,SUV39H1,FKBP4,MNAT1,MAPK6,EIF2AK1,USP42,FAM2	darkgrey	VSMC_M8
GO:0007566	0.28	0.87	4	36	embryo implantation	BP	1	TRIM28,POLR1B,EMP2,TPPP3	darkgrey	VSMC_M8
GO:1901657	0.28	0.85	6	60	glycosyl compound metabolic process	BP	1	AMD1,TK1,UMPS,NUDT1,PRPS1,ERH	darkgrey	VSMC_M8
GO:0043666	0.28	0.86	5	47	regulation of phosphoprotein phosphatase activity	BP	1	HSP90AB1,PPP6R1,MASTL,HSP90B1,PPP1R15B	darkgrey	VSMC_M8
GO:0006023	0.28	0.84	7	68	aminoglycan biosynthetic process	BP	1	SLC35D2,B3GNT2,PXYLP1,SLC10A7,UGDH,XYLT1,HAS2	darkgrey	VSMC_M8
GO:0022617	0.28	0.86	5	47	extracellular matrix disassembly	BP	1	ETS1,ADAMTS4,FSCN1,PDPN,SH3PXD2B	darkgrey	VSMC_M8
GO:0061180	0.29	0.84	6	58	mammary gland epithelium development	BP	1	HOXA5,PGR,ZNF703,TBX3,MSX1,IQGAP3	darkgrey	VSMC_M8

GO:0071241	0.29	0.80	15	165	cellular response to inorganic substance	BP	1	CDK2,CCNA2,PPP5C,FOSB,EIF4A3,CCNB1,RAD51,CHUK,BLM,ECT2,EIF2S1,FUS,SYT4,AIFM1,HNRNPD	darkgrey	VSMC_M8
GO:0001890	0.29	0.81	11	117	placenta development	BP	1	HSP90AB1,TRIM28,GJB3,PLK4,E2F7,HEY1,E2F8,FOSL1,CCNF,DAZAP1,TPPP3	darkgrey	VSMC_M8
GO:0032386	0.29	0.78	25	290	regulation of intracellular transport	BP	1	EZR,NUS1,RANGAP1,HSP90AB1,TRIM28,ANP32B,NUP62,SAE1,PREB,IPO5,AAAS,KIF20B,BAP1,NOLC1,NUP153,NSUN2,ICE1,KHDRBS1,CDK1,DHX9,BARD1,ECT2,NEDD4,MTCL1,UBE2J2	darkgrey	VSMC_M8
GO:0043967	0.29	0.84	6	58	histone H4 acetylation	BP	1	RUVBL2,RUVBL1,NAA50,HAT1,BRCA1,MORF4L2	darkgrey	VSMC_M8
GO:0008406	0.29	0.80	15	166	gonad development	BP	1	NUP107,CASP2,SDC1,PGR,NASP,RRM1,HMGB2,NRIP1,KIF18A,ASPM,SF1,SIX4,NUDT1,BRIP1,FANCA	darkgrey	VSMC_M8
GO:0042176	0.29	0.77	29	342	regulation of protein catabolic process	BP	1	CDK2,EZR,DESI1,CYP51A1,VCP,HSP90AB1,ODC1,NRDC,GRIN2C,CDC20,CHMP6,CHFR,PBK,FAM83D,HMGCR,MDM4,PSMD14,DTL,PSMC5,SMARCC1,BARD1,UBE2K,NEDD4,PSMD3,RAD23A,PLK1,SF3B3,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:0014070	0.29	0.75	58	703	response to organic cyclic compound	BP	1	EZR,HSP90AB1,CDC5L,EZH2,SDC1,RUVBL2,PGR,NAMPT,CCNA2,PPP5C,FOSB,NASP,CAD,DDX18,SRSF2,EIF4A3,ARHGDIA,PCNA,ZNF703,CCNB1,SNAI2,HSP90B1,HMGB2,ATF1,NRIP1,HEY1,RAD51,HMGCR,KIF18A,ETS1,H2AFZ,RGS9,PRMT5,DDX5,BLM,PDE3A,CDK1,PAK2,FOSL1,DHX9,DDX21,EFTUD2,BRCA1,TFPI,CNOT9,HNRNPU,NEDD4,BID,COL1A1,TYMS,AIFM1,TFAP4,G6PD,GCLM,HNRNPD,ACSL3,CASP6,MBD2	darkgrey	VSMC_M8
GO:0071407	0.29	0.76	38	448	cellular response to organic cyclic compound	BP	1	EZR,HSP90AB1,CDC5L,EZH2,RUVBL2,PGR,CCNA2,PPP5C,DDX18,ARHGDIA,ZNF703,CCNB1,SNAI2,HSP90B1,NRIP1,HEY1,RAD51,KIF18A,H2AFZ,RGS9,PRMT5,DDX5,BLM,PDE3A,PAK2,DHX9,BRCA1,TFPI,CNOT9,HNRNPU,NEDD4,COL1A1,AIFM1,TFAP4,GCLM,HNRNPD,CASP6,MBD2	darkgrey	VSMC_M8
GO:0070972	0.30	0.84	6	60	protein localization to endoplasmic reticulum	BP	1	MAN1A1,SEC61A1,SRP68,TRAM1,KDELR2,SPCS3	darkgrey	VSMC_M8
GO:0042773	0.30	0.83	7	83	ATP synthesis coupled electron transport	BP	1	CYC1,CYCS,CCNB1,NDUFAF1,CDK1,NDUFS1,BID	darkgrey	VSMC_M8
GO:0042775	0.30	0.83	7	83	mitochondrial ATP synthesis coupled electron transport	BP	1	CYC1,CYCS,CCNB1,NDUFAF1,CDK1,NDUFS1,BID	darkgrey	VSMC_M8
GO:2000781	0.30	0.86	4	36	positive regulation of double-strand break repair	BP	1	FANCB,RAD51AP1,FOXM1,FUS	darkgrey	VSMC_M8
GO:0030203	0.30	0.81	9	93	glycosaminoglycan metabolic process	BP	1	SLC35D2,B3GNT2,HGF,CD44,PXYLP1,SLC10A7,UGDH,XYLT1,HAS2	darkgrey	VSMC_M8
GO:2001243	0.30	0.82	8	83	negative regulation of intrinsic apoptotic signaling pathway	BP	1	PLAUR,SNAI2,CD44,HELLS,CREB3L1,XBP1,BID,NOC2L	darkgrey	VSMC_M8
GO:0002637	0.30	0.85	5	48	regulation of immunoglobulin production	BP	1	RBP4,XBP1,TFRC,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0035306	0.30	0.84	5	47	positive regulation of dephosphorylation	BP	1	PPP2R5D,HSP90AB1,CDCA2,PPP1R15B,PTBP1	darkgrey	VSMC_M8
GO:0035303	0.30	0.81	10	106	regulation of dephosphorylation	BP	1	PPP2R5D,HSP90AB1,PPP6R1,MASTL,HSP90B1,CDCA2,YWHAB,PPP1R15B,SMG6,PTBP1	darkgrey	VSMC_M8
GO:0031111	0.30	0.86	4	36	negative regulation of microtubule polymerization or depolymerization	BP	1	CKAP2,TPX2,FKBP4,STMN1	darkgrey	VSMC_M8
GO:0120192	0.30	0.84	5	48	tight junction assembly	BP	1	STRN,SNAI2,MTDH,PAK2,ECT2	darkgrey	VSMC_M8
GO:0002381	0.30	0.84	5	48	immunoglobulin production involved in immunoglobulin-mediated immune response	BP	1	MSH6,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0009064	0.30	0.83	6	59	glutamine family amino acid metabolic process	BP	1	CTPS1,CAD,AADAT,ARG2,PFAS,GCLM	darkgrey	VSMC_M8
GO:0097194	0.31	0.83	6	60	execution phase of apoptosis	BP	1	CASP2,PAK2,TOP2A,AIFM1,XKR5,CASP6	darkgrey	VSMC_M8
GO:0008630	0.31	0.81	8	84	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	MSH6,CASP2,SNAI2,CD44,E2F1,BRCA1,BID,TP73	darkgrey	VSMC_M8
GO:2001242	0.31	0.79	12	135	regulation of intrinsic apoptotic signaling pathway	BP	1	BCLAF1,PLAUR,SNAI2,CD44,HELLS,CREB3L1,XBP1,MSX1,EIF5A,BID,NOC2L,ERP29	darkgrey	VSMC_M8
GO:0033673	0.31	0.78	17	191	negative regulation of kinase activity	BP	1	NUP62,CHORDC1,NCAPG2,IPO5,CHMP6,HMGCR,PRKAR2A,NF2,CEP85,PAK2,EPHB2,HNRNPU,UCHL1,PLK1,TFAP4,CDKN2C,DUSP7	darkgrey	VSMC_M8
GO:0046683	0.31	0.80	9	94	response to organophosphorus	BP	1	EZR,SDC1,FOSB,RFC3,HSP90B1,PDE3A,FOSL1,COL1A1,TYMS	darkgrey	VSMC_M8
GO:0009408	0.31	0.81	8	84	response to heat	BP	1	PSIP1,VCP,HSP90AB1,DNAJC2,CHORDC1,EIF2B1,DNAJC7,EIF2S1	darkgrey	VSMC_M8
GO:0001101	0.31	0.80	10	107	response to acid chemical	BP	1	COL1A2,IPO5,PCNA,CHUK,XBP1,COL1A1,DNMT1,AIFM1,GCLM,HNRNPD	darkgrey	VSMC_M8
GO:0018022	0.31	0.80	10	108	peptidyl-lysine methylation	BP	1	PWP1,EZH2,PHF19,SETD4,BRCA1,NSD2,SUV39H1,LMNA,DNMT1,CSKMT	darkgrey	VSMC_M8
GO:0055007	0.31	0.80	9	96	cardiac muscle cell differentiation	BP	1	ALPK2,DDX39B,PARP2,CCNB1,TBX3,CDK1,HNRNPU,LMNA,G6PD	darkgrey	VSMC_M8
GO:0051155	0.31	0.85	4	37	positive regulation of striated muscle cell differentiation	BP	1	DDX39B,PARP2,MORF4L2,FAM129B	darkgrey	VSMC_M8
GO:0060968	0.31	0.82	6	59	regulation of gene silencing	BP	1	CDK2,TRIM28,DDX5,EIF4G1,DHX9,DNMT1	darkgrey	VSMC_M8
GO:0001510	0.31	0.81	7	73	RNA methylation	BP	1	METTL1,THADA,FBL,METTL15,NSUN2,TARBP1,TRMT13	darkgrey	VSMC_M8
GO:0006473	0.32	0.78	15	168	protein acetylation	BP	1	DSCC1,NAA15,RUVBL2,RUVBL1,SPHK1,ESCO2,CHEK1,NAA50,MCM3AP,HAT1,BRCA1,MORF4L2,TADA2A,NOC2L,POLE3	darkgrey	VSMC_M8
GO:0060021	0.32	0.81	7	71	roof of mouth development	BP	1	ANP32B,MSC,LOXL3,TBX3,PAK1IP1,EPHB2,MSX1	darkgrey	VSMC_M8
GO:0048010	0.32	0.83	5	48	vascular endothelial growth factor receptor signaling pathway	BP	1	AXL,PAK2,NEDD4,BCAR1,FAM129B	darkgrey	VSMC_M8
GO:0006400	0.32	0.80	8	85	tRNA modification	BP	1	METTL1,THADA,PUS7,DUS1L,NSUN2,TARBP1,SSB,TRMT13	darkgrey	VSMC_M8
GO:0098727	0.32	0.79	10	108	maintenance of cell number	BP	1	EZH2,PHF19,WDR43,GNL3,TBX3,SMC3,ASPM,MED28,SMC1A,SRRT	darkgrey	VSMC_M8
GO:0010563	0.32	0.74	30	356	negative regulation of phosphorus metabolic process	BP	1	PPP2R5D,PWP1,NUP62,CHORDC1,PPP5C,MASTL,NCAPG2,IPO5,CHMP6,HGF,CCNB1,PBK,YWHAB,HMGCR,PPP1R15B,PRKAR2A,NF2,CEP85,EIF4G1,PAK2,EPHB2,HNRNPU,UCHL1,SPAG9,PLK1,NNT,TFAP4,CDKN2C,PID1,DUSP7	darkgrey	VSMC_M8
GO:0045936	0.32	0.74	30	356	negative regulation of phosphate metabolic process	BP	1	PPP2R5D,PWP1,NUP62,CHORDC1,PPP5C,MASTL,NCAPG2,IPO5,CHMP6,HGF,CCNB1,PBK,YWHAB,HMGCR,PPP1R15B,PRKAR2A,NF2,CEP85,EIF4G1,PAK2,EPHB2,HNRNPU,UCHL1,SPAG9,PLK1,NNT,TFAP4,CDKN2C,PID1,DUSP7	darkgrey	VSMC_M8
GO:0044403	0.32	0.76	18	206	biological process involved in symbiotic interaction	BP	1	DDX39B,TCP1,HSP90AB1,TRIM28,SLC1A5,AXL,ALYREF,VAMP8,PPID,TRIM35,NUP153,NUCKS1,CDK1,TFRC,PPIB,TFAP4,THOC6,TRIM59	darkgrey	VSMC_M8
GO:0070542	0.32	0.83	5	49	response to fatty acid	BP	1	PPP5C,CCNB1,E2F1,ADIPOR2,PID1	darkgrey	VSMC_M8
GO:0045137	0.33	0.77	15	170	development of primary sexual characteristics	BP	1	NUP107,CASP2,SDC1,PGR,NASP,RRM1,HMGB2,NRIP1,KIF18A,ASPM,SF1,SIX4,NUDT1,BRIP1,FANCA	darkgrey	VSMC_M8
GO:0009152	0.33	0.78	12	137	purine ribonucleotide biosynthetic process	BP	1	ATP5F1B,VCP,PAICS,PDHB,ELOVL6,PDHA1,DLAT,PFAS,ACSL4,ACSL3,PID1,GART	darkgrey	VSMC_M8

GO:0007018	0.33	0.75	24	283	microtubule-based movement	BP	1	TTLL1,KIFC1,KIF20A,KIF27,KIF24,KIF2C,KIF20B,KIF2A,KIF11,CFAP298,KIF18A,CENPE,KIF14,KIF18B,KIF15,CABYR,DLGAP5,HNRNPU,UCHL1,KIF4A,KIF22,KIF23,NDE1,BLOC1S2	darkgrey	VSMC_M8
GO:0044706	0.33	0.77	14	159	multi-multicellular organism process	BP	1	TRIM28,PGR,NAMPT,FOSB,CAD,POLR1B,ETS1,UMPS,FOSL1,ADIPOR2,ACSL4,EMP2,DAZAP1,TPPP3	darkgrey	VSMC_M8
GO:1901264	0.33	0.81	6	61	carbohydrate derivative transport	BP	1	SLC35D2,MFSD2A,SLC25A19,SLC10A7,SLC17A9,SLC25A5	darkgrey	VSMC_M8
GO:1902117	0.33	0.81	6	61	positive regulation of organelle assembly	BP	1	CEP135,NUP62,SDC1,PLK4,CENPJ,FSCN1	darkgrey	VSMC_M8
GO:0051146	0.33	0.75	19	220	striated muscle cell differentiation	BP	1	ALPK2,DDX39B,EZH2,SDC1,PARP2,CCNB1,TBX3,CHUK,XBP1,CDK1,SIX4,MSX1,HNRNPU,LMNA,SPAG9,MORF4L2,G6PD,FAM129B,TMOD3	darkgrey	VSMC_M8
GO:0043620	0.33	0.82	5	49	regulation of DNA-templated transcription in response to stress	BP	1	BCLAF1,CREB3L1,GCN1,CHEK1,NEDD4	darkgrey	VSMC_M8
GO:0006513	0.33	0.81	6	61	protein monoubiquitination	BP	1	RAD18,UBE2T,DTL,FANCM,UHRF1,ZNF598	darkgrey	VSMC_M8
GO:0072595	0.33	0.84	4	38	maintenance of protein localization in organelle	BP	1	RANGAP1,BARD1,KDELR2,HNRNPU	darkgrey	VSMC_M8
GO:0007338	0.33	0.79	8	86	single fertilization	BP	1	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,CDK1,CCT3	darkgrey	VSMC_M8
GO:0032964	0.34	0.83	4	38	collagen biosynthetic process	BP	1	SERPINH1,CREB3L1,RUNX1,COL1A1	darkgrey	VSMC_M8
GO:0070059	0.34	0.82	5	50	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP	1	CREB3L1,XBP1,UBE2K,AIFM1,ERP29	darkgrey	VSMC_M8
GO:0010171	0.34	0.83	4	38	body morphogenesis	BP	1	FLVCR1,MSX1,COL1A1,CRISPLD2	darkgrey	VSMC_M8
GO:0045995	0.34	0.82	5	50	regulation of embryonic development	BP	1	RACGAP1,RBM19,UTP25,CDK1,FAM129B	darkgrey	VSMC_M8
GO:0010821	0.34	0.77	11	124	regulation of mitochondrion organization	BP	1	FAM49B,PLAUR,PGAM5,HGF,TFRC,BID,PRELID1,LMNA,SLC25A5,AURKA,PID1	darkgrey	VSMC_M8
GO:0140053	0.34	0.78	9	101	mitochondrial gene expression	BP	1	MRPS18B,MRPL2,GARS,MRPL58,MRPS7,FASTKD3,ELAC2,TRUB2,MRPS15	darkgrey	VSMC_M8
GO:0034968	0.34	0.78	9	98	histone lysine methylation	BP	1	PWP1,EZH2,PHF19,SETD4,BRCA1,NSD2,SUV39H1,LMNA,DNMT1	darkgrey	VSMC_M8
GO:0070228	0.34	0.83	4	38	regulation of lymphocyte apoptotic process	BP	1	ARG2,PRELID1,AURKB,NOC2L	darkgrey	VSMC_M8
GO:2000736	0.34	0.82	5	50	regulation of stem cell differentiation	BP	1	HSPA9,PWP1,PUS7,NSUN2,HNRNPU	darkgrey	VSMC_M8
GO:0045471	0.34	0.79	8	87	response to ethanol	BP	1	GGH,RBP4,HMGCR,PSMD14,CDK1,ADIPOR2,TYMS,G6PD	darkgrey	VSMC_M8
GO:0031099	0.34	0.76	13	150	regeneration	BP	1	EZH2,CCNA2,CAD,AXL,PCNA,HGF,CCNB1,RUNX1,PRMT5,CDK1,SRSF5,TYMS,AURKA	darkgrey	VSMC_M8
GO:0090316	0.34	0.76	12	136	positive regulation of intracellular protein transport	BP	1	HSP90AB1,TRIM28,ANP32B,SAE1,IPO5,KIF20B,BAP1,ICE1,CDK1,ECT2,MTCL1,UBE2J2	darkgrey	VSMC_M8
GO:0002181	0.35	0.77	9	111	cytoplasmic translation	BP	1	EIF3M,EIF4H,EIF4G1,DHX9,RPL22L1,EIF3B,EIF4A1,EIF5,DRG2	darkgrey	VSMC_M8
GO:0042177	0.35	0.77	9	101	negative regulation of protein catabolic process	BP	1	CYP51A1,HSP90AB1,GRIN2C,PBK,HMGCR,MDM4,SMARCC1,SF3B3,MAD2L1	darkgrey	VSMC_M8
GO:0071709	0.35	0.82	4	39	membrane assembly	BP	1	REEP4,RCC1,EPHB2,EMP2	darkgrey	VSMC_M8
GO:0022904	0.35	0.78	8	99	respiratory electron transport chain	BP	1	CYC1,CYCS,CCNB1,NDUFAF1,CDK1,NDUFS1,MYBBP1A,BID	darkgrey	VSMC_M8
GO:0006022	0.35	0.77	9	98	aminoglycan metabolic process	BP	1	SLC35D2,B3GNT2,HGF,CD44,PXYLP1,SLC10A7,UGDH,XYLT1,HAS2	darkgrey	VSMC_M8
GO:2001233	0.36	0.72	24	292	regulation of apoptotic signaling pathway	BP	1	BCLAF1,CASP2,PLAUR,HGF,SNAI2,CD44,HMGB2,HELLS,CREB3L1,XBP1,PAK2,PPP2R1B,BRCA1,MSX1,EIF5A,BID,PRELID1,LMNA,MAZ,SLC25A5,NOC2L,GCLM,CTH,ERP29	darkgrey	VSMC_M8
GO:0048738	0.36	0.74	16	186	cardiac muscle tissue development	BP	1	ALPK2,DDX39B,PRMT1,PARP2,CCNB1,RBP4,MSC,HEY1,TBX3,RUNX1,CDK1,MSX1,HNRNPU,LMNA,TP73,G6PD	darkgrey	VSMC_M8
GO:1901570	0.36	0.82	4	39	fatty acid derivative biosynthetic process	BP	1	ELOVL6,ALOX15B,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0015031	0.36	0.68	103	1301	protein transport	BP	1	TMED9,XPOT,NUP43,NUP107,EZR,TCP1,NUP50,ARFGAP3,MAN1A1,DESI1,RANGAP1,KIF20A,HSPA9,TNPO3,CYP51A1,VCP,HSP90AB1,TRIM28,ANP32B,NUP205,NUP62,NBAS,SEC61A1,SAE1,CHCHD4,NASP,COG3,TOMM40,PREB,KCNN4,NUP85,SRP68,GDI2,SEC23B,RRBP1,IPO5,CHMP6,AAAS,KIF20B,HSP90B1,NECAB3,VAMP8,SLC10A7,TRAM1,RBP4,NUP160,SELENOT,PPID,NUP93,TOMM70,YWHAB,HMGCR,BAP1,HEATR3,NOLC1,NUP153,KIF18A,ICE1,CSE1L,XBP1,MCM3AP,IPO4,NUP133,SEC24D,ARCN1,CENPF,ARFGAP1,CDK1,TFRC,LSG1,ZW10,BARD1,NMD3,UFD1,CDK16,ANKLE1,ECT2,RAC1,KDELR2,MYO5A,RAB27A,NEDD4,EIF5A,BID,LMNA,LTBP2,COL1A1,TIMM8A,NUP62CL,ACSL4,TIMM44,MTCL1,AIFM1,HOOK1,NDC1,NUP188,GLE1,ACD,ARF6,SPCS3,ACSL3,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:0019220	0.36	0.69	86	1074	regulation of phosphate metabolic process	BP	1	PRRC1,CDC25C,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,CKS2,PPP6R1,TTK,MFSD2A,EZH2,NUP62,CLSPN,CCNA2,CHORDC1,PPP5C,MASTL,PLAUR,BORA,AXL,SPHK1,NCAPG2,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,CD44,TPX2,HSP90B1,CCNE1,PBK,RBL1,CCNL1,CDCA2,RAD51,CCNE2,YWHAB,HMGCR,PPP1R15B,GCN1,CENPE,KIF14,PRKAR2A,NF2,BLM,CEP85,EIF4G1,CDC25A,TFRC,PAK2,BARD1,EPHB2,MCM7,CNOT9,CDKN3,ECT2,MNAT1,EIF2AK1,RAC1,HNRNPU,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,CCNB2,IQGAP3,SPAG9,PLK1,NNT,RAP2C,EMP2,TFAP4,SMG6,PKMYT1,CCNF,PTBP1,CDKN2C,ACSL3,ERP29,PID1,DUSP7	darkgrey	VSMC_M8
GO:0051174	0.36	0.69	86	1074	regulation of phosphorus metabolic process	BP	1	PRRC1,CDC25C,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,CKS2,PPP6R1,TTK,MFSD2A,EZH2,NUP62,CLSPN,CCNA2,CHORDC1,PPP5C,MASTL,PLAUR,BORA,AXL,SPHK1,NCAPG2,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,CD44,TPX2,HSP90B1,CCNE1,PBK,RBL1,CCNL1,CDCA2,RAD51,CCNE2,YWHAB,HMGCR,PPP1R15B,GCN1,CENPE,KIF14,PRKAR2A,NF2,BLM,CEP85,EIF4G1,CDC25A,TFRC,PAK2,BARD1,EPHB2,MCM7,CNOT9,CDKN3,ECT2,MNAT1,EIF2AK1,RAC1,HNRNPU,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,CCNB2,IQGAP3,SPAG9,PLK1,NNT,RAP2C,EMP2,TFAP4,SMG6,PKMYT1,CCNF,PTBP1,CDKN2C,ACSL3,ERP29,PID1,DUSP7	darkgrey	VSMC_M8
GO:0045088	0.36	0.75	13	148	regulation of innate immune response	BP	1	MATR3,POLR3B,HSP90AB1,POLR3F,HMGB2,TOMM70,MNDA,RBM14,PAK2,DHX9,LYAR,UBE2K,GBP5	darkgrey	VSMC_M8
GO:0043297	0.36	0.80	5	52	apical junction assembly	BP	1	STRN,SNAI2,MTDH,PAK2,ECT2	darkgrey	VSMC_M8
GO:0046660	0.36	0.77	8	88	female sex differentiation	BP	1	NUP107,CASP2,PGR,AXL,RBP4,NRIP1,TBX3,FANCA	darkgrey	VSMC_M8
GO:0046148	0.36	0.80	5	52	pigment biosynthetic process	BP	1	PAICS,HMBS,FLVCR1,PRPS1,GART	darkgrey	VSMC_M8

GO:0031058	0.36	0.78	7	75	positive regulation of histone modification	BP	1	PHF19,RUVBL2,CCNB1,BRCA1,LMNA,DNMT1,TADA2A	darkgrey	VSMC_M8
GO:1902115	0.36	0.74	14	161	regulation of organelle assembly	BP	1	EZR,CEP135,NUP62,SDC1,PLK4,STIL,CENPJ,RBM14,KIF15,BRCA1,HNRNPU,FSCN1,PLK1,CEP76	darkgrey	VSMC_M8
GO:0061351	0.36	0.75	10	111	neural precursor cell proliferation	BP	1	MELK,SHCBP1,NAP1L1,RRM1,RACGAP1,KIF14,ASPM,NF2,NES,NDE1	darkgrey	VSMC_M8
GO:0021761	0.37	0.77	7	75	limbic system development	BP	1	MFSD2A,EZH2,XRN2,TBX3,ETS1,KIF14,NF2	darkgrey	VSMC_M8
GO:0031056	0.37	0.75	11	124	regulation of histone modification	BP	1	PHF19,RUVBL2,NCAPG2,CCNB1,CHEK1,BRCA1,LMNA,DNMT1,TADA2A,WDR70,NOC2L	darkgrey	VSMC_M8
GO:0021695	0.37	0.81	4	39	cerebellar cortex development	BP	1	TTLL1,EZH2,KIF14,ARCN1	darkgrey	VSMC_M8
GO:0043281	0.37	0.74	13	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	VCP,ANP32B,CYCS,CASP2,PLAUR,BIRC5,HGF,CD44,PAK2,BID,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:0002312	0.37	0.78	6	64	B cell activation involved in immune response	BP	1	MSH6,UNG,XBP1,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0035967	0.37	0.75	9	103	cellular response to topologically incorrect protein	BP	1	HSPA9,VCP,CREB3L1,PPP1R15B,XBP1,UFD1,EIF2S1,TOR1A,CTH	darkgrey	VSMC_M8
GO:0061136	0.37	0.73	14	166	regulation of proteasomal protein catabolic process	BP	1	CDK2,DESI1,VCP,HSP90AB1,CDC20,CHFR,PBK,PSMD14,PSMC5,SMARCC1,UBE2K,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0046622	0.37	0.81	4	41	positive regulation of organ growth	BP	1	DDX39B,PARP2,CCNB1,CDK1	darkgrey	VSMC_M8
GO:0051149	0.38	0.79	5	53	positive regulation of muscle cell differentiation	BP	1	DDX39B,PARP2,MORF4L2,FAM129B,CTH	darkgrey	VSMC_M8
GO:0031670	0.38	0.80	4	40	cellular response to nutrient	BP	1	SNAI2,XBP1,COL1A1,BRIP1	darkgrey	VSMC_M8
GO:0042692	0.38	0.70	25	303	muscle cell differentiation	BP	1	ALPK2,DDX39B,EZH2,SDC1,PARP2,CCNB1,HEY1,TBX3,CHUK,XBP1,CDK1,MED28,SIX4,MSX1,HNRNPU,UCHL1,LMNA,SPAG9,MORF4L2,DNMT1,G6PD,PTBP1,FAM129B,CTH,TMOD3	darkgrey	VSMC_M8
GO:0000266	0.38	0.80	4	40	mitochondrial fission	BP	1	MTFR2,FAM49B,PGAM5,AURKA	darkgrey	VSMC_M8
GO:0061383	0.38	0.80	4	40	trabecula morphogenesis	BP	1	FBN2,RBP4,HEY1,COL1A1	darkgrey	VSMC_M8
GO:0009451	0.38	0.73	12	141	RNA modification	BP	1	METTL1,THADA,PUS7,FBL,DUS1L,METTL15,NSUN2,TARBP1,SSB,DKC1,TRMT13,TRUB2	darkgrey	VSMC_M8
GO:0006637	0.38	0.76	7	78	acyl-CoA metabolic process	BP	1	PDHB,AADAT,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0035383	0.38	0.76	7	78	thioester metabolic process	BP	1	PDHB,AADAT,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0043065	0.38	0.68	33	410	positive regulation of apoptotic process	BP	1	BCLAF1,MELK,HOXA5,CASP2,NET1,E2F1,PPID,TRIM35,CTNNBL1,MYBL2,HMGCR,EEF1E1,MNDA,PAK2,FOSL1,DDX20,PPP2R1B,BARD1,MYBBP1A,ECT2,MSX1,TOP2A,EIF5A,BID,EIF2S1,PRELID1,PTRH2,AIFM1,TFAP4,RNPS1,TP73,PIK3CD,PDCD2	darkgrey	VSMC_M8
GO:0051205	0.39	0.80	4	44	protein insertion into membrane	BP	1	TRAM1,TOMM70,TIMM8A,EMC8	darkgrey	VSMC_M8
GO:0042127	0.39	0.65	97	1230	regulation of cell population proliferation	BP	1	CDK2,DDX39B,FBXO5,MTBP,CDCA7L,TTK,CLEC11A,HOXA5,EZH2,NUP62,PRMT1,SHCBP1,PGR,NAMPT,CCNA2,RNASEH2B,SPHK1,CDC20,BIRC5,GTPBP4,NAP1L1,E2F7,STRN,CDC25B,ZNF703,CCNB1,SNAI2,UTP20,KIF20B,SGK3,E2F1,CCNE1,HMGB2,RBP4,FAM98B,GNL3,TBX3,HMGCR,BAP1,NRAS,EEF1E1,RUNX1,SETD4,MDM4,HMGN1,NOLC1,ETS1,CHEK1,KIF14,ASPM,MNDA,XBP1,PRC1,NF2,CDK1,S100A11,TFRC,FOSL1,DHX9,DDX20,IFT80,SF1,EPHB2,CDKN3,DPT,SIX4,MNAT1,FOXM1,EIF2AK1,MSX1,HNRNPU,CDC6,BID,PDPN,ARG2,IQGAP3,EFNB1,NES,LMNA,ALOX15B,MAZ,BRIP1,DNMT1,SLC25A5,UHRF1,EMP2,TFAP4,TP73,PIK3CD,FANCA,FAM129B,CDKN2C,HAS2,SAAL1,PDCD2,PID1,MBD2	darkgrey	VSMC_M8
GO:0051222	0.39	0.70	20	241	positive regulation of protein transport	BP	1	EZR,HSP90AB1,TRIM28,ANP32B,SAE1,KCNN4,IPO5,KIF20B,RBP4,PPID,BAP1,ICE1,CDK1,ECT2,RAC1,ACSL4,MTCL1,ARF6,ACSL3,UBE2J2	darkgrey	VSMC_M8
GO:0043161	0.39	0.68	30	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	CDK2,MAN1A1,DESI1,VCP,HSP90AB1,CDC20,CHFR,CDC16,ANAPC1,HSP90B1,PBK,UBE2C,PSMD14,KIF14,PSMD4,PSMC5,SMARCC1,UFD1,UCHL1,UBE2K,NEDD4,RAD23A,PLK1,CCNF,ZNF598,PSMA5,AURKA,UBE2S,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0072348	0.39	0.79	4	41	sulfur compound transport	BP	1	SLC25A19,SLC5A6,RACGAP1,SLC19A2	darkgrey	VSMC_M8
GO:2000756	0.39	0.78	5	53	regulation of peptidyl-lysine acetylation	BP	1	RUVBL2,CHEK1,BRCA1,TADA2A,NOC2L	darkgrey	VSMC_M8
GO:0016310	0.39	0.65	114	1440	phosphorylation	BP	1	CDK2,ALPK2,PRRC1,CDC25C,SRPK1,PPP2R5D,PWP1,DBF4,HSP90AB1,CKS2,MELK,TRIM28,TTK,DCK,EZH2,NUP62,CLSPN,PLK4,CCNA2,CHORDC1,PPP5C,MASTL,MAST2,PLAUR,CAD,BORA,AXL,SPHK1,ULK4,NCAPG2,TK1,BIRC5,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,CD44,BUB1,TPX2,SGK3,WEE1,PPIP5K2,CCNE1,PBK,RBL1,BUB1B,CCNL1,RSRC1,RAD51,CCNE2,HMGCR,CHUK,PPP1R15B,CIT,GCN1,CHEK1,CENPE,KIF14,PRKAR2A,NEK2,NF2,BLM,CEP85,EIF4G1,CDK1,CDC25A,TFRC,PAK2,UCK2,GK,BARD1,EPHB2,MCM7,CNOT9,CDKN3,CDK16,ECT2,MNAT1,MAPK6,EIF2AK1,RAC1,HNRNPU,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,EIF2S1,CCNB2,IQGAP3,AURKB,SPAG9,PLK1,ILF3,VRK1,PRPS1,NNT,RAP2C,EMP2,TFAP4,PKMYT1,HASPIN,CCNF,PIK3CD,PKN3,NEK6,CDKN2C,AURKA,ERP29,PID1,DUSP7	darkgrey	VSMC_M8
GO:0016925	0.39	0.79	4	42	protein sumoylation	BP	1	TRIM28,SAE1,UBA2,GNL3	darkgrey	VSMC_M8
GO:0006470	0.39	0.70	19	228	protein dephosphorylation	BP	1	CDC25C,PPP2R5D,HSP90AB1,PPP6R1,PPP5C,MASTL,PGAM5,CDC25B,HSP90B1,CDCA2,YWHAB,PPP1R15B,CDC25A,PPP2R1B,CDKN3,FAM220A,PTBP1,PDP2,DUSP7	darkgrey	VSMC_M8
GO:0015748	0.40	0.73	9	102	organophosphate ester transport	BP	1	MFSD2A,KCNN4,SLC25A19,DBI,PITPNB,SLC17A9,PRELID1,SLC25A5,XKR5	darkgrey	VSMC_M8
GO:0051262	0.40	0.76	6	66	protein tetramerization	BP	1	TK1,RRM1,CPSF7,TP73,CTH,GBP5	darkgrey	VSMC_M8
GO:0051260	0.40	0.72	11	128	protein homooligomerization	BP	1	PRMT1,SLC1A5,TK1,POLQ,BLM,ECT2,FUS,RBMX,CTH,GBP5,SIGMAR1	darkgrey	VSMC_M8
GO:2000514	0.40	0.79	4	41	regulation of CD4-positive, alpha-beta T cell activation	BP	1	LOXL3,RUNX1,ARG2,CBFB	darkgrey	VSMC_M8
GO:2000242	0.40	0.79	4	42	negative regulation of reproductive process	BP	1	FBXO5,TTK,CHFR,TRIP13	darkgrey	VSMC_M8
GO:0043632	0.40	0.66	45	561	modification-dependent macromolecule catabolic process	BP	1	CDK2,MAN1A1,DESI1,VCP,HSP90AB1,CDC20,CHFR,EXOSC8,PSMD13,CDC16,ANAPC1,HSP90B1,PBK,BAP1,UBE2C,PSMD14,KIF14,XBP1,DTL,PSMD4,PSMC5,SMARCC1,PSMA6,UFD1,USP42,UCHL1,UBE2K,NEDD4,PSMD3,EXOSC10,RAD23A,PLK1,PSMD11,COPS3,USP1,UHRF1,CCNF,ZNF598,PSMA5,EXOSC2,USP4,AURKA,UBE2S,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0034250	0.40	0.72	11	130	positive regulation of cellular amide metabolic process	BP	1	DDX39B,EIF4A3,FASTKD3,TENT4A,KHDRBS1,EIF4G1,DHX9,RBM3,EIF5A,TRUB2,HNRNPD	darkgrey	VSMC_M8
GO:0120193	0.40	0.77	5	54	tight junction organization	BP	1	STRN,SNAI2,MTDH,PAK2,ECT2	darkgrey	VSMC_M8

GO:0006119	0.40	0.73	9	119	oxidative phosphorylation	BP	1	ATP5F1B,CYC1,VCP,CYCS,CCNB1,NDUFAF1,CDK1,NDUFS1,BID	darkgrey	VSMC_M8
GO:0051384	0.40	0.73	9	104	response to glucocorticoid	BP	1	SDC1,FOSB,CAD,PCNA,HEY1,FOSL1,HNRNPU,TYMS,TFAP4	darkgrey	VSMC_M8
GO:2000058	0.40	0.71	12	143	regulation of ubiquitin-dependent protein catabolic process	BP	1	CDK2,DESI1,VCP,HSP90AB1,CDC20,CHFR,PBK,SMARCC1,UBE2K,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0006487	0.40	0.77	5	55	protein N-linked glycosylation	BP	1	NUS1,RPN1,ALG8,STT3A,DOLPP1	darkgrey	VSMC_M8
GO:0043631	0.40	0.79	4	41	RNA polyadenylation	BP	1	GRSF1,WDR33,TENT4A,CPSF7	darkgrey	VSMC_M8
GO:0006888	0.40	0.73	9	106	endoplasmic reticulum to Golgi vesicle-mediated transport	BP	1	TMED9,VCP,COG3,PREB,SEC23B,SEC24D,ARCN1,ZW10,KDELR2	darkgrey	VSMC_M8
GO:0032527	0.40	0.78	4	43	protein exit from endoplasmic reticulum	BP	1	VCP,PREB,HSP90B1,UFD1	darkgrey	VSMC_M8
GO:0090407	0.40	0.66	36	452	organophosphate biosynthetic process	BP	1	ATP5F1B,NUS1,VCP,PAICS,CTPS1,DCK,MFSD2A,GARS,NAMPT,CAD,TK1,AFMID,PGS1,RRM1,PDHB,PPIP5K2,AGPAT5,ELOVL6,UMPS,PDHA1,UCK2,GK,DLAT,DUT,MTHFD1,PFAS,PRPS1,ACSL4,TYMS,G6PD,PIK3CD,DOLPP1,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0071887	0.41	0.74	7	79	leukocyte apoptotic process	BP	1	TCP1,AXL,ARG2,PRELID1,AURKB,NOC2L,PIK3CD	darkgrey	VSMC_M8
GO:0031648	0.41	0.78	4	42	protein destabilization	BP	1	CHFR,UTP25,RAD23A,PLK1	darkgrey	VSMC_M8
GO:0006695	0.41	0.78	4	43	cholesterol biosynthetic process	BP	1	CYP51A1,HMGCR,LBR,G6PD	darkgrey	VSMC_M8
GO:1902653	0.41	0.78	4	43	secondary alcohol biosynthetic process	BP	1	CYP51A1,HMGCR,LBR,G6PD	darkgrey	VSMC_M8
GO:0071466	0.41	0.73	8	92	cellular response to xenobiotic stimulus	BP	1	CAD,PCNA,E2F1,UMPS,TFRC,EFTUD2,MCM7,UCHL1	darkgrey	VSMC_M8
GO:0043154	0.41	0.76	5	55	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	PLAUR,BIRC5,HGF,CD44,PAK2	darkgrey	VSMC_M8
GO:0009991	0.41	0.66	31	385	response to extracellular stimulus	BP	1	MIOS,MFSD2A,NAMPT,CAD,AXL,SRSF2,RRP8,SNAI2,HMGCR,GCN1,XBP1,EIF4G1,HAT1,FOSL1,MYBBP1A,EIF2AK1,ADIPOR2,EIF2S1,NUDT1,DCTPP1,COL1A1,BRIP1,ACSL4,TYMS,NNT,AIFM1,LIPG,G6PD,GCLM,ACSL3,MBD2	darkgrey	VSMC_M8
GO:0031668	0.41	0.69	17	205	cellular response to extracellular stimulus	BP	1	MIOS,MFSD2A,NAMPT,AXL,RRP8,SNAI2,GCN1,XBP1,EIF4G1,FOSL1,MYBBP1A,EIF2S1,NUDT1,DCTPP1,COL1A1,BRIP1,AIFM1	darkgrey	VSMC_M8
GO:0031110	0.41	0.74	7	79	regulation of microtubule polymerization or depolymerization	BP	1	CKAP2,TPX2,SKA3,CKAP5,FKBP4,RAC1,STMN1	darkgrey	VSMC_M8
GO:0043966	0.41	0.76	5	54	histone H3 acetylation	BP	1	CHEK1,MCM3AP,BRCA1,TADA2A,POLE3	darkgrey	VSMC_M8
GO:0051130	0.41	0.64	69	870	positive regulation of cellular component organization	BP	1	TMED9,CCT2,TCP1,RAD21,VCP,CEP135,TRIM28,HNRNPA2B1,CCT4,ANLN,EZH2,NUP62,SDC1,PLK4,CDC42EP4,PLAUR,AXL,SPHK1,CDC20,PGAM5,HGF,CDC16,ESPL1,CENPJ,ATF1,TERF1,CCT8,CCT7,GNL3,CKAP5,NUSAP1,RUNX1,CCT5,CCT6A,ICE1,NEK2,NF2,EIF4G1,PSMC5,TFRC,EPHB2,DLGAP5,RAD51AP1,DHX33,MSX1,RAC1,FSCN1,EIF5A,BID,PDPN,NES,CCT3,AURKB,DNMT1,SLC25A5,POLDIP2,SF3A2,DKC1,CDT1,TOR1A,ACD,TPPP3,ARPC4,ARF6,GBP5,HNRNPD,AURKA,FEN1,CLSTN3	darkgrey	VSMC_M8
GO:0007266	0.41	0.71	10	116	Rho protein signal transduction	BP	1	COL1A2,CDC42EP4,NET1,ARHGDIA,CHUK,PHACTR4,CDC42SE1,RAC1,PDPN,STMN1	darkgrey	VSMC_M8
GO:0032774	0.42	0.62	198	2534	RNA biosynthetic process	BP	1	PRIM1,HNRNPAB,BCLAF1,NUP107,DDX39B,EZR,RAD21,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,POLR3B,POLR1C,CDC5L,CKS2,TRIM28,POLR1E,TWISTNB,CDCA7L,HOXA5,PPIE,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,NIFK,NUP85,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,ZNF703,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,POLR1B,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,PSMA6,POLA1,DDX20,AP000944.2,DDX21,SF1,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,NOC2L,RNPS1,TP73,POLR2E,REXO4,FANCA,FAM129B,CBFB,CTH,DEPDC1,PRIM2,SRRT,HNRNPD,DRAP1,HMGB3,ABT1,PID1,LIN52,HOXC8,MBD2	darkgrey	VSMC_M8
GO:2001244	0.42	0.77	4	46	positive regulation of intrinsic apoptotic signaling pathway	BP	1	BCLAF1,MSX1,EIF5A,BID	darkgrey	VSMC_M8
GO:0030968	0.42	0.74	6	69	endoplasmic reticulum unfolded protein response	BP	1	VCP,CREB3L1,PPP1R15B,XBP1,EIF2S1,CTH	darkgrey	VSMC_M8
GO:0033157	0.42	0.68	16	196	regulation of intracellular protein transport	BP	1	RANGAP1,HSP90AB1,TRIM28,ANP32B,NUP62,SAE1,IPO5,KIF20B,BAP1,NOLC1,ICE1,CDK1,BARD1,ECT2,MTCL1,UBE2J2	darkgrey	VSMC_M8
GO:0032922	0.42	0.75	5	55	circadian regulation of gene expression	BP	1	NAMPT,NRIP1,PRMT5,MYBBP1A,HNRNPU	darkgrey	VSMC_M8
GO:0048706	0.43	0.71	9	105	embryonic skeletal system development	BP	1	HOXA5,EIF4A3,RBP4,FLVCR1,SIX4,MTHFD1,HOXB7,COL1A1,XYLT1	darkgrey	VSMC_M8
GO:0009790	0.43	0.62	67	841	embryo development	BP	1	FBN2,TTLL1,BYSL,TRIM28,GRSF1,HOXA5,PRMT1,GJB3,PLK4,STIL,RNASEH2B,NASP,SMG9,NCAPG2,EIF4A3,E2F7,GINS4,POLE,CCNB1,POLR1B,KIF20B,CENPU,RBP4,RACGAP1,LOXL3,HEY1,RBM19,TBX3,E2F8,NOLC1,NSUN2,CHEK1,PHACTR4,UTP25,NEK2,NUP133,HINFP,NF2,SEC24D,FLVCR1,CDK1,FOSL1,TRA2B,EPHB2,BRCA1,SIX4,MSX1,MTHFD1,UGDH,TOP2A,ASF1B,CCNB2,EFNB1,NES,HOXB7,COL1A1,DNMT1,ACSL4,XYLT1,COPS3,NXN,FAM129B,ACD,GINS1,PALB2,SLC30A1,MBD2	darkgrey	VSMC_M8
GO:0043618	0.43	0.76	4	43	regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	CREB3L1,GCN1,CHEK1,NEDD4	darkgrey	VSMC_M8
GO:1901605	0.43	0.68	12	146	alpha-amino acid metabolic process	BP	1	GCAT,CTPS1,ODC1,CAD,AFMID,AADAT,MTHFD1,ARG2,PFAS,GCLM,CTH,GART	darkgrey	VSMC_M8

GO:0043280	0.43	0.71	8	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	VCP,ANP32B,CYCS,CASP2,BID,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:0080134	0.43	0.61	76	970	regulation of response to stress	BP	1	BCLAF1,DDX39B,FBXO5,EZR,MATR3,POLR3B,POLH,HSP90AB1,TRIM28,PRMT1,NAMPT,DNAJC2,CHORDC1,RNASEH2B,SPHK1,ULK4,POLR3F,PCNA,HGF,SNAI2,CD44,PARPBP,VAMP8,HMGB2,PBK,RBL1,RAD51,CREB3L1,TOMM70,HMGCR,BAP1,EEF1E1,SETD4,PPP1R15B,DEK,MANF,ETS1,CHEK1,POLQ,MNDA,DDX5,FANCB,XBP1,RPA2,H2AFX,RBM14,NSMCE4A,EIF4G1,AUNIP,PAK2,DHX9,PSMA6,WDR76,EPHB2,UFD1,BRCA1,TFPI,NSD2,RAD51AP1,ANKLE1,FOXM1,EIF2AK1,LYAR,MSX1,DNAJC7,UBE2K,BID,ARG2,FUS,LMNA,USP1,RSL1D1,FANCA,NEK6,GBP5,ERP29	darkgrey	VSMC_M8
GO:0043412	0.44	0.60	235	3029	macromolecule modification	BP	1	CDK2,ALPK2,METTL1,FBXO5,PRRC1,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,DESI1,CDC25C,FKBP5,SRPK1,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,PUM3,CKS2,MELK,TRIM28,THADA,PPIH,U2AF2,PPP6R1,TTK,PPIE,B3GNT2,EZH2,NUP62,CLSPN,PHF19,PRMT1,NAA15,RUVBL2,PLK4,PUS7,RUVBL1,CCNA2,RPN1,SAE1,CHORDC1,PPP5C,MASTL,MAST2,CHCHD4,COG3,PLAUR,CAD,ALG8,DBI,TRIM47,BORA,AXL,RNF157,SPHK1,ULK4,NCAPG2,CDC20,BIRC5,PARP2,FBL,GTPBP4,RAD18,IPO5,CHMP6,DUS1L,CHFR,PGAM5,CDC25B,METAP2,DCUN1D2,HGF,CDC16,USPL1,CCNB1,SNRPB,CD44,BUB1,TPX2,ANAPC1,UBA2,CWC27,SGK3,WEE1,HSP90B1,CCNE1,GALNT6,HELLS,LOXL3,PBK,ESCO2,NEIL3,FAM98B,PPID,TRIM35,BUB1B,MIS18A,CCNL1,RSRC1,CDCA2,GNL3,RAD51,CCNE2,TRIM33,YWHAB,HMGCR,BAP1,CHUK,SETD4,PPP1R15B,HR,UBE2C,PSMD14,CIT,METTL15,METAP1,NSUN2,UBE2T,CHEK1,NAA50,STT3A,CENPE,TRAIP,KIF14,UNG,PRMT5,TARBP1,FANCI,MCM3AP,PRKAR2A,NEK2,DTL,NF2,HMBS,BLM,RBM14,SSB,CEP85,EIF4G1,HAT1,CDK1,CDC25A,TFRC,PAK2,FANCM,LRR1,PPP2R1B,BARD1,EPHB2,BRCA1,CDCA3,CNOT9,CDKN3,NSD2,CDK16,DCUN1D5,ECT2,AIPL1,SUV39H1,FKBP4,MNAT1,MAPK6,EIF2AK1,USP42,FAM220A,RAC1,DESI2,UCHL1,INCENP,ADIPOR2,UBE2K,NEDD4,CCNB3,CDC6,EIF2S1,DCAF15,CCNB2,IQGAP3,LMNA,AURKB,PPIB,SPAG9,PLK1,ILF3,MORF4L2,VRK1,DNMT1,TADA2A,COPS3,NNT,WDR70,USP1,RAP2C,UHRF1,EMP2,NXN,TFAP4,PKMYT1,NOC2L,HASPIN,CCNF,THOP1,ZNF598,G6PD,DKC1,PTBP1,PIK3CD,TOR1A,DOLPP1,TRMT13,PKN3,TRUB2,FAM129B,NEK6,CBFB,PDP2,CTH,GMPPB,USP4,MAD2L1,CDKN2C,AURKA,UBE2S,CSKMT,ERP29,P	darkgrey	VSMC_M8
GO:0019827	0.44	0.70	9	106	stem cell population maintenance	BP	1	PHF19,WDR43,GNL3,TBX3,SMC3,ASPM,MED28,SMC1A,SRRT	darkgrey	VSMC_M8
GO:0016573	0.44	0.69	11	131	histone acetylation	BP	1	RUVBL2,RUVBL1,CHEK1,NAA50,MCM3AP,HAT1,BRCA1,MORF4L2,TADA2A,NOC2L,POLE3	darkgrey	VSMC_M8
GO:0014855	0.44	0.74	5	56	striated muscle cell proliferation	BP	1	CCNB1,RBP4,RUNX1,CDK1,TP73	darkgrey	VSMC_M8
GO:0044091	0.44	0.75	4	44	membrane biogenesis	BP	1	REEP4,RCC1,EPHB2,EMP2	darkgrey	VSMC_M8
GO:0031397	0.44	0.72	6	72	negative regulation of protein ubiquitination	BP	1	FBXO5,U2AF2,GTPBP4,NXN,USP4,MAD2L1	darkgrey	VSMC_M8
GO:0097035	0.44	0.75	4	43	regulation of membrane lipid distribution	BP	1	MFSD2A,KCNN4,PRELID1,XKR5	darkgrey	VSMC_M8
GO:0051145	0.44	0.73	5	57	smooth muscle cell differentiation	BP	1	HEY1,TBX3,MED28,DNMT1,CTH	darkgrey	VSMC_M8
GO:0042325	0.44	0.61	76	967	regulation of phosphorylation	BP	1	PRRC1,CDC25C,PPP2R5D,PWP1,DBF4,HSP90AB1,CKS2,TTK,EZH2,NUP62,CLSPN,CCNA2,CHORDC1,PPP5C,PLAUR,BORA,AXL,SPHK1,NCAPG2,GTPBP4,IPO5,CHMP6,CDC25B,HGF,CCNB1,CD44,TPX2,CCNE1,PBK,RBL1,CCNL1,RAD51,CCNE2,HMGCR,PPP1R15B,GCN1,CENPE,KIF14,PRKAR2A,NF2,BLM,CEP85,EIF4G1,CDC25A,TFRC,PAK2,BARD1,EPHB2,MCM7,CNOT9,CDKN3,ECT2,MNAT1,EIF2AK1,RAC1,HNRNPU,UCHL1,INCENP,ADIPOR2,UBE2K,CCNB3,CDC6,CCNB2,IQGAP3,SPAG9,PLK1,NNT,RAP2C,EMP2,TFAP4,PKMYT1,CCNF,CDKN2C,ERP29,PID1,DUSP7	darkgrey	VSMC_M8
GO:0009894	0.44	0.61	63	806	regulation of catabolic process	BP	1	CDK2,EZR,DESI1,CYP51A1,VCP,HSP90AB1,GRSF1,MFSD2A,SYNCRIP,PABPC4,THRAP3,ODC1,NBAS,NRDC,NAMPT,GRIN2C,DIS3,CDC20,CHMP6,CHFR,EXOSC8,HGF,E2F1,PBK,FAM83D,MTDH,HMGCR,MDM4,PSMD14,FASTKD3,TENT4A,NSUN2,DTL,EIF4G1,PSMC5,SMARCC1,DHX9,HNRNPR,BARD1,HNRNPU,UCHL1,UBE2K,NEDD4,BID,PSMD3,FUS,RAD23A,PLK1,TAF15,SLC25A5,HNRNPM,SERBP1,NNT,POLDIP2,MTCL1,AIFM1,DKC1,ZC3H18,EXOSC2,SF3B3,HNRNPD,MAD2L1,AURKA	darkgrey	VSMC_M8
GO:0050779	0.44	0.71	7	82	RNA destabilization	BP	1	DIS3,EXOSC8,TENT4A,HNRNPR,ZC3H18,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0007264	0.44	0.63	35	437	small GTPase mediated signal transduction	BP	1	CDK2,FAM49B,COL1A2,TRIM28,NUP62,CCNA2,CDC42EP4,GDI2,NET1,DOCK9,ARHGDIA,SIPA1L3,PSD4,ARHGAP11A,RACGAP1,NRAS,CHUK,RASSF1,KIF14,PHACTR4,CDC42SE1,ARFGAP1,EPHB2,ECT2,FOXM1,RAC1,PDPN,IQGAP3,LRRC59,DNMT1,RAP2C,PLEKHG4,ARF6,RAPGEF6,STMN1	darkgrey	VSMC_M8
GO:0022600	0.45	0.73	5	56	digestive system process	BP	1	EZR,TJP2,KCNN4,RBP4,STRAP	darkgrey	VSMC_M8
GO:0016579	0.45	0.69	9	108	protein deubiquitination	BP	1	VCP,BAP1,PSMD14,CDK1,USP42,DESI2,UCHL1,USP1,USP4	darkgrey	VSMC_M8
GO:1902743	0.45	0.75	4	45	regulation of lamellipodium organization	BP	1	CD44,RAC1,FSCN1,PDPN	darkgrey	VSMC_M8
GO:0006520	0.45	0.65	18	224	cellular amino acid metabolic process	BP	1	NARS,VARS2,VARS,GCAT,CTPS1,GARS,ODC1,CAD,AFMID,AADAT,BCAT1,MTHFD1,ARG2,PFAS,RARS,GCLM,CTH,GART	darkgrey	VSMC_M8
GO:0000959	0.45	0.75	4	44	mitochondrial RNA metabolic process	BP	1	GRSF1,GARS,FASTKD3,ELAC2	darkgrey	VSMC_M8
GO:0031334	0.45	0.65	16	199	positive regulation of protein-containing complex assembly	BP	1	VCP,CDC42EP4,TERF1,CKAP5,ICE1,EIF4G1,TFRC,DHX33,RAC1,FSCN1,BID,CDT1,TPPP3,ARPC4,ARF6,GBP5	darkgrey	VSMC_M8
GO:0043068	0.45	0.62	33	422	positive regulation of programmed cell death	BP	1	BCLAF1,MELK,HOXA5,CASP2,NET1,E2F1,PPID,TRIM35,CTNNBL1,MYBL2,HMGCR,EEF1E1,MNDA,PAK2,FOSL1,DDX20,PPP2R1B,BARD1,MYBBP1A,ECT2,MSX1,TOP2A,EIF5A,BID,EIF2S1,PRELID1,PTRH2,AIFM1,TFAP4,RNPS1,TP73,PIK3CD,PDCD2	darkgrey	VSMC_M8
GO:0010822	0.46	0.72	5	59	positive regulation of mitochondrion organization	BP	1	PLAUR,PGAM5,BID,SLC25A5,AURKA	darkgrey	VSMC_M8

GO:0045892	0.46	0.59	74	943	negative regulation of transcription, DNA-templated	BP	1	BCLAF1,EZR,TRIM28,EZH2,PHF19,RUVBL2,FOSB,SRSF2,BIRC5,E2F7,PCNA,ZNF703,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,HMGB2,MSC,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,PHC2,GMNN,KHDRBS1,PRMT5,DDX5,HINFP,CENPF,STRAP,PSMC5,DDX20,SF1,BRCA1,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,HDGF,MAZ,AURKB,PLK1,ILF3,DNMT1,UHRF1,TFAP4,NOC2L,FAM129B,CBFB,DEPDC1,DRAP1,MBD2	darkgrey	VSMC_M8
GO:0010718	0.46	0.73	4	45	positive regulation of epithelial to mesenchymal transition	BP	1	EZH2,ZNF703,PDPN,COL1A1	darkgrey	VSMC_M8
GO:0018393	0.46	0.66	11	134	internal peptidyl-lysine acetylation	BP	1	RUVBL2,RUVBL1,CHEK1,NAA50,MCM3AP,HAT1,BRCA1,MORF4L2,TADA2A,NOC2L,POLE3	darkgrey	VSMC_M8
GO:0007005	0.46	0.61	33	436	mitochondrion organization	BP	1	MTFR2,FAM49B,HSPA9,CHCHD3,SAE1,CHCHD4,TOMM40,PLAUR,PGAM5,HGF,CEP89,TOMM70,BAP1,NDUFAF1,FASTKD3,TFRC,NDUFS1,DNA2,GABPB1,BID,PRELID1,LMNA,TIMM8A,TOP3A,TIMM44,SLC25A5,POLDIP2,AIFM1,GCLM,AURKA,BLOC1S2,PID1,UBE2J2	darkgrey	VSMC_M8
GO:0015914	0.47	0.70	6	70	phospholipid transport	BP	1	MFSD2A,KCNN4,DBI,PITPNB,PRELID1,XKR5	darkgrey	VSMC_M8
GO:0008284	0.47	0.59	53	681	positive regulation of cell population proliferation	BP	1	CDK2,DDX39B,FBXO5,CDCA7L,TTK,CLEC11A,EZH2,PRMT1,NAMPT,CCNA2,RNASEH2B,SPHK1,CDC20,BIRC5,NAP1L1,CDC25B,ZNF703,CCNB1,KIF20B,E2F1,CCNE1,HMGB2,FAM98B,TBX3,HMGCR,NRAS,NOLC1,ETS1,KIF14,ASPM,XBP1,PRC1,CDK1,TFRC,FOSL1,DHX9,EPHB2,MNAT1,FOXM1,HNRNPU,CDC6,IQGAP3,EFNB1,NES,MAZ,DNMT1,SLC25A5,EMP2,PIK3CD,HAS2,SAAL1,PDCD2,PID1	darkgrey	VSMC_M8
GO:1903507	0.47	0.58	74	945	negative regulation of nucleic acid-templated transcription	BP	1	BCLAF1,EZR,TRIM28,EZH2,PHF19,RUVBL2,FOSB,SRSF2,BIRC5,E2F7,PCNA,ZNF703,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,HMGB2,MSC,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,PHC2,GMNN,KHDRBS1,PRMT5,DDX5,HINFP,CENPF,STRAP,PSMC5,DDX20,SF1,BRCA1,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,HDGF,MAZ,AURKB,PLK1,ILF3,DNMT1,UHRF1,TFAP4,NOC2L,FAM129B,CBFB,DEPDC1,DRAP1,MBD2	darkgrey	VSMC_M8
GO:0034394	0.47	0.71	5	59	protein localization to cell surface	BP	1	HSP90AB1,EMP2,TOR1A,ARF6,USP4	darkgrey	VSMC_M8
GO:0007623	0.47	0.64	13	160	circadian rhythm	BP	1	THRAP3,EZH2,NAMPT,NRIP1,PRMT5,CDK1,HNRNPR,MYBBP1A,SUV39H1,HNRNPU,TOP2A,TYMS,HNRNPD	darkgrey	VSMC_M8
GO:0002244	0.47	0.67	8	96	hematopoietic progenitor cell differentiation	BP	1	HSPA9,PUS7,SIPA1L3,ESCO2,AGPAT5,ANKLE1,TOP2A,PDCD2	darkgrey	VSMC_M8
GO:1902679	0.47	0.58	74	946	negative regulation of RNA biosynthetic process	BP	1	BCLAF1,EZR,TRIM28,EZH2,PHF19,RUVBL2,FOSB,SRSF2,BIRC5,E2F7,PCNA,ZNF703,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,HMGB2,MSC,NRIP1,LOXL3,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,YWHAB,BAP1,RUNX1,MDM4,NCOA5,PHC2,GMNN,KHDRBS1,PRMT5,DDX5,HINFP,CENPF,STRAP,PSMC5,DDX20,SF1,BRCA1,NSD2,MYBBP1A,CREG1,SUV39H1,SIX4,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,HDGF,MAZ,AURKB,PLK1,ILF3,DNMT1,UHRF1,TFAP4,NOC2L,FAM129B,CBFB,DEPDC1,DRAP1,MBD2	darkgrey	VSMC_M8
GO:1990090	0.47	0.73	4	46	cellular response to nerve growth factor stimulus	BP	1	CDC5L,EIF4A3,E2F1,ARF6	darkgrey	VSMC_M8
GO:0034620	0.47	0.68	7	86	cellular response to unfolded protein	BP	1	HSPA9,VCP,CREB3L1,PPP1R15B,XBP1,EIF2S1,CTH	darkgrey	VSMC_M8
GO:0071384	0.48	0.72	4	46	cellular response to corticosteroid stimulus	BP	1	HEY1,HNRNPU,AIFM1,TFAP4	darkgrey	VSMC_M8
GO:0006475	0.48	0.64	11	136	internal protein amino acid acetylation	BP	1	RUVBL2,RUVBL1,CHEK1,NAA50,MCM3AP,HAT1,BRCA1,MORF4L2,TADA2A,NOC2L,POLE3	darkgrey	VSMC_M8
GO:0031050	0.48	0.72	4	46	dsRNA processing	BP	1	HNRNPA2B1,DDX5,DGCR8,SRRT	darkgrey	VSMC_M8
GO:0035196	0.48	0.72	4	46	production of miRNAs involved in gene silencing by miRNA	BP	1	HNRNPA2B1,DDX5,DGCR8,SRRT	darkgrey	VSMC_M8
GO:0070918	0.48	0.72	4	46	production of small RNA involved in gene silencing by RNA	BP	1	HNRNPA2B1,DDX5,DGCR8,SRRT	darkgrey	VSMC_M8
GO:2000117	0.48	0.70	5	60	negative regulation of cysteine-type endopeptidase activity	BP	1	PLAUR,BIRC5,HGF,CD44,PAK2	darkgrey	VSMC_M8
GO:0008037	0.49	0.66	8	97	cell recognition	BP	1	CCT2,TCP1,CCT4,CCT8,CCT7,CCT5,EPHB2,CCT3	darkgrey	VSMC_M8
GO:0010950	0.49	0.64	10	127	positive regulation of endopeptidase activity	BP	1	VCP,ANP32B,CYCS,CASP2,PSMD14,BID,PRELID1,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:0031349	0.49	0.62	14	177	positive regulation of defense response	BP	1	MATR3,POLR3B,POLR3F,VAMP8,HMGB2,TOMM70,SETD4,ETS1,MNDA,RBM14,PAK2,DHX9,UBE2K,GBP5	darkgrey	VSMC_M8
GO:1990089	0.49	0.71	4	47	response to nerve growth factor	BP	1	CDC5L,EIF4A3,E2F1,ARF6	darkgrey	VSMC_M8
GO:0046578	0.49	0.62	13	161	regulation of Ras protein signal transduction	BP	1	NUP62,NET1,ARHGDIA,PSD4,KIF14,CDC42SE1,ARFGAP1,EPHB2,FOXM1,RAC1,LRRC59,ARF6,STMN1	darkgrey	VSMC_M8

GO:0006793	0.49	0.54	167	2169	phosphorus metabolic process	BP	1	CDK2,ALPK2,ATP5F1B,PRRC1,NUS1,CDC25C,SRPK1,PPP2R5D,PWP1,APTX,DBF4,TJP2,VCP,HSP90AB1,CKS2,PAICS,MELK,TRIM28,NANS,PPP6R1,CTPS1,TTK,DCK,MFSD2A,GARS,EZH2,NUP62,CLSPN,PLK4,NAMPT,CCNA2,CHORDC1,RNASEH2B,PPP5C,MASTL,MAST2,PLAUR,CAD,DBI,BORA,AXL,SPHK1,ULK4,NCAPG2,TK1,AFMID,BIRC5,PGS1,GTPBP4,IPO5,CHMP6,RRM1,PGAM5,CDC25B,HGF,CCNB1,CD44,BUB1,TPX2,SLC20A1,PDHB,SGK3,WEE1,HSP90B1,PPIP5K2,CCNE1,PXYLP1,AADAT,PBK,AGPAT5,RBL1,BUB1B,CCNL1,RSRC1,CDCA2,NT5DC2,RAD51,CCNE2,ENTPD7,YWHAB,HMGCR,CHUK,PPP1R15B,CIT,GCN1,CHEK1,CENPE,KIF14,UNG,ELOVL6,PRKAR2A,NEK2,NF2,BLM,UMPS,CEP85,EIF4G1,CDK1,CDC25A,TFRC,PDHA1,PAK2,UAP1,UCK2,GK,DLAT,PPP2R1B,BARD1,DUT,EPHB2,MCM7,CNOT9,CDKN3,CDK16,ECT2,MNAT1,MAPK6,EIF2AK1,FAM220A,RAC1,HNRNPU,UCHL1,INCENP,ADIPOR2,UBE2K,MTHFD1,UGDH,CCNB3,CDC6,EIF2S1,DCTPP1,CCNB2,IQGAP3,ALOX15B,AURKB,PFAS,SPAG9,PLK1,ILF3,VRK1,PRPS1,ACSL4,TYMS,NNT,RAP2C,EMP2,LIPG,TFAP4,SMG6,PKMYT1,HASPIN,CCNF,G6PD,PTBP1,PIK3CD,DOLPP1,PKN3,NEK6,PDP2,CDKN2C,ACSL3,AURKA,ERP29,PID1,GART,PRPSAP1,DUSP7	darkgrey	VSMC_M8
GO:0071496	0.49	0.60	21	267	cellular response to external stimulus	BP	1	MIOS,MFSD2A,CASP2,NAMPT,AXL,ARHGDIA,RRP8,SNAI2,GCN1,CHEK1,XBP1,EIF4G1,FOSL1,MYBBP1A,RAC1,EIF2S1,NUDT1,DCTPP1,COL1A1,BRIP1,AIFM1	darkgrey	VSMC_M8
GO:0006839	0.49	0.61	16	210	mitochondrial transport	BP	1	ATP5F1B,SAE1,CHCHD4,TOMM40,TOMM70,BAP1,SFXN3,SFXN4,FLVCR1,BID,TIMM8A,TIMM44,SLC25A5,AIFM1,BLOC1S2,UBE2J2	darkgrey	VSMC_M8
GO:0061515	0.49	0.69	5	59	myeloid cell development	BP	1	PABPC4,FLVCR1,LYAR,G6PD,TMOD3	darkgrey	VSMC_M8
GO:0006790	0.49	0.60	21	270	sulfur compound metabolic process	BP	1	SLC35D2,HSPA9,B3GNT2,AMD1,SLC25A19,PDHB,AADAT,SLC10A7,ELOVL6,PDHA1,DLAT,SLC19A2,MTHFD1,UGDH,CIAO2A,ACSL4,XYLT1,G6PD,GCLM,CTH,ACSL3	darkgrey	VSMC_M8
GO:0021766	0.50	0.69	5	59	hippocampus development	BP	1	MFSD2A,EZH2,XRN2,KIF14,NF2	darkgrey	VSMC_M8
GO:2000116	0.50	0.62	13	167	regulation of cysteine-type endopeptidase activity	BP	1	VCP,ANP32B,CYCS,CASP2,PLAUR,BIRC5,HGF,CD44,PAK2,BID,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:0006511	0.50	0.57	42	542	ubiquitin-dependent protein catabolic process	BP	1	CDK2,MAN1A1,DESI1,VCP,HSP90AB1,CDC20,CHFR,PSMD13,CDC16,ANAPC1,HSP90B1,PBK,BAP1,UBE2C,PSMD14,KIF14,XBP1,DTL,PSMD4,PSMC5,SMARCC1,PSMA6,UFD1,USP42,UCHL1,UBE2K,NEDD4,PSMD3,RAD23A,PLK1,PSMD11,COPS3,USP1,UHRF1,CCNF,ZNF598,PSMA5,USP4,AURKA,UBE2S,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0019693	0.50	0.59	24	312	ribose phosphate metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,CTPS1,RNASEH2B,CAD,PDHB,AADAT,ENTPD7,HMGCR,ELOVL6,UMPS,PDHA1,UCK2,DLAT,PFAS,PRPS1,ACSL4,G6PD,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0009166	0.50	0.68	5	61	nucleotide catabolic process	BP	1	VCP,ENTPD7,UNG,DUT,DCTPP1	darkgrey	VSMC_M8
GO:0019080	0.50	0.65	7	86	viral gene expression	BP	1	NUCKS1,SSB,DHX9,EIF3B,TFAP4,PTBP1,SPCS3	darkgrey	VSMC_M8
GO:0009566	0.50	0.63	9	113	fertilization	BP	1	CCT2,TCP1,CCT4,AAAS,CCT8,CCT7,CCT5,CDK1,CCT3	darkgrey	VSMC_M8
GO:0043407	0.50	0.70	4	47	negative regulation of MAP kinase activity	BP	1	NUP62,HMGCR,UCHL1,DUSP7	darkgrey	VSMC_M8
GO:1901564	0.50	0.52	365	4789	organonitrogen compound metabolic process	BP	1	CDK2,ALPK2,NARS,ATP5F1B,MRPS18B,VARS2,DDX39B,FBXO5,PRRC1,VARS,EZR,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,DESI1,SLC35D2,CDC25C,FKBP5,SRPK1,GCAT,PPP2R5D,PWP1,MRPL2,DBF4,TJP2,ALDH1L2,CYP51A1,VCP,HSP90AB1,PUM3,CKS2,PAICS,MELK,TRIM28,NCBP1,ANP32B,PPIH,U2AF2,PPP6R1,CTPS1,TTK,CYCS,DCK,MFSD2A,SYNCRIP,PPIE,PABPC4,GARS,B3GNT2,EZH2,ODC1,NUP62,MRPL32,CLSPN,PHF19,PRMT1,CASP2,NAA15,NRDC,RUVBL2,PLK4,AMD1,NAMPT,PUS7,RUVBL1,CCNA2,RPN1,SAE1,CHORDC1,NAALAD2,PPP5C,MASTL,MAST2,CHCHD4,COG3,GRIN2C,PRCP,MRPL58,PLAUR,MRPS7,SLC25A19,CAD,ALG8,DBI,TRIM47,BORA,DIS3,AXL,RNF157,SPHK1,ULK4,NCAPG2,CDC20,TK1,AFMID,BIRC5,SERPINH1,PARP2,FBL,RRBP1,GTPBP4,RAD18,IPO5,EIF4A3,CHMP6,RRM1,CHFR,EXOSC8,PGAM5,CDC25B,METAP2,DCUN1D2,HGF,PSMD13,CDC16,USPL1,CCNB1,SNRPB,CD44,ESPL1,MRPS5,BUB1,TPX2,ANAPC1,GGH,UBA2,CWC27,PDHB,ADAMTS6,SGK3,EIF3M,WEE1,HSP90B1,NECAB3,EIF2B1,ABCE1,CCNE1,PXYLP1,AADAT,SLC10A7,GALNT6,LOXL3,PBK,ESCO2,SELENOT,FAM98B,PPID,TRIM35,BUB1B,CCNL1,RSRC1,CDCA2,GNL3,FAM83D,RAD51,CCNE2,TRIM33,ENTPD7,YWHAB,HMGCR,BAP1,EEF1E1,CHUK,RUNX1,SETD4,PPP1R15B,HR,MDM4,UBE2C,PSMD14,NOLC1,CIT,FASTKD3,GCN1,METAP1,TENT4A,UBE2T,CHEK1,NAA50,KHDRBS1,STT3A,CENPE,NCL,TRAIP,KIF14,UNG,PRMT5,BCAT1,ELOVL6,FANCI,XBP1,SPP2,UTP25,MCM3AP,EIF4H,PRKAR2A,NEK2,DTL,NF2,HMBS,FLVCR1,BLM,UMPS,RBM14,PSMD4,CEP85,EIF4G1,MRPL11,PSMC5,ADAMTS4,HAT1,CDK1,CDC25A,TFRC,PDHA1,PAK2,SMARCC1,DHX9,HNRNPR,PSMA6,UCK2,DLAT,FANCM,ADAMTS14,LRP1,PPP2R1B,BARD1,DUT,EPHB2,HE	darkgrey	VSMC_M8
GO:0015980	0.51	0.59	19	259	energy derivation by oxidation of organic compounds	BP	1	ATP5F1B,MTFR2,CYC1,VCP,CYCS,CCNB1,PDHB,SUCLG1,NDUFAF1,CDK1,PDHA1,NDUFS1,DLAT,MYBBP1A,FH,BID,PRELID1,NNT,PID1	darkgrey	VSMC_M8
GO:0032612	0.51	0.67	5	62	interleukin-1 production	BP	1	PANX2,SPHK1,MNDA,ARG2,GBP5	darkgrey	VSMC_M8
GO:0032652	0.51	0.67	5	62	regulation of interleukin-1 production	BP	1	PANX2,SPHK1,MNDA,ARG2,GBP5	darkgrey	VSMC_M8
GO:0048525	0.51	0.67	5	61	negative regulation of viral process	BP	1	SRPK1,TRIM28,TRIM35,ILF3,TRIM59	darkgrey	VSMC_M8
GO:0016126	0.51	0.69	4	49	sterol biosynthetic process	BP	1	CYP51A1,HMGCR,LBR,G6PD	darkgrey	VSMC_M8
GO:0006605	0.51	0.58	20	262	protein targeting	BP	1	MAN1A1,SEC61A1,SAE1,CHCHD4,TOMM40,SRP68,TRAM1,TOMM70,YWHAB,BAP1,RAB27A,NEDD4,BID,LTBP2,TIMM8A,TIMM44,MTCL1,AIFM1,SPCS3,UBE2J2	darkgrey	VSMC_M8
GO:0002702	0.51	0.65	6	75	positive regulation of production of molecular mediator of immune response	BP	1	RBP4,XBP1,TFRC,DDX21,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0001909	0.52	0.67	5	61	leukocyte mediated cytotoxicity	BP	1	TUBB,FAM49B,RAB27A,EMP2,TUBB4B	darkgrey	VSMC_M8
GO:0003281	0.52	0.67	5	60	ventricular septum development	BP	1	MATR3,HEY1,TBX3,MDM4,NSD2	darkgrey	VSMC_M8
GO:0033273	0.52	0.65	6	75	response to vitamin	BP	1	SRSF2,SNAI2,COL1A1,BRIP1,TYMS,NNT	darkgrey	VSMC_M8

GO:0048732	0.52	0.57	26	335	gland development	BP	1	DDX39B,HOXA5,EZH2,PGR,CAD,E2F7,PCNA,ZNF703,HGF,TBX3,E2F8,ETS1,PRMT5,XBP1,UMPS,SMARCC1,SIX4,MSX1,SRSF5,CCNB2,IQGAP3,ALOX15B,TYMS,ARF6,HNRNPD,AURKA	darkgrey	VSMC_M8
GO:0051100	0.52	0.61	10	129	negative regulation of binding	BP	1	GTPBP4,EIF4A3,E2F1,HEY1,NEK2,MSX1,NES,AURKB,TFAP4,AURKA	darkgrey	VSMC_M8
GO:0030879	0.52	0.62	9	114	mammary gland development	BP	1	HOXA5,PGR,CAD,ZNF703,TBX3,XBP1,UMPS,MSX1,IQGAP3	darkgrey	VSMC_M8
GO:0033865	0.52	0.62	8	102	nucleoside bisphosphate metabolic process	BP	1	PDHB,AADAT,HMGCR,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0033875	0.52	0.62	8	102	ribonucleoside bisphosphate metabolic process	BP	1	PDHB,AADAT,HMGCR,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0034032	0.52	0.62	8	102	purine nucleoside bisphosphate metabolic process	BP	1	PDHB,AADAT,HMGCR,ELOVL6,PDHA1,DLAT,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0031113	0.53	0.68	4	49	regulation of microtubule polymerization	BP	1	CKAP5,FKBP4,RAC1,STMN1	darkgrey	VSMC_M8
GO:0061614	0.53	0.68	4	48	pri-miRNA transcription by RNA polymerase II	BP	1	GNL3,ETS1,DDX5,FOSL1	darkgrey	VSMC_M8
GO:0006414	0.53	0.68	4	50	translational elongation	BP	1	EIF4A3,SELENOT,EIF5A,ZNF598	darkgrey	VSMC_M8
GO:0034976	0.53	0.57	17	222	response to endoplasmic reticulum stress	BP	1	MAN1A1,VCP,HSP90B1,CREB3L1,PPP1R15B,MANF,XBP1,EIF4G1,UFD1,UBE2K,BID,EIF2S1,AIFM1,TOR1A,CTH,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:0052126	0.53	0.60	10	127	movement in host environment	BP	1	TRIM28,SLC1A5,AXL,VAMP8,PPID,TRIM35,NUP153,CDK1,TFRC,TRIM59	darkgrey	VSMC_M8
GO:0051865	0.53	0.65	5	62	protein autoubiquitination	BP	1	RNF157,RAD18,UBE2T,BRCA1,UHRF1	darkgrey	VSMC_M8
GO:0006979	0.53	0.55	27	357	response to oxidative stress	BP	1	PSIP1,APTX,MELK,EZH2,SDC1,PPP5C,AXL,SPHK1,NET1,PCNA,HGF,CHUK,PPP1R15B,ETS1,CDK1,FOSL1,TRA2B,ECT2,EIF2S1,NUDT1,COL1A1,HNRNPM,AIFM1,G6PD,TOR1A,GCLM,SIGMAR1	darkgrey	VSMC_M8
GO:2000177	0.54	0.65	5	62	regulation of neural precursor cell proliferation	BP	1	SHCBP1,NAP1L1,ASPM,NF2,NES	darkgrey	VSMC_M8
GO:0019941	0.54	0.53	42	550	modification-dependent protein catabolic process	BP	1	CDK2,MAN1A1,DESI1,VCP,HSP90AB1,CDC20,CHFR,PSMD13,CDC16,ANAPC1,HSP90B1,PBK,BAP1,UBE2C,PSMD14,KIF14,XBP1,DTL,PSMD4,PSMC5,SMARCC1,PSMA6,UFD1,USP42,UCHL1,UBE2K,NEDD4,PSMD3,RAD23A,PLK1,PSMD11,COPS3,USP1,UHRF1,CCNF,ZNF598,PSMA5,USP4,AURKA,UBE2S,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:2001056	0.54	0.61	8	105	positive regulation of cysteine-type endopeptidase activity	BP	1	VCP,ANP32B,CYCS,CASP2,BID,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:0008333	0.54	0.66	4	50	endosome to lysosome transport	BP	1	HMGXB4,VCP,RNF157,HOOK1	darkgrey	VSMC_M8
GO:0071702	0.54	0.49	144	1891	organic substance transport	BP	1	TMED9,XPOT,NUP43,NUP107,DDX39B,EZR,TCP1,NUP50,NUS1,ARFGAP3,MAN1A1,DESI1,RANGAP1,KIF20A,SLC35D2,HSPA9,SRSF3,TNPO3,CYP51A1,VCP,HSP90AB1,TRIM28,NCBP1,ANP32B,HNRNPA2B1,MFSD2A,NUP205,NUP62,NBAS,SEC61A1,SAE1,SLC1A5,CHCHD4,NASP,COG3,TOMM40,PREB,KCNN4,NUP85,SLC25A19,SLC5A6,DBI,SRP68,GDI2,SEC23B,RRBP1,IPO5,EIF4A3,CHMP6,ALYREF,AAAS,KIF20B,HSP90B1,NECAB3,VAMP8,SLC10A7,TRAM1,RBP4,NUP160,SELENOT,PPID,CKAP5,NUP93,TOMM70,YWHAB,HMGCR,BAP1,SFXN3,HEATR3,NOLC1,NUP153,KIF18A,NSUN2,ICE1,KHDRBS1,CSE1L,PITPNB,XBP1,MCM3AP,IPO4,SFXN4,NUP133,SEC24D,FLVCR1,SSB,ARCN1,CENPF,SLC17A9,ARFGAP1,CDK1,HDLBP,TFRC,DHX9,LSG1,HNRNPA3,ZW10,BARD1,NMD3,UFD1,CDK16,SLBP,SLC19A2,ANKLE1,ECT2,RAC1,KDELR2,MYO5A,RAB27A,ADIPOR2,NEDD4,EIF5A,BID,DDX39A,PRELID1,LMNA,LTBP2,COL1A1,TIMM8A,SYT4,NUP62CL,ACSL4,TIMM44,SLC25A5,MTCL1,AIFM1,HOOK1,LIPG,NDC1,SMG6,THOC6,SLC6A17,TOR1A,NUP188,GLE1,ACD,ARF6,SPCS3,ACSL3,SRSF7,SIGMAR1,ERP29,XKR5,PID1,UBE2J2	darkgrey	VSMC_M8
GO:0010611	0.54	0.66	4	51	regulation of cardiac muscle hypertrophy	BP	1	DDX39B,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0051058	0.54	0.66	4	49	negative regulation of small GTPase mediated signal transduction	BP	1	FAM49B,NUP62,EPHB2,STMN1	darkgrey	VSMC_M8
GO:0006796	0.55	0.49	164	2150	phosphate-containing compound metabolic process	BP	1	CDK2,ALPK2,ATP5F1B,PRRC1,NUS1,CDC25C,SRPK1,PPP2R5D,PWP1,APTX,DBF4,TJP2,VCP,HSP90AB1,CKS2,PAICS,MELK,TRIM28,PPP6R1,CTPS1,TTK,DCK,MFSD2A,GARS,EZH2,NUP62,CLSPN,PLK4,NAMPT,CCNA2,CHORDC1,RNASEH2B,PPP5C,MASTL,MAST2,PLAUR,CAD,DBI,BORA,AXL,SPHK1,ULK4,NCAPG2,TK1,AFMID,BIRC5,PGS1,GTPBP4,IPO5,CHMP6,RRM1,PGAM5,CDC25B,HGF,CCNB1,CD44,BUB1,TPX2,SLC20A1,PDHB,SGK3,WEE1,HSP90B1,PPIP5K2,CCNE1,PXYLP1,AADAT,PBK,AGPAT5,RBL1,BUB1B,CCNL1,RSRC1,CDCA2,NT5DC2,RAD51,CCNE2,ENTPD7,YWHAB,HMGCR,CHUK,PPP1R15B,CIT,GCN1,CHEK1,CENPE,KIF14,UNG,ELOVL6,PRKAR2A,NEK2,NF2,BLM,UMPS,CEP85,EIF4G1,CDK1,CDC25A,TFRC,PDHA1,PAK2,UCK2,GK,DLAT,PPP2R1B,BARD1,DUT,EPHB2,MCM7,CNOT9,CDKN3,CDK16,ECT2,MNAT1,MAPK6,EIF2AK1,FAM220A,RAC1,HNRNPU,UCHL1,INCENP,ADIPOR2,UBE2K,MTHFD1,CCNB3,CDC6,EIF2S1,DCTPP1,CCNB2,IQGAP3,ALOX15B,AURKB,PFAS,SPAG9,PLK1,ILF3,VRK1,PRPS1,ACSL4,TYMS,NNT,RAP2C,EMP2,LIPG,TFAP4,SMG6,PKMYT1,HASPIN,CCNF,G6PD,PTBP1,PIK3CD,DOLPP1,PKN3,NEK6,PDP2,CDKN2C,ACSL3,AURKA,ERP29,PID1,GART,PRPSAP1,DUSP7	darkgrey	VSMC_M8
GO:1901983	0.55	0.64	5	63	regulation of protein acetylation	BP	1	RUVBL2,CHEK1,BRCA1,TADA2A,NOC2L	darkgrey	VSMC_M8

GO:0006351	0.55	0.49	193	2521	transcription, DNA-templated	BP	1	HNRNPAB,BCLAF1,NUP107,DDX39B,EZR,RAD21,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,POLR3B,POLR1C,CDC5L,CKS2,TRIM28,POLR1E,TWISTNB,CDCA7L,HOXA5,PPIE,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,NIFK,NUP85,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,ZNF703,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,POLR1B,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,PSMA6,DDX20,DDX21,SF1,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,NOC2L,RNPS1,TP73,POLR2E,REXO4,FANCA,FAM129B,CBFB,CTH,DEPDC1,SRRT,HNRNPD,DRAP1,HMGB3,ABT1,PID1,LIN52,HOXC8,MBD2	darkgrey	VSMC_M8
GO:0097659	0.55	0.48	193	2522	nucleic acid-templated transcription	BP	1	HNRNPAB,BCLAF1,NUP107,DDX39B,EZR,RAD21,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,POLR3B,POLR1C,CDC5L,CKS2,TRIM28,POLR1E,TWISTNB,CDCA7L,HOXA5,PPIE,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,PPP5C,FOSB,CD3EAP,NUFIP1,NIFK,NUP85,SPHK1,SRSF2,XRN2,NCAPG2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,ZNF703,HGF,ELK3,RRP8,TCERG1,USPL1,CBX5,SNAI2,TCEA1,POLR1B,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,PSMA6,DDX20,DDX21,SF1,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,NOC2L,RNPS1,TP73,POLR2E,REXO4,FANCA,FAM129B,CBFB,CTH,DEPDC1,SRRT,HNRNPD,DRAP1,HMGB3,ABT1,PID1,LIN52,HOXC8,MBD2	darkgrey	VSMC_M8
GO:0007586	0.55	0.63	5	63	digestion	BP	1	EZR,TJP2,KCNN4,RBP4,STRAP	darkgrey	VSMC_M8
GO:0009636	0.55	0.57	13	174	response to toxic substance	BP	1	SDC1,CCNB1,SELENOT,RAD51,CHUK,CDK1,DHX15,BRIP1,TYMS,NNT,AIFM1,NXN,SLC30A1	darkgrey	VSMC_M8
GO:0018394	0.55	0.57	11	143	peptidyl-lysine acetylation	BP	1	RUVBL2,RUVBL1,CHEK1,NAA50,MCM3AP,HAT1,BRCA1,MORF4L2,TADA2A,NOC2L,POLE3	darkgrey	VSMC_M8
GO:0051258	0.55	0.54	19	250	protein polymerization	BP	1	FBXO5,FAM49B,CDC42EP4,DIAPH3,TPX2,CENPJ,CKAP5,UBE2C,FKBP4,RAC1,UBE2K,NDE1,MAP7D3,TPPP3,ARPC4,ARF6,TMOD3,STMN1,UBE2S	darkgrey	VSMC_M8
GO:2000377	0.55	0.59	9	120	regulation of reactive oxygen species metabolic process	BP	1	PRCP,BRCA1,FOXM1,RAC1,RAB27A,ARG2,NNT,G6PD,PID1	darkgrey	VSMC_M8
GO:0001906	0.55	0.61	6	78	cell killing	BP	1	TUBB,FAM49B,HSP90AB1,RAB27A,EMP2,TUBB4B	darkgrey	VSMC_M8
GO:0002011	0.55	0.65	4	50	morphogenesis of an epithelial sheet	BP	1	CD44,PHACTR4,PDPN,TOR1A	darkgrey	VSMC_M8
GO:0052548	0.55	0.54	20	270	regulation of endopeptidase activity	BP	1	VCP,ANP32B,CYCS,CASP2,NRDC,PLAUR,BIRC5,SERPINH1,HGF,CD44,PSMD14,SPP2,PAK2,TFPI,BID,PRELID1,PTTG1,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:2001237	0.56	0.61	6	79	negative regulation of extrinsic apoptotic signaling pathway	BP	1	HGF,SNAI2,HMGB2,BRCA1,LMNA,GCLM	darkgrey	VSMC_M8
GO:0042440	0.56	0.63	5	65	pigment metabolic process	BP	1	PAICS,HMBS,FLVCR1,PRPS1,GART	darkgrey	VSMC_M8
GO:0001503	0.56	0.53	25	328	ossification	BP	1	ATP5F1B,FBXO5,FBN2,COL1A2,CLEC11A,SYNCRIP,FBL,RRBP1,GTPBP4,ALYREF,HGF,SNAI2,CREB3L1,RUNX1,DDX5,DHX9,DDX21,IFT80,MYBBP1A,HNRNPU,COL1A1,XYLT1,RSL1D1,RBMX,CBFB	darkgrey	VSMC_M8
GO:0061053	0.56	0.63	5	63	somite development	BP	1	LOXL3,NUP133,SIX4,MTHFD1,PALB2	darkgrey	VSMC_M8
GO:0014743	0.56	0.64	4	52	regulation of muscle hypertrophy	BP	1	DDX39B,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0021549	0.56	0.61	6	77	cerebellum development	BP	1	TTLL1,EZH2,KIF14,ARCN1,HNRNPD,GART	darkgrey	VSMC_M8

GO:0006464	0.56	0.47	218	2859	cellular protein modification process	BP	1	CDK2,ALPK2,FBXO5,PRRC1,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,DESI1,CDC25C,FKBP5,SRPK1,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,PUM3,CKS2,MELK,TRIM28,PPIH,U2AF2,PPP6R1,TTK,PPIE,B3GNT2,EZH2,NUP62,CLSPN,PHF19,PRMT1,NAA15,RUVBL2,PLK4,RUVBL1,CCNA2,RPN1,SAE1,CHORDC1,PPP5C,MASTL,MAST2,CHCHD4,COG3,PLAUR,CAD,ALG8,DBI,TRIM47,BORA,AXL,RNF157,SPHK1,ULK4,NCAPG2,CDC20,BIRC5,PARP2,FBL,GTPBP4,RAD18,IPO5,CHMP6,CHFR,PGAM5,CDC25B,METAP2,DCUN1D2,HGF,CDC16,USPL1,CCNB1,SNRPB,CD44,BUB1,TPX2,ANAPC1,UBA2,CWC27,SGK3,WEE1,HSP90B1,CCNE1,GALNT6,LOXL3,PBK,ESCO2,FAM98B,PPID,TRIM35,BUB1B,CCNL1,RSRC1,CDCA2,GNL3,RAD51,CCNE2,TRIM33,YWHAB,HMGCR,BAP1,CHUK,SETD4,PPP1R15B,HR,UBE2C,PSMD14,CIT,METAP1,UBE2T,CHEK1,NAA50,STT3A,CENPE,TRAIP,KIF14,PRMT5,FANCI,MCM3AP,PRKAR2A,NEK2,DTL,NF2,HMBS,BLM,RBM14,CEP85,EIF4G1,HAT1,CDK1,CDC25A,TFRC,PAK2,FANCM,LRR1,PPP2R1B,BARD1,EPHB2,BRCA1,CDCA3,CNOT9,CDKN3,NSD2,CDK16,DCUN1D5,ECT2,AIPL1,SUV39H1,FKBP4,MNAT1,MAPK6,EIF2AK1,USP42,FAM220A,RAC1,DESI2,UCHL1,INCENP,ADIPOR2,UBE2K,NEDD4,CCNB3,CDC6,EIF2S1,DCAF15,CCNB2,IQGAP3,LMNA,AURKB,PPIB,SPAG9,PLK1,ILF3,MORF4L2,VRK1,DNMT1,TADA2A,COPS3,NNT,WDR70,USP1,RAP2C,UHRF1,EMP2,NXN,TFAP4,PKMYT1,NOC2L,HASPIN,CCNF,THOP1,ZNF598,G6PD,PTBP1,PIK3CD,TOR1A,DOLPP1,PKN3,NEK6,CBFB,PDP2,CTH,GMPPB,USP4,MAD2L1,CDKN2C,AURKA,UBE2S,CSKMT,ERP29,POLE3,PJA1,PID1,TRIM59,DUSP7,UBE2J2	darkgrey	VSMC_M8
GO:0036211	0.56	0.47	218	2859	protein modification process	BP	1	CDK2,ALPK2,FBXO5,PRRC1,DSCC1,TTLL1,NUS1,MAN1A1,MTBP,DESI1,CDC25C,FKBP5,SRPK1,PPP2R5D,PWP1,DBF4,VCP,HSP90AB1,PUM3,CKS2,MELK,TRIM28,PPIH,U2AF2,PPP6R1,TTK,PPIE,B3GNT2,EZH2,NUP62,CLSPN,PHF19,PRMT1,NAA15,RUVBL2,PLK4,RUVBL1,CCNA2,RPN1,SAE1,CHORDC1,PPP5C,MASTL,MAST2,CHCHD4,COG3,PLAUR,CAD,ALG8,DBI,TRIM47,BORA,AXL,RNF157,SPHK1,ULK4,NCAPG2,CDC20,BIRC5,PARP2,FBL,GTPBP4,RAD18,IPO5,CHMP6,CHFR,PGAM5,CDC25B,METAP2,DCUN1D2,HGF,CDC16,USPL1,CCNB1,SNRPB,CD44,BUB1,TPX2,ANAPC1,UBA2,CWC27,SGK3,WEE1,HSP90B1,CCNE1,GALNT6,LOXL3,PBK,ESCO2,FAM98B,PPID,TRIM35,BUB1B,CCNL1,RSRC1,CDCA2,GNL3,RAD51,CCNE2,TRIM33,YWHAB,HMGCR,BAP1,CHUK,SETD4,PPP1R15B,HR,UBE2C,PSMD14,CIT,METAP1,UBE2T,CHEK1,NAA50,STT3A,CENPE,TRAIP,KIF14,PRMT5,FANCI,MCM3AP,PRKAR2A,NEK2,DTL,NF2,HMBS,BLM,RBM14,CEP85,EIF4G1,HAT1,CDK1,CDC25A,TFRC,PAK2,FANCM,LRR1,PPP2R1B,BARD1,EPHB2,BRCA1,CDCA3,CNOT9,CDKN3,NSD2,CDK16,DCUN1D5,ECT2,AIPL1,SUV39H1,FKBP4,MNAT1,MAPK6,EIF2AK1,USP42,FAM220A,RAC1,DESI2,UCHL1,INCENP,ADIPOR2,UBE2K,NEDD4,CCNB3,CDC6,EIF2S1,DCAF15,CCNB2,IQGAP3,LMNA,AURKB,PPIB,SPAG9,PLK1,ILF3,MORF4L2,VRK1,DNMT1,TADA2A,COPS3,NNT,WDR70,USP1,RAP2C,UHRF1,EMP2,NXN,TFAP4,PKMYT1,NOC2L,HASPIN,CCNF,THOP1,ZNF598,G6PD,PTBP1,PIK3CD,TOR1A,DOLPP1,PKN3,NEK6,CBFB,PDP2,CTH,GMPPB,USP4,MAD2L1,CDKN2C,AURKA,UBE2S,CSKMT,ERP29,POLE3,PJA1,PID1,TRIM59,DUSP7,UBE2J2	darkgrey	VSMC_M8
GO:0032611	0.56	0.64	4	52	interleukin-1 beta production	BP	1	SPHK1,MNDA,ARG2,GBP5	darkgrey	VSMC_M8
GO:0032651	0.56	0.64	4	52	regulation of interleukin-1 beta production	BP	1	SPHK1,MNDA,ARG2,GBP5	darkgrey	VSMC_M8
GO:0008625	0.57	0.62	5	67	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	HGF,HMGB2,BRCA1,BID,BLOC1S2	darkgrey	VSMC_M8
GO:0032963	0.57	0.60	6	78	collagen metabolic process	BP	1	COL1A2,SERPINH1,CREB3L1,RUNX1,ADAMTS14,COL1A1	darkgrey	VSMC_M8
GO:0048863	0.57	0.55	13	171	stem cell differentiation	BP	1	PHF5A,HSPA9,PWP1,PHF19,PUS7,SNAI2,NOLC1,NSUN2,PHACTR4,MSX1,HNRNPU,EFNB1,PSMD11	darkgrey	VSMC_M8
GO:0035556	0.57	0.47	157	2063	intracellular signal transduction	BP	1	CDK2,BCLAF1,DDX39B,EZR,GTSE1,FAM49B,SRPK1,HSP90AB1,CDC5L,COL1A2,MIOS,MELK,TRIM28,MSH6,TTK,EZH2,NUP62,CLSPN,PRMT1,CASP2,ORC1,GEN1,CCNA2,AMOTL1,RNASEH2B,PPP5C,MASTL,MAST2,CDC42EP4,GRIN2C,PLAUR,AXL,RNF157,SPHK1,FANCD2,ULK4,GDI2,NET1,E2F7,DOCK9,ARHGDIA,SIPA1L3,CHFR,HGF,TOPBP1,RRP8,CCNB1,SNAI2,CD44,BUB1,DEPDC1B,SLC20A1,PSD4,SGK3,E2F1,KNTC1,CEP55,HELLS,ARHGAP11A,RACGAP1,PBK,BUB1B,FAM83D,CREB3L1,MTDH,HMGCR,NRAS,EEF1E1,CHUK,MDM4,PAK1IP1,CIT,NSUN2,CHEK1,RASSF1,TRIP13,KIF14,RGS9,PRMT5,EFS,RAD9A,DDX5,PHACTR4,XBP1,TICRR,RPA2,PRKAR2A,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,CDC42SE1,CENPF,BUB3,ARFGAP1,CDK1,TFRC,PAK2,WDR76,DNA2,ZW10,DDX21,EPHB2,CDC45,UFD1,BRCA1,MYBBP1A,ECT2,ZWINT,DHX33,MAPK6,FOXM1,MSX1,RAC1,UCHL1,UBE2K,NEDD4,CDC6,EIF5A,BID,PDPN,IQGAP3,MAZ,SPDL1,AURKB,LRRC59,SPAG9,ZWILCH,PLK1,BRIP1,DNMT1,NDC80,AIFM1,RAP2C,TFAP4,NOC2L,HASPIN,TP73,PTBP1,PIK3CD,CDT1,PKN3,NEK6,PLEKHG4,CTH,DEPDC1,ARF6,RAPGEF6,MAD2L1,STMN1,AURKA,ERP29,TRIM59,DUSP7	darkgrey	VSMC_M8
GO:0035051	0.57	0.57	9	119	cardiocyte differentiation	BP	1	ALPK2,DDX39B,PARP2,CCNB1,TBX3,CDK1,HNRNPU,LMNA,G6PD	darkgrey	VSMC_M8
GO:0035265	0.57	0.56	10	134	organ growth	BP	1	DDX39B,PARP2,CCNB1,RBP4,RUNX1,FLVCR1,CDK1,IFT80,TP73,G6PD	darkgrey	VSMC_M8
GO:1903321	0.57	0.60	6	82	negative regulation of protein modification by small protein conjugation or removal	BP	1	FBXO5,U2AF2,GTPBP4,NXN,USP4,MAD2L1	darkgrey	VSMC_M8
GO:0002931	0.57	0.63	4	51	response to ischemia	BP	1	PANX2,UCHL1,BID,AIFM1	darkgrey	VSMC_M8
GO:0021537	0.57	0.54	14	184	telencephalon development	BP	1	NARS,MFSD2A,EZH2,XRN2,WDR62,KIF14,ASPM,NF2,H2AFX,TRA2B,EPHB2,TACC3,NDE1,GART	darkgrey	VSMC_M8
GO:0061157	0.57	0.60	6	79	mRNA destabilization	BP	1	DIS3,EXOSC8,TENT4A,HNRNPR,EXOSC2,HNRNPD	darkgrey	VSMC_M8

GO:0097190	0.57	0.50	35	471	apoptotic signaling pathway	BP	1	BCLAF1,MELK,MSH6,CASP2,PLAUR,PARP2,HGF,RRP8,SNAI2,CD44,E2F1,HMGB2,HELLS,CREB3L1,DDX5,XBP1,PAK2,PPP2R1B,BRCA1,MYBBP1A,MSX1,UBE2K,EIF5A,BID,PRELID1,LMNA,MAZ,SLC25A5,AIFM1,NOC2L,TP73,GCLM,CTH,BLOC1S2,ERP29	darkgrey	VSMC_M8
GO:0070227	0.57	0.63	4	52	lymphocyte apoptotic process	BP	1	ARG2,PRELID1,AURKB,NOC2L	darkgrey	VSMC_M8
GO:2001236	0.58	0.56	9	121	regulation of extrinsic apoptotic signaling pathway	BP	1	HGF,SNAI2,HMGB2,PAK2,PPP2R1B,BRCA1,BID,LMNA,GCLM	darkgrey	VSMC_M8
GO:0045665	0.58	0.63	4	52	negative regulation of neuron differentiation	BP	1	HEY1,ASPM,SPAG9,TP73	darkgrey	VSMC_M8
GO:1903078	0.58	0.63	4	52	positive regulation of protein localization to plasma membrane	BP	1	EZR,EPHB2,ARF6,ACSL3	darkgrey	VSMC_M8
GO:0031060	0.58	0.63	4	52	regulation of histone methylation	BP	1	PHF19,BRCA1,LMNA,DNMT1	darkgrey	VSMC_M8
GO:0035710	0.58	0.60	5	65	CD4-positive, alpha-beta T cell activation	BP	1	LOXL3,ENTPD7,RUNX1,ARG2,CBFB	darkgrey	VSMC_M8
GO:0045185	0.58	0.59	6	80	maintenance of protein location	BP	1	FBN2,RANGAP1,YWHAB,BARD1,KDELR2,HNRNPU	darkgrey	VSMC_M8
GO:0031667	0.58	0.50	27	362	response to nutrient levels	BP	1	MIOS,MFSD2A,NAMPT,CAD,SRSF2,RRP8,SNAI2,HMGCR,GCN1,XBP1,EIF4G1,HAT1,MYBBP1A,EIF2AK1,ADIPOR2,EIF2S1,COL1A1,BRIP1,ACSL4,TYMS,NNT,AIFM1,LIPG,G6PD,GCLM,ACSL3,MBD2	darkgrey	VSMC_M8
GO:0048872	0.59	0.51	17	229	homeostasis of number of cells	BP	1	HSPA9,HOXA5,EZH2,PRMT1,AXL,NCAPG2,HMGB2,BAP1,ETS1,FLVCR1,LYAR,FH,CCNB2,SLC25A5,G6PD,PIK3CD,TMOD3	darkgrey	VSMC_M8
GO:0045445	0.59	0.60	5	67	myoblast differentiation	BP	1	SDC1,TBX3,HMGCR,DDX5,HINFP	darkgrey	VSMC_M8
GO:0000288	0.59	0.62	4	53	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	BP	1	DIS3,EXOSC8,TENT4A,EXOSC2	darkgrey	VSMC_M8
GO:0032270	0.59	0.46	80	1066	positive regulation of cellular protein metabolic process	BP	1	DDX39B,PRRC1,EZR,PPP2R5D,DBF4,VCP,HSP90AB1,CKS2,ANP32B,TTK,CYCS,EZH2,CLSPN,PHF19,CASP2,NRDC,RUVBL2,SAE1,PLAUR,BORA,SPHK1,CDC20,EIF4A3,CHFR,CDC25B,DCUN1D2,HGF,CCNB1,CD44,TPX2,UBA2,CDCA2,GNL3,PPP1R15B,UBE2C,PSMD14,FASTKD3,TENT4A,KHDRBS1,CENPE,KIF14,FANCI,EIF4G1,PSMC5,TFRC,PAK2,DHX9,FANCM,BRCA1,CNOT9,DCUN1D5,ECT2,RBM3,MNAT1,RAC1,INCENP,ADIPOR2,UBE2K,CDC6,EIF5A,BID,PRELID1,IQGAP3,LMNA,RAD23A,PLK1,DNMT1,TADA2A,AIFM1,RAP2C,UHRF1,EMP2,TFAP4,PTBP1,TRUB2,HNRNPD,AURKA,UBE2S,ERP29,PDCD2	darkgrey	VSMC_M8
GO:1903050	0.59	0.52	14	192	regulation of proteolysis involved in cellular protein catabolic process	BP	1	CDK2,DESI1,VCP,HSP90AB1,CDC20,CHFR,PBK,PSMD14,PSMC5,SMARCC1,UBE2K,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:2001235	0.59	0.56	7	98	positive regulation of apoptotic signaling pathway	BP	1	BCLAF1,CASP2,PAK2,PPP2R1B,MSX1,EIF5A,BID	darkgrey	VSMC_M8
GO:0007589	0.60	0.58	5	68	body fluid secretion	BP	1	KCNN4,CAD,VAMP8,XBP1,UMPS	darkgrey	VSMC_M8
GO:0001892	0.60	0.58	5	67	embryonic placenta development	BP	1	TRIM28,PLK4,E2F7,HEY1,E2F8	darkgrey	VSMC_M8
GO:0043543	0.60	0.50	15	202	protein acylation	BP	1	DSCC1,NAA15,RUVBL2,RUVBL1,SPHK1,ESCO2,CHEK1,NAA50,MCM3AP,HAT1,BRCA1,MORF4L2,TADA2A,NOC2L,POLE3	darkgrey	VSMC_M8
GO:1901568	0.60	0.60	4	54	fatty acid derivative metabolic process	BP	1	ELOVL6,ALOX15B,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0009205	0.60	0.60	4	57	purine ribonucleoside triphosphate metabolic process	BP	1	ATP5F1B,VCP,ENTPD7,PID1	darkgrey	VSMC_M8
GO:0010921	0.61	0.58	5	68	regulation of phosphatase activity	BP	1	HSP90AB1,PPP6R1,MASTL,HSP90B1,PPP1R15B	darkgrey	VSMC_M8
GO:0032436	0.61	0.56	6	83	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	VCP,CDC20,CHFR,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0010498	0.61	0.46	32	434	proteasomal protein catabolic process	BP	1	CDK2,MAN1A1,DESI1,VCP,HSP90AB1,CDC20,CHFR,CDC16,ANAPC1,HSP90B1,PBK,UBE2C,PSMD14,KIF14,PSMD4,PSMC5,SMARCC1,PSMA6,UFD1,UCHL1,UBE2K,NEDD4,RAD23A,PLK1,CCNF,ZNF598,PSMA5,TOR1A,AURKA,UBE2S,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0048545	0.61	0.49	19	258	response to steroid hormone	BP	1	SDC1,PGR,PPP5C,FOSB,CAD,PCNA,HMGB2,HEY1,DDX5,FOSL1,BRCA1,TFPI,CNOT9,HNRNPU,NEDD4,COL1A1,TYMS,AIFM1,TFAP4	darkgrey	VSMC_M8
GO:1901292	0.61	0.57	5	69	nucleoside phosphate catabolic process	BP	1	VCP,ENTPD7,UNG,DUT,DCTPP1	darkgrey	VSMC_M8
GO:0007006	0.61	0.54	7	99	mitochondrial membrane organization	BP	1	HSPA9,CHCHD3,TOMM70,BID,TIMM8A,SLC25A5,BLOC1S2	darkgrey	VSMC_M8
GO:0061014	0.61	0.56	6	82	positive regulation of mRNA catabolic process	BP	1	DIS3,EXOSC8,TENT4A,HNRNPR,EXOSC2,HNRNPD	darkgrey	VSMC_M8
GO:0032507	0.61	0.59	4	55	maintenance of protein location in cell	BP	1	RANGAP1,BARD1,KDELR2,HNRNPU	darkgrey	VSMC_M8
GO:0030900	0.61	0.48	21	282	forebrain development	BP	1	NARS,MFSD2A,EZH2,STIL,AXL,XRN2,RRM1,WDR62,E2F1,TBX3,ETS1,KIF14,ASPM,NF2,H2AFX,TRA2B,EPHB2,TACC3,MSX1,NDE1,GART	darkgrey	VSMC_M8
GO:0000209	0.61	0.49	15	203	protein polyubiquitination	BP	1	CHFR,CDC16,ANAPC1,UBE2C,UBE2T,DTL,BARD1,BRCA1,UBE2K,NEDD4,DCAF15,THOP1,CBFB,UBE2S,UBE2J2	darkgrey	VSMC_M8
GO:0070647	0.61	0.44	60	806	protein modification by small protein conjugation or removal	BP	1	FBXO5,MTBP,DESI1,VCP,HSP90AB1,TRIM28,U2AF2,SAE1,TRIM47,RNF157,SPHK1,CDC20,GTPBP4,RAD18,CHFR,DCUN1D2,CDC16,USPL1,ANAPC1,UBA2,TRIM35,GNL3,TRIM33,BAP1,UBE2C,PSMD14,UBE2T,TRAIP,FANCI,DTL,CDK1,FANCM,LRR1,BARD1,BRCA1,CDCA3,DCUN1D5,USP42,DESI2,UCHL1,UBE2K,NEDD4,DCAF15,PLK1,COPS3,WDR70,USP1,UHRF1,NXN,CCNF,THOP1,ZNF598,TOR1A,CBFB,USP4,MAD2L1,UBE2S,PJA1,TRIM59,UBE2J2	darkgrey	VSMC_M8
GO:1904888	0.61	0.59	4	54	cranial skeletal system development	BP	1	EIF4A3,CEP55,SIX4,MTHFD1	darkgrey	VSMC_M8
GO:0051247	0.62	0.43	85	1140	positive regulation of protein metabolic process	BP	1	DDX39B,PRRC1,EZR,PPP2R5D,DBF4,VCP,HSP90AB1,CKS2,ANP32B,TTK,CYCS,EZH2,CLSPN,PHF19,PRMT1,CASP2,NRDC,RUVBL2,SAE1,PLAUR,BORA,SPHK1,CDC20,EIF4A3,CHFR,CDC25B,DCUN1D2,HGF,CCNB1,CD44,TPX2,UBA2,PXYLP1,CDCA2,GNL3,PPP1R15B,UBE2C,PSMD14,FASTKD3,TENT4A,KHDRBS1,CENPE,KIF14,FANCI,DTL,EIF4G1,PSMC5,TFRC,PAK2,DHX9,FANCM,BARD1,BRCA1,CNOT9,DCUN1D5,ECT2,RBM3,MNAT1,RAC1,INCENP,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,BID,PRELID1,IQGAP3,LMNA,RAD23A,PLK1,DNMT1,TADA2A,AIFM1,RAP2C,UHRF1,EMP2,TFAP4,PTBP1,TRUB2,HNRNPD,AURKA,UBE2S,ERP29,PDCD2	darkgrey	VSMC_M8
GO:1905897	0.62	0.56	5	70	regulation of response to endoplasmic reticulum stress	BP	1	CREB3L1,PPP1R15B,MANF,XBP1,ERP29	darkgrey	VSMC_M8
GO:0014074	0.62	0.52	8	109	response to purine-containing compound	BP	1	EZR,SDC1,FOSB,CAD,HSP90B1,PDE3A,FOSL1,COL1A1	darkgrey	VSMC_M8

GO:0031329	0.62	0.44	51	689	regulation of cellular catabolic process	BP	1	CDK2,EZR,DESI1,VCP,HSP90AB1,GRSF1,MFSD2A,SYNCRIP,PABPC4,THRAP3,NBAS,NRDC,NAMPT,DIS3,CDC20,CHFR,EXOSC8,HGF,E2F1,PBK,MTDH,PSMD14,FASTKD3,TENT4A,NSUN2,EIF4G1,PSMC5,SMARCC1,DHX9,HNRNPR,HNRNPU,UCHL1,UBE2K,NEDD4,BID,FUS,RAD23A,PLK1,TAF15,SLC25A5,HNRNPM,SERBP1,NNT,POLDIP2,MTCL1,AIFM1,DKC1,ZC3H18,EXOSC2,HNRNPD,AURKA	darkgrey	VSMC_M8
GO:0051591	0.62	0.56	5	68	response to cAMP	BP	1	EZR,SDC1,FOSB,FOSL1,COL1A1	darkgrey	VSMC_M8
GO:0071260	0.62	0.56	5	69	cellular response to mechanical stimulus	BP	1	CASP2,ARHGDIA,CHEK1,RAC1,COL1A1	darkgrey	VSMC_M8
GO:0008652	0.63	0.57	4	56	cellular amino acid biosynthetic process	BP	1	CAD,BCAT1,MTHFD1,CTH	darkgrey	VSMC_M8
GO:0048704	0.63	0.54	6	83	embryonic skeletal system morphogenesis	BP	1	HOXA5,EIF4A3,FLVCR1,SIX4,MTHFD1,HOXB7	darkgrey	VSMC_M8
GO:0042100	0.63	0.57	4	56	B cell proliferation	BP	1	CTPS1,MNDA,TFRC,EPHB2	darkgrey	VSMC_M8
GO:1905330	0.63	0.57	4	56	regulation of morphogenesis of an epithelium	BP	1	HGF,SIX4,HOXB7,PIK3CD	darkgrey	VSMC_M8
GO:0010952	0.63	0.49	10	142	positive regulation of peptidase activity	BP	1	VCP,ANP32B,CYCS,CASP2,PSMD14,BID,PRELID1,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:0050789	0.63	0.39	602	7907	regulation of biological process	BP	1	CDK2,ALPK2,ATP5F1B,TMED9,HNRNPAB,BCLAF1,ABRACL,HNRNPH1,NUP107,CCT2,TUBB,TCF19,DDX39B,FBXO5,PRRC1,EZR,FBN2,PANX2,TCP1,GTSE1,RAD21,DSCC1,TTLL1,NUS1,MTBP,ATAD2,DESI1,PHF5A,FAM49B,RANGAP1,KIF20A,ZNF367,CDC25C,HSPA9,MATR3,SRPK1,SRSF3,PSIP1,BYSL,HMGXB4,PPP2R5D,PWP1,DBF4,POLR3B,UBAP2,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,COL1A2,ARHGEF39,CENPQ,CEP135,CKS2,MIOS,MELK,TRIM28,NCBP1,THADA,ANP32B,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,CLEC11A,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,ANLN,YRDC,THRAP3,EZH2,ODC1,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,SHCBP1,NAA15,SMC6,ORC1,GEN1,NRDC,SDC1,RUVBL2,PLK4,PGR,NAMPT,STIL,PUS7,MCM2,RUVBL1,CCNA2,AMOTL1,SAE1,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,MAST2,FOSB,CD3EAP,CDC42EP4,NUFIP1,GRIN2C,PRCP,PREB,KCNN4,SMG9,NUP85,PLAUR,KIF2C,DBI,BORA,DIS3,AXL,RNF157,SPHK1,SRSF2,FANCD2,XRN2,ULK4,NCAPG2,GDI2,NET1,WDR43,CDC20,BIRC5,SERPINH1,PARP2,POLR3F,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,DOCK9,ARHGDIA,ALYREF,CKAP2,STRN,KCNK6,SIPA1L3,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,TOPBP1,ELK3,RRP8,CDC16,TCERG1,MEDAG,CBX5,CCNB1,SFSWAP,SNAI2,API5,CD44,AAAS,UTP20,TCEA1,ESPL1,HNRNPF,BUB1,TPX2,ANAPC1,DEPDC1B,KIF20B,SKA3,KIF2A,SLC20A1,UBA2,PARPBP,PSD4,SGK3,CENPJ,WEE1,HSP90B1,NECAB3,EIF2B1,E2F1,KIF11,ABCE1,CCNE1,PXYLP1,VAMP8,ZNF827,ATP1B3,KNTC1,HMGB2,CEP55,RBP4,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,ARHGAP11A,UTP	darkgrey	VSMC_M8
GO:0051494	0.63	0.49	10	138	negative regulation of cytoskeleton organization	BP	1	FAM49B,CKAP2,TPX2,RBM14,PAK2,BRCA1,FKBP4,CCNF,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0035023	0.64	0.54	5	69	regulation of Rho protein signal transduction	BP	1	NET1,ARHGDIA,CDC42SE1,RAC1,STMN1	darkgrey	VSMC_M8
GO:1903531	0.64	0.52	7	99	negative regulation of secretion by cell	BP	1	CYP51A1,VAMP8,HMGCR,SYT4,STXBP6,ERP29,SLC30A1	darkgrey	VSMC_M8
GO:0007043	0.64	0.51	7	99	cell-cell junction assembly	BP	1	STRN,ZNF703,SNAI2,MTDH,PAK2,ECT2,FSCN1	darkgrey	VSMC_M8
GO:0010942	0.64	0.43	34	470	positive regulation of cell death	BP	1	BCLAF1,MELK,HOXA5,CASP2,NET1,E2F1,PPID,TRIM35,CTNNBL1,MYBL2,HMGCR,EEF1E1,MNDA,EIF4G1,PAK2,FOSL1,DDX20,PPP2R1B,BARD1,MYBBP1A,ECT2,MSX1,TOP2A,EIF5A,BID,EIF2S1,PRELID1,PTRH2,AIFM1,TFAP4,RNPS1,TP73,PIK3CD,PDCD2	darkgrey	VSMC_M8
GO:0150104	0.64	0.54	5	70	transport across blood-brain barrier	BP	1	MFSD2A,SLC1A5,SLC5A6,TFRC,SLC6A17	darkgrey	VSMC_M8
GO:0034109	0.64	0.54	5	71	homotypic cell-cell adhesion	BP	1	TJP2,PLAUR,ZNF703,METAP1,PDPN	darkgrey	VSMC_M8
GO:0009628	0.64	0.41	66	891	response to abiotic stimulus	BP	1	PSIP1,POLH,VCP,HSP90AB1,MSH6,POLD1,CASP2,RUVBL2,NAMPT,CCNA2,DNAJC2,RAD54L,CHORDC1,FOSB,FANCD2,NET1,POLD3,ARHGDIA,RRM1,PCNA,TOPBP1,CCNB1,HSP90B1,EIF2B1,E2F1,PBK,PPID,RAD51,HMGCR,MDM4,HMGN1,NOLC1,NUCKS1,ETS1,CHEK1,RGS9,RAD9A,TICRR,INTS7,DTL,H2AFX,BLM,CDC25A,FOSL1,BRCA1,RAD51AP1,ECT2,AIPL1,SUV39H1,RAC1,DNAJC7,NEDD4,SMC1A,PDPN,EIF2S1,LMNA,AURKB,COL1A1,BRIP1,COPS3,AIFM1,USP1,NOC2L,HNRNPD,FEN1,MBD2	darkgrey	VSMC_M8
GO:0051716	0.64	0.38	382	5042	cellular response to stimulus	BP	1	CDK2,ALPK2,BCLAF1,DDX39B,FBXO5,EZR,FBN2,GTSE1,RAD21,NUS1,MAN1A1,FAM49B,RANGAP1,HSPA9,SRPK1,SRSF3,RECQL4,TONSL,MCM5,HMGXB4,PPP2R5D,PWP1,APTX,POLH,VCP,HSP90AB1,CDC5L,COL1A2,MCM3,MIOS,MELK,TRIM28,MSH6,TTK,CLEC11A,POLD1,MFSD2A,SYNCRIP,B3GNT2,SLC31A1,EZH2,NUP62,MMS22L,CLSPN,PRMT1,GJB3,CASP2,SHCBP1,SMC6,ORC1,GEN1,SDC1,RUVBL2,PGR,NAMPT,STIL,LIG1,MCM2,RUVBL1,CCNA2,AMOTL1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,PPP5C,WDR33,MASTL,MAST2,FOSB,CD3EAP,CDC42EP4,GRIN2C,PRCP,KCNN4,NUP85,PLAUR,MCM10,CAD,DDX18,AXL,RNF157,SPHK1,MCM6,FANCD2,ULK4,NCAPG2,GDI2,NET1,PARP2,POLD3,RAD18,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,GINS4,DOCK9,ARHGDIA,STRN,SIPA1L3,PCNA,CHFR,POLE,ZNF703,RFC3,HGF,TOPBP1,ELK3,RRP8,CBX5,CCNB1,MCM4,SNAI2,CD44,BUB1,DEPDC1B,SLC20A1,PARPBP,PSD4,SGK3,CENPJ,HSP90B1,EIF2B1,E2F1,CCNE1,KNTC1,HMGB2,CEP55,MSC,SSRP1,HELLS,NRIP1,ARHGAP11A,RACGAP1,LOXL3,PBK,ESCO2,HEY1,NEIL3,SELENOT,TUBA1B,PPID,RBL1,MSH3,BUB1B,FAM83D,NUP93,KNSTRN,TBX3,RAD51,DCLRE1B,CREB3L1,MYBL2,TRIM33,MTDH,YWHAB,HMGCR,NRAS,EEF1E1,CHUK,PPP1R15B,MDM4,CHAF1B,PAK1IP1,RFC5,PSMD14,NCOA5,HMGN1,CIT,NUCKS1,DEK,GCN1,KIF18A,MANF,ETS1,TENT4A,NSUN2,UBE2T,CHEK1,H2AFZ,RASSF1,SMC3,KHDRBS1,TRIP13,CHD1L,NCL,TRAIP,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,EFS,RAD9A,FANCI,MNDA,DDX5,PHACTR4,FANCB,XBP1,TICRR,RFC2,RPA2,PRKAR2A,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,CDC42SE1,UMPS,RBM14,NSMCE4A,CENPF,STRAP,EIF4G1,BUB3,AUNIP,ARFG	darkgrey	VSMC_M8
GO:0043367	0.65	0.55	4	56	CD4-positive, alpha-beta T cell differentiation	BP	1	LOXL3,ENTPD7,RUNX1,CBFB	darkgrey	VSMC_M8
GO:0051056	0.65	0.45	19	259	regulation of small GTPase mediated signal transduction	BP	1	FAM49B,NUP62,NET1,ARHGDIA,SIPA1L3,PSD4,ARHGAP11A,RACGAP1,KIF14,CDC42SE1,ARFGAP1,EPHB2,ECT2,FOXM1,RAC1,LRRC59,PLEKHG4,ARF6,STMN1	darkgrey	VSMC_M8

GO:0022037	0.65	0.52	6	84	metencephalon development	BP	1	TTLL1,EZH2,KIF14,ARCN1,HNRNPD,GART	darkgrey	VSMC_M8
GO:0035773	0.65	0.55	4	58	insulin secretion involved in cellular response to glucose stimulus	BP	1	SELENOT,HMGCR,CDK16,RAC1	darkgrey	VSMC_M8
GO:0031669	0.65	0.46	13	182	cellular response to nutrient levels	BP	1	MIOS,MFSD2A,NAMPT,RRP8,SNAI2,GCN1,XBP1,EIF4G1,MYBBP1A,EIF2S1,COL1A1,BRIP1,AIFM1	darkgrey	VSMC_M8
GO:0008585	0.65	0.53	5	72	female gonad development	BP	1	NUP107,CASP2,PGR,NRIP1,FANCA	darkgrey	VSMC_M8
GO:0044344	0.65	0.51	6	86	cellular response to fibroblast growth factor stimulus	BP	1	CDC5L,SHCBP1,CD44,CREB3L1,COL1A1,GCLM	darkgrey	VSMC_M8
GO:0002532	0.65	0.55	4	59	production of molecular mediator involved in inflammatory response	BP	1	EZH2,VAMP8,BAP1,GBP5	darkgrey	VSMC_M8
GO:0010232	0.65	0.52	5	71	vascular transport	BP	1	MFSD2A,SLC1A5,SLC5A6,TFRC,SLC6A17	darkgrey	VSMC_M8
GO:0031401	0.66	0.40	55	747	positive regulation of protein modification process	BP	1	PRRC1,PPP2R5D,DBF4,VCP,HSP90AB1,CKS2,TTK,EZH2,CLSPN,PHF19,RUVBL2,SAE1,PLAUR,BORA,SPHK1,CDC20,CHFR,CDC25B,DCUN1D2,HGF,CCNB1,CD44,TPX2,UBA2,CDCA2,GNL3,PPP1R15B,UBE2C,CENPE,KIF14,FANCI,EIF4G1,TFRC,PAK2,FANCM,BRCA1,CNOT9,DCUN1D5,ECT2,MNAT1,RAC1,INCENP,ADIPOR2,UBE2K,CDC6,IQGAP3,LMNA,PLK1,DNMT1,TADA2A,RAP2C,EMP2,PTBP1,UBE2S,ERP29	darkgrey	VSMC_M8
GO:0043086	0.66	0.41	40	555	negative regulation of catalytic activity	BP	1	FBXO5,NUP62,MCM2,CHORDC1,MASTL,PLAUR,NCAPG2,BIRC5,SERPINH1,IPO5,CHMP6,HGF,CD44,ABCE1,TERF1,YWHAB,HMGCR,CIT,ANP32E,SPP2,PRKAR2A,NF2,CDC42SE1,CEP85,PAK2,HNRNPR,EPHB2,TFPI,MNAT1,HNRNPU,UCHL1,NES,PTTG1,PLK1,FAM122B,TFAP4,MAD2L1,CDKN2C,PRPSAP1,DUSP7	darkgrey	VSMC_M8
GO:0002285	0.66	0.48	9	127	lymphocyte activation involved in immune response	BP	1	MSH6,LOXL3,ENTPD7,UNG,XBP1,TFRC,NSD2,EXO1,RAB27A	darkgrey	VSMC_M8
GO:0050852	0.66	0.50	6	85	T cell receptor signaling pathway	BP	1	EZR,KCNN4,EIF2B1,KHDRBS1,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0036294	0.66	0.47	9	129	cellular response to decreased oxygen levels	BP	1	NAMPT,CCNA2,CCNB1,E2F1,MDM4,SUV39H1,LMNA,BRIP1,AIFM1	darkgrey	VSMC_M8
GO:1904377	0.66	0.54	4	58	positive regulation of protein localization to cell periphery	BP	1	EZR,EPHB2,ARF6,ACSL3	darkgrey	VSMC_M8
GO:0051592	0.66	0.48	8	114	response to calcium ion	BP	1	SDC1,FOSB,ECT2,MNAT1,NEDD4,FUS,SYT4,HNRNPD	darkgrey	VSMC_M8
GO:0090559	0.66	0.54	4	59	regulation of membrane permeability	BP	1	TJP2,BID,SLC25A5,BLOC1S2	darkgrey	VSMC_M8
GO:0050778	0.66	0.42	22	306	positive regulation of immune response	BP	1	EZR,FAM49B,MATR3,POLR3B,KCNN4,POLR3F,EIF2B1,VAMP8,HMGB2,TOMM70,KHDRBS1,MNDA,XBP1,RBM14,TFRC,PAK2,DHX9,NSD2,UBE2K,PIK3CD,BCAR1,GBP5	darkgrey	VSMC_M8
GO:0043648	0.66	0.51	5	73	dicarboxylic acid metabolic process	BP	1	ALDH1L2,AADAT,FH,MTHFD1,GCLM	darkgrey	VSMC_M8
GO:0046718	0.66	0.48	7	100	viral entry into host cell	BP	1	SLC1A5,AXL,VAMP8,NUP153,CDK1,TFRC,TRIM59	darkgrey	VSMC_M8
GO:0050714	0.67	0.48	7	100	positive regulation of protein secretion	BP	1	EZR,KCNN4,RBP4,PPID,RAC1,ACSL4,ARF6	darkgrey	VSMC_M8
GO:0014013	0.67	0.51	5	73	regulation of gliogenesis	BP	1	EZH2,E2F1,PRMT5,NF2,TP73	darkgrey	VSMC_M8
GO:0097191	0.67	0.45	12	173	extrinsic apoptotic signaling pathway	BP	1	CASP2,PARP2,HGF,SNAI2,HMGB2,PAK2,PPP2R1B,BRCA1,BID,LMNA,GCLM,BLOC1S2	darkgrey	VSMC_M8
GO:0001501	0.67	0.40	30	413	skeletal system development	BP	1	FBN2,COL1A2,HOXA5,COL9A2,SERPINH1,EIF4A3,SNAI2,CD44,SLC10A7,RBP4,TBX3,RUNX1,SPP2,FLVCR1,ADAMTS4,IFT80,UFD1,NSD2,SIX4,MSX1,MTHFD1,SH3PXD2B,HOXB7,COL1A1,PPIB,XYLT1,TYMS,USP1,ACD,HAS2	darkgrey	VSMC_M8
GO:0033002	0.67	0.44	12	174	muscle cell proliferation	BP	1	DDX39B,NAMPT,CCNB1,RBP4,HMGCR,RUNX1,CDK1,SF1,MNAT1,DNMT1,POLDIP2,TP73	darkgrey	VSMC_M8
GO:0003073	0.67	0.52	4	60	regulation of systemic arterial blood pressure	BP	1	PRCP,KCNK6,NAV2,EMP2	darkgrey	VSMC_M8
GO:0003300	0.68	0.50	5	75	cardiac muscle hypertrophy	BP	1	DDX39B,EZH2,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0043473	0.68	0.50	5	75	pigmentation	BP	1	SNAI2,ARCN1,MYO5A,RAB27A,BLOC1S2	darkgrey	VSMC_M8
GO:0003170	0.68	0.52	4	58	heart valve development	BP	1	MATR3,SNAI2,HEY1,MDM4	darkgrey	VSMC_M8
GO:0033108	0.68	0.50	5	83	mitochondrial respiratory chain complex assembly	BP	1	CHCHD4,NDUFAF1,FASTKD3,NDUFS1,AIFM1	darkgrey	VSMC_M8
GO:0033138	0.68	0.50	5	74	positive regulation of peptidyl-serine phosphorylation	BP	1	HSP90AB1,CD44,EIF4G1,TFRC,CNOT9	darkgrey	VSMC_M8
GO:1901800	0.68	0.47	7	104	positive regulation of proteasomal protein catabolic process	BP	1	VCP,CDC20,CHFR,PSMC5,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0033209	0.68	0.49	5	75	tumor necrosis factor-mediated signaling pathway	BP	1	SPHK1,CHUK,TRAIP,UBE2K,EIF5A	darkgrey	VSMC_M8
GO:0009144	0.69	0.51	4	63	purine nucleoside triphosphate metabolic process	BP	1	ATP5F1B,VCP,ENTPD7,PID1	darkgrey	VSMC_M8
GO:0046545	0.69	0.49	5	75	development of primary female sexual characteristics	BP	1	NUP107,CASP2,PGR,NRIP1,FANCA	darkgrey	VSMC_M8
GO:0050871	0.69	0.50	4	61	positive regulation of B cell activation	BP	1	XBP1,TFRC,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0009259	0.69	0.39	21	302	ribonucleotide metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,CTPS1,RNASEH2B,CAD,PDHB,AADAT,ENTPD7,HMGCR,ELOVL6,UMPS,PDHA1,UCK2,DLAT,PFAS,ACSL4,ACSL3,PID1,GART	darkgrey	VSMC_M8
GO:0033135	0.69	0.45	7	104	regulation of peptidyl-serine phosphorylation	BP	1	PWP1,HSP90AB1,HGF,CD44,EIF4G1,TFRC,CNOT9	darkgrey	VSMC_M8
GO:0042752	0.70	0.46	6	89	regulation of circadian rhythm	BP	1	THRAP3,EZH2,CDK1,SUV39H1,TOP2A,HNRNPD	darkgrey	VSMC_M8
GO:0043409	0.70	0.43	9	131	negative regulation of MAPK cascade	BP	1	EZR,NUP62,PBK,HMGCR,NF2,EPHB2,FOXM1,UCHL1,DUSP7	darkgrey	VSMC_M8
GO:0071396	0.70	0.37	30	422	cellular response to lipid	BP	1	GJB3,RUVBL2,PGR,CCNA2,PPP5C,DDX18,AXL,ZNF703,CCNB1,SNAI2,E2F1,HMGB2,NRIP1,HEY1,MTDH,KIF18A,H2AFZ,DDX5,XBP1,BRCA1,TFPI,CNOT9,HNRNPU,ADIPOR2,NEDD4,COL1A1,AIFM1,TFAP4,HNRNPD,PID1	darkgrey	VSMC_M8
GO:1903076	0.70	0.46	6	90	regulation of protein localization to plasma membrane	BP	1	EZR,VAMP8,EPHB2,ARF6,ACSL3,PID1	darkgrey	VSMC_M8
GO:0031032	0.70	0.41	12	172	actomyosin structure organization	BP	1	ANLN,FHDC1,RACGAP1,CIT,NF2,PAK2,FRMD6,ECT2,SIX4,RAC1,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0042632	0.70	0.49	4	62	cholesterol homeostasis	BP	1	NUS1,HMGCR,XBP1,LIPG	darkgrey	VSMC_M8
GO:0014897	0.70	0.47	5	77	striated muscle hypertrophy	BP	1	DDX39B,EZH2,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0040008	0.70	0.36	37	518	regulation of growth	BP	1	DDX39B,EZR,NCBP1,MFSD2A,RUVBL2,RUVBL1,RNF157,SPHK1,NET1,PARP2,CCNB1,SGK3,RBP4,BAP1,RUNX1,KIF14,FLVCR1,EIF4G1,CDK1,PAK2,DCUN1D5,CREG1,SIX4,MSX1,ADIPOR2,CCNB2,ALOX15B,PPIB,SPAG9,SYT4,MORF4L2,TP73,G6PD,EXOSC2,BCAR1,CDKN2C,CLSTN3	darkgrey	VSMC_M8
GO:0071774	0.70	0.46	6	91	response to fibroblast growth factor	BP	1	CDC5L,SHCBP1,CD44,CREB3L1,COL1A1,GCLM	darkgrey	VSMC_M8
GO:0031047	0.70	0.43	8	129	gene silencing by RNA	BP	1	NCBP1,HNRNPA2B1,DDX5,EIF4G1,DHX9,DGCR8,CNOT9,SRRT	darkgrey	VSMC_M8
GO:0003279	0.70	0.45	6	88	cardiac septum development	BP	1	MATR3,ADAMTS6,HEY1,TBX3,MDM4,NSD2	darkgrey	VSMC_M8

GO:0097435	0.70	0.35	45	622	supramolecular fiber organization	BP	1	FBXO5,EZR,FAM49B,KIF24,HSP90AB1,COL1A2,CDC42EP4,KIF2C,DIAPH3,SERPINH1,CKAP2,GAS2L3,TPX2,KIF2A,CENPJ,HSP90B1,FHDC1,LOXL3,CKAP5,KIF18A,EFS,NF2,PAK2,KIF18B,ADAMTS14,DPT,FKBP4,SIX4,RAC1,MYO5A,FSCN1,BID,LTBP2,COL1A1,TPM3,NDE1,HOOK1,MAP7D3,EMP2,BCAR1,TPPP3,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0010951	0.70	0.42	9	137	negative regulation of endopeptidase activity	BP	1	PLAUR,BIRC5,SERPINH1,HGF,CD44,SPP2,PAK2,TFPI,PTTG1	darkgrey	VSMC_M8
GO:0048661	0.70	0.47	5	78	positive regulation of smooth muscle cell proliferation	BP	1	DDX39B,NAMPT,HMGCR,MNAT1,DNMT1	darkgrey	VSMC_M8
GO:0032147	0.70	0.44	7	105	activation of protein kinase activity	BP	1	PRRC1,CLSPN,BORA,TPX2,KIF14,ECT2,EMP2	darkgrey	VSMC_M8
GO:0072521	0.70	0.38	22	319	purine-containing compound metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,DCK,AMD1,PDHB,AADAT,ENTPD7,HMGCR,ELOVL6,PDHA1,DLAT,MTHFD1,NUDT1,PFAS,PRPS1,ACSL4,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0030307	0.71	0.42	9	134	positive regulation of cell growth	BP	1	DDX39B,NCBP1,MFSD2A,RNF157,SPHK1,PARP2,EIF4G1,SYT4,EXOSC2	darkgrey	VSMC_M8
GO:0042058	0.71	0.48	4	62	regulation of epidermal growth factor receptor signaling pathway	BP	1	NUP62,PLAUR,CHMP6,CNOT9	darkgrey	VSMC_M8
GO:0052547	0.71	0.38	20	294	regulation of peptidase activity	BP	1	VCP,ANP32B,CYCS,CASP2,NRDC,PLAUR,BIRC5,SERPINH1,HGF,CD44,PSMD14,SPP2,PAK2,TFPI,BID,PRELID1,PTTG1,AIFM1,TFAP4,PDCD2	darkgrey	VSMC_M8
GO:0032418	0.71	0.48	4	62	lysosome localization	BP	1	VAMP8,SPAG9,PIK3CD,BLOC1S2	darkgrey	VSMC_M8
GO:0045639	0.71	0.46	5	77	positive regulation of myeloid cell differentiation	BP	1	HOXA5,PRMT1,HMGB2,RUNX1,ETS1	darkgrey	VSMC_M8
GO:0034599	0.71	0.39	16	234	cellular response to oxidative stress	BP	1	MELK,EZH2,PPP5C,AXL,SPHK1,NET1,PCNA,HGF,CHUK,ETS1,CDK1,ECT2,EIF2S1,AIFM1,G6PD,SIGMAR1	darkgrey	VSMC_M8
GO:0051092	0.71	0.43	8	119	positive regulation of NF-kappaB transcription factor activity	BP	1	SPHK1,MTDH,CHUK,TFRC,DHX9,PSMA6,DHX33,CTH	darkgrey	VSMC_M8
GO:0014896	0.71	0.46	5	78	muscle hypertrophy	BP	1	DDX39B,EZH2,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0098586	0.71	0.48	4	63	cellular response to virus	BP	1	TOMM70,CHUK,UFD1,EIF5A	darkgrey	VSMC_M8
GO:2001141	0.71	0.32	180	2416	regulation of RNA biosynthetic process	BP	1	HNRNPAB,BCLAF1,NUP107,DDX39B,EZR,RAD21,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,CDC5L,CKS2,TRIM28,CDCA7L,HOXA5,PPIE,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,ZNF703,HGF,ELK3,RRP8,TCERG1,CBX5,SNAI2,TCEA1,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,PSMA6,DDX20,SF1,NMD3,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,NOC2L,TP73,REXO4,FANCA,FAM129B,CBFB,CTH,DEPDC1,PRIM2,SRRT,HNRNPD,DRAP1,HMGB3,ABT1,PID1,HOXC8,MBD2	darkgrey	VSMC_M8
GO:1904063	0.71	0.48	4	62	negative regulation of cation transmembrane transport	BP	1	THADA,EPHB2,NEDD4,SLC30A1	darkgrey	VSMC_M8
GO:0048284	0.71	0.42	8	120	organelle fusion	BP	1	CHCHD3,SPHK1,VAMP8,CDK1,TFRC,SYT4,STXBP6,PID1	darkgrey	VSMC_M8
GO:0055092	0.71	0.48	4	63	sterol homeostasis	BP	1	NUS1,HMGCR,XBP1,LIPG	darkgrey	VSMC_M8
GO:0045921	0.72	0.47	4	63	positive regulation of exocytosis	BP	1	SDC1,VAMP8,RAB27A,SYT4	darkgrey	VSMC_M8
GO:0016567	0.72	0.34	47	656	protein ubiquitination	BP	1	FBXO5,MTBP,VCP,HSP90AB1,TRIM28,U2AF2,SAE1,TRIM47,RNF157,SPHK1,CDC20,GTPBP4,RAD18,CHFR,DCUN1D2,CDC16,ANAPC1,TRIM35,TRIM33,UBE2C,UBE2T,TRAIP,FANCI,DTL,FANCM,LRR1,BARD1,BRCA1,CDCA3,DCUN1D5,UBE2K,NEDD4,DCAF15,PLK1,WDR70,UHRF1,NXN,CCNF,THOP1,ZNF598,CBFB,USP4,MAD2L1,UBE2S,PJA1,TRIM59,UBE2J2	darkgrey	VSMC_M8
GO:1903362	0.72	0.38	15	222	regulation of cellular protein catabolic process	BP	1	CDK2,EZR,DESI1,VCP,HSP90AB1,CDC20,CHFR,PBK,PSMD14,PSMC5,SMARCC1,UBE2K,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0035335	0.72	0.45	5	77	peptidyl-tyrosine dephosphorylation	BP	1	CDC25C,CDC25B,CDC25A,CDKN3,DUSP7	darkgrey	VSMC_M8
GO:0060349	0.72	0.45	5	76	bone morphogenesis	BP	1	SERPINH1,IFT80,MSX1,COL1A1,HAS2	darkgrey	VSMC_M8

GO:0050794	0.72	0.30	574	7581	regulation of cellular process	BP	1	CDK2,ALPK2,ATP5F1B,TMED9,HNRNPAB,BCLAF1,ABRACL,HNRNPH1,NUP107,CCT2,TUBB,DDX39B,FBXO5,PRRC1,EZR,FBN2,TCP1,GTSE1,RAD21,DSCC1,NUS1,MTBP,ATAD2,DESI1,PHF5A,FAM49B,RANGAP1,KIF20A,ZNF367,CDC25C,HSPA9,SRPK1,SRSF3,PSIP1,BYSL,HMGXB4,PPP2R5D,PWP1,DBF4,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,COL1A2,ARHGEF39,CENPQ,CEP135,CKS2,MIOS,MELK,TRIM28,NCBP1,THADA,ANP32B,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,CLEC11A,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,ANLN,THRAP3,EZH2,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,SHCBP1,NAA15,SMC6,ORC1,GEN1,NRDC,SDC1,RUVBL2,PLK4,PGR,NAMPT,STIL,PUS7,MCM2,RUVBL1,CCNA2,AMOTL1,SAE1,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,MAST2,FOSB,CD3EAP,CDC42EP4,NUFIP1,GRIN2C,PRCP,PREB,KCNN4,NUP85,PLAUR,KIF2C,DBI,BORA,DIS3,AXL,RNF157,SPHK1,SRSF2,FANCD2,ULK4,NCAPG2,GDI2,NET1,WDR43,CDC20,BIRC5,SERPINH1,PARP2,POLR3F,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,DOCK9,ARHGDIA,ALYREF,CKAP2,STRN,KCNK6,SIPA1L3,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,TOPBP1,ELK3,RRP8,CDC16,TCERG1,MEDAG,CBX5,CCNB1,SFSWAP,SNAI2,API5,CD44,AAAS,UTP20,TCEA1,ESPL1,HNRNPF,BUB1,TPX2,ANAPC1,DEPDC1B,KIF20B,SKA3,KIF2A,SLC20A1,UBA2,PARPBP,PSD4,SGK3,CENPJ,WEE1,HSP90B1,NECAB3,EIF2B1,E2F1,KIF11,ABCE1,CCNE1,PXYLP1,VAMP8,ZNF827,ATP1B3,KNTC1,HMGB2,CEP55,RBP4,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,ARHGAP11A,UTP15,RBM12,RACGAP1,LOXL3,PBK,ESCO2,HEY1,ZBTB10,SELENOT,FAM98B,CCT8,PPI	darkgrey	VSMC_M8
GO:0001819	0.72	0.36	21	304	positive regulation of cytokine production	BP	1	PANX2,FAM49B,POLR3B,SPHK1,POLR3F,HGF,HMGB2,TOMM70,CHUK,RUNX1,SETD4,MNDA,XBP1,DHX9,DDX21,EPHB2,BRCA1,DHX33,ALOX15B,PIK3CD,GBP5	darkgrey	VSMC_M8
GO:1904375	0.72	0.42	7	107	regulation of protein localization to cell periphery	BP	1	EZR,VAMP8,EPHB2,PLK1,ARF6,ACSL3,PID1	darkgrey	VSMC_M8
GO:0006639	0.72	0.43	6	92	acylglycerol metabolic process	BP	1	MFSD2A,PGS1,AGPAT5,GK,ACSL4,LIPG	darkgrey	VSMC_M8
GO:0071383	0.72	0.39	11	163	cellular response to steroid hormone stimulus	BP	1	PGR,PPP5C,HEY1,DDX5,BRCA1,TFPI,CNOT9,HNRNPU,NEDD4,AIFM1,TFAP4	darkgrey	VSMC_M8
GO:0030433	0.72	0.45	5	78	ubiquitin-dependent ERAD pathway	BP	1	MAN1A1,VCP,HSP90B1,UFD1,UBE2J2	darkgrey	VSMC_M8
GO:0033143	0.72	0.46	4	63	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	PPP5C,DDX5,BRCA1,CNOT9	darkgrey	VSMC_M8
GO:0048568	0.72	0.35	24	341	embryonic organ development	BP	1	FBN2,TRIM28,HOXA5,PLK4,STIL,EIF4A3,E2F7,POLE,RBP4,HEY1,TBX3,E2F8,PHACTR4,UTP25,FLVCR1,TRA2B,EPHB2,SIX4,MSX1,MTHFD1,NES,HOXB7,PALB2,MBD2	darkgrey	VSMC_M8
GO:0046165	0.72	0.42	7	108	alcohol biosynthetic process	BP	1	NUS1,CYP51A1,SPHK1,PPIP5K2,HMGCR,LBR,G6PD	darkgrey	VSMC_M8
GO:0044409	0.72	0.42	7	106	entry into host	BP	1	SLC1A5,AXL,VAMP8,NUP153,CDK1,TFRC,TRIM59	darkgrey	VSMC_M8
GO:0006633	0.72	0.42	7	107	fatty acid biosynthetic process	BP	1	ELOVL6,XBP1,BRCA1,ALOX15B,LIPG,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0019646	0.72	0.46	4	75	aerobic electron transport chain	BP	1	CYC1,CYCS,NDUFAF1,NDUFS1	darkgrey	VSMC_M8
GO:0046634	0.73	0.46	4	63	regulation of alpha-beta T cell activation	BP	1	LOXL3,RUNX1,ARG2,CBFB	darkgrey	VSMC_M8
GO:0006576	0.73	0.46	4	64	cellular biogenic amine metabolic process	BP	1	ODC1,AMD1,AFMID,SRM	darkgrey	VSMC_M8
GO:0097581	0.73	0.44	5	78	lamellipodium organization	BP	1	NUP85,CD44,RAC1,FSCN1,PDPN	darkgrey	VSMC_M8
GO:0000122	0.73	0.32	50	694	negative regulation of transcription by RNA polymerase II	BP	1	EZR,TRIM28,EZH2,PHF19,FOSB,E2F7,PCNA,ELK3,TCERG1,CBX5,SNAI2,E2F1,CCNE1,MSC,NRIP1,HEY1,PPID,RBL1,TBX3,CREB3L1,E2F8,TRIM33,MTDH,RUNX1,MDM4,NCOA5,KHDRBS1,DDX5,HINFP,STRAP,DDX20,NSD2,SUV39H1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,RFC1,HDGF,MAZ,AURKB,PLK1,DNMT1,UHRF1,NOC2L,CBFB,DRAP1,MBD2	darkgrey	VSMC_M8
GO:0042113	0.73	0.37	13	193	B cell activation	BP	1	MSH6,CTPS1,EZH2,TXLNA,UNG,MNDA,XBP1,TFRC,EPHB2,NSD2,EXO1,SLC25A5,PIK3CD	darkgrey	VSMC_M8
GO:1901654	0.73	0.39	10	151	response to ketone	BP	1	CDC5L,FOSB,NASP,CAD,PCNA,FOSL1,TYMS,AIFM1,TFAP4,HNRNPD	darkgrey	VSMC_M8
GO:0006638	0.73	0.42	6	93	neutral lipid metabolic process	BP	1	MFSD2A,PGS1,AGPAT5,GK,ACSL4,LIPG	darkgrey	VSMC_M8
GO:0035264	0.73	0.41	7	108	multicellular organism growth	BP	1	EZR,HOXA5,MFSD2A,STIL,FLVCR1,PPIB,PALB2	darkgrey	VSMC_M8
GO:0071277	0.73	0.45	4	63	cellular response to calcium ion	BP	1	FOSB,ECT2,FUS,SYT4	darkgrey	VSMC_M8
GO:0010038	0.73	0.35	19	279	response to metal ion	BP	1	SDC1,PPP5C,FOSB,PCNA,CCNB1,GGH,ATF1,CHUK,CDK1,ECT2,MNAT1,NEDD4,EIF2S1,NUDT1,FUS,SYT4,G6PD,HNRNPD,SLC30A1	darkgrey	VSMC_M8
GO:0007030	0.74	0.39	8	122	Golgi organization	BP	1	TMED9,COG3,FHDC1,PRMT5,CDK1,ZW10,VRK1,HOOK1	darkgrey	VSMC_M8
GO:0001678	0.74	0.39	8	124	cellular glucose homeostasis	BP	1	SELENOT,HMGCR,NUCKS1,XBP1,TRA2B,CDK16,RAC1,GCLM	darkgrey	VSMC_M8
GO:0071333	0.74	0.40	7	110	cellular response to glucose stimulus	BP	1	SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,GCLM	darkgrey	VSMC_M8
GO:2000060	0.74	0.41	6	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	VCP,CDC20,CHFR,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:1901606	0.74	0.44	4	65	alpha-amino acid catabolic process	BP	1	GCAT,AFMID,AADAT,ARG2	darkgrey	VSMC_M8
GO:0014706	0.74	0.33	21	307	striated muscle tissue development	BP	1	ALPK2,DDX39B,PRMT1,PARP2,CCNB1,RBP4,MSC,HEY1,TBX3,HMGCR,RUNX1,DDX5,CENPF,CDK1,SIX4,MSX1,HNRNPU,LMNA,TP73,G6PD,FAM129B	darkgrey	VSMC_M8
GO:1901135	0.74	0.30	56	791	carbohydrate derivative metabolic process	BP	1	ATP5F1B,NUS1,MAN1A1,SLC35D2,TJP2,VCP,PAICS,NANS,CTPS1,DCK,B3GNT2,AMD1,RPN1,RNASEH2B,COG3,CAD,ALG8,TK1,RRM1,HGF,CD44,PDHB,NECAB3,PXYLP1,AADAT,SLC10A7,GALNT6,ENTPD7,HMGCR,STT3A,UNG,ELOVL6,UMPS,PDHA1,UAP1,UCK2,GK,DLAT,DUT,UGDH,NUDT1,DCTPP1,PFAS,PRPS1,ACSL4,XYLT1,TYMS,G6PD,DOLPP1,GMPPB,ACSL3,HAS2,PID1,GART,PRPSAP1,ERH	darkgrey	VSMC_M8
GO:0051048	0.74	0.39	7	110	negative regulation of secretion	BP	1	CYP51A1,VAMP8,HMGCR,SYT4,STXBP6,ERP29,SLC30A1	darkgrey	VSMC_M8
GO:0051493	0.75	0.32	32	457	regulation of cytoskeleton organization	BP	1	FAM49B,NUP62,PLK4,CDC42EP4,BORA,ARHGDIA,CKAP2,TPX2,SKA3,CENPJ,CKAP5,KIF18A,RASSF1,NF2,RBM14,PAK2,KIF15,BRCA1,TACC3,ECT2,FKBP4,RAC1,HNRNPU,FSCN1,IQGAP3,NES,PLK1,CCNF,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0090277	0.75	0.43	4	65	positive regulation of peptide hormone secretion	BP	1	RBP4,SELENOT,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0043123	0.75	0.36	10	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	NUP62,PPP5C,SLC20A1,MTDH,CHUK,TFRC,DDX21,ECT2,NEK6,CTH	darkgrey	VSMC_M8

GO:0002831	0.75	0.34	15	224	regulation of response to biotic stimulus	BP	1	MATR3,POLR3B,HSP90AB1,POLR3F,HMGB2,TOMM70,MNDA,RBM14,PAK2,DHX9,UFD1,LYAR,UBE2K,ARG2,GBP5	darkgrey	VSMC_M8
GO:0043523	0.75	0.36	11	169	regulation of neuron apoptotic process	BP	1	HSP90AB1,CASP2,AXL,MYBL2,KIF14,SIX4,NES,AIFM1,G6PD,GCLM,SIGMAR1	darkgrey	VSMC_M8
GO:0051402	0.75	0.35	13	198	neuron apoptotic process	BP	1	HSP90AB1,CASP2,AXL,MYBL2,CIT,KIF14,SIX4,BID,NES,AIFM1,G6PD,GCLM,SIGMAR1	darkgrey	VSMC_M8
GO:0042593	0.75	0.35	12	183	glucose homeostasis	BP	1	PRCP,RBP4,SELENOT,HMGCR,NCOA5,NUCKS1,XBP1,TRA2B,CDK16,RAC1,ADIPOR2,GCLM	darkgrey	VSMC_M8
GO:0051047	0.75	0.34	14	211	positive regulation of secretion	BP	1	EZR,SDC1,KCNN4,VAMP8,RBP4,SELENOT,PPID,XBP1,RAC1,RAB27A,SYT4,ACSL4,ARF6,ACSL3	darkgrey	VSMC_M8
GO:0030198	0.75	0.33	17	250	extracellular matrix organization	BP	1	COL1A2,COL9A2,SERPINH1,ADAMTS6,LOXL3,CREB3L1,RUNX1,ETS1,ADAMTS4,ADAMTS14,DPT,FSCN1,PDPN,SH3PXD2B,COL1A1,CRISPLD2,HAS2	darkgrey	VSMC_M8
GO:0099518	0.75	0.42	4	65	vesicle cytoskeletal trafficking	BP	1	MYO5A,SYT4,NDE1,BLOC1S2	darkgrey	VSMC_M8
GO:0002793	0.75	0.42	4	66	positive regulation of peptide secretion	BP	1	RBP4,SELENOT,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0001676	0.76	0.42	4	66	long-chain fatty acid metabolic process	BP	1	ELOVL6,ALOX15B,ACSL4,ACSL3	darkgrey	VSMC_M8
GO:0006355	0.76	0.27	178	2411	regulation of transcription, DNA-templated	BP	1	HNRNPAB,BCLAF1,NUP107,DDX39B,EZR,RAD21,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,CDC5L,CKS2,TRIM28,CDCA7L,HOXA5,PPIE,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,ZNF703,HGF,ELK3,RRP8,TCERG1,CBX5,SNAI2,TCEA1,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,PSMA6,DDX20,SF1,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,NOC2L,TP73,REXO4,FANCA,FAM129B,CBFB,CTH,DEPDC1,SRRT,HNRNPD,DRAP1,HMGB3,ABT1,PID1,HOXC8,MBD2	darkgrey	VSMC_M8
GO:0051963	0.76	0.40	5	79	regulation of synapse assembly	BP	1	EIF4G1,EPHB2,SIX4,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0033500	0.76	0.34	12	184	carbohydrate homeostasis	BP	1	PRCP,RBP4,SELENOT,HMGCR,NCOA5,NUCKS1,XBP1,TRA2B,CDK16,RAC1,ADIPOR2,GCLM	darkgrey	VSMC_M8
GO:0071331	0.76	0.37	7	112	cellular response to hexose stimulus	BP	1	SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,GCLM	darkgrey	VSMC_M8
GO:0035195	0.76	0.38	6	107	gene silencing by miRNA	BP	1	HNRNPA2B1,DDX5,EIF4G1,DHX9,DGCR8,SRRT	darkgrey	VSMC_M8
GO:0008277	0.76	0.39	6	96	regulation of G protein-coupled receptor signaling pathway	BP	1	RNF157,YWHAB,RGS9,PRMT5,AIPL1,STMN1	darkgrey	VSMC_M8
GO:1903506	0.76	0.27	178	2412	regulation of nucleic acid-templated transcription	BP	1	HNRNPAB,BCLAF1,NUP107,DDX39B,EZR,RAD21,ATAD2,PHF5A,ZNF367,PSIP1,PWP1,CDC5L,CKS2,TRIM28,CDCA7L,HOXA5,PPIE,THRAP3,EZH2,NUP62,PHF19,NAA15,RUVBL2,PGR,NAMPT,RUVBL1,CCNA2,DNAJC2,FOSB,NUFIP1,NUP85,SPHK1,SRSF2,WDR43,BIRC5,POLR3F,SUPT16H,E2F7,ALYREF,CKAP2,PCNA,ZNF703,HGF,ELK3,RRP8,TCERG1,CBX5,SNAI2,TCEA1,SGK3,CENPJ,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,UTP15,LOXL3,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,YWHAB,BAP1,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NOLC1,NUCKS1,DEK,GCN1,ETS1,PHC2,ICE1,GMNN,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TRAIP,RBM23,PRMT5,NOL11,TARBP1,DDX5,XBP1,EWSR1,HINFP,BLM,RBM14,CENPF,STRAP,PSMC5,TFRC,FOSL1,SMARCC1,DHX9,PSMA6,DDX20,SF1,SMARCAL1,ETV4,BRCA1,CNOT9,PSMC3IP,NSD2,CDK16,GABPB1,MYBBP1A,CREG1,DHX33,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,COL1A1,NFATC2IP,ILF2,PLK1,ILF3,BRIP1,MORF4L2,DNMT1,TADA2A,TAF15,CDCA4,ELF4,RAP2C,UHRF1,RBMX,TFAP4,NOC2L,TP73,REXO4,FANCA,FAM129B,CBFB,CTH,DEPDC1,SRRT,HNRNPD,DRAP1,HMGB3,ABT1,PID1,HOXC8,MBD2	darkgrey	VSMC_M8
GO:0043062	0.76	0.32	17	251	extracellular structure organization	BP	1	COL1A2,COL9A2,SERPINH1,ADAMTS6,LOXL3,CREB3L1,RUNX1,ETS1,ADAMTS4,ADAMTS14,DPT,FSCN1,PDPN,SH3PXD2B,COL1A1,CRISPLD2,HAS2	darkgrey	VSMC_M8
GO:0045229	0.76	0.32	17	251	external encapsulating structure organization	BP	1	COL1A2,COL9A2,SERPINH1,ADAMTS6,LOXL3,CREB3L1,RUNX1,ETS1,ADAMTS4,ADAMTS14,DPT,FSCN1,PDPN,SH3PXD2B,COL1A1,CRISPLD2,HAS2	darkgrey	VSMC_M8
GO:0030518	0.76	0.38	6	96	intracellular steroid hormone receptor signaling pathway	BP	1	PGR,PPP5C,DDX5,BRCA1,CNOT9,NEDD4	darkgrey	VSMC_M8
GO:0032272	0.76	0.42	4	66	negative regulation of protein polymerization	BP	1	FAM49B,FKBP4,TMOD3,STMN1	darkgrey	VSMC_M8
GO:1901701	0.76	0.28	63	887	cellular response to oxygen-containing compound	BP	1	CDK2,EZR,RANGAP1,VCP,CDC5L,COL1A2,EZH2,GJB3,RUVBL2,NAMPT,CCNA2,PPP5C,DDX18,AXL,SPHK1,NET1,IPO5,PCNA,ZNF703,HGF,CCNB1,SNAI2,HSP90B1,E2F1,HMGB2,NRIP1,SELENOT,RAD51,MTDH,HMGCR,CHUK,NCOA5,NUCKS1,KIF18A,ETS1,H2AFZ,RGS9,PRMT5,XBP1,BLM,PDE3A,CDK1,SMARCC1,TRA2B,BRCA1,TFPI,CDK16,ECT2,RAC1,MYO5A,ADIPOR2,CDC6,SRSF5,COL1A1,BRIP1,DNMT1,AIFM1,TFAP4,BCAR1,GCLM,HNRNPD,SIGMAR1,PID1	darkgrey	VSMC_M8
GO:0060322	0.76	0.29	44	624	head development	BP	1	NARS,TTLL1,KIF27,ANP32B,MFSD2A,EZH2,CASP2,STIL,GRIN2C,SMG9,AXL,SPHK1,XRN2,RRM1,WDR62,SNRPB,E2F1,TBX3,ETS1,KIF14,ASPM,NF2,H2AFX,FLVCR1,ARCN1,CENPF,TRA2B,EPHB2,TACC3,MNAT1,MSX1,BID,NES,COL1A1,PFAS,SYT4,NDE1,G6PD,SLC6A17,CRISPLD2,HNRNPD,ACSL3,STMN1,GART	darkgrey	VSMC_M8

GO:0010466	0.76	0.35	9	145	negative regulation of peptidase activity	BP	1	PLAUR,BIRC5,SERPINH1,HGF,CD44,SPP2,PAK2,TFPI,PTTG1	darkgrey	VSMC_M8
GO:1901184	0.76	0.41	4	67	regulation of ERBB signaling pathway	BP	1	NUP62,PLAUR,CHMP6,CNOT9	darkgrey	VSMC_M8
GO:0010507	0.76	0.41	4	67	negative regulation of autophagy	BP	1	NAMPT,HGF,EIF4G1,POLDIP2	darkgrey	VSMC_M8
GO:0006163	0.76	0.31	20	302	purine nucleotide metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,DCK,PDHB,AADAT,ENTPD7,HMGCR,ELOVL6,PDHA1,DLAT,MTHFD1,PFAS,PRPS1,ACSL4,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0045927	0.77	0.33	13	199	positive regulation of growth	BP	1	DDX39B,EZR,NCBP1,MFSD2A,RNF157,SPHK1,PARP2,CCNB1,EIF4G1,CDK1,PPIB,SYT4,EXOSC2	darkgrey	VSMC_M8
GO:0071453	0.77	0.35	9	142	cellular response to oxygen levels	BP	1	NAMPT,CCNA2,CCNB1,E2F1,MDM4,SUV39H1,LMNA,BRIP1,AIFM1	darkgrey	VSMC_M8
GO:0071326	0.77	0.36	7	113	cellular response to monosaccharide stimulus	BP	1	SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,GCLM	darkgrey	VSMC_M8
GO:0051223	0.77	0.30	28	412	regulation of protein transport	BP	1	EZR,RANGAP1,CYP51A1,HSP90AB1,TRIM28,ANP32B,NUP62,SAE1,KCNN4,IPO5,KIF20B,RBP4,PPID,HMGCR,BAP1,NOLC1,ICE1,CDK1,BARD1,CDK16,ECT2,RAC1,ACSL4,MTCL1,ARF6,ACSL3,ERP29,UBE2J2	darkgrey	VSMC_M8
GO:0046631	0.77	0.37	6	97	alpha-beta T cell activation	BP	1	LOXL3,ENTPD7,RUNX1,ARG2,ELF4,CBFB	darkgrey	VSMC_M8
GO:0001655	0.77	0.30	19	283	urogenital system development	BP	1	NUP107,SDC1,SEC61A1,NUP85,ADAMTS6,RBP4,HELLS,NUP160,NUP133,CENPF,SMARCC1,EPHB2,SIX4,ARG2,HOXB7,ALOX15B,TP73,ACD,HAS2	darkgrey	VSMC_M8
GO:0048709	0.77	0.40	4	67	oligodendrocyte differentiation	BP	1	EIF2B1,PRMT5,TP73,CDKN2C	darkgrey	VSMC_M8
GO:1903533	0.77	0.40	4	69	regulation of protein targeting	BP	1	SAE1,BAP1,MTCL1,UBE2J2	darkgrey	VSMC_M8
GO:0009746	0.77	0.33	10	159	response to hexose	BP	1	NAMPT,EIF2B1,SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,ADIPOR2,GCLM	darkgrey	VSMC_M8
GO:1903039	0.78	0.34	9	143	positive regulation of leukocyte cell-cell adhesion	BP	1	FAM49B,CD44,RUNX1,ETS1,XBP1,TFRC,EFNB1,CBFB,HAS2	darkgrey	VSMC_M8
GO:1904950	0.78	0.36	6	100	negative regulation of establishment of protein localization	BP	1	RANGAP1,CYP51A1,TERF1,HMGCR,BARD1,ERP29	darkgrey	VSMC_M8
GO:0044092	0.78	0.27	56	806	negative regulation of molecular function	BP	1	FBXO5,THADA,EZH2,NUP62,MCM2,CHORDC1,MASTL,PLAUR,NCAPG2,BIRC5,SERPINH1,GTPBP4,IPO5,EIF4A3,CHMP6,HGF,CD44,E2F1,ABCE1,TERF1,HEY1,YWHAB,HMGCR,CHUK,CIT,NUCKS1,TRAIP,ANP32E,SPP2,PRKAR2A,NEK2,NF2,CDC42SE1,CEP85,PAK2,HNRNPR,EPHB2,TFPI,MNAT1,MSX1,HNRNPU,UCHL1,NEDD4,EIF2S1,NES,AURKB,PTTG1,PLK1,FAM122B,TFAP4,MAD2L1,CDKN2C,STMN1,AURKA,PRPSAP1,DUSP7	darkgrey	VSMC_M8
GO:0036503	0.78	0.36	6	99	ERAD pathway	BP	1	MAN1A1,VCP,HSP90B1,UFD1,TOR1A,UBE2J2	darkgrey	VSMC_M8
GO:0072593	0.78	0.32	11	176	reactive oxygen species metabolic process	BP	1	PRCP,NDUFS1,BRCA1,FOXM1,RAC1,RAB27A,ARG2,SH3PXD2B,NNT,G6PD,PID1	darkgrey	VSMC_M8
GO:0051250	0.78	0.36	6	99	negative regulation of lymphocyte activation	BP	1	AXL,LOXL3,RUNX1,MNDA,ARG2,CBFB	darkgrey	VSMC_M8
GO:0034766	0.78	0.39	4	68	negative regulation of ion transmembrane transport	BP	1	THADA,EPHB2,NEDD4,SLC30A1	darkgrey	VSMC_M8
GO:0008088	0.78	0.39	4	68	axo-dendritic transport	BP	1	HNRNPU,UCHL1,KIF4A,BLOC1S2	darkgrey	VSMC_M8
GO:0040007	0.78	0.27	52	742	growth	BP	1	DDX39B,EZR,HSP90AB1,TRIM28,NCBP1,HOXA5,MFSD2A,EZH2,RUVBL2,STIL,RUVBL1,RNF157,SPHK1,NCAPG2,NET1,PARP2,GINS4,CCNB1,SGK3,RBP4,BAP1,RUNX1,CHEK1,KIF14,ASPM,EIF4H,FLVCR1,EIF4G1,CDK1,PAK2,IFT80,DCUN1D5,CREG1,SIX4,MSX1,ADIPOR2,CCNB2,ALOX15B,PPIB,SPAG9,SYT4,MORF4L2,TYMS,TP73,G6PD,EXOSC2,BCAR1,CDKN2C,AURKA,GINS1,PALB2,CLSTN3	darkgrey	VSMC_M8
GO:0032446	0.78	0.27	49	703	protein modification by small protein conjugation	BP	1	FBXO5,MTBP,VCP,HSP90AB1,TRIM28,U2AF2,SAE1,TRIM47,RNF157,SPHK1,CDC20,GTPBP4,RAD18,CHFR,DCUN1D2,CDC16,ANAPC1,UBA2,TRIM35,GNL3,TRIM33,UBE2C,UBE2T,TRAIP,FANCI,DTL,FANCM,LRR1,BARD1,BRCA1,CDCA3,DCUN1D5,UBE2K,NEDD4,DCAF15,PLK1,WDR70,UHRF1,NXN,CCNF,THOP1,ZNF598,CBFB,USP4,MAD2L1,UBE2S,PJA1,TRIM59,UBE2J2	darkgrey	VSMC_M8
GO:1903828	0.78	0.36	6	99	negative regulation of cellular protein localization	BP	1	RANGAP1,TERF1,BARD1,CDT1,ARF6,PID1	darkgrey	VSMC_M8
GO:0045580	0.78	0.36	6	98	regulation of T cell differentiation	BP	1	LOXL3,RUNX1,XBP1,PRELID1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0016311	0.78	0.29	23	342	dephosphorylation	BP	1	CDC25C,PPP2R5D,APTX,HSP90AB1,PPP6R1,PPP5C,MASTL,PGAM5,CDC25B,HSP90B1,PXYLP1,CDCA2,NT5DC2,YWHAB,PPP1R15B,CDC25A,PPP2R1B,CDKN3,FAM220A,SMG6,PTBP1,PDP2,DUSP7	darkgrey	VSMC_M8
GO:0030163	0.79	0.26	57	815	protein catabolic process	BP	1	CDK2,EZR,MAN1A1,DESI1,CYP51A1,VCP,HSP90AB1,ODC1,NRDC,GRIN2C,CDC20,CHMP6,CHFR,PSMD13,CDC16,ANAPC1,HSP90B1,PBK,FAM83D,HMGCR,BAP1,MDM4,UBE2C,PSMD14,KIF14,XBP1,UTP25,DTL,PSMD4,PSMC5,SMARCC1,PSMA6,BARD1,UFD1,USP42,UCHL1,UBE2K,NEDD4,PSMD3,RAD23A,PLK1,PSMD11,COPS3,USP1,UHRF1,CCNF,ZNF598,PSMA5,TOR1A,SF3B3,USP4,MAD2L1,AURKA,UBE2S,PJA1,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0048705	0.79	0.31	12	186	skeletal system morphogenesis	BP	1	FBN2,HOXA5,SERPINH1,EIF4A3,FLVCR1,IFT80,SIX4,MSX1,MTHFD1,HOXB7,COL1A1,HAS2	darkgrey	VSMC_M8
GO:0001764	0.79	0.34	7	113	neuron migration	BP	1	AXL,ULK4,KIF20B,NAV1,ASPM,RAC1,NDE1	darkgrey	VSMC_M8
GO:0016064	0.79	0.36	5	85	immunoglobulin mediated immune response	BP	1	MSH6,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0043254	0.79	0.28	24	361	regulation of protein-containing complex assembly	BP	1	FAM49B,VCP,CDC42EP4,PREB,TERF1,CKAP5,ICE1,KIF14,HJURP,EIF4G1,TFRC,DHX33,FKBP4,RAC1,FSCN1,BID,CDT1,TPPP3,ARPC4,ARF6,GBP5,TMOD3,STMN1,STXBP6	darkgrey	VSMC_M8
GO:0051650	0.79	0.32	9	143	establishment of vesicle localization	BP	1	TMED9,ARFGAP3,PREB,MYO5A,RAB27A,SYT4,NDE1,TOR1A,BLOC1S2	darkgrey	VSMC_M8
GO:0002449	0.79	0.31	10	159	lymphocyte mediated immunity	BP	1	TUBB,FAM49B,MSH6,UNG,TFRC,NSD2,EXO1,RAB27A,EMP2,TUBB4B	darkgrey	VSMC_M8
GO:0014032	0.79	0.37	4	69	neural crest cell development	BP	1	SNAI2,NOLC1,PHACTR4,EFNB1	darkgrey	VSMC_M8
GO:0043502	0.79	0.37	4	71	regulation of muscle adaptation	BP	1	DDX39B,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0000041	0.79	0.35	5	86	transition metal ion transport	BP	1	SLC31A1,FLVCR1,TFRC,FKBP4,SLC30A1	darkgrey	VSMC_M8
GO:0006641	0.80	0.37	4	70	triglyceride metabolic process	BP	1	MFSD2A,GK,ACSL4,LIPG	darkgrey	VSMC_M8
GO:0001776	0.80	0.37	4	70	leukocyte homeostasis	BP	1	AXL,BAP1,CCNB2,PIK3CD	darkgrey	VSMC_M8
GO:0046887	0.80	0.34	5	86	positive regulation of hormone secretion	BP	1	VAMP8,RBP4,SELENOT,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0045216	0.80	0.31	9	146	cell-cell junction organization	BP	1	TJP2,STRN,ZNF703,SNAI2,MTDH,NF2,PAK2,ECT2,FSCN1	darkgrey	VSMC_M8
GO:0071356	0.80	0.30	10	163	cellular response to tumor necrosis factor	BP	1	SPHK1,CHUK,TRAIP,DHX9,BRCA1,UBE2K,EIF5A,COL1A1,HAS2,PID1	darkgrey	VSMC_M8
GO:0035194	0.80	0.33	6	112	post-transcriptional gene silencing by RNA	BP	1	HNRNPA2B1,DDX5,EIF4G1,DHX9,DGCR8,SRRT	darkgrey	VSMC_M8
GO:1903052	0.80	0.32	7	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	VCP,CDC20,CHFR,PSMC5,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8

GO:0071345	0.80	0.25	39	574	cellular response to cytokine stimulus	BP	1	SRSF3,HSP90AB1,CDC5L,SYNCRIP,B3GNT2,MCM2,CDC42EP4,AXL,SPHK1,CD44,MSC,HELLS,TUBA1B,MYBL2,CHUK,NCL,TRAIP,MNDA,XBP1,TFRC,DHX9,BRCA1,TFPI,CNOT9,HNRNPU,ADIPOR2,UBE2K,EIF5A,HDGF,COL1A1,SLC25A5,RBMX,GCLM,CTH,GBP5,HAS2,SRSF7,PID1,SRM	darkgrey	VSMC_M8
GO:0045766	0.80	0.31	8	133	positive regulation of angiogenesis	BP	1	SPHK1,HGF,MTDH,RUNX1,ETS1,XBP1,BRCA1,PIK3CD	darkgrey	VSMC_M8
GO:1904018	0.80	0.31	8	133	positive regulation of vasculature development	BP	1	SPHK1,HGF,MTDH,RUNX1,ETS1,XBP1,BRCA1,PIK3CD	darkgrey	VSMC_M8
GO:1990845	0.80	0.31	8	132	adaptive thermogenesis	BP	1	THADA,NRDC,PGAM5,ELOVL6,FH,HNRNPU,ADIPOR2,SLC25A5	darkgrey	VSMC_M8
GO:0022409	0.80	0.29	11	176	positive regulation of cell-cell adhesion	BP	1	FAM49B,PLAUR,CD44,RUNX1,ETS1,XBP1,TFRC,PDPN,EFNB1,CBFB,HAS2	darkgrey	VSMC_M8
GO:0019724	0.80	0.34	5	87	B cell mediated immunity	BP	1	MSH6,UNG,TFRC,NSD2,EXO1	darkgrey	VSMC_M8
GO:0043500	0.80	0.34	5	88	muscle adaptation	BP	1	DDX39B,EZH2,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0001816	0.80	0.25	34	504	cytokine production	BP	1	EZR,PANX2,FAM49B,POLR3B,HSP90AB1,EZH2,MAST2,AXL,SPHK1,POLR3F,HGF,SNAI2,HMGB2,TOMM70,BAP1,CHUK,RUNX1,SETD4,TRAIP,MNDA,XBP1,DHX9,POLA1,DDX21,EPHB2,UFD1,BRCA1,DHX33,RAC1,ARG2,ALOX15B,NFATC2IP,PIK3CD,GBP5	darkgrey	VSMC_M8
GO:0034284	0.81	0.29	10	164	response to monosaccharide	BP	1	NAMPT,EIF2B1,SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,ADIPOR2,GCLM	darkgrey	VSMC_M8
GO:0034763	0.81	0.33	5	88	negative regulation of transmembrane transport	BP	1	THADA,EPHB2,NEDD4,PID1,SLC30A1	darkgrey	VSMC_M8
GO:0055072	0.81	0.35	4	72	iron ion homeostasis	BP	1	STEAP1,FLVCR1,TFRC,EIF2AK1	darkgrey	VSMC_M8
GO:0110020	0.81	0.33	5	86	regulation of actomyosin structure organization	BP	1	NF2,PAK2,ECT2,RAC1,STMN1	darkgrey	VSMC_M8
GO:0010595	0.81	0.32	6	105	positive regulation of endothelial cell migration	BP	1	ATP5F1B,NUS1,ETS1,RAC1,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0033993	0.81	0.23	45	657	response to lipid	BP	1	EZH2,GJB3,SDC1,RUVBL2,PGR,CCNA2,PPP5C,FOSB,NASP,CAD,DDX18,AXL,PCNA,ZNF703,CCNB1,SNAI2,E2F1,HMGB2,RBP4,NRIP1,HEY1,MTDH,HMGCR,CHUK,KIF18A,ETS1,H2AFZ,RGS9,DDX5,XBP1,FOSL1,BRCA1,TFPI,CNOT9,HNRNPU,ADIPOR2,NEDD4,BID,COL1A1,TYMS,AIFM1,TFAP4,HNRNPD,PID1,MBD2	darkgrey	VSMC_M8
GO:0097306	0.81	0.35	4	71	cellular response to alcohol	BP	1	RAD51,BLM,BRCA1,AIFM1	darkgrey	VSMC_M8
GO:0045833	0.81	0.35	4	72	negative regulation of lipid metabolic process	BP	1	MFSD2A,SPHK1,SNAI2,BRCA1	darkgrey	VSMC_M8
GO:0001817	0.81	0.24	33	492	regulation of cytokine production	BP	1	EZR,PANX2,FAM49B,POLR3B,HSP90AB1,EZH2,MAST2,AXL,SPHK1,POLR3F,HGF,SNAI2,HMGB2,TOMM70,BAP1,CHUK,RUNX1,SETD4,TRAIP,MNDA,XBP1,DHX9,POLA1,DDX21,EPHB2,UFD1,BRCA1,DHX33,RAC1,ARG2,ALOX15B,PIK3CD,GBP5	darkgrey	VSMC_M8
GO:1903707	0.81	0.35	4	72	negative regulation of hemopoiesis	BP	1	HSPA9,LOXL3,RUNX1,CBFB	darkgrey	VSMC_M8
GO:0060996	0.81	0.33	5	87	dendritic spine development	BP	1	PAK2,EPHB2,MAPK6,ACSL4,ARF6	darkgrey	VSMC_M8
GO:0045619	0.81	0.30	7	117	regulation of lymphocyte differentiation	BP	1	AXL,LOXL3,RUNX1,XBP1,PRELID1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0051897	0.81	0.33	5	88	positive regulation of protein kinase B signaling	BP	1	HSP90AB1,AXL,MTDH,MAZ,PIK3CD	darkgrey	VSMC_M8
GO:0006575	0.81	0.29	8	136	cellular modified amino acid metabolic process	BP	1	ALDH1L2,MFSD2A,GGH,MTHFD1,TYMS,G6PD,GCLM,GART	darkgrey	VSMC_M8
GO:0050851	0.81	0.30	7	117	antigen receptor-mediated signaling pathway	BP	1	EZR,KCNN4,EIF2B1,KHDRBS1,MNDA,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0046777	0.82	0.27	13	204	protein autophosphorylation	BP	1	MELK,TRIM28,TTK,CAD,NEK2,PAK2,EIF2AK1,EIF2S1,AURKB,VRK1,RAP2C,NEK6,AURKA	darkgrey	VSMC_M8
GO:0071456	0.82	0.30	7	119	cellular response to hypoxia	BP	1	CCNA2,CCNB1,E2F1,MDM4,SUV39H1,LMNA,BRIP1	darkgrey	VSMC_M8
GO:0030099	0.82	0.25	19	293	myeloid cell differentiation	BP	1	HSPA9,HOXA5,PABPC4,PRMT1,NCAPG2,HMGB2,RUNX1,ETS1,FLVCR1,TFRC,EIF2AK1,LYAR,LBR,HOXB7,SLC25A5,G6PD,PIK3CD,CBFB,TMOD3	darkgrey	VSMC_M8
GO:1905477	0.82	0.32	5	88	positive regulation of protein localization to membrane	BP	1	EZR,EPHB2,MTCL1,ARF6,ACSL3	darkgrey	VSMC_M8
GO:0062014	0.82	0.34	4	73	negative regulation of small molecule metabolic process	BP	1	MFSD2A,SNAI2,BRCA1,PID1	darkgrey	VSMC_M8
GO:0072006	0.82	0.30	7	118	nephron development	BP	1	NUP107,SEC61A1,NUP85,NUP160,NUP133,SIX4,HOXB7	darkgrey	VSMC_M8
GO:0050773	0.82	0.32	5	87	regulation of dendrite development	BP	1	MFSD2A,EZH2,CDC20,NEDD4,ARF6	darkgrey	VSMC_M8
GO:0060537	0.82	0.24	21	323	muscle tissue development	BP	1	ALPK2,DDX39B,PRMT1,PARP2,CCNB1,RBP4,MSC,HEY1,TBX3,HMGCR,RUNX1,DDX5,CENPF,CDK1,SIX4,MSX1,HNRNPU,LMNA,TP73,G6PD,FAM129B	darkgrey	VSMC_M8
GO:0048864	0.82	0.33	4	72	stem cell development	BP	1	SNAI2,NOLC1,PHACTR4,EFNB1	darkgrey	VSMC_M8
GO:0048639	0.82	0.29	8	134	positive regulation of developmental growth	BP	1	DDX39B,EZR,RNF157,PARP2,CCNB1,CDK1,PPIB,SYT4	darkgrey	VSMC_M8
GO:0016441	0.82	0.30	6	115	posttranscriptional gene silencing	BP	1	HNRNPA2B1,DDX5,EIF4G1,DHX9,DGCR8,SRRT	darkgrey	VSMC_M8
GO:0007420	0.82	0.23	40	587	brain development	BP	1	NARS,TTLL1,KIF27,ANP32B,MFSD2A,EZH2,CASP2,STIL,GRIN2C,SMG9,AXL,SPHK1,XRN2,RRM1,WDR62,SNRPB,E2F1,TBX3,ETS1,KIF14,ASPM,NF2,H2AFX,ARCN1,CENPF,TRA2B,EPHB2,TACC3,MNAT1,MSX1,BID,NES,SYT4,NDE1,G6PD,SLC6A17,HNRNPD,ACSL3,STMN1,GART	darkgrey	VSMC_M8
GO:0006720	0.82	0.33	4	73	isoprenoid metabolic process	BP	1	NUS1,RBP4,HMGCR,ALDH3A2	darkgrey	VSMC_M8
GO:0022900	0.82	0.29	8	149	electron transport chain	BP	1	CYC1,CYCS,CCNB1,NDUFAF1,CDK1,NDUFS1,MYBBP1A,BID	darkgrey	VSMC_M8
GO:0045621	0.82	0.33	4	72	positive regulation of lymphocyte differentiation	BP	1	AXL,RUNX1,XBP1,CBFB	darkgrey	VSMC_M8
GO:0071322	0.83	0.29	7	121	cellular response to carbohydrate stimulus	BP	1	SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,GCLM	darkgrey	VSMC_M8
GO:0044106	0.83	0.33	4	74	cellular amine metabolic process	BP	1	ODC1,AMD1,AFMID,SRM	darkgrey	VSMC_M8
GO:1903364	0.83	0.28	8	137	positive regulation of cellular protein catabolic process	BP	1	EZR,VCP,CDC20,CHFR,PSMC5,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0014031	0.83	0.32	4	73	mesenchymal cell development	BP	1	SNAI2,NOLC1,PHACTR4,EFNB1	darkgrey	VSMC_M8
GO:0009266	0.83	0.27	8	137	response to temperature stimulus	BP	1	PSIP1,VCP,HSP90AB1,DNAJC2,CHORDC1,EIF2B1,DNAJC7,EIF2S1	darkgrey	VSMC_M8
GO:0061097	0.83	0.32	4	74	regulation of protein tyrosine kinase activity	BP	1	NCAPG2,CHMP6,PAK2,RAP2C	darkgrey	VSMC_M8
GO:0055076	0.83	0.29	6	107	transition metal ion homeostasis	BP	1	STEAP1,SLC31A1,FLVCR1,TFRC,EIF2AK1,SLC30A1	darkgrey	VSMC_M8
GO:0007173	0.83	0.30	5	90	epidermal growth factor receptor signaling pathway	BP	1	NUP62,PLAUR,CHMP6,CNOT9,BCAR1	darkgrey	VSMC_M8
GO:0002366	0.83	0.25	11	181	leukocyte activation involved in immune response	BP	1	MSH6,VAMP8,LOXL3,ENTPD7,UNG,XBP1,TFRC,NSD2,EXO1,RAB27A,PIK3CD	darkgrey	VSMC_M8

GO:0051603	0.83	0.21	43	639	proteolysis involved in cellular protein catabolic process	BP	1	CDK2,MAN1A1,DESI1,VCP,HSP90AB1,CDC20,CHFR,PSMD13,CDC16,ANAPC1,HSP90B1,PBK,BAP1,UBE2C,PSMD14,KIF14,XBP1,DTL,PSMD4,PSMC5,SMARCC1,PSMA6,UFD1,USP42,UCHL1,UBE2K,NEDD4,PSMD3,RAD23A,PLK1,PSMD11,COPS3,USP1,UHRF1,CCNF,ZNF598,PSMA5,TOR1A,USP4,AURKA,UBE2S,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:1903532	0.83	0.25	12	196	positive regulation of secretion by cell	BP	1	EZR,SDC1,KCNN4,VAMP8,RBP4,SELENOT,PPID,RAC1,RAB27A,SYT4,ACSL4,ARF6	darkgrey	VSMC_M8
GO:0002700	0.83	0.28	6	106	regulation of production of molecular mediator of immune response	BP	1	RBP4,XBP1,TFRC,DDX21,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0016050	0.84	0.23	16	255	vesicle organization	BP	1	TMED9,FBXO5,ARFGAP3,SDC1,PREB,SPHK1,SEC23B,CHMP6,VAMP8,KNL1,SEC24D,RAB27A,SYT4,HOOK1,BLOC1S2,STXBP6	darkgrey	VSMC_M8
GO:0046632	0.84	0.31	4	74	alpha-beta T cell differentiation	BP	1	LOXL3,ENTPD7,RUNX1,CBFB	darkgrey	VSMC_M8
GO:0071692	0.84	0.23	17	271	protein localization to extracellular region	BP	1	EZR,FBN2,ARFGAP3,CYP51A1,PREB,KCNN4,NECAB3,RBP4,SELENOT,PPID,HMGCR,CDK16,RAC1,LTBP2,ACSL4,ARF6,ERP29	darkgrey	VSMC_M8
GO:0034446	0.84	0.29	5	89	substrate adhesion-dependent cell spreading	BP	1	AXL,KIF14,RAC1,PDPN,HAS2	darkgrey	VSMC_M8
GO:0044089	0.84	0.21	29	441	positive regulation of cellular component biogenesis	BP	1	VCP,CEP135,TRIM28,ANLN,NUP62,SDC1,PLK4,CDC42EP4,CENPJ,TERF1,CKAP5,ICE1,NF2,EIF4G1,PSMC5,TFRC,EPHB2,DHX33,RAC1,FSCN1,BID,DNMT1,POLDIP2,CDT1,TPPP3,ARPC4,ARF6,GBP5,CLSTN3	darkgrey	VSMC_M8
GO:0120034	0.84	0.29	5	92	positive regulation of plasma membrane bounded cell projection assembly	BP	1	CEP135,ANLN,CDC42EP4,RAC1,FSCN1	darkgrey	VSMC_M8
GO:0070997	0.84	0.22	18	288	neuron death	BP	1	HSP90AB1,CASP2,NAMPT,PPP5C,AXL,PARP2,MYBL2,CIT,KIF14,EIF4G1,SIX4,BID,EIF2S1,NES,AIFM1,G6PD,GCLM,SIGMAR1	darkgrey	VSMC_M8
GO:0007498	0.84	0.29	5	89	mesoderm development	BP	1	PUS7,TBX3,NUP133,NF2,PALB2	darkgrey	VSMC_M8
GO:0048193	0.84	0.23	16	259	Golgi vesicle transport	BP	1	TMED9,ARFGAP3,VCP,NBAS,COG3,PREB,SEC23B,SLC10A7,PITPNB,SEC24D,ARCN1,ZW10,KDELR2,MYO5A,ACSL3,STXBP6	darkgrey	VSMC_M8
GO:0050868	0.84	0.30	4	76	negative regulation of T cell activation	BP	1	LOXL3,RUNX1,ARG2,CBFB	darkgrey	VSMC_M8
GO:0045087	0.84	0.20	30	459	innate immune response	BP	1	TUBB,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,SYNCRIP,SEC61A1,CDC42EP4,AXL,POLR3F,HMGB2,TRIM35,TOMM70,CHUK,MNDA,RBM14,PAK2,DHX9,DDX21,LYAR,RAB27A,UBE2K,ARG2,ELF4,TUBB4B,PIK3CD,GBP5,HMGB3,TRIM59	darkgrey	VSMC_M8
GO:0048638	0.84	0.22	16	257	regulation of developmental growth	BP	1	DDX39B,EZR,MFSD2A,RNF157,PARP2,CCNB1,RBP4,RUNX1,FLVCR1,CDK1,SIX4,PPIB,SPAG9,SYT4,TP73,G6PD	darkgrey	VSMC_M8
GO:0009743	0.85	0.23	11	186	response to carbohydrate	BP	1	NAMPT,EIF2B1,SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,ADIPOR2,CDT1,GCLM	darkgrey	VSMC_M8
GO:0034097	0.85	0.19	44	659	response to cytokine	BP	1	SRSF3,HSP90AB1,CDC5L,SYNCRIP,B3GNT2,MCM2,SEC61A1,CDC42EP4,AXL,SPHK1,CD44,MSC,HELLS,TUBA1B,MYBL2,CHUK,ETS1,NCL,TRAIP,MNDA,XBP1,TFRC,FOSL1,DHX9,BRCA1,TFPI,CNOT9,HNRNPU,ADIPOR2,UBE2K,EIF5A,HDGF,COL1A1,ACSL4,TYMS,SLC25A5,RBMX,GCLM,CTH,GBP5,HAS2,SRSF7,PID1,SRM	darkgrey	VSMC_M8
GO:0002705	0.85	0.29	4	76	positive regulation of leukocyte mediated immunity	BP	1	FAM49B,TFRC,DDX21,NSD2	darkgrey	VSMC_M8
GO:0045446	0.85	0.27	5	91	endothelial cell differentiation	BP	1	EZR,TJP2,HEY1,PDPN,RAP2C	darkgrey	VSMC_M8
GO:1901216	0.85	0.29	4	78	positive regulation of neuron death	BP	1	CASP2,MYBL2,EIF2S1,AIFM1	darkgrey	VSMC_M8
GO:0009308	0.85	0.29	4	77	amine metabolic process	BP	1	ODC1,AMD1,AFMID,SRM	darkgrey	VSMC_M8
GO:1901879	0.85	0.29	4	75	regulation of protein depolymerization	BP	1	CKAP2,TPX2,NES,TMOD3	darkgrey	VSMC_M8
GO:0050864	0.85	0.27	5	93	regulation of B cell activation	BP	1	MNDA,XBP1,TFRC,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0072359	0.85	0.18	62	902	circulatory system development	BP	1	ALPK2,ATP5F1B,DDX39B,NUS1,MATR3,COL1A2,ANP32B,HOXA5,PRMT1,NAA15,STIL,AMOTL1,PRCP,SMG9,CAD,SPHK1,PARP2,E2F7,PCNA,HGF,ELK3,CCNB1,SNAI2,ADAMTS6,RBP4,MSC,HEY1,FMNL3,TBX3,CREB3L1,E2F8,MTDH,RUNX1,MDM4,ETS1,NCL,XBP1,FLVCR1,CDK1,FOSL1,EPHB2,BRCA1,NSD2,MNAT1,MSX1,HNRNPU,ADIPOR2,MTHFD1,PDPN,SH3PXD2B,LMNA,COL1A1,DNMT1,EMP2,NXN,TP73,G6PD,PIK3CD,FAM129B,CTH,HAS2,MBD2	darkgrey	VSMC_M8
GO:1901136	0.85	0.25	7	126	carbohydrate derivative catabolic process	BP	1	MAN1A1,CD44,ENTPD7,UNG,DUT,NUDT1,DCTPP1	darkgrey	VSMC_M8
GO:0071216	0.85	0.24	9	157	cellular response to biotic stimulus	BP	1	FAM49B,AXL,HMGB2,MTDH,PPP1R15B,XBP1,TFPI,BID,SMC1A	darkgrey	VSMC_M8
GO:0002263	0.85	0.23	11	185	cell activation involved in immune response	BP	1	MSH6,VAMP8,LOXL3,ENTPD7,UNG,XBP1,TFRC,NSD2,EXO1,RAB27A,PIK3CD	darkgrey	VSMC_M8
GO:0048659	0.85	0.25	7	128	smooth muscle cell proliferation	BP	1	DDX39B,NAMPT,HMGCR,SF1,MNAT1,DNMT1,POLDIP2	darkgrey	VSMC_M8
GO:0010634	0.85	0.24	8	143	positive regulation of epithelial cell migration	BP	1	ATP5F1B,NUS1,ETS1,RAC1,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0043244	0.85	0.26	6	107	regulation of protein-containing complex disassembly	BP	1	CKAP2,TPX2,EIF5A,NES,GLE1,TMOD3	darkgrey	VSMC_M8
GO:0051648	0.85	0.23	9	154	vesicle localization	BP	1	TMED9,ARFGAP3,PREB,MYO5A,RAB27A,SYT4,NDE1,TOR1A,BLOC1S2	darkgrey	VSMC_M8
GO:0051216	0.85	0.23	9	154	cartilage development	BP	1	HOXA5,SERPINH1,SNAI2,CD44,RUNX1,IFT80,MSX1,COL1A1,TYMS	darkgrey	VSMC_M8

GO:0050896	0.86	0.16	435	5876	response to stimulus	BP	1	CDK2,ALPK2,BCLAF1,TUBB,DDX39B,FBXO5,EZR,FBN2,PANX2,GTSE1,RAD21,TTLL1,NUS1,MAN1A1,FAM49B,RANGAP1,HSPA9,FKBP5,MATR3,SRPK1,SRSF3,CYC1,PSIP1,RECQL4,TONSL,MCM5,HMGXB4,PPP2R5D,PWP1,APTX,POLR3B,POLH,VCP,HSP90AB1,CDC5L,COL1A2,MCM3,MIOS,MELK,TRIM28,MSH6,CTPS1,TTK,CLEC11A,POLD1,MFSD2A,SYNCRIP,PABPC4,B3GNT2,SLC31A1,EZH2,ODC1,NUP62,MMS22L,CLSPN,PRMT1,GJB3,CASP2,SHCBP1,SMC6,ORC1,GEN1,SDC1,RUVBL2,PGR,NAMPT,STIL,LIG1,MCM2,SEC61A1,RUVBL1,CCNA2,AMOTL1,DNAJC2,RAD54L,CHORDC1,RNASEH2B,PPP5C,WDR33,MASTL,MAST2,FOSB,CD3EAP,CDC42EP4,NASP,GRIN2C,PRCP,KCNN4,NUP85,PLAUR,MCM10,CAD,DDX18,HNRNPUL1,SRP68,AXL,RNF157,SPHK1,MCM6,SRSF2,FANCD2,ULK4,NCAPG2,GDI2,NET1,SERPINH1,PARP2,POLR3F,POLD3,RAD18,IPO5,SUPT16H,EIF4A3,CHMP6,E2F7,GINS4,DOCK9,ARHGDIA,STRN,RRM1,SPA1L3,PCNA,CHFR,POLE,ZNF703,RFC3,HGF,TOPBP1,ELK3,RRP8,CBX5,CCNB1,MCM4,SNAI2,CD44,BUB1,DEPDC1B,SLC20A1,GGH,PARPBP,PSD4,SGK3,WDR36,CENPJ,HSP90B1,EIF2B1,E2F1,CCNE1,VAMP8,KNTC1,HMGB2,TRAM1,CEP55,RBP4,MSC,ATF1,SSRP1,TERF1,HELLS,NRIP1,ARHGAP11A,RACGAP1,LOXL3,PBK,ESCO2,HEY1,NEIL3,SELENOT,TUBA1B,PPID,RBL1,TRIM35,MSH3,BUB1B,RSRC1,FAM83D,NUP93,KNSTRN,TBX3,RAD51,DCLRE1B,CREB3L1,TOMM70,MYBL2,TRIM33,ENTPD7,MTDH,YWHAB,HMGCR,BAP1,NRAS,EEF1E1,CHUK,SETD4,PPP1R15B,MDM4,CHAF1B,PAK1IP1,RFC5,PSMD14,NCOA5,HMGN1,NOLC1,CCT5,CIT,NUCKS1,DEK,GCN1,KIF18A,MANF,ETS1,METAP1,TENT4A,NSUN2,UBE2T,CHEK1,H2AFZ,RASSF1,SMC3,KHDRBS1,TRIP13,C	darkgrey	VSMC_M8
GO:0006694	0.86	0.24	7	126	steroid biosynthetic process	BP	1	CYP51A1,SNAI2,HMGCR,DDX20,SF1,LBR,G6PD	darkgrey	VSMC_M8
GO:0071248	0.86	0.24	8	141	cellular response to metal ion	BP	1	PPP5C,FOSB,CCNB1,CHUK,ECT2,EIF2S1,FUS,SYT4	darkgrey	VSMC_M8
GO:0045732	0.86	0.22	12	203	positive regulation of protein catabolic process	BP	1	EZR,VCP,NRDC,CDC20,CHFR,DTL,PSMC5,BARD1,NEDD4,RAD23A,PLK1,AURKA	darkgrey	VSMC_M8
GO:0014033	0.86	0.28	4	77	neural crest cell differentiation	BP	1	SNAI2,NOLC1,PHACTR4,EFNB1	darkgrey	VSMC_M8
GO:0045860	0.86	0.20	19	305	positive regulation of protein kinase activity	BP	1	PRRC1,DBF4,HSP90AB1,CKS2,EZH2,CLSPN,BORA,CDC25B,CCNB1,TPX2,CENPE,KIF14,PAK2,ECT2,MNAT1,INCENP,CDC6,EMP2,ERP29	darkgrey	VSMC_M8
GO:0008286	0.86	0.26	5	93	insulin receptor signaling pathway	BP	1	NCOA5,NUCKS1,SMARCC1,BCAR1,PID1	darkgrey	VSMC_M8
GO:0051017	0.86	0.23	8	139	actin filament bundle assembly	BP	1	EZR,HSP90B1,FHDC1,NF2,PAK2,RAC1,FSCN1,STMN1	darkgrey	VSMC_M8
GO:0051224	0.86	0.26	5	96	negative regulation of protein transport	BP	1	RANGAP1,CYP51A1,HMGCR,BARD1,ERP29	darkgrey	VSMC_M8
GO:0034341	0.86	0.26	5	95	response to interferon-gamma	BP	1	HSP90AB1,SYNCRIP,SEC61A1,CDC42EP4,GBP5	darkgrey	VSMC_M8
GO:1901575	0.86	0.16	114	1628	organic substance catabolic process	BP	1	CDK2,POP1,EZR,MAN1A1,DESI1,GCAT,ALDH1L2,CYP51A1,VCP,HSP90AB1,NCBP1,GRSF1,MFSD2A,SYNCRIP,PABPC4,THRAP3,ODC1,NBAS,NRDC,RNASEH2B,GRIN2C,SMG9,DIS3,SPHK1,XRN2,CDC20,AFMID,EIF4A3,CHMP6,PCCA,CHFR,EXOSC8,PSMD13,CDC16,CD44,ANAPC1,HSP90B1,E2F1,AADAT,PBK,FAM83D,ENTPD7,HMGCR,BAP1,MDM4,UBE2C,PSMD14,FASTKD3,TENT4A,NSUN2,KIF14,UNG,DDX5,XBP1,UTP25,DTL,SSB,PSMD4,PSMC5,SMARCC1,GALE,DHX9,HNRNPR,PSMA6,DNA2,GK,BARD1,DUT,UFD1,CNOT9,USP42,HNRNPU,UCHL1,UBE2K,NEDD4,PSMD3,ARG2,NUDT1,DCTPP1,EXOSC10,FUS,RAD23A,PLK1,ELAC2,EDC3,TAF15,PSMD11,COPS3,HNRNPM,SERBP1,AIFM1,USP1,UHRF1,LIPG,SMG6,CCNF,RNPS1,ZNF598,DKC1,REXO4,PSMA5,ZC3H18,EXOSC2,TOR1A,SF3B3,USP4,HNRNPD,MAD2L1,AURKA,UBE2S,FEN1,PJA1,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0046890	0.86	0.24	7	127	regulation of lipid biosynthetic process	BP	1	MFSD2A,SPHK1,SNAI2,DDX20,SF1,BRCA1,ACSL3	darkgrey	VSMC_M8
GO:0002699	0.86	0.23	8	142	positive regulation of immune effector process	BP	1	FAM49B,VAMP8,RBP4,XBP1,TFRC,DDX21,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0090288	0.86	0.27	4	78	negative regulation of cellular response to growth factor stimulus	BP	1	CREB3L1,TRIM33,NEDD4,FAM129B	darkgrey	VSMC_M8
GO:0042594	0.86	0.22	9	158	response to starvation	BP	1	MIOS,MFSD2A,CAD,RRP8,GCN1,XBP1,MYBBP1A,EIF2AK1,EIF2S1	darkgrey	VSMC_M8
GO:0007507	0.86	0.18	31	474	heart development	BP	1	ALPK2,DDX39B,MATR3,PRMT1,STIL,SMG9,CAD,PARP2,PCNA,CCNB1,SNAI2,ADAMTS6,RBP4,MSC,HEY1,TBX3,RUNX1,MDM4,CDK1,NSD2,MNAT1,MSX1,HNRNPU,ADIPOR2,MTHFD1,SH3PXD2B,LMNA,TP73,G6PD,HAS2,MBD2	darkgrey	VSMC_M8
GO:0001657	0.86	0.27	4	78	ureteric bud development	BP	1	SDC1,SIX4,ARG2,HOXB7	darkgrey	VSMC_M8
GO:0014812	0.86	0.27	4	79	muscle cell migration	BP	1	NET1,S100A11,SIX4,HAS2	darkgrey	VSMC_M8
GO:0030705	0.86	0.22	10	173	cytoskeleton-dependent intracellular transport	BP	1	TUBB,TUBA1B,MYO5A,HNRNPU,UCHL1,KIF4A,SYT4,NDE1,HOOK1,BLOC1S2	darkgrey	VSMC_M8
GO:1902532	0.87	0.18	26	407	negative regulation of intracellular signal transduction	BP	1	DDX39B,EZR,FAM49B,NUP62,PLAUR,RNF157,SNAI2,CD44,HELLS,PBK,CREB3L1,HMGCR,CIT,XBP1,NF2,PDE3A,EPHB2,UFD1,FOXM1,UCHL1,BID,NOC2L,CDT1,STMN1,TRIM59,DUSP7	darkgrey	VSMC_M8
GO:0031214	0.87	0.23	7	126	biomineral tissue development	BP	1	FBXO5,FBN2,COL1A2,SLC20A1,HEY1,IFT80,COL1A1	darkgrey	VSMC_M8
GO:0007029	0.87	0.27	4	80	endoplasmic reticulum organization	BP	1	SEC61A1,TRAM1,REEP4,EMC8	darkgrey	VSMC_M8
GO:0002460	0.87	0.21	10	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	FAM49B,MSH6,LOXL3,ENTPD7,UNG,TFRC,NSD2,EXO1,RAB27A,EMP2	darkgrey	VSMC_M8
GO:0042476	0.87	0.25	5	95	odontogenesis	BP	1	COL1A2,SDC1,NF2,MSX1,COL1A1	darkgrey	VSMC_M8
GO:0045944	0.87	0.16	62	904	positive regulation of transcription by RNA polymerase II	BP	1	BCLAF1,ATAD2,CDC5L,HOXA5,THRAP3,RUVBL2,PGR,NAMPT,FOSB,NUFIP1,SUPT16H,E2F7,CKAP2,HGF,ELK3,TCERG1,TCEA1,E2F1,ZNF827,HMGB2,ATF1,NRIP1,HEY1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,CHUK,RUNX1,PPRC1,NUCKS1,GCN1,ETS1,H2AFZ,NCL,XBP1,HINFP,RBM14,FOSL1,SMARCC1,DHX9,ETV4,BRCA1,GABPB1,SIX4,FOXM1,MSX1,HNRNPU,TOP2A,EIF5A,HOXB7,NFATC2IP,MORF4L2,ELF4,UHRF1,RBMX,TFAP4,TP73,CBFB,DRAP1,PID1	darkgrey	VSMC_M8
GO:0009755	0.87	0.22	8	142	hormone-mediated signaling pathway	BP	1	PGR,PPP5C,PRCP,DDX5,BRCA1,CNOT9,ADIPOR2,NEDD4	darkgrey	VSMC_M8
GO:0043401	0.87	0.24	6	111	steroid hormone mediated signaling pathway	BP	1	PGR,PPP5C,DDX5,BRCA1,CNOT9,NEDD4	darkgrey	VSMC_M8

GO:0032502	0.87	0.15	337	4589	developmental process	BP	1	RTTN,CDK2,ALPK2,NARS,ATP5F1B,HNRNPAB,NUP107,DDX39B,FBXO5,EZR,FBN2,TTLL1,NUS1,KIFC1,PHF5A,FAM49B,CDC25C,HSPA9,MATR3,SRPK1,KIF27,RECQL4,BYSL,PPP2R5D,PWP1,TJP2,HSP90AB1,COL1A2,MELK,TRIM28,ANP32B,MSH6,GRSF1,HOXA5,COL9A2,MFSD2A,SYNCRIP,PABPC4,B3GNT2,EZH2,NUP62,PHF19,PRMT1,GJB3,CASP2,NAA15,SMC6,SDC1,PLK4,PGR,NAMPT,STIL,PUS7,LIG1,MCM2,SEC61A1,RUVBL1,CCNA2,AMOTL1,RADS4L,RNASEH2B,WDR33,MAST2,CDC42EP4,NASP,GRIN2C,PRCP,SMG9,NUP85,CAD,AXL,RNF157,SPHK1,XRN2,ULK4,NCAPG2,WDR43,CDC20,SERPINH1,PARP2,FBL,RRBP1,GTPBP4,EIF4A3,NAP1L1,E2F7,GINS4,ARHGDIA,ALYREF,STRN,RRM1,SIPA1L3,PCNA,PGAM5,CDC25B,POLE,ZNF703,HGF,ELK3,MEDAG,CCNB1,WDR62,SNAI2,SNRPB,CD44,POLR1B,KIF20B,KIF2A,SLC20A1,ADAMTS6,WEE1,EIF2B1,E2F1,CENPU,SLC10A7,HMGB2,CEP55,RBP4,MSC,ATF1,HELLS,NRIP1,NUP160,RACGAP1,LOXL3,ESCO2,HEY1,SELENOT,FMNL3,AGPAT5,RBL1,MSH3,CTNNBL1,GNL3,FAM83D,RBM19,KNL1,TBX3,CREB3L1,E2F8,ENTPD7,MTDH,HMGCR,EEF1E1,CHUK,RUNX1,MDM4,PAK1IP1,NAV2,HMGN1,NOLC1,CIT,KIF18A,MANF,ETS1,NSUN2,GMNN,CHEK1,SNRPA1,NAV1,SMC3,KHDRBS1,TRIP13,NCL,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,IQCB1,CLMP,DDX5,PHACTR4,XBP1,SPP2,UTP25,MCM3AP,EIF4H,NEK2,NUP133,HINFP,NF2,H2AFX,SEC24D,FLVCR1,PDE3A,CDC42SE1,UMPS,ARCN1,CENPF,STRAP,EIF4G1,NHS,ADAMTS4,CDK1,TFRC,PAK2,FOSL1,SMARCC1,DHX9,TRA2B,HNRNPH3,DDX20,DDX21,CABYR,PPP2R1B,IFT80,SF1,EPHB2,ETV4,UFD1,BRCA1,CNOT9,NSD2,TACC3,CDK16,MED28,MYBBP1A,CREG1,ANKLE1,ECT2,SUV39H1,FK	darkgrey	VSMC_M8
GO:0061572	0.87	0.22	8	141	actin filament bundle organization	BP	1	EZR,HSP90B1,FHDC1,NF2,PAK2,RAC1,FSCN1,STMN1	darkgrey	VSMC_M8
GO:0071346	0.87	0.26	4	80	cellular response to interferon-gamma	BP	1	HSP90AB1,SYNCRIP,CDC42EP4,GBP5	darkgrey	VSMC_M8
GO:0060348	0.87	0.21	10	172	bone development	BP	1	SERPINH1,SLC10A7,IFT80,NSD2,MSX1,SH3PXD2B,COL1A1,PPIB,XYLT1,HAS2	darkgrey	VSMC_M8
GO:0110148	0.87	0.22	7	127	biomineralization	BP	1	FBXO5,FBN2,COL1A2,SLC20A1,HEY1,IFT80,COL1A1	darkgrey	VSMC_M8
GO:0072163	0.87	0.26	4	79	mesonephric epithelium development	BP	1	SDC1,SIX4,ARG2,HOXB7	darkgrey	VSMC_M8
GO:0072164	0.87	0.26	4	79	mesonephric tubule development	BP	1	SDC1,SIX4,ARG2,HOXB7	darkgrey	VSMC_M8
GO:0051345	0.87	0.17	28	440	positive regulation of hydrolase activity	BP	1	RANGAP1,VCP,HSP90AB1,ANP32B,CYCS,EZH2,CASP2,NET1,DOCK9,SIPA1L3,PCNA,TCEA1,ATP1B3,HMGB2,ARHGAP11A,PPP1R15B,PSMD14,DNAJC9,ECT2,BID,PRELID1,AHSA1,EIF5,POLDIP2,AIFM1,TFAP4,RAPGEF6,PDCD2	darkgrey	VSMC_M8
GO:1901214	0.87	0.19	15	251	regulation of neuron death	BP	1	HSP90AB1,CASP2,PPP5C,AXL,PARP2,MYBL2,KIF14,EIF4G1,SIX4,EIF2S1,NES,AIFM1,G6PD,GCLM,SIGMAR1	darkgrey	VSMC_M8
GO:0009615	0.87	0.19	15	253	response to virus	BP	1	POLR3B,ODC1,HNRNPUL1,POLR3F,VAMP8,TOMM70,CHUK,CCT5,FOSL1,DHX9,DDX21,UFD1,EIF5A,ILF3,STMN1	darkgrey	VSMC_M8
GO:0043434	0.87	0.18	19	308	response to peptide hormone	BP	1	RANGAP1,CYC1,CDC5L,CCNA2,CAD,GGH,EIF2B1,CHUK,NCOA5,NUCKS1,XBP1,SMARCC1,MYO5A,CDC6,SRSF5,COL1A1,BRIP1,BCAR1,PID1	darkgrey	VSMC_M8
GO:0010717	0.87	0.25	4	80	regulation of epithelial to mesenchymal transition	BP	1	EZH2,ZNF703,PDPN,COL1A1	darkgrey	VSMC_M8
GO:0030038	0.87	0.24	5	95	contractile actin filament bundle assembly	BP	1	FHDC1,NF2,PAK2,RAC1,STMN1	darkgrey	VSMC_M8
GO:0043149	0.87	0.24	5	95	stress fiber assembly	BP	1	FHDC1,NF2,PAK2,RAC1,STMN1	darkgrey	VSMC_M8
GO:0009306	0.87	0.18	16	266	protein secretion	BP	1	EZR,ARFGAP3,CYP51A1,PREB,KCNN4,NECAB3,RBP4,SELENOT,PPID,HMGCR,CDK16,RAC1,LTBP2,ACSL4,ARF6,ERP29	darkgrey	VSMC_M8
GO:0035592	0.87	0.18	16	266	establishment of protein localization to extracellular region	BP	1	EZR,ARFGAP3,CYP51A1,PREB,KCNN4,NECAB3,RBP4,SELENOT,PPID,HMGCR,CDK16,RAC1,LTBP2,ACSL4,ARF6,ERP29	darkgrey	VSMC_M8
GO:0048593	0.87	0.24	5	96	camera-type eye morphogenesis	BP	1	MFSD2A,RBP4,HMGN1,PHACTR4,EPHB2	darkgrey	VSMC_M8
GO:0071375	0.87	0.19	13	219	cellular response to peptide hormone stimulus	BP	1	RANGAP1,CDC5L,CCNA2,NCOA5,NUCKS1,XBP1,SMARCC1,MYO5A,CDC6,SRSF5,BRIP1,BCAR1,PID1	darkgrey	VSMC_M8
GO:0001558	0.87	0.18	21	339	regulation of cell growth	BP	1	DDX39B,NCBP1,MFSD2A,RNF157,SPHK1,NET1,PARP2,SGK3,BAP1,KIF14,EIF4G1,DCUN1D5,MSX1,ADIPOR2,SPAG9,SYT4,G6PD,EXOSC2,BCAR1,CDKN2C,CLSTN3	darkgrey	VSMC_M8
GO:1901699	0.87	0.17	33	508	cellular response to nitrogen compound	BP	1	CDK2,EZR,RANGAP1,CDC5L,COL1A2,EZH2,NAMPT,CCNA2,IPO5,HSP90B1,RAD51,NCOA5,NUCKS1,RGS9,PRMT5,XBP1,BLM,PDE3A,SMARCC1,DHX9,BRCA1,MYO5A,CDC6,SRSF5,COL1A1,BRIP1,DNMT1,AIFM1,BCAR1,GCLM,HNRNPD,PID1,CASP6	darkgrey	VSMC_M8
GO:0030326	0.88	0.23	5	96	embryonic limb morphogenesis	BP	1	FBN2,TBX3,FLVCR1,MSX1,ACD	darkgrey	VSMC_M8
GO:0035113	0.88	0.23	5	96	embryonic appendage morphogenesis	BP	1	FBN2,TBX3,FLVCR1,MSX1,ACD	darkgrey	VSMC_M8
GO:0071417	0.88	0.17	30	466	cellular response to organonitrogen compound	BP	1	EZR,RANGAP1,CDC5L,COL1A2,EZH2,NAMPT,CCNA2,IPO5,HSP90B1,RAD51,NCOA5,NUCKS1,RGS9,PRMT5,XBP1,BLM,PDE3A,SMARCC1,BRCA1,MYO5A,CDC6,SRSF5,COL1A1,BRIP1,DNMT1,BCAR1,GCLM,HNRNPD,PID1,CASP6	darkgrey	VSMC_M8
GO:0002443	0.88	0.19	13	221	leukocyte mediated immunity	BP	1	TUBB,FAM49B,MSH6,VAMP8,UNG,TFRC,DDX21,NSD2,EXO1,RAB27A,EMP2,TUBB4B,PIK3CD	darkgrey	VSMC_M8
GO:0022408	0.88	0.21	7	130	negative regulation of cell-cell adhesion	BP	1	GTPBP4,ZNF703,LOXL3,RUNX1,NF2,ARG2,CBFB	darkgrey	VSMC_M8
GO:0010243	0.88	0.15	53	793	response to organonitrogen compound	BP	1	EZR,MAN1A1,RANGAP1,CYC1,VCP,HSP90AB1,CDC5L,COL1A2,EZH2,SDC1,NAMPT,CCNA2,PPP5C,FOSB,CAD,IPO5,PCNA,GGH,HSP90B1,EIF2B1,RAD51,CHUK,NCOA5,NUCKS1,RGS9,PRMT5,XBP1,BLM,PDE3A,CDK1,FOSL1,SMARCC1,EFTUD2,UFD1,BRCA1,MYO5A,ADIPOR2,CDC6,DHX15,SRSF5,COL1A1,BRIP1,DNMT1,TYMS,AIFM1,TP73,TOR1A,BCAR1,GCLM,HNRNPD,PID1,CASP6,UBE2J2	darkgrey	VSMC_M8
GO:1901215	0.88	0.20	9	161	negative regulation of neuron death	BP	1	HSP90AB1,PPP5C,AXL,PARP2,KIF14,EIF4G1,SIX4,NES,GCLM	darkgrey	VSMC_M8

GO:0065007	0.88	0.14	626	8375	biological regulation	BP	1	CDK2,ALPK2,ATP5F1B,TMED9,HNRNPAB,BCLAF1,ABRACL,HNRNPH1,NUP107,CCT2,TUBB,VARS2,TCF19,DDX39B,FBXO5,PRRC1,VARS,EZR,FBN2,PANX2,TCP1,GTSE1,RAD21,DSCC1,TTLL1,NUS1,ARFGAP3,MTBP,ATAD2,DESI1,PHF5A,FAM49B,RANGAP1,KIF20A,ZNF367,CDC25C,HSPA9,MATR3,SRPK1,SRSF3,PSIP1,BYSL,HMGXB4,PPP2R5D,PWP1,APTX,DBF4,POLR3B,STEAP1,UBAP2,TJP2,POLH,CYP51A1,VCP,HSP90AB1,CDC5L,PUM3,COL1A2,ARHGEF39,CENPQ,CEP135,CKS2,MIOS,MELK,TRIM28,NCBP1,THADA,ANP32B,PPIH,U2AF2,PPP6R1,MSH6,CDCA7L,TTK,CYCS,HNRNPA2B1,GRSF1,CLEC11A,POLD1,HOXA5,MFSD2A,SYNCRIP,PPIE,PABPC4,CCT4,SLC31A1,ANLN,YRDC,THRAP3,EZH2,ODC1,NUP62,CLSPN,PHF19,PRMT1,CASP2,NBAS,ORC6,SHCBP1,NAA15,SMC6,ORC1,GEN1,NRDC,SDC1,RUVBL2,PLK4,PGR,NAMPT,STIL,PUS7,MCM2,RUVBL1,CCNA2,AMOTL1,SAE1,DNAJC2,CHORDC1,RNASEH2B,PPP5C,MASTL,MAST2,FOSB,CD3EAP,CDC42EP4,COG3,NUFIP1,GRIN2C,PRCP,PREB,KCNN4,SMG9,NUP85,PLAUR,CAD,KIF2C,DBI,BORA,DIS3,AXL,RNF157,SPHK1,SRSF2,FANCD2,XRN2,ULK4,NCAPG2,GDI2,NET1,WDR43,CDC20,BIRC5,SERPINH1,PARP2,SEC23B,POLR3F,GTPBP4,RAD18,IPO5,SUPT16H,EIF4A3,NAP1L1,CHMP6,E2F7,DOCK9,ARHGDIA,ALYREF,CKAP2,STRN,KCNK6,SIPA1L3,PCNA,CHFR,EXOSC8,PGAM5,CDC25B,ZNF703,RFC3,DCUN1D2,HGF,TOPBP1,ELK3,RRP8,CDC16,TCERG1,MEDAG,CBX5,CCNB1,SFSWAP,SNAI2,API5,CD44,AAAS,UTP20,TCEA1,ESPL1,HNRNPF,BUB1,TPX2,ANAPC1,DEPDC1B,KIF20B,SKA3,KIF2A,SLC20A1,UBA2,PARPBP,PSD4,SGK3,CENPJ,WEE1,HSP90B1,NECAB3,EIF2B1,E2F1,KIF11,ABCE1,CCNE1,PXYLP1,VAMP8,ZNF827,ATP1B3,SLC10A	darkgrey	VSMC_M8
GO:0045861	0.88	0.19	12	213	negative regulation of proteolysis	BP	1	HSP90AB1,PLAUR,BIRC5,SERPINH1,HGF,CD44,PBK,SPP2,PAK2,SMARCC1,TFPI,PTTG1	darkgrey	VSMC_M8
GO:0009267	0.88	0.21	7	130	cellular response to starvation	BP	1	MIOS,MFSD2A,RRP8,GCN1,XBP1,MYBBP1A,EIF2S1	darkgrey	VSMC_M8
GO:0002253	0.88	0.19	11	191	activation of immune response	BP	1	EZR,MATR3,KCNN4,EIF2B1,TOMM70,KHDRBS1,MNDA,RBM14,PAK2,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0051492	0.88	0.24	4	80	regulation of stress fiber assembly	BP	1	NF2,PAK2,RAC1,STMN1	darkgrey	VSMC_M8
GO:0001823	0.88	0.24	4	81	mesonephros development	BP	1	SDC1,SIX4,ARG2,HOXB7	darkgrey	VSMC_M8
GO:0009612	0.88	0.19	10	176	response to mechanical stimulus	BP	1	CASP2,FOSB,ARHGDIA,CCNB1,ETS1,CHEK1,FOSL1,RAC1,COL1A1,MBD2	darkgrey	VSMC_M8
GO:0043524	0.88	0.21	6	115	negative regulation of neuron apoptotic process	BP	1	HSP90AB1,AXL,KIF14,SIX4,NES,GCLM	darkgrey	VSMC_M8
GO:0070085	0.88	0.18	11	194	glycosylation	BP	1	NUS1,MAN1A1,NANS,B3GNT2,RPN1,COG3,ALG8,GALNT6,STT3A,DOLPP1,GMPPB	darkgrey	VSMC_M8
GO:0032273	0.89	0.21	6	116	positive regulation of protein polymerization	BP	1	CDC42EP4,CKAP5,RAC1,TPPP3,ARPC4,ARF6	darkgrey	VSMC_M8
GO:0055088	0.89	0.21	6	116	lipid homeostasis	BP	1	NUS1,THADA,POLD1,HMGCR,XBP1,LIPG	darkgrey	VSMC_M8
GO:0008285	0.89	0.15	35	548	negative regulation of cell population proliferation	BP	1	MTBP,NUP62,GTPBP4,E2F7,STRN,SNAI2,UTP20,E2F1,RBP4,TBX3,BAP1,EEF1E1,MDM4,ETS1,MNDA,NF2,S100A11,FOSL1,DDX20,IFT80,SF1,CDKN3,DPT,EIF2AK1,MSX1,CDC6,PDPN,ARG2,LMNA,ALOX15B,BRIP1,TFAP4,TP73,FAM129B,CDKN2C	darkgrey	VSMC_M8
GO:0034612	0.89	0.18	10	181	response to tumor necrosis factor	BP	1	SPHK1,CHUK,TRAIP,DHX9,BRCA1,UBE2K,EIF5A,COL1A1,HAS2,PID1	darkgrey	VSMC_M8
GO:1902414	0.89	0.23	4	82	protein localization to cell junction	BP	1	TJP2,GRIN2C,PAK2,CLSTN3	darkgrey	VSMC_M8
GO:0001843	0.89	0.23	4	82	neural tube closure	BP	1	STIL,KIF20B,PHACTR4,MTHFD1	darkgrey	VSMC_M8
GO:1901700	0.89	0.13	84	1234	response to oxygen-containing compound	BP	1	CDK2,EZR,MAN1A1,RANGAP1,CYC1,APTX,VCP,HSP90AB1,CDC5L,COL1A2,EZH2,GJB3,SDC1,RUVBL2,NAMPT,CCNA2,PPP5C,FOSB,NASP,CAD,DDX18,AXL,SPHK1,SRSF2,NET1,IPO5,PCNA,ZNF703,HGF,CCNB1,SNAI2,GGH,HSP90B1,EIF2B1,E2F1,HMGB2,RBP4,NRIP1,SELENOT,RAD51,MTDH,HMGCR,CHUK,PPP1R15B,PSMD14,NCOA5,NUCKS1,KIF18A,ETS1,H2AFZ,RGS9,PRMT5,XBP1,BLM,PDE3A,CDK1,FOSL1,SMARCC1,TRA2B,EFTUD2,BRCA1,TFPI,CDK16,ECT2,RAC1,MYO5A,ADIPOR2,CDC6,BID,SRSF5,COL1A1,BRIP1,DNMT1,TYMS,AIFM1,TFAP4,G6PD,CDT1,BCAR1,GCLM,HNRNPD,SIGMAR1,PID1,MBD2	darkgrey	VSMC_M8
GO:0032872	0.89	0.19	8	148	regulation of stress-activated MAPK cascade	BP	1	EZR,PRMT1,SPHK1,ULK4,HGF,PBK,HMGCR,FOXM1	darkgrey	VSMC_M8
GO:0002695	0.89	0.20	6	118	negative regulation of leukocyte activation	BP	1	AXL,LOXL3,RUNX1,MNDA,ARG2,CBFB	darkgrey	VSMC_M8
GO:1901890	0.89	0.22	4	82	positive regulation of cell junction assembly	BP	1	EPHB2,RAC1,POLDIP2,CLSTN3	darkgrey	VSMC_M8
GO:0060606	0.89	0.22	4	83	tube closure	BP	1	STIL,KIF20B,PHACTR4,MTHFD1	darkgrey	VSMC_M8
GO:0009063	0.89	0.22	4	84	cellular amino acid catabolic process	BP	1	GCAT,AFMID,AADAT,ARG2	darkgrey	VSMC_M8
GO:0072175	0.90	0.19	6	116	epithelial tube formation	BP	1	STIL,KIF20B,PHACTR4,SIX4,MTHFD1,PIK3CD	darkgrey	VSMC_M8
GO:0002429	0.90	0.18	8	148	immune response-activating cell surface receptor signaling pathway	BP	1	EZR,KCNN4,EIF2B1,KHDRBS1,MNDA,PAK2,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0002757	0.90	0.18	8	148	immune response-activating signal transduction	BP	1	EZR,KCNN4,EIF2B1,KHDRBS1,MNDA,PAK2,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0051094	0.90	0.13	66	982	positive regulation of developmental process	BP	1	DDX39B,FBXO5,EZR,FBN2,PWP1,HSP90AB1,HOXA5,EZH2,PRMT1,AXL,RNF157,SPHK1,CDC20,PARP2,NAP1L1,PGAM5,ZNF703,HGF,MEDAG,CCNB1,E2F1,HMGB2,RBM19,MTDH,HMGCR,EEF1E1,RUNX1,ETS1,PRMT5,ASPM,XBP1,UTP25,NF2,PDE3A,EIF4G1,CDK1,TFRC,EPHB2,ETV4,BRCA1,NSD2,ECT2,SIX4,MAPK6,RAC1,HNRNPU,PDPN,ARG2,IQGAP3,HOXB7,LMNA,ALOX15B,COL1A1,PPIB,SPAG9,SYT4,MORF4L2,TP73,PIK3CD,FAM129B,CBFB,CTH,SRRT,AURKA,HAS2,CLSTN3	darkgrey	VSMC_M8
GO:0007041	0.90	0.20	5	100	lysosomal transport	BP	1	HMGXB4,VCP,RNF157,NEDD4,HOOK1	darkgrey	VSMC_M8
GO:0050878	0.90	0.16	16	273	regulation of body fluid levels	BP	1	PABPC4,KCNN4,PLAUR,CAD,AXL,VAMP8,METAP1,XBP1,UMPS,EPHB2,TFPI,RAB27A,PDPN,EMP2,STMN1,HAS2	darkgrey	VSMC_M8
GO:1901698	0.90	0.13	56	845	response to nitrogen compound	BP	1	CDK2,EZR,MAN1A1,RANGAP1,CYC1,VCP,HSP90AB1,CDC5L,COL1A2,EZH2,SDC1,NAMPT,CCNA2,PPP5C,FOSB,CAD,IPO5,PCNA,GGH,HSP90B1,EIF2B1,RAD51,CHUK,NCOA5,NUCKS1,RGS9,PRMT5,XBP1,BLM,PDE3A,CDK1,FOSL1,SMARCC1,DHX9,DDX21,EFTUD2,UFD1,BRCA1,MYO5A,ADIPOR2,CDC6,DHX15,SRSF5,COL1A1,BRIP1,DNMT1,TYMS,AIFM1,TP73,TOR1A,BCAR1,GCLM,HNRNPD,PID1,CASP6,UBE2J2	darkgrey	VSMC_M8
GO:0046394	0.90	0.16	12	213	carboxylic acid biosynthetic process	BP	1	CAD,BCAT1,ELOVL6,XBP1,BRCA1,MTHFD1,UGDH,ALOX15B,LIPG,CTH,SCD5,ACSL3	darkgrey	VSMC_M8

GO:0006486	0.90	0.17	10	182	protein glycosylation	BP	1	NUS1,MAN1A1,B3GNT2,RPN1,COG3,ALG8,GALNT6,STT3A,DOLPP1,GMPPB	darkgrey	VSMC_M8
GO:0043413	0.90	0.17	10	182	macromolecule glycosylation	BP	1	NUS1,MAN1A1,B3GNT2,RPN1,COG3,ALG8,GALNT6,STT3A,DOLPP1,GMPPB	darkgrey	VSMC_M8
GO:0043122	0.90	0.16	11	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	NUP62,PPP5C,SLC20A1,MTDH,CHUK,TFRC,DDX21,ECT2,NEK6,CTH,TRIM59	darkgrey	VSMC_M8
GO:0030902	0.90	0.19	6	116	hindbrain development	BP	1	TTLL1,EZH2,KIF14,ARCN1,HNRNPD,GART	darkgrey	VSMC_M8
GO:0043535	0.90	0.21	4	87	regulation of blood vessel endothelial cell migration	BP	1	ATP5F1B,NUS1,PRCP,ETS1	darkgrey	VSMC_M8
GO:0048562	0.90	0.16	13	225	embryonic organ morphogenesis	BP	1	FBN2,HOXA5,STIL,EIF4A3,RBP4,TBX3,PHACTR4,FLVCR1,EPHB2,SIX4,MSX1,MTHFD1,HOXB7	darkgrey	VSMC_M8
GO:0098754	0.90	0.21	4	90	detoxification	BP	1	SELENOT,NNT,NXN,SLC30A1	darkgrey	VSMC_M8
GO:0007605	0.90	0.20	5	102	sensory perception of sound	BP	1	BIRC5,SNAI2,PPIP5K2,NAV2,COL1A1	darkgrey	VSMC_M8
GO:0008360	0.90	0.18	7	134	regulation of cell shape	BP	1	EZR,CDC42EP4,ARHGDIA,FMNL3,CDC42SE1,RAC1,PDPN	darkgrey	VSMC_M8
GO:1904019	0.90	0.21	4	86	epithelial cell apoptotic process	BP	1	E2F1,BID,EIF2S1,ARF6	darkgrey	VSMC_M8
GO:0009749	0.90	0.17	8	153	response to glucose	BP	1	EIF2B1,SELENOT,HMGCR,XBP1,TRA2B,CDK16,RAC1,GCLM	darkgrey	VSMC_M8
GO:0038127	0.90	0.19	5	102	ERBB signaling pathway	BP	1	NUP62,PLAUR,CHMP6,CNOT9,BCAR1	darkgrey	VSMC_M8
GO:0050807	0.90	0.16	9	165	regulation of synapse organization	BP	1	TUBB,VCP,CDC20,EIF4G1,EPHB2,SIX4,NEDD4,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0016053	0.90	0.15	12	215	organic acid biosynthetic process	BP	1	CAD,BCAT1,ELOVL6,XBP1,BRCA1,MTHFD1,UGDH,ALOX15B,LIPG,CTH,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0046916	0.90	0.20	4	86	cellular transition metal ion homeostasis	BP	1	SLC31A1,FLVCR1,TFRC,SLC30A1	darkgrey	VSMC_M8
GO:0048592	0.90	0.18	6	118	eye morphogenesis	BP	1	FBN2,MFSD2A,RBP4,HMGN1,PHACTR4,EPHB2	darkgrey	VSMC_M8
GO:1903038	0.90	0.20	4	87	negative regulation of leukocyte cell-cell adhesion	BP	1	LOXL3,RUNX1,ARG2,CBFB	darkgrey	VSMC_M8
GO:0009952	0.90	0.17	8	150	anterior/posterior pattern specification	BP	1	GRSF1,HOXA5,HEY1,TBX3,MSX1,HOXB7,AURKA,PALB2	darkgrey	VSMC_M8
GO:0070302	0.90	0.17	8	151	regulation of stress-activated protein kinase signaling cascade	BP	1	EZR,PRMT1,SPHK1,ULK4,HGF,PBK,HMGCR,FOXM1	darkgrey	VSMC_M8
GO:1904064	0.90	0.19	5	103	positive regulation of cation transmembrane transport	BP	1	KCNN4,ATP1B3,RGS9,EPHB2,G6PD	darkgrey	VSMC_M8
GO:0008203	0.91	0.19	5	103	cholesterol metabolic process	BP	1	CYP51A1,HMGCR,HDLBP,LBR,G6PD	darkgrey	VSMC_M8
GO:0003231	0.91	0.19	5	101	cardiac ventricle development	BP	1	MATR3,HEY1,TBX3,MDM4,NSD2	darkgrey	VSMC_M8
GO:0090100	0.91	0.20	4	85	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	HSP90AB1,TTK,NUP93,MSX1	darkgrey	VSMC_M8
GO:0009101	0.91	0.15	14	245	glycoprotein biosynthetic process	BP	1	NUS1,MAN1A1,B3GNT2,RPN1,COG3,ALG8,NECAB3,PXYLP1,GALNT6,STT3A,UGDH,XYLT1,DOLPP1,GMPPB	darkgrey	VSMC_M8
GO:0050708	0.91	0.15	11	200	regulation of protein secretion	BP	1	EZR,CYP51A1,KCNN4,RBP4,PPID,HMGCR,CDK16,RAC1,ACSL4,ARF6,ERP29	darkgrey	VSMC_M8
GO:0002520	0.91	0.12	45	694	immune system development	BP	1	HSPA9,MELK,MSH6,HOXA5,PABPC4,EZH2,PRMT1,PUS7,AXL,NCAPG2,SIPA1L3,HMGB2,LOXL3,ESCO2,AGPAT5,MSH3,CTNNBL1,ENTPD7,RUNX1,ETS1,UNG,POLQ,XBP1,MCM3AP,FLVCR1,TFRC,NSD2,ANKLE1,SIX4,EIF2AK1,LYAR,EXO1,TOP2A,LBR,PDPN,PRELID1,CCNB2,HOXB7,SLC25A5,G6PD,PIK3CD,FANCA,CBFB,TMOD3,PDCD2	darkgrey	VSMC_M8
GO:0017015	0.91	0.18	5	102	regulation of transforming growth factor beta receptor signaling pathway	BP	1	FBN2,HSP90AB1,ZNF703,TRIM33,STRAP	darkgrey	VSMC_M8
GO:0008217	0.91	0.17	6	122	regulation of blood pressure	BP	1	COL1A2,NAMPT,PRCP,KCNK6,NAV2,EMP2	darkgrey	VSMC_M8
GO:0032870	0.91	0.13	28	450	cellular response to hormone stimulus	BP	1	RANGAP1,CDC5L,PGR,CCNA2,PPP5C,FOSB,PRCP,HEY1,NCOA5,NUCKS1,DDX5,XBP1,SMARCC1,BRCA1,TFPI,CNOT9,MYO5A,HNRNPU,ADIPOR2,NEDD4,CDC6,SRSF5,BRIP1,AIFM1,TFAP4,BCAR1,GCLM,PID1	darkgrey	VSMC_M8
GO:0014066	0.91	0.20	4	86	regulation of phosphatidylinositol 3-kinase signaling	BP	1	HGF,CEP55,NEDD4,MAZ	darkgrey	VSMC_M8
GO:0045597	0.91	0.12	41	639	positive regulation of cell differentiation	BP	1	DDX39B,FBXO5,FBN2,PWP1,HSP90AB1,HOXA5,EZH2,PRMT1,AXL,PARP2,NAP1L1,ZNF703,HGF,MEDAG,E2F1,HMGB2,RUNX1,ETS1,PRMT5,ASPM,XBP1,NF2,PDE3A,EIF4G1,EPHB2,ETV4,ECT2,RAC1,HNRNPU,PDPN,ALOX15B,COL1A1,SPAG9,MORF4L2,TP73,FAM129B,CBFB,CTH,SRRT,AURKA,HAS2	darkgrey	VSMC_M8
GO:0031347	0.91	0.13	24	397	regulation of defense response	BP	1	MATR3,POLR3B,HSP90AB1,SPHK1,POLR3F,HGF,VAMP8,HMGB2,PBK,TOMM70,BAP1,SETD4,ETS1,MNDA,RBM14,PAK2,DHX9,PSMA6,UFD1,LYAR,UBE2K,ARG2,FANCA,GBP5	darkgrey	VSMC_M8
GO:0044257	0.91	0.12	44	685	cellular protein catabolic process	BP	1	CDK2,EZR,MAN1A1,DESI1,VCP,HSP90AB1,CDC20,CHFR,PSMD13,CDC16,ANAPC1,HSP90B1,PBK,BAP1,UBE2C,PSMD14,KIF14,XBP1,DTL,PSMD4,PSMC5,SMARCC1,PSMA6,UFD1,USP42,UCHL1,UBE2K,NEDD4,PSMD3,RAD23A,PLK1,PSMD11,COPS3,USP1,UHRF1,CCNF,ZNF598,PSMA5,TOR1A,USP4,AURKA,UBE2S,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0061024	0.91	0.12	38	599	membrane organization	BP	1	TMED9,ARFGAP3,KIF20A,HSPA9,CHCHD3,MFSD2A,PREB,KCNN4,SPHK1,SEC23B,CHMP6,VAMP8,TRAM1,CEP55,NUP93,TOMM70,REEP4,RCC1,PITPNB,SEC24D,EPHB2,RAC1,BID,PRELID1,LMNA,AURKB,TIMM8A,PLK1,SYT4,VRK1,SLC25A5,EMP2,EMC8,TOR1A,NEK6,BLOC1S2,STXBP6,XKR5	darkgrey	VSMC_M8
GO:0048660	0.91	0.17	6	124	regulation of smooth muscle cell proliferation	BP	1	DDX39B,NAMPT,HMGCR,SF1,MNAT1,DNMT1	darkgrey	VSMC_M8
GO:0014020	0.91	0.19	4	86	primary neural tube formation	BP	1	STIL,KIF20B,PHACTR4,MTHFD1	darkgrey	VSMC_M8
GO:0006352	0.91	0.18	5	105	DNA-templated transcription, initiation	BP	1	BCLAF1,POLR1E,TWISTNB,FOSL1,MAZ	darkgrey	VSMC_M8
GO:0003205	0.91	0.16	7	135	cardiac chamber development	BP	1	MATR3,ADAMTS6,RBP4,HEY1,TBX3,MDM4,NSD2	darkgrey	VSMC_M8
GO:0030162	0.91	0.12	33	538	regulation of proteolysis	BP	1	CDK2,DESI1,VCP,HSP90AB1,ANP32B,CYCS,CASP2,NRDC,PLAUR,CDC20,BIRC5,SERPINH1,CHFR,HGF,CD44,PBK,RUNX1,PSMD14,SPP2,PSMC5,PAK2,SMARCC1,TFPI,UBE2K,BID,PRELID1,RAD23A,PTTG1,PLK1,AIFM1,TFAP4,AURKA,PDCD2	darkgrey	VSMC_M8
GO:0071902	0.91	0.15	9	170	positive regulation of protein serine/threonine kinase activity	BP	1	DBF4,HSP90AB1,CKS2,EZH2,CCNB1,MNAT1,INCENP,CDC6,ERP29	darkgrey	VSMC_M8
GO:0045862	0.91	0.13	17	297	positive regulation of proteolysis	BP	1	VCP,ANP32B,CYCS,CASP2,NRDC,CDC20,CHFR,PSMD14,PSMC5,BID,PRELID1,RAD23A,PLK1,AIFM1,TFAP4,AURKA,PDCD2	darkgrey	VSMC_M8

GO:0010562	0.91	0.11	43	669	positive regulation of phosphorus metabolic process	BP	1	PRRC1,PPP2R5D,DBF4,VCP,HSP90AB1,CKS2,TTK,EZH2,CLSPN,PLAUR,BORA,AXL,SPHK1,CDC25B,HGF,CCNB1,CD44,TPX2,CDCA2,PPP1R15B,GCN1,CENPE,KIF14,EIF4G1,TFRC,PAK2,EPHB2,CNOT9,ECT2,MNAT1,RAC1,INCENP,ADIPOR2,UBE2K,CDC6,IQGAP3,PLK1,RAP2C,EMP2,PTBP1,ACSL3,ERP29,PID1	darkgrey	VSMC_M8
GO:0045937	0.91	0.11	43	669	positive regulation of phosphate metabolic process	BP	1	PRRC1,PPP2R5D,DBF4,VCP,HSP90AB1,CKS2,TTK,EZH2,CLSPN,PLAUR,BORA,AXL,SPHK1,CDC25B,HGF,CCNB1,CD44,TPX2,CDCA2,PPP1R15B,GCN1,CENPE,KIF14,EIF4G1,TFRC,PAK2,EPHB2,CNOT9,ECT2,MNAT1,RAC1,INCENP,ADIPOR2,UBE2K,CDC6,IQGAP3,PLK1,RAP2C,EMP2,PTBP1,ACSL3,ERP29,PID1	darkgrey	VSMC_M8
GO:0010594	0.92	0.15	8	157	regulation of endothelial cell migration	BP	1	ATP5F1B,NUS1,PRCP,ETS1,RAC1,EMP2,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:1903844	0.92	0.17	5	104	regulation of cellular response to transforming growth factor beta stimulus	BP	1	FBN2,HSP90AB1,ZNF703,TRIM33,STRAP	darkgrey	VSMC_M8
GO:1902904	0.92	0.15	7	139	negative regulation of supramolecular fiber organization	BP	1	FAM49B,CKAP2,TPX2,PAK2,FKBP4,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0007612	0.92	0.17	5	104	learning	BP	1	EIF4A3,AAAS,HMGCR,FOSL1,EPHB2	darkgrey	VSMC_M8
GO:0062197	0.92	0.13	16	282	cellular response to chemical stress	BP	1	MELK,EZH2,PPP5C,AXL,SPHK1,NET1,PCNA,HGF,CHUK,ETS1,CDK1,ECT2,EIF2S1,AIFM1,G6PD,SIGMAR1	darkgrey	VSMC_M8
GO:0043534	0.92	0.16	5	108	blood vessel endothelial cell migration	BP	1	ATP5F1B,NUS1,PRCP,ETS1,EMP2	darkgrey	VSMC_M8
GO:0048589	0.92	0.11	31	501	developmental growth	BP	1	DDX39B,EZR,HSP90AB1,TRIM28,HOXA5,MFSD2A,EZH2,STIL,RNF157,NCAPG2,PARP2,GINS4,CCNB1,RBP4,RUNX1,CHEK1,ASPM,EIF4H,FLVCR1,CDK1,IFT80,SIX4,PPIB,SPAG9,SYT4,TYMS,TP73,G6PD,AURKA,GINS1,PALB2	darkgrey	VSMC_M8
GO:0050803	0.92	0.14	9	170	regulation of synapse structure or activity	BP	1	TUBB,VCP,CDC20,EIF4G1,EPHB2,SIX4,NEDD4,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0006906	0.92	0.17	4	90	vesicle fusion	BP	1	SPHK1,VAMP8,SYT4,STXBP6	darkgrey	VSMC_M8
GO:1903037	0.92	0.13	11	206	regulation of leukocyte cell-cell adhesion	BP	1	FAM49B,CD44,LOXL3,RUNX1,ETS1,XBP1,TFRC,ARG2,EFNB1,CBFB,HAS2	darkgrey	VSMC_M8
GO:0061448	0.92	0.13	11	203	connective tissue development	BP	1	HOXA5,SERPINH1,SNAI2,CD44,RUNX1,XBP1,IFT80,MSX1,SH3PXD2B,COL1A1,TYMS	darkgrey	VSMC_M8
GO:0007601	0.92	0.15	6	123	visual perception	BP	1	WDR36,RBP4,RGS9,AIPL1,COL1A1,NOB1	darkgrey	VSMC_M8
GO:0009150	0.92	0.12	16	286	purine ribonucleotide metabolic process	BP	1	ATP5F1B,TJP2,VCP,PAICS,PDHB,AADAT,ENTPD7,HMGCR,ELOVL6,PDHA1,DLAT,PFAS,ACSL4,ACSL3,PID1,GART	darkgrey	VSMC_M8
GO:0030177	0.92	0.15	6	124	positive regulation of Wnt signaling pathway	BP	1	VCP,RUVBL1,DEPDC1B,ASPM,COL1A1,MBD2	darkgrey	VSMC_M8
GO:0048640	0.92	0.17	4	90	negative regulation of developmental growth	BP	1	RBP4,SPAG9,TP73,G6PD	darkgrey	VSMC_M8
GO:0046434	0.92	0.15	6	126	organophosphate catabolic process	BP	1	VCP,ENTPD7,UNG,DUT,DCTPP1,LIPG	darkgrey	VSMC_M8
GO:0001894	0.93	0.13	10	189	tissue homeostasis	BP	1	TJP2,MFSD2A,RBP4,IQCB1,STRAP,TFRC,BARD1,AIPL1,FH,RAC1	darkgrey	VSMC_M8
GO:0001838	0.93	0.15	5	107	embryonic epithelial tube formation	BP	1	STIL,KIF20B,PHACTR4,SIX4,MTHFD1	darkgrey	VSMC_M8
GO:0003158	0.93	0.15	5	107	endothelium development	BP	1	EZR,TJP2,HEY1,PDPN,RAP2C	darkgrey	VSMC_M8
GO:0045667	0.93	0.15	5	109	regulation of osteoblast differentiation	BP	1	FBXO5,FBN2,HGF,SNAI2,DDX5	darkgrey	VSMC_M8
GO:0033674	0.93	0.11	22	373	positive regulation of kinase activity	BP	1	PRRC1,DBF4,HSP90AB1,CKS2,EZH2,CLSPN,BORA,AXL,CDC25B,CCNB1,TPX2,GCN1,CENPE,KIF14,PAK2,EPHB2,ECT2,MNAT1,INCENP,CDC6,EMP2,ERP29	darkgrey	VSMC_M8
GO:0060759	0.93	0.14	6	128	regulation of response to cytokine stimulus	BP	1	HSP90AB1,AXL,SPHK1,TRAIP,DHX9,UBE2K	darkgrey	VSMC_M8
GO:0050729	0.93	0.16	4	93	positive regulation of inflammatory response	BP	1	VAMP8,SETD4,ETS1,DHX9	darkgrey	VSMC_M8
GO:0002062	0.93	0.16	4	91	chondrocyte differentiation	BP	1	SERPINH1,SNAI2,RUNX1,IFT80	darkgrey	VSMC_M8
GO:0090263	0.93	0.16	4	92	positive regulation of canonical Wnt signaling pathway	BP	1	VCP,RUVBL1,ASPM,COL1A1	darkgrey	VSMC_M8
GO:2000027	0.93	0.15	5	108	regulation of animal organ morphogenesis	BP	1	HGF,SIX4,MSX1,RAC1,HOXB7	darkgrey	VSMC_M8
GO:0002768	0.93	0.13	8	158	immune response-regulating cell surface receptor signaling pathway	BP	1	EZR,KCNN4,EIF2B1,KHDRBS1,MNDA,PAK2,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0060041	0.93	0.14	5	108	retina development in camera-type eye	BP	1	MFSD2A,CASP2,XRN2,RRM1,RBP4	darkgrey	VSMC_M8
GO:0032640	0.93	0.14	5	111	tumor necrosis factor production	BP	1	AXL,SETD4,DHX9,EPHB2,ARG2	darkgrey	VSMC_M8
GO:0032680	0.93	0.14	5	111	regulation of tumor necrosis factor production	BP	1	AXL,SETD4,DHX9,EPHB2,ARG2	darkgrey	VSMC_M8
GO:0072330	0.93	0.13	7	144	monocarboxylic acid biosynthetic process	BP	1	ELOVL6,XBP1,BRCA1,ALOX15B,LIPG,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0050953	0.93	0.13	6	126	sensory perception of light stimulus	BP	1	WDR36,RBP4,RGS9,AIPL1,COL1A1,NOB1	darkgrey	VSMC_M8
GO:0032368	0.93	0.15	4	95	regulation of lipid transport	BP	1	NUS1,DBI,PRELID1,LIPG	darkgrey	VSMC_M8
GO:1901617	0.93	0.12	9	178	organic hydroxy compound biosynthetic process	BP	1	NUS1,CYP51A1,SPHK1,SNAI2,PPIP5K2,HMGCR,LBR,ALOX15B,G6PD	darkgrey	VSMC_M8
GO:1902652	0.93	0.14	5	111	secondary alcohol metabolic process	BP	1	CYP51A1,HMGCR,HDLBP,LBR,G6PD	darkgrey	VSMC_M8
GO:0001841	0.93	0.15	4	92	neural tube formation	BP	1	STIL,KIF20B,PHACTR4,MTHFD1	darkgrey	VSMC_M8
GO:0032231	0.94	0.15	4	92	regulation of actin filament bundle assembly	BP	1	NF2,PAK2,RAC1,STMN1	darkgrey	VSMC_M8
GO:0048565	0.94	0.15	4	92	digestive tract development	BP	1	HOXA5,CCNB1,CLMP,TYMS	darkgrey	VSMC_M8
GO:0043271	0.94	0.14	4	93	negative regulation of ion transport	BP	1	THADA,EPHB2,NEDD4,SLC30A1	darkgrey	VSMC_M8
GO:0051495	0.94	0.11	10	194	positive regulation of cytoskeleton organization	BP	1	NUP62,PLK4,CDC42EP4,CENPJ,CKAP5,NF2,RAC1,NES,ARPC4,ARF6	darkgrey	VSMC_M8
GO:0090174	0.94	0.14	4	94	organelle membrane fusion	BP	1	SPHK1,VAMP8,SYT4,STXBP6	darkgrey	VSMC_M8
GO:0007229	0.94	0.14	4	92	integrin-mediated signaling pathway	BP	1	LOXL3,PHACTR4,EMP2,BCAR1	darkgrey	VSMC_M8
GO:0072001	0.94	0.10	14	256	renal system development	BP	1	NUP107,SDC1,SEC61A1,NUP85,ADAMTS6,RBP4,NUP160,NUP133,CENPF,SIX4,ARG2,HOXB7,TP73,HAS2	darkgrey	VSMC_M8
GO:0016331	0.94	0.13	6	127	morphogenesis of embryonic epithelium	BP	1	GRSF1,STIL,KIF20B,PHACTR4,SIX4,MTHFD1	darkgrey	VSMC_M8
GO:0031532	0.94	0.14	4	94	actin cytoskeleton reorganization	BP	1	EZR,ARHGDIA,EFS,BCAR1	darkgrey	VSMC_M8
GO:0031331	0.94	0.09	21	366	positive regulation of cellular catabolic process	BP	1	EZR,VCP,GRSF1,NRDC,DIS3,CDC20,CHFR,EXOSC8,MTDH,TENT4A,PSMC5,HNRNPR,BID,RAD23A,PLK1,SLC25A5,NNT,ZC3H18,EXOSC2,HNRNPD,AURKA	darkgrey	VSMC_M8
GO:0045765	0.94	0.10	12	229	regulation of angiogenesis	BP	1	HOXA5,SPHK1,HGF,CREB3L1,MTDH,RUNX1,ETS1,XBP1,BRCA1,EMP2,PIK3CD,FAM129B	darkgrey	VSMC_M8
GO:0014065	0.94	0.13	5	111	phosphatidylinositol 3-kinase signaling	BP	1	HGF,CEP55,NEDD4,MAZ,PIK3CD	darkgrey	VSMC_M8
GO:0050870	0.94	0.12	6	130	positive regulation of T cell activation	BP	1	FAM49B,RUNX1,XBP1,TFRC,EFNB1,CBFB	darkgrey	VSMC_M8
GO:0032869	0.94	0.11	8	161	cellular response to insulin stimulus	BP	1	NCOA5,NUCKS1,XBP1,SMARCC1,MYO5A,SRSF5,BCAR1,PID1	darkgrey	VSMC_M8
GO:0046649	0.94	0.09	28	470	lymphocyte activation	BP	1	FAM49B,MSH6,CTPS1,EZH2,AXL,CD44,HELLS,LOXL3,ENTPD7,RUNX1,TXLNA,UNG,MNDA,XBP1,TFRC,EPHB2,NSD2,EXO1,RAB27A,DCAF15,ARG2,PRELID1,EFNB1,SLC25A5,ELF4,PIK3CD,FANCA,CBFB	darkgrey	VSMC_M8
GO:0090630	0.94	0.14	4	93	activation of GTPase activity	BP	1	RANGAP1,SIPA1L3,ECT2,EIF5	darkgrey	VSMC_M8
GO:0007596	0.94	0.11	8	164	blood coagulation	BP	1	PABPC4,PLAUR,AXL,METAP1,EPHB2,TFPI,RAB27A,PDPN	darkgrey	VSMC_M8

GO:0001934	0.94	0.08	33	543	positive regulation of protein phosphorylation	BP	1	PRRC1,DBF4,HSP90AB1,CKS2,TTK,EZH2,CLSPN,PLAUR,BORA,SPHK1,CDC25B,HGF,CCNB1,CD44,TPX2,CENPE,KIF14,EIF4G1,TFRC,PAK2,CNOT9,ECT2,MNAT1,RAC1,INCENP,ADIPOR2,UBE2K,CDC6,IQGAP3,PLK1,RAP2C,EMP2,ERP29	darkgrey	VSMC_M8
GO:0022612	0.94	0.14	4	95	gland morphogenesis	BP	1	PGR,HGF,TBX3,XBP1	darkgrey	VSMC_M8
GO:1905475	0.94	0.12	7	147	regulation of protein localization to membrane	BP	1	EZR,VAMP8,EPHB2,MTCL1,ARF6,ACSL3,PID1	darkgrey	VSMC_M8
GO:0061041	0.94	0.14	4	96	regulation of wound healing	BP	1	HMGCR,XBP1,EPHB2,TFPI	darkgrey	VSMC_M8
GO:0044782	0.94	0.09	16	288	cilium organization	BP	1	RTTN,TTLL1,KIF27,CEP78,KIF24,CEP135,PLK4,CENPJ,CEP89,FHDC1,CFAP298,IQCB1,IFT80,LRRC49,SEPT6,ODF2	darkgrey	VSMC_M8
GO:0001525	0.94	0.09	25	428	angiogenesis	BP	1	ATP5F1B,NUS1,HOXA5,NAA15,AMOTL1,PRCP,SPHK1,E2F7,HGF,ELK3,HEY1,FMNL3,CREB3L1,E2F8,MTDH,RUNX1,ETS1,NCL,XBP1,EPHB2,BRCA1,ADIPOR2,EMP2,PIK3CD,FAM129B	darkgrey	VSMC_M8
GO:0008643	0.94	0.13	5	112	carbohydrate transport	BP	1	EZR,SLC35D2,MFSD2A,ADIPOR2,PID1	darkgrey	VSMC_M8
GO:0044087	0.94	0.08	51	801	regulation of cellular component biogenesis	BP	1	EZR,FAM49B,VCP,CEP135,TRIM28,ANLN,NUP62,SDC1,PLK4,STIL,CDC42EP4,PREB,SPHK1,SNAI2,CENPJ,TERF1,CKAP5,ICE1,KIF14,HJURP,NF2,RBM14,EIF4G1,PSMC5,TFRC,PAK2,KIF15,EPHB2,BRCA1,ECT2,DHX33,FKBP4,SIX4,RAC1,HNRNPU,FSCN1,BID,PLK1,DNMT1,POLDIP2,CEP76,CDT1,TPPP3,ARPC4,ARF6,GBP5,TMOD3,STMN1,HAS2,STXBP6,CLSTN3	darkgrey	VSMC_M8
GO:0035148	0.94	0.12	6	129	tube formation	BP	1	STIL,KIF20B,PHACTR4,SIX4,MTHFD1,PIK3CD	darkgrey	VSMC_M8
GO:0006909	0.94	0.11	8	163	phagocytosis	BP	1	AXL,SPHK1,CDC42SE1,EIF2AK1,LYAR,RAC1,RAB27A,XKR5	darkgrey	VSMC_M8
GO:0060541	0.94	0.11	8	163	respiratory system development	BP	1	HOXA5,PGR,RBP4,MSC,LOXL3,SIX4,PDPN,CRISPLD2	darkgrey	VSMC_M8
GO:0034767	0.94	0.12	5	114	positive regulation of ion transmembrane transport	BP	1	KCNN4,ATP1B3,RGS9,EPHB2,G6PD	darkgrey	VSMC_M8
GO:0071219	0.94	0.11	6	133	cellular response to molecule of bacterial origin	BP	1	FAM49B,AXL,HMGB2,MTDH,XBP1,TFPI	darkgrey	VSMC_M8
GO:0032635	0.94	0.13	4	96	interleukin-6 production	BP	1	HGF,SETD4,XBP1,DHX9	darkgrey	VSMC_M8
GO:0032675	0.94	0.13	4	96	regulation of interleukin-6 production	BP	1	HGF,SETD4,XBP1,DHX9	darkgrey	VSMC_M8
GO:1901342	0.94	0.10	12	232	regulation of vasculature development	BP	1	HOXA5,SPHK1,HGF,CREB3L1,MTDH,RUNX1,ETS1,XBP1,BRCA1,EMP2,PIK3CD,FAM129B	darkgrey	VSMC_M8
GO:0061061	0.94	0.08	30	504	muscle structure development	BP	1	ALPK2,DDX39B,EZH2,SDC1,PARP2,CCNB1,MSC,HEY1,TBX3,HMGCR,CHUK,DDX5,XBP1,HINFP,CENPF,CDK1,MED28,SIX4,MSX1,HNRNPU,UCHL1,LMNA,SPAG9,MORF4L2,DNMT1,G6PD,PTBP1,FAM129B,CTH,TMOD3	darkgrey	VSMC_M8
GO:0016125	0.94	0.12	5	114	sterol metabolic process	BP	1	CYP51A1,HMGCR,HDLBP,LBR,G6PD	darkgrey	VSMC_M8
GO:0006612	0.94	0.13	4	97	protein targeting to membrane	BP	1	SEC61A1,SRP68,TRAM1,MTCL1	darkgrey	VSMC_M8
GO:0019637	0.94	0.07	46	743	organophosphate metabolic process	BP	1	ATP5F1B,NUS1,TJP2,VCP,PAICS,CTPS1,DCK,MFSD2A,GARS,NAMPT,RNASEH2B,CAD,DBI,TK1,AFMID,PGS1,RRM1,PDHB,PPIP5K2,AADAT,AGPAT5,ENTPD7,HMGCR,UNG,ELOVL6,UMPS,PDHA1,UCK2,GK,DLAT,DUT,MTHFD1,DCTPP1,ALOX15B,PFAS,PRPS1,ACSL4,TYMS,LIPG,G6PD,PIK3CD,DOLPP1,ACSL3,PID1,GART,PRPSAP1	darkgrey	VSMC_M8
GO:0071706	0.94	0.12	5	115	tumor necrosis factor superfamily cytokine production	BP	1	AXL,SETD4,DHX9,EPHB2,ARG2	darkgrey	VSMC_M8
GO:1903555	0.94	0.12	5	115	regulation of tumor necrosis factor superfamily cytokine production	BP	1	AXL,SETD4,DHX9,EPHB2,ARG2	darkgrey	VSMC_M8
GO:0016049	0.94	0.08	23	399	cell growth	BP	1	DDX39B,HSP90AB1,NCBP1,MFSD2A,RNF157,SPHK1,NET1,PARP2,SGK3,BAP1,KIF14,EIF4G1,DCUN1D5,MSX1,ADIPOR2,SPAG9,SYT4,G6PD,EXOSC2,BCAR1,CDKN2C,AURKA,CLSTN3	darkgrey	VSMC_M8
GO:0099111	0.94	0.10	8	165	microtubule-based transport	BP	1	TTLL1,KIF27,CABYR,HNRNPU,UCHL1,KIF4A,NDE1,BLOC1S2	darkgrey	VSMC_M8
GO:0070555	0.94	0.13	4	98	response to interleukin-1	BP	1	ETS1,TFPI,RBMX,HAS2	darkgrey	VSMC_M8
GO:0007599	0.94	0.10	8	166	hemostasis	BP	1	PABPC4,PLAUR,AXL,METAP1,EPHB2,TFPI,RAB27A,PDPN	darkgrey	VSMC_M8
GO:0050817	0.94	0.10	8	166	coagulation	BP	1	PABPC4,PLAUR,AXL,METAP1,EPHB2,TFPI,RAB27A,PDPN	darkgrey	VSMC_M8
GO:1901565	0.95	0.07	69	1069	organonitrogen compound catabolic process	BP	1	CDK2,EZR,MAN1A1,DESI1,GCAT,ALDH1L2,CYP51A1,VCP,HSP90AB1,ODC1,NRDC,GRIN2C,SPHK1,CDC20,AFMID,CHMP6,CHFR,PSMD13,CDC16,CD44,ANAPC1,HSP90B1,AADAT,PBK,FAM83D,ENTPD7,HMGCR,BAP1,MDM4,UBE2C,PSMD14,KIF14,UNG,XBP1,UTP25,DTL,PSMD4,PSMC5,SMARCC1,PSMA6,BARD1,DUT,UFD1,USP42,UCHL1,UBE2K,NEDD4,PSMD3,ARG2,NUDT1,DCTPP1,RAD23A,PLK1,PSMD11,COPS3,USP1,UHRF1,CCNF,ZNF598,PSMA5,TOR1A,SF3B3,USP4,MAD2L1,AURKA,UBE2S,PJA1,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0071363	0.95	0.08	33	545	cellular response to growth factor stimulus	BP	1	FBN2,NUS1,HSP90AB1,CDC5L,COL1A2,SHCBP1,CCNA2,CAD,SPHK1,EIF4A3,ZNF703,HGF,SNAI2,CD44,E2F1,KNSTRN,CREB3L1,TRIM33,NCL,DDX5,PDE3A,STRAP,MCM7,MSX1,NEDD4,LTBP2,COL1A1,PIK3CD,BCAR1,GCLM,FAM129B,ARF6,HAS2	darkgrey	VSMC_M8
GO:0032271	0.95	0.10	10	199	regulation of protein polymerization	BP	1	FAM49B,CDC42EP4,CKAP5,FKBP4,RAC1,TPPP3,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0022407	0.95	0.09	16	293	regulation of cell-cell adhesion	BP	1	FAM49B,PLAUR,GTPBP4,ZNF703,CD44,LOXL3,RUNX1,ETS1,XBP1,NF2,TFRC,PDPN,ARG2,EFNB1,CBFB,HAS2	darkgrey	VSMC_M8
GO:0007162	0.95	0.09	11	215	negative regulation of cell adhesion	BP	1	GTPBP4,ARHGDIA,ZNF703,SNAI2,LOXL3,RUNX1,NF2,EPHB2,ARG2,COL1A1,CBFB	darkgrey	VSMC_M8
GO:0010720	0.95	0.09	12	231	positive regulation of cell development	BP	1	NAP1L1,E2F1,PRMT5,ASPM,PDE3A,EPHB2,RAC1,TP73,FAM129B,SRRT,AURKA,HAS2	darkgrey	VSMC_M8
GO:0031333	0.95	0.11	5	115	negative regulation of protein-containing complex assembly	BP	1	FAM49B,KIF14,FKBP4,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0051051	0.95	0.08	17	314	negative regulation of transport	BP	1	RANGAP1,CYP51A1,THADA,YRDC,VAMP8,HMGCR,NUP153,BARD1,EPHB2,RAC1,NEDD4,SYT4,ARF6,STXBP6,ERP29,PID1,SLC30A1	darkgrey	VSMC_M8
GO:0007159	0.95	0.09	12	234	leukocyte cell-cell adhesion	BP	1	EZR,FAM49B,CD44,LOXL3,RUNX1,ETS1,XBP1,TFRC,ARG2,EFNB1,CBFB,HAS2	darkgrey	VSMC_M8
GO:0009725	0.95	0.07	40	652	response to hormone	BP	1	RANGAP1,CYC1,CDC5L,SDC1,PGR,CCNA2,PPP5C,FOSB,PRCP,CAD,PCNA,GGH,EIF2B1,HMGB2,HEY1,CHUK,NCOA5,NUCKS1,DDX5,XBP1,RBM14,FOSL1,SMARCC1,BRCA1,TFPI,CNOT9,MYO5A,HNRNPU,ADIPOR2,NEDD4,CDC6,SRSF5,COL1A1,BRIP1,TYMS,AIFM1,TFAP4,BCAR1,GCLM,PID1	darkgrey	VSMC_M8

GO:0035107	0.95	0.11	5	115	appendage morphogenesis	BP	1	FBN2,TBX3,FLVCR1,MSX1,ACD	darkgrey	VSMC_M8
GO:0035108	0.95	0.11	5	115	limb morphogenesis	BP	1	FBN2,TBX3,FLVCR1,MSX1,ACD	darkgrey	VSMC_M8
GO:0009896	0.95	0.07	24	420	positive regulation of catabolic process	BP	1	EZR,VCP,GRSF1,NRDC,DIS3,CDC20,CHFR,EXOSC8,MTDH,TENT4A,DTL,PSMC5,HNRNPR,BARD1,NEDD4,BID,RAD23A,PLK1,SLC25A5,NNT,ZC3H18,EXOSC2,HNRNPD,AURKA	darkgrey	VSMC_M8
GO:0001959	0.95	0.11	5	119	regulation of cytokine-mediated signaling pathway	BP	1	HSP90AB1,AXL,SPHK1,TRAIP,UBE2K	darkgrey	VSMC_M8
GO:0001822	0.95	0.08	13	248	kidney development	BP	1	NUP107,SDC1,SEC61A1,NUP85,ADAMTS6,NUP160,NUP133,CENPF,SIX4,ARG2,HOXB7,TP73,HAS2	darkgrey	VSMC_M8
GO:0003007	0.95	0.09	10	197	heart morphogenesis	BP	1	ALPK2,STIL,SNAI2,RBP4,HEY1,TBX3,MDM4,NSD2,MSX1,HAS2	darkgrey	VSMC_M8
GO:0051251	0.95	0.09	9	186	positive regulation of lymphocyte activation	BP	1	FAM49B,AXL,RUNX1,XBP1,TFRC,EPHB2,NSD2,EFNB1,CBFB	darkgrey	VSMC_M8
GO:0048015	0.95	0.10	6	133	phosphatidylinositol-mediated signaling	BP	1	EZR,HGF,CEP55,NEDD4,MAZ,PIK3CD	darkgrey	VSMC_M8
GO:1903008	0.95	0.11	4	101	organelle disassembly	BP	1	VCP,CDK1,VRK1,SLC25A5	darkgrey	VSMC_M8
GO:0050866	0.95	0.10	6	136	negative regulation of cell activation	BP	1	AXL,LOXL3,RUNX1,MNDA,ARG2,CBFB	darkgrey	VSMC_M8
GO:1901888	0.95	0.09	8	165	regulation of cell junction assembly	BP	1	SNAI2,EIF4G1,EPHB2,SIX4,RAC1,POLDIP2,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0046034	0.95	0.08	10	219	ATP metabolic process	BP	1	ATP5F1B,CYC1,VCP,CYCS,CCNB1,NDUFAF1,CDK1,NDUFS1,BID,PID1	darkgrey	VSMC_M8
GO:0030522	0.95	0.08	11	217	intracellular receptor signaling pathway	BP	1	EZH2,PGR,PPP5C,PRCP,SNAI2,DDX5,UFD1,BRCA1,CNOT9,NEDD4,ALOX15B	darkgrey	VSMC_M8
GO:0051050	0.95	0.06	40	660	positive regulation of transport	BP	1	EZR,HSP90AB1,TRIM28,ANP32B,SDC1,SAE1,KCNN4,DBI,AXL,IPO5,KIF20B,VAMP8,ATP1B3,RBP4,SELENOT,PPID,BAP1,ICE1,KHDRBS1,RGS9,XBP1,CDK1,DHX9,EPHB2,ECT2,LYAR,RAC1,RAB27A,ADIPOR2,NEDD4,PRELID1,SYT4,ACSL4,MTCL1,LIPG,G6PD,TOR1A,ARF6,ACSL3,UBE2J2	darkgrey	VSMC_M8
GO:0032103	0.95	0.08	15	286	positive regulation of response to external stimulus	BP	1	MATR3,POLR3B,POLR3F,VAMP8,HMGB2,TOMM70,SETD4,ETS1,MNDA,RBM14,PAK2,DHX9,RAC1,UBE2K,GBP5	darkgrey	VSMC_M8
GO:0015849	0.95	0.08	10	203	organic acid transport	BP	1	MFSD2A,SLC1A5,SLC5A6,SLC10A7,SFXN3,SFXN4,SLC19A2,ACSL4,SLC6A17,ACSL3	darkgrey	VSMC_M8
GO:0042060	0.95	0.07	18	329	wound healing	BP	1	PABPC4,SDC1,PRCP,PLAUR,AXL,ELK3,CD44,HMGCR,ETS1,METAP1,XBP1,EPHB2,TFPI,RAB27A,ADIPOR2,PDPN,COL1A1,TOR1A	darkgrey	VSMC_M8
GO:0001654	0.95	0.07	15	280	eye development	BP	1	FBN2,MFSD2A,CASP2,SMG9,XRN2,RRM1,SIPA1L3,RBP4,HMGN1,PHACTR4,NF2,NHS,EPHB2,NES,SH3PXD2B	darkgrey	VSMC_M8
GO:0043547	0.96	0.08	10	202	positive regulation of GTPase activity	BP	1	RANGAP1,EZH2,NET1,DOCK9,SIPA1L3,ARHGAP11A,ECT2,EIF5,POLDIP2,RAPGEF6	darkgrey	VSMC_M8
GO:0010811	0.96	0.11	4	100	positive regulation of cell-substrate adhesion	BP	1	RAC1,POLDIP2,EMP2,HAS2	darkgrey	VSMC_M8
GO:0006865	0.96	0.11	4	99	amino acid transport	BP	1	SLC1A5,SFXN3,SFXN4,SLC6A17	darkgrey	VSMC_M8
GO:0050679	0.96	0.09	7	154	positive regulation of epithelial cell proliferation	BP	1	ZNF703,HMGB2,NRAS,XBP1,IQGAP3,PIK3CD,HAS2	darkgrey	VSMC_M8
GO:0055123	0.96	0.11	4	99	digestive system development	BP	1	HOXA5,CCNB1,CLMP,TYMS	darkgrey	VSMC_M8
GO:0051091	0.96	0.08	10	204	positive regulation of DNA-binding transcription factor activity	BP	1	SPHK1,MTDH,CHUK,PPRC1,TFRC,FOSL1,DHX9,PSMA6,DHX33,CTH	darkgrey	VSMC_M8
GO:0010256	0.96	0.06	24	422	endomembrane system organization	BP	1	TMED9,SEC61A1,COG3,CHMP6,TRAM1,FHDC1,NUP93,KNL1,REEP4,PRMT5,RCC1,CDK1,ZW10,RAB27A,LMNA,PLK1,SYT4,VRK1,HOOK1,EMC8,TOR1A,NEK6,BLOC1S2,XKR5	darkgrey	VSMC_M8
GO:0051336	0.96	0.06	46	754	regulation of hydrolase activity	BP	1	RANGAP1,VCP,HSP90AB1,ANP32B,PPP6R1,CYCS,EZH2,CASP2,NRDC,MASTL,PLAUR,NET1,BIRC5,SERPINH1,DOCK9,SIPA1L3,PCNA,HGF,CD44,TCEA1,HSP90B1,ABCE1,ATP1B3,HMGB2,TERF1,ARHGAP11A,PPP1R15B,PSMD14,SPP2,PAK2,DNAJC9,TFPI,ECT2,BID,EIF2S1,PRELID1,IQGAP3,AHSA1,PTTG1,EIF5,POLDIP2,AIFM1,TFAP4,RAPGEF6,STMN1,PDCD2	darkgrey	VSMC_M8
GO:0007249	0.96	0.08	11	222	I-kappaB kinase/NF-kappaB signaling	BP	1	NUP62,PPP5C,SLC20A1,MTDH,CHUK,TFRC,DDX21,ECT2,NEK6,CTH,TRIM59	darkgrey	VSMC_M8
GO:0051346	0.96	0.07	12	242	negative regulation of hydrolase activity	BP	1	MASTL,PLAUR,BIRC5,SERPINH1,HGF,CD44,ABCE1,TERF1,SPP2,PAK2,TFPI,PTTG1	darkgrey	VSMC_M8
GO:0150063	0.96	0.07	15	282	visual system development	BP	1	FBN2,MFSD2A,CASP2,SMG9,XRN2,RRM1,SIPA1L3,RBP4,HMGN1,PHACTR4,NF2,NHS,EPHB2,NES,SH3PXD2B	darkgrey	VSMC_M8
GO:0050863	0.96	0.08	10	206	regulation of T cell activation	BP	1	FAM49B,LOXL3,RUNX1,XBP1,TFRC,ARG2,PRELID1,EFNB1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0007034	0.96	0.09	6	137	vacuolar transport	BP	1	HMGXB4,VCP,RNF157,CHMP6,NEDD4,HOOK1	darkgrey	VSMC_M8
GO:0043467	0.96	0.10	4	104	regulation of generation of precursor metabolites and energy	BP	1	VCP,CCNB1,CDK1,PRELID1	darkgrey	VSMC_M8
GO:0010632	0.96	0.08	10	208	regulation of epithelial cell migration	BP	1	ATP5F1B,NUS1,PRCP,ETS1,RAC1,EMP2,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0050954	0.96	0.09	5	120	sensory perception of mechanical stimulus	BP	1	BIRC5,SNAI2,PPIP5K2,NAV2,COL1A1	darkgrey	VSMC_M8
GO:0051249	0.96	0.07	15	287	regulation of lymphocyte activation	BP	1	FAM49B,AXL,LOXL3,RUNX1,MNDA,XBP1,TFRC,EPHB2,NSD2,DCAF15,ARG2,PRELID1,EFNB1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0006366	0.96	0.05	126	1862	transcription by RNA polymerase II	BP	1	BCLAF1,EZR,RAD21,ATAD2,ZNF367,PSIP1,CDC5L,CKS2,TRIM28,HOXA5,THRAP3,EZH2,PHF19,RUVBL2,PGR,NAMPT,RUVBL1,FOSB,NUFIP1,NCAPG2,WDR43,SUPT16H,E2F7,CKAP2,PCNA,HGF,ELK3,TCERG1,CBX5,SNAI2,TCEA1,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NUCKS1,DEK,GCN1,ETS1,ICE1,CHEK1,H2AFZ,KHDRBS1,TRIP13,NCL,TARBP1,DDX5,XBP1,HINFP,RBM14,STRAP,PSMC5,FOSL1,SMARCC1,DHX9,DDX20,DDX21,SMARCAL1,ETV4,BRCA1,NSD2,GABPB1,CREG1,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,PMF1,HOXB7,FUS,MAZ,AURKB,NFATC2IP,PLK1,BRIP1,MORF4L2,DNMT1,TADA2A,CDCA4,ELF4,UHRF1,RBMX,TFAP4,NOC2L,TP73,POLR2E,CBFB,DRAP1,HMGB3,ABT1,PID1,HOXC8,MBD2	darkgrey	VSMC_M8
GO:0016358	0.96	0.08	10	204	dendrite development	BP	1	MFSD2A,EZH2,CDC20,STRN,PAK2,EPHB2,MAPK6,NEDD4,ACSL4,ARF6	darkgrey	VSMC_M8
GO:0003341	0.96	0.10	4	103	cilium movement	BP	1	TTLL1,KIF27,CFAP298,CABYR	darkgrey	VSMC_M8

GO:1901653	0.96	0.07	14	270	cellular response to peptide	BP	1	RANGAP1,CDC5L,NAMPT,CCNA2,NCOA5,NUCKS1,XBP1,SMARCC1,MYO5A,CDC6,SRSF5,BRIP1,BCAR1,PID1	darkgrey	VSMC_M8
GO:0051607	0.96	0.08	8	174	defense response to virus	BP	1	POLR3B,POLR3F,VAMP8,TOMM70,DHX9,DDX21,UFD1,ILF3	darkgrey	VSMC_M8
GO:0140546	0.96	0.08	8	174	defense response to symbiont	BP	1	POLR3B,POLR3F,VAMP8,TOMM70,DHX9,DDX21,UFD1,ILF3	darkgrey	VSMC_M8
GO:0003206	0.96	0.10	4	101	cardiac chamber morphogenesis	BP	1	RBP4,HEY1,TBX3,NSD2	darkgrey	VSMC_M8
GO:0048017	0.96	0.08	6	137	inositol lipid-mediated signaling	BP	1	EZR,HGF,CEP55,NEDD4,MAZ,PIK3CD	darkgrey	VSMC_M8
GO:0098657	0.96	0.08	7	155	import into cell	BP	1	SLC31A1,SLC1A5,SLC5A6,ATP1B3,TOR1A,ACSL3,SLC30A1	darkgrey	VSMC_M8
GO:0002822	0.96	0.10	4	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	FAM49B,LOXL3,TFRC,NSD2	darkgrey	VSMC_M8
GO:0006869	0.96	0.07	14	273	lipid transport	BP	1	NUS1,MFSD2A,KCNN4,DBI,SLC10A7,RBP4,PITPNB,HDLBP,PRELID1,ACSL4,LIPG,ACSL3,SIGMAR1,XKR5	darkgrey	VSMC_M8
GO:0044283	0.96	0.06	23	414	small molecule biosynthetic process	BP	1	NUS1,CYP51A1,AMD1,CAD,SPHK1,SNAI2,PPIP5K2,RBP4,HMGCR,BCAT1,ELOVL6,XBP1,BRCA1,MTHFD1,UGDH,LBR,ALOX15B,PRPS1,LIPG,G6PD,CTH,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0032868	0.96	0.07	10	206	response to insulin	BP	1	CAD,GGH,NCOA5,NUCKS1,XBP1,SMARCC1,MYO5A,SRSF5,BCAR1,PID1	darkgrey	VSMC_M8
GO:0090276	0.96	0.08	6	140	regulation of peptide hormone secretion	BP	1	RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0048754	0.96	0.08	5	121	branching morphogenesis of an epithelial tube	BP	1	HOXA5,PGR,TBX3,SIX4,HOXB7	darkgrey	VSMC_M8
GO:0007519	0.96	0.08	5	122	skeletal muscle tissue development	BP	1	MSC,HMGCR,DDX5,SIX4,FAM129B	darkgrey	VSMC_M8
GO:0001944	0.96	0.05	36	607	vasculature development	BP	1	ATP5F1B,NUS1,COL1A2,ANP32B,HOXA5,NAA15,AMOTL1,PRCP,SPHK1,E2F7,HGF,ELK3,ADAMTS6,HEY1,FMNL3,TBX3,CREB3L1,E2F8,MTDH,RUNX1,ETS1,NCL,XBP1,FLVCR1,FOSL1,EPHB2,BRCA1,ADIPOR2,PDPN,COL1A1,DNMT1,EMP2,PIK3CD,FAM129B,CTH,HAS2	darkgrey	VSMC_M8
GO:0048880	0.96	0.06	15	286	sensory system development	BP	1	FBN2,MFSD2A,CASP2,SMG9,XRN2,RRM1,SIPA1L3,RBP4,HMGN1,PHACTR4,NF2,NHS,EPHB2,NES,SH3PXD2B	darkgrey	VSMC_M8
GO:0106106	0.96	0.08	5	123	cold-induced thermogenesis	BP	1	NRDC,PGAM5,ELOVL6,FH,ADIPOR2	darkgrey	VSMC_M8
GO:0120161	0.96	0.08	5	123	regulation of cold-induced thermogenesis	BP	1	NRDC,PGAM5,ELOVL6,FH,ADIPOR2	darkgrey	VSMC_M8
GO:0051234	0.96	0.04	239	3429	establishment of localization	BP	1	ATP5F1B,TMED9,XPOT,NUP43,NUP107,CCT2,TUBB,DDX39B,EZR,PANX2,TCP1,NUP50,TTLL1,NUS1,ARFGAP3,MAN1A1,KIFC1,DESI1,RANGAP1,KIF20A,SLC35D2,HSPA9,SRSF3,KIF27,CYC1,TNPO3,HMGXB4,STEAP1,TJP2,CYP51A1,VCP,HSP90AB1,CENPQ,CEP135,TRIM28,NCBP1,THADA,ANP32B,HNRNPA2B1,MFSD2A,CCT4,SLC31A1,NUP205,YRDC,CDCA8,NUP62,GJB3,NBAS,SDC1,RUVBL2,SEC61A1,SAE1,SLC1A5,CHCHD4,CENPA,NASP,COG3,GRIN2C,TOMM40,PREB,KCNN4,NUP85,SLC25A19,CAD,KIF2C,SLC5A6,DBI,SRP68,AXL,RNF157,SPHK1,GDI2,SEC23B,RRBP1,IPO5,EIF4A3,CHMP6,ALYREF,KCNK6,CCNB1,AAAS,ESPL1,KIF20B,SLC20A1,CENPJ,HSP90B1,NECAB3,ABCE1,VAMP8,ATP1B3,SLC10A7,TRAM1,CEP55,RBP4,TERF1,NUP160,RACGAP1,LOXL3,SELENOT,TUBA1B,CCT8,PPID,CCT7,RSRC1,FAM83D,CKAP5,NUP93,TBX3,CREB3L1,TOMM70,YWHAB,HMGCR,BAP1,NUSAP1,NIPA2,SFXN3,HEATR3,NOLC1,CCT5,NUP153,CCT6A,KIF18A,NSUN2,ICE1,TXLNA,KHDRBS1,CENPE,KIF14,RGS9,CSE1L,PITPNB,XBP1,MCM3AP,IPO4,SFXN4,NUP133,HINFP,SEC24D,FLVCR1,CDC42SE1,UMPS,SSB,ARCN1,CENPF,SLC17A9,ARFGAP1,CDK1,HDLBP,TFRC,DHX9,NUF2,LSG1,HNRNPA3,ZW10,CDCA5,CABYR,RANBP1,BARD1,EPHB2,NMD3,UFD1,SLC35F2,NSD2,CDK16,SLBP,DLGAP5,SLC19A2,ANKLE1,ECT2,ZWINT,FKBP4,EIF2AK1,LYAR,RAC1,KDELR2,MYO5A,HNRNPU,UCHL1,INCENP,RAB27A,ADIPOR2,NEDD4,EIF5A,BID,DDX39A,PRELID1,CCT3,KIF4A,LMNA,LTBP2,KIF22,SPDL1,AURKB,COL1A1,SPAG9,TIMM8A,PLK1,SYT4,NUP62CL,ACSL4,TIMM44,SLC25A5,NDC80,NNT,MTCL1,NDE1,AIFM1,HOOK1,EMP2,LIPG,NDC1,SMG6,THOC6,G6PD,DKC1,PIK3CD,SLC6A17,CDT1,EMC8,TOR1A,	darkgrey	VSMC_M8
GO:0007417	0.96	0.05	49	795	central nervous system development	BP	1	NARS,TTLL1,KIF27,HSP90AB1,ANP32B,MFSD2A,EZH2,CASP2,STIL,GRIN2C,SMG9,AXL,SPHK1,XRN2,RRM1,WDR62,SNRPB,EIF2B1,E2F1,LOXL3,TBX3,NAV2,ETS1,KIF14,PRMT5,ASPM,NF2,H2AFX,ARCN1,CENPF,TRA2B,EPHB2,TACC3,MNAT1,MSX1,BID,NES,SYT4,ALDH3A2,NDE1,THOC6,TP73,G6PD,SLC6A17,HNRNPD,CDKN2C,ACSL3,STMN1,GART	darkgrey	VSMC_M8
GO:0050678	0.96	0.06	14	275	regulation of epithelial cell proliferation	BP	1	HOXA5,PGR,ZNF703,SNAI2,HMGB2,NRAS,HMGN1,XBP1,IFT80,SIX4,IQGAP3,UHRF1,PIK3CD,HAS2	darkgrey	VSMC_M8
GO:0007179	0.96	0.07	7	156	transforming growth factor beta receptor signaling pathway	BP	1	FBN2,HSP90AB1,COL1A2,ZNF703,TRIM33,STRAP,LTBP2	darkgrey	VSMC_M8
GO:0001818	0.96	0.07	9	195	negative regulation of cytokine production	BP	1	EZR,HSP90AB1,EZH2,AXL,HGF,TRAIP,UFD1,RAC1,ARG2	darkgrey	VSMC_M8
GO:0046651	0.97	0.07	8	177	lymphocyte proliferation	BP	1	CTPS1,HELLS,MNDA,TFRC,EPHB2,ARG2,EFNB1,ELF4	darkgrey	VSMC_M8
GO:0002064	0.97	0.07	8	173	epithelial cell development	BP	1	EZR,TJP2,HOXA5,SDC1,PGR,SIPA1L3,TYMS,RAP2C	darkgrey	VSMC_M8
GO:0030178	0.97	0.08	6	142	negative regulation of Wnt signaling pathway	BP	1	ALPK2,HMGXB4,RUVBL2,SNAI2,IFT80,NXN	darkgrey	VSMC_M8
GO:0002791	0.97	0.08	6	142	regulation of peptide secretion	BP	1	RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0030324	0.97	0.07	6	141	lung development	BP	1	HOXA5,PGR,RBP4,LOXL3,PDPN,CRISPLD2	darkgrey	VSMC_M8
GO:0048736	0.97	0.07	6	140	appendage development	BP	1	FBN2,TBX3,FLVCR1,IFT80,MSX1,ACD	darkgrey	VSMC_M8
GO:0060173	0.97	0.07	6	140	limb development	BP	1	FBN2,TBX3,FLVCR1,IFT80,MSX1,ACD	darkgrey	VSMC_M8
GO:0030856	0.97	0.08	4	106	regulation of epithelial cell differentiation	BP	1	EZH2,TBX3,ETV4,ALOX15B	darkgrey	VSMC_M8
GO:0051896	0.97	0.08	5	125	regulation of protein kinase B signaling	BP	1	HSP90AB1,AXL,MTDH,MAZ,PIK3CD	darkgrey	VSMC_M8
GO:0030041	0.97	0.07	7	160	actin filament polymerization	BP	1	FAM49B,CDC42EP4,DIAPH3,RAC1,ARPC4,ARF6,TMOD3	darkgrey	VSMC_M8
GO:0001952	0.97	0.08	4	105	regulation of cell-matrix adhesion	BP	1	NF2,RAC1,POLDIP2,EMP2	darkgrey	VSMC_M8
GO:0071222	0.97	0.08	5	126	cellular response to lipopolysaccharide	BP	1	AXL,HMGB2,MTDH,XBP1,TFPI	darkgrey	VSMC_M8
GO:0098739	0.97	0.08	5	123	import across plasma membrane	BP	1	SLC31A1,SLC1A5,SLC5A6,ATP1B3,SLC30A1	darkgrey	VSMC_M8
GO:0043010	0.97	0.06	12	242	camera-type eye development	BP	1	FBN2,MFSD2A,CASP2,XRN2,RRM1,RBP4,HMGN1,PHACTR4,NF2,NHS,EPHB2,NES	darkgrey	VSMC_M8
GO:0032943	0.97	0.06	8	179	mononuclear cell proliferation	BP	1	CTPS1,HELLS,MNDA,TFRC,EPHB2,ARG2,EFNB1,ELF4	darkgrey	VSMC_M8
GO:0090087	0.97	0.07	6	144	regulation of peptide transport	BP	1	RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0043393	0.97	0.07	7	162	regulation of protein binding	BP	1	HSP90AB1,NMD3,NES,AURKB,PLK1,POLDIP2,AURKA	darkgrey	VSMC_M8

GO:0002250	0.97	0.06	12	244	adaptive immune response	BP	1	FAM49B,MSH6,LOXL3,ENTPD7,UNG,TFRC,NSD2,EXO1,RAB27A,ARG2,EMP2,PIK3CD	darkgrey	VSMC_M8
GO:0015711	0.97	0.06	11	228	organic anion transport	BP	1	SLC35D2,MFSD2A,SLC1A5,SLC25A19,SLC5A6,SLC10A7,SFXN3,SLC17A9,SLC19A2,SLC25A5,SLC6A17	darkgrey	VSMC_M8
GO:0042327	0.97	0.04	36	612	positive regulation of phosphorylation	BP	1	PRRC1,DBF4,HSP90AB1,CKS2,TTK,EZH2,CLSPN,PLAUR,BORA,AXL,SPHK1,CDC25B,HGF,CCNB1,CD44,TPX2,GCN1,CENPE,KIF14,EIF4G1,TFRC,PAK2,EPHB2,CNOT9,ECT2,MNAT1,RAC1,INCENP,ADIPOR2,UBE2K,CDC6,IQGAP3,PLK1,RAP2C,EMP2,ERP29	darkgrey	VSMC_M8
GO:0042110	0.97	0.05	16	310	T cell activation	BP	1	FAM49B,CTPS1,CD44,LOXL3,ENTPD7,RUNX1,XBP1,TFRC,RAB27A,ARG2,PRELID1,EFNB1,ELF4,PIK3CD,FANCA,CBFB	darkgrey	VSMC_M8
GO:0042098	0.97	0.07	5	127	T cell proliferation	BP	1	CTPS1,TFRC,ARG2,EFNB1,ELF4	darkgrey	VSMC_M8
GO:1902531	0.97	0.04	84	1309	regulation of intracellular signal transduction	BP	1	BCLAF1,DDX39B,EZR,FAM49B,HSP90AB1,MIOS,EZH2,NUP62,PRMT1,GEN1,RNASEH2B,PPP5C,PLAUR,AXL,RNF157,SPHK1,ULK4,NET1,ARHGDIA,SIPA1L3,HGF,CCNB1,SNAI2,CD44,SLC20A1,PSD4,CEP55,HELLS,ARHGAP11A,RACGAP1,PBK,FAM83D,CREB3L1,MTDH,HMGCR,EEF1E1,CHUK,PAK1IP1,CIT,CHEK1,KIF14,PRMT5,DDX5,XBP1,RPA2,NF2,PDE3A,CDC42SE1,ARFGAP1,TFRC,PAK2,WDR76,DDX21,EPHB2,UFD1,ECT2,DHX33,FOXM1,MSX1,RAC1,UCHL1,NEDD4,EIF5A,BID,IQGAP3,MAZ,AURKB,LRRC59,SPAG9,NDC80,NOC2L,PTBP1,PIK3CD,CDT1,NEK6,PLEKHG4,CTH,ARF6,MAD2L1,STMN1,AURKA,ERP29,TRIM59,DUSP7	darkgrey	VSMC_M8
GO:0098542	0.97	0.04	33	574	defense response to other organism	BP	1	TUBB,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,SYNCRIP,SEC61A1,CDC42EP4,AXL,POLR3F,VAMP8,HMGB2,TRIM35,TOMM70,CHUK,MNDA,RBM14,PAK2,DHX9,DDX21,UFD1,LYAR,RAB27A,UBE2K,ARG2,ILF3,ELF4,TUBB4B,PIK3CD,GBP5,HMGB3,TRIM59	darkgrey	VSMC_M8
GO:0098656	0.97	0.06	7	161	anion transmembrane transport	BP	1	SLC35D2,SLC1A5,SLC25A19,SLC5A6,SLC20A1,SFXN3,SLC25A5	darkgrey	VSMC_M8
GO:0050796	0.97	0.07	5	127	regulation of insulin secretion	BP	1	RBP4,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:1902600	0.97	0.07	4	115	proton transmembrane transport	BP	1	ATP5F1B,CYC1,SLC25A5,NNT	darkgrey	VSMC_M8
GO:0070848	0.97	0.04	33	570	response to growth factor	BP	1	FBN2,NUS1,HSP90AB1,CDC5L,COL1A2,SHCBP1,CCNA2,CAD,SPHK1,EIF4A3,ZNF703,HGF,SNAI2,CD44,E2F1,KNSTRN,CREB3L1,TRIM33,NCL,DDX5,PDE3A,STRAP,MCM7,MSX1,NEDD4,LTBP2,COL1A1,PIK3CD,BCAR1,GCLM,FAM129B,ARF6,HAS2	darkgrey	VSMC_M8
GO:0030217	0.97	0.06	8	179	T cell differentiation	BP	1	LOXL3,ENTPD7,RUNX1,XBP1,PRELID1,PIK3CD,FANCA,CBFB	darkgrey	VSMC_M8
GO:1901652	0.97	0.05	20	375	response to peptide	BP	1	RANGAP1,CYC1,CDC5L,NAMPT,CCNA2,CAD,GGH,EIF2B1,CHUK,NCOA5,NUCKS1,XBP1,SMARCC1,MYO5A,CDC6,SRSF5,COL1A1,BRIP1,BCAR1,PID1	darkgrey	VSMC_M8
GO:0006091	0.97	0.05	20	392	generation of precursor metabolites and energy	BP	1	ATP5F1B,MTFR2,CYC1,VCP,CYCS,CCNB1,PDHB,SUCLG1,NDUFAF1,CDK1,PDHA1,NDUFS1,DLAT,MYBBP1A,FH,BID,PRELID1,NNT,G6PD,PID1	darkgrey	VSMC_M8
GO:0009611	0.97	0.04	23	422	response to wounding	BP	1	RANGAP1,PABPC4,SDC1,GRIN2C,PRCP,PLAUR,AXL,ELK3,CD44,HMGCR,ETS1,METAP1,XBP1,CDK1,EPHB2,TFPI,RAC1,RAB27A,ADIPOR2,PDPN,COL1A1,TOR1A,AURKA	darkgrey	VSMC_M8
GO:0030323	0.97	0.06	6	145	respiratory tube development	BP	1	HOXA5,PGR,RBP4,LOXL3,PDPN,CRISPLD2	darkgrey	VSMC_M8
GO:0022604	0.97	0.05	13	261	regulation of cell morphogenesis	BP	1	EZR,MFSD2A,CDC42EP4,RNF157,ARHGDIA,CD44,FMNL3,CDC42SE1,RAC1,PDPN,SPAG9,SYT4,HAS2	darkgrey	VSMC_M8
GO:0048771	0.97	0.07	5	129	tissue remodeling	BP	1	AXL,RUNX1,SPP2,TFRC,RAC1	darkgrey	VSMC_M8
GO:0045664	0.97	0.06	6	145	regulation of neuron differentiation	BP	1	HEY1,ASPM,EIF4G1,ECT2,SPAG9,TP73	darkgrey	VSMC_M8
GO:0045598	0.97	0.07	4	109	regulation of fat cell differentiation	BP	1	MEDAG,E2F1,XBP1,HNRNPU	darkgrey	VSMC_M8
GO:0007015	0.97	0.04	20	373	actin filament organization	BP	1	EZR,FAM49B,CDC42EP4,DIAPH3,GAS2L3,HSP90B1,FHDC1,EFS,NF2,PAK2,RAC1,MYO5A,FSCN1,TPM3,EMP2,BCAR1,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0051179	0.97	0.03	324	4586	localization	BP	1	NARS,ATP5F1B,TMED9,XPOT,NUP43,NUP107,CCT2,TUBB,DDX39B,FBXO5,EZR,FBN2,PANX2,TCP1,RAD21,NUP50,TTLL1,NUS1,ARFGAP3,MAN1A1,MTBP,KIFC1,DESI1,FAM49B,RANGAP1,KIF20A,SLC35D2,HSPA9,SRSF3,KIF27,CYC1,TNPO3,BYSL,HMGXB4,STEAP1,TJP2,CYP51A1,VCP,HSP90AB1,ARHGEF39,CENPQ,CEP135,MIOS,NOL8,TRIM28,NCBP1,THADA,ANP32B,TTK,HNRNPA2B1,HOXA5,MFSD2A,CCT4,SLC31A1,NUP205,ANLN,YRDC,CDCA8,EZH2,NUP62,GJB3,NBAS,SDC1,RUVBL2,STIL,SEC61A1,RUVBL1,AMOTL1,SAE1,SLC1A5,CHCHD4,CENPA,NASP,COG3,GRIN2C,TOMM40,PRCP,PREB,KCNN4,NUP85,SLC25A19,CAD,KIF2C,SLC5A6,DBI,BORA,SRP68,AXL,RNF157,SPHK1,ULK4,GDI2,NET1,BIRC5,SEC23B,FBL,RRBP1,GTPBP4,IPO5,EIF4A3,CHMP6,ARHGDIA,ALYREF,KCNK6,ZNF703,HGF,CCNB1,SNAI2,CD44,AAAS,ESPL1,DEPDC1B,KIF20B,KIF2A,SLC20A1,SGK3,CENPJ,HSP90B1,NECAB3,ABCE1,CCNE1,VAMP8,ATP1B3,SLC10A7,KNTC1,HMGB2,TRAM1,CEP55,RBP4,TERF1,NRIP1,NUP160,RACGAP1,LOXL3,ESCO2,SELENOT,FMNL3,TUBA1B,CCT8,PPID,BUB1B,CCT7,RSRC1,CFAP298,GNL3,FAM83D,CKAP5,NUP93,KNSTRN,KNL1,TBX3,CREB3L1,TOMM70,CCNE2,YWHAB,HMGCR,BAP1,NUSAP1,NIPA2,SFXN3,HEATR3,NOLC1,CCT5,NUP153,CCT6A,KIF18A,ETS1,NSUN2,ICE1,TXLNA,NAV1,KHDRBS1,CENPE,CEP72,KIF14,RGS9,CSE1L,ASPM,EFS,PHACTR4,PITPNB,XBP1,RPA2,UTP25,MCM3AP,IPO4,SFXN4,NUP133,HINFP,NF2,SEC24D,FLVCR1,CDC42SE1,UMPS,SSB,NOP58,ARCN1,CENPF,BUB3,SLC17A9,ARFGAP1,CDK1,HDLBP,S100A11,TFRC,PAK2,DHX9,NUF2,LSG1,HNRNPA3,ZW10,CDCA5,CABYR,RANBP1,IFT80,BARD1,EPHB2,NMD3,UFD1,SLC35F2,NSD2,CDK16,SLBP,DLG	darkgrey	VSMC_M8
GO:0043405	0.97	0.06	6	146	regulation of MAP kinase activity	BP	1	EZH2,NUP62,HMGCR,UCHL1,ERP29,DUSP7	darkgrey	VSMC_M8
GO:0044419	0.97	0.04	58	948	biological process involved in interspecies interaction between organisms	BP	1	TUBB,DDX39B,TCP1,FAM49B,FKBP5,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,SYNCRIP,ODC1,SEC61A1,SLC1A5,CDC42EP4,HNRNPUL1,AXL,POLR3F,ALYREF,VAMP8,HMGB2,PPID,TRIM35,TOMM70,MTDH,CHUK,CCT5,NUP153,NUCKS1,MNDA,XBP1,RBM14,CDK1,TFRC,PAK2,FOSL1,DHX9,DDX21,UFD1,TFPI,LYAR,RAB27A,ADIPOR2,UBE2K,NEDD4,EIF5A,ARG2,PPIB,ILF3,ELF4,TFAP4,THOC6,TUBB4B,PIK3CD,GBP5,HMGB3,STMN1,TRIM59	darkgrey	VSMC_M8

GO:0002696	0.98	0.05	10	218	positive regulation of leukocyte activation	BP	1	FAM49B,AXL,VAMP8,RUNX1,XBP1,TFRC,EPHB2,NSD2,EFNB1,CBFB	darkgrey	VSMC_M8
GO:1902107	0.98	0.07	4	110	positive regulation of leukocyte differentiation	BP	1	AXL,RUNX1,XBP1,CBFB	darkgrey	VSMC_M8
GO:1903708	0.98	0.07	4	110	positive regulation of hemopoiesis	BP	1	AXL,RUNX1,XBP1,CBFB	darkgrey	VSMC_M8
GO:0061138	0.98	0.06	6	147	morphogenesis of a branching epithelium	BP	1	HOXA5,PGR,HGF,TBX3,SIX4,HOXB7	darkgrey	VSMC_M8
GO:0071560	0.98	0.05	9	199	cellular response to transforming growth factor beta stimulus	BP	1	FBN2,HSP90AB1,COL1A2,ZNF703,TRIM33,PDE3A,STRAP,LTBP2,COL1A1	darkgrey	VSMC_M8
GO:0030073	0.98	0.06	6	149	insulin secretion	BP	1	RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0003018	0.98	0.05	9	200	vascular process in circulatory system	BP	1	TJP2,MFSD2A,SLC1A5,SLC5A6,HMGCR,PDE3A,TFRC,SLC6A17,GCLM	darkgrey	VSMC_M8
GO:0060271	0.98	0.04	13	266	cilium assembly	BP	1	TTLL1,KIF27,KIF24,CEP135,PLK4,CENPJ,CEP89,FHDC1,CFAP298,IQCB1,IFT80,LRRC49,SEPT6	darkgrey	VSMC_M8
GO:0002819	0.98	0.06	4	111	regulation of adaptive immune response	BP	1	FAM49B,LOXL3,TFRC,NSD2	darkgrey	VSMC_M8
GO:0010469	0.98	0.06	4	112	regulation of signaling receptor activity	BP	1	NCAPG2,CHMP6,RGS9,EPHB2	darkgrey	VSMC_M8
GO:0060249	0.98	0.05	10	218	anatomical structure homeostasis	BP	1	TJP2,MFSD2A,RBP4,IQCB1,STRAP,TFRC,BARD1,AIPL1,FH,RAC1	darkgrey	VSMC_M8
GO:0021915	0.98	0.06	5	130	neural tube development	BP	1	STIL,KIF20B,PHACTR4,NUP133,MTHFD1	darkgrey	VSMC_M8
GO:0006631	0.98	0.04	13	271	fatty acid metabolic process	BP	1	MFSD2A,PCCA,CRYL1,ELOVL6,XBP1,BRCA1,ADIPOR2,ALOX15B,ACSL4,ALDH3A2,LIPG,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0071495	0.98	0.03	63	1018	cellular response to endogenous stimulus	BP	1	EZR,FBN2,RANGAP1,HSP90AB1,CDC5L,COL1A2,EZH2,SHCBP1,PGR,NAMPT,CCNA2,PPP5C,FOSB,PRCP,CAD,IPO5,EIF4A3,ZNF703,SNAI2,CD44,HSP90B1,E2F1,HEY1,KNSTRN,RAD51,CREB3L1,TRIM33,NCOA5,NUCKS1,NCL,RGS9,PRMT5,DDX5,XBP1,BLM,PDE3A,STRAP,SMARCC1,BRCA1,MCM7,TFPI,CNOT9,MSX1,MYO5A,HNRNPU,ADIPOR2,NEDD4,CDC6,SMC1A,SRSF5,LTBP2,COL1A1,BRIP1,DNMT1,AIFM1,TFAP4,BCAR1,GCLM,ARF6,HNRNPD,HAS2,PID1,CASP6	darkgrey	VSMC_M8
GO:0060538	0.98	0.05	5	132	skeletal muscle organ development	BP	1	MSC,HMGCR,DDX5,SIX4,FAM129B	darkgrey	VSMC_M8
GO:0044248	0.98	0.03	114	1755	cellular catabolic process	BP	1	CDK2,POP1,EZR,MAN1A1,DESI1,GCAT,ALDH1L2,VCP,HSP90AB1,NCBP1,GRSF1,MFSD2A,SYNCRIP,PABPC4,THRAP3,NBAS,NRDC,NAMPT,RNASEH2B,SMG9,DIS3,SPHK1,XRN2,CDC20,AFMID,EIF4A3,CHMP6,PCCA,CHFR,EXOSC8,PGAM5,HGF,PSMD13,CDC16,ANAPC1,ATG101,HSP90B1,E2F1,AADAT,VAMP8,PBK,ENTPD7,MTDH,BAP1,UBE2C,PSMD14,FASTKD3,TENT4A,NSUN2,KIF14,UNG,DDX5,XBP1,DTL,SSB,PSMD4,EIF4G1,PSMC5,SMARCC1,DHX9,HNRNPR,PSMA6,DNA2,GK,DUT,UFD1,CNOT9,USP42,HNRNPU,UCHL1,UBE2K,NEDD4,BID,PSMD3,ARG2,NUDT1,DCTPP1,EXOSC10,FUS,RAD23A,PLK1,ELAC2,EDC3,TAF15,PSMD11,SLC25A5,COPS3,HNRNPM,SERBP1,NNT,POLDIP2,MTCL1,AIFM1,USP1,UHRF1,LIPG,SMG6,CCNF,RNPS1,ZNF598,DKC1,REXO4,PSMA5,ZC3H18,EXOSC2,TOR1A,USP4,HNRNPD,AURKA,UBE2S,FEN1,PSMD7,UBE2J2,EVA1A	darkgrey	VSMC_M8
GO:0006508	0.98	0.03	81	1295	proteolysis	BP	1	CDK2,MAN1A1,DESI1,VCP,HSP90AB1,ANP32B,CYCS,CASP2,NRDC,NAALAD2,PRCP,PLAUR,CDC20,BIRC5,SERPINH1,CHFR,METAP2,HGF,PSMD13,CDC16,USPL1,CD44,ESPL1,ANAPC1,GGH,ADAMTS6,HSP90B1,PBK,BAP1,RUNX1,UBE2C,PSMD14,METAP1,KIF14,XBP1,SPP2,DTL,PSMD4,PSMC5,ADAMTS4,CDK1,TFRC,PAK2,SMARCC1,PSMA6,ADAMTS14,UFD1,TFPI,USP42,DESI2,UCHL1,UBE2K,NEDD4,BID,PSMD3,PRELID1,RAD23A,PTTG1,PLK1,PSMD11,COPS3,AIFM1,USP1,UHRF1,RBMX,DPP9,TFAP4,CCNF,THOP1,ZNF598,PSMA5,TOR1A,USP4,FAM111B,SPCS3,AURKA,UBE2S,PDCD2,CASP6,PSMD7,UBE2J2	darkgrey	VSMC_M8
GO:0030855	0.98	0.03	23	430	epithelial cell differentiation	BP	1	EZR,TJP2,HOXA5,EZH2,SDC1,PLK4,PGR,E2F7,SIPA1L3,PCNA,ZNF703,HEY1,TBX3,E2F8,NF2,CDK1,HNRNPH3,ETV4,PDPN,ALOX15B,TYMS,RAP2C,CASP6	darkgrey	VSMC_M8
GO:0045637	0.98	0.05	6	152	regulation of myeloid cell differentiation	BP	1	HSPA9,HOXA5,PRMT1,HMGB2,RUNX1,ETS1	darkgrey	VSMC_M8
GO:0002684	0.98	0.03	30	542	positive regulation of immune system process	BP	1	EZR,FAM49B,MATR3,POLR3B,KCNN4,AXL,POLR3F,EIF2B1,VAMP8,HMGB2,RBP4,TOMM70,RUNX1,KHDRBS1,MNDA,XBP1,RBM14,TFRC,PAK2,DHX9,DDX21,EPHB2,NSD2,RAC1,UBE2K,EFNB1,PIK3CD,BCAR1,CBFB,GBP5	darkgrey	VSMC_M8
GO:0046879	0.98	0.04	9	206	hormone secretion	BP	1	VAMP8,RBP4,SELENOT,TBX3,HMGCR,CDK16,RAC1,ACSL4,FAM129B	darkgrey	VSMC_M8
GO:1905952	0.98	0.05	4	118	regulation of lipid localization	BP	1	NUS1,DBI,PRELID1,LIPG	darkgrey	VSMC_M8
GO:0090150	0.98	0.04	9	210	establishment of protein localization to membrane	BP	1	SEC61A1,SRP68,TRAM1,TOMM70,BID,TIMM8A,MTCL1,EMC8,ACSL3	darkgrey	VSMC_M8
GO:0071559	0.98	0.04	9	205	response to transforming growth factor beta	BP	1	FBN2,HSP90AB1,COL1A2,ZNF703,TRIM33,PDE3A,STRAP,LTBP2,COL1A1	darkgrey	VSMC_M8
GO:0009968	0.98	0.03	59	973	negative regulation of signal transduction	BP	1	ALPK2,DDX39B,EZR,FBN2,FAM49B,HMGXB4,VCP,EZH2,NUP62,RUVBL2,PLAUR,RNF157,EIF4A3,CHMP6,HGF,SNAI2,CD44,HMGB2,HELLS,PBK,HEY1,CREB3L1,TRIM33,YWHAB,HMGCR,PPP1R15B,PAK1IP1,NCOA5,CIT,TRAIP,RGS9,PHACTR4,XBP1,NF2,PDE3A,STRAP,IFT80,EPHB2,UFD1,BRCA1,CNOT9,FOXM1,UCHL1,NEDD4,BID,PRELID1,LMNA,MAZ,SLC25A5,NXN,NOC2L,CDT1,GCLM,FAM129B,CTH,STMN1,PID1,TRIM59,DUSP7	darkgrey	VSMC_M8
GO:0007416	0.98	0.05	5	132	synapse assembly	BP	1	EIF4G1,EPHB2,SIX4,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0002697	0.98	0.04	9	206	regulation of immune effector process	BP	1	FAM49B,VAMP8,RBP4,LOXL3,XBP1,TFRC,DDX21,EPHB2,NSD2	darkgrey	VSMC_M8
GO:0010631	0.98	0.03	12	261	epithelial cell migration	BP	1	ATP5F1B,NUS1,ANLN,PRCP,ETS1,RAC1,EMP2,PIK3CD,PKN3,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0072073	0.98	0.05	4	115	kidney epithelium development	BP	1	SDC1,SIX4,ARG2,HOXB7	darkgrey	VSMC_M8

GO:0006357	0.98	0.02	117	1784	regulation of transcription by RNA polymerase II	BP	1	BCLAF1,EZR,RAD21,ATAD2,ZNF367,PSIP1,CDC5L,CKS2,TRIM28,HOXA5,THRAP3,EZH2,PHF19,RUVBL2,PGR,NAMPT,RUVBL1,FOSB,NUFIP1,SUPT16H,E2F7,CKAP2,PCNA,HGF,ELK3,TCERG1,CBX5,SNAI2,TCEA1,E2F1,CCNE1,ZNF827,HMGB2,MSC,ATF1,NRIP1,HEY1,ZBTB10,PPID,RBL1,CCNL1,GNL3,TBX3,CREB3L1,MYBL2,E2F8,TRIM33,MTDH,CHUK,RUNX1,HR,MDM4,NCOA5,PPRC1,HMGN1,NUCKS1,DEK,GCN1,ETS1,CHEK1,H2AFZ,KHDRBS1,NCL,TARBP1,DDX5,XBP1,HINFP,RBM14,STRAP,PSMC5,FOSL1,SMARCC1,DHX9,DDX20,SMARCAL1,ETV4,BRCA1,NSD2,GABPB1,CREG1,SUV39H1,SIX4,MNAT1,FOXM1,LYAR,MSX1,FAM220A,HNRNPU,NEDD4,SMARCE1,RFC1,TOP2A,LIN9,EIF5A,HDGF,HOXB7,FUS,MAZ,AURKB,NFATC2IP,PLK1,BRIP1,MORF4L2,DNMT1,TADA2A,ELF4,UHRF1,RBMX,TFAP4,NOC2L,TP73,CBFB,DRAP1,HMGB3,PID1,HOXC8,MBD2	darkgrey	VSMC_M8
GO:0030100	0.98	0.04	7	174	regulation of endocytosis	BP	1	AXL,SPHK1,ARFGAP1,RAC1,SYT4,TOR1A,ARF6	darkgrey	VSMC_M8
GO:1903706	0.98	0.03	12	258	regulation of hemopoiesis	BP	1	HSPA9,HOXA5,PRMT1,AXL,HMGB2,LOXL3,RUNX1,ETS1,XBP1,PRELID1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0051403	0.98	0.04	8	190	stress-activated MAPK cascade	BP	1	EZR,PRMT1,SPHK1,ULK4,HGF,PBK,HMGCR,FOXM1	darkgrey	VSMC_M8
GO:0050670	0.98	0.04	5	137	regulation of lymphocyte proliferation	BP	1	MNDA,TFRC,EPHB2,ARG2,EFNB1	darkgrey	VSMC_M8
GO:0030111	0.98	0.03	13	277	regulation of Wnt signaling pathway	BP	1	ALPK2,HMGXB4,VCP,RUVBL2,RUVBL1,ZNF703,SNAI2,DEPDC1B,ASPM,IFT80,COL1A1,NXN,MBD2	darkgrey	VSMC_M8
GO:0090132	0.98	0.03	12	262	epithelium migration	BP	1	ATP5F1B,NUS1,ANLN,PRCP,ETS1,RAC1,EMP2,PIK3CD,PKN3,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0050867	0.98	0.04	10	226	positive regulation of cell activation	BP	1	FAM49B,AXL,VAMP8,RUNX1,XBP1,TFRC,EPHB2,NSD2,EFNB1,CBFB	darkgrey	VSMC_M8
GO:0048534	0.98	0.03	37	649	hematopoietic or lymphoid organ development	BP	1	HSPA9,MELK,HOXA5,PABPC4,EZH2,PRMT1,PUS7,AXL,NCAPG2,SIPA1L3,HMGB2,LOXL3,ESCO2,AGPAT5,ENTPD7,RUNX1,ETS1,XBP1,FLVCR1,TFRC,ANKLE1,SIX4,EIF2AK1,LYAR,TOP2A,LBR,PDPN,PRELID1,CCNB2,HOXB7,SLC25A5,G6PD,PIK3CD,FANCA,CBFB,TMOD3,PDCD2	darkgrey	VSMC_M8
GO:0034764	0.98	0.04	6	155	positive regulation of transmembrane transport	BP	1	KCNN4,ATP1B3,RGS9,EPHB2,ADIPOR2,G6PD	darkgrey	VSMC_M8
GO:0010876	0.98	0.03	15	311	lipid localization	BP	1	NUS1,MFSD2A,KCNN4,DBI,SLC10A7,RBP4,NRIP1,PITPNB,HDLBP,PRELID1,ACSL4,LIPG,ACSL3,SIGMAR1,XKR5	darkgrey	VSMC_M8
GO:0046883	0.98	0.04	7	174	regulation of hormone secretion	BP	1	VAMP8,RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0043588	0.98	0.04	7	171	skin development	BP	1	COL1A2,GJB3,NSUN2,ETV4,ALOX15B,COL1A1,STMN1	darkgrey	VSMC_M8
GO:0001568	0.98	0.03	32	576	blood vessel development	BP	1	ATP5F1B,NUS1,COL1A2,HOXA5,NAA15,AMOTL1,PRCP,SPHK1,E2F7,HGF,ELK3,ADAMTS6,HEY1,FMNL3,TBX3,CREB3L1,E2F8,MTDH,RUNX1,ETS1,NCL,XBP1,FLVCR1,FOSL1,EPHB2,BRCA1,ADIPOR2,COL1A1,EMP2,PIK3CD,FAM129B,HAS2	darkgrey	VSMC_M8
GO:0046942	0.98	0.04	7	173	carboxylic acid transport	BP	1	SLC35D2,SLC1A5,SLC5A6,SLC10A7,SFXN3,SLC19A2,SLC6A17	darkgrey	VSMC_M8
GO:0032944	0.98	0.04	5	138	regulation of mononuclear cell proliferation	BP	1	MNDA,TFRC,EPHB2,ARG2,EFNB1	darkgrey	VSMC_M8
GO:0002703	0.98	0.04	5	136	regulation of leukocyte mediated immunity	BP	1	FAM49B,VAMP8,TFRC,DDX21,NSD2	darkgrey	VSMC_M8
GO:0043542	0.98	0.03	8	195	endothelial cell migration	BP	1	ATP5F1B,NUS1,PRCP,ETS1,RAC1,EMP2,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0019752	0.98	0.02	37	659	carboxylic acid metabolic process	BP	1	NARS,VARS2,VARS,GCAT,ALDH1L2,CTPS1,MFSD2A,GARS,ODC1,CAD,AFMID,PCCA,CRYL1,PDHB,AADAT,BCAT1,ELOVL6,XBP1,PDHA1,DLAT,BRCA1,FH,ADIPOR2,MTHFD1,UGDH,ARG2,ALOX15B,PFAS,RARS,ACSL4,ALDH3A2,LIPG,GCLM,CTH,SCD5,ACSL3,GART	darkgrey	VSMC_M8
GO:0002252	0.98	0.03	18	360	immune effector process	BP	1	TUBB,FAM49B,MSH6,VAMP8,RBP4,LOXL3,ENTPD7,UNG,XBP1,TFRC,DDX21,EPHB2,NSD2,EXO1,RAB27A,EMP2,TUBB4B,PIK3CD	darkgrey	VSMC_M8
GO:0070482	0.98	0.03	13	280	response to oxygen levels	BP	1	NAMPT,CCNA2,CCNB1,HSP90B1,E2F1,MDM4,ETS1,SUV39H1,PDPN,LMNA,COL1A1,BRIP1,AIFM1	darkgrey	VSMC_M8
GO:1990778	0.98	0.03	13	279	protein localization to cell periphery	BP	1	EZR,GRIN2C,VAMP8,ATP1B3,IFT80,EPHB2,MYO5A,PLK1,EMP2,ARF6,RAPGEF6,ACSL3,PID1	darkgrey	VSMC_M8
GO:0090130	0.98	0.03	12	266	tissue migration	BP	1	ATP5F1B,NUS1,ANLN,PRCP,ETS1,RAC1,EMP2,PIK3CD,PKN3,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0010970	0.98	0.04	5	139	transport along microtubule	BP	1	HNRNPU,UCHL1,KIF4A,NDE1,BLOC1S2	darkgrey	VSMC_M8
GO:0120032	0.98	0.04	6	158	regulation of plasma membrane bounded cell projection assembly	BP	1	CEP135,ANLN,CDC42EP4,RAC1,FSCN1,ARF6	darkgrey	VSMC_M8
GO:0045926	0.98	0.03	8	195	negative regulation of growth	BP	1	RBP4,MSX1,ADIPOR2,ALOX15B,SPAG9,TP73,G6PD,CDKN2C	darkgrey	VSMC_M8
GO:0009914	0.98	0.03	9	212	hormone transport	BP	1	VAMP8,RBP4,SELENOT,TBX3,HMGCR,CDK16,RAC1,ACSL4,FAM129B	darkgrey	VSMC_M8
GO:0010810	0.99	0.03	7	175	regulation of cell-substrate adhesion	BP	1	NF2,RAC1,PDPN,COL1A1,POLDIP2,EMP2,HAS2	darkgrey	VSMC_M8
GO:0001763	0.99	0.04	6	157	morphogenesis of a branching structure	BP	1	HOXA5,PGR,HGF,TBX3,SIX4,HOXB7	darkgrey	VSMC_M8
GO:0071310	0.99	0.02	115	1784	cellular response to organic substance	BP	1	EZR,FBN2,NUS1,RANGAP1,HSPA9,SRSF3,VCP,HSP90AB1,CDC5L,COL1A2,SYNCRIP,B3GNT2,EZH2,GJB3,SHCBP1,RUVBL2,PGR,NAMPT,MCM2,CCNA2,PPP5C,FOSB,CDC42EP4,PRCP,CAD,DDX18,AXL,SPHK1,IPO5,EIF4A3,ARHGDIA,ZNF703,HGF,CCNB1,SNAI2,CD44,HSP90B1,E2F1,HMGB2,MSC,HELLS,NRIP1,HEY1,SELENOT,TUBA1B,KNSTRN,RAD51,CREB3L1,MYBL2,TRIM33,MTDH,HMGCR,CHUK,PPP1R15B,NCOA5,NUCKS1,KIF18A,H2AFZ,NCL,TRAIP,RGS9,PRMT5,MNDA,DDX5,XBP1,BLM,PDE3A,STRAP,TFRC,PAK2,SMARCC1,DHX9,TRA2B,UFD1,BRCA1,MCM7,TFPI,CNOT9,CDK16,MSX1,RAC1,MYO5A,HNRNPU,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,EIF2S1,SRSF5,IQGAP3,HDGF,LTBP2,COL1A1,BRIP1,DNMT1,SLC25A5,AIFM1,RBMX,TFAP4,PIK3CD,TOR1A,BCAR1,GCLM,FAM129B,CTH,ARF6,GBP5,HNRNPD,HAS2,SRSF7,PID1,CASP6,SRM,MBD2	darkgrey	VSMC_M8
GO:0045596	0.99	0.02	26	489	negative regulation of cell differentiation	BP	1	HSPA9,ANP32B,HOXA5,EZH2,PRMT1,SNAI2,E2F1,LOXL3,HEY1,TBX3,RUNX1,PRMT5,ASPM,IQCB1,XBP1,EPHB2,MED28,SIX4,MSX1,HNRNPU,SPAG9,DNMT1,TP73,G6PD,PTBP1,CBFB	darkgrey	VSMC_M8
GO:0060491	0.99	0.03	6	159	regulation of cell projection assembly	BP	1	CEP135,ANLN,CDC42EP4,RAC1,FSCN1,ARF6	darkgrey	VSMC_M8
GO:0048839	0.99	0.04	5	139	inner ear development	BP	1	ANP32B,MCM2,CCNA2,EPHB2,SIX4	darkgrey	VSMC_M8
GO:0090092	0.99	0.03	8	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	FBN2,HSP90AB1,TTK,ZNF703,NUP93,TRIM33,STRAP,MSX1	darkgrey	VSMC_M8

GO:0048588	0.99	0.03	8	195	developmental cell growth	BP	1	DDX39B,HSP90AB1,RNF157,PARP2,SPAG9,SYT4,G6PD,AURKA	darkgrey	VSMC_M8
GO:0050673	0.99	0.03	15	316	epithelial cell proliferation	BP	1	HOXA5,PGR,ZNF703,HGF,SNAI2,HMGB2,NRAS,HMGN1,XBP1,IFT80,SIX4,IQGAP3,UHRF1,PIK3CD,HAS2	darkgrey	VSMC_M8
GO:0001659	0.99	0.04	5	141	temperature homeostasis	BP	1	NRDC,PGAM5,ELOVL6,FH,ADIPOR2	darkgrey	VSMC_M8
GO:1903034	0.99	0.04	4	123	regulation of response to wounding	BP	1	HMGCR,XBP1,EPHB2,TFPI	darkgrey	VSMC_M8
GO:0035725	0.99	0.04	4	120	sodium ion transmembrane transport	BP	1	SLC20A1,ATP1B3,NEDD4,SLC6A17	darkgrey	VSMC_M8
GO:0009100	0.99	0.02	14	299	glycoprotein metabolic process	BP	1	NUS1,MAN1A1,B3GNT2,RPN1,COG3,ALG8,NECAB3,PXYLP1,GALNT6,STT3A,UGDH,XYLT1,DOLPP1,GMPPB	darkgrey	VSMC_M8
GO:0031098	0.99	0.03	8	197	stress-activated protein kinase signaling cascade	BP	1	EZR,PRMT1,SPHK1,ULK4,HGF,PBK,HMGCR,FOXM1	darkgrey	VSMC_M8
GO:0002694	0.99	0.02	17	352	regulation of leukocyte activation	BP	1	FAM49B,AXL,SPHK1,VAMP8,LOXL3,RUNX1,MNDA,XBP1,TFRC,EPHB2,NSD2,DCAF15,ARG2,PRELID1,EFNB1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0051651	0.99	0.03	6	163	maintenance of location in cell	BP	1	RANGAP1,HSP90B1,ASPM,BARD1,KDELR2,HNRNPU	darkgrey	VSMC_M8
GO:0046395	0.99	0.03	7	182	carboxylic acid catabolic process	BP	1	GCAT,ALDH1L2,MFSD2A,AFMID,PCCA,AADAT,ARG2	darkgrey	VSMC_M8
GO:0006814	0.99	0.03	6	161	sodium ion transport	BP	1	SLC5A6,SLC20A1,ATP1B3,SLC10A7,NEDD4,SLC6A17	darkgrey	VSMC_M8
GO:0030097	0.99	0.02	34	618	hemopoiesis	BP	1	HSPA9,MELK,HOXA5,PABPC4,EZH2,PRMT1,PUS7,AXL,NCAPG2,SIPA1L3,HMGB2,LOXL3,ESCO2,AGPAT5,ENTPD7,RUNX1,ETS1,XBP1,FLVCR1,TFRC,ANKLE1,EIF2AK1,LYAR,TOP2A,LBR,PRELID1,HOXB7,SLC25A5,G6PD,PIK3CD,FANCA,CBFB,TMOD3,PDCD2	darkgrey	VSMC_M8
GO:0070661	0.99	0.03	8	201	leukocyte proliferation	BP	1	CTPS1,HELLS,MNDA,TFRC,EPHB2,ARG2,EFNB1,ELF4	darkgrey	VSMC_M8
GO:0050769	0.99	0.03	7	181	positive regulation of neurogenesis	BP	1	NAP1L1,E2F1,PRMT5,ASPM,EPHB2,TP73,SRRT	darkgrey	VSMC_M8
GO:0061025	0.99	0.03	4	125	membrane fusion	BP	1	SPHK1,VAMP8,SYT4,STXBP6	darkgrey	VSMC_M8
GO:0043583	0.99	0.03	6	162	ear development	BP	1	ANP32B,MCM2,CCNA2,EPHB2,SIX4,MSX1	darkgrey	VSMC_M8
GO:0090596	0.99	0.03	8	198	sensory organ morphogenesis	BP	1	FBN2,MFSD2A,RBP4,HMGN1,PHACTR4,EPHB2,SIX4,MSX1	darkgrey	VSMC_M8
GO:0050727	0.99	0.02	10	239	regulation of inflammatory response	BP	1	SPHK1,HGF,VAMP8,PBK,BAP1,SETD4,ETS1,DHX9,PSMA6,FANCA	darkgrey	VSMC_M8
GO:0030833	0.99	0.03	5	145	regulation of actin filament polymerization	BP	1	FAM49B,CDC42EP4,ARPC4,ARF6,TMOD3	darkgrey	VSMC_M8
GO:0043087	0.99	0.02	13	285	regulation of GTPase activity	BP	1	RANGAP1,EZH2,NET1,DOCK9,SIPA1L3,ARHGAP11A,ECT2,EIF2S1,IQGAP3,EIF5,POLDIP2,RAPGEF6,STMN1	darkgrey	VSMC_M8
GO:0048869	0.99	0.01	205	3033	cellular developmental process	BP	1	CDK2,ALPK2,ATP5F1B,HNRNPAB,DDX39B,FBXO5,EZR,FBN2,TTLL1,NUS1,PHF5A,HSPA9,SRPK1,BYSL,PWP1,TJP2,HSP90AB1,TRIM28,ANP32B,HOXA5,MFSD2A,SYNCRIP,PABPC4,B3GNT2,EZH2,NUP62,PHF19,PRMT1,CASP2,NAA15,SMC6,SDC1,PLK4,PGR,NAMPT,PUS7,MAST2,AXL,RNF157,XRN2,ULK4,NCAPG2,CDC20,SERPINH1,PARP2,FBL,RRBP1,GTPBP4,NAP1L1,E2F7,ALYREF,STRN,SIPA1L3,PCNA,CDC25B,ZNF703,HGF,ELK3,MEDAG,CCNB1,WDR62,SNAI2,CD44,POLR1B,KIF20B,KIF2A,WEE1,EIF2B1,E2F1,HMGB2,ATF1,RACGAP1,LOXL3,ESCO2,HEY1,AGPAT5,RBL1,FAM83D,KNL1,TBX3,CREB3L1,E2F8,ENTPD7,HMGCR,EEF1E1,CHUK,RUNX1,NAV2,NOLC1,CIT,MANF,ETS1,NSUN2,CHEK1,NAV1,TRIP13,KIF14,PRMT5,ASPM,IQCB1,DDX5,PHACTR4,XBP1,NUP133,HINFP,NF2,H2AFX,FLVCR1,PDE3A,CENPF,STRAP,EIF4G1,NHS,CDK1,TFRC,PAK2,DHX9,HNRNPH3,DDX20,DDX21,CABYR,IFT80,SF1,EPHB2,ETV4,CDK16,MED28,MYBBP1A,ANKLE1,ECT2,SUV39H1,FKBP4,SIX4,MAPK6,FOXM1,EIF2AK1,LYAR,USP42,MSX1,RAC1,HNRNPU,UCHL1,RAB27A,NEDD4,UGDH,SMARCE1,TOP2A,LBR,PDPN,ARG2,PRELID1,ASF1B,EFNB1,NES,SH3PXD2B,HOXB7,LMNA,ALOX15B,COL1A1,SPAG9,SYT4,BRIP1,MORF4L2,DNMT1,ACSL4,TYMS,PSMD11,SLC25A5,SEPT6,POLDIP2,NDE1,ELF4,RAI14,RAP2C,RSL1D1,HOOK1,EMP2,RBMX,NXN,SF3A2,TP73,DAZAP1,G6PD,PTBP1,PIK3CD,FANCA,TOR1A,ODF2,FAM129B,NEK6,CBFB,CTH,SRRT,ARF6,TMOD3,HNRNPD,CDKN2C,ACSL3,STMN1,AURKA,HAS2,BLOC1S2,PDCD2,PID1,CASP6	darkgrey	VSMC_M8
GO:0008154	0.99	0.02	7	183	actin polymerization or depolymerization	BP	1	FAM49B,CDC42EP4,DIAPH3,RAC1,ARPC4,ARF6,TMOD3	darkgrey	VSMC_M8
GO:0006082	0.99	0.02	38	689	organic acid metabolic process	BP	1	NARS,VARS2,VARS,GCAT,ALDH1L2,CTPS1,MFSD2A,GARS,ODC1,CAD,AFMID,PCCA,CRYL1,PDHB,AADAT,BCAT1,ELOVL6,XBP1,PDHA1,DLAT,BRCA1,FH,ADIPOR2,MTHFD1,UGDH,ARG2,ALOX15B,PFAS,RARS,PRPS1,ACSL4,ALDH3A2,LIPG,GCLM,CTH,SCD5,ACSL3,GART	darkgrey	VSMC_M8
GO:0018108	0.99	0.02	13	287	peptidyl-tyrosine phosphorylation	BP	1	MELK,TTK,AXL,NCAPG2,CHMP6,HGF,CD44,WEE1,PBK,NF2,PAK2,EPHB2,RAP2C	darkgrey	VSMC_M8
GO:0043491	0.99	0.03	5	147	protein kinase B signaling	BP	1	HSP90AB1,AXL,MTDH,MAZ,PIK3CD	darkgrey	VSMC_M8
GO:0045785	0.99	0.02	14	306	positive regulation of cell adhesion	BP	1	FAM49B,PLAUR,CD44,RUNX1,ETS1,XBP1,TFRC,RAC1,PDPN,EFNB1,POLDIP2,EMP2,CBFB,HAS2	darkgrey	VSMC_M8
GO:0120031	0.99	0.02	22	435	plasma membrane bounded cell projection assembly	BP	1	EZR,TTLL1,KIF27,KIF24,CEP135,ANLN,PLK4,CDC42EP4,NUP85,CENPJ,CEP89,FHDC1,CFAP298,IQCB1,IFT80,RAC1,FSCN1,LRRC49,SEPT6,EMP2,ARF6,RAPGEF6	darkgrey	VSMC_M8
GO:0017157	0.99	0.03	5	147	regulation of exocytosis	BP	1	SDC1,VAMP8,RAB27A,SYT4,STXBP6	darkgrey	VSMC_M8
GO:0016054	0.99	0.02	7	186	organic acid catabolic process	BP	1	GCAT,ALDH1L2,MFSD2A,AFMID,PCCA,AADAT,ARG2	darkgrey	VSMC_M8

GO:0010033	0.99	0.01	148	2273	response to organic substance	BP	1	EZR,FBN2,NUS1,MAN1A1,FAM49B,RANGAP1,HSPA9,SRSF3,CYC1,VCP,HSP90AB1,CDC5L,COL1A2,SYNCRIP,B3GNT2,EZH2,GJB3,SHCBP1,SDC1,RUVBL2,PGR,NAMPT,MCM2,SEC61A1,CCNA2,PPP5C,FOSB,CDC42EP4,NASP,PRCP,CAD,DDX18,AXL,SPHK1,SRSF2,SERPINH1,IPO5,EIF4A3,ARHGDIA,PCNA,ZNF703,RFC3,HGF,CCNB1,SNAI2,CD44,GGH,HSP90B1,EIF2B1,E2F1,HMGB2,TRAM1,RBP4,MSC,ATF1,HELLS,NRIP1,HEY1,SELENOT,TUBA1B,KNSTRN,RAD51,CREB3L1,MYBL2,TRIM33,MTDH,HMGCR,CHUK,PPP1R15B,PSMD14,NCOA5,NUCKS1,KIF18A,MANF,ETS1,H2AFZ,NCL,TRAIP,RGS9,PRMT5,MNDA,DDX5,XBP1,BLM,PDE3A,RBM14,STRAP,CDK1,TFRC,PAK2,FOSL1,SMARCC1,DHX9,TRA2B,DDX21,EFTUD2,UFD1,BRCA1,MCM7,TFPI,CNOT9,CDK16,MSX1,RAC1,MYO5A,HNRNPU,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,BID,EIF2S1,DHX15,SRSF5,IQGAP3,HDGF,LTBP2,COL1A1,BRIP1,DNMT1,ACSL4,TYMS,SLC25A5,AIFM1,RBMX,TFAP4,TP73,G6PD,PIK3CD,CDT1,TOR1A,BCAR1,GCLM,FAM129B,CTH,ARF6,GBP5,HNRNPD,ACSL3,HAS2,SRSF7,PID1,GART,CASP6,UBE2J2,SRM,MBD2	darkgrey	VSMC_M8
GO:0016055	0.99	0.02	18	373	Wnt signaling pathway	BP	1	ALPK2,HMGXB4,VCP,SDC1,RUVBL2,RUVBL1,AMOTL1,STRN,ZNF703,SNAI2,DEPDC1B,CCNE1,ASPM,IFT80,RAC1,COL1A1,NXN,MBD2	darkgrey	VSMC_M8
GO:0009719	0.99	0.01	73	1202	response to endogenous stimulus	BP	1	EZR,FBN2,RANGAP1,CYC1,HSP90AB1,CDC5L,COL1A2,EZH2,SHCBP1,SDC1,PGR,NAMPT,CCNA2,PPP5C,FOSB,PRCP,CAD,IPO5,EIF4A3,PCNA,ZNF703,SNAI2,CD44,GGH,HSP90B1,EIF2B1,E2F1,HMGB2,HEY1,KNSTRN,RAD51,CREB3L1,TRIM33,CHUK,NCOA5,NUCKS1,NCL,RGS9,PRMT5,DDX5,XBP1,BLM,PDE3A,RBM14,STRAP,FOSL1,SMARCC1,BRCA1,MCM7,TFPI,CNOT9,MSX1,MYO5A,HNRNPU,ADIPOR2,NEDD4,CDC6,SMC1A,SRSF5,LTBP2,COL1A1,BRIP1,DNMT1,TYMS,AIFM1,TFAP4,BCAR1,GCLM,ARF6,HNRNPD,HAS2,PID1,CASP6	darkgrey	VSMC_M8
GO:0043436	0.99	0.01	37	677	oxoacid metabolic process	BP	1	NARS,VARS2,VARS,GCAT,ALDH1L2,CTPS1,MFSD2A,GARS,ODC1,CAD,AFMID,PCCA,CRYL1,PDHB,AADAT,BCAT1,ELOVL6,XBP1,PDHA1,DLAT,BRCA1,FH,ADIPOR2,MTHFD1,UGDH,ARG2,ALOX15B,PFAS,RARS,ACSL4,ALDH3A2,LIPG,GCLM,CTH,SCD5,ACSL3,GART	darkgrey	VSMC_M8
GO:0198738	0.99	0.02	18	374	cell-cell signaling by wnt	BP	1	ALPK2,HMGXB4,VCP,SDC1,RUVBL2,RUVBL1,AMOTL1,STRN,ZNF703,SNAI2,DEPDC1B,CCNE1,ASPM,IFT80,RAC1,COL1A1,NXN,MBD2	darkgrey	VSMC_M8
GO:0009056	0.99	0.01	128	2000	catabolic process	BP	1	CDK2,POP1,EZR,MAN1A1,DESI1,GCAT,ALDH1L2,CYP51A1,VCP,HSP90AB1,NCBP1,GRSF1,MFSD2A,SYNCRIP,PABPC4,THRAP3,ODC1,NBAS,NRDC,NAMPT,RNASEH2B,GRIN2C,SMG9,DIS3,SPHK1,XRN2,CDC20,AFMID,EIF4A3,CHMP6,PCCA,CHFR,EXOSC8,PGAM5,HGF,PSMD13,CDC16,CD44,ANAPC1,ATG101,HSP90B1,E2F1,AADAT,VAMP8,PBK,FAM83D,ENTPD7,MTDH,HMGCR,BAP1,MDM4,UBE2C,PSMD14,FASTKD3,TENT4A,NSUN2,KIF14,UNG,DDX5,XBP1,UTP25,DTL,SSB,PSMD4,EIF4G1,PSMC5,SMARCC1,GALE,DHX9,HNRNPR,PSMA6,DNA2,GK,ADAMTS14,BARD1,DUT,UFD1,CNOT9,USP42,HNRNPU,UCHL1,UBE2K,NEDD4,BID,PSMD3,ARG2,NUDT1,DCTPP1,EXOSC10,FUS,RAD23A,PLK1,ELAC2,EDC3,TAF15,PSMD11,SLC25A5,COPS3,HNRNPM,SERBP1,NNT,POLDIP2,MTCL1,AIFM1,USP1,UHRF1,LIPG,SMG6,CCNF,RNPS1,ZNF598,DKC1,REXO4,PSMA5,ZC3H18,EXOSC2,TOR1A,SF3B3,USP4,HNRNPD,MAD2L1,AURKA,UBE2S,FEN1,PJA1,PSMD7,UBE2J2,EVA1A	darkgrey	VSMC_M8
GO:0018212	0.99	0.02	13	290	peptidyl-tyrosine modification	BP	1	MELK,TTK,AXL,NCAPG2,CHMP6,HGF,CD44,WEE1,PBK,NF2,PAK2,EPHB2,RAP2C	darkgrey	VSMC_M8
GO:0072659	0.99	0.02	10	239	protein localization to plasma membrane	BP	1	EZR,VAMP8,ATP1B3,EPHB2,MYO5A,EMP2,ARF6,RAPGEF6,ACSL3,PID1	darkgrey	VSMC_M8
GO:0036293	0.99	0.02	11	258	response to decreased oxygen levels	BP	1	NAMPT,CCNA2,CCNB1,HSP90B1,E2F1,MDM4,ETS1,SUV39H1,LMNA,BRIP1,AIFM1	darkgrey	VSMC_M8
GO:0006066	0.99	0.02	11	258	alcohol metabolic process	BP	1	NUS1,CYP51A1,SPHK1,PPIP5K2,RBP4,HMGCR,HDLBP,GK,LBR,ALDH3A2,G6PD	darkgrey	VSMC_M8
GO:0030335	0.99	0.02	22	443	positive regulation of cell migration	BP	1	ATP5F1B,FBXO5,NUS1,ARHGEF39,SPHK1,ZNF703,HGF,SNAI2,KIF20B,ETS1,XBP1,S100A11,EPHB2,RAC1,PDPN,MAZ,COL1A1,SPAG9,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0031348	0.99	0.02	5	149	negative regulation of defense response	BP	1	HGF,PBK,UFD1,LYAR,ARG2	darkgrey	VSMC_M8
GO:0030072	0.99	0.02	6	168	peptide hormone secretion	BP	1	RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0050777	0.99	0.03	4	128	negative regulation of immune response	BP	1	LOXL3,UFD1,LYAR,ARG2	darkgrey	VSMC_M8
GO:0007178	0.99	0.02	12	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	FBN2,HSP90AB1,COL1A2,TTK,ZNF703,NUP93,TRIM33,DDX5,RBM14,STRAP,MSX1,LTBP2	darkgrey	VSMC_M8
GO:0045321	0.99	0.01	31	586	leukocyte activation	BP	1	FAM49B,MSH6,CTPS1,EZH2,NAMPT,AXL,SPHK1,CD44,VAMP8,HELLS,LOXL3,ENTPD7,RUNX1,TXLNA,UNG,MNDA,XBP1,TFRC,EPHB2,NSD2,EXO1,RAB27A,DCAF15,ARG2,PRELID1,EFNB1,SLC25A5,ELF4,PIK3CD,FANCA,CBFB	darkgrey	VSMC_M8
GO:0016241	0.99	0.03	4	128	regulation of macroautophagy	BP	1	UCHL1,NEDD4,SLC25A5,POLDIP2	darkgrey	VSMC_M8
GO:0042180	0.99	0.02	5	150	cellular ketone metabolic process	BP	1	MFSD2A,AFMID,AADAT,HMGCR,BRCA1	darkgrey	VSMC_M8
GO:1990138	0.99	0.02	5	147	neuron projection extension	BP	1	HSP90AB1,RNF157,SPAG9,SYT4,AURKA	darkgrey	VSMC_M8
GO:0048514	0.99	0.01	26	508	blood vessel morphogenesis	BP	1	ATP5F1B,NUS1,HOXA5,NAA15,AMOTL1,PRCP,SPHK1,E2F7,HGF,ELK3,HEY1,FMNL3,CREB3L1,E2F8,MTDH,RUNX1,ETS1,NCL,XBP1,EPHB2,BRCA1,ADIPOR2,EMP2,PIK3CD,FAM129B,HAS2	darkgrey	VSMC_M8
GO:0030098	0.99	0.02	11	259	lymphocyte differentiation	BP	1	EZH2,AXL,LOXL3,ENTPD7,RUNX1,XBP1,PRELID1,SLC25A5,PIK3CD,FANCA,CBFB	darkgrey	VSMC_M8
GO:0051604	0.99	0.02	9	230	protein maturation	BP	1	CASP2,NAA15,CHCHD4,SERPINH1,METAP2,RUNX1,NAA50,CIAO2A,SPCS3	darkgrey	VSMC_M8
GO:0048871	0.99	0.01	18	378	multicellular organismal homeostasis	BP	1	TJP2,MFSD2A,NRDC,PRCP,PGAM5,RBP4,ELOVL6,IQCB1,STRAP,EIF4G1,TFRC,BARD1,AIPL1,FH,RAC1,ADIPOR2,STMN1,HAS2	darkgrey	VSMC_M8

GO:0050776	0.99	0.01	28	538	regulation of immune response	BP	1	EZR,FAM49B,MATR3,POLR3B,HSP90AB1,KCNN4,POLR3F,EIF2B1,VAMP8,HMGB2,LOXL3,TOMM70,ENTPD7,KHDRBS1,MNDA,XBP1,RBM14,TFRC,PAK2,DHX9,UFD1,NSD2,LYAR,UBE2K,ARG2,PIK3CD,BCAR1,GBP5	darkgrey	VSMC_M8
GO:0044281	0.99	0.01	78	1301	small molecule metabolic process	BP	1	NARS,ATP5F1B,VARS2,VARS,NUS1,GCAT,TJP2,ALDH1L2,CYP51A1,VCP,PAICS,NANS,CTPS1,DCK,MFSD2A,GARS,ODC1,AMD1,NAMPT,RNASEH2B,SLC25A19,CAD,SPHK1,TK1,AFMID,PCCA,RRM1,SNAI2,CRYL1,PDHB,PIP5K2,AADAT,RBP4,ENTPD7,HMGCR,SFXN3,UNG,BCAT1,ELOVL6,XBP1,UMPS,HDLBP,PDHA1,UAP1,GALE,UCK2,AGPS,GK,DLAT,DUT,BRCA1,SLC19A2,FH,ADIPOR2,MTHFD1,UGDH,LBR,ARG2,NUDT1,DCTPP1,ALOX15B,PFAS,RARS,PRPS1,ACSL4,ALDH3A2,TYMS,LIPG,G6PD,GCLM,CTH,GMPPB,SCD5,ACSL3,PID1,GART,PRPSAP1,ERH	darkgrey	VSMC_M8
GO:0048856	0.99	0.01	289	4193	anatomical structure development	BP	1	RTTN,ALPK2,NARS,ATP5F1B,HNRNPAB,NUP107,DDX39B,FBXO5,EZR,FBN2,TTLL1,NUS1,FAM49B,HSPA9,MATR3,SRPK1,KIF27,RECQL4,BYSL,PPP2R5D,TJP2,HSP90AB1,COL1A2,MELK,TRIM28,ANP32B,MSH6,GRSF1,HOXA5,COL9A2,MFSD2A,PABPC4,B3GNT2,EZH2,PRMT1,GJB3,CASP2,NAA15,SDC1,PLK4,PGR,STIL,PUS7,LIG1,MCM2,SEC61A1,CCNA2,AMOTL1,RAD54L,RNASEH2B,CDC42EP4,NASP,GRIN2C,PRCP,SMG9,NUP85,CAD,AXL,RNF157,SPHK1,XRN2,ULK4,NCAPG2,CDC20,SERPINH1,PARP2,EIF4A3,NAP1L1,E2F7,GINS4,ARHGDIA,STRN,RRM1,SIPA1L3,PCNA,PGAM5,CDC25B,POLE,ZNF703,HGF,ELK3,CCNB1,WDR62,SNAI2,SNRPB,CD44,POLR1B,KIF20B,KIF2A,SLC20A1,ADAMTS6,WEE1,EIF2B1,E2F1,CENPU,SLC10A7,HMGB2,CEP55,RBP4,MSC,ATF1,HELLS,NRIP1,NUP160,RACGAP1,LOXL3,ESCO2,HEY1,SELENOT,FMNL3,AGPAT5,MSH3,CTNNBL1,FAM83D,RBM19,KNL1,TBX3,CREB3L1,E2F8,ENTPD7,MTDH,HMGCR,CHUK,RUNX1,MDM4,PAK1IP1,NAV2,HMGN1,NOLC1,CIT,KIF18A,MANF,ETS1,NSUN2,GMNN,CHEK1,NAV1,TRIP13,NCL,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,IQCB1,CLMP,DDX5,PHACTR4,XBP1,SPP2,UTP25,MCM3AP,NEK2,NUP133,HINFP,NF2,H2AFX,SEC24D,FLVCR1,PDE3A,CDC42SE1,UMPS,ARCN1,CENPF,STRAP,EIF4G1,NHS,ADAMTS4,CDK1,TFRC,PAK2,FOSL1,SMARCC1,TRA2B,HNRNPH3,DDX20,CABYR,PPP2R1B,IFT80,SF1,EPHB2,ETV4,UFD1,BRCA1,NSD2,TACC3,CDK16,MED28,CREG1,ANKLE1,ECT2,FKBP4,SIX4,MNAT1,MAPK6,EIF2AK1,LYAR,MSX1,RAC1,EXO1,HNRNPU,UCHL1,ADIPOR2,MTHFD1,NEDD4,UGDH,SMARCE1,TOP2A,BID,LBR,PDPN,ARG2,NUDT1,PRELID1,ASF1B,SRSF5,CCNB2,IQGAP3,EFNB1,NES,SH3PXD2B,HOXB7,LMNA,AL	darkgrey	VSMC_M8
GO:0030031	0.99	0.01	22	443	cell projection assembly	BP	1	EZR,TTLL1,KIF27,KIF24,CEP135,ANLN,PLK4,CDC42EP4,NUP85,CENPJ,CEP89,FHDC1,CFAP298,IQCB1,IFT80,RAC1,FSCN1,LRRC49,SEPT6,EMP2,ARF6,RAPGEF6	darkgrey	VSMC_M8
GO:0070663	0.99	0.02	5	153	regulation of leukocyte proliferation	BP	1	MNDA,TFRC,EPHB2,ARG2,EFNB1	darkgrey	VSMC_M8
GO:0002790	0.99	0.02	6	172	peptide secretion	BP	1	RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0042886	0.99	0.02	8	210	amide transport	BP	1	SLC5A6,RBP4,SELENOT,HMGCR,CDK16,SLC19A2,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0051272	0.99	0.01	23	466	positive regulation of cellular component movement	BP	1	ATP5F1B,FBXO5,NUS1,ARHGEF39,SPHK1,ZNF703,HGF,SNAI2,KIF20B,ETS1,XBP1,S100A11,EPHB2,RAC1,PDPN,MAZ,COL1A1,SPAG9,PIK3CD,BCAR1,ARF6,STMN1,HAS2	darkgrey	VSMC_M8
GO:0007626	0.99	0.02	4	132	locomotory behavior	BP	1	STRN,NAV2,ARCN1,UCHL1	darkgrey	VSMC_M8
GO:0030308	0.99	0.02	5	153	negative regulation of cell growth	BP	1	MSX1,ADIPOR2,SPAG9,G6PD,CDKN2C	darkgrey	VSMC_M8
GO:0048513	0.99	0.01	166	2529	animal organ development	BP	1	ALPK2,NARS,HNRNPAB,NUP107,DDX39B,FBXO5,FBN2,TTLL1,HSPA9,MATR3,KIF27,HSP90AB1,COL1A2,MELK,TRIM28,ANP32B,HOXA5,MFSD2A,PABPC4,EZH2,PRMT1,GJB3,CASP2,SDC1,PLK4,PGR,STIL,PUS7,MCM2,SEC61A1,CCNA2,NASP,GRIN2C,SMG9,NUP85,CAD,AXL,SPHK1,XRN2,NCAPG2,SERPINH1,PARP2,EIF4A3,E2F7,RRM1,SIPA1L3,PCNA,POLE,ZNF703,HGF,CCNB1,WDR62,SNAI2,SNRPB,CD44,POLR1B,SLC20A1,ADAMTS6,E2F1,SLC10A7,HMGB2,RBP4,MSC,NRIP1,NUP160,LOXL3,ESCO2,HEY1,SELENOT,AGPAT5,FAM83D,TBX3,E2F8,ENTPD7,HMGCR,RUNX1,MDM4,HMGN1,NOLC1,KIF18A,ETS1,NSUN2,GMNN,KIF14,PRMT5,ASPM,IQCB1,DDX5,PHACTR4,XBP1,UTP25,NUP133,NF2,H2AFX,FLVCR1,UMPS,ARCN1,CENPF,NHS,CDK1,TFRC,FOSL1,SMARCC1,TRA2B,IFT80,SF1,EPHB2,ETV4,NSD2,TACC3,ANKLE1,SIX4,MNAT1,EIF2AK1,LYAR,MSX1,RAC1,HNRNPU,ADIPOR2,MTHFD1,TOP2A,BID,LBR,PDPN,ARG2,NUDT1,PRELID1,SRSF5,CCNB2,IQGAP3,EFNB1,NES,SH3PXD2B,HOXB7,LMNA,ALOX15B,COL1A1,PPIB,SYT4,BRIP1,XYLT1,TYMS,SLC25A5,NDE1,CCNF,TP73,DAZAP1,G6PD,PIK3CD,SLC6A17,FANCA,CRISPLD2,FAM129B,TPPP3,CBFB,ARF6,TMOD3,HNRNPD,ACSL3,STMN1,AURKA,HAS2,PDCD2,PALB2,GART,MBD2	darkgrey	VSMC_M8
GO:0032940	0.99	0.01	30	574	secretion by cell	BP	1	EZR,ARFGAP3,CYP51A1,SDC1,SLC1A5,PREB,KCNN4,AXL,NECAB3,VAMP8,RBP4,SELENOT,PPID,TBX3,CREB3L1,HMGCR,TXLNA,SLC17A9,CDK16,RAC1,RAB27A,LTBP2,SYT4,ACSL4,PIK3CD,FAM129B,ARF6,STXBP6,ERP29,SLC30A1	darkgrey	VSMC_M8
GO:0009607	0.99	0.01	48	856	response to biotic stimulus	BP	1	TUBB,FAM49B,FKBP5,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,SYNCRIP,ODC1,SEC61A1,CDC42EP4,HNRNPUL1,AXL,POLR3F,VAMP8,HMGB2,TRIM35,TOMM70,MTDH,CHUK,PPP1R15B,CCT5,MNDA,XBP1,RBM14,PAK2,FOSL1,DHX9,DDX21,UFD1,TFPI,LYAR,RAB27A,ADIPOR2,UBE2K,EIF5A,BID,SMC1A,ARG2,ILF3,ELF4,TUBB4B,PIK3CD,GBP5,HMGB3,STMN1,TRIM59	darkgrey	VSMC_M8
GO:0016482	0.99	0.02	5	153	cytosolic transport	BP	1	EZR,SPAG9,SYT4,HOOK1,EMP2	darkgrey	VSMC_M8
GO:0050865	0.99	0.01	18	385	regulation of cell activation	BP	1	FAM49B,AXL,SPHK1,VAMP8,LOXL3,RUNX1,MNDA,XBP1,TFRC,EPHB2,NSD2,PDPN,DCAF15,ARG2,PRELID1,EFNB1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0071805	0.99	0.02	4	131	potassium ion transmembrane transport	BP	1	KCNN4,KCNK6,ATP1B3,NEDD4	darkgrey	VSMC_M8
GO:0050730	0.99	0.02	7	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	NCAPG2,CHMP6,HGF,CD44,NF2,PAK2,RAP2C	darkgrey	VSMC_M8

GO:0010648	0.99	0.01	61	1047	negative regulation of cell communication	BP	1	ALPK2,DDX39B,EZR,FBN2,FAM49B,HMGXB4,VCP,EZH2,NUP62,RUVBL2,PLAUR,RNF157,EIF4A3,CHMP6,HGF,SNAI2,CD44,HMGB2,HELLS,PBK,HEY1,CREB3L1,TRIM33,YWHAB,HMGCR,PPP1R15B,PAK1IP1,NCOA5,CIT,TRAIP,RGS9,PHACTR4,XBP1,NF2,PDE3A,STRAP,IFT80,EPHB2,UFD1,BRCA1,CNOT9,FOXM1,UCHL1,NEDD4,BID,PRELID1,LMNA,MAZ,SYT4,SLC25A5,NXN,NOC2L,CDT1,GCLM,FAM129B,CTH,STMN1,PID1,TRIM59,SLC30A1,DUSP7	darkgrey	VSMC_M8
GO:0006006	0.99	0.02	5	155	glucose metabolic process	BP	1	PDHB,RBP4,PDHA1,DLAT,G6PD	darkgrey	VSMC_M8
GO:0023057	0.99	0.01	61	1048	negative regulation of signaling	BP	1	ALPK2,DDX39B,EZR,FBN2,FAM49B,HMGXB4,VCP,EZH2,NUP62,RUVBL2,PLAUR,RNF157,EIF4A3,CHMP6,HGF,SNAI2,CD44,HMGB2,HELLS,PBK,HEY1,CREB3L1,TRIM33,YWHAB,HMGCR,PPP1R15B,PAK1IP1,NCOA5,CIT,TRAIP,RGS9,PHACTR4,XBP1,NF2,PDE3A,STRAP,IFT80,EPHB2,UFD1,BRCA1,CNOT9,FOXM1,UCHL1,NEDD4,BID,PRELID1,LMNA,MAZ,SYT4,SLC25A5,NXN,NOC2L,CDT1,GCLM,FAM129B,CTH,STMN1,PID1,TRIM59,SLC30A1,DUSP7	darkgrey	VSMC_M8
GO:0002573	0.99	0.02	5	154	myeloid leukocyte differentiation	BP	1	RUNX1,TFRC,EIF2AK1,LBR,PIK3CD	darkgrey	VSMC_M8
GO:0007423	0.99	0.01	20	415	sensory organ development	BP	1	FBN2,ANP32B,MFSD2A,CASP2,MCM2,CCNA2,SMG9,XRN2,RRM1,SIPA1L3,RBP4,HMGN1,PHACTR4,NF2,NHS,EPHB2,SIX4,MSX1,NES,SH3PXD2B	darkgrey	VSMC_M8
GO:0016051	0.99	0.02	5	155	carbohydrate biosynthetic process	BP	1	NANS,B3GNT2,RBP4,G6PD,HAS2	darkgrey	VSMC_M8
GO:0032501	0.99	0.01	348	5003	multicellular organismal process	BP	1	RTTN,ALPK2,NARS,ATP5F1B,HNRNPAB,NUP107,DDX39B,FBXO5,EZR,FBN2,PANX2,TTLL1,NUS1,KIFC1,FAM49B,CDC25C,HSPA9,MATR3,SRPK1,KIF27,RECQL4,BYSL,PPP2R5D,POLR3B,TJP2,CYP51A1,HSP90AB1,COL1A2,MELK,TRIM28,ANP32B,MSH6,TTK,GRSF1,CLEC11A,HOXA5,COL9A2,MFSD2A,SYNCRIP,PABPC4,B3GNT2,ANLN,EZH2,NUP62,PHF19,PRMT1,GJB3,CASP2,NAA15,NRDC,SDC1,PLK4,PGR,NAMPT,STIL,PUS7,MCM2,SEC61A1,RUVBL1,CCNA2,AMOTL1,SLC1A5,RAD54L,RNASEH2B,WDR33,MAST2,FOSB,NASP,GRIN2C,PRCP,KCNN4,SMG9,NUP85,PLAUR,CAD,SLC5A6,AXL,RNF157,SPHK1,XRN2,ULK4,NCAPG2,WDR43,CDC20,BIRC5,SERPINH1,PARP2,FBL,POLR3F,RRBP1,GTPBP4,EIF4A3,NAP1L1,E2F7,GINS4,ALYREF,STRN,KCNK6,RRM1,SIPA1L3,PCNA,PGAM5,CDC25B,POLE,ZNF703,HGF,ELK3,CCNB1,WDR62,SNAI2,SNRPB,CD44,AAAS,POLR1B,KIF20B,KIF2A,SLC20A1,ADAMTS6,WDR36,WEE1,EIF2B1,E2F1,PPIP5K2,VAMP8,CENPU,SLC10A7,HMGB2,RBP4,MSC,ATF1,HELLS,NRIP1,NUP160,RACGAP1,LOXL3,ESCO2,HEY1,SELENOT,FMNL3,AGPAT5,MSH3,CTNNBL1,GNL3,FAM83D,RBM19,KNL1,TBX3,CREB3L1,TOMM70,E2F8,ENTPD7,MTDH,HMGCR,BAP1,CHUK,RUNX1,SETD4,MDM4,NAV2,HMGN1,NOLC1,CIT,KIF18A,MANF,ETS1,METAP1,NSUN2,GMNN,CHEK1,SNRPA1,NAV1,SMC3,KHDRBS1,TRIP13,NCL,TRAIP,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,ELOVL6,IQCB1,CLMP,MNDA,DDX5,PHACTR4,XBP1,SPP2,UTP25,MCM3AP,NEK2,NUP133,HINFP,NF2,H2AFX,SEC24D,FLVCR1,PDE3A,UMPS,ARCN1,CENPF,STRAP,EIF4G1,NHS,ADAMTS4,CDK1,TFRC,PAK2,FOSL1,SMARCC1,DHX9,TRA2B,POLA1,DDX20,DDX21,DLAT,CABYR,IFT80,SF1,BARD1,C17orf53,EPHB2,ETV4,	darkgrey	VSMC_M8
GO:2000147	0.99	0.01	22	455	positive regulation of cell motility	BP	1	ATP5F1B,FBXO5,NUS1,ARHGEF39,SPHK1,ZNF703,HGF,SNAI2,KIF20B,ETS1,XBP1,S100A11,EPHB2,RAC1,PDPN,MAZ,COL1A1,SPAG9,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:1902105	0.99	0.01	7	193	regulation of leukocyte differentiation	BP	1	AXL,LOXL3,RUNX1,XBP1,PRELID1,FANCA,CBFB	darkgrey	VSMC_M8
GO:0090287	0.99	0.01	9	230	regulation of cellular response to growth factor stimulus	BP	1	FBN2,HSP90AB1,ZNF703,CREB3L1,TRIM33,STRAP,MSX1,NEDD4,FAM129B	darkgrey	VSMC_M8
GO:0007169	0.99	0.01	25	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	NUS1,NUP62,SHCBP1,CD3EAP,PLAUR,AXL,CHMP6,HGF,CREB3L1,NCOA5,NUCKS1,EFS,PAK2,SMARCC1,EPHB2,CNOT9,RAC1,NEDD4,EFNB1,COL1A1,PIK3CD,BCAR1,FAM129B,STMN1,PID1	darkgrey	VSMC_M8
GO:0042391	0.99	0.01	13	302	regulation of membrane potential	BP	1	VCP,GRIN2C,KCNN4,EIF4A3,KCNK6,ATP1B3,NDUFS1,NEDD4,BID,PRELID1,NNT,GCLM,PID1	darkgrey	VSMC_M8
GO:0032970	0.99	0.01	15	337	regulation of actin filament-based process	BP	1	ABRACL,FAM49B,CDC42EP4,ARHGDIA,NF2,PAK2,ECT2,RAC1,FSCN1,PDPN,IQGAP3,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0051093	0.99	0.01	36	676	negative regulation of developmental process	BP	1	ALPK2,FBXO5,HSPA9,ANP32B,HOXA5,EZH2,PRMT1,NAMPT,SNAI2,E2F1,RBP4,LOXL3,HEY1,RBL1,TBX3,CREB3L1,RUNX1,PRMT5,ASPM,IQCB1,XBP1,TFRC,EPHB2,MED28,SIX4,FOXM1,MSX1,HNRNPU,SPAG9,DNMT1,TP73,G6PD,PTBP1,FAM129B,CBFB,ARF6	darkgrey	VSMC_M8
GO:0015850	0.99	0.01	6	179	organic hydroxy compound transport	BP	1	NUS1,SLC10A7,RBP4,SYT4,LIPG,TOR1A	darkgrey	VSMC_M8
GO:0008202	0.99	0.01	8	217	steroid metabolic process	BP	1	CYP51A1,SNAI2,HMGCR,HDLBP,DDX20,SF1,LBR,G6PD	darkgrey	VSMC_M8
GO:0043207	0.99	0.01	45	820	response to external biotic stimulus	BP	1	TUBB,FAM49B,FKBP5,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,SYNCRIP,ODC1,SEC61A1,CDC42EP4,HNRNPUL1,AXL,POLR3F,VAMP8,HMGB2,TRIM35,TOMM70,MTDH,CHUK,CCT5,MNDA,XBP1,RBM14,PAK2,FOSL1,DHX9,DDX21,UFD1,TFPI,LYAR,RAB27A,ADIPOR2,UBE2K,EIF5A,ARG2,ILF3,ELF4,TUBB4B,PIK3CD,GBP5,HMGB3,STMN1,TRIM59	darkgrey	VSMC_M8
GO:0051707	0.99	0.01	45	820	response to other organism	BP	1	TUBB,FAM49B,FKBP5,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,SYNCRIP,ODC1,SEC61A1,CDC42EP4,HNRNPUL1,AXL,POLR3F,VAMP8,HMGB2,TRIM35,TOMM70,MTDH,CHUK,CCT5,MNDA,XBP1,RBM14,PAK2,FOSL1,DHX9,DDX21,UFD1,TFPI,LYAR,RAB27A,ADIPOR2,UBE2K,EIF5A,ARG2,ILF3,ELF4,TUBB4B,PIK3CD,GBP5,HMGB3,STMN1,TRIM59	darkgrey	VSMC_M8
GO:0034329	0.99	0.01	14	318	cell junction assembly	BP	1	STRN,ZNF703,SNAI2,MTDH,EIF4G1,PAK2,EPHB2,ECT2,SIX4,RAC1,FSCN1,POLDIP2,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0032956	0.99	0.01	13	304	regulation of actin cytoskeleton organization	BP	1	FAM49B,CDC42EP4,ARHGDIA,NF2,PAK2,ECT2,RAC1,FSCN1,IQGAP3,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0003002	0.99	0.01	10	251	regionalization	BP	1	GRSF1,HOXA5,HEY1,TBX3,TRA2B,MSX1,HOXB7,ACD,AURKA,PALB2	darkgrey	VSMC_M8

GO:0060429	0.99	0.01	45	810	epithelium development	BP	1	EZR,TJP2,TRIM28,GRSF1,HOXA5,MFSD2A,EZH2,SDC1,PLK4,PGR,STIL,E2F7,SIPA1L3,PCNA,ZNF703,HGF,SNAI2,CD44,KIF20B,LOXL3,HEY1,TBX3,E2F8,NSUN2,PHACTR4,NUP133,NF2,CDK1,HNRNPH3,ETV4,SIX4,MSX1,RAC1,MTHFD1,PDPN,ARG2,IQGAP3,HOXB7,ALOX15B,TYMS,RAP2C,PIK3CD,TOR1A,PALB2,CASP6	darkgrey	VSMC_M8
GO:0001667	0.99	0.01	16	360	ameboidal-type cell migration	BP	1	ATP5F1B,NUS1,ANLN,AMOTL1,PRCP,ETS1,PHACTR4,RAC1,ADIPOR2,EFNB1,EMP2,PIK3CD,PKN3,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0008064	1.00	0.01	5	159	regulation of actin polymerization or depolymerization	BP	1	FAM49B,CDC42EP4,ARPC4,ARF6,TMOD3	darkgrey	VSMC_M8
GO:1902533	1.00	0.01	39	731	positive regulation of intracellular signal transduction	BP	1	BCLAF1,HSP90AB1,MIOS,EZH2,NUP62,PRMT1,GEN1,PPP5C,AXL,SPHK1,NET1,HGF,CD44,SLC20A1,MTDH,HMGCR,EEF1E1,CHUK,DDX5,TFRC,DDX21,ECT2,DHX33,MSX1,RAC1,NEDD4,EIF5A,BID,IQGAP3,MAZ,LRRC59,SPAG9,NDC80,PTBP1,PIK3CD,NEK6,CTH,MAD2L1,ERP29	darkgrey	VSMC_M8
GO:0097529	1.00	0.02	4	142	myeloid leukocyte migration	BP	1	NUP85,RAC1,PPIB,PIK3CD	darkgrey	VSMC_M8
GO:0051962	1.00	0.01	8	216	positive regulation of nervous system development	BP	1	NAP1L1,E2F1,PRMT5,ASPM,EPHB2,TP73,SRRT,CLSTN3	darkgrey	VSMC_M8
GO:1902905	1.00	0.01	6	179	positive regulation of supramolecular fiber organization	BP	1	CDC42EP4,CKAP5,NF2,RAC1,ARPC4,ARF6	darkgrey	VSMC_M8
GO:0048584	1.00	0.01	90	1488	positive regulation of response to stimulus	BP	1	BCLAF1,EZR,FAM49B,MATR3,POLR3B,VCP,HSP90AB1,MIOS,TRIM28,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL1,PPP5C,KCNN4,PLAUR,AXL,SPHK1,NET1,POLR3F,PCNA,HGF,CD44,DEPDC1B,SLC20A1,CENPJ,EIF2B1,VAMP8,HMGB2,LOXL3,NUP93,TOMM70,MTDH,HMGCR,EEF1E1,CHUK,SETD4,NUCKS1,ETS1,KHDRBS1,PRMT5,ASPM,MNDA,DDX5,FANCB,XBP1,H2AFX,RBM14,NSMCE4A,TFRC,PAK2,DHX9,DDX21,PPP2R1B,BRCA1,CNOT9,NSD2,RAD51AP1,ANKLE1,ECT2,DHX33,FOXM1,MSX1,RAC1,UBE2K,NEDD4,EIF5A,BID,ARG2,IQGAP3,FUS,ALOX15B,MAZ,COL1A1,LRRC59,SPAG9,NDC80,EMP2,PTBP1,PIK3CD,BCAR1,NEK6,CTH,GBP5,MAD2L1,ERP29,MBD2	darkgrey	VSMC_M8
GO:0030832	1.00	0.01	5	160	regulation of actin filament length	BP	1	FAM49B,CDC42EP4,ARPC4,ARF6,TMOD3	darkgrey	VSMC_M8
GO:0140352	1.00	0.01	32	618	export from cell	BP	1	EZR,ARFGAP3,CYP51A1,SDC1,SLC1A5,PREB,KCNN4,AXL,NECAB3,VAMP8,ATP1B3,RBP4,SELENOT,PPID,TBX3,CREB3L1,HMGCR,TXLNA,RGS9,SLC17A9,CDK16,RAC1,RAB27A,LTBP2,SYT4,ACSL4,PIK3CD,FAM129B,ARF6,STXBP6,ERP29,SLC30A1	darkgrey	VSMC_M8
GO:0040017	1.00	0.01	22	462	positive regulation of locomotion	BP	1	ATP5F1B,FBXO5,NUS1,ARHGEF39,SPHK1,ZNF703,HGF,SNAI2,KIF20B,ETS1,XBP1,S100A11,EPHB2,RAC1,PDPN,MAZ,COL1A1,SPAG9,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0043270	1.00	0.01	6	182	positive regulation of ion transport	BP	1	KCNN4,VAMP8,ATP1B3,RGS9,EPHB2,G6PD	darkgrey	VSMC_M8
GO:0030036	1.00	0.01	31	600	actin cytoskeleton organization	BP	1	EZR,FAM49B,ANLN,AMOTL1,CDC42EP4,DIAPH3,ARHGDIA,GAS2L3,HSP90B1,FHDC1,RACGAP1,FMNL3,CIT,EFS,PHACTR4,NF2,PAK2,FRMD6,ECT2,SIX4,RAC1,MYO5A,FSCN1,IQGAP3,TPM3,EMP2,BCAR1,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0051090	1.00	0.01	14	328	regulation of DNA-binding transcription factor activity	BP	1	EZH2,SPHK1,SGK3,MTDH,CHUK,PPRC1,TRAIP,TFRC,FOSL1,DHX9,PSMA6,DHX33,FANCA,CTH	darkgrey	VSMC_M8
GO:0006836	1.00	0.01	4	139	neurotransmitter transport	BP	1	SYT4,SLC6A17,TOR1A,SLC30A1	darkgrey	VSMC_M8
GO:0010976	1.00	0.01	4	140	positive regulation of neuron projection development	BP	1	EZH2,HGF,ATF1,SF3A2	darkgrey	VSMC_M8
GO:0110053	1.00	0.01	9	237	regulation of actin filament organization	BP	1	FAM49B,CDC42EP4,NF2,PAK2,RAC1,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0007275	1.00	0.01	258	3815	multicellular organism development	BP	1	RTTN,ALPK2,NARS,ATP5F1B,HNRNPAB,NUP107,DDX39B,FBXO5,FBN2,TTLL1,NUS1,HSPA9,MATR3,KIF27,RECQL4,BYSL,PPP2R5D,HSP90AB1,COL1A2,MELK,TRIM28,ANP32B,MSH6,GRSF1,HOXA5,COL9A2,MFSD2A,PABPC4,B3GNT2,EZH2,PRMT1,GJB3,CASP2,NAA15,SDC1,PLK4,PGR,STIL,PUS7,MCM2,SEC61A1,CCNA2,AMOTL1,RAD54L,RNASEH2B,NASP,GRIN2C,PRCP,SMG9,NUP85,CAD,AXL,RNF157,SPHK1,XRN2,ULK4,NCAPG2,CDC20,SERPINH1,PARP2,EIF4A3,NAP1L1,E2F7,GINS4,STRN,RRM1,SIPA1L3,PCNA,POLE,ZNF703,HGF,ELK3,CCNB1,WDR62,SNAI2,SNRPB,CD44,POLR1B,KIF20B,KIF2A,SLC20A1,ADAMTS6,WEE1,EIF2B1,E2F1,CENPU,SLC10A7,HMGB2,RBP4,MSC,ATF1,HELLS,NRIP1,NUP160,RACGAP1,LOXL3,ESCO2,HEY1,SELENOT,FMNL3,AGPAT5,MSH3,CTNNBL1,FAM83D,RBM19,TBX3,CREB3L1,E2F8,ENTPD7,MTDH,HMGCR,RUNX1,MDM4,NAV2,HMGN1,NOLC1,CIT,KIF18A,MANF,ETS1,NSUN2,GMNN,CHEK1,NAV1,NCL,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,IQCB1,CLMP,DDX5,PHACTR4,XBP1,SPP2,UTP25,MCM3AP,NEK2,NUP133,HINFP,NF2,H2AFX,SEC24D,FLVCR1,UMPS,ARCN1,CENPF,STRAP,EIF4G1,NHS,ADAMTS4,CDK1,TFRC,PAK2,FOSL1,SMARCC1,TRA2B,IFT80,SF1,EPHB2,ETV4,UFD1,BRCA1,NSD2,TACC3,CDK16,CREG1,ANKLE1,ECT2,FKBP4,SIX4,MNAT1,MAPK6,EIF2AK1,LYAR,MSX1,RAC1,EXO1,HNRNPU,UCHL1,ADIPOR2,MTHFD1,NEDD4,UGDH,SMARCE1,TOP2A,BID,LBR,PDPN,ARG2,NUDT1,PRELID1,ASF1B,SRSF5,CCNB2,IQGAP3,EFNB1,NES,SH3PXD2B,HOXB7,LMNA,ALOX15B,AURKB,COL1A1,PPIB,SPAG9,TIMM8A,SYT4,BRIP1,DNMT1,PRPS1,ACSL4,ALDH3A2,XYLT1,TYMS,SLC25A5,COPS3,NDE1,USP1,EMP2,NXN,THOC6,CCNF,SF3A2,TP	darkgrey	VSMC_M8
GO:0072657	1.00	0.01	22	466	protein localization to membrane	BP	1	EZR,SEC61A1,GRIN2C,SRP68,VAMP8,ATP1B3,TRAM1,TOMM70,IFT80,EPHB2,MYO5A,BID,SH3PXD2B,TIMM8A,MTCL1,EMP2,NDC1,EMC8,ARF6,RAPGEF6,ACSL3,PID1	darkgrey	VSMC_M8
GO:0060326	1.00	0.01	7	206	cell chemotaxis	BP	1	NUP85,HGF,HMGB2,RAC1,PPIB,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0060560	1.00	0.01	7	200	developmental growth involved in morphogenesis	BP	1	HSP90AB1,TRIM28,RNF157,SIX4,SPAG9,SYT4,AURKA	darkgrey	VSMC_M8
GO:0006813	1.00	0.01	4	140	potassium ion transport	BP	1	KCNN4,KCNK6,ATP1B3,NEDD4	darkgrey	VSMC_M8
GO:0019318	1.00	0.01	6	185	hexose metabolic process	BP	1	PDHB,RBP4,PDHA1,GALE,DLAT,G6PD	darkgrey	VSMC_M8
GO:1903530	1.00	0.01	18	399	regulation of secretion by cell	BP	1	EZR,CYP51A1,SDC1,KCNN4,VAMP8,RBP4,SELENOT,PPID,HMGCR,CDK16,RAC1,RAB27A,SYT4,ACSL4,ARF6,STXBP6,ERP29,SLC30A1	darkgrey	VSMC_M8

GO:0051046	1.00	0.01	20	434	regulation of secretion	BP	1	EZR,CYP51A1,SDC1,KCNN4,VAMP8,RBP4,SELENOT,PPID,HMGCR,XBP1,CDK16,RAC1,RAB27A,SYT4,ACSL4,ARF6,ACSL3,STXBP6,ERP29,SLC30A1	darkgrey	VSMC_M8
GO:0015833	1.00	0.01	6	186	peptide transport	BP	1	RBP4,SELENOT,HMGCR,CDK16,RAC1,ACSL4	darkgrey	VSMC_M8
GO:0007611	1.00	0.01	6	183	learning or memory	BP	1	EIF4A3,AAAS,HMGCR,FOSL1,EPHB2,FEN1	darkgrey	VSMC_M8
GO:0048731	1.00	0.00	238	3556	system development	BP	1	ALPK2,NARS,ATP5F1B,HNRNPAB,NUP107,DDX39B,FBXO5,FBN2,TTLL1,NUS1,HSPA9,MATR3,KIF27,PPP2R5D,HSP90AB1,COL1A2,MELK,TRIM28,ANP32B,MSH6,HOXA5,COL9A2,MFSD2A,PABPC4,B3GNT2,EZH2,PRMT1,GJB3,CASP2,NAA15,SDC1,PLK4,PGR,STIL,PUS7,MCM2,SEC61A1,CCNA2,AMOTL1,NASP,GRIN2C,PRCP,SMG9,NUP85,CAD,AXL,RNF157,SPHK1,XRN2,ULK4,NCAPG2,CDC20,SERPINH1,PARP2,EIF4A3,NAP1L1,E2F7,STRN,RRM1,SIPA1L3,PCNA,POLE,ZNF703,HGF,ELK3,CCNB1,WDR62,SNAI2,SNRPB,CD44,POLR1B,KIF20B,KIF2A,SLC20A1,ADAMTS6,WEE1,EIF2B1,E2F1,SLC10A7,HMGB2,RBP4,MSC,ATF1,HELLS,NRIP1,NUP160,RACGAP1,LOXL3,ESCO2,HEY1,SELENOT,FMNL3,AGPAT5,MSH3,CTNNBL1,FAM83D,TBX3,CREB3L1,E2F8,ENTPD7,MTDH,HMGCR,RUNX1,MDM4,NAV2,HMGN1,NOLC1,CIT,KIF18A,MANF,ETS1,NSUN2,GMNN,NAV1,NCL,KIF14,UNG,RGS9,PRMT5,ASPM,POLQ,IQCB1,CLMP,DDX5,PHACTR4,XBP1,SPP2,UTP25,MCM3AP,NUP133,NF2,H2AFX,FLVCR1,UMPS,ARCN1,CENPF,STRAP,EIF4G1,NHS,ADAMTS4,CDK1,TFRC,PAK2,FOSL1,SMARCC1,TRA2B,IFT80,SF1,EPHB2,ETV4,UFD1,BRCA1,NSD2,TACC3,CDK16,ANKLE1,ECT2,FKBP4,SIX4,MNAT1,MAPK6,EIF2AK1,LYAR,MSX1,RAC1,EXO1,HNRNPU,UCHL1,ADIPOR2,MTHFD1,NEDD4,UGDH,SMARCE1,TOP2A,BID,LBR,PDPN,ARG2,NUDT1,PRELID1,SRSF5,CCNB2,IQGAP3,EFNB1,NES,SH3PXD2B,HOXB7,LMNA,ALOX15B,COL1A1,PPIB,SPAG9,TIMM8A,SYT4,BRIP1,DNMT1,PRPS1,ACSL4,ALDH3A2,XYLT1,TYMS,SLC25A5,NDE1,USP1,EMP2,NXN,THOC6,CCNF,SF3A2,TP73,DAZAP1,G6PD,PIK3CD,SLC6A17,FANCA,CRISPLD2,TOR1A,FAM129B,ACD,TPPP3,CBFB,CTH,SRRT,ARF6,TMOD3,HNRNPD,CDK	darkgrey	VSMC_M8
GO:0001666	1.00	0.01	9	244	response to hypoxia	BP	1	CCNA2,CCNB1,HSP90B1,E2F1,MDM4,ETS1,SUV39H1,LMNA,BRIP1	darkgrey	VSMC_M8
GO:0070371	1.00	0.01	8	227	ERK1 and ERK2 cascade	BP	1	EZR,CD44,FAM83D,HMGCR,PRMT5,CDK1,EPHB2,IQGAP3	darkgrey	VSMC_M8
GO:0044282	1.00	0.01	11	284	small molecule catabolic process	BP	1	GCAT,ALDH1L2,MFSD2A,AFMID,PCCA,AADAT,ENTPD7,GALE,GK,ARG2,NUDT1	darkgrey	VSMC_M8
GO:0060284	1.00	0.01	17	384	regulation of cell development	BP	1	EZH2,NAP1L1,E2F1,HMGB2,HEY1,KIF14,PRMT5,ASPM,NF2,PDE3A,EPHB2,RAC1,TP73,FAM129B,SRRT,AURKA,HAS2	darkgrey	VSMC_M8
GO:0035295	1.00	0.00	46	849	tube development	BP	1	ATP5F1B,NUS1,HOXA5,NAA15,SDC1,PGR,STIL,AMOTL1,PRCP,SPHK1,E2F7,HGF,ELK3,CCNB1,KIF20B,RBP4,LOXL3,HEY1,FMNL3,TBX3,CREB3L1,E2F8,MTDH,RUNX1,KIF18A,ETS1,NCL,CLMP,PHACTR4,XBP1,NUP133,EPHB2,BRCA1,SIX4,ADIPOR2,MTHFD1,PDPN,ARG2,HOXB7,BRIP1,TYMS,EMP2,PIK3CD,CRISPLD2,FAM129B,HAS2	darkgrey	VSMC_M8
GO:0030595	1.00	0.01	4	150	leukocyte chemotaxis	BP	1	NUP85,RAC1,PPIB,PIK3CD	darkgrey	VSMC_M8
GO:0051235	1.00	0.01	9	248	maintenance of location	BP	1	FBN2,RANGAP1,HSP90B1,NRIP1,YWHAB,ASPM,BARD1,KDELR2,HNRNPU	darkgrey	VSMC_M8
GO:0051240	1.00	0.00	59	1050	positive regulation of multicellular organismal process	BP	1	DDX39B,FBXO5,EZR,FBN2,PANX2,FAM49B,POLR3B,EZH2,AXL,SPHK1,PARP2,POLR3F,NAP1L1,ZNF703,HGF,CCNB1,E2F1,VAMP8,HMGB2,RBM19,TOMM70,MTDH,HMGCR,CHUK,RUNX1,SETD4,ETS1,PRMT5,ASPM,ELOVL6,MNDA,XBP1,UTP25,CDK1,TFRC,DHX9,DDX21,EPHB2,ETV4,BRCA1,NSD2,DHX33,SIX4,FH,ADIPOR2,PDPN,IQGAP3,HOXB7,ALOX15B,COL1A1,PPIB,LIPG,TP73,PIK3CD,FAM129B,CBFB,SRRT,GBP5,CLSTN3	darkgrey	VSMC_M8
GO:0060828	1.00	0.01	7	210	regulation of canonical Wnt signaling pathway	BP	1	VCP,RUVBL2,RUVBL1,ZNF703,SNAI2,ASPM,COL1A1	darkgrey	VSMC_M8
GO:0006820	1.00	0.01	13	319	anion transport	BP	1	SLC35D2,MFSD2A,SLC1A5,SLC25A19,SLC5A6,SLC20A1,SLC10A7,RACGAP1,SFXN3,SLC17A9,SLC19A2,SLC25A5,SLC6A17	darkgrey	VSMC_M8
GO:0006952	1.00	0.00	52	949	defense response	BP	1	TUBB,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,SYNCRIP,EZH2,SDC1,SEC61A1,CDC42EP4,PRCP,KCNN4,AXL,SPHK1,POLR3F,HGF,CD44,VAMP8,HMGB2,LOXL3,PBK,TRIM35,TOMM70,BAP1,CHUK,SETD4,ETS1,MNDA,RBM14,EIF4G1,PAK2,FOSL1,DHX9,PSMA6,DDX21,UFD1,EIF2AK1,LYAR,RAC1,RAB27A,UBE2K,ARG2,ILF3,ELF4,TUBB4B,PIK3CD,FANCA,LY75,GBP5,HMGB3,TRIM59	darkgrey	VSMC_M8
GO:0042063	1.00	0.01	8	230	gliogenesis	BP	1	EZH2,EIF2B1,E2F1,PRMT5,NF2,CDK1,TP73,CDKN2C	darkgrey	VSMC_M8
GO:0006954	1.00	0.00	23	497	inflammatory response	BP	1	EZH2,SDC1,PRCP,AXL,SPHK1,HGF,CD44,VAMP8,HMGB2,LOXL3,PBK,BAP1,CHUK,SETD4,ETS1,DHX9,PSMA6,EIF2AK1,RAC1,PIK3CD,FANCA,LY75,GBP5	darkgrey	VSMC_M8
GO:0050767	1.00	0.01	11	285	regulation of neurogenesis	BP	1	EZH2,NAP1L1,E2F1,HMGB2,HEY1,PRMT5,ASPM,NF2,EPHB2,TP73,SRRT	darkgrey	VSMC_M8
GO:0010506	1.00	0.01	10	268	regulation of autophagy	BP	1	NAMPT,HGF,MTDH,EIF4G1,UCHL1,NEDD4,BID,SLC25A5,POLDIP2,MTCL1	darkgrey	VSMC_M8
GO:0045017	1.00	0.01	7	214	glycerolipid biosynthetic process	BP	1	MFSD2A,PGS1,AGPAT5,GK,ACSL4,PIK3CD,ACSL3	darkgrey	VSMC_M8
GO:0046903	1.00	0.00	34	673	secretion	BP	1	EZR,ARFGAP3,CYP51A1,SDC1,SLC1A5,PREB,KCNN4,CAD,AXL,NECAB3,VAMP8,RBP4,SELENOT,PPID,TBX3,CREB3L1,HMGCR,TXLNA,XBP1,UMPS,SLC17A9,CDK16,RAC1,RAB27A,LTBP2,SYT4,ACSL4,PIK3CD,FAM129B,ARF6,ACSL3,STXBP6,ERP29,SLC30A1	darkgrey	VSMC_M8
GO:0001775	1.00	0.00	35	692	cell activation	BP	1	FAM49B,MSH6,CTPS1,EZH2,NAMPT,AXL,SPHK1,CD44,VAMP8,HELLS,LOXL3,ENTPD7,RUNX1,METAP1,TXLNA,UNG,PRMT5,MNDA,XBP1,TFRC,EPHB2,NSD2,EXO1,RAB27A,PDPN,DCAF15,ARG2,PRELID1,EFNB1,SLC25A5,ELF4,PIK3CD,FANCA,GCLM,CBFB	darkgrey	VSMC_M8
GO:0010001	1.00	0.01	5	173	glial cell differentiation	BP	1	EIF2B1,PRMT5,CDK1,TP73,CDKN2C	darkgrey	VSMC_M8
GO:0060562	1.00	0.00	10	269	epithelial tube morphogenesis	BP	1	HOXA5,PGR,STIL,KIF20B,TBX3,PHACTR4,SIX4,MTHFD1,HOXB7,PIK3CD	darkgrey	VSMC_M8

GO:0016477	1.00	0.00	63	1120	cell migration	BP	1	NARS,ATP5F1B,FBXO5,NUS1,FAM49B,ARHGEF39,HOXA5,ANLN,SDC1,AMOTL1,PRCP,NUP85,AXL,SPHK1,ULK4,NET1,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,CD44,DEPDC1B,KIF20B,KIF2A,SGK3,HMGB2,FMNL3,FAM83D,KNSTRN,ETS1,NAV1,KIF14,ASPM,EFS,PHACTR4,XBP1,NF2,CDK1,S100A11,EPHB2,SIX4,RAC1,ADIPOR2,FSCN1,PDPN,EFNB1,LMNA,ALOX15B,MAZ,SPDL1,COL1A1,PPIB,SPAG9,NDE1,RAP2C,EMP2,PIK3CD,TOR1A,PKN3,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0002237	1.00	0.01	8	236	response to molecule of bacterial origin	BP	1	FAM49B,AXL,HMGB2,MTDH,CHUK,XBP1,TFPI,ADIPOR2	darkgrey	VSMC_M8
GO:0048585	1.00	0.00	70	1229	negative regulation of response to stimulus	BP	1	ALPK2,DDX39B,FBXO5,EZR,FBN2,FAM49B,HMGXB4,VCP,EZH2,NUP62,RUVBL2,NAMPT,PLAUR,RNF157,EIF4A3,CHMP6,HGF,SNAI2,CD44,PARPBP,HMGB2,HELLS,LOXL3,PBK,HEY1,RBL1,CREB3L1,TRIM33,YWHAB,HMGCR,PPP1R15B,PAK1IP1,NCOA5,CIT,TRAIP,RGS9,POLQ,PHACTR4,FANCB,XBP1,NF2,PDE3A,STRAP,AUNIP,IFT80,EPHB2,UFD1,BRCA1,TFPI,CNOT9,FOXM1,LYAR,UCHL1,NEDD4,BID,ARG2,PRELID1,LMNA,MAZ,SLC25A5,NXN,NOC2L,CDT1,GCLM,FAM129B,CTH,STMN1,PID1,TRIM59,DUSP7	darkgrey	VSMC_M8
GO:1902903	1.00	0.00	13	327	regulation of supramolecular fiber organization	BP	1	FAM49B,CDC42EP4,CKAP2,TPX2,CKAP5,NF2,PAK2,FKBP4,RAC1,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:0032879	1.00	0.00	128	2074	regulation of localization	BP	1	ATP5F1B,CCT2,FBXO5,EZR,TCP1,NUS1,FAM49B,RANGAP1,BYSL,CYP51A1,VCP,HSP90AB1,ARHGEF39,CENPQ,CEP135,TRIM28,THADA,ANP32B,CCT4,YRDC,NUP62,SDC1,RUVBL2,RUVBL1,AMOTL1,SAE1,PRCP,PREB,KCNN4,DBI,BORA,AXL,SPHK1,ULK4,GTPBP4,IPO5,ARHGDIA,KCNK6,ZNF703,HGF,SNAI2,AAAS,KIF20B,KIF2A,SGK3,CENPJ,CCNE1,VAMP8,ATP1B3,RBP4,TERF1,SELENOT,CCT8,PPID,CCT7,CFAP298,GNL3,CCNE2,HMGCR,BAP1,NOLC1,CCT5,NUP153,CCT6A,ETS1,NSUN2,ICE1,KHDRBS1,CEP72,KIF14,RGS9,XBP1,NF2,ARFGAP1,CDK1,S100A11,TFRC,DHX9,CDCA5,BARD1,EPHB2,NMD3,NSD2,CDK16,ECT2,SIX4,LYAR,RAC1,HNRNPU,RAB27A,ADIPOR2,NEDD4,PDPN,PRELID1,EXOSC10,CCT3,LMNA,ALOX15B,MAZ,AURKB,COL1A1,SPAG9,PLK1,SYT4,ACSL4,SLC25A5,NDC80,MTCL1,RAP2C,RSL1D1,EMP2,LIPG,G6PD,DKC1,PIK3CD,CDT1,TOR1A,BCAR1,ARF6,ACSL3,STMN1,HAS2,STXBP6,ERP29,PID1,CLSTN3,SLC30A1,UBE2J2	darkgrey	VSMC_M8
GO:0002274	1.00	0.01	4	156	myeloid leukocyte activation	BP	1	NAMPT,SPHK1,VAMP8,PIK3CD	darkgrey	VSMC_M8
GO:0051960	1.00	0.00	14	344	regulation of nervous system development	BP	1	EZH2,NAP1L1,HGF,E2F1,HMGB2,HEY1,KIF14,PRMT5,ASPM,NF2,EPHB2,TP73,SRRT,CLSTN3	darkgrey	VSMC_M8
GO:0050890	1.00	0.01	7	214	cognition	BP	1	MFSD2A,EIF4A3,AAAS,HMGCR,FOSL1,EPHB2,FEN1	darkgrey	VSMC_M8
GO:1905114	1.00	0.00	20	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	ALPK2,HMGXB4,VCP,SDC1,RUVBL2,RUVBL1,AMOTL1,GRIN2C,EIF4A3,STRN,ZNF703,SNAI2,DEPDC1B,CCNE1,ASPM,IFT80,RAC1,COL1A1,NXN,MBD2	darkgrey	VSMC_M8
GO:0005996	1.00	0.01	6	199	monosaccharide metabolic process	BP	1	PDHB,RBP4,PDHA1,GALE,DLAT,G6PD	darkgrey	VSMC_M8
GO:0090257	1.00	0.01	5	179	regulation of muscle system process	BP	1	DDX39B,SPHK1,PARP2,LMNA,G6PD	darkgrey	VSMC_M8
GO:0032412	1.00	0.01	5	178	regulation of ion transmembrane transporter activity	BP	1	THADA,ATP1B3,RGS9,EPHB2,NEDD4	darkgrey	VSMC_M8
GO:0007389	1.00	0.00	13	329	pattern specification process	BP	1	RTTN,GRSF1,HOXA5,STIL,HEY1,TBX3,TRA2B,MSX1,EFNB1,HOXB7,ACD,AURKA,PALB2	darkgrey	VSMC_M8
GO:0030029	1.00	0.00	33	662	actin filament-based process	BP	1	ABRACL,EZR,FAM49B,ANLN,AMOTL1,CDC42EP4,DIAPH3,ARHGDIA,GAS2L3,HSP90B1,FHDC1,RACGAP1,FMNL3,CIT,EFS,PHACTR4,NF2,PAK2,FRMD6,ECT2,SIX4,RAC1,MYO5A,FSCN1,PDPN,IQGAP3,TPM3,EMP2,BCAR1,ARPC4,ARF6,TMOD3,STMN1	darkgrey	VSMC_M8
GO:1904062	1.00	0.00	8	241	regulation of cation transmembrane transport	BP	1	THADA,KCNN4,ATP1B3,RGS9,EPHB2,NEDD4,G6PD,SLC30A1	darkgrey	VSMC_M8
GO:0008654	1.00	0.00	7	222	phospholipid biosynthetic process	BP	1	NUS1,MFSD2A,PGS1,AGPAT5,PIK3CD,DOLPP1,ACSL3	darkgrey	VSMC_M8
GO:0030334	1.00	0.00	37	735	regulation of cell migration	BP	1	ATP5F1B,FBXO5,NUS1,FAM49B,ARHGEF39,AMOTL1,PRCP,SPHK1,ULK4,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,KIF20B,KIF2A,SGK3,ETS1,KIF14,XBP1,NF2,S100A11,EPHB2,RAC1,ADIPOR2,PDPN,LMNA,ALOX15B,MAZ,COL1A1,SPAG9,RAP2C,EMP2,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0008361	1.00	0.01	4	157	regulation of cell size	BP	1	HSP90AB1,KCNN4,RAC1,IQGAP3	darkgrey	VSMC_M8
GO:0030336	1.00	0.00	7	223	negative regulation of cell migration	BP	1	GTPBP4,ARHGDIA,NF2,RAC1,ADIPOR2,ALOX15B,RAP2C	darkgrey	VSMC_M8
GO:1903131	1.00	0.00	11	297	mononuclear cell differentiation	BP	1	EZH2,AXL,LOXL3,ENTPD7,RUNX1,XBP1,PRELID1,SLC25A5,PIK3CD,FANCA,CBFB	darkgrey	VSMC_M8
GO:0050793	1.00	0.00	112	1852	regulation of developmental process	BP	1	ALPK2,DDX39B,FBXO5,EZR,FBN2,TTLL1,FAM49B,HSPA9,PWP1,HSP90AB1,ANP32B,HOXA5,MFSD2A,EZH2,PRMT1,NAMPT,PUS7,CDC42EP4,AXL,RNF157,SPHK1,WDR43,CDC20,PARP2,NAP1L1,ARHGDIA,PGAM5,ZNF703,HGF,MEDAG,CCNB1,SNAI2,CD44,E2F1,HMGB2,RBP4,RACGAP1,LOXL3,HEY1,FMNL3,RBL1,RBM19,TBX3,CREB3L1,MTDH,HMGCR,EEF1E1,RUNX1,HMGN1,ETS1,NSUN2,KIF14,PRMT5,ASPM,IQCB1,DDX5,XBP1,UTP25,NF2,FLVCR1,PDE3A,CDC42SE1,CENPF,EIF4G1,CDK1,TFRC,PAK2,EPHB2,ETV4,BRCA1,NSD2,MED28,ANKLE1,ECT2,SIX4,MAPK6,FOXM1,MSX1,RAC1,HNRNPU,NEDD4,PDPN,ARG2,PRELID1,IQGAP3,HOXB7,LMNA,ALOX15B,COL1A1,PPIB,SPAG9,SYT4,MORF4L2,DNMT1,RSL1D1,EMP2,TP73,G6PD,PTBP1,PIK3CD,FANCA,FAM129B,NEK6,CBFB,CTH,SRRT,ARF6,AURKA,HAS2,PDCD2,PID1,CLSTN3	darkgrey	VSMC_M8

GO:0048583	1.00	0.00	181	2834	regulation of response to stimulus	BP	1	ALPK2,BCLAF1,DDX39B,FBXO5,EZR,FBN2,FAM49B,MATR3,HMGXB4,PWP1,POLR3B,POLH,VCP,HSP90AB1,MIOS,TRIM28,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL2,NAMPT,RUVBL1,DNAJC2,CHORDC1,RNASEH2B,PPP5C,PRCP,KCNN4,PLAUR,AXL,RNF157,SPHK1,ULK4,NCAPG2,NET1,PARP2,POLR3F,EIF4A3,CHMP6,ARHGDIA,SIPA1L3,PCNA,ZNF703,HGF,CCNB1,SNAI2,CD44,DEPDC1B,SLC20A1,PARPBP,PSD4,CENPJ,EIF2B1,VAMP8,HMGB2,CEP55,HELLS,ARHGAP11A,RACGAP1,LOXL3,PBK,HEY1,RBL1,FAM83D,NUP93,RAD51,CREB3L1,TOMM70,TRIM33,ENTPD7,MTDH,YWHAB,HMGCR,BAP1,EEF1E1,CHUK,SETD4,PPP1R15B,PAK1IP1,NCOA5,CIT,NUCKS1,DEK,MANF,ETS1,CHEK1,KHDRBS1,TRAIP,KIF14,RGS9,PRMT5,ASPM,POLQ,MNDA,DDX5,PHACTR4,FANCB,XBP1,RPA2,NF2,H2AFX,PDE3A,CDC42SE1,RBM14,NSMCE4A,STRAP,EIF4G1,AUNIP,ARFGAP1,TFRC,PAK2,DHX9,PSMA6,WDR76,DDX21,PPP2R1B,IFT80,EPHB2,UFD1,BRCA1,TFPI,CNOT9,NSD2,RAD51AP1,ANKLE1,ECT2,AIPL1,DHX33,FOXM1,EIF2AK1,LYAR,MSX1,RAC1,DNAJC7,UCHL1,UBE2K,NEDD4,EIF5A,BID,ARG2,PRELID1,IQGAP3,FUS,LMNA,ALOX15B,MAZ,AURKB,COL1A1,LRRC59,SPAG9,SLC25A5,NDC80,USP1,RSL1D1,EMP2,NXN,NOC2L,G6PD,PTBP1,PIK3CD,FANCA,CDT1,BCAR1,GCLM,FAM129B,NEK6,PLEKHG4,CTH,ARF6,GBP5,MAD2L1,STMN1,AURKA,ERP29,PID1,TRIM59,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0032101	1.00	0.00	31	646	regulation of response to external stimulus	BP	1	FAM49B,MATR3,POLR3B,HSP90AB1,SPHK1,POLR3F,HGF,SNAI2,VAMP8,HMGB2,PBK,TOMM70,HMGCR,BAP1,SETD4,ETS1,MNDA,RBM14,PAK2,DHX9,PSMA6,EPHB2,UFD1,TFPI,AIPL1,LYAR,RAC1,UBE2K,ARG2,FANCA,GBP5	darkgrey	VSMC_M8
GO:0032496	1.00	0.00	7	225	response to lipopolysaccharide	BP	1	AXL,HMGB2,MTDH,CHUK,XBP1,TFPI,ADIPOR2	darkgrey	VSMC_M8
GO:0007411	1.00	0.00	5	181	axon guidance	BP	1	B3GNT2,EPHB2,RAC1,EFNB1,FAM129B	darkgrey	VSMC_M8
GO:0045595	1.00	0.00	64	1153	regulation of cell differentiation	BP	1	DDX39B,FBXO5,FBN2,HSPA9,PWP1,HSP90AB1,ANP32B,HOXA5,EZH2,PRMT1,PUS7,AXL,PARP2,NAP1L1,ZNF703,HGF,MEDAG,SNAI2,E2F1,HMGB2,LOXL3,HEY1,TBX3,RUNX1,ETS1,NSUN2,KIF14,PRMT5,ASPM,IQCB1,DDX5,XBP1,NF2,PDE3A,EIF4G1,CDK1,EPHB2,ETV4,MED28,ANKLE1,ECT2,SIX4,MSX1,RAC1,HNRNPU,PDPN,PRELID1,ALOX15B,COL1A1,SPAG9,MORF4L2,DNMT1,EMP2,TP73,G6PD,PTBP1,FANCA,FAM129B,CBFB,CTH,SRRT,AURKA,HAS2,PDCD2	darkgrey	VSMC_M8
GO:0009888	1.00	0.00	80	1389	tissue development	BP	1	ALPK2,HNRNPAB,DDX39B,FBXO5,EZR,FBN2,TJP2,COL1A2,TRIM28,GRSF1,HOXA5,MFSD2A,EZH2,PRMT1,SDC1,PLK4,PGR,STIL,PUS7,SERPINH1,PARP2,E2F7,SIPA1L3,PCNA,ZNF703,HGF,CCNB1,SNAI2,CD44,POLR1B,KIF20B,SLC20A1,RBP4,MSC,LOXL3,HEY1,FAM83D,TBX3,E2F8,HMGCR,RUNX1,MDM4,NOLC1,NSUN2,DDX5,PHACTR4,XBP1,NUP133,NF2,CENPF,CDK1,HNRNPH3,IFT80,ETV4,SIX4,MSX1,RAC1,HNRNPU,MTHFD1,PDPN,ARG2,IQGAP3,EFNB1,SH3PXD2B,HOXB7,LMNA,ALOX15B,COL1A1,ALDH3A2,TYMS,RAP2C,TP73,G6PD,PIK3CD,TOR1A,FAM129B,TPPP3,HAS2,PALB2,CASP6	darkgrey	VSMC_M8
GO:0016236	1.00	0.00	9	265	macroautophagy	BP	1	VCP,CHMP6,PGAM5,ATG101,VAMP8,UCHL1,NEDD4,SLC25A5,POLDIP2	darkgrey	VSMC_M8
GO:0046474	1.00	0.00	5	185	glycerophospholipid biosynthetic process	BP	1	MFSD2A,PGS1,AGPAT5,PIK3CD,ACSL3	darkgrey	VSMC_M8
GO:0007600	1.00	0.00	12	320	sensory perception	BP	1	B3GNT2,BIRC5,SNAI2,WDR36,PPIP5K2,RBP4,NAV2,RGS9,AIPL1,UCHL1,COL1A1,NOB1	darkgrey	VSMC_M8
GO:0048729	1.00	0.00	22	490	tissue morphogenesis	BP	1	TRIM28,GRSF1,HOXA5,PGR,STIL,HGF,SNAI2,CD44,KIF20B,HEY1,TBX3,MDM4,PHACTR4,NF2,SIX4,MSX1,RAC1,MTHFD1,PDPN,HOXB7,PIK3CD,TOR1A	darkgrey	VSMC_M8
GO:0097485	1.00	0.00	5	182	neuron projection guidance	BP	1	B3GNT2,EPHB2,RAC1,EFNB1,FAM129B	darkgrey	VSMC_M8
GO:0070887	1.00	0.00	137	2230	cellular response to chemical stimulus	BP	1	CDK2,EZR,FBN2,NUS1,RANGAP1,HSPA9,SRSF3,VCP,HSP90AB1,CDC5L,COL1A2,MELK,SYNCRIP,B3GNT2,SLC31A1,EZH2,GJB3,SHCBP1,RUVBL2,PGR,NAMPT,MCM2,CCNA2,PPP5C,FOSB,CDC42EP4,PRCP,NUP85,CAD,DDX18,AXL,SPHK1,NET1,IPO5,EIF4A3,ARHGDIA,PCNA,ZNF703,HGF,CCNB1,SNAI2,CD44,HSP90B1,E2F1,HMGB2,MSC,HELLS,NRIP1,HEY1,SELENOT,TUBA1B,KNSTRN,RAD51,CREB3L1,MYBL2,TRIM33,MTDH,HMGCR,CHUK,PPP1R15B,MDM4,NCOA5,NUCKS1,KIF18A,ETS1,H2AFZ,NCL,TRAIP,RGS9,PRMT5,MNDA,DDX5,XBP1,BLM,PDE3A,UMPS,STRAP,CDK1,TFRC,PAK2,SMARCC1,DHX9,TRA2B,EFTUD2,UFD1,BRCA1,MCM7,TFPI,CNOT9,CDK16,ECT2,SUV39H1,MSX1,RAC1,MYO5A,HNRNPU,UCHL1,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,EIF2S1,SRSF5,IQGAP3,HDGF,FUS,LMNA,LTBP2,COL1A1,PPIB,SYT4,BRIP1,DNMT1,SLC25A5,NNT,AIFM1,RBMX,NXN,TFAP4,G6PD,PIK3CD,TOR1A,BCAR1,GCLM,FAM129B,CTH,ARF6,GBP5,HNRNPD,HAS2,SRSF7,SIGMAR1,PID1,CASP6,SRM,MBD2	darkgrey	VSMC_M8
GO:0044242	1.00	0.00	4	164	cellular lipid catabolic process	BP	1	MFSD2A,SPHK1,PCCA,LIPG	darkgrey	VSMC_M8
GO:0022898	1.00	0.00	5	186	regulation of transmembrane transporter activity	BP	1	THADA,ATP1B3,RGS9,EPHB2,NEDD4	darkgrey	VSMC_M8
GO:0002376	1.00	0.00	97	1656	immune system process	BP	1	TUBB,EZR,TTLL1,FAM49B,HSPA9,MATR3,SRPK1,POLR3B,HSP90AB1,MELK,TRIM28,MSH6,CTPS1,HOXA5,SYNCRIP,PABPC4,EZH2,PRMT1,NAMPT,PUS7,SEC61A1,CDC42EP4,KCNN4,NUP85,AXL,SPHK1,NCAPG2,POLR3F,SIPA1L3,CD44,EIF2B1,VAMP8,HMGB2,RBP4,HELLS,LOXL3,ESCO2,AGPAT5,TRIM35,MSH3,CTNNBL1,TOMM70,ENTPD7,BAP1,CHUK,RUNX1,ETS1,TXLNA,KHDRBS1,UNG,POLQ,MNDA,XBP1,MCM3AP,FLVCR1,RBM14,TFRC,PAK2,DHX9,DDX21,EPHB2,UFD1,NSD2,ANKLE1,SIX4,EIF2AK1,LYAR,RAC1,EXO1,RAB27A,UBE2K,TOP2A,LBR,PDPN,DCAF15,ARG2,PRELID1,CCNB2,EFNB1,HOXB7,PPIB,ILF3,SLC25A5,ELF4,EMP2,TUBB4B,G6PD,PIK3CD,FANCA,BCAR1,CBFB,LY75,GBP5,TMOD3,HMGB3,PDCD2,TRIM59	darkgrey	VSMC_M8

GO:0006887	1.00	0.00	9	266	exocytosis	BP	1	SDC1,VAMP8,TXLNA,SLC17A9,CDK16,RAB27A,SYT4,PIK3CD,STXBP6	darkgrey	VSMC_M8
GO:0043408	1.00	0.00	22	502	regulation of MAPK cascade	BP	1	EZR,EZH2,NUP62,PRMT1,SPHK1,ULK4,HGF,CD44,PBK,FAM83D,HMGCR,PRMT5,NF2,PAK2,EPHB2,DHX33,FOXM1,UCHL1,IQGAP3,SPAG9,ERP29,DUSP7	darkgrey	VSMC_M8
GO:0030154	1.00	0.00	190	2966	cell differentiation	BP	1	ALPK2,ATP5F1B,HNRNPAB,DDX39B,FBXO5,EZR,FBN2,TTLL1,NUS1,PHF5A,HSPA9,SRPK1,BYSL,PWP1,TJP2,HSP90AB1,TRIM28,ANP32B,HOXA5,MFSD2A,SYNCRIP,PABPC4,B3GNT2,EZH2,PHF19,PRMT1,CASP2,NAA15,SDC1,PLK4,PGR,PUS7,MAST2,AXL,RNF157,XRN2,ULK4,NCAPG2,CDC20,SERPINH1,PARP2,FBL,RRBP1,GTPBP4,NAP1L1,E2F7,ALYREF,STRN,SIPA1L3,PCNA,CDC25B,ZNF703,HGF,ELK3,MEDAG,CCNB1,WDR62,SNAI2,POLR1B,KIF20B,KIF2A,WEE1,EIF2B1,E2F1,HMGB2,ATF1,RACGAP1,LOXL3,ESCO2,HEY1,AGPAT5,RBL1,FAM83D,KNL1,TBX3,CREB3L1,E2F8,ENTPD7,HMGCR,CHUK,RUNX1,NAV2,NOLC1,CIT,MANF,ETS1,NSUN2,NAV1,TRIP13,KIF14,PRMT5,ASPM,IQCB1,DDX5,PHACTR4,XBP1,NUP133,HINFP,NF2,FLVCR1,PDE3A,CENPF,STRAP,EIF4G1,NHS,CDK1,TFRC,PAK2,DHX9,HNRNPH3,DDX20,DDX21,CABYR,IFT80,SF1,EPHB2,ETV4,CDK16,MED28,MYBBP1A,ANKLE1,ECT2,SUV39H1,FKBP4,SIX4,MAPK6,EIF2AK1,LYAR,USP42,MSX1,RAC1,HNRNPU,UCHL1,RAB27A,NEDD4,UGDH,SMARCE1,TOP2A,LBR,PDPN,PRELID1,ASF1B,EFNB1,SH3PXD2B,HOXB7,LMNA,ALOX15B,COL1A1,SPAG9,SYT4,BRIP1,MORF4L2,DNMT1,ACSL4,TYMS,PSMD11,SLC25A5,SEPT6,NDE1,ELF4,RAI14,RAP2C,RSL1D1,HOOK1,EMP2,RBMX,NXN,SF3A2,TP73,DAZAP1,G6PD,PTBP1,PIK3CD,FANCA,TOR1A,ODF2,FAM129B,CBFB,CTH,SRRT,ARF6,TMOD3,CDKN2C,ACSL3,STMN1,AURKA,HAS2,BLOC1S2,PDCD2,CASP6	darkgrey	VSMC_M8
GO:0051668	1.00	0.00	24	537	localization within membrane	BP	1	EZR,SEC61A1,GRIN2C,SRP68,VAMP8,ATP1B3,TRAM1,TOMM70,IFT80,EPHB2,RAC1,MYO5A,BID,SH3PXD2B,TIMM8A,MTCL1,EMP2,NDC1,EMC8,ARF6,RAPGEF6,ACSL3,STXBP6,PID1	darkgrey	VSMC_M8
GO:0002683	1.00	0.00	10	290	negative regulation of immune system process	BP	1	EZR,HSPA9,AXL,LOXL3,RUNX1,MNDA,UFD1,LYAR,ARG2,CBFB	darkgrey	VSMC_M8
GO:0070372	1.00	0.00	6	211	regulation of ERK1 and ERK2 cascade	BP	1	EZR,CD44,FAM83D,HMGCR,PRMT5,EPHB2	darkgrey	VSMC_M8
GO:0060070	1.00	0.00	8	250	canonical Wnt signaling pathway	BP	1	VCP,SDC1,RUVBL2,RUVBL1,ZNF703,SNAI2,ASPM,COL1A1	darkgrey	VSMC_M8
GO:0035239	1.00	0.00	34	699	tube morphogenesis	BP	1	ATP5F1B,NUS1,HOXA5,NAA15,PGR,STIL,AMOTL1,PRCP,SPHK1,E2F7,HGF,ELK3,KIF20B,HEY1,FMNL3,TBX3,CREB3L1,E2F8,MTDH,RUNX1,ETS1,NCL,PHACTR4,XBP1,EPHB2,BRCA1,SIX4,ADIPOR2,MTHFD1,HOXB7,EMP2,PIK3CD,FAM129B,HAS2	darkgrey	VSMC_M8
GO:0002009	1.00	0.00	17	412	morphogenesis of an epithelium	BP	1	TRIM28,GRSF1,HOXA5,PGR,STIL,HGF,CD44,KIF20B,TBX3,PHACTR4,SIX4,RAC1,MTHFD1,PDPN,HOXB7,PIK3CD,TOR1A	darkgrey	VSMC_M8
GO:0009967	1.00	0.00	61	1127	positive regulation of signal transduction	BP	1	BCLAF1,VCP,HSP90AB1,MIOS,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL1,PPP5C,KCNN4,PLAUR,AXL,SPHK1,NET1,HGF,CD44,DEPDC1B,SLC20A1,CENPJ,LOXL3,NUP93,MTDH,HMGCR,EEF1E1,CHUK,NUCKS1,PRMT5,ASPM,DDX5,XBP1,TFRC,PAK2,DDX21,PPP2R1B,CNOT9,ECT2,DHX33,MSX1,RAC1,UBE2K,NEDD4,EIF5A,BID,IQGAP3,ALOX15B,MAZ,COL1A1,LRRC59,SPAG9,NDC80,EMP2,PTBP1,PIK3CD,NEK6,CTH,MAD2L1,ERP29,MBD2	darkgrey	VSMC_M8
GO:0016485	1.00	0.00	4	170	protein processing	BP	1	CASP2,METAP2,RUNX1,SPCS3	darkgrey	VSMC_M8
GO:0006898	1.00	0.00	5	192	receptor-mediated endocytosis	BP	1	EZR,TFRC,RAC1,NEDD4,ARF6	darkgrey	VSMC_M8
GO:2000146	1.00	0.00	7	234	negative regulation of cell motility	BP	1	GTPBP4,ARHGDIA,NF2,RAC1,ADIPOR2,ALOX15B,RAP2C	darkgrey	VSMC_M8
GO:0045055	1.00	0.00	4	167	regulated exocytosis	BP	1	VAMP8,RAB27A,SYT4,PIK3CD	darkgrey	VSMC_M8
GO:0032787	1.00	0.00	16	404	monocarboxylic acid metabolic process	BP	1	MFSD2A,PCCA,CRYL1,PDHB,ELOVL6,XBP1,PDHA1,DLAT,BRCA1,ADIPOR2,ALOX15B,ACSL4,ALDH3A2,LIPG,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0030258	1.00	0.00	4	171	lipid modification	BP	1	MFSD2A,SPHK1,ADIPOR2,ALOX15B	darkgrey	VSMC_M8
GO:0008610	1.00	0.00	24	544	lipid biosynthetic process	BP	1	NUS1,CYP51A1,MFSD2A,SPHK1,PGS1,SNAI2,AGPAT5,HMGCR,ELOVL6,XBP1,AGPS,DDX20,GK,SF1,BRCA1,LBR,ALOX15B,ACSL4,LIPG,G6PD,PIK3CD,DOLPP1,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0048646	1.00	0.00	45	877	anatomical structure formation involved in morphogenesis	BP	1	ATP5F1B,FBN2,TTLL1,NUS1,BYSL,HOXA5,NAA15,STIL,AMOTL1,PRCP,SPHK1,E2F7,HGF,ELK3,SNAI2,POLR1B,KIF20B,RBP4,HEY1,FMNL3,KNL1,TBX3,CREB3L1,E2F8,MTDH,RUNX1,NOLC1,ETS1,NCL,PHACTR4,XBP1,NF2,EPHB2,BRCA1,SIX4,MSX1,ADIPOR2,MTHFD1,PDPN,COL1A1,EMP2,PIK3CD,FAM129B,TMOD3,PALB2	darkgrey	VSMC_M8
GO:0030155	1.00	0.00	24	541	regulation of cell adhesion	BP	1	FAM49B,PLAUR,GTPBP4,ARHGDIA,ZNF703,SNAI2,CD44,LOXL3,RUNX1,ETS1,KIF14,XBP1,NF2,TFRC,EPHB2,RAC1,PDPN,ARG2,EFNB1,COL1A1,POLDIP2,EMP2,CBFB,HAS2	darkgrey	VSMC_M8

GO:0042221	1.00	0.00	184	2921	response to chemical	BP	1	CDK2,EZR,FBN2,NUS1,MAN1A1,FAM49B,RANGAP1,HSPA9,SRSF3,CYC1,APTX,VCP,HSP90AB1,CDC5L,COL1A2,MELK,CTPS1,SYNCRIP,B3GNT2,SLC31A1,EZH2,GJB3,SHCBP1,SDC1,RUVBL2,PGR,NAMPT,MCM2,SEC61A1,CCNA2,RAD54L,PPP5C,FOSB,CDC42EP4,NASP,PRCP,NUP85,PLAUR,CAD,DDX18,SRP68,AXL,SPHK1,SRSF2,NET1,SERPINH1,IPO5,EIF4A3,ARHGDIA,PCNA,ZNF703,RFC3,HGF,CCNB1,SNAI2,CD44,GGH,HSP90B1,EIF2B1,E2F1,HMGB2,TRAM1,RBP4,MSC,ATF1,TERF1,HELLS,NRIP1,HEY1,SELENOT,TUBA1B,RSRC1,KNSTRN,RAD51,CREB3L1,MYBL2,TRIM33,MTDH,HMGCR,BAP1,CHUK,PPP1R15B,MDM4,PSMD14,NCOA5,NUCKS1,KIF18A,MANF,ETS1,TENT4A,H2AFZ,NCL,TRAIP,RGS9,PRMT5,MNDA,DDX5,XBP1,BLM,PDE3A,UMPS,RBM14,CENPF,STRAP,HAT1,CDK1,TFRC,PAK2,FOSL1,SMARCC1,DHX9,TRA2B,DDX21,EFTUD2,EPHB2,UFD1,BRCA1,MCM7,TFPI,CNOT9,CDK16,ECT2,SUV39H1,MNAT1,MSX1,RAC1,MYO5A,HNRNPU,UCHL1,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,BID,EIF2S1,NUDT1,DHX15,SRSF5,IQGAP3,EFNB1,HDGF,FUS,LMNA,LTBP2,COL1A1,PFAS,PPIB,SYT4,BRIP1,DNMT1,ACSL4,TYMS,SLC25A5,NNT,AIFM1,RBMX,LIPG,NXN,TFAP4,TP73,G6PD,PIK3CD,CDT1,TOR1A,BCAR1,GCLM,FAM129B,CTH,SRRT,ARF6,GBP5,HNRNPD,ACSL3,HAS2,SRSF7,SIGMAR1,PID1,GART,CASP6,SLC30A1,UBE2J2,SRM,MBD2	darkgrey	VSMC_M8
GO:0000165	1.00	0.00	26	579	MAPK cascade	BP	1	EZR,EZH2,NUP62,PRMT1,PPP5C,SPHK1,ULK4,HGF,CD44,PBK,FAM83D,HMGCR,NRAS,PRMT5,NF2,CDK1,PAK2,EPHB2,DHX33,MAPK6,FOXM1,UCHL1,IQGAP3,SPAG9,ERP29,DUSP7	darkgrey	VSMC_M8
GO:0007167	1.00	0.00	37	752	enzyme linked receptor protein signaling pathway	BP	1	FBN2,NUS1,HSP90AB1,COL1A2,TTK,NUP62,SHCBP1,CD3EAP,PLAUR,AXL,CHMP6,ZNF703,HGF,NUP93,CREB3L1,TRIM33,NCOA5,NUCKS1,EFS,DDX5,RBM14,STRAP,PAK2,SMARCC1,EPHB2,CNOT9,MSX1,RAC1,NEDD4,EFNB1,LTBP2,COL1A1,PIK3CD,BCAR1,FAM129B,STMN1,PID1	darkgrey	VSMC_M8
GO:0051924	1.00	0.00	4	172	regulation of calcium ion transport	BP	1	THADA,RGS9,G6PD,SLC30A1	darkgrey	VSMC_M8
GO:0007160	1.00	0.00	5	192	cell-matrix adhesion	BP	1	CD44,NF2,RAC1,POLDIP2,EMP2	darkgrey	VSMC_M8
GO:0031589	1.00	0.00	10	294	cell-substrate adhesion	BP	1	AXL,CD44,KIF14,NF2,RAC1,PDPN,COL1A1,POLDIP2,EMP2,HAS2	darkgrey	VSMC_M8
GO:0007517	1.00	0.00	8	259	muscle organ development	BP	1	MSC,HMGCR,DDX5,XBP1,CENPF,SIX4,MSX1,FAM129B	darkgrey	VSMC_M8
GO:0032409	1.00	0.00	5	198	regulation of transporter activity	BP	1	THADA,ATP1B3,RGS9,EPHB2,NEDD4	darkgrey	VSMC_M8
GO:0002764	1.00	0.00	9	278	immune response-regulating signaling pathway	BP	1	EZR,KCNN4,EIF2B1,KHDRBS1,MNDA,PAK2,UFD1,PIK3CD,BCAR1	darkgrey	VSMC_M8
GO:0051271	1.00	0.00	7	241	negative regulation of cellular component movement	BP	1	GTPBP4,ARHGDIA,NF2,RAC1,ADIPOR2,ALOX15B,RAP2C	darkgrey	VSMC_M8
GO:0010647	1.00	0.00	68	1251	positive regulation of cell communication	BP	1	BCLAF1,VCP,HSP90AB1,MIOS,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL1,PPP5C,GRIN2C,KCNN4,PLAUR,AXL,SPHK1,NET1,HGF,CD44,DEPDC1B,SLC20A1,CENPJ,VAMP8,RBP4,LOXL3,SELENOT,NUP93,MTDH,HMGCR,EEF1E1,CHUK,NUCKS1,PRMT5,ASPM,DDX5,XBP1,TFRC,PAK2,DDX21,PPP2R1B,EPHB2,CNOT9,ECT2,DHX33,MSX1,RAC1,UBE2K,NEDD4,EIF5A,BID,IQGAP3,ALOX15B,MAZ,COL1A1,LRRC59,SPAG9,ACSL4,NDC80,EMP2,PTBP1,PIK3CD,NEK6,CTH,MAD2L1,ERP29,CLSTN3,MBD2	darkgrey	VSMC_M8
GO:0019221	1.00	0.00	10	306	cytokine-mediated signaling pathway	BP	1	HSP90AB1,AXL,SPHK1,CD44,CHUK,TRAIP,CNOT9,ADIPOR2,UBE2K,EIF5A	darkgrey	VSMC_M8
GO:0048468	1.00	0.00	91	1587	cell development	BP	1	ALPK2,DDX39B,FBXO5,EZR,TTLL1,SRPK1,TJP2,HSP90AB1,HOXA5,MFSD2A,PABPC4,B3GNT2,EZH2,PRMT1,CASP2,SDC1,PGR,AXL,RNF157,ULK4,CDC20,SERPINH1,PARP2,NAP1L1,STRN,SIPA1L3,CDC25B,HGF,CCNB1,SNAI2,KIF20B,WEE1,EIF2B1,E2F1,HMGB2,ATF1,HEY1,KNL1,TBX3,RUNX1,NOLC1,MANF,NSUN2,TRIP13,KIF14,PRMT5,ASPM,PHACTR4,XBP1,NF2,FLVCR1,PDE3A,CDK1,PAK2,DDX20,CABYR,EPHB2,CDK16,FKBP4,SIX4,MAPK6,LYAR,RAC1,HNRNPU,UCHL1,NEDD4,UGDH,PDPN,EFNB1,LMNA,SPAG9,SYT4,BRIP1,ACSL4,TYMS,RAP2C,HOOK1,SF3A2,TP73,G6PD,TOR1A,ODF2,FAM129B,CBFB,SRRT,ARF6,TMOD3,STMN1,AURKA,HAS2,BLOC1S2	darkgrey	VSMC_M8
GO:2000145	1.00	0.00	37	772	regulation of cell motility	BP	1	ATP5F1B,FBXO5,NUS1,FAM49B,ARHGEF39,AMOTL1,PRCP,SPHK1,ULK4,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,KIF20B,KIF2A,SGK3,ETS1,KIF14,XBP1,NF2,S100A11,EPHB2,RAC1,ADIPOR2,PDPN,LMNA,ALOX15B,MAZ,COL1A1,SPAG9,RAP2C,EMP2,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0006955	1.00	0.00	52	1012	immune response	BP	1	TUBB,EZR,TTLL1,FAM49B,MATR3,SRPK1,POLR3B,HSP90AB1,TRIM28,MSH6,SYNCRIP,SEC61A1,CDC42EP4,KCNN4,AXL,POLR3F,EIF2B1,VAMP8,HMGB2,LOXL3,TRIM35,TOMM70,ENTPD7,CHUK,ETS1,KHDRBS1,UNG,MNDA,XBP1,RBM14,TFRC,PAK2,DHX9,DDX21,UFD1,NSD2,LYAR,EXO1,RAB27A,UBE2K,ARG2,PRELID1,ILF3,ELF4,EMP2,TUBB4B,PIK3CD,BCAR1,LY75,GBP5,HMGB3,TRIM59	darkgrey	VSMC_M8
GO:0023056	1.00	0.00	68	1258	positive regulation of signaling	BP	1	BCLAF1,VCP,HSP90AB1,MIOS,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL1,PPP5C,GRIN2C,KCNN4,PLAUR,AXL,SPHK1,NET1,HGF,CD44,DEPDC1B,SLC20A1,CENPJ,VAMP8,RBP4,LOXL3,SELENOT,NUP93,MTDH,HMGCR,EEF1E1,CHUK,NUCKS1,PRMT5,ASPM,DDX5,XBP1,TFRC,PAK2,DDX21,PPP2R1B,EPHB2,CNOT9,ECT2,DHX33,MSX1,RAC1,UBE2K,NEDD4,EIF5A,BID,IQGAP3,ALOX15B,MAZ,COL1A1,LRRC59,SPAG9,ACSL4,NDC80,EMP2,PTBP1,PIK3CD,NEK6,CTH,MAD2L1,ERP29,CLSTN3,MBD2	darkgrey	VSMC_M8
GO:0008544	1.00	0.00	5	201	epidermis development	BP	1	EZH2,NSUN2,ETV4,ALOX15B,ALDH3A2	darkgrey	VSMC_M8
GO:0023061	1.00	0.00	11	325	signal release	BP	1	VAMP8,RBP4,SELENOT,TBX3,HMGCR,CDK16,RAC1,SYT4,ACSL4,FAM129B,SLC30A1	darkgrey	VSMC_M8
GO:0060627	1.00	0.00	15	403	regulation of vesicle-mediated transport	BP	1	EZR,SDC1,PREB,AXL,SPHK1,VAMP8,ARFGAP1,LYAR,RAC1,RAB27A,SYT4,TOR1A,ARF6,ACSL3,STXBP6	darkgrey	VSMC_M8

GO:0002521	1.00	0.00	14	383	leukocyte differentiation	BP	1	EZH2,AXL,LOXL3,ENTPD7,RUNX1,XBP1,TFRC,EIF2AK1,LBR,PRELID1,SLC25A5,PIK3CD,FANCA,CBFB	darkgrey	VSMC_M8
GO:0048598	1.00	0.00	19	469	embryonic morphogenesis	BP	1	FBN2,TRIM28,GRSF1,HOXA5,STIL,EIF4A3,KIF20B,RBP4,TBX3,PHACTR4,NF2,FLVCR1,EPHB2,SIX4,MSX1,MTHFD1,UGDH,HOXB7,ACD	darkgrey	VSMC_M8
GO:0019216	1.00	0.00	7	251	regulation of lipid metabolic process	BP	1	MFSD2A,SPHK1,SNAI2,DDX20,SF1,BRCA1,ACSL3	darkgrey	VSMC_M8
GO:0022603	1.00	0.00	36	761	regulation of anatomical structure morphogenesis	BP	1	EZR,FAM49B,HOXA5,MFSD2A,CDC42EP4,RNF157,SPHK1,ARHGDIA,PGAM5,HGF,CD44,FMNL3,CREB3L1,MTDH,RUNX1,ETS1,XBP1,CDC42SE1,TFRC,PAK2,EPHB2,BRCA1,SIX4,MSX1,RAC1,NEDD4,PDPN,HOXB7,SPAG9,SYT4,EMP2,PIK3CD,FAM129B,AURKA,HAS2,PID1	darkgrey	VSMC_M8
GO:0003012	1.00	0.00	11	332	muscle system process	BP	1	DDX39B,EZH2,SPHK1,PARP2,TBX3,CHUK,ARG2,LMNA,TPM3,G6PD,TMOD3	darkgrey	VSMC_M8
GO:0006644	1.00	0.00	10	314	phospholipid metabolic process	BP	1	NUS1,MFSD2A,DBI,PGS1,AGPAT5,ALOX15B,LIPG,PIK3CD,DOLPP1,ACSL3	darkgrey	VSMC_M8
GO:0016197	1.00	0.00	5	209	endosomal transport	BP	1	VCP,CHMP6,SPAG9,ARF6,BLOC1S2	darkgrey	VSMC_M8
GO:0045444	1.00	0.00	4	188	fat cell differentiation	BP	1	MEDAG,E2F1,XBP1,HNRNPU	darkgrey	VSMC_M8
GO:0009966	1.00	0.00	133	2237	regulation of signal transduction	BP	1	ALPK2,BCLAF1,DDX39B,EZR,FBN2,FAM49B,HMGXB4,PWP1,VCP,HSP90AB1,MIOS,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL2,RUVBL1,RNASEH2B,PPP5C,PRCP,KCNN4,PLAUR,AXL,RNF157,SPHK1,ULK4,NCAPG2,NET1,EIF4A3,CHMP6,ARHGDIA,SIPA1L3,ZNF703,HGF,CCNB1,SNAI2,CD44,DEPDC1B,SLC20A1,PSD4,CENPJ,HMGB2,CEP55,HELLS,ARHGAP11A,RACGAP1,LOXL3,PBK,HEY1,FAM83D,NUP93,CREB3L1,TRIM33,MTDH,YWHAB,HMGCR,EEF1E1,CHUK,PPP1R15B,PAK1IP1,NCOA5,CIT,NUCKS1,CHEK1,TRAIP,KIF14,RGS9,PRMT5,ASPM,DDX5,PHACTR4,XBP1,RPA2,NF2,PDE3A,CDC42SE1,STRAP,ARFGAP1,TFRC,PAK2,WDR76,DDX21,PPP2R1B,IFT80,EPHB2,UFD1,BRCA1,CNOT9,ECT2,AIPL1,DHX33,FOXM1,MSX1,RAC1,UCHL1,UBE2K,NEDD4,EIF5A,BID,PRELID1,IQGAP3,LMNA,ALOX15B,MAZ,AURKB,COL1A1,LRRC59,SPAG9,SLC25A5,NDC80,EMP2,NXN,NOC2L,PTBP1,PIK3CD,FANCA,CDT1,GCLM,FAM129B,NEK6,PLEKHG4,CTH,ARF6,MAD2L1,STMN1,AURKA,ERP29,PID1,TRIM59,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0006914	1.00	0.00	17	450	autophagy	BP	1	VCP,NAMPT,CHMP6,PGAM5,HGF,ATG101,VAMP8,MTDH,XBP1,EIF4G1,UCHL1,NEDD4,BID,SLC25A5,POLDIP2,MTCL1,EVA1A	darkgrey	VSMC_M8
GO:0061919	1.00	0.00	17	450	process utilizing autophagic mechanism	BP	1	VCP,NAMPT,CHMP6,PGAM5,HGF,ATG101,VAMP8,MTDH,XBP1,EIF4G1,UCHL1,NEDD4,BID,SLC25A5,POLDIP2,MTCL1,EVA1A	darkgrey	VSMC_M8
GO:0070588	1.00	0.00	5	211	calcium ion transmembrane transport	BP	1	THADA,SEC61A1,GRIN2C,RGS9,G6PD	darkgrey	VSMC_M8
GO:0006928	1.00	0.00	87	1565	movement of cell or subcellular component	BP	1	NARS,ATP5F1B,FBXO5,TTLL1,NUS1,KIFC1,FAM49B,KIF20A,KIF27,KIF24,ARHGEF39,HOXA5,B3GNT2,ANLN,SDC1,AMOTL1,PRCP,NUP85,KIF2C,AXL,SPHK1,ULK4,NET1,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,CD44,DEPDC1B,KIF20B,KIF2A,SGK3,KIF11,HMGB2,FMNL3,CFAP298,FAM83D,KNSTRN,KIF18A,ETS1,NAV1,CENPE,KIF14,ASPM,EFS,PHACTR4,XBP1,NF2,CDK1,S100A11,KIF18B,KIF15,CABYR,EPHB2,DLGAP5,SIX4,RAC1,MYO5A,HNRNPU,UCHL1,ADIPOR2,FSCN1,PDPN,EFNB1,KIF4A,LMNA,ALOX15B,KIF22,MAZ,SPDL1,COL1A1,PPIB,SPAG9,KIF23,NDE1,RAP2C,EMP2,PIK3CD,TOR1A,PKN3,BCAR1,FAM129B,ARF6,STMN1,HAS2,BLOC1S2	darkgrey	VSMC_M8
GO:0032990	1.00	0.00	22	536	cell part morphogenesis	BP	1	HSP90AB1,MFSD2A,B3GNT2,RNF157,CD44,KIF20B,WEE1,PAK2,EPHB2,RAC1,UCHL1,NEDD4,PDPN,EFNB1,NES,SPAG9,SYT4,POLDIP2,FAM129B,STMN1,AURKA,PID1	darkgrey	VSMC_M8
GO:0040012	1.00	0.00	37	796	regulation of locomotion	BP	1	ATP5F1B,FBXO5,NUS1,FAM49B,ARHGEF39,AMOTL1,PRCP,SPHK1,ULK4,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,KIF20B,KIF2A,SGK3,ETS1,KIF14,XBP1,NF2,S100A11,EPHB2,RAC1,ADIPOR2,PDPN,LMNA,ALOX15B,MAZ,COL1A1,SPAG9,RAP2C,EMP2,PIK3CD,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0051270	1.00	0.00	39	830	regulation of cellular component movement	BP	1	ATP5F1B,FBXO5,NUS1,FAM49B,ARHGEF39,AMOTL1,PRCP,SPHK1,ULK4,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,KIF20B,KIF2A,SGK3,CFAP298,ETS1,KIF14,XBP1,NF2,S100A11,EPHB2,RAC1,ADIPOR2,PDPN,LMNA,ALOX15B,MAZ,COL1A1,SPAG9,RAP2C,EMP2,PIK3CD,BCAR1,ARF6,STMN1,HAS2	darkgrey	VSMC_M8
GO:0040013	1.00	0.00	7	261	negative regulation of locomotion	BP	1	GTPBP4,ARHGDIA,NF2,RAC1,ADIPOR2,ALOX15B,RAP2C	darkgrey	VSMC_M8
GO:0031346	1.00	0.00	9	302	positive regulation of cell projection organization	BP	1	CEP135,ANLN,EZH2,CDC42EP4,HGF,ATF1,RAC1,FSCN1,SF3A2	darkgrey	VSMC_M8
GO:0002682	1.00	0.00	44	915	regulation of immune system process	BP	1	EZR,FAM49B,HSPA9,MATR3,POLR3B,HSP90AB1,HOXA5,PRMT1,KCNN4,AXL,SPHK1,POLR3F,EIF2B1,VAMP8,HMGB2,RBP4,LOXL3,TOMM70,ENTPD7,RUNX1,ETS1,KHDRBS1,MNDA,XBP1,RBM14,TFRC,PAK2,DHX9,DDX21,EPHB2,UFD1,NSD2,LYAR,RAC1,UBE2K,DCAF15,ARG2,PRELID1,EFNB1,PIK3CD,FANCA,BCAR1,CBFB,GBP5	darkgrey	VSMC_M8

GO:0006810	1.00	0.00	206	3300	transport	BP	1	ATP5F1B,TMED9,XPOT,NUP43,NUP107,CCT2,TUBB,DDX39B,EZR,PANX2,TCP1,NUP50,TTLL1,NUS1,ARFGAP3,MAN1A1,DESI1,RANGAP1,KIF20A,SLC35D2,HSPA9,SRSF3,KIF27,CYC1,TNPO3,HMGXB4,STEAP1,TJP2,CYP51A1,VCP,HSP90AB1,TRIM28,NCBP1,THADA,ANP32B,HNRNPA2B1,MFSD2A,CCT4,SLC31A1,NUP205,YRDC,NUP62,GJB3,NBAS,SDC1,SEC61A1,SAE1,SLC1A5,CHCHD4,NASP,COG3,GRIN2C,TOMM40,PREB,KCNN4,NUP85,SLC25A19,CAD,SLC5A6,DBI,SRP68,AXL,RNF157,SPHK1,GDI2,SEC23B,RRBP1,IPO5,EIF4A3,CHMP6,ALYREF,KCNK6,AAAS,KIF20B,SLC20A1,HSP90B1,NECAB3,ABCE1,VAMP8,ATP1B3,SLC10A7,TRAM1,RBP4,NUP160,RACGAP1,LOXL3,SELENOT,TUBA1B,CCT8,PPID,CCT7,RSRC1,CKAP5,NUP93,TBX3,CREB3L1,TOMM70,YWHAB,HMGCR,BAP1,NIPA2,SFXN3,HEATR3,NOLC1,CCT5,NUP153,KIF18A,NSUN2,ICE1,TXLNA,KHDRBS1,RGS9,CSE1L,PITPNB,XBP1,MCM3AP,IPO4,SFXN4,NUP133,SEC24D,FLVCR1,CDC42SE1,UMPS,SSB,ARCN1,CENPF,SLC17A9,ARFGAP1,CDK1,HDLBP,TFRC,DHX9,LSG1,HNRNPA3,ZW10,CABYR,RANBP1,BARD1,EPHB2,NMD3,UFD1,SLC35F2,CDK16,SLBP,SLC19A2,ANKLE1,ECT2,FKBP4,EIF2AK1,LYAR,RAC1,KDELR2,MYO5A,HNRNPU,UCHL1,RAB27A,ADIPOR2,NEDD4,EIF5A,BID,DDX39A,PRELID1,CCT3,KIF4A,LMNA,LTBP2,COL1A1,SPAG9,TIMM8A,SYT4,NUP62CL,ACSL4,TIMM44,SLC25A5,NNT,MTCL1,NDE1,AIFM1,HOOK1,EMP2,LIPG,NDC1,SMG6,THOC6,G6PD,PIK3CD,SLC6A17,TOR1A,NUP188,GLE1,FAM129B,ACD,LY75,ARF6,SPCS3,ACSL3,HAS2,BLOC1S2,STXBP6,SRSF7,SIGMAR1,ERP29,XKR5,PID1,SLC30A1,UBE2J2	darkgrey	VSMC_M8
GO:1901615	1.00	0.00	13	382	organic hydroxy compound metabolic process	BP	1	NUS1,CYP51A1,SPHK1,SNAI2,PPIP5K2,RBP4,HMGCR,HDLBP,GK,LBR,ALOX15B,ALDH3A2,G6PD	darkgrey	VSMC_M8
GO:0010959	1.00	0.00	7	263	regulation of metal ion transport	BP	1	THADA,KCNN4,ATP1B3,RGS9,NEDD4,G6PD,SLC30A1	darkgrey	VSMC_M8
GO:0019932	1.00	0.00	5	218	second-messenger-mediated signaling	BP	1	GRIN2C,RNF157,SPHK1,PDE3A,PTBP1	darkgrey	VSMC_M8
GO:0032102	1.00	0.00	7	266	negative regulation of response to external stimulus	BP	1	HGF,PBK,HMGCR,UFD1,TFPI,LYAR,ARG2	darkgrey	VSMC_M8
GO:0032535	1.00	0.00	10	325	regulation of cellular component size	BP	1	EZR,FAM49B,HSP90AB1,CDC42EP4,KCNN4,RAC1,IQGAP3,ARPC4,ARF6,TMOD3	darkgrey	VSMC_M8
GO:0048870	1.00	0.00	64	1234	cell motility	BP	1	NARS,ATP5F1B,FBXO5,TTLL1,NUS1,FAM49B,ARHGEF39,HOXA5,ANLN,SDC1,AMOTL1,PRCP,NUP85,AXL,SPHK1,ULK4,NET1,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,CD44,DEPDC1B,KIF20B,KIF2A,SGK3,HMGB2,FMNL3,FAM83D,KNSTRN,ETS1,NAV1,KIF14,ASPM,EFS,PHACTR4,XBP1,NF2,CDK1,S100A11,EPHB2,SIX4,RAC1,ADIPOR2,FSCN1,PDPN,EFNB1,LMNA,ALOX15B,MAZ,SPDL1,COL1A1,PPIB,SPAG9,NDE1,RAP2C,EMP2,PIK3CD,TOR1A,PKN3,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0051674	1.00	0.00	64	1234	localization of cell	BP	1	NARS,ATP5F1B,FBXO5,TTLL1,NUS1,FAM49B,ARHGEF39,HOXA5,ANLN,SDC1,AMOTL1,PRCP,NUP85,AXL,SPHK1,ULK4,NET1,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,CD44,DEPDC1B,KIF20B,KIF2A,SGK3,HMGB2,FMNL3,FAM83D,KNSTRN,ETS1,NAV1,KIF14,ASPM,EFS,PHACTR4,XBP1,NF2,CDK1,S100A11,EPHB2,SIX4,RAC1,ADIPOR2,FSCN1,PDPN,EFNB1,LMNA,ALOX15B,MAZ,SPDL1,COL1A1,PPIB,SPAG9,NDE1,RAP2C,EMP2,PIK3CD,TOR1A,PKN3,BCAR1,ARF6,HAS2	darkgrey	VSMC_M8
GO:0046486	1.00	0.00	9	317	glycerolipid metabolic process	BP	1	MFSD2A,DBI,PGS1,AGPAT5,GK,ACSL4,LIPG,PIK3CD,ACSL3	darkgrey	VSMC_M8
GO:0048858	1.00	0.00	20	520	cell projection morphogenesis	BP	1	HSP90AB1,MFSD2A,B3GNT2,RNF157,CD44,KIF20B,WEE1,PAK2,EPHB2,RAC1,UCHL1,NEDD4,PDPN,EFNB1,NES,SPAG9,SYT4,FAM129B,STMN1,AURKA	darkgrey	VSMC_M8
GO:0032989	1.00	0.00	25	609	cellular component morphogenesis	BP	1	HSP90AB1,MFSD2A,B3GNT2,RNF157,CD44,KIF20B,WEE1,KNL1,PAK2,EPHB2,SIX4,RAC1,UCHL1,NEDD4,PDPN,EFNB1,NES,SPAG9,SYT4,POLDIP2,FAM129B,TMOD3,STMN1,AURKA,PID1	darkgrey	VSMC_M8
GO:0120035	1.00	0.00	20	524	regulation of plasma membrane bounded cell projection organization	BP	1	EZR,CEP135,MFSD2A,ANLN,EZH2,CDC42EP4,ULK4,CDC20,HGF,CD44,ATF1,PAK2,EPHB2,FKBP4,RAC1,NEDD4,FSCN1,PDPN,SF3A2,ARF6	darkgrey	VSMC_M8
GO:0010975	1.00	0.00	12	376	regulation of neuron projection development	BP	1	MFSD2A,EZH2,ULK4,CDC20,HGF,ATF1,PAK2,EPHB2,FKBP4,NEDD4,SF3A2,ARF6	darkgrey	VSMC_M8
GO:0003013	1.00	0.00	15	437	circulatory system process	BP	1	TJP2,COL1A2,MFSD2A,NAMPT,SLC1A5,PRCP,SLC5A6,KCNK6,HMGCR,NAV2,PDE3A,TFRC,EMP2,SLC6A17,GCLM	darkgrey	VSMC_M8
GO:0006650	1.00	0.00	6	257	glycerophospholipid metabolic process	BP	1	MFSD2A,DBI,PGS1,AGPAT5,PIK3CD,ACSL3	darkgrey	VSMC_M8
GO:0006936	1.00	0.00	6	256	muscle contraction	BP	1	SPHK1,TBX3,CHUK,ARG2,TPM3,TMOD3	darkgrey	VSMC_M8
GO:0034765	1.00	0.00	9	323	regulation of ion transmembrane transport	BP	1	THADA,KCNN4,KCNK6,ATP1B3,RGS9,EPHB2,NEDD4,G6PD,SLC30A1	darkgrey	VSMC_M8
GO:0006935	1.00	0.00	14	426	chemotaxis	BP	1	FAM49B,B3GNT2,NUP85,PLAUR,HGF,HMGB2,FOSL1,EPHB2,RAC1,EFNB1,PPIB,PIK3CD,BCAR1,FAM129B	darkgrey	VSMC_M8
GO:0042330	1.00	0.00	14	427	taxis	BP	1	FAM49B,B3GNT2,NUP85,PLAUR,HGF,HMGB2,FOSL1,EPHB2,RAC1,EFNB1,PPIB,PIK3CD,BCAR1,FAM129B	darkgrey	VSMC_M8
GO:0006816	1.00	0.00	7	282	calcium ion transport	BP	1	THADA,SEC61A1,GRIN2C,KCNN4,RGS9,G6PD,SLC30A1	darkgrey	VSMC_M8
GO:2000026	1.00	0.00	48	1014	regulation of multicellular organismal development	BP	1	DDX39B,FBXO5,FBN2,HSPA9,HOXA5,EZH2,PRMT1,AXL,SPHK1,PARP2,NAP1L1,HGF,CCNB1,SNAI2,E2F1,HMGB2,RBP4,RACGAP1,LOXL3,HEY1,RBM19,TBX3,CREB3L1,MTDH,RUNX1,ETS1,KIF14,PRMT5,ASPM,XBP1,UTP25,NF2,CDK1,EPHB2,ETV4,BRCA1,SIX4,PRELID1,ALOX15B,EMP2,TP73,G6PD,PIK3CD,FANCA,FAM129B,CBFB,SRRT,CLSTN3	darkgrey	VSMC_M8

GO:0040011	1.00	0.00	69	1349	locomotion	BP	1	NARS,ATP5F1B,FBXO5,TTLL1,NUS1,FAM49B,ARHGEF39,HOXA5,B3GNT2,ANLN,SDC1,AMOTL1,GRIN2C,PRCP,NUP85,PLAUR,AXL,SPHK1,ULK4,NET1,GTPBP4,ARHGDIA,ZNF703,HGF,SNAI2,CD44,DEPDC1B,KIF20B,KIF2A,SGK3,HMGB2,FMNL3,FAM83D,KNSTRN,ETS1,NAV1,KIF14,ASPM,EFS,PHACTR4,XBP1,NF2,CDK1,S100A11,FOSL1,EPHB2,SIX4,RAC1,ADIPOR2,FSCN1,PDPN,EFNB1,LMNA,ALOX15B,MAZ,SPDL1,COL1A1,PPIB,SPAG9,NDE1,RAP2C,EMP2,PIK3CD,TOR1A,PKN3,BCAR1,FAM129B,ARF6,HAS2	darkgrey	VSMC_M8
GO:0031344	1.00	0.00	20	538	regulation of cell projection organization	BP	1	EZR,CEP135,MFSD2A,ANLN,EZH2,CDC42EP4,ULK4,CDC20,HGF,CD44,ATF1,PAK2,EPHB2,FKBP4,RAC1,NEDD4,FSCN1,PDPN,SF3A2,ARF6	darkgrey	VSMC_M8
GO:0007610	1.00	0.00	13	406	behavior	BP	1	MFSD2A,EIF4A3,STRN,AAAS,HMGCR,NAV2,ARCN1,EIF4G1,FOSL1,EPHB2,UCHL1,FEN1,MBD2	darkgrey	VSMC_M8
GO:0120039	1.00	0.00	19	517	plasma membrane bounded cell projection morphogenesis	BP	1	HSP90AB1,MFSD2A,B3GNT2,RNF157,CD44,KIF20B,WEE1,PAK2,EPHB2,RAC1,UCHL1,NEDD4,PDPN,EFNB1,SPAG9,SYT4,FAM129B,STMN1,AURKA	darkgrey	VSMC_M8
GO:0098609	1.00	0.00	23	592	cell-cell adhesion	BP	1	EZR,FAM49B,TJP2,PLAUR,GTPBP4,ZNF703,CD44,LOXL3,RUNX1,ETS1,METAP1,XBP1,NF2,S100A11,TFRC,PDPN,ARG2,EFNB1,CBFB,TMOD3,HAS2,STXBP6,CLSTN3	darkgrey	VSMC_M8
GO:0010817	1.00	0.00	9	331	regulation of hormone levels	BP	1	VAMP8,RBP4,SELENOT,TBX3,HMGCR,CDK16,RAC1,ACSL4,FAM129B	darkgrey	VSMC_M8
GO:0062012	1.00	0.00	5	243	regulation of small molecule metabolic process	BP	1	VCP,MFSD2A,SNAI2,BRCA1,PID1	darkgrey	VSMC_M8
GO:0043410	1.00	0.00	10	356	positive regulation of MAPK cascade	BP	1	EZH2,PRMT1,SPHK1,HGF,CD44,HMGCR,DHX33,IQGAP3,SPAG9,ERP29	darkgrey	VSMC_M8
GO:0009887	1.00	0.00	34	784	animal organ morphogenesis	BP	1	ALPK2,FBN2,COL1A2,HOXA5,MFSD2A,SDC1,PGR,STIL,SERPINH1,EIF4A3,HGF,SNAI2,RBP4,HEY1,TBX3,MDM4,HMGN1,GMNN,PHACTR4,XBP1,NF2,FLVCR1,SMARCC1,IFT80,EPHB2,NSD2,SIX4,MSX1,RAC1,MTHFD1,HOXB7,COL1A1,HAS2,PALB2	darkgrey	VSMC_M8
GO:0050808	1.00	0.00	9	329	synapse organization	BP	1	TUBB,VCP,CDC20,EIF4G1,EPHB2,SIX4,NEDD4,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0034330	1.00	0.00	20	541	cell junction organization	BP	1	TUBB,TJP2,VCP,CDC20,STRN,ZNF703,SNAI2,MTDH,NF2,EIF4G1,PAK2,EPHB2,ECT2,SIX4,RAC1,NEDD4,FSCN1,POLDIP2,ARF6,CLSTN3	darkgrey	VSMC_M8
GO:0007399	1.00	0.00	103	1867	nervous system development	BP	1	NARS,TTLL1,KIF27,PPP2R5D,HSP90AB1,ANP32B,MFSD2A,B3GNT2,EZH2,PRMT1,CASP2,STIL,GRIN2C,SMG9,AXL,RNF157,SPHK1,XRN2,ULK4,CDC20,NAP1L1,STRN,RRM1,HGF,WDR62,SNRPB,KIF20B,KIF2A,WEE1,EIF2B1,E2F1,HMGB2,ATF1,RACGAP1,LOXL3,HEY1,TBX3,RUNX1,NAV2,CIT,MANF,ETS1,NAV1,KIF14,RGS9,PRMT5,ASPM,PHACTR4,XBP1,NUP133,NF2,H2AFX,ARCN1,CENPF,STRAP,EIF4G1,CDK1,PAK2,SMARCC1,TRA2B,EPHB2,TACC3,CDK16,ECT2,FKBP4,SIX4,MNAT1,MAPK6,MSX1,RAC1,UCHL1,MTHFD1,NEDD4,UGDH,SMARCE1,BID,EFNB1,NES,SPAG9,TIMM8A,SYT4,PRPS1,ACSL4,ALDH3A2,NDE1,THOC6,SF3A2,TP73,G6PD,SLC6A17,TOR1A,FAM129B,SRRT,ARF6,HNRNPD,CDKN2C,ACSL3,STMN1,AURKA,BLOC1S2,SIGMAR1,GART,CLSTN3	darkgrey	VSMC_M8
GO:0022008	1.00	0.00	64	1272	neurogenesis	BP	1	TTLL1,HSP90AB1,MFSD2A,B3GNT2,EZH2,PRMT1,AXL,RNF157,XRN2,ULK4,CDC20,NAP1L1,STRN,HGF,WDR62,KIF20B,WEE1,EIF2B1,E2F1,HMGB2,ATF1,RACGAP1,HEY1,RUNX1,NAV2,CIT,MANF,NAV1,PRMT5,ASPM,XBP1,NUP133,NF2,STRAP,EIF4G1,CDK1,PAK2,EPHB2,CDK16,ECT2,FKBP4,SIX4,MAPK6,RAC1,UCHL1,NEDD4,UGDH,SMARCE1,EFNB1,SPAG9,SYT4,ACSL4,NDE1,SF3A2,TP73,TOR1A,FAM129B,SRRT,ARF6,CDKN2C,ACSL3,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8
GO:0016042	1.00	0.00	4	225	lipid catabolic process	BP	1	MFSD2A,SPHK1,PCCA,LIPG	darkgrey	VSMC_M8
GO:0009617	1.00	0.00	10	362	response to bacterium	BP	1	FAM49B,FKBP5,AXL,HMGB2,MTDH,CHUK,XBP1,TFPI,ADIPOR2,ARG2	darkgrey	VSMC_M8
GO:0009605	1.00	0.00	95	1770	response to external stimulus	BP	1	TUBB,FAM49B,FKBP5,MATR3,SRPK1,POLR3B,HSP90AB1,MIOS,TRIM28,MFSD2A,SYNCRIP,B3GNT2,ODC1,CASP2,NAMPT,SEC61A1,FOSB,CDC42EP4,NUP85,PLAUR,CAD,HNRNPUL1,AXL,SPHK1,SRSF2,POLR3F,ARHGDIA,HGF,RRP8,CCNB1,SNAI2,VAMP8,HMGB2,PBK,TRIM35,TOMM70,MTDH,HMGCR,BAP1,CHUK,SETD4,CCT5,GCN1,ETS1,CHEK1,MNDA,XBP1,RBM14,EIF4G1,HAT1,PAK2,FOSL1,DHX9,PSMA6,DDX21,EPHB2,UFD1,TFPI,MYBBP1A,AIPL1,EIF2AK1,LYAR,RAC1,RAB27A,ADIPOR2,UBE2K,EIF5A,EIF2S1,ARG2,NUDT1,DCTPP1,EFNB1,COL1A1,PPIB,ILF3,BRIP1,ACSL4,TYMS,NNT,ELF4,AIFM1,LIPG,TUBB4B,G6PD,PIK3CD,FANCA,BCAR1,GCLM,FAM129B,GBP5,HMGB3,ACSL3,STMN1,TRIM59,MBD2	darkgrey	VSMC_M8
GO:0031175	1.00	0.00	33	784	neuron projection development	BP	1	HSP90AB1,MFSD2A,B3GNT2,EZH2,PRMT1,RNF157,ULK4,CDC20,STRN,HGF,KIF20B,WEE1,ATF1,MANF,PAK2,EPHB2,CDK16,FKBP4,MAPK6,RAC1,UCHL1,NEDD4,EFNB1,SPAG9,SYT4,ACSL4,SF3A2,TOR1A,FAM129B,ARF6,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8
GO:0120036	1.00	0.00	58	1193	plasma membrane bounded cell projection organization	BP	1	RTTN,EZR,TTLL1,KIF27,CEP78,KIF24,HSP90AB1,CEP135,MFSD2A,B3GNT2,ANLN,EZH2,PRMT1,PLK4,CDC42EP4,NUP85,RNF157,ULK4,CDC20,STRN,HGF,CD44,KIF20B,CENPJ,WEE1,CEP89,ATF1,FHDC1,CFAP298,MANF,IQCB1,PAK2,IFT80,EPHB2,CDK16,FKBP4,MAPK6,RAC1,UCHL1,NEDD4,FSCN1,PDPN,EFNB1,SPAG9,LRRC49,SYT4,ACSL4,SEPT6,EMP2,SF3A2,TOR1A,ODF2,FAM129B,ARF6,RAPGEF6,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8
GO:0030030	1.00	0.00	60	1226	cell projection organization	BP	1	RTTN,EZR,TTLL1,KIF27,CEP78,KIF24,HSP90AB1,CEP135,MFSD2A,B3GNT2,ANLN,EZH2,PRMT1,PLK4,CDC42EP4,NUP85,RNF157,ULK4,CDC20,STRN,HGF,CD44,KIF20B,CENPJ,WEE1,CEP89,ATF1,FHDC1,CFAP298,MANF,IQCB1,PAK2,IFT80,EPHB2,CDK16,FKBP4,MAPK6,RAC1,UCHL1,NEDD4,FSCN1,PDPN,EFNB1,NES,SPAG9,LRRC49,SYT4,ACSL4,SEPT6,EMP2,SF3A2,TOR1A,ODF2,FAM129B,POC1A,ARF6,RAPGEF6,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8

GO:0048699	1.00	0.00	57	1177	generation of neurons	BP	1	TTLL1,HSP90AB1,MFSD2A,B3GNT2,EZH2,PRMT1,AXL,RNF157,XRN2,ULK4,CDC20,NAP1L1,STRN,HGF,KIF20B,WEE1,E2F1,HMGB2,ATF1,RACGAP1,HEY1,RUNX1,CIT,MANF,NAV1,PRMT5,ASPM,XBP1,NF2,STRAP,EIF4G1,PAK2,EPHB2,CDK16,ECT2,FKBP4,SIX4,MAPK6,RAC1,UCHL1,NEDD4,UGDH,EFNB1,SPAG9,SYT4,ACSL4,NDE1,SF3A2,TP73,TOR1A,FAM129B,SRRT,ARF6,ACSL3,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8
GO:0044262	1.00	0.00	4	229	cellular carbohydrate metabolic process	BP	1	B3GNT2,PPIP5K2,GK,HAS2	darkgrey	VSMC_M8
GO:0007409	1.00	0.00	9	341	axonogenesis	BP	1	HSP90AB1,B3GNT2,PAK2,EPHB2,RAC1,UCHL1,EFNB1,FAM129B,STMN1	darkgrey	VSMC_M8
GO:0008015	1.00	0.00	10	369	blood circulation	BP	1	TJP2,COL1A2,NAMPT,PRCP,KCNK6,HMGCR,NAV2,PDE3A,EMP2,GCLM	darkgrey	VSMC_M8
GO:0098655	1.00	0.00	23	623	cation transmembrane transport	BP	1	ATP5F1B,CYC1,THADA,SLC31A1,SEC61A1,SLC1A5,GRIN2C,KCNN4,SLC25A19,KCNK6,SLC20A1,ATP1B3,NIPA2,SFXN3,RGS9,EPHB2,SLC19A2,NEDD4,SLC25A5,NNT,G6PD,SLC6A17,SLC30A1	darkgrey	VSMC_M8
GO:0051049	1.00	0.00	62	1276	regulation of transport	BP	1	EZR,NUS1,RANGAP1,CYP51A1,HSP90AB1,TRIM28,THADA,ANP32B,YRDC,NUP62,SDC1,SAE1,PREB,KCNN4,DBI,AXL,SPHK1,IPO5,KCNK6,AAAS,KIF20B,VAMP8,ATP1B3,RBP4,SELENOT,PPID,HMGCR,BAP1,NOLC1,NUP153,NSUN2,ICE1,KHDRBS1,RGS9,XBP1,ARFGAP1,CDK1,DHX9,BARD1,EPHB2,CDK16,ECT2,LYAR,RAC1,RAB27A,ADIPOR2,NEDD4,PRELID1,SYT4,ACSL4,SLC25A5,MTCL1,LIPG,G6PD,TOR1A,ARF6,ACSL3,STXBP6,ERP29,PID1,SLC30A1,UBE2J2	darkgrey	VSMC_M8
GO:0048812	1.00	0.00	17	503	neuron projection morphogenesis	BP	1	HSP90AB1,MFSD2A,B3GNT2,RNF157,KIF20B,WEE1,PAK2,EPHB2,RAC1,UCHL1,NEDD4,EFNB1,SPAG9,SYT4,FAM129B,STMN1,AURKA	darkgrey	VSMC_M8
GO:0006874	1.00	0.00	6	283	cellular calcium ion homeostasis	BP	1	THADA,GRIN2C,HSP90B1,SLC10A7,SELENOT,SLC30A1	darkgrey	VSMC_M8
GO:0034762	1.00	0.00	11	396	regulation of transmembrane transport	BP	1	THADA,KCNN4,KCNK6,ATP1B3,RGS9,EPHB2,ADIPOR2,NEDD4,G6PD,PID1,SLC30A1	darkgrey	VSMC_M8
GO:0098662	1.00	0.00	18	541	inorganic cation transmembrane transport	BP	1	ATP5F1B,CYC1,THADA,SLC31A1,SEC61A1,GRIN2C,KCNN4,KCNK6,SLC20A1,ATP1B3,NIPA2,RGS9,NEDD4,SLC25A5,NNT,G6PD,SLC6A17,SLC30A1	darkgrey	VSMC_M8
GO:0090066	1.00	0.00	12	418	regulation of anatomical structure size	BP	1	EZR,FAM49B,HSP90AB1,CDC42EP4,KCNN4,HMGCR,RAC1,IQGAP3,GCLM,ARPC4,ARF6,TMOD3	darkgrey	VSMC_M8
GO:0010646	1.00	0.00	143	2513	regulation of cell communication	BP	1	ALPK2,BCLAF1,DDX39B,EZR,FBN2,FAM49B,HMGXB4,PWP1,VCP,HSP90AB1,MIOS,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL2,RUVBL1,RNASEH2B,PPP5C,GRIN2C,PRCP,KCNN4,PLAUR,AXL,RNF157,SPHK1,ULK4,NCAPG2,NET1,CDC20,EIF4A3,CHMP6,ARHGDIA,SIPA1L3,ZNF703,HGF,CCNB1,SNAI2,CD44,DEPDC1B,SLC20A1,PSD4,CENPJ,VAMP8,HMGB2,CEP55,RBP4,HELLS,ARHGAP11A,RACGAP1,LOXL3,PBK,HEY1,SELENOT,FAM83D,NUP93,CREB3L1,TRIM33,MTDH,YWHAB,HMGCR,EEF1E1,CHUK,PPP1R15B,PAK1IP1,NCOA5,CIT,NUCKS1,CHEK1,TRAIP,KIF14,RGS9,PRMT5,ASPM,DDX5,PHACTR4,XBP1,RPA2,NF2,PDE3A,CDC42SE1,STRAP,ARFGAP1,TFRC,PAK2,WDR76,DDX21,PPP2R1B,IFT80,EPHB2,UFD1,BRCA1,CNOT9,CDK16,ECT2,AIPL1,DHX33,FOXM1,MSX1,RAC1,UCHL1,UBE2K,NEDD4,EIF5A,BID,PRELID1,IQGAP3,LMNA,ALOX15B,MAZ,AURKB,COL1A1,LRRC59,SPAG9,SYT4,ACSL4,SLC25A5,NDC80,EMP2,NXN,NOC2L,PTBP1,PIK3CD,FANCA,CDT1,GCLM,FAM129B,NEK6,PLEKHG4,CTH,ARF6,MAD2L1,STMN1,AURKA,ERP29,PID1,TRIM59,CLSTN3,SLC30A1,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0006812	1.00	0.00	32	796	cation transport	BP	1	ATP5F1B,PANX2,CYC1,THADA,SLC31A1,SEC61A1,SLC1A5,GRIN2C,KCNN4,SLC25A19,SLC5A6,KCNK6,SLC20A1,VAMP8,ATP1B3,SLC10A7,NIPA2,SFXN3,RGS9,FLVCR1,TFRC,EPHB2,SLC19A2,FKBP4,NEDD4,SYT4,SLC25A5,NNT,G6PD,SLC6A17,TOR1A,SLC30A1	darkgrey	VSMC_M8
GO:0051241	1.00	0.00	29	743	negative regulation of multicellular organismal process	BP	1	ALPK2,EZR,HSPA9,CYP51A1,HSP90AB1,HOXA5,EZH2,NRDC,AXL,PGAM5,HGF,SNAI2,RBP4,LOXL3,HEY1,CREB3L1,HMGCR,RUNX1,TRAIP,EPHB2,UFD1,TFPI,RAC1,ARG2,LMNA,TP73,G6PD,FAM129B,CBFB	darkgrey	VSMC_M8
GO:0055074	1.00	0.00	6	291	calcium ion homeostasis	BP	1	THADA,GRIN2C,HSP90B1,SLC10A7,SELENOT,SLC30A1	darkgrey	VSMC_M8
GO:0006875	1.00	0.00	10	381	cellular metal ion homeostasis	BP	1	THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,FLVCR1,TFRC,SLC30A1	darkgrey	VSMC_M8
GO:0050900	1.00	0.00	4	245	leukocyte migration	BP	1	NUP85,RAC1,PPIB,PIK3CD	darkgrey	VSMC_M8
GO:0006897	1.00	0.00	13	444	endocytosis	BP	1	EZR,AXL,SPHK1,LOXL3,ARFGAP1,TFRC,RAC1,NEDD4,SYT4,TOR1A,LY75,ARF6,XKR5	darkgrey	VSMC_M8
GO:0023051	1.00	0.00	143	2524	regulation of signaling	BP	1	ALPK2,BCLAF1,DDX39B,EZR,FBN2,FAM49B,HMGXB4,PWP1,VCP,HSP90AB1,MIOS,TTK,EZH2,NUP62,PRMT1,CASP2,GEN1,RUVBL2,RUVBL1,RNASEH2B,PPP5C,GRIN2C,PRCP,KCNN4,PLAUR,AXL,RNF157,SPHK1,ULK4,NCAPG2,NET1,CDC20,EIF4A3,CHMP6,ARHGDIA,SIPA1L3,ZNF703,HGF,CCNB1,SNAI2,CD44,DEPDC1B,SLC20A1,PSD4,CENPJ,VAMP8,HMGB2,CEP55,RBP4,HELLS,ARHGAP11A,RACGAP1,LOXL3,PBK,HEY1,SELENOT,FAM83D,NUP93,CREB3L1,TRIM33,MTDH,YWHAB,HMGCR,EEF1E1,CHUK,PPP1R15B,PAK1IP1,NCOA5,CIT,NUCKS1,CHEK1,TRAIP,KIF14,RGS9,PRMT5,ASPM,DDX5,PHACTR4,XBP1,RPA2,NF2,PDE3A,CDC42SE1,STRAP,ARFGAP1,TFRC,PAK2,WDR76,DDX21,PPP2R1B,IFT80,EPHB2,UFD1,BRCA1,CNOT9,CDK16,ECT2,AIPL1,DHX33,FOXM1,MSX1,RAC1,UCHL1,UBE2K,NEDD4,EIF5A,BID,PRELID1,IQGAP3,LMNA,ALOX15B,MAZ,AURKB,COL1A1,LRRC59,SPAG9,SYT4,ACSL4,SLC25A5,NDC80,EMP2,NXN,NOC2L,PTBP1,PIK3CD,FANCA,CDT1,GCLM,FAM129B,NEK6,PLEKHG4,CTH,ARF6,MAD2L1,STMN1,AURKA,ERP29,PID1,TRIM59,CLSTN3,SLC30A1,DUSP7,MBD2	darkgrey	VSMC_M8
GO:0019725	1.00	0.00	23	638	cellular homeostasis	BP	1	ATP5F1B,THADA,SLC31A1,GRIN2C,KCNN4,HSP90B1,ATP1B3,SLC10A7,SELENOT,HMGCR,UBE2C,NUCKS1,XBP1,FLVCR1,TFRC,TRA2B,CDK16,RAC1,UBE2K,NNT,GCLM,UBE2S,SLC30A1	darkgrey	VSMC_M8

GO:0050804	1.00	0.00	7	317	modulation of chemical synaptic transmission	BP	1	GRIN2C,CDC20,EIF4A3,EPHB2,SYT4,CLSTN3,SLC30A1	darkgrey	VSMC_M8
GO:0099177	1.00	0.00	7	318	regulation of trans-synaptic signaling	BP	1	GRIN2C,CDC20,EIF4A3,EPHB2,SYT4,CLSTN3,SLC30A1	darkgrey	VSMC_M8
GO:0098660	1.00	0.00	19	574	inorganic ion transmembrane transport	BP	1	ATP5F1B,CYC1,THADA,SLC31A1,SEC61A1,GRIN2C,KCNN4,SLC5A6,KCNK6,SLC20A1,ATP1B3,NIPA2,RGS9,NEDD4,SLC25A5,NNT,G6PD,SLC6A17,SLC30A1	darkgrey	VSMC_M8
GO:0000902	1.00	0.00	32	799	cell morphogenesis	BP	1	EZR,HSP90AB1,MFSD2A,B3GNT2,CDC42EP4,AXL,RNF157,ARHGDIA,SIPA1L3,HGF,CD44,KIF20B,WEE1,FMNL3,KIF14,CDC42SE1,PAK2,EPHB2,ECT2,MSX1,RAC1,UCHL1,NEDD4,PDPN,EFNB1,NES,SPAG9,SYT4,FAM129B,STMN1,AURKA,HAS2	darkgrey	VSMC_M8
GO:0005975	1.00	0.00	13	458	carbohydrate metabolic process	BP	1	MAN1A1,NANS,B3GNT2,PDHB,PPIP5K2,RBP4,PDHA1,GALE,GK,DLAT,UGDH,G6PD,HAS2	darkgrey	VSMC_M8
GO:0048666	1.00	0.00	36	877	neuron development	BP	1	HSP90AB1,MFSD2A,B3GNT2,EZH2,PRMT1,RNF157,ULK4,CDC20,STRN,HGF,KIF20B,WEE1,ATF1,RUNX1,MANF,XBP1,PAK2,EPHB2,CDK16,FKBP4,MAPK6,RAC1,UCHL1,NEDD4,UGDH,EFNB1,SPAG9,SYT4,ACSL4,SF3A2,TOR1A,FAM129B,ARF6,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8
GO:0007186	1.00	0.00	13	458	G protein-coupled receptor signaling pathway	BP	1	EZR,RNF157,SPHK1,YWHAB,RGS9,PRMT5,PDE3A,AIPL1,RAC1,ALOX15B,BCAR1,STMN1,SIGMAR1	darkgrey	VSMC_M8
GO:0055065	1.00	0.00	12	438	metal ion homeostasis	BP	1	STEAP1,THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,FLVCR1,TFRC,EIF2AK1,SLC30A1	darkgrey	VSMC_M8
GO:0072503	1.00	0.00	6	306	cellular divalent inorganic cation homeostasis	BP	1	THADA,GRIN2C,HSP90B1,SLC10A7,SELENOT,SLC30A1	darkgrey	VSMC_M8
GO:0043269	1.00	0.00	12	444	regulation of ion transport	BP	1	THADA,KCNN4,KCNK6,VAMP8,ATP1B3,RGS9,EPHB2,NEDD4,SYT4,G6PD,TOR1A,SLC30A1	darkgrey	VSMC_M8
GO:0042592	1.00	0.00	60	1295	homeostatic process	BP	1	ATP5F1B,NUS1,HSPA9,STEAP1,TJP2,THADA,POLD1,HOXA5,MFSD2A,SLC31A1,EZH2,PRMT1,NRDC,GRIN2C,PRCP,KCNN4,AXL,NCAPG2,PGAM5,HSP90B1,ATP1B3,SLC10A7,HMGB2,RBP4,SELENOT,HMGCR,BAP1,UBE2C,NCOA5,NUCKS1,ETS1,ELOVL6,IQCB1,XBP1,FLVCR1,STRAP,EIF4G1,TFRC,TRA2B,BARD1,CDK16,AIPL1,EIF2AK1,LYAR,FH,RAC1,ADIPOR2,UBE2K,CCNB2,SLC25A5,NNT,LIPG,G6PD,PIK3CD,GCLM,TMOD3,STMN1,UBE2S,HAS2,SLC30A1	darkgrey	VSMC_M8
GO:0055082	1.00	0.00	18	564	cellular chemical homeostasis	BP	1	ATP5F1B,THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,HMGCR,NUCKS1,XBP1,FLVCR1,TFRC,TRA2B,CDK16,RAC1,GCLM,SLC30A1	darkgrey	VSMC_M8
GO:0061564	1.00	0.00	9	380	axon development	BP	1	HSP90AB1,B3GNT2,PAK2,EPHB2,RAC1,UCHL1,EFNB1,FAM129B,STMN1	darkgrey	VSMC_M8
GO:0030001	1.00	0.00	19	587	metal ion transport	BP	1	THADA,SLC31A1,SEC61A1,GRIN2C,KCNN4,SLC5A6,KCNK6,SLC20A1,ATP1B3,SLC10A7,NIPA2,RGS9,FLVCR1,TFRC,FKBP4,NEDD4,G6PD,SLC6A17,SLC30A1	darkgrey	VSMC_M8
GO:0051239	1.00	0.00	100	1937	regulation of multicellular organismal process	BP	1	ALPK2,ATP5F1B,DDX39B,FBXO5,EZR,FBN2,PANX2,NUS1,FAM49B,HSPA9,POLR3B,CYP51A1,HSP90AB1,HOXA5,MFSD2A,EZH2,PRMT1,NRDC,MAST2,PRCP,AXL,SPHK1,WDR43,PARP2,POLR3F,EIF4A3,NAP1L1,PGAM5,ZNF703,HGF,CCNB1,SNAI2,E2F1,VAMP8,HMGB2,RBP4,RACGAP1,LOXL3,HEY1,RBM19,TBX3,CREB3L1,TOMM70,MTDH,HMGCR,BAP1,CHUK,RUNX1,SETD4,ETS1,TRAIP,KIF14,PRMT5,ASPM,ELOVL6,MNDA,XBP1,UTP25,NF2,FLVCR1,PDE3A,CDK1,TFRC,DHX9,POLA1,DDX21,EPHB2,ETV4,UFD1,BRCA1,TFPI,NSD2,DHX33,SIX4,FH,RAC1,ADIPOR2,PDPN,ARG2,PRELID1,IQGAP3,HOXB7,LMNA,ALOX15B,COL1A1,PPIB,EMP2,LIPG,TP73,G6PD,PIK3CD,FANCA,BCAR1,FAM129B,CBFB,SRRT,ARF6,GBP5,HAS2,CLSTN3	darkgrey	VSMC_M8
GO:0030003	1.00	0.00	11	434	cellular cation homeostasis	BP	1	ATP5F1B,THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,FLVCR1,TFRC,SLC30A1	darkgrey	VSMC_M8
GO:0072507	1.00	0.00	6	323	divalent inorganic cation homeostasis	BP	1	THADA,GRIN2C,HSP90B1,SLC10A7,SELENOT,SLC30A1	darkgrey	VSMC_M8
GO:0044057	1.00	0.00	9	398	regulation of system process	BP	1	DDX39B,SPHK1,PARP2,EIF4A3,HGF,HMGCR,LMNA,EMP2,G6PD	darkgrey	VSMC_M8
GO:0030182	1.00	0.00	45	1067	neuron differentiation	BP	1	TTLL1,HSP90AB1,MFSD2A,B3GNT2,EZH2,PRMT1,RNF157,XRN2,ULK4,CDC20,STRN,HGF,KIF20B,WEE1,ATF1,HEY1,RUNX1,MANF,ASPM,XBP1,STRAP,EIF4G1,PAK2,EPHB2,CDK16,ECT2,FKBP4,MAPK6,RAC1,UCHL1,NEDD4,UGDH,EFNB1,SPAG9,SYT4,ACSL4,SF3A2,TP73,TOR1A,FAM129B,ARF6,ACSL3,STMN1,AURKA,BLOC1S2	darkgrey	VSMC_M8
GO:0006873	1.00	0.00	11	444	cellular ion homeostasis	BP	1	ATP5F1B,THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,FLVCR1,TFRC,SLC30A1	darkgrey	VSMC_M8

GO:0007165	1.00	0.00	234	3919	signal transduction	BP	1	CDK2,ALPK2,BCLAF1,DDX39B,EZR,FBN2,GTSE1,NUS1,FAM49B,RANGAP1,SRPK1,HMGXB4,PPP2R5D,PWP1,VCP,HSP90AB1,CDC5L,COL1A2,MIOS,MELK,TRIM28,MSH6,TTK,CLEC11A,EZH2,NUP62,CLSPN,PRMT1,CASP2,SHCBP1,ORC1,GEN1,SDC1,RUVBL2,PGR,NAMPT,STIL,RUVBL1,CCNA2,AMOTL1,RNASEH2B,PPP5C,MASTL,MAST2,CD3EAP,CDC42EP4,GRIN2C,PRCP,KCNN4,PLAUR,AXL,RNF157,SPHK1,FANCD2,ULK4,NCAPG2,GDI2,NET1,PARP2,EIF4A3,CHMP6,E2F7,DOCK9,ARHGDIA,STRN,SIPA1L3,CHFR,ZNF703,HGF,TOPBP1,ELK3,RRP8,CCNB1,SNAI2,CD44,BUB1,DEPDC1B,SLC20A1,PSD4,SGK3,CENPJ,EIF2B1,E2F1,CCNE1,KNTC1,HMGB2,CEP55,HELLS,ARHGAP11A,RACGAP1,LOXL3,PBK,HEY1,BUB1B,FAM83D,NUP93,CREB3L1,TRIM33,MTDH,YWHAB,HMGCR,NRAS,EEF1E1,CHUK,PPP1R15B,MDM4,PAK1IP1,NCOA5,CIT,NUCKS1,DEK,MANF,NSUN2,CHEK1,RASSF1,KHDRBS1,TRIP13,TRAIP,KIF14,RGS9,PRMT5,ASPM,EFS,RAD9A,MNDA,DDX5,PHACTR4,XBP1,TICRR,RPA2,PRKAR2A,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,CDC42SE1,RBM14,CENPF,STRAP,BUB3,ARFGAP1,CDK1,S100A11,TFRC,PAK2,SMARCC1,WDR76,DNA2,ZW10,DDX21,RANBP1,PPP2R1B,IFT80,EPHB2,CDC45,UFD1,BRCA1,CNOT9,PDAP1,MYBBP1A,ECT2,AIPL1,ZWINT,DHX33,MAPK6,FOXM1,MSX1,RAC1,UCHL1,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,BID,PDPN,EIF2S1,PRELID1,IQGAP3,EFNB1,HDGF,LMNA,ALOX15B,LTBP2,MAZ,SPDL1,AURKB,COL1A1,LRRC59,SPAG9,ZWILCH,PLK1,BRIP1,DNMT1,DRG2,SLC25A5,NDC80,COPS3,AIFM1,RAP2C,EMP2,NXN,TFAP4,NOC2L,HASPIN,TP73,PTBP1,PIK3CD,FANCA,CDT1,PKN3,BCAR1,GCLM,FAM129B,NEK6,RANBP10,PLEKHG4,CTH,DEPDC1,ARF6,RAPG	darkgrey	VSMC_M8
GO:0048667	1.00	0.00	11	446	cell morphogenesis involved in neuron differentiation	BP	1	HSP90AB1,MFSD2A,B3GNT2,PAK2,EPHB2,RAC1,UCHL1,NEDD4,EFNB1,FAM129B,STMN1	darkgrey	VSMC_M8
GO:0055080	1.00	0.00	13	494	cation homeostasis	BP	1	ATP5F1B,STEAP1,THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,FLVCR1,TFRC,EIF2AK1,SLC30A1	darkgrey	VSMC_M8
GO:0055085	1.00	0.00	42	1047	transmembrane transport	BP	1	ATP5F1B,PANX2,SLC35D2,CYC1,STEAP1,THADA,MFSD2A,SLC31A1,GJB3,SEC61A1,SLC1A5,CHCHD4,GRIN2C,TOMM40,KCNN4,SLC25A19,SLC5A6,KCNK6,SLC20A1,ATP1B3,SLC10A7,TRAM1,TOMM70,NIPA2,SFXN3,RGS9,SFXN4,FLVCR1,SLC17A9,EPHB2,SLC35F2,SLC19A2,ADIPOR2,NEDD4,TIMM44,SLC25A5,NNT,AIFM1,G6PD,SLC6A17,PID1,SLC30A1	darkgrey	VSMC_M8
GO:0044255	1.00	0.00	25	743	cellular lipid metabolic process	BP	1	NUS1,MFSD2A,ALG8,DBI,SPHK1,PGS1,PCCA,CRYL1,RBP4,AGPAT5,HMGCR,ELOVL6,XBP1,AGPS,GK,BRCA1,ADIPOR2,ALOX15B,ACSL4,ALDH3A2,LIPG,PIK3CD,DOLPP1,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0048878	1.00	0.00	30	832	chemical homeostasis	BP	1	ATP5F1B,NUS1,STEAP1,THADA,POLD1,SLC31A1,GRIN2C,PRCP,HSP90B1,ATP1B3,SLC10A7,RBP4,SELENOT,HMGCR,NCOA5,NUCKS1,XBP1,FLVCR1,TFRC,TRA2B,CDK16,EIF2AK1,RAC1,ADIPOR2,NNT,LIPG,GCLM,STMN1,HAS2,SLC30A1	darkgrey	VSMC_M8
GO:0050877	1.00	0.00	22	678	nervous system process	BP	1	MFSD2A,B3GNT2,GRIN2C,BIRC5,EIF4A3,HGF,SNAI2,AAAS,WDR36,PPIP5K2,RBP4,HMGCR,CHUK,NAV2,RGS9,FOSL1,EPHB2,AIPL1,UCHL1,COL1A1,NOB1,FEN1	darkgrey	VSMC_M8
GO:0098771	1.00	0.00	13	502	inorganic ion homeostasis	BP	1	ATP5F1B,STEAP1,THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,FLVCR1,TFRC,EIF2AK1,SLC30A1	darkgrey	VSMC_M8
GO:0034220	1.00	0.00	26	765	ion transmembrane transport	BP	1	ATP5F1B,SLC35D2,CYC1,THADA,SLC31A1,SEC61A1,SLC1A5,GRIN2C,KCNN4,SLC25A19,SLC5A6,KCNK6,SLC20A1,ATP1B3,NIPA2,SFXN3,RGS9,SFXN4,EPHB2,SLC19A2,NEDD4,SLC25A5,NNT,G6PD,SLC6A17,SLC30A1	darkgrey	VSMC_M8
GO:0000904	1.00	0.00	16	562	cell morphogenesis involved in differentiation	BP	1	HSP90AB1,MFSD2A,B3GNT2,AXL,SIPA1L3,KIF14,PAK2,EPHB2,RAC1,UCHL1,NEDD4,PDPN,EFNB1,FAM129B,STMN1,HAS2	darkgrey	VSMC_M8
GO:0065008	1.00	0.00	151	2770	regulation of biological quality	BP	1	ATP5F1B,CCT2,TUBB,VARS2,VARS,EZR,TCP1,NUS1,FAM49B,HSPA9,APTX,STEAP1,TJP2,VCP,HSP90AB1,COL1A2,THADA,POLD1,HOXA5,MFSD2A,SYNCRIP,PABPC4,CCT4,SLC31A1,YRDC,THRAP3,EZH2,PRMT1,NAA15,NRDC,NAMPT,DNAJC2,CDC42EP4,COG3,GRIN2C,PRCP,KCNN4,PLAUR,CAD,DIS3,AXL,NCAPG2,CDC20,GTPBP4,EIF4A3,ARHGDIA,KCNK6,CHFR,EXOSC8,PGAM5,HSP90B1,E2F1,VAMP8,ATP1B3,SLC10A7,HMGB2,RBP4,SELENOT,FMNL3,CCT8,CCT7,TBX3,HMGCR,BAP1,MDM4,UBE2C,NAV2,NCOA5,CCT5,FASTKD3,CCT6A,NUCKS1,ETS1,METAP1,TENT4A,NSUN2,ELOVL6,IQCB1,XBP1,UTP25,NF2,FLVCR1,PDE3A,CDC42SE1,UMPS,STRAP,EIF4G1,TFRC,DHX9,HNRNPR,NDUFS1,TRA2B,BARD1,EPHB2,TFPI,CDK16,AIPL1,SIX4,EIF2AK1,LYAR,FH,MSX1,RAC1,HNRNPU,RAB27A,ADIPOR2,UBE2K,NEDD4,BID,PDPN,PRELID1,CCNB2,IQGAP3,CCT3,FUS,LMNA,PPIB,RAD23A,PLK1,SYT4,ACSL4,ZSWIM7,TAF15,SLC25A5,HNRNPM,SERBP1,NNT,EMP2,LIPG,G6PD,DKC1,PIK3CD,ZC3H18,EXOSC2,TOR1A,GCLM,FAM129B,ARPC4,ARF6,USP4,TMOD3,HNRNPD,STMN1,AURKA,UBE2S,HAS2,BLOC1S2,XKR5,PID1,CLSTN3,SLC30A1	darkgrey	VSMC_M8
GO:0050801	1.00	0.00	14	542	ion homeostasis	BP	1	ATP5F1B,STEAP1,THADA,SLC31A1,GRIN2C,HSP90B1,ATP1B3,SLC10A7,SELENOT,FLVCR1,TFRC,EIF2AK1,GCLM,SLC30A1	darkgrey	VSMC_M8
GO:0006811	1.00	0.00	39	1026	ion transport	BP	1	ATP5F1B,PANX2,SLC35D2,CYC1,STEAP1,THADA,MFSD2A,SLC31A1,SEC61A1,SLC1A5,GRIN2C,TOMM40,KCNN4,SLC25A19,SLC5A6,KCNK6,SLC20A1,VAMP8,ATP1B3,SLC10A7,RACGAP1,NIPA2,SFXN3,RGS9,SFXN4,FLVCR1,SLC17A9,TFRC,EPHB2,SLC19A2,FKBP4,NEDD4,SYT4,SLC25A5,NNT,G6PD,SLC6A17,TOR1A,SLC30A1	darkgrey	VSMC_M8

GO:0007154	1.00	0.00	256	4300	cell communication	BP	1	CDK2,ALPK2,BCLAF1,DDX39B,EZR,FBN2,PANX2,GTSE1,NUS1,FAM49B,RANGAP1,SRPK1,HMGXB4,PPP2R5D,PWP1,VCP,HSP90AB1,CDC5L,COL1A2,MIOS,MELK,TRIM28,MSH6,TTK,CLEC11A,HOXA5,MFSD2A,EZH2,NUP62,CLSPN,PRMT1,GJB3,CASP2,SHCBP1,ORC1,GEN1,SDC1,RUVBL2,PGR,NAMPT,STIL,RUVBL1,CCNA2,AMOTL1,RNASEH2B,PPP5C,MASTL,MAST2,CD3EAP,CDC42EP4,GRIN2C,PRCP,KCNN4,PLAUR,AXL,RNF157,SPHK1,FANCD2,ULK4,NCAPG2,GDI2,NET1,CDC20,PARP2,EIF4A3,CHMP6,E2F7,DOCK9,ARHGDIA,STRN,SIPA1L3,CHFR,ZNF703,HGF,TOPBP1,ELK3,RRP8,CCNB1,SNAI2,CD44,BUB1,DEPDC1B,SLC20A1,PSD4,SGK3,CENPJ,EIF2B1,E2F1,CEP89,CCNE1,VAMP8,KNTC1,HMGB2,CEP55,RBP4,HELLS,ARHGAP11A,RACGAP1,LOXL3,PBK,HEY1,SELENOT,BUB1B,FAM83D,NUP93,TBX3,CREB3L1,TRIM33,MTDH,YWHAB,HMGCR,OIP5,NRAS,EEF1E1,CHUK,PPP1R15B,MDM4,PAK1IP1,NCOA5,CIT,NUCKS1,DEK,GCN1,MANF,NSUN2,CHEK1,RASSF1,KHDRBS1,TRIP13,TRAIP,KIF14,RGS9,PRMT5,ASPM,EFS,RAD9A,MNDA,DDX5,PHACTR4,XBP1,TICRR,RPA2,PRKAR2A,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,CDC42SE1,RBM14,CENPF,STRAP,EIF4G1,BUB3,ARFGAP1,CDK1,S100A11,TFRC,PAK2,FOSL1,SMARCC1,WDR76,DNA2,ZW10,DDX21,RANBP1,PPP2R1B,IFT80,EPHB2,CDC45,UFD1,BRCA1,CNOT9,CDK16,PDAP1,MYBBP1A,ECT2,AIPL1,ZWINT,DHX33,MAPK6,FOXM1,MSX1,RAC1,UCHL1,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,BID,PDPN,EIF2S1,NUDT1,PRELID1,DCTPP1,IQGAP3,EFNB1,HDGF,LMNA,ALOX15B,LTBP2,MAZ,SPDL1,AURKB,COL1A1,LRRC59,SPAG9,ZWILCH,PLK1,SYT4,BRIP1,DNMT1,ACSL4,DRG2,SLC25A5,NDC80,COPS3,AIFM1,RAP2C,EMP2,NXN,T	darkgrey	VSMC_M8
GO:0016192	1.00	0.00	48	1192	vesicle-mediated transport	BP	1	TMED9,EZR,ARFGAP3,HMGXB4,VCP,MFSD2A,NBAS,SDC1,COG3,PREB,AXL,RNF157,SPHK1,GDI2,SEC23B,CHMP6,VAMP8,SLC10A7,LOXL3,TXLNA,PITPNB,SEC24D,CDC42SE1,ARCN1,SLC17A9,ARFGAP1,TFRC,ZW10,CDK16,EIF2AK1,LYAR,RAC1,KDELR2,MYO5A,RAB27A,NEDD4,SPAG9,SYT4,HOOK1,EMP2,PIK3CD,TOR1A,LY75,ARF6,ACSL3,BLOC1S2,STXBP6,XKR5	darkgrey	VSMC_M8
GO:0003008	1.00	0.00	51	1240	system process	BP	1	DDX39B,EZR,TTLL1,TJP2,COL1A2,HOXA5,MFSD2A,B3GNT2,EZH2,NAMPT,SLC1A5,GRIN2C,PRCP,KCNN4,SLC5A6,SPHK1,BIRC5,PARP2,EIF4A3,KCNK6,HGF,SNAI2,AAAS,WDR36,PPIP5K2,RBP4,TBX3,HMGCR,CHUK,NAV2,RGS9,PDE3A,STRAP,TFRC,FOSL1,EPHB2,AIPL1,UCHL1,ARG2,LMNA,COL1A1,TPM3,EMP2,G6PD,SLC6A17,GCLM,FAM129B,NOB1,TMOD3,HAS2,FEN1	darkgrey	VSMC_M8
GO:0022610	1.00	0.00	40	1050	biological adhesion	BP	1	EZR,FAM49B,TJP2,HSP90AB1,PLAUR,AXL,GTPBP4,ARHGDIA,ZNF703,SNAI2,CD44,LOXL3,TROAP,RUNX1,ETS1,METAP1,KIF14,EFS,XBP1,NF2,S100A11,TFRC,PNN,EPHB2,DPT,RAC1,PDPN,ARG2,EFNB1,COL1A1,POLDIP2,EMP2,TOR1A,BCAR1,CBFB,ARF6,TMOD3,HAS2,STXBP6,CLSTN3	darkgrey	VSMC_M8
GO:0007268	1.00	0.00	10	471	chemical synaptic transmission	BP	1	EZH2,GRIN2C,CDC20,EIF4A3,CEP89,EPHB2,SYT4,TOR1A,CLSTN3,SLC30A1	darkgrey	VSMC_M8
GO:0098916	1.00	0.00	10	471	anterograde trans-synaptic signaling	BP	1	EZH2,GRIN2C,CDC20,EIF4A3,CEP89,EPHB2,SYT4,TOR1A,CLSTN3,SLC30A1	darkgrey	VSMC_M8
GO:0023052	1.00	0.00	250	4258	signaling	BP	1	CDK2,ALPK2,BCLAF1,DDX39B,EZR,FBN2,PANX2,GTSE1,NUS1,FAM49B,RANGAP1,SRPK1,HMGXB4,PPP2R5D,PWP1,VCP,HSP90AB1,CDC5L,COL1A2,MIOS,MELK,TRIM28,MSH6,TTK,CLEC11A,HOXA5,EZH2,NUP62,CLSPN,PRMT1,GJB3,CASP2,SHCBP1,ORC1,GEN1,SDC1,RUVBL2,PGR,NAMPT,STIL,RUVBL1,CCNA2,AMOTL1,RNASEH2B,PPP5C,MASTL,MAST2,CD3EAP,CDC42EP4,GRIN2C,PRCP,KCNN4,PLAUR,AXL,RNF157,SPHK1,FANCD2,ULK4,NCAPG2,GDI2,NET1,CDC20,PARP2,EIF4A3,CHMP6,E2F7,DOCK9,ARHGDIA,STRN,SIPA1L3,CHFR,ZNF703,HGF,TOPBP1,ELK3,RRP8,CCNB1,SNAI2,CD44,BUB1,DEPDC1B,SLC20A1,PSD4,SGK3,CENPJ,EIF2B1,E2F1,CEP89,CCNE1,VAMP8,KNTC1,HMGB2,CEP55,RBP4,HELLS,ARHGAP11A,RACGAP1,LOXL3,PBK,HEY1,SELENOT,BUB1B,FAM83D,NUP93,TBX3,CREB3L1,TRIM33,MTDH,YWHAB,HMGCR,NRAS,EEF1E1,CHUK,PPP1R15B,MDM4,PAK1IP1,NCOA5,CIT,NUCKS1,DEK,MANF,NSUN2,CHEK1,RASSF1,KHDRBS1,TRIP13,TRAIP,KIF14,RGS9,PRMT5,ASPM,EFS,RAD9A,MNDA,DDX5,PHACTR4,XBP1,TICRR,RPA2,PRKAR2A,INTS7,HINFP,DTL,NF2,H2AFX,BLM,PDE3A,CDC42SE1,RBM14,CENPF,STRAP,BUB3,ARFGAP1,CDK1,S100A11,TFRC,PAK2,SMARCC1,WDR76,DNA2,ZW10,DDX21,RANBP1,PPP2R1B,IFT80,EPHB2,CDC45,UFD1,BRCA1,CNOT9,CDK16,DLGAP5,PDAP1,MYBBP1A,ECT2,AIPL1,ZWINT,DHX33,MAPK6,FOXM1,MSX1,RAC1,UCHL1,ADIPOR2,UBE2K,NEDD4,CDC6,EIF5A,BID,PDPN,EIF2S1,PRELID1,IQGAP3,EFNB1,HDGF,LMNA,ALOX15B,LTBP2,MAZ,SPDL1,AURKB,COL1A1,LRRC59,SPAG9,ZWILCH,PLK1,SYT4,BRIP1,DNMT1,ACSL4,DRG2,SLC25A5,NDC80,COPS3,AIFM1,RAP2C,EMP2,NXN,TFAP4,NOC2L,HASPIN,TP73,PTBP1,PIK3CD,FA	darkgrey	VSMC_M8
GO:0007155	1.00	0.00	39	1044	cell adhesion	BP	1	EZR,FAM49B,TJP2,PLAUR,AXL,GTPBP4,ARHGDIA,ZNF703,SNAI2,CD44,LOXL3,TROAP,RUNX1,ETS1,METAP1,KIF14,EFS,XBP1,NF2,S100A11,TFRC,PNN,EPHB2,DPT,RAC1,PDPN,ARG2,EFNB1,COL1A1,POLDIP2,EMP2,TOR1A,BCAR1,CBFB,ARF6,TMOD3,HAS2,STXBP6,CLSTN3	darkgrey	VSMC_M8
GO:0099537	1.00	0.00	10	477	trans-synaptic signaling	BP	1	EZH2,GRIN2C,CDC20,EIF4A3,CEP89,EPHB2,SYT4,TOR1A,CLSTN3,SLC30A1	darkgrey	VSMC_M8
GO:0006629	1.00	0.00	34	982	lipid metabolic process	BP	1	NUS1,CYP51A1,MFSD2A,ALG8,DBI,SPHK1,PGS1,PCCA,SNAI2,CRYL1,RBP4,AGPAT5,HMGCR,ELOVL6,PITPNB,XBP1,PDE3A,HDLBP,AGPS,DDX20,GK,SF1,BRCA1,ADIPOR2,LBR,ALOX15B,ACSL4,ALDH3A2,LIPG,G6PD,PIK3CD,DOLPP1,SCD5,ACSL3	darkgrey	VSMC_M8
GO:0099536	1.00	0.00	10	494	synaptic signaling	BP	1	EZH2,GRIN2C,CDC20,EIF4A3,CEP89,EPHB2,SYT4,TOR1A,CLSTN3,SLC30A1	darkgrey	VSMC_M8

GO:0007267	1.00	0.00	43	1146	cell-cell signaling	BP	1	ALPK2,PANX2,HMGXB4,VCP,HOXA5,EZH2,GJB3,SDC1,RUVBL2,PGR,NAMPT,RUVBL1,AMOTL1,GRIN2C,CDC20,EIF4A3,STRN,ZNF703,HGF,SNAI2,DEPDC1B,CEP89,CCNE1,VAMP8,RBP4,SELENOT,TBX3,HMGCR,ASPM,IFT80,EPHB2,CDK16,RAC1,EFNB1,COL1A1,SYT4,ACSL4,NXN,TOR1A,FAM129B,CLSTN3,SLC30A1,MBD2	darkgrey	VSMC_M8
GO:0009653	1.00	0.00	98	2050	anatomical structure morphogenesis	BP	1	ALPK2,ATP5F1B,EZR,FBN2,TTLL1,NUS1,FAM49B,BYSL,HSP90AB1,COL1A2,TRIM28,GRSF1,HOXA5,MFSD2A,B3GNT2,NAA15,SDC1,PGR,STIL,LIG1,AMOTL1,CDC42EP4,PRCP,AXL,RNF157,SPHK1,SERPINH1,EIF4A3,E2F7,ARHGDIA,SIPA1L3,PGAM5,HGF,ELK3,SNAI2,CD44,POLR1B,KIF20B,WEE1,RBP4,HEY1,FMNL3,KNL1,TBX3,CREB3L1,E2F8,MTDH,CHUK,RUNX1,MDM4,HMGN1,NOLC1,ETS1,GMNN,NCL,KIF14,PHACTR4,XBP1,NF2,FLVCR1,CDC42SE1,TFRC,PAK2,SMARCC1,PPP2R1B,IFT80,EPHB2,BRCA1,NSD2,ECT2,SIX4,MSX1,RAC1,UCHL1,ADIPOR2,MTHFD1,NEDD4,UGDH,PDPN,EFNB1,NES,HOXB7,COL1A1,SPAG9,SYT4,POLDIP2,EMP2,PIK3CD,CRISPLD2,TOR1A,FAM129B,ACD,TMOD3,STMN1,AURKA,HAS2,PID1,PALB2	darkgrey	VSMC_M8
GO:0007166	1.00	0.00	88	1935	cell surface receptor signaling pathway	BP	1	ALPK2,EZR,FBN2,NUS1,HMGXB4,PWP1,VCP,HSP90AB1,COL1A2,TTK,NUP62,PRMT1,CASP2,SHCBP1,SDC1,RUVBL2,STIL,RUVBL1,AMOTL1,CD3EAP,GRIN2C,KCNN4,PLAUR,AXL,SPHK1,PARP2,EIF4A3,CHMP6,ARHGDIA,STRN,ZNF703,HGF,SNAI2,CD44,DEPDC1B,CENPJ,EIF2B1,CCNE1,HMGB2,LOXL3,HEY1,NUP93,CREB3L1,TRIM33,MTDH,CHUK,NCOA5,NUCKS1,KHDRBS1,TRAIP,ASPM,EFS,MNDA,DDX5,PHACTR4,NF2,RBM14,STRAP,PAK2,SMARCC1,PPP2R1B,IFT80,EPHB2,BRCA1,CNOT9,MSX1,RAC1,ADIPOR2,UBE2K,NEDD4,EIF5A,BID,EFNB1,LMNA,LTBP2,COL1A1,EMP2,NXN,PIK3CD,FANCA,BCAR1,GCLM,FAM129B,RANBP10,STMN1,BLOC1S2,PID1,MBD2	darkgrey	VSMC_M8
GO:0032501	0.00	1.00	435	5003	multicellular organismal process	BP	6.2E-05	CTDP1,TSHZ1,MMP19,MYL6B,STAT6,TCF21,ADAMTS2,AKAP12,FLOT1,EHMT2,PLXNB2,ZFPM2,RPS6KA2,IRF1,CYB5R3,FBXO32,TGFBI,PTPRK,ST3GAL1,GSDMD,TEAD3,NPTXR,MTCH1,TLE1,CARD10,NFIB,GCNT1,HMOX1,LRRC19,MEA1,ACO1,KIAA1324L,TRPM3,APPL2,PLA2G7,MLIP,IARS,ZBTB45,ITGB8,P3H1,GPNMB,SLC44A1,EFEMP1,TRIL,BBS9,MEIS1,STK40,COBL,GLI3,SIM1,AP2A1,IRF3,RRAS,FLT3LG,GSN,SLC17A7,NRP1,KLF15,RHOB,BAX,DBP,MEIS3,LRRC17,LURAP1,FZD4,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,SLC6A9,COQ8B,LTBP4,SLITRK6,SOCS3,CAMK1,EHD3,PLD3,PNP,DZIP1,TPPP2,RPS16,TIMP2,ZFP36,GAA,PAK4,RNF213,NPTX1,GPAT4,FOLR2,HGS,KAT2B,RFTN1,RHOG,RFNG,CATSPERG,FGFR1,IL5RA,EFNB2,TRIM21,POC1B,EPYC,RAB11FIP1,ADGRA2,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,HSPB6,PRICKLE2,SLC15A4,ANGPT4,SLC7A2,RARG,SCN1B,IGF1,CYP4V2,TLR3,SNTA1,MAN2A1,WT1,EFNA5,RHPN2,CHMP4B,TP53INP2,TSHZ3,GGT7,GGCX,POU6F1,SERPING1,CTSB,ARRDC3,PLSCR1,HEXB,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,DECR1,PLCG1,ZHX3,BBS2,FOXF2,GNAO1,SFRP5,PDLIM2,NISCH,MMP2,EXT2,SLC5A3,LZTS2,STAT1,PHACTR1,HPS6,GFRA2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,CAPN3,TJP1,TIRAP,AGFG1,CTTN,PCSK6,BOC,CSTB,TUSC2,TPCN2,SEMA3B,NFKB1,GNAI2,SPOCD1,ADGRB2,TPPP,LGALS8,RGMA,BCL9,LRP10,HADH,IP6K1,LEF1,STS,DISP1,PTGIS,B4GALT5,SOX5,RLBP1,ATRNL1,LAMB2,APH1A,MN1,VEGFD,ECM1,REC8,SEMA4B,CTSK,RHBDD3,NCKIPSD,ADCY1,FES,PRUNE1,FURIN,BCL9L,SEMA6C,TACC2,HEG1,VANGL2,GATA5,KIF1A,CLCN2,STK25,FIBP,CTNNA3	cyan	VSMC_M2
GO:0051239	0.00	1.00	197	1937	regulation of multicellular organismal process	BP	8.5E-05	CTDP1,STAT6,AKAP12,FLOT1,PLXNB2,ZFPM2,IRF1,FBXO32,GSDMD,NPTXR,CARD10,NFIB,HMOX1,LRRC19,KIAA1324L,APPL2,MLIP,ITGB8,GPNMB,EFEMP1,TRIL,MEIS1,GLI3,IRF3,RRAS,NRP1,RHOB,LRRC17,LURAP1,TMEM176B,BIN1,APOE,BCL3,ATRAID,SLITRK6,EHD3,PLD3,PNP,ZFP36,GAA,PAK4,NPTX1,GPAT4,HGS,RFTN1,FGFR1,IL5RA,EFNB2,TRIM21,RAB11FIP1,ADGRA2,TMEM108,PKDCC,HSPB6,ANGPT4,RARG,SCN1B,IGF1,TLR3,SNTA1,MAN2A1,WT1,TSHZ3,SERPING1,ARRDC3,SFRP2,WWTR1,PRKCD,SRC,CACNB3,TGM2,BPI,LRP4,DECR1,PLCG1,BBS2,GNAO1,SLC5A3,STAT1,CD81,CHRNA7,CAPN3,TJP1,TIRAP,CTTN,TUSC2,SEMA3B,NFKB1,GNAI2,ADGRB2,TPPP,RGMA,HADH,IP6K1,LEF1,PTGIS,B4GALT5,SOX5,VEGFD,ECM1,SEMA4B,CTSK,FES,PRUNE1,FURIN,BCL9L,SEMA6C,HEG1,GATA5,STK25,CTNNA3,ELL3,NFKBIA,LTBP3,LINC02210-CRHR1,FRMD8,B2M,WNT2B,KCND3,ADORA2A,ADAMTS7,GRN,HDAC5,HOMER3,VEGFB,TMEM106A,RND2,TMBIM1,WNK4,ADD1,BMP4,RARRES3,STAT5A,DLG5,HDAC6,PQBP1,DHX58,ARRB2,JUP,EPHA2,MYRF,IL17RA,SERPINE2,MCC,ERBB2,PRKACA,ZFP36L1,IL27RA,NTRK1,SLIT2,AR,TP53,GBA,NUPR1,ACP5,SIGLEC15,WARS,GPRC5B,EPN2,TMEM98,MAP2K3,PTPRS,SH3GL1,CPT2,ABCD1,DVL1,ASPA,AGRN,ISG15,TNFRSF14,PTGDS,RAB11FIP3,CLSTN1,FOXC2,ABL1,IL34,PBX3,IST1,LCAT,MIR197,OAS2,SLC8A3,SERPINF1,CD55,PML,RPS19,PLPP3,GATA4,CALM3,CARD8,CLIC2,CDK9,NFKBIL1,RNLS,BST2,TMEM176A,ZFPM1	cyan	VSMC_M2

GO:0035295	0.00	1.00	98	849	tube development	BP	0.00063	MMP19,TCF21,ADAMTS2,PLXNB2,ZFPM2,TGFBI,CARD10,NFIB,HMOX1,ITGB8,GPNMB,MEIS1,STK40,COBL,GLI3,RRAS,NRP1,RHOB,BAX,FZD4,APOE,PAK4,RNF213,HGS,EFNB2,ADGRA2,PKDCC,HSPB6,ANGPT4,RARG,TLR3,MAN2A1,WT1,SFRP2,WWTR1,NDRG4,SRC,TGM2,PLCG1,FOXF2,SFRP5,MMP2,LZTS2,STAT1,CHRNA7,TJP1,ADGRB2,RGMA,LEF1,PTGIS,VEGFD,ECM1,REC8,HEG1,VANGL2,GATA5,PHEX,LTBP3,WNT2B,PLCD3,GRN,HDAC5,ACAT1,VEGFB,WNK4,BMP4,CC2D2A,DLG5,FKBP10,JUP,EPHA2,SERPINE2,ERBB2,PRKACA,ZFP36L1,SLIT2,AR,MED12,ADAM15,SHC1,WARS,EPN2,PDGFRB,TRAF4,DVL1,TSC2,NPRL3,FOXC2,ABL1,DNAAF1,SERPINF1,PML,JUNB,GATA4,SAT1,SDC4,COL8A1,EN1	cyan	VSMC_M2
GO:0048731	0.00	1.00	315	3556	system development	BP	0.00063	CTDP1,TSHZ1,MMP19,MYL6B,STAT6,TCF21,ADAMTS2,FLOT1,EHMT2,PLXNB2,ZFPM2,RPS6KA2,IRF1,TGFBI,PTPRK,ST3GAL1,TEAD3,MTCH1,TLE1,CARD10,NFIB,GCNT1,HMOX1,MEA1,KIAA1324L,APPL2,ZBTB45,ITGB8,P3H1,GPNMB,EFEMP1,MEIS1,STK40,COBL,GLI3,SIM1,AP2A1,RRAS,FLT3LG,GSN,SLC17A7,NRP1,KLF15,RHOB,BAX,DBP,MEIS3,LRRC17,FZD4,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,COQ8B,SLITRK6,SOCS3,CAMK1,PNP,RPS16,TIMP2,ZFP36,GAA,PAK4,RNF213,NPTX1,GPAT4,HGS,KAT2B,RHOG,RFNG,FGFR1,EFNB2,EPYC,ADGRA2,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,HSPB6,PRICKLE2,SLC15A4,ANGPT4,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,POU6F1,CTSB,ARRDC3,HEXB,SFRP2,WWTR1,NDRG4,GLRB,EPHA3,SRC,CPE,TGM2,LRP4,PLCG1,BBS2,FOXF2,GNAO1,SFRP5,PDLIM2,MMP2,EXT2,SLC5A3,LZTS2,STAT1,PHACTR1,GFRA2,CD81,NDN,SLC45A3,CHRNA7,CAPN3,TJP1,TIRAP,CTTN,BOC,TUSC2,SEMA3B,ADGRB2,TPPP,LGALS8,RGMA,BCL9,LRP10,LEF1,DISP1,PTGIS,B4GALT5,SOX5,ATRNL1,LAMB2,APH1A,VEGFD,ECM1,REC8,SEMA4B,CTSK,RHBDD3,NCKIPSD,ADCY1,FES,PRUNE1,BCL9L,SEMA6C,TACC2,HEG1,VANGL2,GATA5,KIF1A,CLCN2,STK25,PHEX,ARPC5,ELL3,PTCHD1,NFKBIA,MOV10,LTBP3,B2M,WNT2B,DPF2,ARHGEF10,BCR,ADORA2A,CAPN1,PLCD3,CLEC3B,CCDC141,ADAMTS7,GRN,ASTN1,HDAC5,PSAP,GPC2,ACAT1,VEGFB,RND2,WNK4,DGCR2,BMP4,NAGLU,MAEA,RARRES3,QDPR,LDB2,NBL1,MAP1S,CC2D2A,STAT5A,NR2F6,DLG5,CPAMD8,HDAC6,TMEM223,PQBP1,DNAJB6,FKBP10,ARRB2,JUP,ALOX15,EPHA2,MYRF,DAGLA,TCF12,SERPINE2,CASP9,KAZN,ERBB2,PRKACA,ZFP36L1,IL27RA,NTRK1,PCGF2,	cyan	VSMC_M2
GO:0009605	0.00	1.00	177	1770	response to external stimulus	BP	0.00063	ULBP2,AKAP12,EHMT2,PLXNB2,CFB,IRF1,GSDMD,NFIB,HMOX1,LRRC19,CNPY3,TRPM3,APPL2,PLA2G7,TRIM14,ITGB8,GPNMB,BCKDHB,TRIL,RRAGC,COLEC11,GLI3,IRF3,GSN,NRP1,BAX,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,RHBDF2,SLITRK6,SOCS3,ZFP36,FOLR2,TBC1D5,RHOG,FGFR1,EFNB2,TRIM21,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,WDFY4,SLC15A4,SCN1B,IGF1,TLR3,EFNA5,GGT7,SERPING1,PLSCR1,SFRP2,GLRB,PRKCD,EPHA3,SRC,CACNB3,TGM2,BPI,PLCG1,BBS2,STAT1,CD81,TRIM8,IKBKE,CAPN3,TIRAP,BOC,TUSC2,SEMA3B,NFKB1,GNAI2,LGALS8,RGMA,LEF1,PTGIS,LAMB2,MN1,VEGFD,SEMA4B,RHBDD3,GAS2L1,FES,FURIN,SEMA6C,RNASEL,PHEX,NFKBIA,MOV10,B2M,WNT2B,ADORA2A,GRN,C1R,C1S,ACAT1,VEGFB,TMEM106A,BMP4,NBL1,NR2F6,PQBP1,DHX58,WDR45,ARRB2,JUP,ALOX15,EPHA2,DAGLA,IL17RA,GABARAP,PLEKHM2,SERPINE2,CASP9,PLSCR3,VWCE,ERBB2,IL27RA,NTRK1,CLCN6,SLIT2,TP53,HSD3B7,NPC2,PDK2,GBA,PPP1R9B,ADAM15,NUPR1,SHC1,ADAR,ACP5,KANK2,NEO1,GPRC5B,ABCC1,PDGFRB,MTA1,C6,PIEZO2,PTPRS,EEF2,DVL1,ISG15,TNFRSF14,TSC2,NDOR1,SBNO2,FAM3A,NPRL3,RNF166,ABL1,IL34,GBP6,OAS2,HEXIM1,SERPINF1,CD55,TRIM26,RAB43,NMT2,PML,RPS19,GATA4,CARD8,VPS26B,STX3,NFKBIL1,IL22RA1,OCIAD2,BST2	cyan	VSMC_M2
GO:0065007	0.00	1.00	663	8375	biological regulation	BP	0.00063	CTDP1,TSHZ1,ZADH2,PYM1,RAB5B,STAT6,MOXD1,TCF21,ARHGEF25,OS9,AKAP12,FLOT1,DDAH2,PPP6R2,EHMT2,PLXNB2,ZFPM2,CFB,TBC1D22A,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,TAPBP,TCF20,DAXX,FBXO32,TGFBI,TEF,PTPRK,ARHGAP18,ST3GAL1,CDC14C,GSDMD,TEAD3,NPTXR,MTCH1,GRINA,TLE1,GGA1,CARD10,KCTD17,NFIB,TRERF1,ARHGAP39,HMOX1,LRRC19,ACO1,KIAA1324L,CUL9,KLF9,APPL2,ATP10D,HIGD2A,PLA2G7,CARD19,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,TBC1D2,ITGB8,P3H1,NAT14,KCNQ5,GPNMB,EFEMP1,TRIL,RRAGC,EEPD1,MEIS1,COLEC11,ELMO1,RNF144A,STK40,COBL,TBC1D17,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,CADPS2,IRF3,RRAS,FLT3LG,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,HS1BP3,BAX,DBP,HBP1,DENND2A,NOP53,BICRA,MEIS3,LRRC17,LURAP1,TRIM13,TSPAN1,FZD4,CAB39L,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,MIF4GD,AGAP3,ATRAID,SLC6A9,ATG7,EXOC7,CYP2S1,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,PLB1,SLITRK6,SOCS3,CAMK1,EHD3,PLD3,CMTM6,PNP,DZIP1,TPPP2,TIMP2,ZFP36,LGALS3BP,CANT1,SAMD4B,GAA,PAK4,RNF213,ARAP1,NPTX1,GPAT4,SLC4A9,FOLR2,HGS,KAT2B,TBC1D5,PPP1R27,EIF3K,RFTN1,RHOG,ITGBL1,DCXR,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,POC1B,RAB11FIP1,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,MMP17,ADGRD1,CLIP3,HSPB6,PRICKLE2,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,ATP4A,RARG,SCN1B,IGF1,REEP5,TLR3,SNTA1,MAN2A1,WT1,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,TSHZ3,GGT7,GGCX,POU6F1,SERPING1,CAST,EDEM2,CTSB,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR	cyan	VSMC_M2

GO:0006952	0.00	1.00	108	949	defense response	BP	0.00063	STAT6,ULBP2,CFB,IRF1,GSDMD,HMOX1,LRRC19,CNPY3,APPL2,PLA2G7,TRIM14,TRIL,COLEC11,IRF3,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,RHBDF2,IL17RC,SOCS3,PLD3,ZFP36,LGALS3BP,FOLR2,IL5RA,TRIM21,LAMP1,SMPD1,SLC15A4,IGF1,TLR3,SERPING1,PLSCR1,PRKCD,SRC,TGM2,BPI,PLCG1,STAT1,CD81,TRIM8,IKBKE,TIRAP,TUSC2,NFKB1,LGALS8,PTGIS,ECM1,RHBDD3,ADCY1,FES,FURIN,RNASEL,NFKBIA,MOV10,ADORA2A,GRN,C1R,HDAC5,C1S,TMEM106A,STAT5A,PQBP1,DHX58,ARRB2,ALOX15,EPHA2,DAGLA,IL17RA,PLEKHM2,IL27RA,TP53,GBA,ADAM15,NUPR1,SHC1,PBXIP1,ADAR,ACP5,GPRC5B,ABCC1,MAP2K3,C6,ABCD1,ISG15,TNFRSF14,SBNO2,FAM3A,RNF166,IL34,GBP6,MIR197,OAS2,HEXIM1,SERPINF1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,IL22RA1,BST2	cyan	VSMC_M2
GO:0035239	0.00	1.00	84	699	tube morphogenesis	BP	0.00063	MMP19,TCF21,PLXNB2,ZFPM2,TGFBI,CARD10,NFIB,HMOX1,ITGB8,GPNMB,MEIS1,COBL,GLI3,RRAS,NRP1,RHOB,BAX,FZD4,APOE,PAK4,RNF213,HGS,EFNB2,ADGRA2,HSPB6,ANGPT4,RARG,TLR3,WT1,SFRP2,NDRG4,SRC,TGM2,PLCG1,SFRP5,MMP2,LZTS2,STAT1,CHRNA7,TJP1,ADGRB2,RGMA,LEF1,PTGIS,VEGFD,ECM1,HEG1,VANGL2,WNT2B,PLCD3,GRN,HDAC5,VEGFB,WNK4,BMP4,CC2D2A,DLG5,FKBP10,JUP,EPHA2,ERBB2,PRKACA,ZFP36L1,SLIT2,AR,MED12,ADAM15,SHC1,WARS,EPN2,PDGFRB,DVL1,TSC2,NPRL3,FOXC2,ABL1,DNAAF1,SERPINF1,PML,JUNB,GATA4,SAT1,SDC4,COL8A1	cyan	VSMC_M2
GO:0032879	0.00	1.00	200	2074	regulation of localization	BP	0.00063	RAB5B,OS9,AKAP12,FLOT1,PLXNB2,AFDN,PACSIN2,PTPRK,ARHGAP18,CARD10,HMOX1,APPL2,PLA2G7,TRIM14,P3H1,KCNQ5,GPNMB,EEPD1,GLI3,AP2A1,CADPS2,RRAS,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,BAX,FZD4,MARK4,BIN1,APOE,SLC6A9,RHBDF2,CAMK1,EHD3,TPPP2,ZFP36,ARAP1,HGS,TBC1D5,RHOG,FGFR1,TRIM21,RAB11FIP1,ADGRA2,DCLK1,LAMP1,SMPD1,APBB1,PKDCC,CLIP3,ANGPT4,SCN1B,IGF1,REEP5,SNTA1,EFNA5,CHMP3,TP53INP2,EDEM2,PLSCR1,SFRP2,WWTR1,NDRG4,PRKCD,EPHA3,SRC,CACNB3,TGM2,LRP4,PLCG1,BBS2,ARHGAP1,GNAO1,NISCH,SLC5A3,PNPLA2,CRACR2B,LZTS2,PHACTR1,CD81,TRIM8,IKBKE,CAPN3,TJP1,CACNA2D2,TIRAP,TPCN2,SEMA3B,NFKB1,GNAI2,XG,HADH,LEF1,DISP1,SV2A,VEGFD,ECM1,SEMA4B,RHBDD3,ADCY1,FES,FURIN,VPS11,ERFE,SEMA6C,CLCN2,RNASEL,CTNNA3,NFKBIA,FAM89B,LINC02210-CRHR1,B2M,KCND3,ADORA2A,CAPN1,GRN,HDAC5,HOMER3,GPC2,VEGFB,TMBIM1,WNK4,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,B3GAT3,CROCC,DNAJB6,ARRB2,JUP,ALOX15,EPHA2,AKAP5,PLEKHM2,SERPINE2,MCC,GIPC1,ERBB2,PRKACA,ZFP36L1,IL27RA,UBQLN2,MLLT6,SLIT2,AR,CPLX2,PPP1R9B,ADAM15,SLC51B,STON2,SNX33,RASL10B,PDGFRB,MCOLN1,LLGL1,TMEM98,MAP2K3,SH3GL1,PODN,GLIS2,DVL1,TNFRSF14,TSC2,PHPT1,INPP5E,RAB11FIP3,ENTR1,RHBDF1,FOXC2,ABL1,DNAAF1,OSGIN1,IL34,OAS2,ABCA2,GAS1,ZNF205,CBARP,SERPINF1,KCND2,GRASP,PML,RPS19,PLPP3,GATA4,CALM3,CLIC2,CLIC3,SDC4,STX3,BST2,RAB11B,EMD,UBLS	cyan	VSMC_M2
GO:0006914	0.00	1.00	60	450	autophagy	BP	0.00143	EHMT2,HMOX1,TRIM14,TMEM150B,RRAGC,TBC1D17,TRIM13,ATG7,EXOC7,HGS,TBC1D5,TRIM21,WDFY4,CHMP4B,CHMP3,TP53INP2,CAMKK2,STBD1,SRC,CTSA,TRIM8,CTTN,TPCN2,LGALS8,EXOC8,WDR6,CTSK,VPS11,ATG4B,CAPN1,FYCO1,PSAP,MAP1S,TECPR1,HDAC6,WDR45,GABARAP,PRKACA,UBQLN2,TP53,KAT8,UBQLN4,GBA,NUPR1,ULK3,MCOLN1,UBXN6,RETREG1,WDR81,TSC2,NPRL3,RNF166,ABL1,ATP6V0D1,RAB43,EEF1A2,GATA4,BMF,VPS26B,RGS19	cyan	VSMC_M2
GO:0061919	0.00	1.00	60	450	process utilizing autophagic mechanism	BP	0.00143	EHMT2,HMOX1,TRIM14,TMEM150B,RRAGC,TBC1D17,TRIM13,ATG7,EXOC7,HGS,TBC1D5,TRIM21,WDFY4,CHMP4B,CHMP3,TP53INP2,CAMKK2,STBD1,SRC,CTSA,TRIM8,CTTN,TPCN2,LGALS8,EXOC8,WDR6,CTSK,VPS11,ATG4B,CAPN1,FYCO1,PSAP,MAP1S,TECPR1,HDAC6,WDR45,GABARAP,PRKACA,UBQLN2,TP53,KAT8,UBQLN4,GBA,NUPR1,ULK3,MCOLN1,UBXN6,RETREG1,WDR81,TSC2,NPRL3,RNF166,ABL1,ATP6V0D1,RAB43,EEF1A2,GATA4,BMF,VPS26B,RGS19	cyan	VSMC_M2

GO:0050789	0.00	1.00	628	7907	regulation of biological process	BP	0.0016	CTDP1,TSHZ1,ZADH2,PYM1,RAB5B,STAT6,TCF21,ARHGEF25,OS9,AKAP12,FLOT1,DDAH2,PPP6R2,EHMT2,PLXNB2,ZFPM2,CFB,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,TAPBP,TCF20,DAXX,FBXO32,TGFBI,TEF,PTPRK,ARHGAP18,ST3GAL1,CDC14C,GSDMD,TEAD3,NPTXR,MTCH1,GRINA,TLE1,GGA1,CARD10,KCTD17,NFIB,TRERF1,ARHGAP39,HMOX1,LRRC19,ACO1,KIAA1324L,CUL9,KLF9,APPL2,HIGD2A,PLA2G7,CARD19,MLIP,ZBTB45,ZSCAN18,TRIM14,ITGB8,P3H1,NAT14,KCNQ5,GPNMB,EFEMP1,TRIL,RRAGC,EEPD1,MEIS1,COLEC11,ELMO1,RNF144A,STK40,COBL,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,CADPS2,IRF3,RRAS,FLT3LG,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,HS1BP3,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,LRRC17,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,EXOC7,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,PLB1,SLITRK6,SOCS3,CAMK1,EHD3,PLD3,PNP,DZIP1,TPPP2,TIMP2,ZFP36,LGALS3BP,CANT1,SAMD4B,GAA,PAK4,RNF213,ARAP1,NPTX1,GPAT4,FOLR2,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,ITGBL1,DCXR,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,RAB11FIP1,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,ADGRD1,CLIP3,HSPB6,PRICKLE2,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,SCN1B,IGF1,REEP5,TLR3,SNTA1,MAN2A1,WT1,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,TSHZ3,GGT7,POU6F1,SERPING1,CAST,EDEM2,CTSB,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,DECR1,PLCG1,ZHX3,RIOX2,BBS2,MMS19,ARHGAP1,EXOC2,FOXF2,G	cyan	VSMC_M2
GO:0051241	0.00	1.00	87	743	negative regulation of multicellular organismal process	BP	0.002	CTDP1,ZFPM2,IRF1,CARD10,NFIB,HMOX1,KIAA1324L,APPL2,MLIP,GPNMB,EFEMP1,MEIS1,GLI3,NRP1,LRRC17,TMEM176B,BIN1,APOE,BCL3,ZFP36,HGS,RAB11FIP1,ANGPT4,RARG,IGF1,TLR3,WT1,SERPING1,ARRDC3,SFRP2,PRKCD,CACNB3,BPI,LRP4,BBS2,STAT1,CHRNA7,TUSC2,SEMA3B,NFKB1,GNAI2,ADGRB2,RGMA,IP6K1,LEF1,ECM1,SEMA4B,CTSK,FURIN,SEMA6C,GATA5,LTBP3,B2M,ADAMTS7,GRN,HDAC5,HOMER3,WNK4,BMP4,DHX58,ARRB2,JUP,EPHA2,SERPINE2,MCC,ERBB2,IL27RA,SLIT2,TP53,GBA,ACP5,EPN2,TMEM98,PTPRS,ABCD1,RAB11FIP3,FOXC2,MIR197,SERPINF1,PML,RPS19,CARD8,NFKBIL1,RNLS,BST2,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0044419	0.00	1.00	105	948	biological process involved in interspecies interaction between organisms	BP	0.00284	CTDP1,ULBP2,AKAP12,CFB,IRF1,GSDMD,NFIB,LRRC19,CNPY3,APPL2,TRIM14,ITGB8,TRIL,COLEC11,IRF3,GSN,STOM,NRP1,BAX,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,EXOC7,ZFP36,EFNB2,TRIM21,DCLK1,LAMP1,SMPD1,WDFY4,SLC15A4,TLR3,CHMP4B,CHMP3,GGT7,SERPING1,CTSB,PLSCR1,PRKCD,SRC,BPI,EXOC2,STAT1,CD81,TRIM8,IKBKE,TIRAP,TUSC2,TPCN2,NFKB1,LGALS8,LEF1,VEGFD,FES,RNASEL,NFKBIA,MOV10,B2M,GRN,C1R,C1S,TMEM106A,PQBP1,DHX58,ARRB2,EPHA2,IL17RA,PLEKHM2,CASP9,PLSCR3,VWCE,IL27RA,TP53,NPC2,ADAM15,SHC1,ADAR,ACP5,C6,ISG15,TNFRSF14,SBNO2,FAM3A,RNF166,ABL1,IL34,GBP6,IST1,OAS2,HEXIM1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,NFKBIL1,IL22RA1,OCIAD2,BST2	cyan	VSMC_M2
GO:0002376	0.00	1.00	165	1656	immune system process	BP	0.00284	RAB5B,STAT6,TCF21,ULBP2,FLOT1,CFB,IRF1,TAPBP,PTPRK,ST3GAL1,GSDMD,GCNT1,HMOX1,LRRC19,CNPY3,APPL2,PLA2G7,TRIM14,ITGB8,GPNMB,TRIL,MEIS1,COLEC11,GLI3,IRF3,RRAS,FLT3LG,GSN,BAX,NOP53,LRRC17,TRIM13,VIM,AGBL5,TMEM176B,APOE,BCL3,ATG7,RHBDF2,PLD3,PNP,ZFP36,RFTN1,RHOG,IL5RA,TRIM21,LAMP1,ACKR4,SMPD1,WDFY4,SLC15A4,LMO1,RBCK1,RARG,IGF1,TLR3,SERPING1,PLSCR1,SFRP2,PRKCD,SRC,CACNB3,BPI,PLCG1,MAPK8IP1,STAT1,CD81,TRIM8,IKBKE,TIRAP,TUSC2,LGALS8,XG,LEF1,VEGFD,ECM1,CTSK,RHBDD3,FES,FURIN,RNASEL,NFKBIA,MOV10,LINC02210-CRHR1,B2M,WNT2B,DPF2,ADORA2A,GRN,C1R,HDAC5,C1S,VEGFB,TMEM106A,PIANP,BMP4,IFI30,MAEA,NBL1,DLG5,PQBP1,DHX58,PLD2,ARRB2,ALOX15,EPHA2,IL17RA,PLEKHM2,TCF12,CASP9,ERBB2,ZFP36L1,IL27RA,RFX1,NTRK1,SLIT2,TP53,CPLX2,HSD3B7,KAT8,HOXB4,GBA,ADAM15,SHC1,ADAR,ACP5,SIGLEC15,GPRC5B,MCOLN1,TMEM98,CRIP2,C6,PTPRS,EEF2,ISG15,TNFRSF14,TCF3,PTGDS,SBNO2,PHPT1,FAM3A,CBFA2T3,RNF166,ABL1,IL34,GBP6,OAS2,SLC8A3,HEXIM1,ZBTB7A,CD55,TRIM26,RAB43,PML,RPS19,JUNB,CARD8,VPS26B,SDC4,NFKBIL1,IL22RA1,PSMB9,BST2,TMEM176A,ZFPM1	cyan	VSMC_M2

GO:0007275	0.00	1.00	330	3815	multicellular organism development	BP	0.00331	CTDP1,TSHZ1,MMP19,MYL6B,STAT6,TCF21,ADAMTS2,FLOT1,EHMT2,PLXNB2,ZFPM2,RPS6KA2,IRF1,TGFBI,PTPRK,ST3GAL1,TEAD3,MTCH1,TLE1,CARD10,NFIB,GCNT1,HMOX1,MEA1,ACO1,KIAA1324L,APPL2,ZBTB45,ITGB8,P3H1,GPNMB,EFEMP1,MEIS1,STK40,COBL,GLI3,SIM1,AP2A1,RRAS,FLT3LG,GSN,SLC17A7,NRP1,KLF15,RHOB,BAX,DBP,MEIS3,LRRC17,FZD4,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,COQ8B,LTBP4,SLITRK6,SOCS3,CAMK1,PNP,RPS16,TIMP2,ZFP36,GAA,PAK4,RNF213,NPTX1,GPAT4,HGS,KAT2B,RHOG,RFNG,FGFR1,EFNB2,EPYC,ADGRA2,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,HSPB6,PRICKLE2,SLC15A4,ANGPT4,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,POU6F1,CTSB,ARRDC3,HEXB,SFRP2,WWTR1,NDRG4,GLRB,EPHA3,SRC,CPE,TGM2,LRP4,PLCG1,BBS2,FOXF2,GNAO1,SFRP5,PDLIM2,MMP2,EXT2,SLC5A3,LZTS2,STAT1,PHACTR1,GFRA2,CD81,NDN,SLC45A3,CHRNA7,CAPN3,TJP1,TIRAP,CTTN,PCSK6,BOC,TUSC2,SEMA3B,ADGRB2,TPPP,LGALS8,RGMA,BCL9,LRP10,LEF1,DISP1,PTGIS,B4GALT5,SOX5,ATRNL1,LAMB2,APH1A,VEGFD,ECM1,REC8,SEMA4B,CTSK,RHBDD3,NCKIPSD,ADCY1,FES,PRUNE1,FURIN,BCL9L,SEMA6C,TACC2,HEG1,VANGL2,GATA5,KIF1A,CLCN2,STK25,PHEX,ARPC5,ELL3,PTCHD1,NFKBIA,MOV10,LTBP3,B2M,WNT2B,DPF2,ARHGEF10,BCR,ADORA2A,CAPN1,PLCD3,CLEC3B,CCDC141,ADAMTS7,GRN,ASTN1,PCOLCE,HDAC5,PSAP,GPC2,ACAT1,VEGFB,RND2,WNK4,ADD1,DGCR2,BMP4,NAGLU,MAEA,RARRES3,QDPR,LDB2,NBL1,MAP1S,CC2D2A,STAT5A,NR2F6,DLG5,CPAMD8,HDAC6,TMEM223,PQBP1,DNAJB6,FKBP10,ARRB2,JUP,ALOX15,EPHA2,MYRF,DAGLA,ZBTB17,TCF12,SERPINE2,CASP9,K	cyan	VSMC_M2
GO:0048525	0.00	1.00	16	61	negative regulation of viral process	BP	0.00331	TRIM14,GSN,TRIM13,ZFP36,TRIM21,CHMP3,PLSCR1,STAT1,TRIM8,RNASEL,ISG15,OAS2,HEXIM1,TRIM26,PML,BST2	cyan	VSMC_M2
GO:0007165	0.00	1.00	339	3919	signal transduction	BP	0.00331	STAT6,TCF21,ARHGEF25,OS9,AKAP12,FLOT1,DDAH2,PLXNB2,RPS6KA2,IRF1,AFDN,DEPTOR,DAXX,PTPRK,ARHGAP18,TEAD3,NPTXR,MTCH1,GRINA,TLE1,CARD10,TRERF1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,APPL2,CARD19,TRIM14,ITGB8,GPNMB,EFEMP1,TRIL,RRAGC,ELMO1,STK40,AKT1S1,STK17A,GLI3,IRF3,RRAS,FLT3LG,NRP1,KLF15,RHOB,BAX,HBP1,NOP53,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,APOE,BCL3,SLC6A9,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,SOCS3,CAMK1,DZIP1,TIMP2,ZFP36,LGALS3BP,CANT1,PAK4,RNF213,ARAP1,NPTX1,HGS,RFTN1,RHOG,ITGBL1,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,ADGRD1,PRICKLE2,SLC15A4,ANGPT4,MAP3K12,RBCK1,RARG,IGF1,TLR3,EFNA5,RHPN2,ARRDC3,PLSCR1,CAMKK2,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,PLCG1,BBS2,MMS19,ARHGAP1,GNAO1,SFRP5,C15orf62,MAPK8IP1,SORBS3,NISCH,MMP2,PTPN13,EXT2,PIK3C2B,LZTS2,STAT1,FAM13A,MOB2,GFRA2,CD81,NDN,FIBIN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,BOC,TPCN2,SEMA3B,MRGPRF,NFKB1,GNAI2,ADGRB2,RGMA,BCL9,LEF1,PTGIS,SIPA1L2,ATRNL1,APH1A,MN1,ARHGEF12,VEGFD,KIF7,ECM1,SEMA4B,RHBDD3,GRK5,CASP10,ADCY1,FES,FURIN,VPS11,ERFE,BCL9L,SEMA6C,HEG1,VANGL2,LMO3,GATA5,FAM53B,RERG,STK25,SAMD10,FIBP,MUS81,ELL3,PTCHD1,RGL1,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,DTX2,FRMD8,WNT2B,DPF2,GNAZ,ARHGEF10,BCR,ADORA2A,CAPN1,PLCD3,ADAM11,CDC42BPG,GRN,TMEM161A,TMEM101,PSAP,HOMER3,GPC2,VEG	cyan	VSMC_M2
GO:0006955	0.00	1.00	110	1012	immune response	BP	0.00334	STAT6,ULBP2,FLOT1,CFB,IRF1,TAPBP,ST3GAL1,GSDMD,HMOX1,LRRC19,CNPY3,APPL2,TRIM14,ITGB8,TRIL,COLEC11,IRF3,BAX,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,RHBDF2,PNP,RFTN1,IL5RA,TRIM21,LAMP1,ACKR4,SMPD1,SLC15A4,RBCK1,TLR3,SERPING1,PLSCR1,PRKCD,SRC,CACNB3,BPI,PLCG1,STAT1,CD81,TRIM8,IKBKE,TIRAP,TUSC2,LGALS8,LEF1,ECM1,CTSK,FES,FURIN,RNASEL,NFKBIA,MOV10,LINC02210-CRHR1,B2M,GRN,C1R,C1S,TMEM106A,PIANP,PQBP1,DHX58,PLD2,ARRB2,ALOX15,EPHA2,IL17RA,PLEKHM2,TCF12,IL27RA,RFX1,TP53,CPLX2,ADAM15,SHC1,ADAR,ACP5,GPRC5B,MCOLN1,TMEM98,C6,PTPRS,ISG15,TNFRSF14,PTGDS,SBNO2,PHPT1,FAM3A,RNF166,ABL1,IL34,GBP6,OAS2,HEXIM1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,NFKBIL1,IL22RA1,BST2,ZFPM1	cyan	VSMC_M2
GO:0032101	0.00	1.00	77	646	regulation of response to external stimulus	BP	0.0035	IRF1,LRRC19,APPL2,PLA2G7,IRF3,NRP1,NOP53,APOE,RHBDF2,SOCS3,ZFP36,FGFR1,EFNB2,TRIM21,ADGRA2,LAMP1,SLC15A4,IGF1,TLR3,SERPING1,PLSCR1,PRKCD,SRC,CACNB3,TGM2,PLCG1,BBS2,STAT1,CD81,IKBKE,CAPN3,TIRAP,SEMA3B,NFKB1,RGMA,PTGIS,MN1,VEGFD,SEMA4B,RHBDD3,FURIN,SEMA6C,NFKBIA,ADORA2A,GRN,VEGFB,NBL1,PQBP1,DHX58,ARRB2,ALOX15,DAGLA,IL17RA,SERPINE2,SLIT2,GBA,NUPR1,ADAR,ACP5,KANK2,GPRC5B,ABCC1,PDGFRB,PTPRS,DVL1,ISG15,SBNO2,FAM3A,IL34,HEXIM1,SERPINF1,CD55,NMT2,RPS19,CARD8,STX3,NFKBIL1	cyan	VSMC_M2
GO:0016032	0.00	1.00	46	325	viral process	BP	0.00406	CTDP1,MGAT4B,ST3GAL1,TRIM14,GSN,STOM,NRP1,TRIM13,APOE,ATG7,ZFP36,EFNB2,TRIM21,LAMP1,SMPD1,EIF3F,MAN2A1,CHMP4B,CHMP3,EDEM2,CTSB,PLSCR1,STAT1,CD81,TRIM8,TPCN2,LEF1,FURIN,RNASEL,EPHA2,TP53,ADAR,ISG15,TNFRSF14,MON1B,IST1,OAS2,NFIA,HEXIM1,CD55,TRIM26,RAB43,NMT2,PML,TMEM250,BST2	cyan	VSMC_M2

GO:0009653	0.00	1.00	192	2050	anatomical structure morphogenesis	BP	0.00452	TSHZ1,MMP19,STAT6,TCF21,FLOT1,PLXNB2,ZFPM2,PACSIN2,TGFBI,ARHGAP18,TLE1,CARD10,NFIB,GCNT1,HMOX1,ITGB8,GPNMB,EFEMP1,MEIS1,STK40,COBL,GLI3,RRAS,NRP1,RHOB,BAX,MEIS3,TRIM13,FZD4,TMEM176B,APOE,BCL3,COQ8B,SLITRK6,SOCS3,CAMK1,GAA,PAK4,RNF213,ARAP1,NPTX1,HGS,RHOG,RFNG,FGFR1,EFNB2,ADGRA2,DCLK1,TMEM108,LZTS3,APBB1,PKDCC,HSPB6,PRICKLE2,ANGPT4,RARG,SCN1B,TLR3,MAN2A1,WT1,EFNA5,HEXB,SFRP2,WWTR1,NDRG4,EPHA3,SRC,CPE,TGM2,LRP4,PLCG1,BBS2,FOXF2,GNAO1,SFRP5,C15orf62,MMP2,EXT2,LZTS2,STAT1,PHACTR1,CD81,NDN,CHRNA7,CAPN3,TJP1,CTTN,BOC,SEMA3B,ADGRB2,TPPP,LGALS8,RGMA,LEF1,PTGIS,B4GALT5,SOX5,ATRNL1,LAMB2,VEGFD,ECM1,SEMA4B,ADCY1,FES,FURIN,BCL9L,SEMA6C,HEG1,VANGL2,GATA5,KIF1A,STK25,PHEX,MOV10,LTBP3,WNT2B,ADORA2A,CAPN1,PLCD3,GRN,HDAC5,VEGFB,RND2,VAT1,TMBIM1,WNK4,DGCR2,BMP4,NAGLU,NBL1,CAPZB,MAP1S,CC2D2A,DLG5,HDAC6,PQBP1,DNAJB6,FKBP10,JUP,EPHA2,ZBTB17,SERPINE2,CASP9,ERBB2,PRKACA,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,GBA,ZMYM3,ADAM15,SHC1,ACP5,NEO1,WARS,EPN2,PDGFRB,FLII,LLGL1,ROR1,PTPRS,DVL1,AGRN,TSC2,SBNO2,RERE,NPRL3,FOXC2,ABL1,DNAAF1,HSBP1,PBX3,IST1,ABCA2,KRT25,PTGFRN,SERPINF1,PML,JUNB,GATA4,SAT1,SDC4,COL8A1,ZFPM1,EN1	cyan	VSMC_M2
GO:0098542	0.00	1.00	70	574	defense response to other organism	BP	0.00497	ULBP2,CFB,IRF1,GSDMD,CNPY3,APPL2,TRIM14,TRIL,COLEC11,IRF3,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,TRIM21,LAMP1,SMPD1,SLC15A4,TLR3,SERPING1,PLSCR1,PRKCD,SRC,BPI,STAT1,TRIM8,IKBKE,TIRAP,TUSC2,LGALS8,FES,RNASEL,MOV10,GRN,C1R,C1S,TMEM106A,PQBP1,DHX58,ARRB2,EPHA2,IL17RA,PLEKHM2,IL27RA,TP53,ADAM15,SHC1,ADAR,ACP5,C6,ISG15,TNFRSF14,FAM3A,RNF166,IL34,GBP6,OAS2,HEXIM1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,IL22RA1,BST2	cyan	VSMC_M2
GO:0007154	0.00	1.00	365	4300	cell communication	BP	0.00566	STAT6,TCF21,ARHGEF25,OS9,AKAP12,FLOT1,DDAH2,EHMT2,PLXNB2,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,DAXX,PTPRK,ARHGAP18,GSDMD,TEAD3,NPTXR,MTCH1,GRINA,TLE1,CARD10,TRERF1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,APPL2,CARD19,TRIM14,ITGB8,GPNMB,EFEMP1,TRIL,RRAGC,ELMO1,STK40,AKT1S1,STK17A,GLI3,CADPS2,IRF3,RRAS,FLT3LG,SLC17A7,NRP1,KLF15,RHOB,BAX,HBP1,NOP53,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,APOE,BCL3,SLC6A9,ATG7,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,SOCS3,CAMK1,DZIP1,TIMP2,ZFP36,LGALS3BP,CANT1,PAK4,RNF213,ARAP1,NPTX1,FOLR2,HGS,RFTN1,RHOG,ITGBL1,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,RAB11FIP1,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,ADGRD1,RIMBP2,PRICKLE2,SLC15A4,ANGPT4,MAP3K12,RBCK1,RARG,SCN1B,IGF1,TLR3,EFNA5,RHPN2,TSHZ3,ARRDC3,PLSCR1,CAMKK2,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,PLCG1,BBS2,MMS19,ARHGAP1,GNAO1,SFRP5,C15orf62,MAPK8IP1,SORBS3,NISCH,MMP2,PTPN13,EXT2,PIK3C2B,LZTS2,STAT1,FAM13A,MOB2,GFRA2,CD81,NDN,FIBIN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,BOC,TPCN2,SEMA3B,MRGPRF,NFKB1,GNAI2,ADGRB2,RGMA,BCL9,HADH,LEF1,PTGIS,SV2A,SIPA1L2,ATRNL1,APH1A,MN1,ARHGEF12,VEGFD,KIF7,ECM1,SEMA4B,RHBDD3,GRK5,CASP10,GAS2L1,ADCY1,FES,ANXA9,FURIN,VPS11,ERFE,BCL9L,SEMA6C,HEG1,VANGL2,LMO3,GATA5,FAM53B,RERG,STK25,SAMD10,FIBP,MUS81,CTNNA3,PHEX,ELL3,PTCHD1,RGL1,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,DTX2,FRMD8,WNT2B,DPF2,GNAZ,ARHGEF10,	cyan	VSMC_M2
GO:0052126	0.00	1.00	24	127	movement in host environment	BP	0.00576	TRIM14,GSN,NRP1,TRIM13,EXOC7,EFNB2,TRIM21,LAMP1,SMPD1,CHMP4B,CHMP3,CTSB,PLSCR1,SRC,EXOC2,CD81,TRIM8,TPCN2,EPHA2,TNFRSF14,IST1,CD55,TRIM26,PML	cyan	VSMC_M2
GO:0007166	0.00	1.00	183	1935	cell surface receptor signaling pathway	BP	0.00674	STAT6,PLXNB2,IRF1,DEPTOR,DAXX,PTPRK,TLE1,HMOX1,KIAA1324L,APPL2,ITGB8,EFEMP1,AKT1S1,GLI3,IRF3,NRP1,KLF15,BAX,HBP1,FZD4,VIM,APOE,BCL3,RHBDF2,LTBP4,SHKBP1,IL17RC,SOCS3,DZIP1,RNF213,HGS,RFTN1,ITGBL1,RFNG,FGFR1,IL5RA,EFNB2,ADGRA2,ACKR4,TMEM108,ADGRD1,PRICKLE2,ANGPT4,RBCK1,RARG,IGF1,TLR3,EFNA5,PLSCR1,SFRP2,WWTR1,NDRG4,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,BPI,LRP4,PLCG1,BBS2,SFRP5,MMP2,LZTS2,STAT1,GFRA2,CD81,NDN,CHRNA7,IKBKE,TIRAP,CTTN,TM2D3,PCSK6,BOC,SEMA3B,NFKB1,GNAI2,ADGRB2,RGMA,BCL9,LEF1,APH1A,VEGFD,KIF7,ECM1,SEMA4B,GRK5,FES,FURIN,ERFE,BCL9L,SEMA6C,VANGL2,GATA5,FAM53B,SAMD10,FIBP,PTCHD1,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,DTX2,FRMD8,WNT2B,BCR,ADORA2A,ADAM11,HOMER3,GPC2,VEGFB,TMBIM1,BMP4,NBL1,CC2D2A,STAT5A,PORCN,DLG5,CHRNE,PLD2,ARRB2,JUP,EPHA2,DAGLA,IL17RA,GABARAP,SERPINE2,MCC,GIPC1,ERBB2,PRKACA,IL27RA,NTRK1,SLIT2,AR,TP53,PDK2,MED12,ADAM15,SHC1,PBXIP1,ADAR,GRIA1,NEO1,ULK3,GPRC5B,EPN2,PDGFRB,LLGL1,IL13RA1,ROR1,SH3GL1,GLIS2,DVL1,ISG15,TRAF7,TNFRSF14,TSC2,NPHP4,PHPT1,AXIN1,RHBDF1,FOXC2,ABL1,SLC2A8,IL34,OAS2,GAS1,DTX3,SLC8A3,ZBTB7A,CD55,PML,PLPP3,GATA4,CARD8,NFKBIL1,IL22RA1,OCIAD2,PYGO2,EMD	cyan	VSMC_M2

GO:0023052	0.00	1.00	361	4258	signaling	BP	0.00674	STAT6,TCF21,ARHGEF25,OS9,AKAP12,FLOT1,DDAH2,PLXNB2,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,DAXX,PTPRK,ARHGAP18,TEAD3,NPTXR,MTCH1,GRINA,TLE1,CARD10,TRERF1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,APPL2,CARD19,TRIM14,ITGB8,GPNMB,EFEMP1,TRIL,RRAGC,ELMO1,STK40,AKT1S1,STK17A,GLI3,CADPS2,IRF3,RRAS,FLT3LG,SLC17A7,NRP1,KLF15,RHOB,BAX,HBP1,NOP53,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,BIN1,APOE,BCL3,SLC6A9,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,SOCS3,CAMK1,EHD3,DZIP1,TIMP2,ZFP36,LGALS3BP,CANT1,PAK4,RNF213,ARAP1,NPTX1,HGS,RFTN1,RHOG,ITGBL1,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,RAB11FIP1,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,ADGRD1,RIMBP2,PRICKLE2,SLC15A4,ANGPT4,MAP3K12,RBCK1,RARG,SCN1B,IGF1,TLR3,EFNA5,RHPN2,TSHZ3,ARRDC3,PLSCR1,CAMKK2,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,PLCG1,BBS2,MMS19,ARHGAP1,GNAO1,SFRP5,C15orf62,MAPK8IP1,SORBS3,NISCH,MMP2,PTPN13,EXT2,PIK3C2B,LZTS2,STAT1,FAM13A,MOB2,GFRA2,CD81,NDN,FIBIN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,BOC,TPCN2,SEMA3B,MRGPRF,NFKB1,GNAI2,ADGRB2,RGMA,BCL9,HADH,LEF1,PTGIS,SV2A,SIPA1L2,ATRNL1,APH1A,MN1,ARHGEF12,VEGFD,KIF7,ECM1,SEMA4B,RHBDD3,GRK5,CASP10,ADCY1,FES,ANXA9,FURIN,VPS11,ERFE,BCL9L,SEMA6C,HEG1,VANGL2,LMO3,GATA5,FAM53B,RERG,STK25,SAMD10,FIBP,MUS81,CTNNA3,PHEX,ELL3,PTCHD1,RGL1,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,DTX2,FRMD8,WNT2B,DPF2,GNAZ,KCND3,ARH	cyan	VSMC_M2
GO:0048513	0.00	1.00	229	2529	animal organ development	BP	0.00702	CTDP1,TSHZ1,MYL6B,STAT6,TCF21,ADAMTS2,FLOT1,PLXNB2,ZFPM2,RPS6KA2,IRF1,TGFBI,PTPRK,ST3GAL1,TEAD3,TLE1,NFIB,GCNT1,HMOX1,MEA1,ITGB8,P3H1,GPNMB,EFEMP1,MEIS1,STK40,COBL,GLI3,RRAS,FLT3LG,SLC17A7,NRP1,KLF15,BAX,DBP,MEIS3,LRRC17,FZD4,VIM,TMEM176B,BCL3,ATRAID,COQ8B,SLITRK6,SOCS3,PNP,RPS16,ZFP36,GAA,GPAT4,KAT2B,RFNG,FGFR1,EFNB2,EPYC,DCLK1,TMEM108,PKDCC,PRICKLE2,RARG,IGF1,TLR3,MAN2A1,WT1,POU6F1,CTSB,ARRDC3,SFRP2,WWTR1,NDRG4,EPHA3,SRC,CPE,TGM2,LRP4,BBS2,FOXF2,GNAO1,PDLIM2,MMP2,EXT2,LZTS2,STAT1,PHACTR1,CD81,CAPN3,TIRAP,TUSC2,SEMA3B,BCL9,LRP10,LEF1,DISP1,SOX5,ATRNL1,LAMB2,APH1A,ECM1,REC8,SEMA4B,CTSK,RHBDD3,ADCY1,FES,BCL9L,SEMA6C,TACC2,HEG1,VANGL2,GATA5,KIF1A,CLCN2,PHEX,ARPC5,ELL3,PTCHD1,NFKBIA,LTBP3,B2M,WNT2B,DPF2,BCR,CAPN1,PLCD3,CLEC3B,CCDC141,ADAMTS7,HDAC5,PSAP,ACAT1,VEGFB,WNK4,DGCR2,BMP4,NAGLU,MAEA,RARRES3,QDPR,LDB2,NBL1,MAP1S,CC2D2A,STAT5A,DLG5,CPAMD8,DNAJB6,ARRB2,JUP,ALOX15,EPHA2,TCF12,SERPINE2,CASP9,KAZN,ERBB2,ZFP36L1,NTRK1,PCGF2,SMOC1,SLIT2,AR,TP53,KAT8,HOXB1,HOXB2,HOXB4,MED12,GBA,PPP1R9B,ADAM15,NUPR1,SHC1,PBXIP1,ADAR,ACP5,KANK2,PRKCSH,SIGLEC15,PDGFRB,TMEM98,CRIP2,ROR1,TRAF4,PTPRS,PLAC1,DYM,EEF2,GLIS2,DVL1,AGRN,ISG15,TSC2,TCF3,NPHP4,SBNO2,RERE,NPRL3,TCF25,RPL13,CBFA2T3,FOXC2,ABL1,DNAAF1,FPGS,IL34,PBX3,ATP6V0D1,OAS2,NFIA,RPS15,KRT25,SLC8A3,HEXIM1,SERPINF1,ZBTB7A,PML,RPS19,SELENOP,JUNB,GATA4,CALM3,SDC4,PYGO2,TMEM176A,COL8A1,MPV17,ZFPM1,EN1,EMD	cyan	VSMC_M2
GO:0006687	0.00	1.00	13	47	glycosphingolipid metabolic process	BP	0.00939	NEU1,B3GALT4,NAGA,ST3GAL1,ITGB8,BAX,SMPD1,HEXB,PRKCD,B4GALT5,GBA,ABCA2,AL157935.2	cyan	VSMC_M2
GO:0048519	0.00	1.00	338	3961	negative regulation of biological process	BP	0.00975	CTDP1,ZADH2,PYM1,STAT6,TCF21,OS9,DDAH2,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,DAXX,TGFBI,PTPRK,ST3GAL1,GRINA,TLE1,CARD10,NFIB,TRERF1,HMOX1,KIAA1324L,KLF9,APPL2,HIGD2A,CARD19,MLIP,ZBTB45,TRIM14,ITGB8,P3H1,GPNMB,EFEMP1,MEIS1,STK40,AKT1S1,AASS,GLI3,AP2A1,IRF3,RRAS,GSN,NRP1,KLF15,RHOB,BAX,NOP53,MEIS3,LRRC17,TRIM13,FZD4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,SLC6A9,ATG7,RHBDF2,SOCS3,TIMP2,ZFP36,SAMD4B,PAK4,RNF213,ARAP1,HGS,KAT2B,EFNB2,SH3BP5,TRIM21,RAB11FIP1,ADGRA2,DCLK1,SMPD1,APBB1,PKDCC,CLIP3,HSPB6,ANGPT4,LMO1,RBCK1,RARG,IGF1,TLR3,SNTA1,WT1,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,TSHZ3,GGT7,POU6F1,SERPING1,CAST,ARRDC3,PLSCR1,SPON1,SFRP2,WWTR1,NDRG4,NDRG3,PRKCD,EPHA3,SRC,CACNB3,BPI,LRP4,PLCG1,ZHX3,RIOX2,BBS2,ARHGAP1,FOXF2,GNAO1,SFRP5,MAPK8IP1,SORBS3,NISCH,PTPN13,PNPLA2,LZTS2,STAT1,CTSA,GFRA2,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,TJP1,TIRAP,CTTN,TMEM115,CSTB,TUSC2,TPCN2,SEMA3B,NFKB1,GNAI2,SPOCD1,ADGRB2,TPPP,HIST1H1C,RGMA,HADH,IP6K1,LEF1,TBL1Y,PTGIS,SSH3,MN1,KIF7,WDR6,ECM1,SEMA4B,CTSK,RHBDD3,GRK5,NELFCD,FURIN,VPS11,ERFE,BCL9L,SEMA6C,HEG1,LMO3,RFX5,GATA5,RERG,HELZ2,RNASEL,MAGEF1,MUS81,ELL3,NFKBIA,MOV10,FAM89B,LTBP3,LINC02210-CRHR1,FRMD8,B2M,DPF2,ADORA2A,AIFM2,ADAMTS7,GRN,HDAC5,TMEM161A,TSC22D4,HOMER3,VAT1,TMBIM1,WNK4,ADD1,MXD4,BMP4,IFI30,MAEA,RARRES3,LDB2,NBL1,CAPZB,ZNF503,NR2F6,DLG5,CPAMD8,HDAC6,DHX58,DNAJB6,ARRB2,JUP,ALOX15,EPHA2,	cyan	VSMC_M2

GO:0050896	0.00	1.00	478	5876	response to stimulus	BP	0.01106	CTDP1,STAT6,TCF21,ARHGEF25,OS9,ULBP2,AKAP12,FLOT1,DDAH2,MSH5,EHMT2,PLXNB2,CFB,RPS6KA2,IRF1,AFDN,DEPTOR,TAPBP,DAXX,FBXO32,CUTA,TGFBI,PTPRK,ARHGAP18,ST3GAL1,GSDMD,TEAD3,NPTXR,MTCH1,GRINA,TLE1,CARD10,NFIB,TRERF1,GCNT1,ARHGAP39,HMOX1,LRRC19,CNPY3,ACO1,KIAA1324L,TRPM3,KLF9,APPL2,PLA2G7,CARD19,MLIP,TRIM14,ITGB8,GPNMB,BCKDHB,EFEMP1,TRIL,BBS9,RRAGC,EEPD1,COLEC11,ELMO1,STK40,AKT1S1,STK17A,GLI3,IRF3,RRAS,FLT3LG,GSN,NRP1,KLF15,RHOB,BAX,HBP1,SELENOW,NOP53,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,AGBL5,APOE,BCL3,AGAP3,SLC6A9,ACAA1,ATG7,CYP2S1,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,SLITRK6,SOCS3,CAMK1,PLD3,PNP,DZIP1,RPS16,TIMP2,ZFP36,LGALS3BP,CANT1,PAK4,RNF213,ARAP1,NPTX1,RPL15,FOLR2,HGS,KAT2B,TBC1D5,RFTN1,RHOG,ITGBL1,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,WDFY4,ADGRD1,PRICKLE2,SLC15A4,ANGPT4,MAP3K12,RBCK1,RARG,SCN1B,IGF1,CYP4V2,TLR3,WT1,EFNA5,RHPN2,GGT7,GGCX,SERPING1,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,CAMKK2,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,PLCG1,BBS2,MMS19,ARHGAP1,GNAO1,SFRP5,C15orf62,MAPK8IP1,SORBS3,NISCH,MMP2,PTPN13,EXT2,PIK3C2B,LZTS2,STAT1,FAM13A,HPS6,MOB2,GFRA2,CD81,NDN,FIBIN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,BOC,TUSC2,TPCN2,SEMA3B,MRGPRF,NFKB1,GNAI2,ADGRB2,LGALS8,RGMA,BCL9,UBA7,HADH,LEF1,PTGIS,SOX5,RLBP1,SIPA1L2,ATRNL1,LAMB2,APH1A,MN1,ARHGEF12,VEGFD,KIF7,ECM1,	cyan	VSMC_M2
GO:0048583	0.00	1.00	252	2834	regulation of response to stimulus	BP	0.01124	CTDP1,STAT6,TCF21,ARHGEF25,AKAP12,FLOT1,CFB,IRF1,DEPTOR,FBXO32,ARHGAP18,NPTXR,MTCH1,GRINA,TLE1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,APPL2,PLA2G7,CARD19,MLIP,TRIM14,GPNMB,TRIL,RRAGC,COLEC11,STK40,AKT1S1,GLI3,IRF3,RRAS,NRP1,KLF15,BAX,NOP53,MEIS3,LURAP1,TRIM13,FZD4,APOE,BCL3,SLC6A9,ATG7,RHBDF2,LTBP4,SHKBP1,SOCS3,TIMP2,ZFP36,CANT1,PAK4,RNF213,ARAP1,NPTX1,HGS,RFTN1,RFNG,FGFR1,EFNB2,TRIM21,ADGRA2,LAMP1,SMPD1,TMEM108,APBB1,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,GGT7,SERPING1,ARRDC3,PLSCR1,SFRP2,WWTR1,NDRG4,PRKCD,SRC,CACNB3,TGM2,LRP4,PLCG1,BBS2,MMS19,ARHGAP1,SFRP5,MAPK8IP1,SORBS3,PTPN13,LZTS2,STAT1,FAM13A,CD81,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,SEMA3B,NFKB1,GNAI2,RGMA,LEF1,PTGIS,SIPA1L2,MN1,ARHGEF12,VEGFD,KIF7,ECM1,SEMA4B,RHBDD3,GRK5,CASP10,FES,FURIN,VPS11,ERFE,BCL9L,SEMA6C,HEG1,LMO3,GATA5,FAM53B,STK25,MAGEF1,ELL3,NFKBIA,FAM89B,FRMD8,B2M,ARHGEF10,BCR,ADORA2A,CAPN1,AIFM2,GRN,C1R,C1S,TMEM161A,TMEM101,HOMER3,GPC2,VEGFB,TMEM106A,TMBIM1,PIANP,BMP4,NBL1,DLG5,HDAC6,PQBP1,DHX58,ARHGEF10L,PLD2,DNAJB6,ARRB2,JUP,ALOX15,EPHA2,AKAP5,DAGLA,IL17RA,GABARAP,SERPINE2,MCC,CGNL1,CASP9,GIPC1,ERBB2,PRKACA,IL27RA,UBQLN2,NTRK1,PCGF2,SLIT2,AR,TP53,UBQLN4,PDK2,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,ACP5,KANK2,DENND4B,ARHGAP17,SLC44A2,NEO1,ULK3,GPRC5B,ABCC1,EPN2,PDGFRB,LLGL1,MAP2K3,C6,ROR1,TRAF4,PTPRS,SH3GL1,GLIS2,ABCD1,DVL1,ISG15,TRAF7,TNFRSF14,TSC2,NPHP4,SBNO2,PHPT1	cyan	VSMC_M2
GO:0048514	0.00	1.00	61	508	blood vessel morphogenesis	BP	0.01124	MMP19,TCF21,ZFPM2,TGFBI,CARD10,HMOX1,ITGB8,GPNMB,MEIS1,RRAS,NRP1,RHOB,BAX,FZD4,APOE,PAK4,RNF213,HGS,EFNB2,ADGRA2,HSPB6,ANGPT4,TLR3,WT1,SFRP2,PLCG1,MMP2,STAT1,CHRNA7,TJP1,ADGRB2,LEF1,PTGIS,VEGFD,ECM1,HEG1,PLCD3,GRN,HDAC5,VEGFB,BMP4,FKBP10,JUP,EPHA2,ERBB2,ZFP36L1,SLIT2,ADAM15,SHC1,WARS,EPN2,PDGFRB,NPRL3,FOXC2,ABL1,SERPINF1,PML,JUNB,GATA4,SAT1,COL8A1	cyan	VSMC_M2
GO:0043207	0.00	1.00	90	820	response to external biotic stimulus	BP	0.01124	ULBP2,AKAP12,CFB,IRF1,GSDMD,NFIB,CNPY3,APPL2,TRIM14,ITGB8,TRIL,COLEC11,IRF3,BAX,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,ZFP36,TRIM21,DCLK1,LAMP1,SMPD1,WDFY4,SLC15A4,TLR3,GGT7,SERPING1,PLSCR1,PRKCD,SRC,BPI,STAT1,TRIM8,IKBKE,TIRAP,TUSC2,NFKB1,LGALS8,VEGFD,FES,RNASEL,NFKBIA,MOV10,B2M,GRN,C1R,C1S,TMEM106A,PQBP1,DHX58,ARRB2,EPHA2,IL17RA,PLEKHM2,CASP9,PLSCR3,VWCE,IL27RA,TP53,NPC2,ADAM15,SHC1,ADAR,ACP5,C6,ISG15,TNFRSF14,SBNO2,FAM3A,RNF166,ABL1,IL34,GBP6,OAS2,HEXIM1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,NFKBIL1,IL22RA1,OCIAD2,BST2	cyan	VSMC_M2
GO:0051707	0.00	1.00	90	820	response to other organism	BP	0.01124	ULBP2,AKAP12,CFB,IRF1,GSDMD,NFIB,CNPY3,APPL2,TRIM14,ITGB8,TRIL,COLEC11,IRF3,BAX,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,ZFP36,TRIM21,DCLK1,LAMP1,SMPD1,WDFY4,SLC15A4,TLR3,GGT7,SERPING1,PLSCR1,PRKCD,SRC,BPI,STAT1,TRIM8,IKBKE,TIRAP,TUSC2,NFKB1,LGALS8,VEGFD,FES,RNASEL,NFKBIA,MOV10,B2M,GRN,C1R,C1S,TMEM106A,PQBP1,DHX58,ARRB2,EPHA2,IL17RA,PLEKHM2,CASP9,PLSCR3,VWCE,IL27RA,TP53,NPC2,ADAM15,SHC1,ADAR,ACP5,C6,ISG15,TNFRSF14,SBNO2,FAM3A,RNF166,ABL1,IL34,GBP6,OAS2,HEXIM1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,NFKBIL1,IL22RA1,OCIAD2,BST2	cyan	VSMC_M2
GO:0032102	0.00	1.00	38	266	negative regulation of response to external stimulus	BP	0.01124	NRP1,APOE,RHBDF2,SOCS3,ZFP36,TRIM21,IGF1,SERPING1,PRKCD,SRC,CACNB3,PLCG1,BBS2,SEMA3B,NFKB1,RGMA,PTGIS,SEMA4B,FURIN,SEMA6C,ADORA2A,GRN,NBL1,DHX58,ARRB2,SERPINE2,SLIT2,GBA,ADAR,ACP5,PTPRS,DVL1,ISG15,FAM3A,SERPINF1,RPS19,CARD8,NFKBIL1	cyan	VSMC_M2

GO:0003008	0.00	1.00	124	1240	system process	BP	0.01124	CTDP1,MYL6B,AKAP12,EHMT2,RPS6KA2,CYB5R3,FBXO32,TGFBI,NPTXR,HMOX1,ACO1,TRPM3,MLIP,SLC44A1,EFEMP1,BBS9,STK40,GSN,KLF15,FZD4,BIN1,APOE,SLC6A9,SLITRK6,EHD3,GAA,NPTX1,EPYC,RAB11FIP1,TMEM108,APBB1,TPP1,HSPB6,SLC7A2,SCN1B,IGF1,CYP4V2,SNTA1,RHPN2,TSHZ3,SERPING1,HEXB,WWTR1,NDRG4,GLRB,SRC,CACNB3,BBS2,GNAO1,SFRP5,NISCH,EXT2,SLC5A3,STAT1,NDN,CHRNA7,TJP1,CTTN,TPCN2,GNAI2,TPPP,LEF1,RLBP1,LAMB2,ADCY1,HEG1,GATA5,CTNNA3,PTCHD1,LINC02210-CRHR1,B2M,KCND3,ADORA2A,RPGR,NYX,VEGFB,WNK4,DGCR2,BMP4,NR2F6,CHRNE,ARRB2,JUP,MYRF,SERPINE2,PRKACA,NTRK1,MLLT6,SLIT2,AR,HOXB2,GBA,PPP1R9B,SLC16A2,GRIA1,RASL10B,ABCC1,TMEM98,MAP2K3,ROR1,PIEZO2,SH3GL1,RETREG1,EEF2,DVL1,RENBP,RAB11FIP3,FOXC2,ABL1,HSBP1,PBX3,ABCA2,SLC8A3,SERPINF1,KCND2,LRRN4,SERPINB6,GATA4,CALM3,CLIC2,CDK9,RNLS,EN1,EMD	cyan	VSMC_M2
GO:0001817	0.00	1.00	60	492	regulation of cytokine production	BP	0.01233	AKAP12,FLOT1,IRF1,GSDMD,HMOX1,LRRC19,APPL2,ITGB8,GPNMB,TRIL,IRF3,LURAP1,BCL3,PLD3,PNP,ZFP36,RFTN1,IL5RA,TRIM21,IGF1,TLR3,SRC,BPI,STAT1,CD81,CHRNA7,TIRAP,TUSC2,NFKB1,LEF1,FURIN,HEG1,FRMD8,B2M,HOMER3,TMEM106A,PQBP1,DHX58,ARRB2,EPHA2,IL17RA,IL27RA,GBA,ACP5,GPRC5B,MAP2K3,PTPRS,ABCD1,ISG15,TNFRSF14,ABL1,MIR197,OAS2,CD55,PML,GATA4,CARD8,NFKBIL1,BST2,ZFPM1	cyan	VSMC_M2
GO:0001816	0.00	1.00	61	504	cytokine production	BP	0.01247	AKAP12,FLOT1,IRF1,GSDMD,HMOX1,LRRC19,APPL2,ITGB8,GPNMB,TRIL,IRF3,LURAP1,BCL3,PLD3,PNP,ZFP36,RFTN1,IL5RA,TRIM21,IGF1,TLR3,SRC,BPI,STAT1,CD81,CHRNA7,TIRAP,TUSC2,NFKB1,LEF1,FURIN,HEG1,LTBP3,FRMD8,B2M,HOMER3,TMEM106A,PQBP1,DHX58,ARRB2,EPHA2,IL17RA,IL27RA,GBA,ACP5,GPRC5B,MAP2K3,PTPRS,ABCD1,ISG15,TNFRSF14,ABL1,MIR197,OAS2,CD55,PML,GATA4,CARD8,NFKBIL1,BST2,ZFPM1	cyan	VSMC_M2
GO:0048518	0.00	1.00	378	4533	positive regulation of biological process	BP	0.01747	PYM1,STAT6,TCF21,AKAP12,FLOT1,DDAH2,PLXNB2,ZFPM2,CFB,RPS6KA2,IRF1,AFDN,TCF20,DAXX,TEF,CDC14C,GSDMD,TEAD3,MTCH1,TLE1,GGA1,CARD10,KCTD17,NFIB,TRERF1,HMOX1,LRRC19,KIAA1324L,APPL2,PLA2G7,MLIP,TRIM14,ITGB8,P3H1,NAT14,GPNMB,RRAGC,EEPD1,MEIS1,COLEC11,RNF144A,COBL,STK17A,PTOV1,GLI3,AP2A1,CADPS2,IRF3,RRAS,FLT3LG,GSN,STOM,NRP1,KLF15,RHOB,BAX,DBP,NOP53,BICRA,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,SHKBP1,PLB1,SLITRK6,SOCS3,CAMK1,EHD3,PNP,DZIP1,TPPP2,TIMP2,ZFP36,CANT1,SAMD4B,PAK4,ARAP1,FOLR2,HGS,KAT2B,TBC1D5,RFTN1,RHOG,DCXR,RFNG,FGFR1,IL5RA,EFNB2,TRIM21,ADGRA2,LAMP1,SMPD1,TMEM108,APBB1,PKDCC,CLIP3,HSPB6,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,CHMP3,TP53INP2,PATL1,TSHZ3,SERPING1,EDEM2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,NDRG4,PRKCD,EPHA3,SRC,CACNB3,TGM2,LRP4,DECR1,PLCG1,ZHX3,MMS19,FOXF2,C15orf62,MAPK8IP1,SORBS3,MMP2,SLC5A3,PNPLA2,STAT1,ABHD14B,MOB2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,IKBKE,CAPN3,TJP1,TIRAP,CTTN,TM2D3,BOC,TUSC2,ZNF496,SEMA3B,NFKB1,GNAI2,TPPP,RGMA,BCL9,XG,HADH,LEF1,PTGIS,B4GALT5,SOX5,EGFL6,APH1A,MN1,VEGFD,KIF7,ECM1,SEMA4B,RHBDD3,GRK5,NCKIPSD,CASP10,ADCY1,FES,FURIN,VPS11,ERFE,BCL9L,SEMA6C,HEG1,LMO3,RFX5,GATA5,FAM53B,HELZ2,STK25,ATG4B,RNASEL,MAGEF1,ARPC5,ELL3,NFKBIA,MOV10,FAM89B,LTBP3,FRMD8,B2M,WNT2B,DPF2,ARHGEF10,ADORA2A,CAPN1,FYCO1,AIFM2,CLEC3B,PCB	cyan	VSMC_M2
GO:0016236	0.00	1.00	37	265	macroautophagy	BP	0.02036	EHMT2,HMOX1,TRIM13,ATG7,EXOC7,HGS,TBC1D5,CHMP4B,CHMP3,TP53INP2,STBD1,SRC,LGALS8,EXOC8,ATG4B,CAPN1,FYCO1,TECPR1,HDAC6,WDR45,GABARAP,PRKACA,UBQLN2,TP53,UBQLN4,GBA,NUPR1,ULK3,MCOLN1,UBXN6,RETREG1,WDR81,TSC2,NPRL3,ATP6V0D1,RAB43,VPS26B	cyan	VSMC_M2
GO:0051701	0.00	1.00	25	150	biological process involved in interaction with host	BP	0.02092	TRIM14,GSN,NRP1,TRIM13,ATG7,EXOC7,EFNB2,TRIM21,LAMP1,SMPD1,CHMP4B,CHMP3,CTSB,PLSCR1,SRC,EXOC2,CD81,TRIM8,TPCN2,EPHA2,TNFRSF14,IST1,CD55,TRIM26,PML	cyan	VSMC_M2
GO:0044403	0.00	1.00	31	206	biological process involved in symbiotic interaction	BP	0.02092	CTDP1,LRRC19,TRIM14,GSN,STOM,NRP1,TRIM13,APOE,ATG7,EXOC7,EFNB2,TRIM21,LAMP1,SMPD1,CHMP4B,CHMP3,CTSB,PLSCR1,SRC,EXOC2,CD81,TRIM8,TUSC2,TPCN2,LEF1,EPHA2,TNFRSF14,IST1,CD55,TRIM26,PML	cyan	VSMC_M2

GO:1901564	0.00	1.00	398	4789	organonitrogen compound metabolic process	BP	0.02092	CTDP1,MMP19,PYM1,MOXD1,OS9,ADAMTS2,MGAT4B,GNS,FLOT1,CHKB,DDAH2,PPP6R2,NEU1,EHMT2,PLXNB2,CFB,EIF3H,RPS6KA2,DEPTOR,B3GALT4,TAPBP,DAXX,NAGA,FBXO32,PTPRK,ST3GAL1,IBA57,CDC14C,MTCH1,GGA1,OPLAH,CARD10,KCTD17,TRERF1,GCNT1,HMOX1,ACO1,CUL9,PLA2G7,IARS,TRIM14,GALNT12,ITGB8,P3H1,GPNMB,SLC44A1,BCKDHB,EFEMP1,RNF144A,STK40,AKT1S1,STK17A,AASS,GLI3,AP2A1,GSN,NRP1,KLF15,BAX,RPL18,PARP12,NOP53,ABTB1,FKRP,TRIM13,ACSS1,FZD4,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,UROD,BCL3,ETHE1,MIF4GD,AGAP3,ATRAID,SLC6A9,ATG7,LTBP4,CAPN5,PLB1,SOCS3,CAMK1,OSBPL10,RNF170,PNP,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,PAK4,SGSH,RNF213,GPAT4,RPL15,HGS,KAT2B,EIF3K,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,TPP1,MMP17,CLIP3,ANGPT4,EIF3F,MAP3K12,RBCK1,GNPTAB,IGF1,TLR3,SNTA1,MAN2A1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,GGT7,ACSS2,GALNT18,GGCX,LPCAT4,SERPING1,CAST,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,RIOX2,MMS19,CHST14,FOXF2,MAPK8IP1,MMP2,PTPN13,PTDSS1,EXT2,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,PHKG1,GUSB,CHRNA7,TRIM8,IKBKE,OSBPL5,CAPN3,NADSYN1,TIRAP,MRPL36,PCSK6,RNPEP,CSTB,NFKB1,GNAI2,TPPP,B4GALT4,HIST1H1C,RGMA,UBA7,LEF1,TBL1Y,PTGIS,B4GALT5,SSH3,APH1A,DCAF11,VEGFD,GCNT7,ECM1,CTSK,RHBDD3,GRK5,CASP10,ADCY1,FES,MINDY1,FURIN,VPS11,SCLY,CCS,HEG1,RNPEPL1,B4GAT1,STK25,ATG4B,FUCA1,UCKL1,RNASEL,MAGEF1,NMNAT2,PHEX,ECHS1,NFKBIA,MOV10,DTX2,B2M,BCR,ADORA2A,CA	cyan	VSMC_M2
GO:0045087	0.00	1.00	56	459	innate immune response	BP	0.02124	ULBP2,CFB,IRF1,GSDMD,CNPY3,APPL2,TRIM14,TRIL,COLEC11,IRF3,TRIM13,VIM,APOE,TRIM21,LAMP1,SMPD1,SLC15A4,TLR3,SERPING1,PLSCR1,SRC,BPI,STAT1,TRIM8,IKBKE,TIRAP,FES,GRN,C1R,C1S,TMEM106A,PQBP1,DHX58,ARRB2,IL17RA,PLEKHM2,TP53,ADAM15,ADAR,C6,ISG15,TNFRSF14,FAM3A,RNF166,IL34,GBP6,OAS2,HEXIM1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,BST2	cyan	VSMC_M2
GO:0045765	0.00	1.00	33	229	regulation of angiogenesis	BP	0.02292	HMOX1,ITGB8,GPNMB,RRAS,NRP1,RHOB,PAK4,HGS,ADGRA2,HSPB6,ANGPT4,TLR3,SFRP2,PLCG1,STAT1,CHRNA7,TJP1,ADGRB2,PTGIS,VEGFD,ECM1,GRN,VEGFB,JUP,EPHA2,ERBB2,WARS,EPN2,FOXC2,ABL1,SERPINF1,PML,GATA4	cyan	VSMC_M2
GO:1902187	0.00	1.00	6	12	negative regulation of viral release from host cell	BP	0.02292	TRIM13,TRIM21,CHMP3,TRIM8,TRIM26,PML	cyan	VSMC_M2
GO:0048668	0.00	1.00	8	22	collateral sprouting	BP	0.02292	COBL,RGMA,RND2,HDAC6,PTPRS,DVL1,ABL1,IST1	cyan	VSMC_M2
GO:0065009	0.00	1.00	208	2307	regulation of molecular function	BP	0.02292	ARHGEF25,FLOT1,DDAH2,PPP6R2,PLXNB2,TBC1D22A,AFDN,DEPTOR,DAXX,ARHGAP18,NPTXR,MTCH1,CARD10,ARHGAP39,HMOX1,TRIM14,TBC1D2,ELMO1,TBC1D17,AKT1S1,GSN,STOM,NRP1,BAX,DENND2A,TRIM13,FZD4,CAB39L,BIN1,APOE,BCL3,AGAP3,SLC6A9,SOCS3,CAMK1,EHD3,DZIP1,TIMP2,ZFP36,ARAP1,NPTX1,HGS,KAT2B,TBC1D5,PPP1R27,RHOG,RFNG,FGFR1,SH3BP5,TRIM21,SMPD1,MMP17,ANGPT4,MAP3K12,RBCK1,SCN1B,IGF1,TLR3,EFNA5,SERPING1,CAST,CTSB,ARRDC3,PLSCR1,CAMKK2,SPON1,SFRP2,WWTR1,PRKCD,EPHA3,SRC,CACNB3,TGM2,ARHGAP1,GNAO1,SFRP5,MAPK8IP1,SLC5A3,PHACTR1,CTSA,FAM13A,CD81,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,AGFG1,PCSK6,CSTB,NFKB1,GNAI2,RGMA,LEF1,PTGIS,SGSM1,SIPA1L2,APH1A,ARHGEF12,ECM1,CASP10,ADCY1,ANXA9,FURIN,CCS,HEG1,RGL1,NFKBIA,LINC02210-CRHR1,B2M,ARHGEF10,BCR,ADORA2A,CAPN1,RPGR,PCBD1,GRN,PCOLCE,HDAC5,PSAP,TMBIM1,WNK4,ADD1,BMP4,RARRES3,LDB2,CPAMD8,HDAC6,ARHGEF10L,B3GAT3,DNAJB6,ARRB2,JUP,EPHA2,AKAP5,SERPINE2,CASP9,ERBB2,PRKACA,NTRK1,SLIT2,AR,TP53,GBA,PPP1R9B,ADAM15,NUPR1,SHC1,PBXIP1,ADAR,DENND4B,ARHGAP17,DOCK6,TEX14,WARS,GPRC5B,PDGFRB,LLGL1,MAP2K3,ROR1,MLLT1,TRAF4,GLIS2,WDR81,DVL1,SGSM2,AGRN,RENBP,TSC2,TCF3,EDF1,PHPT1,AXIN1,NPRL3,RALGDS,ABL1,CNN3,IL34,OAS2,INCA1,ABCA2,RPS15,SLC8A3,CBARP,HEXIM1,SERPINF1,ZBTB7A,TRIM26,PML,SERPINB6,PLPP3,EEF1A2,CALM3,CARD8,CLIC2,GCHFR,CDK9,SDC4,NFKBIL1,PSMB9,RGS8,RGS10,BST2,PYGO2,INKA1,GTF2H4,ZFPM1	cyan	VSMC_M2
GO:0060627	0.00	1.00	50	403	regulation of vesicle-mediated transport	BP	0.02292	RAB5B,FLOT1,PACSIN2,HMOX1,APPL2,AP2A1,CADPS2,SLC17A7,NRP1,BIN1,APOE,HGS,TBC1D5,LAMP1,SMPD1,PKDCC,CLIP3,CHMP3,PLSCR1,NDRG4,EPHA3,SRC,TGM2,ARHGAP1,TPCN2,GNAI2,ADCY1,FES,VPS11,B2M,ADORA2A,ARRB2,ALOX15,AKAP5,GIPC1,UBQLN2,CPLX2,STON2,SNX33,SH3GL1,DVL1,TSC2,ABL1,ABCA2,GAS1,CBARP,GRASP,CALM3,SDC4,RAB11B	cyan	VSMC_M2
GO:0009607	0.00	1.00	91	856	response to biotic stimulus	BP	0.02292	ULBP2,AKAP12,CFB,IRF1,GSDMD,NFIB,CNPY3,APPL2,TRIM14,ITGB8,TRIL,COLEC11,IRF3,BAX,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,ATG7,ZFP36,TRIM21,DCLK1,LAMP1,SMPD1,WDFY4,SLC15A4,TLR3,GGT7,SERPING1,PLSCR1,PRKCD,SRC,BPI,STAT1,TRIM8,IKBKE,TIRAP,TUSC2,NFKB1,LGALS8,VEGFD,FES,RNASEL,MUS81,NFKBIA,MOV10,B2M,GRN,C1R,C1S,TMEM106A,PQBP1,DHX58,ARRB2,EPHA2,IL17RA,PLEKHM2,CASP9,PLSCR3,VWCE,IL27RA,TP53,NPC2,ADAM15,SHC1,ADAR,ACP5,C6,ISG15,TNFRSF14,SBNO2,FAM3A,RNF166,ABL1,IL34,GBP6,OAS2,HEXIM1,CD55,TRIM26,RAB43,PML,RPS19,CARD8,VPS26B,NFKBIL1,IL22RA1,OCIAD2,BST2	cyan	VSMC_M2

GO:0050794	0.00	1.00	594	7581	regulation of cellular process	BP	0.02343	CTDP1,TSHZ1,ZADH2,PYM1,RAB5B,STAT6,TCF21,ARHGEF25,OS9,AKAP12,FLOT1,DDAH2,PPP6R2,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,TCF20,DAXX,TGFBI,TEF,PTPRK,ARHGAP18,ST3GAL1,CDC14C,TEAD3,NPTXR,MTCH1,GRINA,TLE1,CARD10,KCTD17,NFIB,TRERF1,ARHGAP39,HMOX1,LRRC19,ACO1,KIAA1324L,CUL9,KLF9,APPL2,HIGD2A,PLA2G7,CARD19,MLIP,ZBTB45,ZSCAN18,TRIM14,ITGB8,P3H1,NAT14,KCNQ5,GPNMB,EFEMP1,TRIL,RRAGC,MEIS1,ELMO1,RNF144A,STK40,COBL,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,CADPS2,IRF3,RRAS,FLT3LG,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,HS1BP3,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,LRRC17,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,EXOC7,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,SLITRK6,SOCS3,CAMK1,EHD3,PNP,DZIP1,TPPP2,TIMP2,ZFP36,LGALS3BP,CANT1,SAMD4B,PAK4,RNF213,ARAP1,NPTX1,FOLR2,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,ITGBL1,DCXR,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,RAB11FIP1,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,ADGRD1,CLIP3,HSPB6,PRICKLE2,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,SCN1B,IGF1,REEP5,TLR3,SNTA1,MAN2A1,WT1,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,TSHZ3,POU6F1,SERPING1,CAST,EDEM2,CTSB,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,PLCG1,ZHX3,RIOX2,BBS2,MMS19,ARHGAP1,FOXF2,GNAO1,SFRP5,C15orf62,MAPK8IP1,SORBS3,NISCH,MMP2,PTPN13,EXT2,SLC5A3,PNPLA2,PIK3C2B,L	cyan	VSMC_M2
GO:1901342	0.00	1.00	33	232	regulation of vasculature development	BP	0.026	HMOX1,ITGB8,GPNMB,RRAS,NRP1,RHOB,PAK4,HGS,ADGRA2,HSPB6,ANGPT4,TLR3,SFRP2,PLCG1,STAT1,CHRNA7,TJP1,ADGRB2,PTGIS,VEGFD,ECM1,GRN,VEGFB,JUP,EPHA2,ERBB2,WARS,EPN2,FOXC2,ABL1,SERPINF1,PML,GATA4	cyan	VSMC_M2
GO:0009056	0.00	1.00	184	2000	catabolic process	BP	0.02849	MMP19,PYM1,MOXD1,OS9,ADAMTS2,GNS,DDAH2,NEU1,EHMT2,EIF3H,NAGA,GGA1,KCTD17,HMOX1,CUL9,PLA2G7,TRIM14,TMEM150B,SLC44A1,BCKDHB,RRAGC,RNF144A,IAH1,TBC1D17,AASS,BAX,NOP53,TRIM13,VIM,APOE,AGAP3,ATRAID,ACAA1,ATG7,EXOC7,CYP2S1,PNP,TIMP2,ZFP36,SAMD4B,GAA,SGSH,ECH1,RNF213,HGS,TBC1D5,TRIM21,SMPD1,TPP1,MMP17,WDFY4,RBCK1,IGF1,CHMP4B,CHMP3,TP53INP2,PATL1,GGT7,EDEM2,CTSB,NEIL2,HEXB,CAMKK2,WWTR1,STBD1,PRKCD,SRC,LRP4,DECR1,PLBD2,PLCG1,FOXF2,MMP2,PNPLA2,CTSA,CD81,GUSB,TRIM8,IKBKE,CAPN3,TIRAP,ACADS,CTTN,TPCN2,LGALS8,RGMA,UBA7,HADH,STS,EXOC8,DCAF11,WDR6,CTSK,RHBDD3,FURIN,VPS11,SCLY,NIT1,HELZ2,ATG4B,FUCA1,RNASEL,MAGEF1,MUS81,ECHS1,MOV10,CAPN1,FYCO1,PLCD3,ADAMTS7,PSAP,ACAT1,NUDT13,NAGLU,MAEA,RARRES3,QDPR,MAP1S,TECPR1,USE1,HDAC6,WDR45,PLD2,ARRB2,DAGLA,GABARAP,SERPINE2,GIPC1,PRKACA,ZFP36L1,UBQLN2,TP53,KAT8,UBQLN4,GBA,ADAM15,NUPR1,ULK3,MAN2C1,SNX33,ABCC1,MCOLN1,MTA1,CLPP,UBXN6,RETREG1,CPT2,WDR81,ABCD1,DVL1,ASPA,ISG15,ELOB,PNPLA7,RENBP,TSC2,HAGH,FBXW5,INPP5E,AXIN1,NPRL3,RHBDF1,GSTM4,CBFA2T3,RNF166,ABL1,CRAT,DPYD,LDHD,ATP6V0D1,OAS2,ABCA2,MEX3D,ZBTB7A,RAB43,PML,EEF1A2,GATA4,SAT1,BMF,VPS26B,NAGK,PSMB9,RGS19	cyan	VSMC_M2
GO:0048589	0.00	1.00	58	501	developmental growth	BP	0.02852	CTDP1,EHMT2,ZFPM2,MEIS1,STK40,COBL,GLI3,NRP1,APOE,SLITRK6,GPAT4,DCLK1,TMEM108,PKDCC,RARG,IGF1,WT1,SFRP2,WWTR1,NDRG4,LRP4,BBS2,LZTS2,CD81,NDN,CAPN3,CTTN,SEMA3B,RGMA,BCL9,LAMB2,ECM1,SEMA4B,SEMA6C,HEG1,PSAP,RND2,BMP4,STAT5A,HDAC6,ZFP36L1,SLIT2,AR,TP53,MED12,ADAM15,PDGFRB,PTPRS,DVL1,AGRN,FOXC2,ABL1,IST1,GAS1,PTGFRN,GATA4,PYGO2,EN1	cyan	VSMC_M2
GO:0048523	0.00	1.00	309	3647	negative regulation of cellular process	BP	0.02852	CTDP1,ZADH2,STAT6,TCF21,OS9,DDAH2,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,DAXX,TGFBI,PTPRK,ST3GAL1,GRINA,TLE1,CARD10,NFIB,TRERF1,HMOX1,KLF9,APPL2,HIGD2A,CARD19,MLIP,ZBTB45,P3H1,GPNMB,EFEMP1,MEIS1,STK40,AKT1S1,AASS,GLI3,IRF3,RRAS,GSN,NRP1,KLF15,RHOB,BAX,NOP53,MEIS3,LRRC17,FZD4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,SLC6A9,ATG7,RHBDF2,SOCS3,TIMP2,ZFP36,SAMD4B,PAK4,RNF213,ARAP1,HGS,KAT2B,EFNB2,SH3BP5,TRIM21,RAB11FIP1,ADGRA2,DCLK1,SMPD1,APBB1,PKDCC,CLIP3,HSPB6,ANGPT4,LMO1,RBCK1,RARG,IGF1,TLR3,SNTA1,WT1,EFNA5,RHPN2,CHMP4B,TP53INP2,PATL1,TSHZ3,POU6F1,SERPING1,CAST,ARRDC3,PLSCR1,SPON1,SFRP2,WWTR1,NDRG4,NDRG3,PRKCD,EPHA3,SRC,CACNB3,BPI,LRP4,PLCG1,ZHX3,RIOX2,ARHGAP1,FOXF2,SFRP5,MAPK8IP1,SORBS3,NISCH,PTPN13,LZTS2,STAT1,CTSA,GFRA2,NDN,CHRNA7,IKBKE,CAPN3,TJP1,TIRAP,CTTN,TMEM115,CSTB,TPCN2,SEMA3B,NFKB1,GNAI2,SPOCD1,TPPP,HIST1H1C,RGMA,HADH,LEF1,TBL1Y,PTGIS,SSH3,MN1,KIF7,WDR6,ECM1,SEMA4B,RHBDD3,GRK5,NELFCD,FURIN,VPS11,ERFE,BCL9L,SEMA6C,HEG1,LMO3,RFX5,RERG,MAGEF1,MUS81,ELL3,NFKBIA,MOV10,FAM89B,LTBP3,LINC02210-CRHR1,FRMD8,B2M,DPF2,ADORA2A,AIFM2,ADAMTS7,GRN,HDAC5,TMEM161A,TSC22D4,HOMER3,VAT1,TMBIM1,ADD1,MXD4,BMP4,IFI30,MAEA,RARRES3,LDB2,NBL1,CAPZB,ZNF503,NR2F6,DLG5,CPAMD8,HDAC6,DHX58,DNAJB6,ARRB2,JUP,EPHA2,ZBTB17,SERPINE2,MCC,CGNL1,GIPC1,ERBB2,TP53BP2,PRKACA,ZFP36L1,IL27RA,UBQLN2,NTRK1,PCGF2,MLLT6,SLIT2,AR,TP	cyan	VSMC_M2

GO:0032502	0.00	1.00	377	4589	developmental process	BP	0.0324	CTDP1,TSHZ1,ZADH2,MMP19,MYL6B,STAT6,TCF21,ADAMTS2,FLOT1,EHMT2,PLXNB2,ZFPM2,RPS6KA2,IRF1,AFDN,PACSIN2,TGFBI,PTPRK,ARHGAP18,ST3GAL1,TEAD3,MTCH1,TLE1,CARD10,NFIB,GCNT1,HMOX1,MEA1,ACO1,KIAA1324L,APPL2,IARS,ZBTB45,ITGB8,P3H1,GPNMB,EFEMP1,BBS9,MEIS1,COLEC11,STK40,COBL,GLI3,SIM1,AP2A1,RRAS,FLT3LG,GSN,SLC17A7,NRP1,KLF15,RHOB,BAX,DBP,MEIS3,LRRC17,TRIM13,FZD4,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,ATG7,COQ8B,LTBP4,SLITRK6,SOCS3,CAMK1,PLD3,PNP,DZIP1,TPPP2,RPS16,TIMP2,ZFP36,GAA,PAK4,RNF213,ARAP1,NPTX1,GPAT4,HGS,KAT2B,RHOG,RFNG,CATSPERG,FGFR1,EFNB2,EPYC,ADGRA2,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,CLIP3,HSPB6,PRICKLE2,SLC15A4,ANGPT4,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,TP53INP2,GGT7,POU6F1,SERPING1,CTSB,ARRDC3,HEXB,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,PLCG1,ZHX3,BBS2,FOXF2,GNAO1,SFRP5,PDLIM2,C15orf62,MMP2,EXT2,SLC5A3,LZTS2,STAT1,PHACTR1,HPS6,GFRA2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,CAPN3,TJP1,TIRAP,AGFG1,CTTN,TM2D3,PCSK6,BOC,TUSC2,SEMA3B,NFKB1,SPOCD1,ADGRB2,TPPP,LGALS8,RGMA,BCL9,LRP10,LEF1,STS,DISP1,PTGIS,B4GALT5,SOX5,ATRNL1,EGFL6,LAMB2,APH1A,VEGFD,ECM1,REC8,SEMA4B,CTSK,RHBDD3,NCKIPSD,ADCY1,FES,PRUNE1,FURIN,BCL9L,SEMA6C,TACC2,HEG1,VANGL2,LMO3,GATA5,KIF1A,CLCN2,STK25,RNASEL,PHEX,ARPC5,ELL3,PTCHD1,NFKBIA,MOV10,LTBP3,B2M,WNT2B,DPF2,ARHGEF10,BCR,ADORA2A,CAPN1,PLCD3,CLEC3B,CCDC141,ADAMTS7,GRN,ASTN1,PCOLCE,HDAC5,PSAP,GPC2,ACAT1,VEGFB,	cyan	VSMC_M2
GO:0031347	0.00	1.00	49	397	regulation of defense response	BP	0.0324	IRF1,LRRC19,APPL2,PLA2G7,IRF3,APOE,RHBDF2,SOCS3,ZFP36,TRIM21,LAMP1,SLC15A4,IGF1,TLR3,SERPING1,PLSCR1,PRKCD,SRC,TGM2,PLCG1,STAT1,CD81,IKBKE,TIRAP,NFKB1,PTGIS,RHBDD3,FURIN,NFKBIA,ADORA2A,GRN,PQBP1,DHX58,ARRB2,ALOX15,DAGLA,IL17RA,GBA,NUPR1,ADAR,ACP5,GPRC5B,ABCC1,ISG15,SBNO2,FAM3A,HEXIM1,SERPINF1,RPS19	cyan	VSMC_M2
GO:0032897	0.00	1.00	6	13	negative regulation of viral transcription	BP	0.03519	TRIM14,TRIM13,ZFP36,TRIM21,TRIM8,HEXIM1	cyan	VSMC_M2
GO:0031348	0.00	1.00	24	149	negative regulation of defense response	BP	0.03519	APOE,RHBDF2,SOCS3,ZFP36,TRIM21,IGF1,SERPING1,PRKCD,SRC,PLCG1,NFKB1,PTGIS,FURIN,ADORA2A,GRN,DHX58,ARRB2,GBA,ADAR,ACP5,ISG15,FAM3A,SERPINF1,RPS19	cyan	VSMC_M2
GO:0045766	0.00	1.00	22	133	positive regulation of angiogenesis	BP	0.0367	HMOX1,ITGB8,RRAS,NRP1,RHOB,PAK4,HSPB6,ANGPT4,TLR3,SFRP2,PLCG1,CHRNA7,TJP1,PTGIS,VEGFD,ECM1,GRN,VEGFB,JUP,FOXC2,ABL1,GATA4	cyan	VSMC_M2
GO:1904018	0.00	1.00	22	133	positive regulation of vasculature development	BP	0.0367	HMOX1,ITGB8,RRAS,NRP1,RHOB,PAK4,HSPB6,ANGPT4,TLR3,SFRP2,PLCG1,CHRNA7,TJP1,PTGIS,VEGFD,ECM1,GRN,VEGFB,JUP,FOXC2,ABL1,GATA4	cyan	VSMC_M2
GO:0001525	0.00	1.00	51	428	angiogenesis	BP	0.03703	MMP19,TCF21,TGFBI,CARD10,HMOX1,ITGB8,GPNMB,MEIS1,RRAS,NRP1,RHOB,PAK4,RNF213,HGS,EFNB2,ADGRA2,HSPB6,ANGPT4,TLR3,SFRP2,PLCG1,MMP2,STAT1,CHRNA7,TJP1,ADGRB2,LEF1,PTGIS,VEGFD,ECM1,PLCD3,GRN,HDAC5,VEGFB,BMP4,JUP,EPHA2,ERBB2,SLIT2,ADAM15,SHC1,WARS,EPN2,PDGFRB,FOXC2,ABL1,SERPINF1,PML,GATA4,SAT1,COL8A1	cyan	VSMC_M2
GO:0051240	0.00	1.00	105	1050	positive regulation of multicellular organismal process	BP	0.0374	STAT6,AKAP12,FLOT1,PLXNB2,ZFPM2,IRF1,GSDMD,HMOX1,APPL2,ITGB8,GLI3,IRF3,RRAS,NRP1,RHOB,LURAP1,BIN1,APOE,BCL3,ATRAID,SLITRK6,PNP,PAK4,RFTN1,EFNB2,PKDCC,HSPB6,ANGPT4,IGF1,TLR3,MAN2A1,WT1,SFRP2,WWTR1,SRC,TGM2,DECR1,PLCG1,STAT1,CD81,CHRNA7,TJP1,TIRAP,CTTN,TUSC2,GNAI2,TPPP,HADH,LEF1,PTGIS,B4GALT5,SOX5,VEGFD,ECM1,FES,FURIN,BCL9L,HEG1,GATA5,STK25,ELL3,FRMD8,B2M,WNT2B,ADORA2A,GRN,VEGFB,TMEM106A,RND2,TMBIM1,BMP4,RARRES3,DLG5,PQBP1,DHX58,ARRB2,JUP,MYRF,IL17RA,SERPINE2,ZFP36L1,IL27RA,NTRK1,SLIT2,AR,GBA,GPRC5B,CPT2,ASPA,AGRN,ISG15,TNFRSF14,CLSTN1,FOXC2,ABL1,IL34,IST1,OAS2,SERPINF1,CD55,RPS19,GATA4,CARD8,CDK9,ZFPM1	cyan	VSMC_M2
GO:0044409	0.00	1.00	19	106	entry into host	BP	0.03746	TRIM14,GSN,NRP1,EXOC7,EFNB2,TRIM21,LAMP1,SMPD1,CTSB,PLSCR1,SRC,EXOC2,CD81,TRIM8,TPCN2,EPHA2,TNFRSF14,CD55,TRIM26	cyan	VSMC_M2
GO:0019377	0.00	1.00	6	13	glycolipid catabolic process	BP	0.03746	NEU1,NAGA,HEXB,PRKCD,FUCA1,GBA	cyan	VSMC_M2
GO:0001573	0.00	1.00	8	24	ganglioside metabolic process	BP	0.03746	NEU1,B3GALT4,ST3GAL1,ITGB8,HEXB,B4GALT5,ABCA2,AL157935.2	cyan	VSMC_M2
GO:0044248	0.00	1.00	163	1755	cellular catabolic process	BP	0.03746	PYM1,MOXD1,OS9,GNS,DDAH2,NEU1,EHMT2,EIF3H,NAGA,KCTD17,HMOX1,CUL9,PLA2G7,TRIM14,TMEM150B,BCKDHB,RRAGC,RNF144A,TBC1D17,AASS,BAX,NOP53,TRIM13,VIM,APOE,AGAP3,ATRAID,ACAA1,ATG7,EXOC7,CYP2S1,PNP,TIMP2,ZFP36,SAMD4B,GAA,SGSH,ECH1,RNF213,HGS,TBC1D5,TRIM21,SMPD1,TPP1,WDFY4,RBCK1,IGF1,CHMP4B,CHMP3,TP53INP2,PATL1,GGT7,EDEM2,CTSB,NEIL2,HEXB,CAMKK2,WWTR1,STBD1,PRKCD,SRC,LRP4,DECR1,PLBD2,PLCG1,FOXF2,PNPLA2,CTSA,CD81,GUSB,TRIM8,IKBKE,TIRAP,ACADS,CTTN,TPCN2,LGALS8,RGMA,UBA7,HADH,EXOC8,DCAF11,WDR6,CTSK,FURIN,VPS11,SCLY,NIT1,HELZ2,ATG4B,FUCA1,RNASEL,MAGEF1,MUS81,ECHS1,MOV10,CAPN1,FYCO1,ADAMTS7,PSAP,ACAT1,NUDT13,MAEA,QDPR,MAP1S,TECPR1,HDAC6,WDR45,ARRB2,DAGLA,GABARAP,GIPC1,PRKACA,ZFP36L1,UBQLN2,TP53,KAT8,UBQLN4,GBA,NUPR1,ULK3,SNX33,ABCC1,MCOLN1,MTA1,CLPP,UBXN6,RETREG1,CPT2,WDR81,ABCD1,DVL1,ASPA,ISG15,ELOB,PNPLA7,RENBP,TSC2,HAGH,FBXW5,AXIN1,NPRL3,RHBDF1,GSTM4,CBFA2T3,RNF166,ABL1,CRAT,DPYD,LDHD,ATP6V0D1,OAS2,ABCA2,MEX3D,RAB43,PML,EEF1A2,GATA4,BMF,VPS26B,NAGK,PSMB9,RGS19	cyan	VSMC_M2

GO:0048856	0.00	1.00	346	4193	anatomical structure development	BP	0.03964	CTDP1,TSHZ1,MMP19,MYL6B,STAT6,TCF21,ADAMTS2,FLOT1,EHMT2,PLXNB2,ZFPM2,RPS6KA2,IRF1,AFDN,PACSIN2,TGFBI,PTPRK,ARHGAP18,ST3GAL1,TEAD3,MTCH1,TLE1,CARD10,NFIB,GCNT1,HMOX1,MEA1,ACO1,KIAA1324L,APPL2,ZBTB45,ITGB8,P3H1,GPNMB,EFEMP1,MEIS1,STK40,COBL,GLI3,SIM1,AP2A1,RRAS,FLT3LG,GSN,SLC17A7,NRP1,KLF15,RHOB,BAX,DBP,MEIS3,LRRC17,TRIM13,FZD4,MARK4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,COQ8B,LTBP4,SLITRK6,SOCS3,CAMK1,PLD3,PNP,DZIP1,RPS16,TIMP2,ZFP36,GAA,PAK4,RNF213,ARAP1,NPTX1,GPAT4,HGS,KAT2B,RHOG,RFNG,FGFR1,EFNB2,EPYC,ADGRA2,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,HSPB6,PRICKLE2,SLC15A4,ANGPT4,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,POU6F1,CTSB,ARRDC3,HEXB,SFRP2,WWTR1,NDRG4,GLRB,EPHA3,SRC,CPE,TGM2,LRP4,PLCG1,BBS2,FOXF2,GNAO1,SFRP5,PDLIM2,C15orf62,MMP2,EXT2,SLC5A3,LZTS2,STAT1,PHACTR1,GFRA2,CD81,NDN,SLC45A3,CHRNA7,CAPN3,TJP1,TIRAP,CTTN,PCSK6,BOC,TUSC2,SEMA3B,ADGRB2,TPPP,LGALS8,RGMA,BCL9,LRP10,LEF1,STS,DISP1,PTGIS,B4GALT5,SOX5,ATRNL1,LAMB2,APH1A,VEGFD,ECM1,REC8,SEMA4B,CTSK,RHBDD3,NCKIPSD,ADCY1,FES,PRUNE1,FURIN,BCL9L,SEMA6C,TACC2,HEG1,VANGL2,GATA5,KIF1A,CLCN2,STK25,PHEX,ARPC5,ELL3,PTCHD1,NFKBIA,MOV10,LTBP3,B2M,WNT2B,DPF2,ARHGEF10,BCR,ADORA2A,CAPN1,PLCD3,CLEC3B,CCDC141,ADAMTS7,GRN,ASTN1,PCOLCE,HDAC5,PSAP,GPC2,ACAT1,VEGFB,RND2,VAT1,TMBIM1,WNK4,ADD1,DGCR2,BMP4,NAGLU,MAEA,RARRES3,QDPR,LDB2,NBL1,CAPZB,MAP1S,CC2D2A,STAT5A,NR2F6,DLG5,CPAMD8,HDAC6,TMEM223,PQBP1,	cyan	VSMC_M2
GO:0009966	0.00	1.00	199	2237	regulation of signal transduction	BP	0.04504	TCF21,ARHGEF25,AKAP12,FLOT1,IRF1,DEPTOR,ARHGAP18,NPTXR,MTCH1,GRINA,TLE1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,APPL2,CARD19,TRIM14,GPNMB,RRAGC,STK40,AKT1S1,GLI3,IRF3,RRAS,NRP1,KLF15,BAX,NOP53,MEIS3,LURAP1,TRIM13,FZD4,APOE,BCL3,SLC6A9,RHBDF2,LTBP4,SHKBP1,SOCS3,TIMP2,CANT1,PAK4,RNF213,ARAP1,NPTX1,HGS,RFNG,FGFR1,TRIM21,ADGRA2,SMPD1,TMEM108,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,ARRDC3,PLSCR1,SFRP2,WWTR1,NDRG4,PRKCD,SRC,CACNB3,TGM2,LRP4,ARHGAP1,SFRP5,MAPK8IP1,SORBS3,PTPN13,LZTS2,STAT1,FAM13A,CD81,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,NFKB1,GNAI2,RGMA,LEF1,PTGIS,SIPA1L2,MN1,ARHGEF12,KIF7,ECM1,GRK5,CASP10,FURIN,VPS11,ERFE,BCL9L,HEG1,LMO3,GATA5,FAM53B,STK25,ELL3,NFKBIA,FAM89B,FRMD8,ARHGEF10,BCR,ADORA2A,CAPN1,TMEM161A,TMEM101,HOMER3,GPC2,TMEM106A,TMBIM1,BMP4,NBL1,DLG5,HDAC6,DHX58,ARHGEF10L,ARRB2,JUP,ALOX15,EPHA2,AKAP5,GABARAP,SERPINE2,MCC,CGNL1,GIPC1,ERBB2,PRKACA,UBQLN2,NTRK1,PCGF2,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,KANK2,DENND4B,ARHGAP17,SLC44A2,NEO1,ULK3,GPRC5B,EPN2,PDGFRB,LLGL1,MAP2K3,ROR1,TRAF4,PTPRS,SH3GL1,GLIS2,DVL1,ISG15,TRAF7,TSC2,NPHP4,PHPT1,INPP5E,AXIN1,NPRL3,RHBDF1,ABL1,IL34,INCA1,RPS15,GAS1,SLC8A3,HEXIM1,ZBTB7A,CD55,NMT2,PML,PLPP3,GATA4,CALM3,CARD8,NFKBIL1,RGS19,RGS8,RGS10,OCIAD2,BST2,EMD	cyan	VSMC_M2
GO:0002683	0.00	1.00	38	290	negative regulation of immune system process	BP	0.04529	STAT6,IRF1,HMOX1,GPNMB,GLI3,LRRC17,TMEM176B,RHBDF2,TRIM21,TLR3,SERPING1,SRC,BPI,PLCG1,RHBDD3,FURIN,ADORA2A,GRN,BMP4,NBL1,DLG5,DHX58,ARRB2,ALOX15,ERBB2,IL27RA,SLIT2,ADAR,ISG15,TNFRSF14,PHPT1,FAM3A,CD55,RPS19,SDC4,BST2,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0030162	0.00	1.00	61	538	regulation of proteolysis	BP	0.04582	EIF3H,RPS6KA2,MTCH1,RNF144A,GSN,BAX,NOP53,BIN1,APOE,LTBP4,TIMP2,TRIM21,SERPING1,CAST,SPON1,SFRP2,SRC,FOXF2,CAPN3,CSTB,RGMA,APH1A,ECM1,CASP10,FURIN,MAGEF1,ADORA2A,CLEC3B,GRN,PCOLCE,CPAMD8,HDAC6,DNAJB6,ARRB2,GABARAP,SERPINE2,CASP9,GIPC1,PRKACA,UBQLN2,TP53,UBQLN4,GBA,NUPR1,SNX33,TMEM98,DVL1,ELOB,RENBP,AXIN1,RHBDF1,CBFA2T3,IST1,ABCA2,GAS1,SERPINF1,PML,SERPINB6,CARD8,PSMB9,BST2	cyan	VSMC_M2
GO:0050728	0.00	1.00	17	91	negative regulation of inflammatory response	BP	0.04582	APOE,RHBDF2,SOCS3,ZFP36,IGF1,PRKCD,SRC,PLCG1,NFKB1,PTGIS,FURIN,ADORA2A,GRN,GBA,ACP5,SERPINF1,RPS19	cyan	VSMC_M2
GO:0009888	0.00	1.00	131	1389	tissue development	BP	0.04739	CTDP1,MYL6B,STAT6,TCF21,FLOT1,PLXNB2,ZFPM2,AFDN,TGFBI,NFIB,GCNT1,KIAA1324L,ITGB8,GPNMB,EFEMP1,MEIS1,COBL,GLI3,NRP1,KLF15,RHOB,BAX,LRRC17,VIM,ATRAID,SLITRK6,SOCS3,ZFP36,GAA,GPAT4,FGFR1,EFNB2,EPYC,PKDCC,TPP1,PRICKLE2,RARG,IGF1,WT1,CTSB,ARRDC3,SFRP2,WWTR1,NDRG4,EPHA3,SRC,TGM2,LRP4,FOXF2,MMP2,EXT2,LZTS2,STAT1,TJP1,SEMA3B,RGMA,BCL9,LEF1,STS,SOX5,ATRNL1,LAMB2,ECM1,SEMA4B,CTSK,BCL9L,SEMA6C,HEG1,VANGL2,GATA5,PHEX,ELL3,LTBP3,WNT2B,BCR,CLEC3B,ADAMTS7,PSAP,ACAT1,WNK4,ADD1,BMP4,RARRES3,LDB2,CC2D2A,DLG5,ARRB2,ALOX15,EPHA2,ZBTB17,SERPINE2,KAZN,PRKACA,ZFP36L1,NTRK1,SLIT2,AR,TP53,HOXB2,HOXB4,MED12,ADAM15,NUPR1,PBXIP1,KANK2,PDGFRB,ROR1,PTPRS,EEF2,DVL1,AGRN,ISG15,TSC2,SBNO2,EDF1,NPRL3,FOXC2,ABL1,DNAAF1,HSBP1,CNN3,KRT25,PML,JUNB,GATA4,SDC4,PYGO2,COL8A1,ZFPM1,EN1,EMD	cyan	VSMC_M2

GO:0044092	0.00	1.00	84	806	negative regulation of molecular function	BP	0.04846	DEPTOR,HMOX1,AKT1S1,BAX,BIN1,APOE,BCL3,SLC6A9,SOCS3,CAMK1,TIMP2,ZFP36,KAT2B,PPP1R27,SH3BP5,TRIM21,SMPD1,RBCK1,SERPING1,CAST,SFRP2,WWTR1,PRKCD,SRC,CACNB3,SFRP5,MAPK8IP1,PHACTR1,NDN,CSTB,NFKB1,GNAI2,RGMA,LEF1,PTGIS,ECM1,ANXA9,FURIN,HEG1,NFKBIA,LINC02210-CRHR1,B2M,ADORA2A,TMBIM1,BMP4,CPAMD8,HDAC6,DNAJB6,ARRB2,AKAP5,SERPINE2,SLIT2,TP53,GBA,PPP1R9B,ADAM15,NUPR1,ADAR,TEX14,WARS,MLLT1,GLIS2,DVL1,RENBP,TSC2,PHPT1,ABL1,CNN3,INCA1,ABCA2,RPS15,SLC8A3,CBARP,HEXIM1,SERPINF1,SERPINB6,CALM3,CARD8,CLIC2,GCHFR,NFKBIL1,BST2,INKA1,ZFPM1	cyan	VSMC_M2
GO:0007249	0.00	1.00	31	222	I-kappaB kinase/NF-kappaB signaling	BP	0.05276	TLE1,HMOX1,CARD19,TRIM14,IRF3,LURAP1,TRIM13,BCL3,CANT1,TRIM21,RBCK1,TLR3,TGM2,STAT1,TRIM8,IKBKE,CAPN3,TIRAP,ECM1,CASP10,NFKBIA,TMEM101,TMEM106A,SLC44A2,GPRC5B,ROR1,TRAF4,ABL1,CARD8,NFKBIL1,BST2	cyan	VSMC_M2
GO:0051179	0.00	1.00	375	4586	localization	BP	0.05398	RAB5B,OS9,AKAP12,FLOT1,RABL2A,PLXNB2,TBC1D22A,AFDN,PACSIN2,TAPBP,CUTA,PTPRK,ARHGAP18,GGA1,CARD10,GCNT1,HMOX1,ACO1,TRPM3,APPL2,ATP10D,RSPH9,PLA2G7,TRIM14,TBC1D2,ITGB8,P3H1,KCNQ5,GPNMB,SLC44A1,BBS9,RRAGC,EEPD1,ELMO1,TBC1D17,GLI3,AP2A1,CADPS2,RRAS,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,BAX,DENND2A,NOP53,UQCRH,LURAP1,FZD4,MARK4,BIN1,APOE,BCL3,ABCB8,SLC6A9,ATG7,EXOC7,RHBDF2,LTBP4,CAMK1,EHD3,CMTM6,OSBPL10,DZIP1,TPPP2,ZFP36,LGALS3BP,GAA,PAK4,SLC26A11,STARD10,ARAP1,GPAT4,SLC4A9,FOLR2,HGS,TBC1D5,RFTN1,RHOG,ITGBL1,FGFR1,EFNB2,TRIM21,RAB11FIP1,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,PKDCC,TPP1,CLIP3,SLC15A4,ANGPT4,SLC7A2,ATP4A,SCN1B,GNPTAB,IGF1,REEP5,SNTA1,EFNA5,CHMP4B,CHMP3,TP53INP2,EDEM2,ERGIC3,ARRDC3,PLSCR1,HEXB,SFRP2,WWTR1,SLC38A7,NDRG4,GLRB,STBD1,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,LRP4,PLCG1,BBS2,ARHGAP1,EXOC2,GNAO1,MAPK8IP1,NISCH,EXT2,SLC5A3,PNPLA2,CRACR2B,PIK3C2B,SYS1,LZTS2,PHACTR1,CTSA,HPS6,CD81,NDN,SLC45A3,CHRNA7,TRIM8,IKBKE,OSBPL5,CAPN3,TJP1,CACNA2D2,TIRAP,AGFG1,CTTN,PCSK6,TMEM115,TUSC2,TPCN2,SEMA3B,NFKB1,GNAI2,LGALS8,XG,LRP10,HADH,LEF1,DISP1,SGSM1,SV2A,ATRNL1,LAMB2,EXOC8,VEGFD,ECM1,SEMA4B,RHBDD3,NCKIPSD,GAS2L1,ADCY1,FES,ANXA9,FURIN,VPS11,ERFE,SLC16A9,SEMA6C,HEG1,VANGL2,KIF1A,FAM53B,CLCN2,TCN2,TMEM50A,PARD3B,STK25,ATG4B,RNASEL,CTNNA3,ARPC5,NFKBIA,FAM89B,LINC02210-CRHR1,B2M,KCND3,ORAI2,M6PR,ADORA2A,CAPN1,F	cyan	VSMC_M2
GO:0001568	0.00	1.00	63	576	blood vessel development	BP	0.05458	MMP19,TCF21,ZFPM2,TGFBI,CARD10,HMOX1,ITGB8,GPNMB,MEIS1,GLI3,RRAS,NRP1,RHOB,BAX,FZD4,APOE,SOCS3,PAK4,RNF213,HGS,EFNB2,ADGRA2,HSPB6,ANGPT4,TLR3,WT1,SFRP2,PLCG1,MMP2,STAT1,CHRNA7,TJP1,ADGRB2,LEF1,PTGIS,VEGFD,ECM1,HEG1,PLCD3,GRN,HDAC5,VEGFB,BMP4,FKBP10,JUP,EPHA2,ERBB2,ZFP36L1,SLIT2,ADAM15,SHC1,WARS,EPN2,PDGFRB,NPRL3,FOXC2,ABL1,SERPINF1,PML,JUNB,GATA4,SAT1,COL8A1	cyan	VSMC_M2
GO:0010506	0.00	1.00	35	268	regulation of autophagy	BP	0.05491	EHMT2,HMOX1,TRIM14,RRAGC,TRIM13,ATG7,EXOC7,TRIM21,CHMP4B,TP53INP2,CAMKK2,CTSA,TRIM8,CTTN,TPCN2,EXOC8,WDR6,CAPN1,FYCO1,PSAP,HDAC6,PRKACA,UBQLN2,TP53,KAT8,UBQLN4,GBA,NUPR1,TSC2,ABL1,ATP6V0D1,EEF1A2,GATA4,BMF,VPS26B	cyan	VSMC_M2
GO:0007033	0.00	1.00	24	157	vacuole organization	BP	0.05706	EHMT2,ATG7,GAA,TPP1,GNPTAB,MAN2A1,CHMP4B,CHMP3,TP53INP2,HEXB,TPCN2,VPS11,GRN,NAGLU,WDR45,GABARAP,UBQLN2,TMEM175,GBA,NUPR1,ULK3,NAGPA,NPRL3,RAB43	cyan	VSMC_M2
GO:0048585	0.00	1.00	118	1229	negative regulation of response to stimulus	BP	0.06268	STAT6,TCF21,DEPTOR,GRINA,TLE1,HMOX1,APPL2,CARD19,MLIP,AKT1S1,GLI3,NRP1,BAX,NOP53,MEIS3,FZD4,APOE,BCL3,RHBDF2,SOCS3,TIMP2,ZFP36,RNF213,HGS,TRIM21,ADGRA2,SMPD1,IGF1,GGT7,SERPING1,ARRDC3,SFRP2,WWTR1,NDRG4,PRKCD,SRC,CACNB3,LRP4,PLCG1,BBS2,SFRP5,MAPK8IP1,LZTS2,STAT1,CTTN,SEMA3B,NFKB1,GNAI2,RGMA,PTGIS,KIF7,ECM1,SEMA4B,FURIN,VPS11,BCL9L,SEMA6C,HEG1,LMO3,MAGEF1,ELL3,NFKBIA,FAM89B,FRMD8,ADORA2A,GRN,TMEM161A,HOMER3,TMBIM1,BMP4,NBL1,DLG5,DHX58,ARRB2,ALOX15,EPHA2,SERPINE2,MCC,CGNL1,PRKACA,IL27RA,UBQLN2,PCGF2,SLIT2,AR,TP53,UBQLN4,GBA,ADAR,ACP5,KANK2,ULK3,EPN2,MAP2K3,PTPRS,GLIS2,DVL1,ISG15,TNFRSF14,TSC2,NPHP4,PHPT1,FAM3A,INPP5E,AXIN1,NPRL3,ABL1,SERPINF1,ZBTB7A,CD55,RPS19,GATA4,CARD8,NFKBIL1,RGS19,RGS8,RGS10,EMD	cyan	VSMC_M2

GO:0048522	0.00	1.00	347	4212	positive regulation of cellular process	BP	0.06268	PYM1,STAT6,TCF21,AKAP12,FLOT1,DDAH2,PLXNB2,ZFPM2,RPS6KA2,IRF1,AFDN,TCF20,DAXX,TEF,CDC14C,TEAD3,MTCH1,CARD10,KCTD17,NFIB,TRERF1,HMOX1,LRRC19,KIAA1324L,APPL2,PLA2G7,MLIP,TRIM14,P3H1,NAT14,GPNMB,RRAGC,MEIS1,RNF144A,COBL,STK17A,PTOV1,GLI3,AP2A1,CADPS2,IRF3,RRAS,FLT3LG,GSN,STOM,NRP1,KLF15,RHOB,BAX,DBP,NOP53,BICRA,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,SHKBP1,SLITRK6,SOCS3,CAMK1,EHD3,PNP,DZIP1,TPPP2,TIMP2,ZFP36,CANT1,SAMD4B,ARAP1,FOLR2,HGS,KAT2B,TBC1D5,RHOG,DCXR,RFNG,FGFR1,IL5RA,EFNB2,TRIM21,ADGRA2,LAMP1,SMPD1,TMEM108,APBB1,PKDCC,CLIP3,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,CHMP3,TP53INP2,PATL1,TSHZ3,EDEM2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,NDRG4,PRKCD,EPHA3,SRC,CACNB3,TGM2,LRP4,PLCG1,ZHX3,MMS19,FOXF2,C15orf62,MAPK8IP1,SORBS3,MMP2,SLC5A3,PNPLA2,STAT1,ABHD14B,MOB2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,IKBKE,CAPN3,TJP1,TIRAP,CTTN,TM2D3,BOC,ZNF496,SEMA3B,NFKB1,GNAI2,TPPP,RGMA,BCL9,XG,LEF1,PTGIS,SOX5,EGFL6,APH1A,MN1,VEGFD,KIF7,ECM1,SEMA4B,GRK5,NCKIPSD,CASP10,ADCY1,FES,FURIN,VPS11,ERFE,BCL9L,SEMA6C,LMO3,RFX5,GATA5,FAM53B,HELZ2,STK25,RNASEL,MAGEF1,ARPC5,ELL3,NFKBIA,MOV10,FAM89B,LTBP3,B2M,DPF2,ARHGEF10,ADORA2A,CAPN1,FYCO1,AIFM2,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,TMEM101,GPC2,VEGFB,TMEM106A,RND2,WNK4,ADD1,BMP4,RARRES3,LDB2,NBL1,TCEA2,STAT5A,DLG5,HDAC6,PQ	cyan	VSMC_M2
GO:0006672	0.00	1.00	15	78	ceramide metabolic process	BP	0.0656	NEU1,B3GALT4,NAGA,ST3GAL1,ITGB8,SMPD1,HEXB,PRKCD,B4GALT5,GBA,CERS4,PLPP2,ABCA2,PLPP3,AL157935.2	cyan	VSMC_M2
GO:0048646	0.00	1.00	88	877	anatomical structure formation involved in morphogenesis	BP	0.0656	MMP19,TCF21,FLOT1,PLXNB2,TGFBI,CARD10,NFIB,HMOX1,ITGB8,GPNMB,MEIS1,COBL,GLI3,RRAS,NRP1,RHOB,BCL3,CAMK1,PAK4,RNF213,HGS,EFNB2,ADGRA2,HSPB6,ANGPT4,RARG,TLR3,WT1,SFRP2,TGM2,PLCG1,MMP2,EXT2,STAT1,CD81,CHRNA7,CAPN3,TJP1,ADGRB2,TPPP,RGMA,LEF1,PTGIS,VEGFD,ECM1,FURIN,VANGL2,GATA5,WNT2B,PLCD3,GRN,HDAC5,VEGFB,BMP4,CC2D2A,JUP,EPHA2,CASP9,ERBB2,PRKACA,SLIT2,AR,TP53,HOXB1,MED12,GBA,ADAM15,SHC1,WARS,EPN2,PDGFRB,FLII,DVL1,TSC2,SBNO2,FOXC2,ABL1,HSBP1,ABCA2,PTGFRN,SERPINF1,PML,JUNB,GATA4,SAT1,SDC4,COL8A1,ZFPM1	cyan	VSMC_M2
GO:0043122	0.00	1.00	28	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	0.06762	TLE1,HMOX1,CARD19,TRIM14,IRF3,LURAP1,TRIM13,CANT1,TRIM21,RBCK1,TLR3,TGM2,STAT1,TRIM8,IKBKE,CAPN3,TIRAP,ECM1,CASP10,TMEM101,TMEM106A,SLC44A2,GPRC5B,ROR1,TRAF4,ABL1,CARD8,BST2	cyan	VSMC_M2
GO:0040007	0.00	1.00	77	742	growth	BP	0.06762	CTDP1,EHMT2,ZFPM2,MEIS1,STK40,COBL,GLI3,NRP1,APOE,LTBP4,SLITRK6,SOCS3,PAK4,GPAT4,RFTN1,DCLK1,TMEM108,PKDCC,RARG,IGF1,WT1,SFRP2,WWTR1,NDRG4,NDRG3,SRC,LRP4,BBS2,LZTS2,CD81,NDN,CAPN3,CTTN,SEMA3B,RGMA,BCL9,LAMB2,ECM1,SEMA4B,SEMA6C,HEG1,RERG,PSAP,RND2,BMP4,STAT5A,HDAC6,SERPINE2,ERBB2,BRAT1,ZFP36L1,SLIT2,AR,TP53,MED12,PPP1R9B,ADAM15,SHC1,PDGFRB,PTPRS,DVL1,AGRN,E4F1,CLSTN1,FOXC2,ABL1,OSGIN1,IST1,GAS1,PTGFRN,PML,SELENOP,GATA4,BST2,PYGO2,OGFR,EN1	cyan	VSMC_M2
GO:0007409	0.00	1.00	41	341	axonogenesis	BP	0.06833	FLOT1,PLXNB2,NFIB,COBL,GLI3,NRP1,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,APBB1,SCN1B,EFNA5,EPHA3,LRP4,NDN,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,STK25,RND2,MAP1S,HDAC6,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,LLGL1,PTPRS,DVL1,ABL1,IST1	cyan	VSMC_M2
GO:0006928	0.00	1.00	143	1565	movement of cell or subcellular component	BP	0.07075	MYL6B,AKAP12,PLXNB2,AFDN,PTPRK,ARHGAP18,CARD10,NFIB,KIFC2,GCNT1,HMOX1,APPL2,RSPH9,PLA2G7,ITGB8,GPNMB,ELMO1,GLI3,RRAS,GSN,NRP1,RHOB,BAX,CCDC114,LURAP1,FZD4,BIN1,APOE,TPPP2,PAK4,ARAP1,RHOG,ITGBL1,FGFR1,EFNB2,ADGRA2,DCLK1,LAMP1,ACKR4,TMEM108,CLIP3,ANGPT4,SCN1B,IGF1,SNTA1,EFNA5,HEXB,SFRP2,NDRG4,PRKCD,EPHA3,SRC,PLCG1,BBS2,NISCH,PIK3C2B,PHACTR1,CD81,NDN,TJP1,TIRAP,CTTN,BOC,SEMA3B,GNAI2,LGALS8,XG,LEF1,ATRNL1,LAMB2,VEGFD,KIF7,ECM1,SEMA4B,FES,SEMA6C,VANGL2,KIF1A,CTNNA3,WIPF1,ARPC5,FAM89B,KCND3,FYCO1,RPGR,CCDC141,GRN,ASTN1,HDAC5,GPC2,VEGFB,RND2,BMP4,LDB2,NBL1,MAP1S,STAT5A,DLG5,HDAC6,PLD2,ARRB2,JUP,EPHA2,SERPINE2,MCC,GIPC1,ERBB2,BRAT1,IL27RA,NTRK1,SLIT2,HSD3B7,GBA,PPP1R9B,ADAM15,PBXIP1,KANK2,NEO1,CENPV,ABCC1,PDGFRB,MAP2K3,PODN,DVL1,TNFRSF14,NPHP4,PHPT1,RHOT2,RERE,RHBDF1,FOXC2,ABL1,DNAAF1,OSGIN1,HSBP1,IL34,SERPINF1,PML,RPS19,PLPP3,GATA4,SDC4,BST2	cyan	VSMC_M2
GO:1901135	0.00	1.00	82	791	carbohydrate derivative metabolic process	BP	0.07141	MGAT4B,GNS,NEU1,B3GALT4,NAGA,ST3GAL1,GCNT1,GALNT12,ITGB8,AASS,AP2A1,BAX,FKRP,TRIM13,ACSS1,PNP,CANT1,SGSH,GPAT4,SMPD1,GNPTAB,IGF1,MAN2A1,DPY19L3,ACSS2,GALNT18,EDEM2,NEIL2,HEXB,PRKCD,CHST14,EXT2,ABHD14B,GUSB,PCSK6,NFKB1,B4GALT4,B4GALT5,GCNT7,ADCY1,B4GAT1,FUCA1,UCKL1,G6PC3,ACAT1,VEGFB,TMEM106A,MACROD1,NAGLU,PGLS,PORCN,GANAB,B3GAT3,EPHA2,TP53,PDK2,GBA,XYLT2,SLC51B,NUPR1,PRKCSH,PPCDC,PDGFRB,NUDT14,NAGPA,ABCD1,RENBP,UAP1L1,PIGQ,H6PD,CBFA2T3,DPYD,TK2,ABCA2,ACOT6,CHST8,ZBTB7A,DGAT1,HS3ST3B1,NAGK,MACROD2,AL157935.2	cyan	VSMC_M2

GO:0040011	0.00	1.00	126	1349	locomotion	BP	0.07141	AKAP12,PLXNB2,AFDN,PTPRK,ARHGAP18,CARD10,NFIB,GCNT1,HMOX1,APPL2,RSPH9,PLA2G7,ITGB8,GPNMB,ELMO1,GLI3,RRAS,NRP1,RHOB,BAX,LURAP1,FZD4,APOE,TPPP2,PAK4,RHOG,ITGBL1,FGFR1,EFNB2,ADGRA2,DCLK1,ACKR4,ANGPT4,SCN1B,IGF1,EFNA5,ARRDC3,HEXB,SFRP2,NDRG4,PRKCD,EPHA3,SRC,PLCG1,BBS2,NISCH,PIK3C2B,PHACTR1,CD81,NDN,TJP1,TIRAP,CTTN,BOC,SEMA3B,GNAI2,LGALS8,XG,LEF1,ATRNL1,LAMB2,VEGFD,ECM1,SEMA4B,FES,SEMA6C,VANGL2,CTNNA3,ARPC5,FAM89B,ADORA2A,CCDC141,GRN,ASTN1,HDAC5,GPC2,VEGFB,RND2,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,PLD2,ARRB2,JUP,EPHA2,SERPINE2,MCC,GIPC1,ERBB2,BRAT1,IL27RA,NTRK1,SLIT2,HSD3B7,GBA,PPP1R9B,ADAM15,PBXIP1,KANK2,NEO1,CENPV,ABCC1,PDGFRB,MAP2K3,PODN,DVL1,TNFRSF14,TSC2,NPHP4,PHPT1,RERE,RHBDF1,FOXC2,ABL1,OSGIN1,IL34,SERPINF1,PML,RPS19,PLPP3,SDC4,STX3,BST2	cyan	VSMC_M2
GO:0019058	0.00	1.00	32	239	viral life cycle	BP	0.07141	TRIM14,GSN,STOM,NRP1,TRIM13,APOE,EFNB2,TRIM21,LAMP1,SMPD1,CHMP4B,CHMP3,CTSB,PLSCR1,CD81,TRIM8,TPCN2,FURIN,RNASEL,EPHA2,ADAR,ISG15,TNFRSF14,IST1,OAS2,NFIA,CD55,TRIM26,RAB43,NMT2,PML,BST2	cyan	VSMC_M2
GO:0050727	0.00	1.00	32	239	regulation of inflammatory response	BP	0.07399	LRRC19,PLA2G7,IRF3,APOE,RHBDF2,SOCS3,ZFP36,IGF1,TLR3,PRKCD,SRC,TGM2,PLCG1,CD81,NFKB1,PTGIS,RHBDD3,FURIN,NFKBIA,ADORA2A,GRN,ALOX15,DAGLA,IL17RA,GBA,NUPR1,ACP5,GPRC5B,ABCC1,SBNO2,SERPINF1,RPS19	cyan	VSMC_M2
GO:1905114	0.00	1.00	51	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	0.07433	TLE1,GLI3,KLF15,HBP1,FZD4,APOE,RNF213,ADGRA2,TMEM108,PRICKLE2,RARG,SFRP2,WWTR1,GLRB,SRC,CACNB3,CPE,LRP4,SFRP5,LZTS2,CHRNA7,NFKB1,BCL9,LEF1,GRK5,BCL9L,VANGL2,FAM53B,FRMD8,WNT2B,ADORA2A,BMP4,PORCN,CHRNE,ARRB2,JUP,MCC,MED12,PBXIP1,GPRC5B,ROR1,SH3GL1,DVL1,TSC2,NPHP4,AXIN1,ABL1,SLC8A3,PLPP3,PYGO2,EMD	cyan	VSMC_M2
GO:0043393	0.00	1.00	24	162	regulation of protein binding	BP	0.07503	FLOT1,NRP1,BAX,APOE,CAMK1,DZIP1,RFNG,TRIM21,SPON1,PRKCD,SRC,RGMA,B2M,PCBD1,HDAC5,ADD1,BMP4,ARRB2,PRKACA,ADAM15,TEX14,DVL1,ABL1,ZFPM1	cyan	VSMC_M2
GO:0010001	0.00	1.00	25	173	glial cell differentiation	BP	0.07525	NFIB,GLI3,KLF15,VIM,BIN1,SLC45A3,TPPP,LEF1,B4GALT5,LAMB2,ARHGEF10,ADORA2A,GRN,MYRF,SERPINE2,ERBB2,MED12,GBA,TMEM98,ROR1,ASPA,ABL1,IL34,ABCA2,SLC8A3	cyan	VSMC_M2
GO:0051716	0.00	1.00	406	5042	cellular response to stimulus	BP	0.07637	STAT6,TCF21,ARHGEF25,OS9,AKAP12,FLOT1,DDAH2,MSH5,EHMT2,PLXNB2,RPS6KA2,IRF1,AFDN,DEPTOR,DAXX,FBXO32,PTPRK,ARHGAP18,GSDMD,TEAD3,NPTXR,MTCH1,GRINA,TLE1,CARD10,TRERF1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,KLF9,APPL2,PLA2G7,CARD19,TRIM14,ITGB8,GPNMB,EFEMP1,TRIL,RRAGC,EEPD1,ELMO1,STK40,AKT1S1,STK17A,GLI3,IRF3,RRAS,FLT3LG,NRP1,KLF15,RHOB,BAX,HBP1,SELENOW,NOP53,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,APOE,BCL3,AGAP3,SLC6A9,ACAA1,ATG7,CYP2S1,RHBDF2,LTBP4,SHKBP1,CAPN5,IL17RC,SOCS3,CAMK1,DZIP1,RPS16,TIMP2,ZFP36,LGALS3BP,CANT1,PAK4,RNF213,ARAP1,NPTX1,FOLR2,HGS,KAT2B,RFTN1,RHOG,ITGBL1,RFNG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,ADGRA2,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,ADGRD1,PRICKLE2,SLC15A4,ANGPT4,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,EFNA5,RHPN2,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,CAMKK2,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,TGM2,BPI,LRP4,PLCG1,BBS2,MMS19,ARHGAP1,GNAO1,SFRP5,C15orf62,MAPK8IP1,SORBS3,NISCH,MMP2,PTPN13,EXT2,PIK3C2B,LZTS2,STAT1,FAM13A,MOB2,GFRA2,CD81,NDN,FIBIN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,BOC,TPCN2,SEMA3B,MRGPRF,NFKB1,GNAI2,ADGRB2,RGMA,BCL9,UBA7,LEF1,PTGIS,SOX5,SIPA1L2,ATRNL1,LAMB2,APH1A,MN1,ARHGEF12,VEGFD,KIF7,ECM1,REC8,SEMA4B,RHBDD3,GRK5,CASP10,GAS2L1,ADCY1,FES,FURIN,VPS11,ERFE,CCS,BCL9L,SEMA6C,HEG1,VANGL2,LMO3,GATA5,FAM53B,RERG,STK25,SAMD10,FIBP,MAGEF1,MUS81,PHEX,ELL3,PTCHD1,RGL1,NFKBIA,FAM89B,LTBP3,LINC02212	cyan	VSMC_M2
GO:0006022	0.00	1.00	17	98	aminoglycan metabolic process	BP	0.07675	GNS,ST3GAL1,AP2A1,SGSH,HEXB,CHST14,EXT2,GUSB,NFKB1,B4GALT5,B4GAT1,FUCA1,NAGLU,B3GAT3,XYLT2,PDGFRB,HS3ST3B1	cyan	VSMC_M2
GO:2000026	0.00	1.00	99	1014	regulation of multicellular organismal development	BP	0.0776	CTDP1,PLXNB2,ZFPM2,IRF1,HMOX1,KIAA1324L,APPL2,ITGB8,GPNMB,EFEMP1,MEIS1,GLI3,RRAS,NRP1,RHOB,LRRC17,TMEM176B,BIN1,ATRAID,SLITRK6,PNP,ZFP36,PAK4,HGS,ADGRA2,PKDCC,HSPB6,ANGPT4,RARG,IGF1,TLR3,MAN2A1,WT1,SFRP2,WWTR1,TGM2,LRP4,PLCG1,STAT1,CHRNA7,CAPN3,TJP1,SEMA3B,ADGRB2,TPPP,RGMA,LEF1,PTGIS,B4GALT5,SOX5,VEGFD,ECM1,SEMA4B,CTSK,FES,PRUNE1,SEMA6C,STK25,ELL3,NFKBIA,LTBP3,B2M,WNT2B,ADAMTS7,GRN,VEGFB,RND2,ADD1,BMP4,RARRES3,DLG5,JUP,EPHA2,MYRF,SERPINE2,ERBB2,ZFP36L1,NTRK1,SLIT2,TP53,NUPR1,WARS,EPN2,TMEM98,PTPRS,ASPA,AGRN,ISG15,CLSTN1,FOXC2,ABL1,IL34,IST1,OAS2,SERPINF1,PML,GATA4,TMEM176A,ZFPM1	cyan	VSMC_M2

GO:0007399	0.00	1.00	166	1867	nervous system development	BP	0.07809	FLOT1,EHMT2,PLXNB2,PTPRK,TEAD3,MTCH1,NFIB,KIAA1324L,APPL2,ZBTB45,P3H1,MEIS1,COBL,GLI3,SIM1,AP2A1,GSN,SLC17A7,NRP1,KLF15,BAX,MEIS3,FZD4,MARK4,VIM,BIN1,APOE,COQ8B,SLITRK6,CAMK1,TIMP2,NPTX1,RHOG,RFNG,FGFR1,EFNB2,ADGRA2,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,TPP1,RARG,SCN1B,MAN2A1,EFNA5,POU6F1,HEXB,SFRP2,NDRG4,GLRB,EPHA3,SRC,TGM2,LRP4,BBS2,GNAO1,SLC5A3,PHACTR1,GFRA2,NDN,SLC45A3,CHRNA7,CTTN,BOC,SEMA3B,ADGRB2,TPPP,RGMA,LEF1,B4GALT5,SOX5,LAMB2,VEGFD,SEMA4B,NCKIPSD,ADCY1,FES,PRUNE1,SEMA6C,TACC2,VANGL2,KIF1A,STK25,ARPC5,ELL3,PTCHD1,MOV10,B2M,WNT2B,DPF2,ARHGEF10,ADORA2A,CCDC141,GRN,ASTN1,GPC2,ACAT1,RND2,BMP4,NAGLU,LDB2,NBL1,MAP1S,CC2D2A,NR2F6,DLG5,HDAC6,TMEM223,PQBP1,ARRB2,EPHA2,MYRF,DAGLA,TCF12,SERPINE2,ERBB2,PRKACA,ZFP36L1,NTRK1,SLIT2,TP53,CPLX2,HOXB1,HOXB2,MED12,GBA,PPP1R9B,NEO1,GPRC5B,LLGL1,TMEM98,ROR1,PTPRS,SH3GL1,EEF2,GLIS2,ABCD1,DVL1,ASPA,AGRN,TSC2,TCF3,NPHP4,RERE,CLSTN1,ABL1,FPGS,IL34,PBX3,IST1,ATP6V0D1,NFIA,ABCA2,SLC8A3,CHST8,SERPINF1,ATN1,SELENOP,CALM3,LRRC7,SDC4,STX3,PYGO2,EN1	cyan	VSMC_M2
GO:0031329	0.00	1.00	72	689	regulation of cellular catabolic process	BP	0.07915	EHMT2,EIF3H,HMOX1,TRIM14,RRAGC,RNF144A,BAX,NOP53,TRIM13,VIM,APOE,ATRAID,ATG7,EXOC7,TIMP2,ZFP36,SAMD4B,TRIM21,IGF1,CHMP4B,TP53INP2,PATL1,CAMKK2,PRKCD,FOXF2,PNPLA2,CTSA,CD81,TRIM8,IKBKE,TIRAP,CTTN,TPCN2,RGMA,EXOC8,WDR6,FURIN,VPS11,RNASEL,MAGEF1,MOV10,CAPN1,FYCO1,PSAP,HDAC6,GABARAP,GIPC1,PRKACA,ZFP36L1,UBQLN2,TP53,KAT8,UBQLN4,GBA,NUPR1,SNX33,ABCD1,DVL1,ELOB,TSC2,AXIN1,RHBDF1,CBFA2T3,ABL1,ATP6V0D1,ABCA2,MEX3D,PML,EEF1A2,GATA4,BMF,VPS26B	cyan	VSMC_M2
GO:0008283	0.00	1.00	134	1442	cell population proliferation	BP	0.09472	STAT6,PLXNB2,ZFPM2,RPS6KA2,IRF1,TGFBI,PTPRK,TEAD3,NFIB,HMOX1,KLF9,APPL2,P3H1,GPNMB,MEIS1,GLI3,FLT3LG,NRP1,BAX,MEIS3,APOE,ATRAID,PNP,TIMP2,ZFP36,FOLR2,HGS,KAT2B,RHOG,FGFR1,IL5RA,EFNB2,POC1B,LMO1,RARG,IGF1,WT1,SFRP2,WWTR1,NDRG4,PRKCD,SRC,TGM2,PLCG1,SFRP5,MAPK8IP1,MMP2,LZTS2,STAT1,CD81,NDN,CHRNA7,TJP1,TIRAP,TMEM115,GNAI2,LEF1,SOX5,MN1,VEGFD,WDR6,ECM1,GRK5,FES,TACC2,KIF1A,RERG,MUS81,ELL3,NFKBIA,LTBP3,B2M,WNT2B,ADORA2A,CAPN1,PLCD3,GRN,VEGFB,BMP4,IFI30,RARRES3,STAT5A,ZNF503,DLG5,JUP,EPHA2,DAGLA,ZBTB17,SERPINE2,MCC,ERBB2,BRAT1,ZFP36L1,IL27RA,NTRK1,AR,TP53,HOXB4,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,SLC16A2,KANK2,WARS,PDGFRB,IL13RA1,CRIP2,EEF2,PODN,TNFRSF14,TSC2,NELFB,RERE,RHBDF1,CBFA2T3,FOXC2,ABL1,OSGIN1,IL34,INCA1,SERPINF1,CD55,PML,JUNB,TMEM250,CDK9,SDC4,STX3,BST2,PYGO2,COL8A1,EMD	cyan	VSMC_M2
GO:0061438	0.00	1.00	4	7	renal system vasculature morphogenesis	BP	0.09472	TCF21,NRP1,BMP4,PDGFRB	cyan	VSMC_M2
GO:0061439	0.00	1.00	4	7	kidney vasculature morphogenesis	BP	0.09472	TCF21,NRP1,BMP4,PDGFRB	cyan	VSMC_M2
GO:0001944	0.00	1.00	64	607	vasculature development	BP	0.09877	MMP19,TCF21,ZFPM2,TGFBI,CARD10,HMOX1,ITGB8,GPNMB,MEIS1,GLI3,RRAS,NRP1,RHOB,BAX,FZD4,APOE,SOCS3,PAK4,RNF213,HGS,EFNB2,ADGRA2,HSPB6,ANGPT4,TLR3,WT1,SFRP2,PLCG1,MMP2,STAT1,CHRNA7,TJP1,ADGRB2,LGALS8,LEF1,PTGIS,VEGFD,ECM1,HEG1,PLCD3,GRN,HDAC5,VEGFB,BMP4,FKBP10,JUP,EPHA2,ERBB2,ZFP36L1,SLIT2,ADAM15,SHC1,WARS,EPN2,PDGFRB,NPRL3,FOXC2,ABL1,SERPINF1,PML,JUNB,GATA4,SAT1,COL8A1	cyan	VSMC_M2
GO:0042742	0.00	1.00	18	109	defense response to bacterium	BP	0.09895	GSDMD,BCL3,TLR3,PRKCD,BPI,TIRAP,TUSC2,GRN,EPHA2,IL27RA,SHC1,ACP5,ISG15,TNFRSF14,GBP6,OAS2,RPS19,IL22RA1	cyan	VSMC_M2
GO:0019076	0.00	1.00	8	29	viral release from host cell	BP	0.10141	TRIM13,TRIM21,CHMP4B,CHMP3,TRIM8,IST1,TRIM26,PML	cyan	VSMC_M2
GO:0035890	0.00	1.00	8	29	exit from host	BP	0.10141	TRIM13,TRIM21,CHMP4B,CHMP3,TRIM8,IST1,TRIM26,PML	cyan	VSMC_M2
GO:0035891	0.00	1.00	8	29	exit from host cell	BP	0.10141	TRIM13,TRIM21,CHMP4B,CHMP3,TRIM8,IST1,TRIM26,PML	cyan	VSMC_M2
GO:0001818	0.00	1.00	27	195	negative regulation of cytokine production	BP	0.10141	HMOX1,APPL2,GPNMB,BCL3,ZFP36,IGF1,BPI,CHRNA7,TUSC2,NFKB1,LEF1,FURIN,HOMER3,DHX58,ARRB2,EPHA2,IL27RA,GBA,ACP5,PTPRS,ABCD1,MIR197,PML,CARD8,NFKBIL1,BST2,ZFPM1	cyan	VSMC_M2
GO:0050792	0.00	1.00	19	119	regulation of viral process	BP	0.10141	TRIM14,GSN,STOM,TRIM13,ZFP36,TRIM21,CHMP3,PLSCR1,STAT1,TRIM8,RNASEL,ADAR,ISG15,OAS2,HEXIM1,TRIM26,PML,TMEM250,BST2	cyan	VSMC_M2
GO:0030203	0.00	1.00	16	93	glycosaminoglycan metabolic process	BP	0.10473	GNS,ST3GAL1,AP2A1,SGSH,HEXB,CHST14,EXT2,GUSB,NFKB1,B4GAT1,FUCA1,NAGLU,B3GAT3,XYLT2,PDGFRB,HS3ST3B1	cyan	VSMC_M2
GO:0046782	0.00	1.00	6	17	regulation of viral transcription	BP	0.10473	TRIM14,TRIM13,ZFP36,TRIM21,TRIM8,HEXIM1	cyan	VSMC_M2
GO:0016477	0.00	1.00	106	1120	cell migration	BP	0.11137	AKAP12,PLXNB2,AFDN,PTPRK,CARD10,GCNT1,HMOX1,APPL2,PLA2G7,ITGB8,GPNMB,ELMO1,GLI3,RRAS,NRP1,RHOB,BAX,LURAP1,FZD4,APOE,PAK4,RHOG,ITGBL1,FGFR1,EFNB2,ADGRA2,DCLK1,ACKR4,ANGPT4,IGF1,HEXB,SFRP2,NDRG4,PRKCD,EPHA3,SRC,PLCG1,NISCH,PIK3C2B,PHACTR1,CD81,NDN,TJP1,TIRAP,CTTN,SEMA3B,GNAI2,LGALS8,XG,LEF1,ATRNL1,LAMB2,VEGFD,ECM1,SEMA4B,SEMA6C,VANGL2,CTNNA3,ARPC5,FAM89B,CCDC141,GRN,ASTN1,HDAC5,GPC2,VEGFB,RND2,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,ARRB2,JUP,EPHA2,SERPINE2,MCC,GIPC1,BRAT1,IL27RA,SLIT2,HSD3B7,GBA,PPP1R9B,ADAM15,PBXIP1,KANK2,CENPV,ABCC1,PDGFRB,MAP2K3,PODN,TNFRSF14,RERE,RHBDF1,FOXC2,ABL1,OSGIN1,IL34,SERPINF1,PML,RPS19,PLPP3,SDC4,BST2	cyan	VSMC_M2
GO:0060443	0.00	1.00	9	37	mammary gland morphogenesis	BP	0.1127	STAT6,GLI3,BAX,SRC,CAPN1,BMP4,EPHA2,AR,PML	cyan	VSMC_M2

GO:0007626	0.00	1.00	20	132	locomotory behavior	BP	0.1127	MEIS1,FZD4,APOE,SLITRK6,GAA,ARRDC3,HEXB,GLRB,GNAO1,CSTB,ADORA2A,ASTN1,NAGLU,ARRB2,MTA1,PBX3,ABCA2,KCND2,SELENOP,EN1	cyan	VSMC_M2
GO:0007417	0.00	1.00	79	795	central nervous system development	BP	0.11573	PLXNB2,NFIB,MEIS1,GLI3,GSN,SLC17A7,NRP1,BAX,MEIS3,FZD4,VIM,BIN1,COQ8B,TIMP2,NPTX1,ADGRA2,DCLK1,TMEM108,TPP1,SCN1B,POU6F1,SFRP2,NDRG4,SRC,BBS2,GNAO1,PHACTR1,NDN,SLC45A3,TPPP,LEF1,B4GALT5,LAMB2,ADCY1,TACC2,KIF1A,ARPC5,PTCHD1,B2M,WNT2B,ADORA2A,CCDC141,GRN,ACAT1,BMP4,NAGLU,MAP1S,DLG5,ARRB2,MYRF,SERPINE2,ERBB2,SLIT2,TP53,HOXB1,HOXB2,MED12,GBA,PPP1R9B,TMEM98,ROR1,PTPRS,SH3GL1,GLIS2,ASPA,RERE,ABL1,FPGS,IL34,PBX3,ATP6V0D1,ABCA2,SLC8A3,CHST8,ATN1,SELENOP,CALM3,PYGO2,EN1	cyan	VSMC_M2
GO:0070887	0.00	1.00	194	2230	cellular response to chemical stimulus	BP	0.11994	STAT6,TCF21,OS9,AKAP12,FLOT1,EHMT2,RPS6KA2,IRF1,DAXX,FBXO32,PTPRK,TRERF1,HMOX1,KIAA1324L,KLF9,APPL2,PLA2G7,ITGB8,RRAGC,AKT1S1,IRF3,NRP1,KLF15,RHOB,BAX,SELENOW,NOP53,FZD4,VIM,APOE,AGAP3,ACAA1,ATG7,CYP2S1,LTBP4,IL17RC,SOCS3,RPS16,ZFP36,FOLR2,HGS,KAT2B,RHOG,FGFR1,IL5RA,ADGRA2,ACKR4,SMPD1,TMEM108,ANGPT4,RARG,IGF1,TLR3,WT1,EFNA5,CTSB,CAMKK2,SFRP2,PRKCD,EPHA3,SRC,CACNB3,TGM2,BPI,PLCG1,BBS2,GNAO1,SFRP5,MMP2,EXT2,STAT1,NDN,CHRNA7,IKBKE,CAPN3,TIRAP,PCSK6,SEMA3B,NFKB1,GNAI2,RGMA,LEF1,PTGIS,SOX5,MN1,VEGFD,ECM1,GAS2L1,ADCY1,FES,FURIN,VPS11,ERFE,CCS,BCL9L,LMO3,GATA5,STK25,FIBP,PHEX,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,B2M,AIFM2,CLEC3B,ADAMTS7,HDAC5,TMEM161A,VEGFB,ADD1,BMP4,QDPR,NBL1,STAT5A,HDAC6,PQBP1,ARRB2,JUP,ALOX15,EPHA2,IL17RA,CASP9,PLSCR3,GIPC1,ERBB2,PRKACA,ZFP36L1,IL27RA,NTRK1,PCGF2,UBIAD1,SLIT2,AR,TP53,HSD3B7,PDK2,GBA,PPP1R9B,ADAM15,SHC1,ADAR,KANK2,TEX14,GRIA1,NEO1,ABCC1,EPN2,PDGFRB,MCOLN1,IL13RA1,MAP2K3,EEF2,ABCD1,AGRN,ISG15,TNFRSF14,TSC2,NDOR1,SBNO2,PHPT1,GSTM4,FOXC2,ABL1,SLC2A8,IL34,GBP6,ATP6V0D1,OAS2,GAS1,SLC8A3,SERPINF1,KCND2,ZBTB7A,CD55,RAB43,PML,SERPINB6,RPS19,JUNB,GATA4,CARD8,CLIC2,VPS26B,CDK9,NFKBIL1,ADPRHL2,IL22RA1,RGS8,RGS10,RAB11B,MPV17,EMD	cyan	VSMC_M2
GO:0019080	0.00	1.00	15	86	viral gene expression	BP	0.12832	CTDP1,MGAT4B,ST3GAL1,TRIM14,TRIM13,ZFP36,TRIM21,EIF3F,MAN2A1,EDEM2,TRIM8,LEF1,FURIN,MON1B,HEXIM1	cyan	VSMC_M2
GO:0009887	0.00	1.00	78	784	animal organ morphogenesis	BP	0.12832	TSHZ1,STAT6,TCF21,ZFPM2,TLE1,NFIB,GCNT1,EFEMP1,MEIS1,STK40,GLI3,NRP1,BAX,MEIS3,TMEM176B,SLITRK6,GAA,RFNG,FGFR1,PRICKLE2,RARG,MAN2A1,WT1,SFRP2,WWTR1,NDRG4,SRC,CPE,TGM2,LRP4,BBS2,FOXF2,GNAO1,MMP2,EXT2,LZTS2,STAT1,LEF1,SOX5,ATRNL1,LAMB2,HEG1,VANGL2,GATA5,PHEX,LTBP3,WNT2B,CAPN1,WNK4,DGCR2,BMP4,NAGLU,NBL1,DLG5,EPHA2,PCGF2,SLIT2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,GBA,ADAM15,ACP5,PDGFRB,ROR1,DVL1,AGRN,FOXC2,ABL1,DNAAF1,PBX3,PML,GATA4,COL8A1,ZFPM1	cyan	VSMC_M2
GO:0022008	0.00	1.00	117	1272	neurogenesis	BP	0.13067	FLOT1,EHMT2,PLXNB2,PTPRK,TEAD3,MTCH1,NFIB,APPL2,P3H1,MEIS1,COBL,GLI3,AP2A1,NRP1,KLF15,BAX,FZD4,VIM,BIN1,APOE,SLITRK6,CAMK1,TIMP2,NPTX1,RHOG,FGFR1,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,MAN2A1,EFNA5,HEXB,SFRP2,NDRG4,EPHA3,TGM2,LRP4,GNAO1,PHACTR1,NDN,SLC45A3,CHRNA7,CTTN,BOC,SEMA3B,TPPP,RGMA,LEF1,B4GALT5,SOX5,LAMB2,VEGFD,SEMA4B,NCKIPSD,ADCY1,FES,PRUNE1,SEMA6C,KIF1A,STK25,ELL3,MOV10,B2M,WNT2B,ARHGEF10,ADORA2A,GRN,ASTN1,GPC2,RND2,BMP4,NAGLU,NBL1,MAP1S,NR2F6,DLG5,HDAC6,PQBP1,EPHA2,MYRF,DAGLA,TCF12,SERPINE2,ERBB2,NTRK1,SLIT2,TP53,MED12,GBA,PPP1R9B,NEO1,GPRC5B,LLGL1,TMEM98,ROR1,PTPRS,EEF2,DVL1,ASPA,AGRN,TCF3,NPHP4,RERE,ABL1,IL34,PBX3,IST1,ABCA2,SLC8A3,SERPINF1,LRRC7,SDC4,STX3,EN1	cyan	VSMC_M2
GO:0070613	0.00	1.00	11	52	regulation of protein processing	BP	0.1309	RPS6KA2,GSN,CAST,SPON1,SRC,CLEC3B,SERPINE2,PRKACA,TMEM98,GAS1,CARD8	cyan	VSMC_M2
GO:0046479	0.00	1.00	5	12	glycosphingolipid catabolic process	BP	0.1309	NEU1,NAGA,HEXB,PRKCD,GBA	cyan	VSMC_M2
GO:0031346	0.00	1.00	36	302	positive regulation of cell projection organization	BP	0.13523	PLXNB2,KCTD17,P3H1,COBL,AP2A1,NRP1,FZD4,MARK4,APOE,CAMK1,DZIP1,ARAP1,APBB1,SCN1B,NDRG4,EPHA3,SRC,C15orf62,RGMA,NCKIPSD,FES,STK25,GRN,GPC2,RND2,CROCC,NTRK1,SLIT2,ROR1,DVL1,AGRN,ENTR1,ATMIN,IST1,SERPINF1,LRRC7	cyan	VSMC_M2
GO:0002252	0.00	1.00	42	360	immune effector process	BP	0.13841	STAT6,ULBP2,CFB,ST3GAL1,HMOX1,APPL2,TRIL,COLEC11,BCL3,RFTN1,LAMP1,SLC15A4,TLR3,SERPING1,PRKCD,SRC,CD81,TUSC2,LEF1,FES,B2M,GRN,C1R,C1S,DHX58,PLD2,ARRB2,PLEKHM2,IL27RA,TP53,CPLX2,GPRC5B,TMEM98,C6,TNFRSF14,PTGDS,SBNO2,ABL1,CD55,RPS19,BST2,ZFPM1	cyan	VSMC_M2
GO:0051098	0.00	1.00	36	296	regulation of binding	BP	0.13929	FLOT1,HMOX1,NRP1,BAX,APOE,BCL3,CAMK1,DZIP1,RFNG,TRIM21,IGF1,SPON1,PRKCD,SRC,RGMA,LEF1,NFKBIA,B2M,PCBD1,HDAC5,ADD1,BMP4,ARRB2,PRKACA,ADAM15,PBXIP1,TEX14,DVL1,EDF1,ABL1,ZBTB7A,CALM3,CLIC2,CDK9,PYGO2,ZFPM1	cyan	VSMC_M2

GO:0023051	0.00	1.00	215	2524	regulation of signaling	BP	0.14103	TCF21,ARHGEF25,AKAP12,FLOT1,IRF1,DEPTOR,PACSIN2,ARHGAP18,NPTXR,MTCH1,GRINA,TLE1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,APPL2,CARD19,TRIM14,GPNMB,RRAGC,STK40,AKT1S1,GLI3,IRF3,RRAS,NRP1,KLF15,BAX,NOP53,MEIS3,LURAP1,TRIM13,FZD4,APOE,BCL3,SLC6A9,RHBDF2,LTBP4,SHKBP1,SOCS3,EHD3,TIMP2,CANT1,PAK4,RNF213,ARAP1,NPTX1,HGS,RFNG,FGFR1,TRIM21,RAB11FIP1,ADGRA2,SMPD1,TMEM108,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,EFNA5,TSHZ3,ARRDC3,PLSCR1,SFRP2,WWTR1,NDRG4,PRKCD,SRC,CACNB3,TGM2,LRP4,PLCG1,ARHGAP1,SFRP5,MAPK8IP1,SORBS3,NISCH,PTPN13,LZTS2,STAT1,FAM13A,CD81,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,NFKB1,GNAI2,RGMA,HADH,LEF1,PTGIS,SIPA1L2,MN1,ARHGEF12,KIF7,ECM1,GRK5,CASP10,ADCY1,FURIN,VPS11,ERFE,BCL9L,HEG1,LMO3,GATA5,FAM53B,STK25,ELL3,NFKBIA,FAM89B,LINC02210-CRHR1,FRMD8,ARHGEF10,BCR,ADORA2A,CAPN1,TMEM161A,TMEM101,HOMER3,GPC2,TMEM106A,TMBIM1,BMP4,NBL1,DLG5,HDAC6,DHX58,ARHGEF10L,ARRB2,JUP,ALOX15,EPHA2,AKAP5,GABARAP,SERPINE2,MCC,CGNL1,GIPC1,ERBB2,PRKACA,UBQLN2,NTRK1,PCGF2,SLIT2,AR,TP53,CPLX2,PDK2,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,KANK2,DENND4B,ARHGAP17,SLC44A2,GRIA1,NEO1,ULK3,GPRC5B,RASL10B,EPN2,PDGFRB,LLGL1,MAP2K3,ROR1,TRAF4,PTPRS,SH3GL1,GLIS2,DVL1,ISG15,TRAF7,TSC2,NPHP4,PHPT1,INPP5E,RAB11FIP3,AXIN1,NPRL3,RHBDF1,CLSTN1,ABL1,IL34,INCA1,RPS15,GAS1,SLC8A3,HEXIM1,ZBTB7A,CD55,NMT2,PML,PLPP3,GATA4,CALM3,CARD8,STX3,NFKBIL1,RGS19,RGS8,RGS10,OCIAD2,BST2,EMD	cyan	VSMC_M2
GO:0048870	0.00	1.00	114	1234	cell motility	BP	0.14103	AKAP12,PLXNB2,AFDN,PTPRK,ARHGAP18,CARD10,GCNT1,HMOX1,APPL2,RSPH9,PLA2G7,ITGB8,GPNMB,ELMO1,GLI3,RRAS,NRP1,RHOB,BAX,LURAP1,FZD4,APOE,TPPP2,PAK4,RHOG,ITGBL1,FGFR1,EFNB2,ADGRA2,DCLK1,ACKR4,ANGPT4,IGF1,HEXB,SFRP2,NDRG4,PRKCD,EPHA3,SRC,PLCG1,BBS2,NISCH,PIK3C2B,PHACTR1,CD81,NDN,TJP1,TIRAP,CTTN,SEMA3B,GNAI2,LGALS8,XG,LEF1,ATRNL1,LAMB2,VEGFD,ECM1,SEMA4B,FES,SEMA6C,VANGL2,CTNNA3,ARPC5,FAM89B,CCDC141,GRN,ASTN1,HDAC5,GPC2,VEGFB,RND2,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,PLD2,ARRB2,JUP,EPHA2,SERPINE2,MCC,GIPC1,BRAT1,IL27RA,SLIT2,HSD3B7,GBA,PPP1R9B,ADAM15,PBXIP1,KANK2,CENPV,ABCC1,PDGFRB,MAP2K3,PODN,TNFRSF14,NPHP4,PHPT1,RERE,RHBDF1,FOXC2,ABL1,OSGIN1,IL34,SERPINF1,PML,RPS19,PLPP3,SDC4,BST2	cyan	VSMC_M2
GO:0051674	0.00	1.00	114	1234	localization of cell	BP	0.14103	AKAP12,PLXNB2,AFDN,PTPRK,ARHGAP18,CARD10,GCNT1,HMOX1,APPL2,RSPH9,PLA2G7,ITGB8,GPNMB,ELMO1,GLI3,RRAS,NRP1,RHOB,BAX,LURAP1,FZD4,APOE,TPPP2,PAK4,RHOG,ITGBL1,FGFR1,EFNB2,ADGRA2,DCLK1,ACKR4,ANGPT4,IGF1,HEXB,SFRP2,NDRG4,PRKCD,EPHA3,SRC,PLCG1,BBS2,NISCH,PIK3C2B,PHACTR1,CD81,NDN,TJP1,TIRAP,CTTN,SEMA3B,GNAI2,LGALS8,XG,LEF1,ATRNL1,LAMB2,VEGFD,ECM1,SEMA4B,FES,SEMA6C,VANGL2,CTNNA3,ARPC5,FAM89B,CCDC141,GRN,ASTN1,HDAC5,GPC2,VEGFB,RND2,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,PLD2,ARRB2,JUP,EPHA2,SERPINE2,MCC,GIPC1,BRAT1,IL27RA,SLIT2,HSD3B7,GBA,PPP1R9B,ADAM15,PBXIP1,KANK2,CENPV,ABCC1,PDGFRB,MAP2K3,PODN,TNFRSF14,NPHP4,PHPT1,RERE,RHBDF1,FOXC2,ABL1,OSGIN1,IL34,SERPINF1,PML,RPS19,PLPP3,SDC4,BST2	cyan	VSMC_M2
GO:0045861	0.00	1.00	28	213	negative regulation of proteolysis	BP	0.14103	EIF3H,NOP53,BIN1,TIMP2,TRIM21,SERPING1,CAST,SFRP2,SRC,CSTB,ECM1,FURIN,ADORA2A,CPAMD8,HDAC6,DNAJB6,ARRB2,SERPINE2,GIPC1,TP53,TMEM98,RENBP,GAS1,SERPINF1,PML,SERPINB6,CARD8,BST2	cyan	VSMC_M2
GO:0030574	0.00	1.00	8	31	collagen catabolic process	BP	0.14103	MMP19,ADAMTS2,MMP17,CTSB,MMP2,CTSK,FURIN,ADAM15	cyan	VSMC_M2
GO:0060562	0.00	1.00	33	269	epithelial tube morphogenesis	BP	0.14103	TCF21,PLXNB2,COBL,GLI3,NRP1,RHOB,RARG,WT1,SFRP2,NDRG4,SRC,LZTS2,RGMA,LEF1,VANGL2,WNT2B,WNK4,BMP4,CC2D2A,DLG5,EPHA2,PRKACA,SLIT2,AR,MED12,DVL1,TSC2,FOXC2,ABL1,DNAAF1,PML,GATA4,SDC4	cyan	VSMC_M2
GO:0010646	0.00	1.00	214	2513	regulation of cell communication	BP	0.14103	TCF21,ARHGEF25,AKAP12,FLOT1,IRF1,DEPTOR,PACSIN2,ARHGAP18,NPTXR,MTCH1,GRINA,TLE1,ARHGAP39,HMOX1,LRRC19,KIAA1324L,APPL2,CARD19,TRIM14,GPNMB,RRAGC,STK40,AKT1S1,GLI3,IRF3,RRAS,NRP1,KLF15,BAX,NOP53,MEIS3,LURAP1,TRIM13,FZD4,APOE,BCL3,SLC6A9,RHBDF2,LTBP4,SHKBP1,SOCS3,TIMP2,CANT1,PAK4,RNF213,ARAP1,NPTX1,HGS,RFNG,FGFR1,TRIM21,RAB11FIP1,ADGRA2,SMPD1,TMEM108,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,EFNA5,TSHZ3,ARRDC3,PLSCR1,SFRP2,WWTR1,NDRG4,PRKCD,SRC,CACNB3,TGM2,LRP4,PLCG1,ARHGAP1,SFRP5,MAPK8IP1,SORBS3,NISCH,PTPN13,LZTS2,STAT1,FAM13A,CD81,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,TM2D3,PCSK6,NFKB1,GNAI2,RGMA,HADH,LEF1,PTGIS,SIPA1L2,MN1,ARHGEF12,KIF7,ECM1,GRK5,CASP10,ADCY1,FURIN,VPS11,ERFE,BCL9L,HEG1,LMO3,GATA5,FAM53B,STK25,ELL3,NFKBIA,FAM89B,LINC02210-CRHR1,FRMD8,ARHGEF10,BCR,ADORA2A,CAPN1,TMEM161A,TMEM101,HOMER3,GPC2,TMEM106A,TMBIM1,BMP4,NBL1,DLG5,HDAC6,DHX58,ARHGEF10L,ARRB2,JUP,ALOX15,EPHA2,AKAP5,GABARAP,SERPINE2,MCC,CGNL1,GIPC1,ERBB2,PRKACA,UBQLN2,NTRK1,PCGF2,SLIT2,AR,TP53,CPLX2,PDK2,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,KANK2,DENND4B,ARHGAP17,SLC44A2,GRIA1,NEO1,ULK3,GPRC5B,RASL10B,EPN2,PDGFRB,LLGL1,MAP2K3,ROR1,TRAF4,PTPRS,SH3GL1,GLIS2,DVL1,ISG15,TRAF7,TSC2,NPHP4,PHPT1,INPP5E,RAB11FIP3,AXIN1,NPRL3,RHBDF1,CLSTN1,ABL1,IL34,INCA1,RPS15,GAS1,SLC8A3,HEXIM1,ZBTB7A,CD55,NMT2,PML,PLPP3,GATA4,CALM3,CARD8,STX3,NFKBIL1,RGS19,RGS8,RGS10,OCIAD2,BST2,EMD	cyan	VSMC_M2

GO:0002455	0.00	1.00	7	24	humoral immune response mediated by circulating immunoglobulin	BP	0.14103	BCL3,SERPING1,CD81,C1R,C1S,C6,CD55	cyan	VSMC_M2
GO:0030100	0.00	1.00	24	174	regulation of endocytosis	BP	0.14103	RAB5B,FLOT1,PACSIN2,APPL2,AP2A1,SLC17A7,BIN1,APOE,TBC1D5,SMPD1,CLIP3,EPHA3,SRC,B2M,ARRB2,ALOX15,UBQLN2,STON2,SNX33,SH3GL1,TSC2,ABL1,ABCA2,CALM3	cyan	VSMC_M2
GO:0060341	0.00	1.00	69	675	regulation of cellular localization	BP	0.14103	OS9,CARD10,HMOX1,GLI3,GSN,STOM,BAX,MARK4,SLC6A9,CAMK1,ZFP36,RHOG,DCLK1,LAMP1,PKDCC,CLIP3,REEP5,EFNA5,CHMP3,TP53INP2,EDEM2,WWTR1,NDRG4,PRKCD,EPHA3,SRC,CACNB3,LRP4,PLCG1,ARHGAP1,SLC5A3,LZTS2,CD81,TRIM8,CAPN3,FES,VPS11,GPC2,TMBIM1,BMP4,B3GAT3,CROCC,JUP,EPHA2,AKAP5,ERBB2,PRKACA,ZFP36L1,AR,PPP1R9B,SLC51B,SNX33,TMEM98,GLIS2,DVL1,PHPT1,INPP5E,ENTR1,ABL1,ABCA2,GAS1,GRASP,PML,CALM3,CLIC2,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0050793	0.00	1.00	163	1852	regulation of developmental process	BP	0.14103	CTDP1,ZADH2,STAT6,FLOT1,PLXNB2,ZFPM2,IRF1,ARHGAP18,NFIB,HMOX1,KIAA1324L,APPL2,ITGB8,GPNMB,EFEMP1,MEIS1,COBL,GLI3,RRAS,NRP1,RHOB,BAX,LRRC17,FZD4,TMEM176B,BIN1,APOE,ATRAID,LTBP4,SLITRK6,SOCS3,CAMK1,PNP,TIMP2,ZFP36,PAK4,ARAP1,GPAT4,HGS,RHOG,FGFR1,EFNB2,ADGRA2,LZTS3,PKDCC,HSPB6,PRICKLE2,ANGPT4,RARG,IGF1,TLR3,MAN2A1,WT1,EFNA5,HEXB,SFRP2,WWTR1,EPHA3,SRC,TGM2,LRP4,PLCG1,ZHX3,BBS2,SFRP5,C15orf62,STAT1,SLC45A3,CHRNA7,CAPN3,TJP1,CTTN,BOC,SEMA3B,NFKB1,ADGRB2,TPPP,RGMA,LEF1,PTGIS,B4GALT5,SOX5,VEGFD,ECM1,SEMA4B,CTSK,FES,PRUNE1,BCL9L,SEMA6C,VANGL2,LMO3,GATA5,KIF1A,STK25,ELL3,NFKBIA,MOV10,LTBP3,B2M,WNT2B,DPF2,ADAMTS7,GRN,HDAC5,VEGFB,RND2,VAT1,TMBIM1,ADD1,BMP4,RARRES3,NBL1,CAPZB,STAT5A,DLG5,HDAC6,PQBP1,ARRB2,JUP,EPHA2,MYRF,TCF12,SERPINE2,ERBB2,PRKACA,ZFP36L1,NTRK1,SMOC1,SLIT2,AR,TP53,HOXB4,MED12,ZMYM3,NUPR1,SIGLEC15,WARS,GPRC5B,EPN2,TMEM98,ROR1,PTPRS,DVL1,ASPA,AGRN,ISG15,NELFB,TCF3,CLSTN1,FOXC2,ABL1,IL34,IST1,OAS2,SERPINF1,PML,RPS19,JUNB,GATA4,CDK9,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0006664	0.00	1.00	15	87	glycolipid metabolic process	BP	0.14452	NEU1,B3GALT4,NAGA,ST3GAL1,ITGB8,BAX,SMPD1,HEXB,PRKCD,B4GALT5,FUCA1,GBA,PIGQ,ABCA2,AL157935.2	cyan	VSMC_M2
GO:1903509	0.00	1.00	15	87	liposaccharide metabolic process	BP	0.14452	NEU1,B3GALT4,NAGA,ST3GAL1,ITGB8,BAX,SMPD1,HEXB,PRKCD,B4GALT5,FUCA1,GBA,PIGQ,ABCA2,AL157935.2	cyan	VSMC_M2
GO:0007034	0.00	1.00	20	137	vacuolar transport	BP	0.14538	RHOB,BIN1,EHD3,HGS,LAMP1,SLC15A4,GNPTAB,CHMP4B,CHMP3,TPCN2,VPS11,TMEM50A,M6PR,GRN,PSAP,USE1,UBXN6,NAGPA,MON1B,ATP6V0D1	cyan	VSMC_M2
GO:0043123	0.00	1.00	22	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	0.14677	HMOX1,TRIM14,IRF3,LURAP1,TRIM13,CANT1,TRIM21,RBCK1,TLR3,TGM2,TRIM8,IKBKE,TIRAP,ECM1,CASP10,TMEM101,TMEM106A,SLC44A2,GPRC5B,ROR1,ABL1,BST2	cyan	VSMC_M2
GO:0032269	0.00	1.00	76	760	negative regulation of cellular protein metabolic process	BP	0.14677	EIF3H,DEPTOR,P3H1,AKT1S1,AASS,KLF15,BAX,NOP53,BIN1,APOE,ATRAID,SOCS3,TIMP2,ZFP36,SAMD4B,KAT2B,SH3BP5,TRIM21,SMPD1,SNTA1,PATL1,SERPING1,CAST,SFRP2,WWTR1,PRKCD,SRC,MAPK8IP1,PTPN13,GFRA2,CAPN3,CSTB,NFKB1,GNAI2,TPPP,ECM1,FURIN,HEG1,MOV10,ADORA2A,BMP4,CPAMD8,HDAC6,DNAJB6,ARRB2,SERPINE2,GIPC1,ZFP36L1,MLLT6,SLIT2,TP53,GBA,PPP1R9B,ADAR,WARS,TMEM98,MLLT1,DVL1,ISG15,RENBP,TSC2,INPP5E,ABL1,INCA1,RPS15,GAS1,MEX3D,SLC8A3,HEXIM1,SERPINF1,PML,SERPINB6,PLPP3,CALM3,CARD8,BST2	cyan	VSMC_M2
GO:0001655	0.00	1.00	34	283	urogenital system development	BP	0.14677	TCF21,GCNT1,GLI3,NRP1,KLF15,BAX,RARG,WT1,WWTR1,LRP4,LZTS2,STAT1,LAMB2,APH1A,VANGL2,WNT2B,PSAP,ACAT1,WNK4,BMP4,CC2D2A,DLG5,CASP9,SLIT2,AR,KANK2,PDGFRB,GLIS2,FOXC2,NFIA,SERPINF1,SDC4,PYGO2,MPV17	cyan	VSMC_M2
GO:1903317	0.00	1.00	11	54	regulation of protein maturation	BP	0.15045	RPS6KA2,GSN,CAST,SPON1,SRC,CLEC3B,SERPINE2,PRKACA,TMEM98,GAS1,CARD8	cyan	VSMC_M2
GO:0009100	0.00	1.00	36	299	glycoprotein metabolic process	BP	0.15045	MGAT4B,B3GALT4,ST3GAL1,GCNT1,GALNT12,FKRP,TRIM13,CANT1,SGSH,GNPTAB,IGF1,MAN2A1,DPY19L3,GALNT18,EDEM2,CHST14,EXT2,PCSK6,B4GALT4,B4GALT5,GCNT7,B4GAT1,VEGFB,TMEM106A,PORCN,GANAB,B3GAT3,XYLT2,SLC51B,PRKCSH,NUDT14,NAGPA,ABCA2,CHST8,HS3ST3B1,AL157935.2	cyan	VSMC_M2

GO:0030154	0.00	1.00	247	2966	cell differentiation	BP	0.15045	CTDP1,ZADH2,MMP19,STAT6,TCF21,FLOT1,EHMT2,PLXNB2,ZFPM2,RPS6KA2,IRF1,AFDN,TGFBI,PTPRK,ST3GAL1,TEAD3,MTCH1,NFIB,MEA1,APPL2,IARS,ITGB8,P3H1,GPNMB,EFEMP1,BBS9,MEIS1,COBL,GLI3,SIM1,AP2A1,RRAS,NRP1,KLF15,RHOB,BAX,LRRC17,FZD4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,LTBP4,SLITRK6,SOCS3,CAMK1,PLD3,PNP,DZIP1,TPPP2,TIMP2,ZFP36,NPTX1,GPAT4,RHOG,RFNG,CATSPERG,FGFR1,EFNB2,ADGRA2,DCLK1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,CLIP3,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,TP53INP2,CTSB,HEXB,SFRP2,WWTR1,NDRG4,NDRG3,EPHA3,SRC,TGM2,LRP4,ZHX3,BBS2,FOXF2,GNAO1,SFRP5,MMP2,EXT2,STAT1,PHACTR1,HPS6,CD81,NDN,SLC45A3,CHRNA7,CAPN3,TJP1,TIRAP,AGFG1,CTTN,TM2D3,BOC,TUSC2,SEMA3B,NFKB1,SPOCD1,TPPP,RGMA,BCL9,LEF1,B4GALT5,SOX5,ATRNL1,EGFL6,LAMB2,VEGFD,ECM1,REC8,SEMA4B,NCKIPSD,ADCY1,FES,PRUNE1,BCL9L,SEMA6C,HEG1,LMO3,GATA5,KIF1A,CLCN2,STK25,RNASEL,ELL3,NFKBIA,MOV10,LTBP3,B2M,WNT2B,DPF2,ARHGEF10,BCR,ADORA2A,ADAMTS7,GRN,ASTN1,HDAC5,PSAP,GPC2,RND2,ADD1,BMP4,NAGLU,MAEA,RARRES3,NBL1,MAP1S,ZNF503,NR2F6,DLG5,HDAC6,PQBP1,DNAJB6,ARRB2,EPHA2,MYRF,DAGLA,TCF12,SERPINE2,CASP9,KAZN,ERBB2,PRKACA,ZFP36L1,NTRK1,SMOC1,SLIT2,AR,TP53,CPLX2,KAT8,HOXB4,MED12,GBA,PPP1R9B,ADAM15,NUPR1,PBXIP1,ADAR,SIGLEC15,NEO1,GPRC5B,PDGFRB,FLII,LLGL1,TMEM98,ROR1,PTPRS,MOSPD1,RETREG1,EEF2,GLIS2,DVL1,ASPA,AGRN,ISG15,NELFB,TCF3,NPHP4,SBNO2,EDF1,RERE,CBFA2T3,FOXC2,ABL1,OSGIN1,HSBP1,CNN3,IL34,PBX3,IST1,ABCA2,RPS15,GAS1,PTGFRN,SLC8A3,SERPIN	cyan	VSMC_M2
GO:0033036	0.00	1.00	202	2356	macromolecule localization	BP	0.15302	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,AFDN,PACSIN2,CUTA,PTPRK,GGA1,CARD10,APPL2,ATP10D,TRIM14,TBC1D2,P3H1,BBS9,RRAGC,EEPD1,TBC1D17,GLI3,AP2A1,CADPS2,GSN,STOM,NRP1,RHOB,BAX,DENND2A,NOP53,FZD4,MARK4,APOE,BCL3,ATG7,EXOC7,RHBDF2,CAMK1,EHD3,CMTM6,OSBPL10,DZIP1,ZFP36,STARD10,HGS,TBC1D5,RFTN1,RHOG,TRIM21,RAB11FIP1,DCLK1,LAMP1,APBB1,PKDCC,TPP1,CLIP3,SLC15A4,GNPTAB,IGF1,EFNA5,CHMP4B,CHMP3,TP53INP2,EDEM2,ARRDC3,PLSCR1,HEXB,WWTR1,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,LRP4,BBS2,ARHGAP1,EXOC2,SLC5A3,PNPLA2,CRACR2B,SYS1,LZTS2,CTSA,HPS6,CD81,TRIM8,IKBKE,OSBPL5,CAPN3,TJP1,AGFG1,CTTN,TMEM115,TPCN2,NFKB1,LRP10,HADH,DISP1,SGSM1,EXOC8,RHBDD3,GAS2L1,FURIN,VPS11,ERFE,HEG1,VANGL2,KIF1A,FAM53B,PARD3B,ATG4B,NFKBIA,LINC02210-CRHR1,M6PR,ADORA2A,RPGR,PSAP,HOMER3,GPC2,TMBIM1,WNK4,BMP4,NBL1,CC2D2A,PORCN,DLG5,USE1,HDAC6,B3GAT3,WDR45,CROCC,DNAJB6,ARRB2,JUP,EPHA2,AKAP5,GABARAP,PLEKHM2,MCC,CGNL1,PLSCR3,GIPC1,ERBB2,STARD3,PRKACA,ZFP36L1,AR,TP53,GLMP,NPC2,GBA,PPP1R9B,SLC51B,ATP8B2,SPNS1,SNX33,ABCC1,MCOLN1,LLGL1,TMEM98,ZDHHC9,NAGPA,CPT2,GLIS2,ABCD1,DVL1,SGSM2,AGRN,ISG15,TSC2,SLC9A3R2,NPHP4,PHPT1,SLC10A3,INPP5E,RAB11FIP3,ENTR1,RHBDF1,CLSTN1,ABL1,MON1B,IST1,LCAT,APOL5,ABCA2,MEX3D,ZBTB7A,RAB43,DGAT1,GRASP,PML,CALM3,SCAMP4,LRRC7,VPS26B,TMEM250,STX3,RAB11B,MCFD2,EMD,UBL5	cyan	VSMC_M2
GO:0050790	0.00	1.00	161	1823	regulation of catalytic activity	BP	0.15457	ARHGEF25,DDAH2,PPP6R2,PLXNB2,TBC1D22A,AFDN,DEPTOR,DAXX,ARHGAP18,MTCH1,CARD10,ARHGAP39,TBC1D2,ELMO1,TBC1D17,AKT1S1,GSN,NRP1,BAX,DENND2A,FZD4,CAB39L,BIN1,APOE,AGAP3,SOCS3,CAMK1,TIMP2,ZFP36,ARAP1,HGS,KAT2B,TBC1D5,PPP1R27,RHOG,FGFR1,SH3BP5,SMPD1,MMP17,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,SERPING1,CAST,CTSB,ARRDC3,PLSCR1,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,TGM2,ARHGAP1,GNAO1,MAPK8IP1,SLC5A3,PHACTR1,CTSA,FAM13A,CD81,CHRNA7,CAPN3,TIRAP,AGFG1,PCSK6,CSTB,NFKB1,GNAI2,RGMA,SGSM1,SIPA1L2,APH1A,ARHGEF12,ECM1,CASP10,ANXA9,FURIN,CCS,HEG1,RGL1,LINC02210-CRHR1,ARHGEF10,BCR,ADORA2A,CAPN1,RPGR,GRN,PCOLCE,PSAP,TMBIM1,BMP4,RARRES3,LDB2,CPAMD8,HDAC6,ARHGEF10L,B3GAT3,DNAJB6,ARRB2,EPHA2,AKAP5,SERPINE2,CASP9,ERBB2,NTRK1,SLIT2,TP53,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,DENND4B,ARHGAP17,DOCK6,WARS,GPRC5B,PDGFRB,LLGL1,MAP2K3,ROR1,MLLT1,TRAF4,WDR81,DVL1,SGSM2,AGRN,RENBP,TSC2,PHPT1,AXIN1,NPRL3,RALGDS,ABL1,CNN3,IL34,OAS2,INCA1,ABCA2,RPS15,SLC8A3,HEXIM1,SERPINF1,PML,SERPINB6,EEF1A2,CALM3,CARD8,GCHFR,SDC4,PSMB9,RGS8,RGS10,BST2,INKA1,GTF2H4	cyan	VSMC_M2

GO:0065008	0.00	1.00	233	2770	regulation of biological quality	BP	0.15864	STAT6,MOXD1,AKAP12,FLOT1,PLXNB2,RPS6KA2,DEPTOR,TAPBP,ARHGAP18,GRINA,KCTD17,HMOX1,LRRC19,ACO1,APPL2,ATP10D,IARS,P3H1,AKT1S1,CADPS2,GSN,SLC17A7,NRP1,KLF15,RHOB,BAX,NOP53,TSPAN1,FZD4,VIM,BIN1,APOE,SLC6A9,CYP2S1,LTBP4,PLB1,SLITRK6,CAMK1,EHD3,CMTM6,ZFP36,SAMD4B,GAA,ARAP1,GPAT4,SLC4A9,RHOG,TRIM21,POC1B,RAB11FIP1,LAMP1,ACKR4,TMEM108,LZTS3,TPP1,SLC15A4,LMO1,ATP4A,RARG,SCN1B,IGF1,SNTA1,EFNA5,CHMP4B,CHMP3,TP53INP2,PATL1,TSHZ3,GGCX,SERPING1,CTSB,ARRDC3,PLSCR1,HEXB,WWTR1,GLRB,PRKCD,SRC,CACNB3,TGM2,LRP4,DECR1,PLCG1,BBS2,C15orf62,NISCH,EXT2,PNPLA2,STAT1,CTSA,HPS6,CD81,NDN,CHRNA7,IKBKE,CAPN3,TJP1,TIRAP,CTTN,PCSK6,TUSC2,TPCN2,SEMA3B,NFKB1,GNAI2,RGMA,HADH,IP6K1,B4GALT5,SV2A,SSH3,SEMA4B,CTSK,ADCY1,FES,FURIN,VPS11,ERFE,SEMA6C,HEG1,KIF1A,CLCN2,CYB561,RNASEL,FIBP,CTNNA3,ARPC5,MOV10,LTBP3,LINC02210-CRHR1,B2M,KCND3,ADORA2A,GRN,RND2,WNK4,ADD1,BMP4,IFI30,MAEA,LDB2,CAPZB,STAT5A,PORCN,DLG5,HDAC6,CHRNE,CROCC,ARRB2,JUP,ALOX15,WIZ,AKAP5,DAGLA,SERPINE2,PLSCR3,GIPC1,STARD3,PRKACA,ZFP36L1,NTRK1,CLCN6,MLLT6,SLIT2,AR,TMEM175,TP53,CPLX2,GLMP,NPC2,PDK2,GBA,SLC51B,ADAR,SLC16A2,ATP8B2,ACP5,SIGLEC15,GRIA1,NEO1,RASL10B,ABCC1,MCOLN1,FLII,PIEZO2,DHRS13,PTPRS,SH3GL1,CPT2,GLIS2,WDR81,ABCD1,DVL1,AGRN,ISG15,RENBP,NPHP4,PHPT1,RHOT2,RAB11FIP3,H6PD,CLSTN1,FOXC2,ABL1,IST1,LCAT,ATP6V0D1,OAS2,ABCA2,CNNM3,MEX3D,ZNF205,SLC8A3,CHST8,SERPINF1,KCND2,ZBTB7A,CD55,DGAT1,GRASP,PML,RPS19,PLPP3,GATA4,C	cyan	VSMC_M2
GO:0016139	0.00	1.00	4	8	glycoside catabolic process	BP	0.15864	NAGA,GUSB,FUCA1,GBA	cyan	VSMC_M2
GO:0044242	0.00	1.00	23	164	cellular lipid catabolic process	BP	0.15864	NEU1,NAGA,PLA2G7,ACAA1,ECH1,SMPD1,HEXB,PRKCD,DECR1,PLBD2,PLCG1,PNPLA2,ACADS,HADH,FUCA1,ECHS1,ACAT1,DAGLA,GBA,CPT2,ABCD1,PNPLA7,CRAT	cyan	VSMC_M2
GO:0010594	0.00	1.00	22	157	regulation of endothelial cell migration	BP	0.15933	CARD10,HMOX1,RRAS,NRP1,RHOB,APOE,FGFR1,ADGRA2,ANGPT4,PLCG1,GRN,HDAC5,BMP4,STAT5A,JUP,EPHA2,SLIT2,MAP2K3,FOXC2,ABL1,SERPINF1,PLPP3	cyan	VSMC_M2
GO:0044255	0.00	1.00	75	743	cellular lipid metabolic process	BP	0.15955	ZADH2,CHKB,NEU1,B3GALT4,NAGA,ST3GAL1,APPL2,PLA2G7,ITGB8,SLC44A1,BAX,ACSS1,APOE,ACAA1,CYP2S1,PLB1,SOCS3,OSBPL10,ECH1,GPAT4,SMPD1,CYP4V2,ACSS2,LPCAT4,PLSCR1,HEXB,PRKCD,DECR1,PLBD2,PLCG1,PTDSS1,PNPLA2,PIK3C2B,SLC45A3,OSBPL5,ACADS,B4GALT4,HADH,IP6K1,PTGIS,B4GALT5,RLBP1,ERFE,FUCA1,ECHS1,PSAP,ACAT1,RARRES3,PORCN,PLD2,ALOX15,DAGLA,PLSCR3,NPC2,PDK2,GBA,SLC44A2,PDGFRB,CERS4,DHRS13,CPT2,ABCD1,PNPLA7,PTGDS,PIGQ,INPP5E,PLPP2,GSTM4,CRAT,LCAT,ABCA2,ACOT6,DGAT1,PLPP3,AL157935.2	cyan	VSMC_M2
GO:0051248	0.00	1.00	80	813	negative regulation of protein metabolic process	BP	0.15955	EIF3H,DEPTOR,P3H1,AKT1S1,AASS,KLF15,BAX,NOP53,BIN1,APOE,ATRAID,SOCS3,TIMP2,ZFP36,SAMD4B,KAT2B,SH3BP5,TRIM21,SMPD1,IGF1,SNTA1,PATL1,SERPING1,CAST,SPON1,SFRP2,WWTR1,PRKCD,SRC,MAPK8IP1,PTPN13,CTSA,GFRA2,CHRNA7,CAPN3,CSTB,NFKB1,GNAI2,TPPP,ECM1,FURIN,HEG1,MOV10,ADORA2A,BMP4,CPAMD8,HDAC6,DNAJB6,ARRB2,SERPINE2,GIPC1,ZFP36L1,MLLT6,SLIT2,TP53,GBA,PPP1R9B,ADAR,WARS,TMEM98,MLLT1,DVL1,ISG15,RENBP,TSC2,INPP5E,ABL1,INCA1,RPS15,GAS1,MEX3D,SLC8A3,HEXIM1,SERPINF1,PML,SERPINB6,PLPP3,CALM3,CARD8,BST2	cyan	VSMC_M2
GO:0032880	0.00	1.00	70	693	regulation of protein localization	BP	0.15955	OS9,AFDN,CARD10,TRIM14,P3H1,GLI3,GSN,STOM,MARK4,APOE,RHBDF2,CAMK1,RHOG,TRIM21,RAB11FIP1,DCLK1,APBB1,PKDCC,CLIP3,IGF1,EFNA5,TP53INP2,EDEM2,WWTR1,PRKCD,EPHA3,SRC,CACNB3,LRP4,SLC5A3,LZTS2,CD81,TRIM8,HADH,DISP1,RHBDD3,VPS11,ADORA2A,GPC2,TMBIM1,BMP4,HDAC6,B3GAT3,CROCC,DNAJB6,JUP,EPHA2,AKAP5,PLEKHM2,ERBB2,PRKACA,AR,PPP1R9B,SLC51B,SNX33,LLGL1,TMEM98,GLIS2,DVL1,PHPT1,INPP5E,RAB11FIP3,ENTR1,RHBDF1,ABCA2,GRASP,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0016042	0.00	1.00	29	225	lipid catabolic process	BP	0.15955	NEU1,NAGA,PLA2G7,IAH1,APOE,ACAA1,ECH1,SMPD1,HEXB,PRKCD,DECR1,PLBD2,PLCG1,PNPLA2,ACADS,HADH,STS,FUCA1,ECHS1,PLCD3,ACAT1,RARRES3,PLD2,DAGLA,GBA,CPT2,ABCD1,PNPLA7,CRAT	cyan	VSMC_M2
GO:0001843	0.00	1.00	14	82	neural tube closure	BP	0.16209	PLXNB2,COBL,RARG,SFRP2,RGMA,VANGL2,BMP4,CC2D2A,PRKACA,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0002682	0.00	1.00	89	915	regulation of immune system process	BP	0.16497	STAT6,FLOT1,CFB,IRF1,HMOX1,LRRC19,APPL2,PLA2G7,GPNMB,TRIL,MEIS1,COLEC11,GLI3,IRF3,BAX,NOP53,LRRC17,TMEM176B,APOE,RHBDF2,PNP,ZFP36,RFTN1,RHOG,TRIM21,LAMP1,SLC15A4,LMO1,RBCK1,RARG,IGF1,TLR3,SERPING1,PLSCR1,PRKCD,SRC,CACNB3,BPI,PLCG1,MAPK8IP1,STAT1,CD81,IKBKE,TIRAP,XG,LEF1,VEGFD,ECM1,RHBDD3,FES,FURIN,NFKBIA,B2M,ADORA2A,GRN,C1R,C1S,VEGFB,PIANP,BMP4,NBL1,DLG5,PQBP1,DHX58,PLD2,ARRB2,ALOX15,ERBB2,ZFP36L1,IL27RA,SLIT2,ADAR,GPRC5B,C6,PTPRS,ISG15,TNFRSF14,PHPT1,FAM3A,ABL1,IL34,HEXIM1,CD55,RPS19,SDC4,NFKBIL1,BST2,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0051348	0.00	1.00	28	219	negative regulation of transferase activity	BP	0.16623	DEPTOR,AKT1S1,APOE,ZFP36,KAT2B,SH3BP5,SMPD1,SFRP2,WWTR1,PRKCD,SRC,MAPK8IP1,HEG1,ADORA2A,BMP4,TP53,GBA,ADAR,WARS,MLLT1,DVL1,TSC2,PHPT1,ABL1,INCA1,RPS15,SLC8A3,HEXIM1	cyan	VSMC_M2
GO:0035456	0.00	1.00	6	19	response to interferon-beta	BP	0.16638	IRF1,TLR3,PLSCR1,STAT1,IKBKE,BST2	cyan	VSMC_M2
GO:0098876	0.00	1.00	19	129	vesicle-mediated transport to the plasma membrane	BP	0.16638	GGA1,EHD3,CMTM6,PKDCC,NDRG4,BBS2,ARHGAP1,EXOC2,SYS1,OSBPL5,EXOC8,AKAP5,LLGL1,RAB11FIP3,ENTR1,CLSTN1,GRASP,STX3,RAB11B	cyan	VSMC_M2
GO:0061005	0.00	1.00	10	49	cell differentiation involved in kidney development	BP	0.16646	TCF21,GLI3,KLF15,WT1,WWTR1,STAT1,LAMB2,BMP4,GLIS2,FOXC2	cyan	VSMC_M2

GO:0050776	0.00	1.00	57	538	regulation of immune response	BP	0.16707	STAT6,FLOT1,CFB,IRF1,HMOX1,LRRC19,APPL2,TRIL,COLEC11,IRF3,BAX,NOP53,APOE,RHBDF2,RFTN1,TRIM21,LAMP1,SLC15A4,RBCK1,TLR3,SERPING1,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,STAT1,CD81,IKBKE,TIRAP,ECM1,FES,FURIN,NFKBIA,B2M,GRN,C1R,C1S,PIANP,PQBP1,DHX58,PLD2,ARRB2,ALOX15,IL27RA,ADAR,C6,PTPRS,ISG15,TNFRSF14,PHPT1,FAM3A,ABL1,HEXIM1,CD55,RPS19,NFKBIL1	cyan	VSMC_M2
GO:0048858	0.00	1.00	54	520	cell projection morphogenesis	BP	0.16707	FLOT1,PLXNB2,PACSIN2,NFIB,COBL,GLI3,NRP1,FZD4,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,EPHA3,SRC,LRP4,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,KIF1A,STK25,MOV10,ADORA2A,RND2,NBL1,MAP1S,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1	cyan	VSMC_M2
GO:0005975	0.00	1.00	50	458	carbohydrate metabolic process	BP	0.16806	NEU1,B3GALT4,NAGA,STK40,AP2A1,GAA,KAT2B,DCXR,PGGHG,GNPTAB,IGF1,MAN2A1,EDEM2,HEXB,STBD1,SRC,CHST14,NISCH,EXT2,SLC5A3,SLC45A3,PHKG1,GUSB,NFKB1,B4GALT4,B4GALT5,ERFE,FUCA1,G6PC3,PGLS,GANAB,B3GAT3,BRAT1,TP53,PDK2,NUPR1,MAN2C1,NAGPA,IDH3G,RENBP,FAM3A,PIGQ,INPP5E,H6PD,CBFA2T3,SLC2A8,CHST8,ZBTB7A,NAGK,AL157935.2	cyan	VSMC_M2
GO:0010976	0.00	1.00	20	140	positive regulation of neuron projection development	BP	0.16806	PLXNB2,P3H1,COBL,AP2A1,APOE,CAMK1,APBB1,SCN1B,NDRG4,EPHA3,RGMA,NCKIPSD,FES,GRN,GPC2,NTRK1,ROR1,DVL1,SERPINF1,LRRC7	cyan	VSMC_M2
GO:0050777	0.00	1.00	19	128	negative regulation of immune response	BP	0.16806	STAT6,HMOX1,RHBDF2,TRIM21,SERPING1,SRC,PLCG1,FURIN,GRN,DHX58,ARRB2,ALOX15,IL27RA,ADAR,ISG15,TNFRSF14,FAM3A,CD55,RPS19	cyan	VSMC_M2
GO:0072001	0.00	1.00	31	256	renal system development	BP	0.16806	TCF21,GCNT1,GLI3,NRP1,KLF15,BAX,WT1,WWTR1,LRP4,LZTS2,STAT1,LAMB2,APH1A,VANGL2,WNT2B,ACAT1,WNK4,BMP4,CC2D2A,DLG5,CASP9,SLIT2,KANK2,PDGFRB,GLIS2,FOXC2,NFIA,SERPINF1,SDC4,PYGO2,MPV17	cyan	VSMC_M2
GO:0046718	0.00	1.00	16	100	viral entry into host cell	BP	0.16806	TRIM14,GSN,NRP1,EFNB2,TRIM21,LAMP1,SMPD1,CTSB,PLSCR1,CD81,TRIM8,TPCN2,EPHA2,TNFRSF14,CD55,TRIM26	cyan	VSMC_M2
GO:0060606	0.00	1.00	14	83	tube closure	BP	0.16854	PLXNB2,COBL,RARG,SFRP2,RGMA,VANGL2,BMP4,CC2D2A,PRKACA,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0048869	0.00	1.00	251	3033	cellular developmental process	BP	0.16854	CTDP1,ZADH2,MMP19,STAT6,TCF21,FLOT1,EHMT2,PLXNB2,ZFPM2,RPS6KA2,IRF1,AFDN,PACSIN2,TGFBI,PTPRK,ST3GAL1,TEAD3,MTCH1,NFIB,MEA1,APPL2,IARS,ITGB8,P3H1,GPNMB,EFEMP1,BBS9,MEIS1,COBL,GLI3,SIM1,AP2A1,RRAS,NRP1,KLF15,RHOB,BAX,LRRC17,FZD4,VIM,TMEM176B,BIN1,APOE,BCL3,ATRAID,LTBP4,SLITRK6,SOCS3,CAMK1,PLD3,PNP,DZIP1,TPPP2,TIMP2,ZFP36,NPTX1,GPAT4,RHOG,RFNG,CATSPERG,FGFR1,EFNB2,ADGRA2,DCLK1,TMEM108,LZTS3,APBB1,PKDCC,TPP1,CLIP3,RARG,SCN1B,IGF1,TLR3,MAN2A1,WT1,EFNA5,TP53INP2,CTSB,HEXB,SFRP2,WWTR1,NDRG4,NDRG3,PRKCD,EPHA3,SRC,TGM2,LRP4,ZHX3,BBS2,FOXF2,GNAO1,SFRP5,MMP2,EXT2,STAT1,PHACTR1,HPS6,CD81,NDN,SLC45A3,CHRNA7,CAPN3,TJP1,TIRAP,AGFG1,CTTN,TM2D3,BOC,TUSC2,SEMA3B,NFKB1,SPOCD1,TPPP,RGMA,BCL9,LEF1,B4GALT5,SOX5,ATRNL1,EGFL6,LAMB2,VEGFD,ECM1,REC8,SEMA4B,NCKIPSD,ADCY1,FES,PRUNE1,BCL9L,SEMA6C,HEG1,LMO3,GATA5,KIF1A,CLCN2,STK25,RNASEL,ELL3,NFKBIA,MOV10,LTBP3,B2M,WNT2B,DPF2,ARHGEF10,BCR,ADORA2A,ADAMTS7,GRN,ASTN1,HDAC5,PSAP,GPC2,RND2,ADD1,BMP4,NAGLU,MAEA,RARRES3,NBL1,MAP1S,ZNF503,NR2F6,DLG5,HDAC6,PQBP1,DNAJB6,ARRB2,EPHA2,MYRF,DAGLA,TCF12,SERPINE2,CASP9,KAZN,ERBB2,PRKACA,ZFP36L1,NTRK1,SMOC1,SLIT2,AR,TP53,CPLX2,KAT8,HOXB4,MED12,GBA,PPP1R9B,ADAM15,NUPR1,PBXIP1,ADAR,SIGLEC15,NEO1,ULK3,GPRC5B,PDGFRB,FLII,LLGL1,TMEM98,MAP2K3,ROR1,PTPRS,MOSPD1,RETREG1,EEF2,GLIS2,DVL1,ASPA,AGRN,ISG15,NELFB,TCF3,NPHP4,SBNO2,EDF1,RERE,CBFA2T3,FOXC2,ABL1,OSGIN1,HSBP1,CNN3,IL34,PBX3,IST1,ABCA2,RPS	cyan	VSMC_M2
GO:0061564	0.00	1.00	42	380	axon development	BP	0.16954	FLOT1,PLXNB2,NFIB,COBL,GLI3,NRP1,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,APBB1,SCN1B,EFNA5,EPHA3,LRP4,NDN,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,STK25,GRN,RND2,MAP1S,HDAC6,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,LLGL1,PTPRS,DVL1,ABL1,IST1	cyan	VSMC_M2
GO:0031324	0.00	1.00	166	1896	negative regulation of cellular metabolic process	BP	0.16954	STAT6,TCF21,EHMT2,ZFPM2,EIF3H,IRF1,DEPTOR,DAXX,PTPRK,TLE1,NFIB,TRERF1,HMOX1,APPL2,MLIP,ZBTB45,P3H1,AKT1S1,AASS,GLI3,IRF3,KLF15,BAX,NOP53,BIN1,APOE,BCL3,ATRAID,ATG7,SOCS3,TIMP2,ZFP36,SAMD4B,KAT2B,SH3BP5,TRIM21,SMPD1,APBB1,LMO1,RARG,IGF1,SNTA1,WT1,CHMP4B,PATL1,TSHZ3,POU6F1,SERPING1,CAST,SPON1,SFRP2,WWTR1,PRKCD,SRC,ZHX3,RIOX2,FOXF2,MAPK8IP1,SORBS3,PTPN13,STAT1,CTSA,GFRA2,NDN,CHRNA7,IKBKE,CAPN3,TIRAP,CSTB,NFKB1,GNAI2,TPPP,HIST1H1C,LEF1,TBL1Y,PTGIS,WDR6,ECM1,NELFCD,FURIN,ERFE,HEG1,RFX5,MAGEF1,MOV10,DPF2,ADORA2A,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,CPAMD8,HDAC6,DNAJB6,ARRB2,ZBTB17,SERPINE2,GIPC1,ZFP36L1,UBQLN2,PCGF2,MLLT6,SLIT2,AR,TP53,KAT8,HOXB4,ELMSAN1,UBQLN4,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,ACP5,KANK2,WARS,TMEM98,MTA1,MLLT1,MOSPD1,MFSD12,GLIS2,ABCD1,DVL1,ISG15,E4F1,RENBP,TSC2,NELFB,TCF3,SBNO2,FAM3A,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,ABL1,HSBP1,INCA1,ABCA2,RPS15,GAS1,MEX3D,ZNF205,SLC8A3,HEXIM1,SERPINF1,ZBTB7A,ATN1,PML,SERPINB6,PLPP3,GATA4,CALM3,CARD8,BMF,CDK9,BST2,ZFPM1,EN1	cyan	VSMC_M2
GO:0045088	0.00	1.00	21	148	regulation of innate immune response	BP	0.1759	IRF1,APPL2,IRF3,APOE,TRIM21,LAMP1,SLC15A4,SERPING1,PLSCR1,SRC,IKBKE,TIRAP,GRN,PQBP1,DHX58,ARRB2,ADAR,ISG15,FAM3A,HEXIM1,RPS19	cyan	VSMC_M2

GO:0043086	0.00	1.00	58	555	negative regulation of catalytic activity	BP	0.17612	DEPTOR,AKT1S1,BIN1,APOE,SOCS3,TIMP2,ZFP36,KAT2B,PPP1R27,SH3BP5,SMPD1,SERPING1,CAST,SFRP2,WWTR1,PRKCD,SRC,MAPK8IP1,PHACTR1,CSTB,NFKB1,GNAI2,ECM1,ANXA9,FURIN,HEG1,ADORA2A,TMBIM1,BMP4,CPAMD8,HDAC6,DNAJB6,ARRB2,AKAP5,SERPINE2,SLIT2,TP53,GBA,PPP1R9B,ADAR,WARS,MLLT1,DVL1,RENBP,TSC2,PHPT1,ABL1,CNN3,INCA1,RPS15,SLC8A3,HEXIM1,SERPINF1,SERPINB6,CARD8,GCHFR,BST2,INKA1	cyan	VSMC_M2
GO:0046466	0.00	1.00	7	26	membrane lipid catabolic process	BP	0.17869	NEU1,NAGA,SMPD1,HEXB,PRKCD,FUCA1,GBA	cyan	VSMC_M2
GO:0032720	0.00	1.00	9	41	negative regulation of tumor necrosis factor production	BP	0.17869	GPNMB,BCL3,IGF1,BPI,CHRNA7,ARRB2,IL27RA,ACP5,NFKBIL1	cyan	VSMC_M2
GO:1903827	0.00	1.00	49	454	regulation of cellular protein localization	BP	0.18039	OS9,CARD10,GLI3,GSN,STOM,MARK4,CAMK1,RHOG,DCLK1,PKDCC,CLIP3,TP53INP2,EDEM2,WWTR1,PRKCD,EPHA3,SRC,CACNB3,LRP4,SLC5A3,LZTS2,CD81,TRIM8,VPS11,GPC2,TMBIM1,BMP4,B3GAT3,CROCC,JUP,EPHA2,AKAP5,ERBB2,PRKACA,AR,PPP1R9B,SLC51B,SNX33,TMEM98,GLIS2,DVL1,INPP5E,ENTR1,ABCA2,GRASP,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0045724	0.00	1.00	6	21	positive regulation of cilium assembly	BP	0.18039	KCTD17,MARK4,DZIP1,CROCC,ENTR1,ATMIN	cyan	VSMC_M2
GO:0032990	0.00	1.00	55	536	cell part morphogenesis	BP	0.18039	FLOT1,PLXNB2,PACSIN2,NFIB,COBL,GLI3,NRP1,BAX,FZD4,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,EPHA3,SRC,LRP4,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,KIF1A,STK25,MOV10,ADORA2A,RND2,NBL1,MAP1S,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1	cyan	VSMC_M2
GO:0007267	0.00	1.00	106	1146	cell-cell signaling	BP	0.18039	AKAP12,FLOT1,RPS6KA2,AFDN,PACSIN2,NPTXR,TLE1,GPNMB,GLI3,CADPS2,SLC17A7,NRP1,KLF15,HBP1,FZD4,APOE,LTBP4,RNF213,NPTX1,EFNB2,RAB11FIP1,ADGRA2,TMEM108,RIMBP2,PRICKLE2,RARG,SCN1B,EFNA5,TSHZ3,SFRP2,WWTR1,GLRB,SRC,CACNB3,CPE,LRP4,PLCG1,SFRP5,NISCH,LZTS2,CHRNA7,TM2D3,SEMA3B,NFKB1,GNAI2,BCL9,HADH,LEF1,SV2A,GRK5,ADCY1,ANXA9,BCL9L,VANGL2,FAM53B,PHEX,PTCHD1,LINC02210-CRHR1,FRMD8,WNT2B,BCR,ADORA2A,BMP4,PORCN,CHRNE,ARRB2,JUP,AKAP5,DAGLA,GABARAP,SERPINE2,MCC,GIPC1,PRKACA,NTRK1,AR,CPLX2,MED12,PPP1R9B,PBXIP1,GRIA1,GPRC5B,RASL10B,ROR1,PTPRS,SH3GL1,DVL1,AGRN,TSC2,NPHP4,PHPT1,RAB11FIP3,AXIN1,CLSTN1,ABL1,SLC8A3,KCND2,PLPP3,GATA4,CALM3,STX3,RGS8,RGS10,PYGO2,RAB11B,EMD	cyan	VSMC_M2
GO:0010507	0.00	1.00	12	67	negative regulation of autophagy	BP	0.18039	EHMT2,HMOX1,ATG7,CHMP4B,CTSA,WDR6,TP53,UBQLN4,NUPR1,TSC2,GATA4,BMF	cyan	VSMC_M2
GO:0006508	0.00	1.00	119	1295	proteolysis	BP	0.18039	MMP19,OS9,ADAMTS2,CFB,EIF3H,RPS6KA2,MTCH1,KCTD17,CUL9,RNF144A,GLI3,GSN,BAX,NOP53,FKRP,TRIM13,AGBL5,BIN1,APOE,AGAP3,LTBP4,CAPN5,TIMP2,RNF213,TRIM21,TPP1,MMP17,EIF3F,RBCK1,CHMP4B,TP53INP2,GGT7,SERPING1,CAST,EDEM2,CTSB,SPON1,SFRP2,WWTR1,SRC,CPE,TGM2,FOXF2,MMP2,CTSA,CAPN3,PCSK6,RNPEP,CSTB,RGMA,UBA7,APH1A,DCAF11,ECM1,CTSK,RHBDD3,CASP10,MINDY1,FURIN,RNPEPL1,ATG4B,MAGEF1,PHEX,ADORA2A,CAPN1,CLEC3B,ADAM11,ADAMTS7,GRN,C1R,PCOLCE,C1S,MAEA,CPAMD8,HDAC6,DNAJB6,ARRB2,MYRF,GABARAP,SERPINE2,CASP9,GIPC1,PRKACA,UBQLN2,TP53,SCRN2,UBQLN4,GBA,ADAM15,NUPR1,SNX33,TMEM98,MTA1,CLPP,XPNPEP2,UBXN6,MPND,WDR81,DVL1,ISG15,ELOB,RENBP,DPP7,FBXW5,CAPN15,AXIN1,RHBDF1,CBFA2T3,RNF166,IST1,ABCA2,GAS1,CNDP2,SERPINF1,PML,SERPINB6,CARD8,PSMB9,BST2	cyan	VSMC_M2
GO:0001822	0.00	1.00	30	248	kidney development	BP	0.18039	TCF21,GCNT1,GLI3,NRP1,KLF15,BAX,WT1,WWTR1,LRP4,LZTS2,STAT1,LAMB2,APH1A,VANGL2,WNT2B,ACAT1,WNK4,BMP4,CC2D2A,DLG5,CASP9,SLIT2,KANK2,PDGFRB,GLIS2,FOXC2,SERPINF1,SDC4,PYGO2,MPV17	cyan	VSMC_M2
GO:0043903	0.00	1.00	10	49	regulation of biological process involved in symbiotic interaction	BP	0.18039	TRIM14,GSN,TRIM13,EXOC7,TRIM21,CHMP3,EXOC2,TRIM8,TRIM26,PML	cyan	VSMC_M2
GO:0048709	0.00	1.00	12	67	oligodendrocyte differentiation	BP	0.18315	GLI3,SLC45A3,TPPP,B4GALT5,MYRF,ERBB2,MED12,TMEM98,ASPA,IL34,ABCA2,SLC8A3	cyan	VSMC_M2
GO:0009615	0.00	1.00	31	253	response to virus	BP	0.1834	IRF1,ITGB8,IRF3,BAX,NOP53,AGBL5,BCL3,ATG7,DCLK1,SMPD1,WDFY4,TLR3,PLSCR1,SRC,STAT1,IKBKE,NFKB1,LGALS8,RNASEL,MOV10,PQBP1,DHX58,IL17RA,VWCE,NPC2,ADAR,ISG15,OAS2,PML,CARD8,BST2	cyan	VSMC_M2
GO:0006469	0.00	1.00	23	172	negative regulation of protein kinase activity	BP	0.18793	DEPTOR,AKT1S1,APOE,KAT2B,SH3BP5,SMPD1,SFRP2,WWTR1,PRKCD,MAPK8IP1,HEG1,ADORA2A,BMP4,GBA,ADAR,WARS,MLLT1,DVL1,TSC2,ABL1,INCA1,SLC8A3,HEXIM1	cyan	VSMC_M2
GO:0006954	0.00	1.00	53	497	inflammatory response	BP	0.18984	GSDMD,HMOX1,LRRC19,APPL2,PLA2G7,TRIL,IRF3,APOE,RHBDF2,IL17RC,SOCS3,PLD3,ZFP36,FOLR2,IL5RA,IGF1,TLR3,PLSCR1,PRKCD,SRC,TGM2,PLCG1,CD81,TIRAP,TUSC2,NFKB1,PTGIS,ECM1,RHBDD3,ADCY1,FURIN,NFKBIA,ADORA2A,GRN,HDAC5,ALOX15,EPHA2,DAGLA,IL17RA,GBA,NUPR1,PBXIP1,ACP5,GPRC5B,ABCC1,MAP2K3,ABCD1,SBNO2,IL34,MIR197,SERPINF1,RPS19,CARD8	cyan	VSMC_M2
GO:0048812	0.00	1.00	52	503	neuron projection morphogenesis	BP	0.18984	FLOT1,PLXNB2,NFIB,COBL,GLI3,NRP1,FZD4,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,EPHA3,LRP4,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,KIF1A,STK25,MOV10,ADORA2A,RND2,NBL1,MAP1S,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1	cyan	VSMC_M2
GO:0032691	0.00	1.00	5	14	negative regulation of interleukin-1 beta production	BP	0.18984	IGF1,ARRB2,ACP5,PML,CARD8	cyan	VSMC_M2

GO:0048699	0.00	1.00	107	1177	generation of neurons	BP	0.19458	FLOT1,EHMT2,PLXNB2,PTPRK,TEAD3,MTCH1,NFIB,APPL2,P3H1,MEIS1,COBL,GLI3,AP2A1,NRP1,BAX,FZD4,VIM,BIN1,APOE,SLITRK6,CAMK1,TIMP2,NPTX1,RHOG,FGFR1,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,MAN2A1,EFNA5,SFRP2,NDRG4,EPHA3,TGM2,LRP4,GNAO1,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,LEF1,B4GALT5,SOX5,LAMB2,VEGFD,SEMA4B,NCKIPSD,ADCY1,FES,PRUNE1,SEMA6C,KIF1A,STK25,ELL3,MOV10,B2M,WNT2B,ADORA2A,GRN,ASTN1,GPC2,RND2,BMP4,NAGLU,NBL1,MAP1S,NR2F6,DLG5,HDAC6,PQBP1,EPHA2,DAGLA,TCF12,SERPINE2,ERBB2,NTRK1,SLIT2,TP53,GBA,PPP1R9B,NEO1,GPRC5B,LLGL1,TMEM98,ROR1,PTPRS,DVL1,ASPA,AGRN,TCF3,NPHP4,RERE,ABL1,IL34,PBX3,IST1,SERPINF1,LRRC7,SDC4,STX3,EN1	cyan	VSMC_M2
GO:0042221	0.00	1.00	243	2921	response to chemical	BP	0.19458	STAT6,TCF21,OS9,AKAP12,FLOT1,EHMT2,PLXNB2,RPS6KA2,IRF1,DAXX,FBXO32,CUTA,PTPRK,NFIB,TRERF1,GCNT1,HMOX1,ACO1,KIAA1324L,KLF9,APPL2,PLA2G7,ITGB8,GPNMB,BCKDHB,RRAGC,AKT1S1,GLI3,IRF3,NRP1,KLF15,RHOB,BAX,SELENOW,NOP53,TRIM13,FZD4,VIM,APOE,AGAP3,ACAA1,ATG7,CYP2S1,LTBP4,IL17RC,SOCS3,PNP,RPS16,TIMP2,ZFP36,RPL15,FOLR2,HGS,KAT2B,RFTN1,RHOG,FGFR1,IL5RA,EFNB2,TRIM21,ADGRA2,ACKR4,SMPD1,TMEM108,APBB1,ANGPT4,RARG,SCN1B,IGF1,TLR3,WT1,EFNA5,GGT7,EDEM2,CTSB,PLSCR1,CAMKK2,SFRP2,GLRB,PRKCD,EPHA3,SRC,CACNB3,TGM2,BPI,PLCG1,BBS2,MMS19,GNAO1,SFRP5,MMP2,EXT2,STAT1,CD81,NDN,FIBIN,CHRNA7,IKBKE,CAPN3,TIRAP,PCSK6,BOC,SEMA3B,NFKB1,GNAI2,RGMA,HADH,LEF1,PTGIS,SOX5,LAMB2,MN1,VEGFD,ECM1,SEMA4B,RHBDD3,GAS2L1,ADCY1,FES,FURIN,VPS11,ERFE,CCS,BCL9L,SEMA6C,LMO3,GATA5,RERG,STK25,FIBP,PHEX,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,B2M,ADORA2A,AIFM2,CLEC3B,ADAMTS7,HDAC5,TMEM161A,ACAT1,VEGFB,ADD1,BMP4,QDPR,NBL1,STAT5A,HDAC6,PQBP1,ARRB2,JUP,ALOX15,EPHA2,IL17RA,CASP9,PLSCR3,GIPC1,ERBB2,PRKACA,ZFP36L1,IL27RA,UBQLN2,NTRK1,PCGF2,UBIAD1,SLIT2,AR,TP53,HSD3B7,PDK2,GBA,PPP1R9B,ADAM15,NUPR1,SHC1,ADAR,ACP5,KANK2,TEX14,GRIA1,NEO1,ABCC1,EPN2,PDGFRB,MCOLN1,IL13RA1,MAP2K3,SNN,UBXN6,EEF2,ABCD1,DVL1,AGRN,ISG15,TNFRSF14,TSC2,NDOR1,SBNO2,PHPT1,SLC10A3,H6PD,GSTM4,FOXC2,ABL1,SLC2A8,IL34,GBP6,ATP6V0D1,OAS2,ABCA2,GAS1,SLC8A3,SERPINF1,KCND2,ZBTB7A,CD55,RAB43,PML,SERPINB6,RPS19,JUNB,EEF1A2,GATA4,CALM3,CARD8,	cyan	VSMC_M2
GO:0006956	0.00	1.00	7	27	complement activation	BP	0.19758	CFB,COLEC11,SERPING1,C1R,C1S,C6,CD55	cyan	VSMC_M2
GO:0014067	0.00	1.00	4	9	negative regulation of phosphatidylinositol 3-kinase signaling	BP	0.19845	NOP53,SERPINE2,TSC2,INPP5E	cyan	VSMC_M2
GO:0120039	0.00	1.00	53	517	plasma membrane bounded cell projection morphogenesis	BP	0.20102	FLOT1,PLXNB2,NFIB,COBL,GLI3,NRP1,FZD4,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,EPHA3,SRC,LRP4,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,KIF1A,STK25,MOV10,ADORA2A,RND2,NBL1,MAP1S,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1	cyan	VSMC_M2
GO:0002040	0.00	1.00	17	114	sprouting angiogenesis	BP	0.20102	CARD10,HMOX1,NRP1,RNF213,EFNB2,ADGRA2,TJP1,LEF1,VEGFD,HDAC5,VEGFB,BMP4,EPHA2,SLIT2,EPN2,FOXC2,ABL1	cyan	VSMC_M2
GO:0014020	0.00	1.00	14	86	primary neural tube formation	BP	0.20443	PLXNB2,COBL,RARG,SFRP2,RGMA,VANGL2,BMP4,CC2D2A,PRKACA,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0048667	0.00	1.00	47	446	cell morphogenesis involved in neuron differentiation	BP	0.20443	FLOT1,PLXNB2,NFIB,COBL,GLI3,NRP1,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,LZTS3,APBB1,SCN1B,EFNA5,EPHA3,LRP4,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,KIF1A,STK25,RND2,MAP1S,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1	cyan	VSMC_M2
GO:0072359	0.00	1.00	85	902	circulatory system development	BP	0.2075	CTDP1,MMP19,TCF21,ZFPM2,RPS6KA2,TGFBI,CARD10,HMOX1,ITGB8,GPNMB,MEIS1,GLI3,RRAS,NRP1,RHOB,BAX,FZD4,APOE,SOCS3,GAA,PAK4,RNF213,HGS,KAT2B,EFNB2,ADGRA2,HSPB6,ANGPT4,IGF1,TLR3,WT1,POU6F1,SFRP2,NDRG4,CPE,PLCG1,PDLIM2,MMP2,STAT1,CHRNA7,TJP1,ADGRB2,LGALS8,LEF1,PTGIS,VEGFD,ECM1,HEG1,VANGL2,GATA5,PLCD3,GRN,HDAC5,VEGFB,BMP4,CC2D2A,FKBP10,ARRB2,JUP,EPHA2,ERBB2,ZFP36L1,SLIT2,TP53,MED12,ADAM15,SHC1,WARS,EPN2,PDGFRB,DVL1,TSC2,NPRL3,TCF25,FOXC2,ABL1,DNAAF1,HEXIM1,SERPINF1,PML,JUNB,GATA4,SAT1,COL8A1,ZFPM1	cyan	VSMC_M2
GO:0051172	0.00	1.00	155	1770	negative regulation of nitrogen compound metabolic process	BP	0.2075	STAT6,TCF21,EHMT2,ZFPM2,EIF3H,IRF1,DEPTOR,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,P3H1,AKT1S1,AASS,GLI3,AP2A1,IRF3,KLF15,BAX,NOP53,BIN1,APOE,BCL3,ATRAID,SOCS3,TIMP2,ZFP36,SAMD4B,KAT2B,SH3BP5,TRIM21,SMPD1,APBB1,LMO1,RARG,IGF1,SNTA1,WT1,PATL1,TSHZ3,POU6F1,SERPING1,CAST,SPON1,SFRP2,WWTR1,PRKCD,SRC,ZHX3,RIOX2,FOXF2,MAPK8IP1,SORBS3,PTPN13,STAT1,CTSA,GFRA2,NDN,CHRNA7,IKBKE,CAPN3,TIRAP,CSTB,NFKB1,GNAI2,TPPP,HIST1H1C,LEF1,TBL1Y,PTGIS,ECM1,NELFCD,FURIN,HEG1,RFX5,MAGEF1,MOV10,DPF2,ADORA2A,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,CPAMD8,HDAC6,DNAJB6,ARRB2,ZBTB17,SERPINE2,GIPC1,ZFP36L1,PCGF2,MLLT6,SLIT2,AR,TP53,KAT8,HOXB4,ELMSAN1,UBQLN4,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,ACP5,KANK2,WARS,TMEM98,MTA1,MLLT1,MOSPD1,GLIS2,DVL1,ISG15,E4F1,RENBP,TSC2,NELFB,TCF3,SBNO2,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,ABL1,HSBP1,INCA1,ABCA2,RPS15,GAS1,MEX3D,ZNF205,SLC8A3,HEXIM1,SERPINF1,ZBTB7A,ATN1,PML,SERPINB6,PLPP3,CALM3,CARD8,CDK9,BST2,ZFPM1,EN1	cyan	VSMC_M2

GO:0009894	0.00	1.00	78	806	regulation of catabolic process	BP	0.20938	EHMT2,EIF3H,GGA1,HMOX1,TRIM14,RRAGC,RNF144A,BAX,NOP53,TRIM13,VIM,APOE,ATRAID,ATG7,EXOC7,TIMP2,ZFP36,SAMD4B,HGS,TRIM21,IGF1,CHMP4B,TP53INP2,PATL1,CAMKK2,PRKCD,FOXF2,PNPLA2,CTSA,CD81,TRIM8,IKBKE,TIRAP,CTTN,TPCN2,RGMA,EXOC8,WDR6,RHBDD3,FURIN,VPS11,ATG4B,RNASEL,MAGEF1,MOV10,CAPN1,FYCO1,PSAP,HDAC6,GABARAP,SERPINE2,GIPC1,PRKACA,ZFP36L1,UBQLN2,TP53,KAT8,UBQLN4,GBA,NUPR1,SNX33,ABCD1,DVL1,ELOB,TSC2,AXIN1,RHBDF1,CBFA2T3,ABL1,ATP6V0D1,ABCA2,MEX3D,ZBTB7A,PML,EEF1A2,GATA4,BMF,VPS26B	cyan	VSMC_M2
GO:0051049	0.00	1.00	116	1276	regulation of transport	BP	0.20938	RAB5B,OS9,FLOT1,PACSIN2,HMOX1,APPL2,P3H1,KCNQ5,EEPD1,GLI3,AP2A1,CADPS2,SLC17A7,STOM,NRP1,KLF15,BAX,BIN1,APOE,SLC6A9,RHBDF2,CAMK1,EHD3,HGS,TBC1D5,RAB11FIP1,LAMP1,SMPD1,APBB1,PKDCC,CLIP3,SCN1B,IGF1,REEP5,SNTA1,EFNA5,CHMP3,EDEM2,PLSCR1,NDRG4,PRKCD,EPHA3,SRC,CACNB3,TGM2,PLCG1,ARHGAP1,GNAO1,CRACR2B,CD81,CAPN3,CACNA2D2,TPCN2,NFKB1,GNAI2,HADH,DISP1,SV2A,RHBDD3,ADCY1,FES,FURIN,VPS11,ERFE,CLCN2,RNASEL,NFKBIA,LINC02210-CRHR1,B2M,KCND3,ADORA2A,CAPN1,HOMER3,WNK4,BMP4,B3GAT3,ARRB2,JUP,ALOX15,AKAP5,SERPINE2,GIPC1,ERBB2,PRKACA,UBQLN2,MLLT6,CPLX2,SLC51B,STON2,SNX33,RASL10B,PDGFRB,LLGL1,SH3GL1,DVL1,TSC2,PHPT1,RAB11FIP3,RHBDF1,ABL1,OAS2,ABCA2,GAS1,ZNF205,CBARP,KCND2,GRASP,PML,CALM3,CLIC2,CLIC3,SDC4,BST2,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0043542	0.00	1.00	25	195	endothelial cell migration	BP	0.21189	CARD10,HMOX1,RRAS,NRP1,RHOB,APOE,FGFR1,EFNB2,ADGRA2,ANGPT4,PLCG1,LGALS8,GRN,HDAC5,BMP4,STAT5A,JUP,EPHA2,GIPC1,SLIT2,MAP2K3,FOXC2,ABL1,SERPINF1,PLPP3	cyan	VSMC_M2
GO:0060070	0.00	1.00	30	250	canonical Wnt signaling pathway	BP	0.21189	TLE1,GLI3,FZD4,APOE,ADGRA2,RARG,SFRP2,WWTR1,SRC,LRP4,SFRP5,LZTS2,NFKB1,BCL9,LEF1,BCL9L,FAM53B,FRMD8,WNT2B,PORCN,JUP,MCC,MED12,GPRC5B,DVL1,NPHP4,AXIN1,PLPP3,PYGO2,EMD	cyan	VSMC_M2
GO:0043067	0.00	1.00	104	1119	regulation of programmed cell death	BP	0.21189	AKAP12,DDAH2,RPS6KA2,DEPTOR,DAXX,ST3GAL1,MTCH1,GRINA,TLE1,CARD10,HMOX1,HIGD2A,STK40,AKT1S1,STK17A,GLI3,IRF3,GSN,NRP1,RHOB,HS1BP3,BAX,NOP53,MEIS3,MARK4,BIN1,APOE,BCL3,ATG7,SOCS3,ZFP36,PAK4,FGFR1,SMPD1,APBB1,CLIP3,HSPB6,ANGPT4,RBCK1,RARG,IGF1,TLR3,WT1,CAST,CTSB,SFRP2,PRKCD,SRC,TGM2,PLCG1,MAPK8IP1,STAT1,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,PTGIS,GRK5,CASP10,ELL3,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,DLG5,HDAC6,DNAJB6,ARRB2,CASP9,PLSCR3,TP53BP2,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,GBA,NUPR1,SHC1,ADAR,KANK2,ATOX1,PDGFRB,TRAF4,RETREG1,TRAF7,FOXC2,ABL1,OSGIN1,INCA1,GAS1,ZBTB7A,PML,EEF1A2,GATA4,CARD8,BMF,EN1	cyan	VSMC_M2
GO:0043535	0.00	1.00	14	87	regulation of blood vessel endothelial cell migration	BP	0.21189	CARD10,HMOX1,NRP1,APOE,FGFR1,ANGPT4,PLCG1,HDAC5,STAT5A,JUP,EPHA2,MAP2K3,FOXC2,ABL1	cyan	VSMC_M2
GO:0016192	0.00	1.00	109	1192	vesicle-mediated transport	BP	0.21189	RAB5B,FLOT1,PACSIN2,TAPBP,GGA1,HMOX1,APPL2,ELMO1,TBC1D17,AP2A1,CADPS2,GSN,SLC17A7,NRP1,RHOB,DENND2A,BIN1,APOE,EXOC7,EHD3,CMTM6,LGALS3BP,HGS,TBC1D5,RHOG,RAB11FIP1,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,PKDCC,CLIP3,CHMP4B,CHMP3,ERGIC3,PLSCR1,NDRG4,PRKCD,EPHA3,SRC,TGM2,LRP4,BBS2,ARHGAP1,EXOC2,MAPK8IP1,SYS1,CD81,OSBPL5,CTTN,TMEM115,TUSC2,TPCN2,GNAI2,LRP10,SV2A,EXOC8,NCKIPSD,ADCY1,FES,VPS11,KIF1A,TMEM50A,B2M,M6PR,ADORA2A,USE1,PLD2,ARRB2,ALOX15,AKAP5,GIPC1,STARD3,UBQLN2,TMEM175,CPLX2,ERGIC1,C1orf43,STON2,GRIA1,SNX33,EPN2,LLGL1,UBXN6,SH3GL1,WDR81,DVL1,SGSM2,TSC2,PTGDS,RAB11FIP3,ENTR1,CLSTN1,ABL1,MON1B,ABCA2,GAS1,CBARP,RAB43,GRASP,PLPP3,CALM3,VPS26B,SDC4,STX3,OCIAD2,RAB11B,MCFD2	cyan	VSMC_M2
GO:0016055	0.00	1.00	41	373	Wnt signaling pathway	BP	0.21189	TLE1,GLI3,KLF15,HBP1,FZD4,APOE,RNF213,ADGRA2,PRICKLE2,RARG,SFRP2,WWTR1,SRC,CPE,LRP4,SFRP5,LZTS2,NFKB1,BCL9,LEF1,GRK5,BCL9L,VANGL2,FAM53B,FRMD8,WNT2B,PORCN,JUP,MCC,MED12,PBXIP1,GPRC5B,ROR1,DVL1,TSC2,NPHP4,AXIN1,ABL1,PLPP3,PYGO2,EMD	cyan	VSMC_M2
GO:1903556	0.00	1.00	9	43	negative regulation of tumor necrosis factor superfamily cytokine production	BP	0.21189	GPNMB,BCL3,IGF1,BPI,CHRNA7,ARRB2,IL27RA,ACP5,NFKBIL1	cyan	VSMC_M2
GO:0051094	0.00	1.00	92	982	positive regulation of developmental process	BP	0.21689	STAT6,FLOT1,PLXNB2,ZFPM2,HMOX1,KIAA1324L,ITGB8,COBL,GLI3,RRAS,NRP1,RHOB,BAX,FZD4,BIN1,APOE,ATRAID,SLITRK6,SOCS3,CAMK1,PNP,TIMP2,ZFP36,PAK4,FGFR1,EFNB2,PKDCC,HSPB6,ANGPT4,IGF1,TLR3,MAN2A1,WT1,SFRP2,WWTR1,SRC,TGM2,PLCG1,ZHX3,STAT1,CHRNA7,CAPN3,TJP1,BOC,NFKB1,LEF1,PTGIS,B4GALT5,SOX5,VEGFD,ECM1,FES,BCL9L,LMO3,GATA5,STK25,ELL3,LTBP3,B2M,WNT2B,GRN,VEGFB,RND2,ADD1,BMP4,RARRES3,NBL1,DLG5,ARRB2,JUP,TCF12,SERPINE2,ZFP36L1,NTRK1,SLIT2,AR,TP53,HOXB4,GPRC5B,DVL1,ASPA,AGRN,ISG15,TCF3,CLSTN1,FOXC2,ABL1,IL34,IST1,SERPINF1,JUNB,GATA4	cyan	VSMC_M2
GO:0198738	0.00	1.00	41	374	cell-cell signaling by wnt	BP	0.22031	TLE1,GLI3,KLF15,HBP1,FZD4,APOE,RNF213,ADGRA2,PRICKLE2,RARG,SFRP2,WWTR1,SRC,CPE,LRP4,SFRP5,LZTS2,NFKB1,BCL9,LEF1,GRK5,BCL9L,VANGL2,FAM53B,FRMD8,WNT2B,PORCN,JUP,MCC,MED12,PBXIP1,GPRC5B,ROR1,DVL1,TSC2,NPHP4,AXIN1,ABL1,PLPP3,PYGO2,EMD	cyan	VSMC_M2
GO:0120254	0.00	1.00	14	86	olefinic compound metabolic process	BP	0.22496	ACAA1,CYP2S1,PLB1,PNPLA2,PTGIS,CLCN2,ALOX15,DAGLA,STARD3,DHRS13,ABCD1,PTGDS,H6PD,DGAT1	cyan	VSMC_M2

GO:1905477	0.00	1.00	14	88	positive regulation of protein localization to membrane	BP	0.22496	STOM,RHOG,CLIP3,EPHA3,CACNB3,LRP4,SLC5A3,CD81,EPHA2,AKAP5,ERBB2,PPP1R9B,SLC51B,STX3	cyan	VSMC_M2
GO:0061318	0.00	1.00	5	16	renal filtration cell differentiation	BP	0.22496	KLF15,WT1,LAMB2,BMP4,FOXC2	cyan	VSMC_M2
GO:0072112	0.00	1.00	5	16	glomerular visceral epithelial cell differentiation	BP	0.22496	KLF15,WT1,LAMB2,BMP4,FOXC2	cyan	VSMC_M2
GO:0042063	0.00	1.00	28	230	gliogenesis	BP	0.22496	NFIB,GLI3,KLF15,VIM,BIN1,HEXB,NDN,SLC45A3,TPPP,LEF1,B4GALT5,LAMB2,ARHGEF10,ADORA2A,GRN,MYRF,SERPINE2,ERBB2,MED12,GBA,TMEM98,ROR1,EEF2,ASPA,ABL1,IL34,ABCA2,SLC8A3	cyan	VSMC_M2
GO:0007040	0.00	1.00	11	61	lysosome organization	BP	0.22496	GAA,TPP1,GNPTAB,CHMP3,HEXB,TPCN2,GRN,NAGLU,TMEM175,GBA,NAGPA	cyan	VSMC_M2
GO:0080171	0.00	1.00	11	61	lytic vacuole organization	BP	0.22496	GAA,TPP1,GNPTAB,CHMP3,HEXB,TPCN2,GRN,NAGLU,TMEM175,GBA,NAGPA	cyan	VSMC_M2
GO:0032989	0.00	1.00	60	609	cellular component morphogenesis	BP	0.22496	FLOT1,PLXNB2,PACSIN2,NFIB,COBL,GLI3,NRP1,BAX,FZD4,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,EPHA3,SRC,LRP4,PHACTR1,NDN,CHRNA7,CAPN3,CTTN,BOC,SEMA3B,TPP,RGMA,B4GALT5,LAMB2,SEMA4B,ADCY1,SEMA6C,KIF1A,STK25,MOV10,ADORA2A,RND2,NBL1,MAP1S,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,PDGFRB,FLII,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1,ABCA2	cyan	VSMC_M2
GO:1902186	0.00	1.00	6	22	regulation of viral release from host cell	BP	0.22496	TRIM13,TRIM21,CHMP3,TRIM8,TRIM26,PML	cyan	VSMC_M2
GO:0046631	0.00	1.00	15	97	alpha-beta T cell activation	BP	0.22496	STAT6,IRF1,GLI3,BCL3,PNP,WDFY4,MAPK8IP1,CD81,LEF1,ADORA2A,TMEM98,TNFRSF14,ABL1,CD55,ZFPM1	cyan	VSMC_M2
GO:0032963	0.00	1.00	13	78	collagen metabolic process	BP	0.22496	MMP19,ADAMTS2,P3H1,VIM,MMP17,CTSB,MMP2,CTSK,FURIN,BMP4,ARRB2,ADAM15,PDGFRB	cyan	VSMC_M2
GO:0032608	0.00	1.00	9	44	interferon-beta production	BP	0.22496	FLOT1,IRF1,IRF3,TLR3,TIRAP,DHX58,PTPRS,ISG15,OAS2	cyan	VSMC_M2
GO:0032648	0.00	1.00	9	44	regulation of interferon-beta production	BP	0.22496	FLOT1,IRF1,IRF3,TLR3,TIRAP,DHX58,PTPRS,ISG15,OAS2	cyan	VSMC_M2
GO:0007264	0.00	1.00	46	437	small GTPase mediated signal transduction	BP	0.2267	ARHGEF25,FLOT1,ARHGAP18,ARHGAP39,HMOX1,RRAGC,ELMO1,RRAS,NRP1,RHOB,APOE,TIMP2,ARAP1,RHOG,IGF1,SRC,TGM2,ARHGAP1,C15orf62,NISCH,FAM13A,SIPA1L2,ARHGEF12,HEG1,RERG,RGL1,ARHGEF10,BCR,RND2,ARHGEF10L,PLD2,GABARAP,CGNL1,NTRK1,SLIT2,TP53,KANK2,DENND4B,ARHGAP17,DOCK6,PDGFRB,TSC2,RHOT2,RALGDS,ABL1,RGS19	cyan	VSMC_M2
GO:0072537	0.00	1.00	4	10	fibroblast activation	BP	0.23103	AKAP12,IL17RA,ULK3,PDGFRB	cyan	VSMC_M2
GO:0016241	0.00	1.00	18	128	regulation of macroautophagy	BP	0.23344	EHMT2,HMOX1,TRIM13,EXOC7,CHMP4B,EXOC8,CAPN1,FYCO1,HDAC6,PRKACA,UBQLN2,TP53,UBQLN4,GBA,NUPR1,TSC2,ATP6V0D1,VPS26B	cyan	VSMC_M2
GO:0043534	0.00	1.00	16	108	blood vessel endothelial cell migration	BP	0.23571	CARD10,HMOX1,NRP1,APOE,FGFR1,EFNB2,ANGPT4,PLCG1,HDAC5,STAT5A,JUP,EPHA2,SLIT2,MAP2K3,FOXC2,ABL1	cyan	VSMC_M2
GO:1905475	0.00	1.00	20	147	regulation of protein localization to membrane	BP	0.23571	GSN,STOM,RHOG,PKDCC,CLIP3,EPHA3,CACNB3,LRP4,SLC5A3,CD81,GPC2,TMBIM1,EPHA2,AKAP5,ERBB2,AR,PPP1R9B,SLC51B,GRASP,STX3	cyan	VSMC_M2
GO:1901615	0.00	1.00	42	382	organic hydroxy compound metabolic process	BP	0.23644	PMEL,MOXD1,CYB5R3,ACSS1,APOE,ACAA1,PLB1,SMPD1,IGF1,CYP4V2,ACSS2,CTSB,SLC5A3,PNPLA2,OSBPL5,NFKB1,IP6K1,CTSK,CLCN2,PCBD1,QDPR,ALOX15,GIPC1,STARD3,TP53,HSD3B7,NPC2,GBA,SLC16A2,DHRS13,MFSD12,IDH3G,HAGH,INPP5E,H6PD,PLPP2,LDHD,LCAT,ABCA2,DGAT1,PLPP3,PDXK	cyan	VSMC_M2
GO:0003015	0.00	1.00	23	180	heart process	BP	0.23698	RPS6KA2,GSN,BIN1,EHD3,GAA,SCN1B,SNTA1,WWTR1,SRC,GNAO1,EXT2,GNAI2,CTNNA3,KCND3,VEGFB,JUP,PRKACA,MAP2K3,SLC8A3,GATA4,CALM3,CLIC2,RNLS	cyan	VSMC_M2
GO:0019083	0.00	1.00	9	45	viral transcription	BP	0.23948	CTDP1,TRIM14,TRIM13,ZFP36,TRIM21,TRIM8,LEF1,MON1B,HEXIM1	cyan	VSMC_M2
GO:0034311	0.00	1.00	6	22	diol metabolic process	BP	0.23948	PCBD1,QDPR,GBA,PLPP2,ABCA2,PLPP3	cyan	VSMC_M2
GO:0071363	0.00	1.00	55	545	cellular response to growth factor stimulus	BP	0.23971	PTPRK,KIAA1324L,APPL2,ITGB8,AKT1S1,NRP1,FZD4,LTBP4,ZFP36,HGS,FGFR1,ADGRA2,TMEM108,SFRP2,SRC,PLCG1,SFRP5,EXT2,NDN,PCSK6,RGMA,LEF1,SOX5,VEGFD,FURIN,BCL9L,GATA5,FIBP,FAM89B,LTBP3,CLEC3B,ADAMTS7,VEGFB,BMP4,NBL1,ARRB2,GIPC1,ERBB2,ZFP36L1,NTRK1,SLIT2,TP53,PPP1R9B,SHC1,NEO1,EPN2,PDGFRB,MAP2K3,EEF2,ABL1,GAS1,ZBTB7A,PML,GATA4,EMD	cyan	VSMC_M2
GO:0042981	0.00	1.00	101	1092	regulation of apoptotic process	BP	0.23971	AKAP12,DDAH2,RPS6KA2,DEPTOR,DAXX,ST3GAL1,MTCH1,GRINA,TLE1,CARD10,HMOX1,HIGD2A,STK40,AKT1S1,STK17A,GLI3,IRF3,GSN,NRP1,RHOB,HS1BP3,BAX,NOP53,MEIS3,BIN1,APOE,BCL3,ATG7,SOCS3,ZFP36,PAK4,FGFR1,SMPD1,APBB1,CLIP3,HSPB6,ANGPT4,RBCK1,RARG,IGF1,TLR3,WT1,CAST,CTSB,SFRP2,PRKCD,SRC,TGM2,PLCG1,MAPK8IP1,STAT1,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,PTGIS,GRK5,CASP10,ELL3,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,DLG5,DNAJB6,ARRB2,CASP9,PLSCR3,TP53BP2,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,GBA,NUPR1,SHC1,ADAR,ATOX1,PDGFRB,TRAF4,RETREG1,TRAF7,FOXC2,ABL1,OSGIN1,INCA1,GAS1,ZBTB7A,PML,EEF1A2,GATA4,CARD8,BMF,EN1	cyan	VSMC_M2
GO:0007041	0.00	1.00	15	100	lysosomal transport	BP	0.23971	RHOB,BIN1,EHD3,HGS,LAMP1,GNPTAB,CHMP3,TPCN2,VPS11,M6PR,GRN,PSAP,USE1,UBXN6,NAGPA	cyan	VSMC_M2
GO:0003013	0.00	1.00	46	437	circulatory system process	BP	0.24103	AKAP12,RPS6KA2,CYB5R3,HMOX1,SLC44A1,GSN,BIN1,APOE,SLC6A9,EHD3,GAA,SLC7A2,SCN1B,SNTA1,SERPING1,WWTR1,SRC,GNAO1,NISCH,EXT2,SLC5A3,STAT1,TJP1,GNAI2,HEG1,CTNNA3,KCND3,ADORA2A,VEGFB,JUP,PRKACA,SLIT2,AR,HOXB2,SLC16A2,RASL10B,ABCC1,MAP2K3,RENBP,FOXC2,ABCA2,SLC8A3,GATA4,CALM3,CLIC2,RNLS	cyan	VSMC_M2

GO:0007167	0.00	1.00	72	752	enzyme linked receptor protein signaling pathway	BP	0.24108	STAT6,PTPRK,KIAA1324L,APPL2,ITGB8,EFEMP1,AKT1S1,NRP1,FZD4,VIM,RHBDF2,LTBP4,SHKBP1,SOCS3,HGS,FGFR1,EFNB2,ADGRA2,TMEM108,ANGPT4,IGF1,EFNA5,SFRP2,WWTR1,NDRG4,PRKCD,EPHA3,SRC,PLCG1,SFRP5,MMP2,GFRA2,NDN,PCSK6,GNAI2,RGMA,LEF1,VEGFD,FES,FURIN,ERFE,BCL9L,SAMD10,FIBP,FAM89B,LTBP3,BCR,VEGFB,BMP4,NBL1,STAT5A,ARRB2,EPHA2,GIPC1,ERBB2,NTRK1,AR,TP53,PDK2,SHC1,NEO1,EPN2,PDGFRB,IL13RA1,TSC2,RHBDF1,FOXC2,ABL1,SLC2A8,ZBTB7A,PML,GATA4	cyan	VSMC_M2
GO:0070848	0.00	1.00	57	570	response to growth factor	BP	0.24108	PTPRK,KIAA1324L,APPL2,ITGB8,AKT1S1,NRP1,FZD4,LTBP4,ZFP36,HGS,FGFR1,ADGRA2,TMEM108,SFRP2,SRC,PLCG1,SFRP5,EXT2,NDN,PCSK6,RGMA,LEF1,SOX5,VEGFD,FURIN,BCL9L,GATA5,FIBP,FAM89B,LTBP3,CLEC3B,ADAMTS7,VEGFB,BMP4,NBL1,HDAC6,ARRB2,EPHA2,GIPC1,ERBB2,ZFP36L1,NTRK1,SLIT2,TP53,PPP1R9B,SHC1,NEO1,EPN2,PDGFRB,MAP2K3,EEF2,ABL1,GAS1,ZBTB7A,PML,GATA4,EMD	cyan	VSMC_M2
GO:0008285	0.00	1.00	56	548	negative regulation of cell population proliferation	BP	0.24108	RPS6KA2,IRF1,PTPRK,NFIB,HMOX1,KLF9,APPL2,P3H1,GPNMB,MEIS1,GLI3,BAX,APOE,ATRAID,TIMP2,HGS,KAT2B,RARG,WT1,SFRP2,NDRG4,SFRP5,LZTS2,STAT1,NDN,TMEM115,MN1,WDR6,RERG,B2M,ADORA2A,BMP4,IFI30,RARRES3,ZNF503,DLG5,ZBTB17,SERPINE2,MCC,ERBB2,NTRK1,AR,TP53,NUPR1,SLC16A2,KANK2,WARS,PODN,TNFRSF14,TSC2,CBFA2T3,INCA1,SERPINF1,PML,SDC4,EMD	cyan	VSMC_M2
GO:1901136	0.00	1.00	18	126	carbohydrate derivative catabolic process	BP	0.2434	GNS,NEU1,NAGA,PNP,SGSH,EDEM2,NEIL2,HEXB,PRKCD,GUSB,FUCA1,ACAT1,NAGLU,GBA,ABCD1,RENBP,DPYD,NAGK	cyan	VSMC_M2
GO:0009952	0.00	1.00	20	150	anterior/posterior pattern specification	BP	0.24642	TSHZ1,COBL,GLI3,RARG,WT1,SFRP2,PCSK6,LEF1,WNT2B,BMP4,PCGF2,TP53,HOXB1,HOXB2,HOXB4,MED12,FOXC2,PBX3,GATA4,EN1	cyan	VSMC_M2
GO:0045893	0.00	1.00	112	1244	positive regulation of transcription, DNA-templated	BP	0.24642	STAT6,TCF21,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,MMS19,FOXF2,STAT1,ABHD14B,CD81,NDN,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,DPF2,PCBD1,HDAC5,BMP4,LDB2,TCEA2,PQBP1,JUP,MYRF,ZBTB17,TCF12,ERBB2,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,NUPR1,SHC1,PBXIP1,MTA1,MAP2K3,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:1903508	0.00	1.00	112	1244	positive regulation of nucleic acid-templated transcription	BP	0.24642	STAT6,TCF21,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,MMS19,FOXF2,STAT1,ABHD14B,CD81,NDN,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,DPF2,PCBD1,HDAC5,BMP4,LDB2,TCEA2,PQBP1,JUP,MYRF,ZBTB17,TCF12,ERBB2,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,NUPR1,SHC1,PBXIP1,MTA1,MAP2K3,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0021915	0.00	1.00	18	130	neural tube development	BP	0.25118	PLXNB2,COBL,GLI3,RARG,SFRP2,RGMA,VANGL2,BMP4,CC2D2A,EPHA2,PRKACA,ZFP36L1,MED12,DVL1,TSC2,ABL1,SDC4,EN1	cyan	VSMC_M2
GO:0032970	0.00	1.00	37	337	regulation of actin filament-based process	BP	0.25638	ARHGAP18,GSN,NRP1,RHOB,BIN1,ARAP1,RHOG,EFNA5,RHPN2,PRKCD,EPHA3,C15orf62,SORBS3,TJP1,CTTN,SSH3,FES,CTNNA3,ARPC5,ARHGEF10,RND2,ADD1,CAPZB,ARHGEF10L,JUP,ALOX15,CGNL1,SLIT2,ARHGAP17,SIGLEC15,PDGFRB,FLII,PHPT1,ABL1,GATA4,SDC4,BST2	cyan	VSMC_M2
GO:1902680	0.00	1.00	112	1246	positive regulation of RNA biosynthetic process	BP	0.25666	STAT6,TCF21,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,MMS19,FOXF2,STAT1,ABHD14B,CD81,NDN,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,DPF2,PCBD1,HDAC5,BMP4,LDB2,TCEA2,PQBP1,JUP,MYRF,ZBTB17,TCF12,ERBB2,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,NUPR1,SHC1,PBXIP1,MTA1,MAP2K3,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0048732	0.00	1.00	37	335	gland development	BP	0.25963	STAT6,TCF21,NFIB,HMOX1,COBL,GLI3,NRP1,BAX,DBP,RPS16,GPAT4,RARG,MAN2A1,WT1,SRC,TGM2,LEF1,RHBDD3,CLCN2,CAPN1,PSAP,ACAT1,BMP4,QDPR,STAT5A,EPHA2,SERPINE2,AR,PRKCSH,ABL1,DNAAF1,FPGS,OAS2,RPS15,SERPINF1,PML,PYGO2	cyan	VSMC_M2
GO:0006958	0.00	1.00	5	16	complement activation, classical pathway	BP	0.26047	SERPING1,C1R,C1S,C6,CD55	cyan	VSMC_M2
GO:0046514	0.00	1.00	5	16	ceramide catabolic process	BP	0.26047	NEU1,NAGA,HEXB,PRKCD,GBA	cyan	VSMC_M2
GO:0010876	0.00	1.00	35	311	lipid localization	BP	0.26047	ATP10D,EEPD1,FZD4,APOE,OSBPL10,STARD10,PLSCR1,HEXB,PRKCD,PNPLA2,IKBKE,OSBPL5,TPCN2,NFKB1,LRP10,FURIN,ERFE,NFKBIA,LINC02210-CRHR1,PSAP,PLSCR3,STARD3,NPC2,GBA,SLC51B,ATP8B2,SPNS1,ABCC1,CPT2,ABCD1,SLC10A3,LCAT,APOL5,ABCA2,DGAT1	cyan	VSMC_M2

GO:0098586	0.00	1.00	11	63	cellular response to virus	BP	0.26047	IRF3,BAX,NOP53,WDFY4,TLR3,IKBKE,NFKB1,LGALS8,DHX58,VWCE,ADAR	cyan	VSMC_M2
GO:0072311	0.00	1.00	5	17	glomerular epithelial cell differentiation	BP	0.2618	KLF15,WT1,LAMB2,BMP4,FOXC2	cyan	VSMC_M2
GO:0032692	0.00	1.00	5	16	negative regulation of interleukin-1 production	BP	0.2618	IGF1,ARRB2,ACP5,PML,CARD8	cyan	VSMC_M2
GO:0010941	0.00	1.00	111	1223	regulation of cell death	BP	0.2618	AKAP12,DDAH2,ZFPM2,RPS6KA2,DEPTOR,DAXX,ST3GAL1,MTCH1,GRINA,TLE1,CARD10,HMOX1,HIGD2A,GPNMB,STK40,AKT1S1,STK17A,GLI3,IRF3,GSN,NRP1,RHOB,HS1BP3,BAX,NOP53,MEIS3,TRIM13,MARK4,BIN1,APOE,BCL3,ATG7,SOCS3,ZFP36,PAK4,FGFR1,EFNB2,SMPD1,APBB1,CLIP3,HSPB6,ANGPT4,RBCK1,RARG,IGF1,TLR3,WT1,CHMP4B,CAST,CTSB,SFRP2,PRKCD,SRC,TGM2,PLCG1,MAPK8IP1,STAT1,CHRNA7,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,PTGIS,GRK5,CASP10,ELL3,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,DLG5,HDAC6,DNAJB6,ARRB2,CASP9,PLSCR3,TP53BP2,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,GBA,NUPR1,SHC1,ADAR,KANK2,ATOX1,PDGFRB,TRAF4,RETREG1,TRAF7,FOXC2,ABL1,OSGIN1,INCA1,GAS1,SERPINF1,ZBTB7A,PML,EEF1A2,GATA4,CARD8,BMF,EN1	cyan	VSMC_M2
GO:0052372	0.00	1.00	7	30	modulation by symbiont of entry into host	BP	0.2618	TRIM14,GSN,EXOC7,TRIM21,EXOC2,TRIM8,TRIM26	cyan	VSMC_M2
GO:0001656	0.00	1.00	12	74	metanephros development	BP	0.26398	TCF21,GLI3,WT1,WWTR1,STAT1,LAMB2,APH1A,ACAT1,BMP4,DLG5,PDGFRB,FOXC2	cyan	VSMC_M2
GO:0007528	0.00	1.00	8	39	neuromuscular junction development	BP	0.26398	PPFIBP2,SNTA1,CACNB3,LRP4,LAMB2,ERBB2,DVL1,AGRN	cyan	VSMC_M2
GO:0006629	0.00	1.00	92	982	lipid metabolic process	BP	0.26419	ZADH2,CHKB,NEU1,B3GALT4,CYB5R3,NAGA,ST3GAL1,APPL2,PLA2G7,ITGB8,SLC44A1,IAH1,BAX,ACSS1,APOE,ACAA1,CYP2S1,PLB1,SOCS3,OSBPL10,ECH1,GPAT4,SMPD1,TPP1,CYP4V2,ACSS2,LPCAT4,PLSCR1,HEXB,PRKCD,SRC,DECR1,PLBD2,PLCG1,PTDSS1,PNPLA2,PIK3C2B,CD81,SLC45A3,OSBPL5,ACADS,NFKB1,B4GALT4,LRP10,HADH,IP6K1,STS,PTGIS,B4GALT5,RLBP1,ERFE,CLCN2,FUCA1,ECHS1,PLCD3,PSAP,ACAT1,RARRES3,PORCN,PLD2,ALOX15,DAGLA,PLSCR3,STARD3,HSD3B7,NPC2,PDK2,GBA,SLC44A2,PDGFRB,CERS4,DHRS13,CPT2,ABCD1,PNPLA7,PTGDS,EDF1,FAM3A,PIGQ,INPP5E,H6PD,PLPP2,GSTM4,CRAT,LCAT,APOL5,ABCA2,ACOT6,DGAT1,PLPP3,EEF1A2,AL157935.2	cyan	VSMC_M2
GO:0009892	0.00	1.00	190	2254	negative regulation of metabolic process	BP	0.26735	PYM1,STAT6,TCF21,EHMT2,ZFPM2,EIF3H,IRF1,DEPTOR,DAXX,PTPRK,TLE1,NFIB,TRERF1,HMOX1,APPL2,MLIP,ZBTB45,ITGB8,P3H1,GPNMB,AKT1S1,AASS,GLI3,AP2A1,IRF3,KLF15,BAX,NOP53,VIM,BIN1,APOE,BCL3,ATRAID,ATG7,SOCS3,TIMP2,ZFP36,SAMD4B,KAT2B,SH3BP5,TRIM21,SMPD1,APBB1,LMO1,RARG,IGF1,SNTA1,WT1,CHMP4B,PATL1,TSHZ3,POU6F1,SERPING1,CAST,ARRDC3,SPON1,SFRP2,WWTR1,PRKCD,SRC,BPI,ZHX3,RIOX2,FOXF2,MAPK8IP1,SORBS3,PTPN13,STAT1,CTSA,GFRA2,NDN,CHRNA7,IKBKE,CAPN3,TIRAP,CSTB,TUSC2,NFKB1,GNAI2,SPOCD1,TPPP,HIST1H1C,IP6K1,LEF1,TBL1Y,PTGIS,WDR6,ECM1,NELFCD,FURIN,ERFE,HEG1,RFX5,GATA5,HELZ2,RNASEL,MAGEF1,MOV10,DPF2,ADORA2A,GRN,HDAC5,TSC22D4,HOMER3,MXD4,BMP4,LDB2,ZNF503,NR2F6,CPAMD8,HDAC6,DHX58,DNAJB6,ARRB2,EPHA2,ZBTB17,SERPINE2,GIPC1,ZFP36L1,IL27RA,UBQLN2,PCGF2,MLLT6,SLIT2,AR,TP53,KAT8,HOXB4,ELMSAN1,UBQLN4,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,ACP5,KANK2,WARS,CENPV,TMEM98,MTA1,MLLT1,PTPRS,MOSPD1,MFSD12,GLUS2,ABCD1,DVL1,ISG15,E4F1,RENBP,TSC2,NELFB,TCF3,SBNO2,FAM3A,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,ABL1,HSBP1,MIR197,INCA1,ABCA2,RPS15,GAS1,MEX3D,ZNF205,SLC8A3,HEXIM1,SERPINF1,ZBTB7A,ATN1,PML,SERPINB6,RPS19,PLPP3,GATA4,CALM3,CARD8,BMF,GCHFR,CDK9,NFKBIL1,BST2,ZFPM1,EN1	cyan	VSMC_M2
GO:0032956	0.00	1.00	34	304	regulation of actin cytoskeleton organization	BP	0.26735	ARHGAP18,GSN,NRP1,RHOB,BIN1,ARAP1,RHOG,EFNA5,RHPN2,PRKCD,EPHA3,C15orf62,SORBS3,TJP1,CTTN,SSH3,FES,ARPC5,ARHGEF10,RND2,ADD1,CAPZB,ARHGEF10L,ALOX15,CGNL1,SLIT2,ARHGAP17,SIGLEC15,PDGFRB,FLII,PHPT1,ABL1,SDC4,BST2	cyan	VSMC_M2
GO:0001841	0.00	1.00	14	92	neural tube formation	BP	0.26735	PLXNB2,COBL,RARG,SFRP2,RGMA,VANGL2,BMP4,CC2D2A,PRKACA,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0034440	0.00	1.00	14	90	lipid oxidation	BP	0.26735	APPL2,PLA2G7,ACAA1,ECH1,CYP4V2,DECR1,ACADS,HADH,ECHS1,ACAT1,ALOX15,CPT2,ABCD1,CRAT	cyan	VSMC_M2
GO:0042127	0.00	1.00	111	1230	regulation of cell population proliferation	BP	0.26735	STAT6,ZFPM2,RPS6KA2,IRF1,PTPRK,NFIB,HMOX1,KLF9,APPL2,P3H1,GPNMB,MEIS1,GLI3,FLT3LG,NRP1,BAX,MEIS3,APOE,ATRAID,PNP,TIMP2,ZFP36,FOLR2,HGS,KAT2B,RHOG,FGFR1,IL5RA,EFNB2,LMO1,RARG,IGF1,WT1,SFRP2,WWTR1,NDRG4,TGM2,PLCG1,SFRP5,MAPK8IP1,MMP2,LZTS2,STAT1,CD81,NDN,CHRNA7,TJP1,TIRAP,TMEM115,GNAI2,LEF1,MN1,VEGFD,WDR6,ECM1,GRK5,FES,RERG,ELL3,NFKBIA,LTBP3,B2M,ADORA2A,CAPN1,PLCD3,GRN,VEGFB,BMP4,IFI30,RARRES3,STAT5A,ZNF503,DLG5,JUP,ZBTB17,SERPINE2,MCC,ERBB2,ZFP36L1,IL27RA,NTRK1,AR,TP53,PPP1R9B,NUPR1,SHC1,PBXIP1,SLC16A2,KANK2,WARS,PDGFRB,IL13RA1,CRIP2,PODN,TNFRSF14,TSC2,CBFA2T3,ABL1,OSGIN1,IL34,INCA1,SERPINF1,CD55,PML,JUNB,TMEM250,SDC4,STX3,BST2,PYGO2,EMD	cyan	VSMC_M2
GO:1901658	0.01	1.00	6	23	glycosyl compound catabolic process	BP	0.26735	NAGA,PNP,GUSB,FUCA1,GBA,DPYD	cyan	VSMC_M2
GO:0030149	0.01	1.00	6	23	sphingolipid catabolic process	BP	0.26735	NEU1,NAGA,SMPD1,HEXB,PRKCD,GBA	cyan	VSMC_M2
GO:0032640	0.01	1.00	16	111	tumor necrosis factor production	BP	0.26735	AKAP12,GPNMB,BCL3,ZFP36,IGF1,TLR3,BPI,CHRNA7,TIRAP,FRMD8,TMEM106A,ARRB2,IL27RA,ACP5,OAS2,NFKBIL1	cyan	VSMC_M2
GO:0032680	0.01	1.00	16	111	regulation of tumor necrosis factor production	BP	0.26735	AKAP12,GPNMB,BCL3,ZFP36,IGF1,TLR3,BPI,CHRNA7,TIRAP,FRMD8,TMEM106A,ARRB2,IL27RA,ACP5,OAS2,NFKBIL1	cyan	VSMC_M2
GO:0072074	0.01	1.00	5	17	kidney mesenchyme development	BP	0.26735	TCF21,WT1,STAT1,BMP4,PDGFRB	cyan	VSMC_M2

GO:0010033	0.01	1.00	191	2273	response to organic substance	BP	0.26735	STAT6,TCF21,OS9,AKAP12,FLOT1,EHMT2,RPS6KA2,IRF1,DAXX,FBXO32,PTPRK,TRERF1,GCNT1,HMOX1,KIAA1324L,KLF9,APPL2,ITGB8,RRAGC,AKT1S1,GLI3,IRF3,NRP1,KLF15,BAX,TRIM13,FZD4,VIM,APOE,ATG7,LTBP4,IL17RC,SOCS3,RPS16,TIMP2,ZFP36,RPL15,FOLR2,HGS,KAT2B,RFTN1,FGFR1,IL5RA,TRIM21,ADGRA2,ACKR4,SMPD1,TMEM108,RARG,IGF1,TLR3,WT1,EFNA5,GGT7,EDEM2,CTSB,PLSCR1,SFRP2,GLRB,PRKCD,EPHA3,SRC,TGM2,BPI,PLCG1,BBS2,MMS19,GNAO1,SFRP5,MMP2,EXT2,STAT1,CD81,NDN,FIBIN,CHRNA7,IKBKE,TIRAP,PCSK6,NFKB1,GNAI2,RGMA,HADH,LEF1,PTGIS,SOX5,MN1,VEGFD,ECM1,GAS2L1,ADCY1,FES,FURIN,VPS11,ERFE,BCL9L,LMO3,GATA5,RERG,FIBP,PHEX,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,B2M,ADORA2A,CLEC3B,ADAMTS7,HDAC5,TMEM161A,ACAT1,VEGFB,BMP4,QDPR,NBL1,STAT5A,HDAC6,PQBP1,ARRB2,JUP,ALOX15,EPHA2,IL17RA,CASP9,PLSCR3,GIPC1,ERBB2,PRKACA,ZFP36L1,IL27RA,UBQLN2,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,ADAM15,SHC1,ADAR,ACP5,KANK2,TEX14,NEO1,ABCC1,EPN2,PDGFRB,IL13RA1,MAP2K3,UBXN6,EEF2,AGRN,ISG15,TNFRSF14,TSC2,NDOR1,SBNO2,PHPT1,SLC10A3,H6PD,FOXC2,ABL1,SLC2A8,IL34,GBP6,OAS2,ABCA2,GAS1,SLC8A3,SERPINF1,ZBTB7A,CD55,RAB43,PML,GATA4,CALM3,CARD8,VPS26B,CDK9,NFKBIL1,IL22RA1,RGS19,RNLS,RGS8,RGS10,BST2,RAB11B,EN1,EMD	cyan	VSMC_M2
GO:0060048	0.01	1.00	15	103	cardiac muscle contraction	BP	0.26735	GSN,BIN1,EHD3,GAA,SCN1B,SNTA1,CTNNA3,KCND3,VEGFB,JUP,PRKACA,MAP2K3,GATA4,CALM3,CLIC2	cyan	VSMC_M2
GO:1901701	0.01	1.00	83	887	cellular response to oxygen-containing compound	BP	0.26735	STAT6,EHMT2,RPS6KA2,FBXO32,PTPRK,TRERF1,KLF9,APPL2,RRAGC,IRF3,KLF15,RHOB,FZD4,VIM,AGAP3,SOCS3,ZFP36,FOLR2,KAT2B,RARG,IGF1,WT1,EFNA5,CAMKK2,PRKCD,EPHA3,SRC,TGM2,BPI,GNAO1,MMP2,STAT1,CHRNA7,TIRAP,NFKB1,GNAI2,MN1,ADCY1,FES,ERFE,CCS,STK25,PHEX,NFKBIA,LINC02210-CRHR1,HDAC5,STAT5A,HDAC6,ARRB2,JUP,CASP9,PLSCR3,PRKACA,ZFP36L1,PCGF2,SLIT2,AR,TP53,PDK2,PPP1R9B,ADAM15,SHC1,KANK2,ABCC1,AGRN,TSC2,NDOR1,SBNO2,PHPT1,FOXC2,ABL1,SLC2A8,SLC8A3,SERPINF1,CD55,GATA4,CARD8,NFKBIL1,ADPRHL2,RGS8,RGS10,RAB11B,MPV17	cyan	VSMC_M2
GO:0006665	0.01	1.00	17	120	sphingolipid metabolic process	BP	0.26809	NEU1,B3GALT4,NAGA,ST3GAL1,ITGB8,BAX,SMPD1,HEXB,PRKCD,B4GALT5,PSAP,GBA,CERS4,PLPP2,ABCA2,PLPP3,AL157935.2	cyan	VSMC_M2
GO:0022603	0.01	1.00	72	761	regulation of anatomical structure morphogenesis	BP	0.27155	PLXNB2,ARHGAP18,HMOX1,ITGB8,GPNMB,RRAS,NRP1,RHOB,FZD4,PAK4,ARAP1,HGS,RHOG,ADGRA2,LZTS3,HSPB6,PRICKLE2,ANGPT4,TLR3,WT1,EFNA5,HEXB,SFRP2,SRC,LRP4,PLCG1,C15orf62,STAT1,CHRNA7,TJP1,SEMA3B,ADGRB2,RGMA,PTGIS,VEGFD,ECM1,SEMA4B,FES,BCL9L,SEMA6C,VANGL2,GATA5,KIF1A,STK25,MOV10,WNT2B,GRN,VEGFB,RND2,VAT1,TMBIM1,BMP4,CAPZB,PQBP1,JUP,EPHA2,ERBB2,SLIT2,AR,MED12,ZMYM3,WARS,EPN2,ROR1,PTPRS,DVL1,FOXC2,ABL1,IST1,SERPINF1,PML,GATA4	cyan	VSMC_M2
GO:0045824	0.01	1.00	9	47	negative regulation of innate immune response	BP	0.27155	TRIM21,SERPING1,GRN,DHX58,ARRB2,ADAR,ISG15,FAM3A,RPS19	cyan	VSMC_M2
GO:0046470	0.01	1.00	10	55	phosphatidylcholine metabolic process	BP	0.27155	CHKB,PLA2G7,SLC44A1,PLB1,GPAT4,LPCAT4,RARRES3,SLC44A2,PNPLA7,LCAT	cyan	VSMC_M2
GO:0006027	0.01	1.00	5	17	glycosaminoglycan catabolic process	BP	0.27155	GNS,SGSH,GUSB,FUCA1,NAGLU	cyan	VSMC_M2
GO:0060429	0.01	1.00	76	810	epithelium development	BP	0.27233	STAT6,TCF21,PLXNB2,AFDN,NFIB,COBL,GLI3,NRP1,KLF15,RHOB,BAX,VIM,SLITRK6,SOCS3,ZFP36,GPAT4,TPP1,PRICKLE2,RARG,WT1,CTSB,SFRP2,WWTR1,NDRG4,SRC,TGM2,LRP4,FOXF2,LZTS2,STAT1,TJP1,RGMA,LEF1,LAMB2,HEG1,VANGL2,GATA5,WNT2B,BCR,PSAP,ACAT1,WNK4,ADD1,BMP4,RARRES3,LDB2,CC2D2A,DLG5,EPHA2,SERPINE2,KAZN,PRKACA,ZFP36L1,NTRK1,SLIT2,AR,TP53,HOXB2,HOXB4,MED12,KANK2,ROR1,PTPRS,DVL1,TSC2,EDF1,FOXC2,ABL1,DNAAF1,CNN3,KRT25,PML,GATA4,SDC4,PYGO2,EN1	cyan	VSMC_M2
GO:0016242	0.01	1.00	7	32	negative regulation of macroautophagy	BP	0.27753	EHMT2,HMOX1,CHMP4B,TP53,UBQLN4,NUPR1,TSC2	cyan	VSMC_M2
GO:0030258	0.01	1.00	22	171	lipid modification	BP	0.28021	APPL2,PLA2G7,APOE,ACAA1,ECH1,CYP4V2,DECR1,ACADS,HADH,ECHS1,ACAT1,PORCN,ALOX15,GBA,CPT2,ABCD1,INPP5E,PLPP2,CRAT,LCAT,ABCA2,PLPP3	cyan	VSMC_M2
GO:0002224	0.01	1.00	14	92	toll-like receptor signaling pathway	BP	0.28021	FLOT1,IRF1,LRRC19,APPL2,TRIL,IRF3,RFTN1,SLC15A4,TLR3,TIRAP,NFKBIA,ARRB2,PTPRS,NFKBIL1	cyan	VSMC_M2
GO:1901565	0.01	1.00	98	1069	organonitrogen compound catabolic process	BP	0.28021	MOXD1,OS9,GNS,DDAH2,NEU1,EIF3H,NAGA,GGA1,KCTD17,HMOX1,CUL9,PLA2G7,SLC44A1,BCKDHB,RNF144A,AASS,NOP53,TRIM13,APOE,AGAP3,ATRAID,ATG7,PNP,TIMP2,SGSH,RNF213,HGS,SMPD1,TPP1,RBCK1,CHMP4B,TP53INP2,GGT7,EDEM2,CTSB,NEIL2,HEXB,WWTR1,PRKCD,FOXF2,CTSA,CD81,GUSB,CAPN3,RGMA,UBA7,DCAF11,CTSK,RHBDD3,FURIN,VPS11,SCLY,ATG4B,FUCA1,MAGEF1,ECHS1,ADAMTS7,ACAT1,NUDT13,NAGLU,MAEA,QDPR,USE1,HDAC6,ARRB2,GABARAP,SERPINE2,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,SNX33,ABCC1,MTA1,CLPP,UBXN6,WDR81,ABCD1,DVL1,ASPA,ISG15,ELOB,PNPLA7,RENBP,FBXW5,AXIN1,RHBDF1,CBFA2T3,RNF166,DPYD,ABCA2,PML,EEF1A2,SAT1,NAGK,PSMB9	cyan	VSMC_M2
GO:0008630	0.01	1.00	13	84	intrinsic apoptotic signaling pathway in response to DNA damage	BP	0.28213	HMOX1,BAX,BCL3,SFRP2,IKBKE,ELL3,TMEM161A,EPHA2,CASP9,TP53,NUPR1,ABL1,PML	cyan	VSMC_M2
GO:0048568	0.01	1.00	37	341	embryonic organ development	BP	0.28239	TSHZ1,TCF21,ZFPM2,TEAD3,EFEMP1,COBL,GLI3,FLT3LG,SLITRK6,SOCS3,PKDCC,RARG,NDRG4,FOXF2,LEF1,VANGL2,PLCD3,BMP4,NAGLU,CC2D2A,DNAJB6,EPHA2,ZFP36L1,PCGF2,TP53,HOXB1,HOXB2,HOXB4,MED12,DVL1,FOXC2,DNAAF1,PBX3,JUNB,GATA4,ZFPM1,EN1	cyan	VSMC_M2

GO:0051668	0.01	1.00	54	537	localization within membrane	BP	0.28239	FLOT1,AFDN,GGA1,GSN,STOM,BAX,APOE,EHD3,CMTM6,HGS,RFTN1,RHOG,PKDCC,CLIP3,CHMP4B,NDRG4,GLRB,EPHA3,CACNB3,CPE,LRP4,BBS2,ARHGAP1,EXOC2,SLC5A3,SYS1,HPS6,CD81,OSBPL5,CAPN3,EXOC8,PSAP,GPC2,TMBIM1,JUP,EPHA2,AKAP5,ERBB2,AR,PPP1R9B,SLC51B,LLGL1,ZDHHC9,DVL1,AGRN,SLC9A3R2,RAB11FIP3,ENTR1,CLSTN1,GRASP,CALM3,LRRC7,STX3,RAB11B	cyan	VSMC_M2
GO:0044057	0.01	1.00	42	398	regulation of system process	BP	0.28471	CTDP1,FBXO32,NPTXR,MLIP,BIN1,APOE,EHD3,GAA,NPTX1,TMEM108,HSPB6,SCN1B,IGF1,SNTA1,TSHZ3,SRC,CACNB3,GNAO1,CHRNA7,CTTN,GNAI2,TPPP,GATA5,CTNNA3,LINC02210-CRHR1,KCND3,ADORA2A,WNK4,JUP,MYRF,PRKACA,GBA,TMEM98,SH3GL1,DVL1,PBX3,SLC8A3,GATA4,CALM3,CLIC2,CDK9,RNLS	cyan	VSMC_M2
GO:0072073	0.01	1.00	16	115	kidney epithelium development	BP	0.28589	TCF21,GLI3,KLF15,WT1,WWTR1,LZTS2,STAT1,LAMB2,WNT2B,ACAT1,WNK4,BMP4,SLIT2,KANK2,FOXC2,SDC4	cyan	VSMC_M2
GO:0009719	0.01	1.00	107	1202	response to endogenous stimulus	BP	0.28589	STAT6,TCF21,EHMT2,DAXX,FBXO32,PTPRK,TRERF1,GCNT1,HMOX1,KIAA1324L,KLF9,APPL2,ITGB8,RRAGC,GLI3,KLF15,VIM,APOE,ATG7,LTBP4,SOCS3,TIMP2,ZFP36,FOLR2,KAT2B,FGFR1,TMEM108,RARG,IGF1,WT1,CTSB,SFRP2,PRKCD,SRC,TGM2,PLCG1,BBS2,MMS19,GNAO1,SFRP5,MMP2,EXT2,STAT1,CD81,FIBIN,PCSK6,NFKB1,GNAI2,RGMA,HADH,LEF1,SOX5,GAS2L1,FURIN,VPS11,ERFE,BCL9L,LMO3,GATA5,RERG,FIBP,MUS81,PHEX,FAM89B,LTBP3,LINC02210-CRHR1,CLEC3B,ADAMTS7,HDAC5,ACAT1,BMP4,QDPR,NBL1,STAT5A,HDAC6,ARRB2,JUP,CASP9,GIPC1,ERBB2,PRKACA,ZFP36L1,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,SHC1,KANK2,NEO1,ABCC1,PDGFRB,EEF2,TSC2,FOXC2,ABL1,SLC2A8,ABCA2,SLC8A3,SERPINF1,ZBTB7A,PML,GATA4,CALM3,RGS8	cyan	VSMC_M2
GO:0007009	0.01	1.00	14	94	plasma membrane organization	BP	0.28861	FLOT1,PACSIN2,GSN,BIN1,FOLR2,SMPD1,PLSCR1,PRKCD,MYRF,PLEKHM2,PLSCR3,AR,SNX33,ABCD1	cyan	VSMC_M2
GO:0000904	0.01	1.00	55	562	cell morphogenesis involved in differentiation	BP	0.28943	FLOT1,PLXNB2,NFIB,COBL,GLI3,NRP1,FZD4,APOE,SLITRK6,NPTX1,RHOG,EFNB2,DCLK1,LZTS3,APBB1,SCN1B,EFNA5,EPHA3,SRC,LRP4,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,LEF1,B4GALT5,ATRNL1,LAMB2,SEMA4B,ADCY1,SEMA6C,HEG1,KIF1A,STK25,RND2,MAP1S,HDAC6,PQBP1,EPHA2,CASP9,ERBB2,NTRK1,SLIT2,AR,NEO1,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1,ZFPM1	cyan	VSMC_M2
GO:0060560	0.01	1.00	24	200	developmental growth involved in morphogenesis	BP	0.28943	COBL,NRP1,APOE,DCLK1,TMEM108,RARG,SFRP2,LZTS2,NDN,CTTN,SEMA3B,RGMA,LAMB2,SEMA4B,SEMA6C,RND2,BMP4,HDAC6,SLIT2,MED12,PTPRS,DVL1,ABL1,IST1	cyan	VSMC_M2
GO:1901386	0.01	1.00	4	11	negative regulation of voltage-gated calcium channel activity	BP	0.28952	CACNB3,LINC02210-CRHR1,CBARP,CALM3	cyan	VSMC_M2
GO:0032481	0.01	1.00	9	48	positive regulation of type I interferon production	BP	0.28952	FLOT1,IRF1,IRF3,TLR3,STAT1,PQBP1,DHX58,ISG15,OAS2	cyan	VSMC_M2
GO:0031670	0.01	1.00	8	40	cellular response to nutrient	BP	0.28952	HMOX1,FOLR2,MN1,FES,PHEX,PDK2,KANK2,NDOR1	cyan	VSMC_M2
GO:0032479	0.01	1.00	12	75	regulation of type I interferon production	BP	0.28952	FLOT1,IRF1,IRF3,TRIM21,TLR3,STAT1,TIRAP,PQBP1,DHX58,PTPRS,ISG15,OAS2	cyan	VSMC_M2
GO:0032606	0.01	1.00	12	75	type I interferon production	BP	0.28952	FLOT1,IRF1,IRF3,TRIM21,TLR3,STAT1,TIRAP,PQBP1,DHX58,PTPRS,ISG15,OAS2	cyan	VSMC_M2
GO:1903829	0.01	1.00	28	241	positive regulation of cellular protein localization	BP	0.28952	CARD10,GLI3,STOM,MARK4,RHOG,CLIP3,WWTR1,PRKCD,EPHA3,SRC,CACNB3,LRP4,SLC5A3,CD81,TRIM8,VPS11,CROCC,JUP,EPHA2,AKAP5,ERBB2,PPP1R9B,SLC51B,SNX33,GLIS2,ENTR1,STX3,UBL5	cyan	VSMC_M2
GO:0072207	0.01	1.00	5	18	metanephric epithelium development	BP	0.28952	WT1,WWTR1,STAT1,LAMB2,ACAT1	cyan	VSMC_M2
GO:0032268	0.01	1.00	156	1819	regulation of cellular protein metabolic process	BP	0.29039	PYM1,FLOT1,PPP6R2,EHMT2,PLXNB2,EIF3H,DEPTOR,DAXX,MTCH1,CARD10,ACO1,P3H1,GPNMB,RNF144A,AKT1S1,AASS,GSN,NRP1,KLF15,BAX,NOP53,FZD4,CAB39L,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,ATG7,SOCS3,CAMK1,TIMP2,ZFP36,SAMD4B,HGS,KAT2B,EIF3K,FGFR1,SH3BP5,TRIM21,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,SNTA1,EFNA5,PATL1,SERPING1,CAST,ARRDC3,CAMKK2,SPON1,SFRP2,WWTR1,PRKCD,SRC,LRP4,FOXF2,MAPK8IP1,PTPN13,MOB2,GFRA2,CD81,NDN,CHRNA7,CAPN3,TIRAP,CSTB,NFKB1,GNAI2,TPPP,RGMA,APH1A,VEGFD,ECM1,CASP10,FURIN,VPS11,HEG1,MAGEF1,NFKBIA,MOV10,ADORA2A,CLEC3B,GRN,PCOLCE,VEGFB,BMP4,CPAMD8,HDAC6,DNAJB6,ARRB2,GABARAP,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PRKACA,ZFP36L1,UBQLN2,NTRK1,MLLT6,SLIT2,TP53,UBQLN4,GBA,PPP1R9B,SLC51B,NUPR1,SHC1,ADAR,WARS,GPRC5B,SNX33,PDGFRB,TMEM98,MTA1,MAP2K3,MLLT1,TRAF4,EEF2,DVL1,ISG15,ELOB,DPH7,RENBP,TNFRSF14,TSC2,INPP5E,AXIN1,RHBDF1,CBFA2T3,ABL1,IL34,IST1,INCA1,ABCA2,RPS15,GAS1,MEX3D,SLC8A3,HEXIM1,SERPINF1,PML,SERPINB6,PLPP3,CALM3,CARD8,CDK9,SDC4,BST2,PYGO2	cyan	VSMC_M2
GO:0010632	0.01	1.00	25	208	regulation of epithelial cell migration	BP	0.29298	CARD10,HMOX1,RRAS,NRP1,RHOB,APOE,FGFR1,ADGRA2,ANGPT4,SRC,PLCG1,GRN,HDAC5,BMP4,STAT5A,HDAC6,JUP,EPHA2,MCC,SLIT2,MAP2K3,FOXC2,ABL1,SERPINF1,PLPP3	cyan	VSMC_M2
GO:2001135	0.01	1.00	5	18	regulation of endocytic recycling	BP	0.29298	NDRG4,ARHGAP1,AKAP5,GRASP,RAB11B	cyan	VSMC_M2
GO:0001819	0.01	1.00	34	304	positive regulation of cytokine production	BP	0.29371	AKAP12,FLOT1,IRF1,GSDMD,HMOX1,IRF3,LURAP1,BCL3,PNP,RFTN1,TLR3,SRC,STAT1,CD81,TIRAP,TUSC2,FURIN,HEG1,FRMD8,B2M,TMEM106A,PQBP1,DHX58,IL17RA,IL27RA,GPRC5B,ISG15,TNFRSF14,ABL1,OAS2,CD55,GATA4,CARD8,ZFPM1	cyan	VSMC_M2

GO:0009893	0.01	0.99	231	2815	positive regulation of metabolic process	BP	0.29371	PYM1,STAT6,TCF21,AKAP12,FLOT1,DDAH2,PLXNB2,ZFPM2,RPS6KA2,IRF1,AFDN,TCF20,DAXX,TEF,GSDMD,TEAD3,MTCH1,TLE1,GGA1,CARD10,NFIB,TRERF1,HMOX1,APPL2,MLIP,TRIM14,ITGB8,NAT14,GPNMB,MEIS1,RNF144A,PTOV1,GLI3,IRF3,GSN,NRP1,KLF15,BAX,DBP,NOP53,BICRA,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,PNP,ZFP36,SAMD4B,ARAP1,HGS,KAT2B,TBC1D5,RFTN1,RHOG,DCXR,FGFR1,TRIM21,SMPD1,APBB1,CLIP3,ANGPT4,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,EFNA5,TP53INP2,PATL1,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,EPHA3,SRC,LRP4,DECR1,MMS19,FOXF2,SLC5A3,PNPLA2,STAT1,ABHD14B,MOB2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,TUSC2,ZNF496,NFKB1,GNAI2,RGMA,BCL9,HADH,LEF1,APH1A,VEGFD,RHBDD3,CASP10,FURIN,VPS11,BCL9L,HEG1,RFX5,GATA5,HELZ2,ATG4B,RNASEL,MAGEF1,ELL3,NFKBIA,MOV10,FRMD8,B2M,DPF2,FYCO1,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,VEGFB,TMEM106A,BMP4,LDB2,TCEA2,HDAC6,PQBP1,DHX58,ARRB2,JUP,WIZ,EPHA2,MYRF,IL17RA,GABARAP,ZBTB17,TCF12,CASP9,GIPC1,ERBB2,BRAT1,ZFP36L1,IL27RA,UBQLN2,NTRK1,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,ADAR,WARS,GPRC5B,SNX33,PDGFRB,MTA1,MAP2K3,ROR1,TRAF4,MOSPD1,MPND,EEF2,CPT2,GLIS2,ABCD1,DVL1,AGRN,ISG15,ELOB,E4F1,TNFRSF14,TSC2,TCF3,SBNO2,EDF1,AXIN1,RERE,CBFA2T3,FOXC2,ABL1,ATMIN,IL34,PBX3,IST1,OAS2,NFIA,ABCA2,MEX3D,ZNF205,CD55,PML,RPS19,JUNB,EEF1A2,GATA4,CALM3,CARD8,CDK9,SDC4,ZFPM1,EN1	cyan	VSMC_M2
GO:0051056	0.01	1.00	29	259	regulation of small GTPase mediated signal transduction	BP	0.29456	ARHGEF25,FLOT1,ARHGAP18,ARHGAP39,NRP1,APOE,TIMP2,ARAP1,IGF1,SRC,TGM2,ARHGAP1,FAM13A,SIPA1L2,ARHGEF12,HEG1,ARHGEF10,BCR,ARHGEF10L,GABARAP,CGNL1,NTRK1,SLIT2,KANK2,DENND4B,ARHGAP17,PDGFRB,TSC2,ABL1	cyan	VSMC_M2
GO:0061437	0.01	1.00	6	25	renal system vasculature development	BP	0.29456	TCF21,NRP1,WT1,BMP4,PDGFRB,FOXC2	cyan	VSMC_M2
GO:0061440	0.01	1.00	6	25	kidney vasculature development	BP	0.29456	TCF21,NRP1,WT1,BMP4,PDGFRB,FOXC2	cyan	VSMC_M2
GO:0071495	0.01	1.00	92	1018	cellular response to endogenous stimulus	BP	0.29998	STAT6,TCF21,EHMT2,DAXX,FBXO32,PTPRK,TRERF1,KIAA1324L,KLF9,APPL2,ITGB8,RRAGC,KLF15,VIM,ATG7,LTBP4,SOCS3,ZFP36,FOLR2,KAT2B,FGFR1,TMEM108,RARG,IGF1,WT1,CTSB,SFRP2,PRKCD,SRC,TGM2,PLCG1,BBS2,GNAO1,SFRP5,MMP2,EXT2,STAT1,PCSK6,NFKB1,GNAI2,RGMA,LEF1,SOX5,GAS2L1,FURIN,VPS11,ERFE,BCL9L,LMO3,GATA5,FIBP,MUS81,PHEX,FAM89B,LTBP3,LINC02210-CRHR1,CLEC3B,ADAMTS7,HDAC5,BMP4,NBL1,STAT5A,HDAC6,ARRB2,JUP,CASP9,GIPC1,ERBB2,PRKACA,ZFP36L1,NTRK1,SLIT2,AR,TP53,PDK2,PPP1R9B,SHC1,KANK2,NEO1,ABCC1,PDGFRB,EEF2,TSC2,FOXC2,ABL1,SLC2A8,SLC8A3,SERPINF1,ZBTB7A,PML,GATA4,RGS8	cyan	VSMC_M2
GO:0061458	0.01	1.00	36	333	reproductive system development	BP	0.29998	TCF21,ZFPM2,MEA1,ITGB8,GLI3,BAX,FZD4,SOCS3,RARG,TLR3,WT1,CTSB,SFRP2,SRC,FOXF2,LEF1,REC8,WNT2B,PLCD3,PSAP,BMP4,DNAJB6,ARRB2,SERPINE2,ZFP36L1,NTRK1,SLIT2,AR,PPP1R9B,ADAM15,NUPR1,PDGFRB,PLAC1,SERPINF1,JUNB,GATA4	cyan	VSMC_M2
GO:0051270	0.01	1.00	77	830	regulation of cellular component movement	BP	0.3054	AKAP12,PLXNB2,AFDN,PTPRK,ARHGAP18,CARD10,HMOX1,APPL2,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,BIN1,APOE,TPPP2,ARAP1,RHOG,FGFR1,ADGRA2,LAMP1,ANGPT4,IGF1,SFRP2,NDRG4,SRC,PLCG1,BBS2,NISCH,PHACTR1,CD81,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,ECM1,SEMA4B,FES,SEMA6C,CTNNA3,FAM89B,GRN,HDAC5,VEGFB,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,JUP,EPHA2,SERPINE2,MCC,IL27RA,SLIT2,ADAM15,PDGFRB,MAP2K3,PODN,TNFRSF14,PHPT1,FOXC2,ABL1,DNAAF1,OSGIN1,IL34,SERPINF1,RPS19,PLPP3,GATA4,SDC4,BST2	cyan	VSMC_M2
GO:0007271	0.01	1.00	5	18	synaptic transmission, cholinergic	BP	0.30971	APOE,CHRNA7,ANXA9,ADORA2A,CHRNE	cyan	VSMC_M2
GO:0031331	0.01	1.00	39	366	positive regulation of cellular catabolic process	BP	0.31084	HMOX1,TRIM14,RNF144A,BAX,NOP53,TRIM13,APOE,ATG7,ZFP36,SAMD4B,TRIM21,IGF1,TP53INP2,PATL1,CAMKK2,PRKCD,PNPLA2,CD81,TRIM8,RGMA,FURIN,VPS11,MAGEF1,MOV10,FYCO1,GABARAP,ZFP36L1,UBQLN2,GBA,NUPR1,SNX33,ABCD1,DVL1,ELOB,TSC2,AXIN1,CBFA2T3,ABCA2,MEX3D	cyan	VSMC_M2
GO:0009891	0.01	0.99	133	1533	positive regulation of biosynthetic process	BP	0.31421	PYM1,STAT6,TCF21,AKAP12,DDAH2,PLXNB2,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,CAMK1,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,MMS19,FOXF2,SLC5A3,STAT1,ABHD14B,CD81,NDN,SLC45A3,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,DPF2,PCBD1,HDAC5,TMEM106A,BMP4,LDB2,TCEA2,PQBP1,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,PDGFRB,MTA1,MAP2K3,MOSPD1,MPND,EEF2,GLIS2,ABCD1,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0001933	0.01	1.00	31	276	negative regulation of protein phosphorylation	BP	0.31425	DEPTOR,AKT1S1,BAX,APOE,SOCS3,KAT2B,SH3BP5,SMPD1,SFRP2,WWTR1,PRKCD,MAPK8IP1,PTPN13,GFRA2,HEG1,ADORA2A,BMP4,ARRB2,SLIT2,GBA,ADAR,WARS,MLLT1,DVL1,TSC2,ABL1,INCA1,SLC8A3,HEXIM1,PLPP3,CALM3	cyan	VSMC_M2
GO:0006491	0.01	1.00	5	18	N-glycan processing	BP	0.31782	MGAT4B,GNPTAB,MAN2A1,GANAB,PRKCSH	cyan	VSMC_M2
GO:0071706	0.01	1.00	16	115	tumor necrosis factor superfamily cytokine production	BP	0.31782	AKAP12,GPNMB,BCL3,ZFP36,IGF1,TLR3,BPI,CHRNA7,TIRAP,FRMD8,TMEM106A,ARRB2,IL27RA,ACP5,OAS2,NFKBIL1	cyan	VSMC_M2

GO:1903555	0.01	1.00	16	115	regulation of tumor necrosis factor superfamily cytokine production	BP	0.31782	AKAP12,GPNMB,BCL3,ZFP36,IGF1,TLR3,BPI,CHRNA7,TIRAP,FRMD8,TMEM106A,ARRB2,IL27RA,ACP5,OAS2,NFKBIL1	cyan	VSMC_M2
GO:0010595	0.01	1.00	15	105	positive regulation of endothelial cell migration	BP	0.31782	HMOX1,RRAS,NRP1,RHOB,FGFR1,ADGRA2,ANGPT4,PLCG1,GRN,BMP4,STAT5A,MAP2K3,FOXC2,ABL1,PLPP3	cyan	VSMC_M2
GO:0010557	0.01	0.99	125	1433	positive regulation of macromolecule biosynthetic process	BP	0.31856	PYM1,STAT6,TCF21,AKAP12,PLXNB2,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,CAMK1,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,MMS19,FOXF2,STAT1,ABHD14B,CD81,NDN,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,DPF2,PCBD1,HDAC5,TMEM106A,BMP4,LDB2,TCEA2,PQBP1,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,SLC51B,NUPR1,SHC1,PBXIP1,PDGFRB,MTA1,MAP2K3,MOSPD1,MPND,EEF2,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,ABCA2,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0010466	0.01	1.00	19	145	negative regulation of peptidase activity	BP	0.32371	BIN1,TIMP2,SERPING1,CAST,SFRP2,SRC,CSTB,ECM1,FURIN,ADORA2A,CPAMD8,DNAJB6,ARRB2,SERPINE2,RENBP,SERPINF1,SERPINB6,CARD8,BST2	cyan	VSMC_M2
GO:0006023	0.01	1.00	11	68	aminoglycan biosynthetic process	BP	0.32397	ST3GAL1,AP2A1,CHST14,EXT2,NFKB1,B4GALT5,B4GAT1,B3GAT3,XYLT2,PDGFRB,HS3ST3B1	cyan	VSMC_M2
GO:0031344	0.01	1.00	53	538	regulation of cell projection organization	BP	0.32397	PLXNB2,KCTD17,P3H1,COBL,AP2A1,NRP1,FZD4,MARK4,VIM,APOE,CAMK1,DZIP1,ARAP1,RHOG,EFNB2,LZTS3,APBB1,SCN1B,SFRP2,NDRG4,PRKCD,EPHA3,SRC,LRP4,C15orf62,SEMA3B,RGMA,SEMA4B,NCKIPSD,FES,SEMA6C,KIF1A,STK25,MOV10,B2M,GRN,GPC2,RND2,CAPZB,PQBP1,CROCC,EPHA2,NTRK1,SLIT2,ROR1,PTPRS,DVL1,AGRN,ENTR1,ATMIN,IST1,SERPINF1,LRRC7	cyan	VSMC_M2
GO:1902531	0.01	0.99	115	1309	regulation of intracellular signal transduction	BP	0.32397	ARHGEF25,AKAP12,FLOT1,DEPTOR,ARHGAP18,GRINA,TLE1,ARHGAP39,HMOX1,LRRC19,CARD19,TRIM14,GPNMB,RRAGC,STK40,AKT1S1,IRF3,RRAS,NRP1,BAX,NOP53,MEIS3,LURAP1,TRIM13,FZD4,APOE,BCL3,TIMP2,CANT1,PAK4,ARAP1,FGFR1,TRIM21,SMPD1,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,SFRP2,NDRG4,PRKCD,SRC,TGM2,ARHGAP1,SFRP5,MAPK8IP1,SORBS3,PTPN13,STAT1,FAM13A,CD81,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,GNAI2,SIPA1L2,ARHGEF12,ECM1,CASP10,HEG1,LMO3,STK25,ELL3,NFKBIA,ARHGEF10,BCR,TMEM161A,TMEM101,HOMER3,TMEM106A,BMP4,DLG5,DHX58,ARHGEF10L,ARRB2,ALOX15,EPHA2,AKAP5,GABARAP,SERPINE2,CGNL1,ERBB2,NTRK1,SLIT2,AR,TP53,PDK2,GBA,NUPR1,SHC1,KANK2,DENND4B,ARHGAP17,SLC44A2,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,TRAF7,TSC2,INPP5E,AXIN1,NPRL3,ABL1,IL34,RPS15,HEXIM1,GATA4,CALM3,CARD8,BST2	cyan	VSMC_M2
GO:0071359	0.01	1.00	5	18	cellular response to dsRNA	BP	0.32397	FLOT1,IRF3,TLR3,NFKB1,PQBP1	cyan	VSMC_M2
GO:0044093	0.01	0.99	103	1151	positive regulation of molecular function	BP	0.32397	FLOT1,TBC1D22A,AFDN,DAXX,MTCH1,CARD10,TRIM14,TBC1D2,TBC1D17,GSN,NRP1,BAX,TRIM13,FZD4,CAB39L,APOE,SLC6A9,CAMK1,EHD3,TIMP2,ARAP1,TBC1D5,RHOG,RFNG,FGFR1,TRIM21,ANGPT4,MAP3K12,RBCK1,IGF1,TLR3,EFNA5,ARRDC3,PLSCR1,SPON1,SFRP2,PRKCD,EPHA3,SRC,CACNB3,TGM2,GNAO1,SLC5A3,CD81,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,GNAI2,RGMA,SGSM1,SIPA1L2,APH1A,CASP10,ADCY1,CCS,B2M,ARHGEF10,BCR,GRN,PCOLCE,HDAC5,PSAP,WNK4,ADD1,BMP4,RARRES3,HDAC6,B3GAT3,JUP,EPHA2,AKAP5,CASP9,ERBB2,NTRK1,AR,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,SGSM2,AGRN,TSC2,TCF3,EDF1,AXIN1,ABL1,IL34,ZBTB7A,TRIM26,PML,PLPP3,EEF1A2,CALM3,CARD8,CLIC2,CDK9,SDC4,RGS8,RGS10,PYGO2	cyan	VSMC_M2
GO:0012501	0.01	0.99	129	1474	programmed cell death	BP	0.32397	AKAP12,DDAH2,RPS6KA2,IRF1,DEPTOR,DAXX,ST3GAL1,GSDMD,MTCH1,GRINA,TLE1,CARD10,HMOX1,HIGD2A,RRAGC,COLEC11,ELMO1,STK40,AKT1S1,STK17A,GLI3,IRF3,GSN,NRP1,RHOB,HS1BP3,BAX,C6orf120,NOP53,MEIS3,MARK4,BIN1,APOE,BCL3,ATG7,SOCS3,ZFP36,PAK4,FGFR1,LAMP1,SMPD1,APBB1,CLIP3,HSPB6,ANGPT4,RBCK1,RARG,IGF1,TLR3,WT1,CHMP3,CAST,CTSB,PLSCR1,SFRP2,PRKCD,SRC,TGM2,PLCG1,SFRP5,MAPK8IP1,NISCH,STAT1,IKBKE,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,PTGIS,GRK5,CASP10,STK25,ELL3,NFKBIA,DPF2,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,MAP1S,DLG5,HDAC6,DNAJB6,ARRB2,EPHA2,GABARAP,CASP9,PLSCR3,BRAT1,TP53BP2,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,PDK2,GBA,NUPR1,SHC1,ADAR,KANK2,ATOX1,PDGFRB,TRAF4,RETREG1,TRAF7,TSC2,RHOT2,AXIN1,FOXC2,ABL1,OSGIN1,INCA1,GAS1,ZNF205,ZBTB7A,ATN1,PML,EEF1A2,GATA4,CARD8,BMF,EN1	cyan	VSMC_M2
GO:0032728	0.01	1.00	7	33	positive regulation of interferon-beta production	BP	0.32526	FLOT1,IRF1,IRF3,TLR3,DHX58,ISG15,OAS2	cyan	VSMC_M2
GO:0006941	0.01	1.00	17	128	striated muscle contraction	BP	0.33048	GSN,BIN1,EHD3,GAA,SCN1B,SNTA1,CTNNA3,KCND3,VEGFB,JUP,PRKACA,MAP2K3,EEF2,SLC8A3,GATA4,CALM3,CLIC2	cyan	VSMC_M2
GO:0070374	0.01	1.00	19	145	positive regulation of ERK1 and ERK2 cascade	BP	0.33048	AKAP12,GPNMB,NRP1,APOE,MAP3K12,IGF1,NDRG4,SRC,CHRNA7,TIRAP,GNAI2,BMP4,ARRB2,ALOX15,NTRK1,SHC1,PDGFRB,ABL1,GATA4	cyan	VSMC_M2
GO:0072010	0.01	1.00	5	19	glomerular epithelium development	BP	0.33048	KLF15,WT1,LAMB2,BMP4,FOXC2	cyan	VSMC_M2

GO:0040012	0.01	0.99	74	796	regulation of locomotion	BP	0.33048	AKAP12,PLXNB2,AFDN,PTPRK,ARHGAP18,CARD10,HMOX1,APPL2,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,APOE,TPPP2,RHOG,FGFR1,EFNB2,ADGRA2,ANGPT4,IGF1,ARRDC3,SFRP2,NDRG4,SRC,PLCG1,BBS2,NISCH,PHACTR1,CD81,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,ECM1,SEMA4B,FES,SEMA6C,FAM89B,ADORA2A,GRN,HDAC5,VEGFB,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,JUP,EPHA2,SERPINE2,MCC,IL27RA,SLIT2,ADAM15,PDGFRB,MAP2K3,PODN,TNFRSF14,PHPT1,FOXC2,ABL1,OSGIN1,IL34,SERPINF1,PLPP3,SDC4,STX3,BST2	cyan	VSMC_M2
GO:0032835	0.01	1.00	9	52	glomerulus development	BP	0.33517	TCF21,KLF15,WT1,WWTR1,LAMB2,BMP4,PDGFRB,FOXC2,MPV17	cyan	VSMC_M2
GO:0072009	0.01	1.00	13	89	nephron epithelium development	BP	0.34628	TCF21,GLI3,KLF15,WT1,WWTR1,LZTS2,STAT1,LAMB2,WNT2B,ACAT1,WNK4,BMP4,FOXC2	cyan	VSMC_M2
GO:0033673	0.01	1.00	23	191	negative regulation of kinase activity	BP	0.34759	DEPTOR,AKT1S1,APOE,KAT2B,SH3BP5,SMPD1,SFRP2,WWTR1,PRKCD,MAPK8IP1,HEG1,ADORA2A,BMP4,GBA,ADAR,WARS,MLLT1,DVL1,TSC2,ABL1,INCA1,SLC8A3,HEXIM1	cyan	VSMC_M2
GO:0000302	0.01	1.00	22	177	response to reactive oxygen species	BP	0.34759	STAT6,PTPRK,HMOX1,RHOB,APOE,AGAP3,CAMKK2,PRKCD,SRC,GNAO1,MMP2,STAT1,CCS,STK25,HDAC6,PCGF2,PDK2,PDGFRB,EEF2,ABL1,ADPRHL2,MPV17	cyan	VSMC_M2
GO:0006677	0.01	1.00	4	12	glycosylceramide metabolic process	BP	0.34857	NAGA,PRKCD,GBA,AL157935.2	cyan	VSMC_M2
GO:0050830	0.01	1.00	7	33	defense response to Gram-positive bacterium	BP	0.34857	GSDMD,TIRAP,EPHA2,IL27RA,ACP5,TNFRSF14,GBP6	cyan	VSMC_M2
GO:0043113	0.01	1.00	8	43	receptor clustering	BP	0.3493	GSN,APOE,GLRB,LRP4,CD81,DVL1,AGRN,LRRC7	cyan	VSMC_M2
GO:0060348	0.01	1.00	21	172	bone development	BP	0.3493	P3H1,MEIS1,GLI3,LRRC17,EPYC,RARG,IGF1,SFRP2,SRC,TGM2,EXT2,PHEX,LTBP3,BMP4,TP53,HOXB4,ACP5,SIGLEC15,DYM,RPL13,ZFPM1	cyan	VSMC_M2
GO:0031328	0.01	0.99	130	1503	positive regulation of cellular biosynthetic process	BP	0.35194	PYM1,STAT6,TCF21,DDAH2,PLXNB2,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,CAMK1,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,MMS19,FOXF2,STAT1,ABHD14B,CD81,NDN,SLC45A3,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,DPF2,PCBD1,HDAC5,BMP4,LDB2,TCEA2,PQBP1,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,PDGFRB,MTA1,MAP2K3,MOSPD1,MPND,EEF2,GLIS2,ABCD1,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0046459	0.01	1.00	4	12	short-chain fatty acid metabolic process	BP	0.35331	ACSS1,ACSS2,ACADS,CRAT	cyan	VSMC_M2
GO:0016137	0.01	1.00	4	12	glycoside metabolic process	BP	0.35462	NAGA,GUSB,FUCA1,GBA	cyan	VSMC_M2
GO:0010605	0.01	0.99	175	2090	negative regulation of macromolecule metabolic process	BP	0.35519	PYM1,STAT6,TCF21,EHMT2,ZFPM2,EIF3H,IRF1,DEPTOR,DAXX,PTPRK,TLE1,NFIB,TRERF1,HMOX1,APPL2,MLIP,ZBTB45,ITGB8,P3H1,GPNMB,AKT1S1,AASS,GLI3,AP2A1,IRF3,KLF15,BAX,NOP53,VIM,BIN1,APOE,BCL3,ATRAID,ATG7,SOCS3,TIMP2,ZFP36,SAMD4B,KAT2B,SH3BP5,TRIM21,SMPD1,APBB1,LMO1,RARG,IGF1,SNTA1,WT1,PATL1,TSHZ3,POU6F1,SERPING1,CAST,SPON1,SFRP2,WWTR1,PRKCD,SRC,BPI,ZHX3,RIOX2,FOXF2,MAPK8IP1,SORBS3,PTPN13,STAT1,CTSA,GFRA2,NDN,CHRNA7,IKBKE,CAPN3,TIRAP,CSTB,TUSC2,NFKB1,GNAI2,SPOCD1,TPPP,HIST1H1C,LEF1,TBL1Y,ECM1,NELFCD,FURIN,HEG1,RFX5,GATA5,HELZ2,RNASEL,MAGEF1,MOV10,DPF2,ADORA2A,HDAC5,TSC22D4,HOMER3,MXD4,BMP4,LDB2,ZNF503,NR2F6,CPAMD8,HDAC6,DHX58,DNAJB6,ARRB2,EPHA2,ZBTB17,SERPINE2,GIPC1,ZFP36L1,IL27RA,UBQLN2,PCGF2,MLLT6,SLIT2,AR,TP53,KAT8,HOXB4,ELMSAN1,UBQLN4,GBA,PPP1R9B,SHC1,PBXIP1,ADAR,ACP5,KANK2,WARS,CENPV,TMEM98,MTA1,MLLT1,PTPRS,MOSPD1,GLIS2,ABCD1,DVL1,ISG15,E4F1,RENBP,TSC2,NELFB,TCF3,SBNO2,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,ABL1,HSBP1,MIR197,INCA1,RPS15,GAS1,MEX3D,ZNF205,SLC8A3,HEXIM1,SERPINF1,ZBTB7A,ATN1,PML,SERPINB6,PLPP3,CALM3,CARD8,CDK9,NFKBIL1,BST2,ZFPM1,EN1	cyan	VSMC_M2

GO:0008150	0.01	0.99	888	12183	biological_process	BP	0.35519	CTDP1,TSHZ1,ZADH2,MMP19,PYM1,PMEL,RAB5B,MYL6B,RBMS2,STAT6,MOXD1,TCF21,ARHGEF25,OS9,ADAMTS2,MGAT4B,GNS,ULBP2,AKAP12,FLOT1,RABL2A,CHKB,DDAH2,PPP6R2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,CFB,TBC1D22A,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,B3GALT4,CYB5R3,TAPBP,TCF20,DAXX,NAGA,FBXO32,CUTA,HDDC2,TGFBI,TEF,PTPRK,ARHGAP18,ST3GAL1,IBA57,CDC14C,GSDMD,TEAD3,NPTXR,MTCH1,GRINA,TLE1,GGA1,OPLAH,CARD10,KCTD17,NFIB,KIFC2,TRERF1,GCNT1,ARHGAP39,HMOX1,LRRC19,CNPY3,MEA1,ACO1,KIAA1324L,CUL9,TRPM3,KLF9,APPL2,ATP10D,RSPH9,HIGD2A,PLA2G7,CARD19,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,TBC1D2,GALNT12,ITGB8,P3H1,NAT14,TMEM150B,KCNQ5,GPNMB,SLC44A1,BCKDHB,EFEMP1,TRIL,BBS9,RRAGC,EEPD1,MEIS1,COLEC11,ELMO1,RNF144A,IAH1,STK40,COBL,TBC1D17,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,CADPS2,IRF3,RRAS,FLT3LG,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,HS1BP3,BAX,DBP,HBP1,DENND2A,RPL18,PARP12,CCDC114,C6orf120,SELENOW,NOP53,ABTB1,BICRA,MEIS3,FKRP,UQCRH,LRRC17,LURAP1,TRIM13,TSPAN1,ACSS1,FZD4,ME3,CAB39L,MARK4,VIM,AGBL5,TMEM176B,BIN1,APOE,UROD,BCL3,ABCB8,ETHE1,MIF4GD,AGAP3,ATRAID,SLC6A9,ACAA1,ATG7,EXOC7,CYP2S1,RHBDF2,COQ8B,LTBP4,SHKBP1,CAPN5,IL17RC,PLB1,SLITRK6,SOCS3,CAMK1,EHD3,PLD3,CMTM6,TEP1,OSBPL10,RNF170,PNP,DZIP1,TPPP2,RPS16,TIMP2,ZFP36,LGALS3BP,CANT1,SAMD4B,GAA,PAK4,SGSH,SLC26A11,ECH1,STARD10,RNF213,ARAP1,NPTX1,GPAT4,SLC4A9,RPL15,FOLR2,HGS,KAT2B,TBC1D5,PPP1R27,EIF3K,RFTN1,RHOG,ITGBL1,DCXR,RFNG,CATS	cyan	VSMC_M2
GO:0010951	0.01	1.00	18	137	negative regulation of endopeptidase activity	BP	0.35541	BIN1,TIMP2,SERPING1,CAST,SFRP2,SRC,CSTB,FURIN,ADORA2A,CPAMD8,DNAJB6,ARRB2,SERPINE2,RENBP,SERPINF1,SERPINB6,CARD8,BST2	cyan	VSMC_M2
GO:0051246	0.01	0.99	165	1953	regulation of protein metabolic process	BP	0.35545	PYM1,FLOT1,PPP6R2,EHMT2,PLXNB2,EIF3H,RPS6KA2,DEPTOR,DAXX,MTCH1,GGA1,CARD10,ACO1,P3H1,GPNMB,RNF144A,AKT1S1,AASS,GSN,NRP1,KLF15,BAX,NOP53,FZD4,CAB39L,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,LTBP4,SOCS3,CAMK1,TIMP2,ZFP36,SAMD4B,HGS,KAT2B,EIF3K,FGFR1,SH3BP5,TRIM21,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,SNTA1,EFNA5,PATL1,SERPING1,CAST,ARRDC3,CAMKK2,SPON1,SFRP2,WWTR1,PRKCD,SRC,LRP4,FOXF2,MAPK8IP1,PTPN13,CTSA,MOB2,GFRA2,CD81,NDN,CHRNA7,CAPN3,TIRAP,CSTB,NFKB1,GNAI2,TPPP,RGMA,APH1A,VEGFD,ECM1,RHBDD3,CASP10,FURIN,VPS11,HEG1,ATG4B,MAGEF1,NFKBIA,MOV10,ADORA2A,CLEC3B,GRN,PCOLCE,VEGFB,BMP4,CPAMD8,HDAC6,DNAJB6,ARRB2,GABARAP,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PRKACA,ZFP36L1,UBQLN2,NTRK1,MLLT6,SLIT2,TP53,UBQLN4,GBA,PPP1R9B,SLC51B,NUPR1,SHC1,ADAR,WARS,GPRC5B,SNX33,PDGFRB,TMEM98,MTA1,MAP2K3,MLLT1,TRAF4,EEF2,DVL1,ISG15,ELOB,DPH7,RENBP,TNFRSF14,TSC2,INPP5E,AXIN1,RHBDF1,CBFA2T3,ABL1,IL34,IST1,INCA1,ABCA2,RPS15,GAS1,MEX3D,SLC8A3,HEXIM1,SERPINF1,PML,SERPINB6,PLPP3,EEF1A2,CALM3,CARD8,CDK9,SDC4,PSMB9,BST2,PYGO2	cyan	VSMC_M2
GO:0048588	0.01	1.00	23	195	developmental cell growth	BP	0.35598	CTDP1,COBL,NRP1,APOE,DCLK1,TMEM108,RARG,IGF1,NDN,CTTN,SEMA3B,RGMA,LAMB2,SEMA4B,SEMA6C,RND2,HDAC6,SLIT2,PTPRS,DVL1,ABL1,IST1,GATA4	cyan	VSMC_M2
GO:0048584	0.01	0.99	129	1488	positive regulation of response to stimulus	BP	0.35852	STAT6,AKAP12,FLOT1,CFB,HMOX1,LRRC19,KIAA1324L,APPL2,PLA2G7,TRIM14,GPNMB,RRAGC,COLEC11,IRF3,NRP1,BAX,MEIS3,LURAP1,TRIM13,FZD4,APOE,SHKBP1,TIMP2,CANT1,RFTN1,RFNG,FGFR1,TRIM21,ADGRA2,LAMP1,TMEM108,APBB1,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,SERPING1,PLSCR1,SFRP2,NDRG4,PRKCD,SRC,CACNB3,TGM2,PLCG1,MMS19,MAPK8IP1,SORBS3,CD81,CHRNA7,TRIM8,IKBKE,TIRAP,TM2D3,NFKB1,GNAI2,LEF1,PTGIS,MN1,VEGFD,KIF7,ECM1,CASP10,ERFE,LMO3,GATA5,FAM53B,STK25,NFKBIA,B2M,ADORA2A,GRN,C1R,C1S,TMEM161A,TMEM101,VEGFB,TMEM106A,BMP4,DLG5,HDAC6,PQBP1,DHX58,PLD2,ARRB2,JUP,ALOX15,IL17RA,GIPC1,ERBB2,IL27RA,UBQLN2,NTRK1,SLIT2,AR,TP53,NUPR1,SHC1,PBXIP1,SLC44A2,NEO1,ULK3,GPRC5B,ABCC1,EPN2,PDGFRB,MAP2K3,C6,ROR1,TRAF4,DVL1,TRAF7,PHPT1,AXIN1,FOXC2,ABL1,IL34,INCA1,RPS15,HEXIM1,CD55,PML,RPS19,PLPP3,GATA4,STX3,OCIAD2,BST2	cyan	VSMC_M2
GO:0050804	0.01	0.99	34	317	modulation of chemical synaptic transmission	BP	0.35856	AKAP12,FLOT1,PACSIN2,NPTXR,APOE,NPTX1,TMEM108,TSHZ3,SRC,CACNB3,PLCG1,NISCH,CHRNA7,GNAI2,ADCY1,BCR,ADORA2A,ARRB2,AKAP5,SERPINE2,GIPC1,PRKACA,NTRK1,CPLX2,PPP1R9B,GRIA1,PTPRS,SH3GL1,DVL1,CLSTN1,ABL1,SLC8A3,CALM3,STX3	cyan	VSMC_M2
GO:0002009	0.01	0.99	42	412	morphogenesis of an epithelium	BP	0.35896	TCF21,PLXNB2,COBL,GLI3,NRP1,RHOB,SOCS3,PRICKLE2,RARG,WT1,SFRP2,NDRG4,SRC,TGM2,FOXF2,LZTS2,STAT1,RGMA,LEF1,VANGL2,WNT2B,WNK4,BMP4,CC2D2A,DLG5,EPHA2,PRKACA,SLIT2,AR,HOXB2,HOXB4,MED12,ROR1,DVL1,TSC2,FOXC2,ABL1,DNAAF1,KRT25,PML,GATA4,SDC4	cyan	VSMC_M2

GO:1901700	0.01	0.99	109	1234	response to oxygen-containing compound	BP	0.35903	STAT6,AKAP12,EHMT2,RPS6KA2,FBXO32,PTPRK,TRERF1,GCNT1,HMOX1,KLF9,APPL2,RRAGC,IRF3,KLF15,RHOB,FZD4,VIM,APOE,AGAP3,ATG7,SOCS3,ZFP36,RPL15,FOLR2,KAT2B,SMPD1,RARG,IGF1,WT1,EFNA5,GGT7,EDEM2,CAMKK2,GLRB,PRKCD,EPHA3,SRC,TGM2,BPI,GNAO1,MMP2,STAT1,FIBIN,CHRNA7,TIRAP,NFKB1,GNAI2,HADH,MN1,ADCY1,FES,ERFE,CCS,STK25,PHEX,NFKBIA,LINC02210-CRHR1,HDAC5,TMEM161A,QDPR,STAT5A,HDAC6,ARRB2,JUP,CASP9,PLSCR3,PRKACA,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,ADAM15,SHC1,ACP5,KANK2,ABCC1,PDGFRB,EEF2,AGRN,TSC2,NDOR1,SBNO2,PHPT1,SLC10A3,H6PD,FOXC2,ABL1,SLC2A8,ABCA2,SLC8A3,SERPINF1,CD55,GATA4,CALM3,CARD8,NFKBIL1,ADPRHL2,RGS19,RNLS,RGS8,RGS10,RAB11B,MPV17,EN1	cyan	VSMC_M2
GO:0019395	0.01	1.00	13	87	fatty acid oxidation	BP	0.35945	APPL2,ACAA1,ECH1,CYP4V2,DECR1,ACADS,HADH,ECHS1,ACAT1,ALOX15,CPT2,ABCD1,CRAT	cyan	VSMC_M2
GO:0071310	0.01	0.99	151	1784	cellular response to organic substance	BP	0.35945	STAT6,TCF21,OS9,AKAP12,FLOT1,EHMT2,RPS6KA2,IRF1,DAXX,FBXO32,PTPRK,TRERF1,KIAA1324L,KLF9,APPL2,ITGB8,RRAGC,AKT1S1,IRF3,NRP1,KLF15,BAX,FZD4,VIM,ATG7,LTBP4,IL17RC,SOCS3,RPS16,ZFP36,FOLR2,HGS,KAT2B,FGFR1,IL5RA,ADGRA2,ACKR4,TMEM108,RARG,IGF1,TLR3,WT1,EFNA5,CTSB,SFRP2,PRKCD,EPHA3,SRC,TGM2,BPI,PLCG1,BBS2,GNAO1,SFRP5,MMP2,EXT2,STAT1,NDN,IKBKE,PCSK6,NFKB1,GNAI2,RGMA,LEF1,PTGIS,SOX5,MN1,VEGFD,ECM1,GAS2L1,ADCY1,FES,FURIN,VPS11,ERFE,BCL9L,LMO3,GATA5,FIBP,PHEX,NFKBIA,FAM89B,LTBP3,LINC02210-CRHR1,CLEC3B,ADAMTS7,HDAC5,VEGFB,BMP4,NBL1,STAT5A,HDAC6,PQBP1,ARRB2,JUP,ALOX15,IL17RA,CASP9,PLSCR3,GIPC1,ERBB2,PRKACA,ZFP36L1,IL27RA,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,ADAM15,SHC1,ADAR,KANK2,TEX14,NEO1,ABCC1,EPN2,PDGFRB,IL13RA1,MAP2K3,EEF2,ISG15,TNFRSF14,TSC2,NDOR1,SBNO2,PHPT1,FOXC2,ABL1,SLC2A8,IL34,GBP6,OAS2,GAS1,SLC8A3,SERPINF1,ZBTB7A,CD55,RAB43,PML,GATA4,CARD8,VPS26B,CDK9,NFKBIL1,IL22RA1,RGS8,RAB11B,EMD	cyan	VSMC_M2
GO:0022010	0.01	1.00	4	13	central nervous system myelination	BP	0.35945	B4GALT5,MYRF,ASPA,ABCA2	cyan	VSMC_M2
GO:0032291	0.01	1.00	4	13	axon ensheathment in central nervous system	BP	0.35945	B4GALT5,MYRF,ASPA,ABCA2	cyan	VSMC_M2
GO:0009101	0.01	0.99	28	245	glycoprotein biosynthetic process	BP	0.35945	MGAT4B,B3GALT4,ST3GAL1,GCNT1,GALNT12,FKRP,CANT1,IGF1,MAN2A1,DPY19L3,GALNT18,CHST14,EXT2,B4GALT4,B4GALT5,GCNT7,B4GAT1,VEGFB,TMEM106A,B3GAT3,XYLT2,SLC51B,NUDT14,NAGPA,ABCA2,CHST8,HS3ST3B1,AL157935.2	cyan	VSMC_M2
GO:0006026	0.01	1.00	5	19	aminoglycan catabolic process	BP	0.35945	GNS,SGSH,GUSB,FUCA1,NAGLU	cyan	VSMC_M2
GO:0007616	0.01	1.00	6	27	long-term memory	BP	0.35945	EHMT2,APOE,ADCY1,PTCHD1,GRIA1,LRRN4	cyan	VSMC_M2
GO:0000422	0.01	1.00	11	71	autophagy of mitochondrion	BP	0.36065	ATG7,CAMKK2,CTTN,CTSK,HDAC6,WDR45,GABARAP,TP53,GBA,RETREG1,TSC2	cyan	VSMC_M2
GO:0061726	0.01	1.00	11	71	mitochondrion disassembly	BP	0.36065	ATG7,CAMKK2,CTTN,CTSK,HDAC6,WDR45,GABARAP,TP53,GBA,RETREG1,TSC2	cyan	VSMC_M2
GO:0014003	0.01	1.00	6	27	oligodendrocyte development	BP	0.3618	TPPP,B4GALT5,MYRF,MED12,ASPA,ABCA2	cyan	VSMC_M2
GO:0008219	0.01	0.99	137	1587	cell death	BP	0.36186	AKAP12,DDAH2,ZFPM2,RPS6KA2,IRF1,DEPTOR,DAXX,ST3GAL1,GSDMD,MTCH1,GRINA,TLE1,CARD10,HMOX1,HIGD2A,GPNMB,RRAGC,COLEC11,ELMO1,STK40,AKT1S1,STK17A,GLI3,IRF3,GSN,NRP1,RHOB,HS1BP3,BAX,C6orf120,NOP53,MEIS3,TRIM13,MARK4,BIN1,APOE,BCL3,ATG7,SOCS3,ZFP36,PAK4,FGFR1,EFNB2,LAMP1,SMPD1,APBB1,CLIP3,HSPB6,ANGPT4,RBCK1,RARG,IGF1,TLR3,WT1,CHMP4B,CHMP3,CAST,CTSB,PLSCR1,SFRP2,PRKCD,SRC,TGM2,PLCG1,SFRP5,MAPK8IP1,NISCH,STAT1,CHRNA7,IKBKE,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,PTGIS,GRK5,CASP10,STK25,ELL3,NFKBIA,DPF2,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,MAP1S,DLG5,HDAC6,DNAJB6,ARRB2,EPHA2,GABARAP,CASP9,PLSCR3,BRAT1,TP53BP2,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,PDK2,GBA,NUPR1,SHC1,ADAR,KANK2,ATOX1,PDGFRB,TRAF4,RETREG1,TRAF7,TSC2,NDOR1,RHOT2,AXIN1,FOXC2,ABL1,OSGIN1,INCA1,GAS1,ZNF205,SERPINF1,ZBTB7A,ATN1,PML,EEF1A2,GATA4,CARD8,BMF,EN1	cyan	VSMC_M2
GO:0099177	0.01	0.99	34	318	regulation of trans-synaptic signaling	BP	0.36201	AKAP12,FLOT1,PACSIN2,NPTXR,APOE,NPTX1,TMEM108,TSHZ3,SRC,CACNB3,PLCG1,NISCH,CHRNA7,GNAI2,ADCY1,BCR,ADORA2A,ARRB2,AKAP5,SERPINE2,GIPC1,PRKACA,NTRK1,CPLX2,PPP1R9B,GRIA1,PTPRS,SH3GL1,DVL1,CLSTN1,ABL1,SLC8A3,CALM3,STX3	cyan	VSMC_M2
GO:0006575	0.01	1.00	18	136	cellular modified amino acid metabolic process	BP	0.36339	OPLAH,ETHE1,OSBPL10,GGT7,LPCAT4,CTSB,PLSCR1,PTDSS1,OSBPL5,CTSK,SLC16A2,CPT2,HAGH,GSTM4,CRAT,FPGS,CLIC2,CLIC3	cyan	VSMC_M2
GO:0031175	0.01	0.99	72	784	neuron projection development	BP	0.36339	FLOT1,PLXNB2,PTPRK,NFIB,P3H1,COBL,GLI3,AP2A1,NRP1,FZD4,VIM,APOE,SLITRK6,CAMK1,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,SFRP2,NDRG4,EPHA3,LRP4,GNAO1,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,NCKIPSD,ADCY1,FES,SEMA6C,KIF1A,STK25,MOV10,B2M,ADORA2A,GRN,GPC2,RND2,NBL1,MAP1S,DLG5,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,PPP1R9B,NEO1,LLGL1,ROR1,PTPRS,DVL1,RERE,ABL1,IST1,SERPINF1,LRRC7,SDC4,STX3	cyan	VSMC_M2
GO:0099536	0.01	0.99	49	494	synaptic signaling	BP	0.36339	AKAP12,FLOT1,RPS6KA2,PACSIN2,NPTXR,CADPS2,SLC17A7,APOE,NPTX1,TMEM108,RIMBP2,TSHZ3,GLRB,SRC,CACNB3,PLCG1,NISCH,CHRNA7,GNAI2,SV2A,ADCY1,ANXA9,PTCHD1,BCR,ADORA2A,CHRNE,ARRB2,AKAP5,DAGLA,GABARAP,SERPINE2,GIPC1,PRKACA,NTRK1,CPLX2,PPP1R9B,GRIA1,PTPRS,SH3GL1,DVL1,AGRN,CLSTN1,ABL1,SLC8A3,KCND2,CALM3,STX3,RGS8,RGS10	cyan	VSMC_M2
GO:0048512	0.01	1.00	6	27	circadian behavior	BP	0.36406	ADORA2A,NAGLU,TP53,MTA1,PTGDS,KCND2	cyan	VSMC_M2

GO:0042098	0.01	1.00	17	127	T cell proliferation	BP	0.36785	IRF1,GPNMB,BAX,PNP,LMO1,IGF1,MAPK8IP1,CD81,BMP4,DLG5,ERBB2,IL27RA,TP53,TNFRSF14,ABL1,CD55,SDC4	cyan	VSMC_M2
GO:0002831	0.01	0.99	26	224	regulation of response to biotic stimulus	BP	0.36875	IRF1,APPL2,IRF3,NOP53,APOE,TRIM21,LAMP1,SLC15A4,SERPING1,PLSCR1,SRC,STAT1,IKBKE,TIRAP,GRN,PQBP1,DHX58,ARRB2,ADAR,ISG15,FAM3A,HEXIM1,CD55,RPS19,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0051254	0.01	0.99	118	1357	positive regulation of RNA metabolic process	BP	0.36875	STAT6,TCF21,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,SAMD4B,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,MMS19,FOXF2,STAT1,ABHD14B,CD81,NDN,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,MOV10,DPF2,PCBD1,HDAC5,BMP4,LDB2,TCEA2,PQBP1,JUP,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,NUPR1,SHC1,PBXIP1,MTA1,MAP2K3,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,MEX3D,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0048608	0.01	0.99	35	330	reproductive structure development	BP	0.36922	TCF21,ZFPM2,MEA1,ITGB8,GLI3,BAX,FZD4,SOCS3,RARG,TLR3,WT1,CTSB,SFRP2,SRC,FOXF2,LEF1,REC8,WNT2B,PLCD3,PSAP,BMP4,DNAJB6,ARRB2,SERPINE2,ZFP36L1,NTRK1,SLIT2,AR,ADAM15,NUPR1,PDGFRB,PLAC1,SERPINF1,JUNB,GATA4	cyan	VSMC_M2
GO:0072224	0.01	1.00	4	13	metanephric glomerulus development	BP	0.36922	TCF21,WT1,LAMB2,PDGFRB	cyan	VSMC_M2
GO:0070661	0.01	0.99	24	201	leukocyte proliferation	BP	0.36922	IRF1,GPNMB,BAX,PNP,IL5RA,LMO1,IGF1,PRKCD,MAPK8IP1,CD81,TIRAP,LEF1,BMP4,DLG5,ERBB2,IL27RA,TP53,GBA,TNFRSF14,ABL1,IL34,CD55,SDC4,BST2	cyan	VSMC_M2
GO:0030099	0.01	0.99	32	293	myeloid cell differentiation	BP	0.36975	ITGB8,MEIS1,LRRC17,ZFP36,RARG,TLR3,SRC,STAT1,CD81,TIRAP,LEF1,FES,NFKBIA,B2M,BMP4,MAEA,EPHA2,CASP9,ZFP36L1,KAT8,GBA,ADAR,SIGLEC15,ISG15,SBNO2,CBFA2T3,IL34,ZBTB7A,PML,RPS19,JUNB,ZFPM1	cyan	VSMC_M2
GO:0001501	0.01	0.99	42	413	skeletal system development	BP	0.37013	TGFBI,NFIB,ITGB8,P3H1,EFEMP1,MEIS1,GLI3,LRRC17,FGFR1,EPYC,PKDCC,RARG,IGF1,HEXB,SFRP2,SRC,TGM2,MMP2,EXT2,SOX5,ECM1,CTSK,PHEX,LTBP3,WNT2B,ADAMTS7,BMP4,EPHA2,PCGF2,TP53,HOXB1,HOXB2,HOXB4,MED12,PBXIP1,ACP5,SIGLEC15,DYM,RPL13,FOXC2,ZFPM1,EN1	cyan	VSMC_M2
GO:0006915	0.01	0.99	125	1436	apoptotic process	BP	0.37013	AKAP12,DDAH2,RPS6KA2,IRF1,DEPTOR,DAXX,ST3GAL1,MTCH1,GRINA,TLE1,CARD10,HMOX1,HIGD2A,RRAGC,COLEC11,ELMO1,STK40,AKT1S1,STK17A,GLI3,IRF3,GSN,NRP1,RHOB,HS1BP3,BAX,C6orf120,NOP53,MEIS3,BIN1,APOE,BCL3,ATG7,SOCS3,ZFP36,PAK4,FGFR1,SMPD1,APBB1,CLIP3,HSPB6,ANGPT4,RBCK1,RARG,IGF1,TLR3,WT1,CHMP3,CAST,CTSB,PLSCR1,SFRP2,PRKCD,SRC,TGM2,PLCG1,SFRP5,MAPK8IP1,NISCH,STAT1,IKBKE,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,PTGIS,GRK5,CASP10,STK25,ELL3,NFKBIA,DPF2,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,MAP1S,DLG5,DNAJB6,ARRB2,EPHA2,GABARAP,CASP9,PLSCR3,BRAT1,TP53BP2,ZFP36L1,NTRK1,PCGF2,SLIT2,AR,TP53,PDK2,GBA,NUPR1,SHC1,ADAR,KANK2,ATOX1,PDGFRB,TRAF4,RETREG1,TRAF7,TSC2,RHOT2,AXIN1,FOXC2,ABL1,OSGIN1,INCA1,GAS1,ZNF205,ZBTB7A,ATN1,PML,EEF1A2,GATA4,CARD8,BMF,EN1	cyan	VSMC_M2
GO:0060541	0.01	0.99	20	163	respiratory system development	BP	0.37013	TCF21,ADAMTS2,ZFPM2,NFIB,STK40,GLI3,PKDCC,RARG,MAN2A1,WT1,LEF1,DISP1,HEG1,PHEX,LTBP3,WNT2B,BMP4,DLG5,PDGFRB,DNAAF1	cyan	VSMC_M2
GO:0001964	0.01	1.00	4	13	startle response	BP	0.37013	SLITRK6,GLRB,ADORA2A,DVL1	cyan	VSMC_M2
GO:0060384	0.01	1.00	5	20	innervation	BP	0.37013	NRP1,SLITRK6,NPTX1,SERPINE2,NTRK1	cyan	VSMC_M2
GO:0019538	0.01	0.99	326	4113	protein metabolic process	BP	0.37013	CTDP1,MMP19,PYM1,OS9,ADAMTS2,MGAT4B,FLOT1,PPP6R2,EHMT2,PLXNB2,CFB,EIF3H,RPS6KA2,DEPTOR,B3GALT4,DAXX,FBXO32,PTPRK,ST3GAL1,CDC14C,MTCH1,GGA1,CARD10,KCTD17,TRERF1,GCNT1,ACO1,CUL9,IARS,TRIM14,GALNT12,P3H1,GPNMB,EFEMP1,RNF144A,STK40,AKT1S1,STK17A,AASS,GLI3,GSN,NRP1,KLF15,BAX,RPL18,PARP12,NOP53,ABTB1,FKRP,TRIM13,FZD4,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,BCL3,MIF4GD,AGAP3,ATRAID,SLC6A9,ATG7,LTBP4,CAPN5,SOCS3,CAMK1,RNF170,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,PAK4,SGSH,RNF213,RPL15,HGS,KAT2B,EIF3K,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,TPP1,MMP17,CLIP3,ANGPT4,EIF3F,MAP3K12,RBCK1,GNPTAB,IGF1,TLR3,SNTA1,MAN2A1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,GGT7,GALNT18,GGCX,SERPING1,CAST,EDEM2,CTSB,ARRDC3,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,RIOX2,MMS19,CHST14,FOXF2,MAPK8IP1,MMP2,PTPN13,EXT2,CTSA,MOB2,GFRA2,CD81,NDN,PHKG1,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,MRPL36,PCSK6,RNPEP,CSTB,NFKB1,GNAI2,TPPP,B4GALT4,HIST1H1C,RGMA,UBA7,LEF1,TBL1Y,B4GALT5,SSH3,APH1A,DCAF11,VEGFD,GCNT7,ECM1,CTSK,RHBDD3,GRK5,CASP10,FES,MINDY1,FURIN,VPS11,CCS,HEG1,RNPEPL1,B4GAT1,STK25,ATG4B,RNASEL,MAGEF1,PHEX,NFKBIA,MOV10,DTX2,B2M,BCR,ADORA2A,CAPN1,CLEC3B,ADAM11,ADAMTS7,CDC42BPG,GRN,C1R,PCOLCE,HDAC5,C1S,VEGFB,TMEM106A,MACROD1,WNK4,BMP4,MAEA,PORCN,USE1,CPAMD8,HDAC6,GANAB,B3GAT3,WDR45,DNAJB6,FKBP10,ARRB2,EPHA2,MYRF,GABARAP,FNTB,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PRKACA,	cyan	VSMC_M2
GO:0048754	0.01	1.00	16	121	branching morphogenesis of an epithelial tube	BP	0.375	TCF21,GLI3,NRP1,WT1,SFRP2,SRC,LEF1,WNT2B,BMP4,DLG5,EPHA2,SLIT2,AR,FOXC2,ABL1,PML	cyan	VSMC_M2
GO:0010631	0.01	0.99	29	261	epithelial cell migration	BP	0.37594	CARD10,HMOX1,RRAS,NRP1,RHOB,APOE,FGFR1,EFNB2,ADGRA2,ANGPT4,SRC,PLCG1,LGALS8,GRN,HDAC5,BMP4,STAT5A,HDAC6,JUP,EPHA2,MCC,GIPC1,SLIT2,KANK2,MAP2K3,FOXC2,ABL1,SERPINF1,PLPP3	cyan	VSMC_M2

GO:0002431	0.01	1.00	6	27	Fc receptor mediated stimulatory signaling pathway	BP	0.37814	APPL2,PLSCR1,PRKCD,SRC,PLD2,ABL1	cyan	VSMC_M2
GO:0016485	0.01	0.99	21	170	protein processing	BP	0.37814	ADAMTS2,RPS6KA2,GLI3,GSN,FKRP,CAST,SPON1,SRC,CPE,PCSK6,APH1A,FURIN,PHEX,CLEC3B,C1R,MYRF,SERPINE2,PRKACA,TMEM98,GAS1,CARD8	cyan	VSMC_M2
GO:1903901	0.01	1.00	4	13	negative regulation of viral life cycle	BP	0.38481	GSN,TRIM8,TRIM26,BST2	cyan	VSMC_M2
GO:0043062	0.01	0.99	28	251	extracellular structure organization	BP	0.38481	MMP19,ADAMTS2,FLOT1,TGFBI,BCL3,MMP17,WT1,SFRP2,FOXF2,MMP2,EGFL6,LAMB2,EXOC8,CTSK,FURIN,OLFML2B,LTBP3,ADAMTS7,DNAJB6,FKBP10,SMOC1,ADAM15,PBXIP1,TEX14,FOXC2,ABL1,COL8A1,MPV17	cyan	VSMC_M2
GO:0090132	0.01	0.99	29	262	epithelium migration	BP	0.38481	CARD10,HMOX1,RRAS,NRP1,RHOB,APOE,FGFR1,EFNB2,ADGRA2,ANGPT4,SRC,PLCG1,LGALS8,GRN,HDAC5,BMP4,STAT5A,HDAC6,JUP,EPHA2,MCC,GIPC1,SLIT2,KANK2,MAP2K3,FOXC2,ABL1,SERPINF1,PLPP3	cyan	VSMC_M2
GO:0045944	0.01	0.99	82	904	positive regulation of transcription by RNA polymerase II	BP	0.38481	STAT6,TCF21,ZFPM2,IRF1,TCF20,TEF,TEAD3,NFIB,TRERF1,MLIP,MEIS1,PTOV1,GLI3,IRF3,KLF15,DBP,MEIS3,BCL3,CAMK1,KAT2B,APBB1,LMO1,RARG,IGF1,TLR3,WT1,PLSCR1,HEXB,SFRP2,WWTR1,FOXF2,STAT1,ABHD14B,CD81,NDN,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,DPF2,HDAC5,BMP4,LDB2,TCEA2,JUP,ZBTB17,TCF12,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,PBXIP1,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,FOXC2,ABL1,ATMIN,PBX3,NFIA,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0120035	0.01	0.99	51	524	regulation of plasma membrane bounded cell projection organization	BP	0.38481	PLXNB2,KCTD17,P3H1,COBL,AP2A1,NRP1,MARK4,VIM,APOE,CAMK1,DZIP1,ARAP1,RHOG,EFNB2,LZTS3,APBB1,SCN1B,SFRP2,NDRG4,PRKCD,EPHA3,SRC,LRP4,C15orf62,SEMA3B,RGMA,SEMA4B,NCKIPSD,FES,SEMA6C,KIF1A,STK25,B2M,GRN,GPC2,RND2,CAPZB,PQBP1,CROCC,EPHA2,NTRK1,SLIT2,ROR1,PTPRS,DVL1,AGRN,ENTR1,ATMIN,IST1,SERPINF1,LRRC7	cyan	VSMC_M2
GO:0140058	0.01	1.00	6	28	neuron projection arborization	BP	0.38481	NRP1,FZD4,PHACTR1,CHRNA7,MOV10,DVL1	cyan	VSMC_M2
GO:0060291	0.01	1.00	10	62	long-term synaptic potentiation	BP	0.38481	APOE,TSHZ3,CHRNA7,ADCY1,ADORA2A,AKAP5,SERPINE2,ABL1,SLC8A3,STX3	cyan	VSMC_M2
GO:0009617	0.01	0.99	38	362	response to bacterium	BP	0.38481	AKAP12,GSDMD,NFIB,IRF3,VIM,BCL3,ZFP36,TLR3,GGT7,PRKCD,SRC,BPI,TIRAP,TUSC2,NFKB1,VEGFD,NFKBIA,B2M,GRN,DHX58,EPHA2,CASP9,PLSCR3,IL27RA,SHC1,ACP5,ISG15,TNFRSF14,SBNO2,ABL1,GBP6,OAS2,CD55,RPS19,CARD8,NFKBIL1,IL22RA1,OCIAD2	cyan	VSMC_M2
GO:1901657	0.01	1.00	10	60	glycosyl compound metabolic process	BP	0.38481	NAGA,PNP,GUSB,FUCA1,UCKL1,MACROD1,GBA,DPYD,TK2,MACROD2	cyan	VSMC_M2
GO:0043331	0.01	1.00	7	35	response to dsRNA	BP	0.38509	FLOT1,IRF3,RFTN1,TLR3,NFKB1,NFKBIA,PQBP1	cyan	VSMC_M2
GO:0048666	0.01	0.99	79	877	neuron development	BP	0.38509	FLOT1,PLXNB2,PTPRK,MTCH1,NFIB,P3H1,COBL,GLI3,AP2A1,NRP1,FZD4,VIM,APOE,SLITRK6,CAMK1,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,SFRP2,NDRG4,EPHA3,LRP4,GNAO1,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,NCKIPSD,ADCY1,FES,SEMA6C,KIF1A,STK25,MOV10,B2M,ADORA2A,GRN,GPC2,RND2,NAGLU,NBL1,MAP1S,NR2F6,DLG5,HDAC6,PQBP1,EPHA2,ERBB2,NTRK1,SLIT2,PPP1R9B,NEO1,LLGL1,ROR1,PTPRS,DVL1,AGRN,NPHP4,RERE,ABL1,PBX3,IST1,SERPINF1,LRRC7,SDC4,STX3,EN1	cyan	VSMC_M2
GO:0008584	0.01	1.00	15	111	male gonad development	BP	0.38661	TCF21,ZFPM2,MEA1,BAX,TLR3,WT1,SFRP2,REC8,WNT2B,NTRK1,AR,ADAM15,NUPR1,PDGFRB,GATA4	cyan	VSMC_M2
GO:0051044	0.01	1.00	4	13	positive regulation of membrane protein ectodomain proteolysis	BP	0.38938	APOE,RGMA,FURIN,SNX33	cyan	VSMC_M2
GO:0051043	0.01	1.00	5	20	regulation of membrane protein ectodomain proteolysis	BP	0.38938	APOE,TIMP2,RGMA,FURIN,SNX33	cyan	VSMC_M2
GO:0006869	0.01	0.99	30	273	lipid transport	BP	0.38938	ATP10D,EEPD1,FZD4,APOE,OSBPL10,STARD10,PLSCR1,PRKCD,OSBPL5,TPCN2,NFKB1,LRP10,FURIN,ERFE,NFKBIA,LINC02210-CRHR1,PSAP,PLSCR3,STARD3,NPC2,SLC51B,ATP8B2,SPNS1,ABCC1,CPT2,ABCD1,SLC10A3,LCAT,APOL5,ABCA2	cyan	VSMC_M2
GO:0048729	0.01	0.99	48	490	tissue morphogenesis	BP	0.38938	TCF21,PLXNB2,ZFPM2,GCNT1,COBL,GLI3,NRP1,RHOB,SOCS3,PRICKLE2,RARG,WT1,SFRP2,NDRG4,SRC,TGM2,FOXF2,EXT2,LZTS2,STAT1,RGMA,LEF1,HEG1,VANGL2,GATA5,WNT2B,WNK4,BMP4,CC2D2A,DLG5,EPHA2,PRKACA,SLIT2,AR,HOXB2,HOXB4,MED12,ROR1,DVL1,TSC2,FOXC2,ABL1,DNAAF1,KRT25,PML,GATA4,SDC4,ZFPM1	cyan	VSMC_M2
GO:0048468	0.01	0.99	134	1587	cell development	BP	0.38938	CTDP1,FLOT1,EHMT2,PLXNB2,RPS6KA2,AFDN,PTPRK,MTCH1,NFIB,APPL2,P3H1,MEIS1,COBL,GLI3,AP2A1,NRP1,BAX,FZD4,VIM,BIN1,APOE,SLITRK6,CAMK1,DZIP1,NPTX1,GPAT4,RHOG,EFNB2,ADGRA2,DCLK1,TMEM108,LZTS3,APBB1,RARG,SCN1B,IGF1,MAN2A1,WT1,EFNA5,HEXB,SFRP2,NDRG4,EPHA3,SRC,TGM2,LRP4,BBS2,GNAO1,PHACTR1,NDN,CHRNA7,CAPN3,TJP1,CTTN,BOC,TUSC2,SEMA3B,TPPP,RGMA,LEF1,B4GALT5,ATRNL1,LAMB2,ECM1,REC8,SEMA4B,NCKIPSD,ADCY1,FES,PRUNE1,SEMA6C,HEG1,KIF1A,STK25,ELL3,MOV10,B2M,ARHGEF10,ADORA2A,GRN,GPC2,RND2,ADD1,BMP4,NAGLU,MAEA,NBL1,MAP1S,NR2F6,DLG5,HDAC6,PQBP1,EPHA2,MYRF,SERPINE2,CASP9,ERBB2,PRKACA,NTRK1,SLIT2,AR,TP53,MED12,GBA,PPP1R9B,SIGLEC15,NEO1,PDGFRB,FLII,LLGL1,TMEM98,ROR1,PTPRS,DVL1,ASPA,AGRN,NPHP4,RERE,FOXC2,ABL1,IL34,PBX3,IST1,ABCA2,SERPINF1,ZBTB7A,RPS19,GATA4,LRRC7,SDC4,STX3,PYGO2,ZFPM1,EN1	cyan	VSMC_M2
GO:0002062	0.01	1.00	13	91	chondrocyte differentiation	BP	0.39163	TGFBI,NFIB,EFEMP1,GLI3,PKDCC,RARG,SFRP2,SOX5,ECM1,LTBP3,WNT2B,ADAMTS7,BMP4	cyan	VSMC_M2

GO:0006790	0.01	0.99	30	270	sulfur compound metabolic process	BP	0.39253	GNS,ST3GAL1,IBA57,OPLAH,AASS,ACSS1,ETHE1,GPAT4,GGT7,ACSS2,MMS19,CHST14,EXT2,ABHD14B,B4GAT1,ACAT1,STAT5A,MRI1,PDK2,XYLT2,ABCD1,NDOR1,HAGH,GSTM4,ACOT6,CHST8,DGAT1,HS3ST3B1,CLIC2,CLIC3	cyan	VSMC_M2
GO:0043536	0.01	1.00	9	53	positive regulation of blood vessel endothelial cell migration	BP	0.39409	HMOX1,NRP1,FGFR1,ANGPT4,PLCG1,STAT5A,MAP2K3,FOXC2,ABL1	cyan	VSMC_M2
GO:0007622	0.01	1.00	6	28	rhythmic behavior	BP	0.39503	ADORA2A,NAGLU,TP53,MTA1,PTGDS,KCND2	cyan	VSMC_M2
GO:0043068	0.01	0.99	43	422	positive regulation of programmed cell death	BP	0.39503	AKAP12,RPS6KA2,MTCH1,HMOX1,STK17A,GSN,RHOB,BAX,MARK4,BIN1,ATG7,SMPD1,APBB1,CLIP3,RBCK1,RARG,TLR3,SFRP2,PRKCD,SRC,TGM2,PLCG1,PTGIS,ADORA2A,AIFM2,GRN,BMP4,HDAC6,ARRB2,CASP9,TP53BP2,NTRK1,SLIT2,TP53,NUPR1,PDGFRB,TRAF7,ABL1,OSGIN1,INCA1,PML,EEF1A2,BMF	cyan	VSMC_M2
GO:0007250	0.01	1.00	4	13	activation of NF-kappaB-inducing kinase activity	BP	0.39503	CARD10,TLR3,TIRAP,TRAF4	cyan	VSMC_M2
GO:0070242	0.01	1.00	4	13	thymocyte apoptotic process	BP	0.39928	GLI3,BAX,BMP4,TP53	cyan	VSMC_M2
GO:0031400	0.01	0.99	43	426	negative regulation of protein modification process	BP	0.40021	DEPTOR,P3H1,AKT1S1,AASS,KLF15,BAX,APOE,SOCS3,KAT2B,SH3BP5,TRIM21,SMPD1,SNTA1,SFRP2,WWTR1,PRKCD,MAPK8IP1,PTPN13,GFRA2,CAPN3,GNAI2,TPPP,HEG1,ADORA2A,BMP4,ARRB2,MLLT6,SLIT2,GBA,PPP1R9B,ADAR,WARS,MLLT1,DVL1,ISG15,TSC2,ABL1,INCA1,RPS15,SLC8A3,HEXIM1,PLPP3,CALM3	cyan	VSMC_M2
GO:0030308	0.01	0.99	19	153	negative regulation of cell growth	BP	0.40341	CTDP1,NRP1,WT1,SFRP2,NDRG3,SEMA3B,RGMA,SEMA4B,SEMA6C,RERG,SERPINE2,SLIT2,TP53,PPP1R9B,ADAM15,PTPRS,OSGIN1,PML,BST2	cyan	VSMC_M2
GO:0046546	0.01	0.99	15	112	development of primary male sexual characteristics	BP	0.40341	TCF21,ZFPM2,MEA1,BAX,TLR3,WT1,SFRP2,REC8,WNT2B,NTRK1,AR,ADAM15,NUPR1,PDGFRB,GATA4	cyan	VSMC_M2
GO:0030097	0.01	0.99	59	618	hemopoiesis	BP	0.40395	STAT6,IRF1,PTPRK,ST3GAL1,ITGB8,MEIS1,GLI3,RRAS,FLT3LG,BAX,LRRC17,TMEM176B,BCL3,PNP,ZFP36,RARG,TLR3,SFRP2,SRC,STAT1,CD81,TIRAP,TUSC2,LEF1,FES,NFKBIA,B2M,WNT2B,DPF2,HDAC5,BMP4,MAEA,EPHA2,CASP9,ERBB2,ZFP36L1,NTRK1,TP53,KAT8,HOXB4,GBA,ADAR,SIGLEC15,TMEM98,CRIP2,EEF2,ISG15,TCF3,SBNO2,CBFA2T3,ABL1,IL34,SLC8A3,ZBTB7A,PML,RPS19,JUNB,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0018108	0.01	0.99	31	287	peptidyl-tyrosine phosphorylation	BP	0.40395	EFEMP1,NRP1,SOCS3,FGFR1,SH3BP5,PKDCC,ANGPT4,IGF1,EFNA5,CAMKK2,SFRP2,PRKCD,EPHA3,SRC,LRP4,CD81,FES,BCR,ARRB2,EPHA2,ERBB2,NTRK1,TP53,SHC1,GPRC5B,PDGFRB,MAP2K3,ROR1,TNFRSF14,ABL1,IL34	cyan	VSMC_M2
GO:0010563	0.01	0.99	37	356	negative regulation of phosphorus metabolic process	BP	0.40395	DEPTOR,AKT1S1,BAX,APOE,SOCS3,KAT2B,SH3BP5,SMPD1,SFRP2,WWTR1,PRKCD,MAPK8IP1,PTPN13,GFRA2,GNAI2,HEG1,ADORA2A,BMP4,ARRB2,SLIT2,TP53,GBA,PPP1R9B,NUPR1,ADAR,WARS,MLLT1,DVL1,TSC2,CBFA2T3,ABL1,INCA1,ABCA2,SLC8A3,HEXIM1,PLPP3,CALM3	cyan	VSMC_M2
GO:0045936	0.01	0.99	37	356	negative regulation of phosphate metabolic process	BP	0.40395	DEPTOR,AKT1S1,BAX,APOE,SOCS3,KAT2B,SH3BP5,SMPD1,SFRP2,WWTR1,PRKCD,MAPK8IP1,PTPN13,GFRA2,GNAI2,HEG1,ADORA2A,BMP4,ARRB2,SLIT2,TP53,GBA,PPP1R9B,NUPR1,ADAR,WARS,MLLT1,DVL1,TSC2,CBFA2T3,ABL1,INCA1,ABCA2,SLC8A3,HEXIM1,PLPP3,CALM3	cyan	VSMC_M2
GO:0010604	0.01	0.99	211	2586	positive regulation of macromolecule metabolic process	BP	0.40508	PYM1,STAT6,TCF21,AKAP12,FLOT1,PLXNB2,ZFPM2,RPS6KA2,IRF1,AFDN,TCF20,DAXX,TEF,GSDMD,TEAD3,MTCH1,TLE1,GGA1,CARD10,NFIB,TRERF1,HMOX1,MLIP,TRIM14,ITGB8,NAT14,GPNMB,MEIS1,RNF144A,PTOV1,GLI3,IRF3,GSN,NRP1,KLF15,BAX,DBP,NOP53,BICRA,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,PNP,ZFP36,SAMD4B,ARAP1,HGS,KAT2B,TBC1D5,RFTN1,RHOG,FGFR1,TRIM21,SMPD1,APBB1,CLIP3,ANGPT4,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,EFNA5,TP53INP2,PATL1,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,LRP4,MMS19,FOXF2,STAT1,ABHD14B,MOB2,CD81,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,TUSC2,ZNF496,NFKB1,RGMA,BCL9,LEF1,APH1A,VEGFD,RHBDD3,CASP10,FURIN,VPS11,BCL9L,HEG1,RFX5,GATA5,HELZ2,ATG4B,RNASEL,MAGEF1,ELL3,NFKBIA,MOV10,FRMD8,B2M,DPF2,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,VEGFB,TMEM106A,BMP4,LDB2,TCEA2,HDAC6,PQBP1,DHX58,ARRB2,JUP,WIZ,MYRF,IL17RA,GABARAP,ZBTB17,TCF12,CASP9,ERBB2,BRAT1,ZFP36L1,IL27RA,UBQLN2,NTRK1,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,ADAR,WARS,GPRC5B,SNX33,PDGFRB,MTA1,MAP2K3,TRAF4,MOSPD1,MPND,EEF2,GLIS2,DVL1,AGRN,ISG15,ELOB,E4F1,TNFRSF14,TCF3,SBNO2,EDF1,AXIN1,RERE,CBFA2T3,FOXC2,ABL1,ATMIN,IL34,PBX3,IST1,OAS2,NFIA,ABCA2,MEX3D,CD55,PML,JUNB,GATA4,CALM3,CARD8,CDK9,SDC4,ZFPM1,EN1	cyan	VSMC_M2
GO:0001654	0.01	0.99	30	280	eye development	BP	0.40508	EFEMP1,MEIS1,GLI3,SLC17A7,NRP1,BAX,MEIS3,FZD4,VIM,SLITRK6,RARG,MAN2A1,WT1,FOXF2,LAMB2,CLCN2,WNT2B,BMP4,NAGLU,CC2D2A,CPAMD8,EPHA2,SMOC1,PDGFRB,NPHP4,FOXC2,PBX3,SERPINF1,PYGO2,COL8A1	cyan	VSMC_M2
GO:0061512	0.01	1.00	9	54	protein localization to cilium	BP	0.40676	GGA1,BBS9,DZIP1,CC2D2A,CROCC,NPHP4,INPP5E,RAB11FIP3,ENTR1	cyan	VSMC_M2
GO:0010656	0.01	1.00	7	36	negative regulation of muscle cell apoptotic process	BP	0.41441	HMOX1,HSPB6,IGF1,SFRP2,ARRB2,NUPR1,GATA4	cyan	VSMC_M2
GO:0042326	0.01	0.99	33	311	negative regulation of phosphorylation	BP	0.41469	DEPTOR,AKT1S1,BAX,APOE,SOCS3,KAT2B,SH3BP5,SMPD1,SFRP2,WWTR1,PRKCD,MAPK8IP1,PTPN13,GFRA2,HEG1,ADORA2A,BMP4,ARRB2,SLIT2,GBA,NUPR1,ADAR,WARS,MLLT1,DVL1,TSC2,CBFA2T3,ABL1,INCA1,SLC8A3,HEXIM1,PLPP3,CALM3	cyan	VSMC_M2

GO:0097190	0.01	0.99	47	471	apoptotic signaling pathway	BP	0.41469	DEPTOR,DAXX,GRINA,HMOX1,NRP1,BAX,MEIS3,BCL3,FGFR1,RBCK1,IGF1,TLR3,SFRP2,PRKCD,SRC,MAPK8IP1,IKBKE,CTTN,GNAI2,PTGIS,CASP10,STK25,ELL3,DPF2,ADORA2A,TMEM161A,TMBIM1,BMP4,ARRB2,EPHA2,GABARAP,CASP9,PLSCR3,TP53BP2,PCGF2,AR,TP53,PDK2,NUPR1,TRAF7,RHOT2,ABL1,INCA1,ZNF205,PML,GATA4,BMF	cyan	VSMC_M2
GO:0009968	0.01	0.99	87	973	negative regulation of signal transduction	BP	0.42297	TCF21,DEPTOR,GRINA,TLE1,HMOX1,CARD19,AKT1S1,GLI3,NRP1,BAX,NOP53,MEIS3,FZD4,APOE,BCL3,SOCS3,TIMP2,RNF213,HGS,ADGRA2,SMPD1,IGF1,ARRDC3,SFRP2,WWTR1,NDRG4,PRKCD,SRC,LRP4,SFRP5,MAPK8IP1,LZTS2,STAT1,CTTN,GNAI2,KIF7,ECM1,VPS11,BCL9L,HEG1,LMO3,ELL3,NFKBIA,FAM89B,FRMD8,TMEM161A,HOMER3,TMBIM1,BMP4,NBL1,DLG5,DHX58,ARRB2,EPHA2,SERPINE2,MCC,CGNL1,PRKACA,UBQLN2,PCGF2,SLIT2,AR,TP53,GBA,ADAR,KANK2,ULK3,EPN2,MAP2K3,PTPRS,GLIS2,ISG15,TSC2,NPHP4,PHPT1,INPP5E,AXIN1,NPRL3,ABL1,ZBTB7A,GATA4,CARD8,NFKBIL1,RGS19,RGS8,RGS10,EMD	cyan	VSMC_M2
GO:1901575	0.01	0.99	139	1628	organic substance catabolic process	BP	0.42297	PYM1,MOXD1,OS9,GNS,DDAH2,NEU1,EIF3H,NAGA,GGA1,KCTD17,HMOX1,CUL9,PLA2G7,SLC44A1,BCKDHB,RNF144A,IAH1,AASS,BAX,NOP53,TRIM13,VIM,APOE,AGAP3,ATRAID,ACAA1,ATG7,PNP,TIMP2,ZFP36,SAMD4B,GAA,SGSH,ECH1,RNF213,HGS,SMPD1,TPP1,RBCK1,IGF1,CHMP4B,TP53INP2,PATL1,GGT7,EDEM2,CTSB,NEIL2,HEXB,WWTR1,STBD1,PRKCD,DECR1,PLBD2,PLCG1,FOXF2,PNPLA2,CTSA,CD81,GUSB,IKBKE,CAPN3,TIRAP,ACADS,RGMA,UBA7,HADH,STS,DCAF11,CTSK,RHBDD3,FURIN,VPS11,SCLY,HELZ2,ATG4B,FUCA1,RNASEL,MAGEF1,MUS81,ECHS1,MOV10,CAPN1,PLCD3,ADAMTS7,ACAT1,NUDT13,NAGLU,MAEA,RARRES3,QDPR,USE1,HDAC6,PLD2,ARRB2,DAGLA,GABARAP,SERPINE2,GIPC1,PRKACA,ZFP36L1,UBQLN2,TP53,UBQLN4,GBA,NUPR1,MAN2C1,SNX33,ABCC1,MTA1,CLPP,UBXN6,CPT2,WDR81,ABCD1,DVL1,ASPA,ISG15,ELOB,PNPLA7,RENBP,HAGH,FBXW5,INPP5E,AXIN1,RHBDF1,CBFA2T3,RNF166,CRAT,DPYD,LDHD,OAS2,ABCA2,MEX3D,ZBTB7A,PML,EEF1A2,SAT1,NAGK,PSMB9	cyan	VSMC_M2
GO:0090130	0.01	0.99	29	266	tissue migration	BP	0.42886	CARD10,HMOX1,RRAS,NRP1,RHOB,APOE,FGFR1,EFNB2,ADGRA2,ANGPT4,SRC,PLCG1,LGALS8,GRN,HDAC5,BMP4,STAT5A,HDAC6,JUP,EPHA2,MCC,GIPC1,SLIT2,KANK2,MAP2K3,FOXC2,ABL1,SERPINF1,PLPP3	cyan	VSMC_M2
GO:0072075	0.01	1.00	4	14	metanephric mesenchyme development	BP	0.42886	TCF21,WT1,STAT1,PDGFRB	cyan	VSMC_M2
GO:0044087	0.01	0.99	73	801	regulation of cellular component biogenesis	BP	0.42886	FLOT1,EHMT2,ARHGAP18,KCTD17,COBL,GSN,NRP1,BAX,NOP53,MARK4,BIN1,APOE,SLITRK6,DZIP1,TPPP2,ARAP1,HGS,KAT2B,RHOG,CLIP3,EFNA5,RHPN2,CHMP4B,PRKCD,EPHA3,SRC,C15orf62,SORBS3,IKBKE,TJP1,TIRAP,CTTN,TPPP,SSH3,FES,PRUNE1,VPS11,ARPC5,ARHGEF10,ADD1,LDB2,CAPZB,DLG5,HDAC6,ARHGEF10L,CROCC,DNAJB6,ALOX15,EPHA2,CGNL1,PRKACA,UBQLN2,NTRK1,SLIT2,TP53,GBA,NUPR1,WARS,FLII,PTPRS,AGRN,ISG15,NPHP4,ENTR1,NPRL3,CLSTN1,ABL1,ATMIN,LCAT,ABCA2,CARD8,BMF,SDC4	cyan	VSMC_M2
GO:0150063	0.01	0.99	30	282	visual system development	BP	0.42931	EFEMP1,MEIS1,GLI3,SLC17A7,NRP1,BAX,MEIS3,FZD4,VIM,SLITRK6,RARG,MAN2A1,WT1,FOXF2,LAMB2,CLCN2,WNT2B,BMP4,NAGLU,CC2D2A,CPAMD8,EPHA2,SMOC1,PDGFRB,NPHP4,FOXC2,PBX3,SERPINF1,PYGO2,COL8A1	cyan	VSMC_M2
GO:0045879	0.01	1.00	6	29	negative regulation of smoothened signaling pathway	BP	0.43266	GLI3,KIF7,SERPINE2,PRKACA,ULK3,GLIS2	cyan	VSMC_M2
GO:0009987	0.01	0.99	854	11676	cellular process	BP	0.43266	CTDP1,TSHZ1,ZADH2,MMP19,PYM1,PMEL,RAB5B,MYL6B,RBMS2,STAT6,MOXD1,TCF21,ARHGEF25,OS9,ADAMTS2,MGAT4B,GNS,ULBP2,AKAP12,FLOT1,RABL2A,CHKB,DDAH2,PPP6R2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,TBC1D22A,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,PACSIN2,B3GALT4,CYB5R3,TAPBP,TCF20,DAXX,NAGA,FBXO32,HDDC2,TGFBI,TEF,PTPRK,ARHGAP18,ST3GAL1,IBA57,CDC14C,GSDMD,TEAD3,NPTXR,MTCH1,GRINA,TLE1,GGA1,OPLAH,CARD10,KCTD17,NFIB,KIFC2,TRERF1,GCNT1,ARHGAP39,HMOX1,LRRC19,MEA1,ACO1,KIAA1324L,CUL9,TRPM3,KLF9,APPL2,ATP10D,RSPH9,HIGD2A,PLA2G7,CARD19,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,TBC1D2,GALNT12,ITGB8,P3H1,NAT14,TMEM150B,KCNQ5,GPNMB,SLC44A1,BCKDHB,EFEMP1,TRIL,BBS9,RRAGC,EEPD1,MEIS1,COLEC11,ELMO1,RNF144A,STK40,COBL,TBC1D17,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,CADPS2,IRF3,RRAS,FLT3LG,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,HS1BP3,BAX,DBP,HBP1,DENND2A,RPL18,PARP12,CCDC114,C6orf120,SELENOW,NOP53,ABTB1,BICRA,MEIS3,FKRP,UQCRH,LRRC17,LURAP1,TRIM13,ACSS1,FZD4,ME3,CAB39L,MARK4,VIM,AGBL5,TMEM176B,BIN1,APOE,UROD,BCL3,ABCB8,ETHE1,MIF4GD,AGAP3,ATRAID,SLC6A9,ACAA1,ATG7,EXOC7,CYP2S1,RHBDF2,COQ8B,LTBP4,SHKBP1,CAPN5,IL17RC,PLB1,SLITRK6,SOCS3,CAMK1,EHD3,PLD3,CMTM6,TEP1,OSBPL10,RNF170,PNP,DZIP1,TPPP2,RPS16,TIMP2,ZFP36,LGALS3BP,CANT1,SAMD4B,GAA,PAK4,SGSH,SLC26A11,ECH1,RNF213,ARAP1,NPTX1,GPAT4,SLC4A9,RPL15,FOLR2,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,ITGBL1,DCXR,RFNG,CATSPERG,FGFR1,IL5RA,EFNB2,SH3BP5,TRIM21,POC1B,	cyan	VSMC_M2
GO:0072524	0.01	1.00	6	28	pyridine-containing compound metabolic process	BP	0.43266	PNP,NADSYN1,PTGIS,NMNAT2,NUDT13,PDXK	cyan	VSMC_M2
GO:0071901	0.01	0.99	13	93	negative regulation of protein serine/threonine kinase activity	BP	0.43446	APOE,KAT2B,SMPD1,SFRP2,PRKCD,MAPK8IP1,HEG1,BMP4,GBA,ABL1,INCA1,SLC8A3,HEXIM1	cyan	VSMC_M2
GO:0034121	0.01	1.00	9	54	regulation of toll-like receptor signaling pathway	BP	0.43446	FLOT1,IRF1,APPL2,SLC15A4,TLR3,TIRAP,ARRB2,PTPRS,NFKBIL1	cyan	VSMC_M2
GO:0001763	0.01	0.99	19	157	morphogenesis of a branching structure	BP	0.43502	TCF21,GLI3,NRP1,SOCS3,WT1,SFRP2,SRC,TGM2,LEF1,WNT2B,BMP4,DLG5,EPHA2,SLIT2,AR,RERE,FOXC2,ABL1,PML	cyan	VSMC_M2

GO:0001667	0.01	0.99	37	360	ameboidal-type cell migration	BP	0.43502	AKAP12,CARD10,HMOX1,APPL2,RRAS,NRP1,RHOB,APOE,FGFR1,EFNB2,ADGRA2,ANGPT4,SRC,PLCG1,SEMA3B,LGALS8,SEMA4B,SEMA6C,GRN,HDAC5,BMP4,STAT5A,HDAC6,JUP,EPHA2,MCC,GIPC1,SLIT2,KANK2,CENPV,MAP2K3,FOXC2,ABL1,SERPINF1,PML,PLPP3,SDC4	cyan	VSMC_M2
GO:0018212	0.01	0.99	31	290	peptidyl-tyrosine modification	BP	0.43552	EFEMP1,NRP1,SOCS3,FGFR1,SH3BP5,PKDCC,ANGPT4,IGF1,EFNA5,CAMKK2,SFRP2,PRKCD,EPHA3,SRC,LRP4,CD81,FES,BCR,ARRB2,EPHA2,ERBB2,NTRK1,TP53,SHC1,GPRC5B,PDGFRB,MAP2K3,ROR1,TNFRSF14,ABL1,IL34	cyan	VSMC_M2
GO:0120036	0.01	0.99	103	1193	plasma membrane bounded cell projection organization	BP	0.43728	FLOT1,PLXNB2,PTPRK,CDC14C,KCTD17,NFIB,RSPH9,P3H1,BBS9,COBL,GLI3,AP2A1,GSN,NRP1,CCDC114,FZD4,MARK4,VIM,APOE,SLITRK6,CAMK1,EHD3,DZIP1,ARAP1,NPTX1,RHOG,EFNB2,POC1B,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,SFRP2,WWTR1,NDRG4,PRKCD,EPHA3,SRC,LRP4,BBS2,GNAO1,C15orf62,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,NCKIPSD,ADCY1,FES,SEMA6C,VANGL2,KIF1A,STK25,ARPC5,MOV10,B2M,ADORA2A,RPGR,GRN,GPC2,RND2,NBL1,CAPZB,MAP1S,CC2D2A,DLG5,HDAC6,PQBP1,CROCC,EPHA2,ERBB2,NTRK1,SLIT2,PPP1R9B,NEO1,LLGL1,ROR1,PTPRS,ABCD1,DVL1,AGRN,WDR90,ENTR1,RERE,AIF1L,ABL1,DNAAF1,ATMIN,IST1,ATP6V0D1,SERPINF1,LRRC7,TMEM250,SDC4,STX3	cyan	VSMC_M2
GO:0070727	0.01	0.99	125	1462	cellular macromolecule localization	BP	0.43749	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,AFDN,PACSIN2,PTPRK,GGA1,CARD10,APPL2,TBC1D2,BBS9,RRAGC,TBC1D17,GLI3,AP2A1,GSN,STOM,NRP1,RHOB,BAX,NOP53,MARK4,APOE,BCL3,CAMK1,EHD3,DZIP1,ZFP36,HGS,TBC1D5,RFTN1,RHOG,DCLK1,LAMP1,PKDCC,TPP1,CLIP3,GNPTAB,CHMP4B,TP53INP2,EDEM2,WWTR1,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,LRP4,BBS2,SLC5A3,CRACR2B,SYS1,LZTS2,CTSA,HPS6,CD81,TRIM8,CAPN3,CTTN,SGSM1,EXOC8,GAS2L1,VPS11,KIF1A,FAM53B,NFKBIA,M6PR,RPGR,HOMER3,GPC2,TMBIM1,BMP4,CC2D2A,HDAC6,B3GAT3,WDR45,CROCC,DNAJB6,JUP,EPHA2,AKAP5,GABARAP,GIPC1,ERBB2,PRKACA,ZFP36L1,AR,TP53,GLMP,PPP1R9B,SLC51B,SNX33,TMEM98,ZDHHC9,NAGPA,GLIS2,DVL1,SGSM2,AGRN,ISG15,TSC2,SLC9A3R2,NPHP4,INPP5E,RAB11FIP3,ENTR1,CLSTN1,MON1B,ABCA2,MEX3D,ZBTB7A,RAB43,GRASP,PML,CALM3,LRRC7,VPS26B,TMEM250,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0051128	0.01	0.99	156	1877	regulation of cellular component organization	BP	0.43999	CTDP1,RAB5B,FLOT1,EHMT2,PLXNB2,RPS6KA2,PACSIN2,ARHGAP18,KCTD17,CUL9,APPL2,P3H1,COBL,AP2A1,GSN,SLC17A7,NRP1,RHOB,BAX,NOP53,FZD4,MARK4,VIM,BIN1,APOE,LTBP4,SLITRK6,CAMK1,EHD3,DZIP1,TPPP2,PAK4,ARAP1,KAT2B,TBC1D5,RHOG,EFNB2,SMPD1,LZTS3,APBB1,CLIP3,SCN1B,IGF1,WT1,EFNA5,RHPN2,CHMP4B,CHMP3,CAMKK2,SFRP2,NDRG4,NDRG3,PRKCD,EPHA3,SRC,LRP4,C15orf62,SORBS3,CHRNA7,IKBKE,TJP1,TIRAP,CTTN,SEMA3B,TPPP,RGMA,SSH3,SEMA4B,NCKIPSD,GAS2L1,FES,PRUNE1,VPS11,SEMA6C,KIF1A,RERG,STK25,ARPC5,MOV10,B2M,ARHGEF10,FYCO1,GRN,GPC2,RND2,VAT1,ADD1,BMP4,CAPZB,MAP1S,DLG5,HDAC6,PQBP1,ARHGEF10L,CROCC,DNAJB6,ARRB2,ALOX15,EPHA2,PLEKHM2,SERPINE2,CGNL1,PLSCR3,ERBB2,BRAT1,PRKACA,UBQLN2,NTRK1,SLIT2,AR,TP53,CPLX2,UBQLN4,GBA,PPP1R9B,ADAM15,NUPR1,STON2,ARHGAP17,TEX14,SIGLEC15,WARS,CENPV,SNX33,PDGFRB,FLII,ROR1,PTPRS,SH3GL1,DVL1,AGRN,ISG15,TSC2,NPHP4,FBXW5,PHPT1,RHOT2,ENTR1,NPRL3,CLSTN1,ABL1,OSGIN1,ATMIN,IST1,LCAT,ABCA2,ZNF205,SERPINF1,PML,CALM3,CARD8,LRRC7,BMF,SDC4,BST2,OGFR	cyan	VSMC_M2
GO:0008104	0.01	0.99	168	2028	protein localization	BP	0.43999	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,AFDN,PACSIN2,CUTA,PTPRK,GGA1,CARD10,APPL2,TRIM14,TBC1D2,P3H1,BBS9,RRAGC,TBC1D17,GLI3,AP2A1,CADPS2,GSN,STOM,NRP1,RHOB,BAX,DENND2A,NOP53,MARK4,APOE,BCL3,ATG7,EXOC7,RHBDF2,CAMK1,EHD3,CMTM6,DZIP1,HGS,TBC1D5,RFTN1,RHOG,TRIM21,RAB11FIP1,DCLK1,LAMP1,APBB1,PKDCC,TPP1,CLIP3,SLC15A4,GNPTAB,IGF1,EFNA5,CHMP4B,CHMP3,TP53INP2,EDEM2,ARRDC3,WWTR1,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,LRP4,BBS2,ARHGAP1,EXOC2,SLC5A3,CRACR2B,SYS1,LZTS2,CTSA,HPS6,CD81,TRIM8,CAPN3,TJP1,CTTN,TMEM115,HADH,DISP1,SGSM1,EXOC8,RHBDD3,GAS2L1,VPS11,HEG1,VANGL2,KIF1A,FAM53B,PARD3B,ATG4B,NFKBIA,M6PR,ADORA2A,RPGR,HOMER3,GPC2,TMBIM1,WNK4,BMP4,NBL1,CC2D2A,PORCN,DLG5,USE1,HDAC6,B3GAT3,WDR45,CROCC,DNAJB6,ARRB2,JUP,EPHA2,AKAP5,GABARAP,PLEKHM2,MCC,CGNL1,GIPC1,ERBB2,PRKACA,AR,TP53,GLMP,PPP1R9B,SLC51B,SNX33,MCOLN1,LLGL1,TMEM98,ZDHHC9,NAGPA,GLIS2,DVL1,SGSM2,AGRN,ISG15,TSC2,SLC9A3R2,NPHP4,PHPT1,INPP5E,RAB11FIP3,ENTR1,RHBDF1,CLSTN1,ABL1,MON1B,IST1,ABCA2,ZBTB7A,RAB43,GRASP,PML,CALM3,SCAMP4,LRRC7,VPS26B,TMEM250,STX3,RAB11B,MCFD2,EMD,UBL5	cyan	VSMC_M2
GO:0006643	0.01	0.99	20	164	membrane lipid metabolic process	BP	0.44071	NEU1,B3GALT4,NAGA,ST3GAL1,ITGB8,BAX,SMPD1,HEXB,PRKCD,B4GALT4,B4GALT5,FUCA1,PSAP,GBA,CERS4,PIGQ,PLPP2,ABCA2,PLPP3,AL157935.2	cyan	VSMC_M2
GO:0071295	0.01	1.00	6	29	cellular response to vitamin	BP	0.44148	FOLR2,MN1,FES,PHEX,KANK2,NDOR1	cyan	VSMC_M2
GO:0042129	0.01	0.99	14	102	regulation of T cell proliferation	BP	0.44148	IRF1,GPNMB,PNP,LMO1,IGF1,MAPK8IP1,CD81,BMP4,DLG5,ERBB2,IL27RA,TNFRSF14,CD55,SDC4	cyan	VSMC_M2

GO:0009896	0.01	0.99	42	420	positive regulation of catabolic process	BP	0.44148	GGA1,HMOX1,TRIM14,RNF144A,BAX,NOP53,TRIM13,APOE,ATG7,ZFP36,SAMD4B,TRIM21,IGF1,TP53INP2,PATL1,CAMKK2,PRKCD,PNPLA2,CD81,TRIM8,RGMA,RHBDD3,FURIN,VPS11,ATG4B,MAGEF1,MOV10,FYCO1,GABARAP,ZFP36L1,UBQLN2,GBA,NUPR1,SNX33,ABCD1,DVL1,ELOB,TSC2,AXIN1,CBFA2T3,ABCA2,MEX3D	cyan	VSMC_M2
GO:0006670	0.01	1.00	4	14	sphingosine metabolic process	BP	0.44148	GBA,PLPP2,ABCA2,PLPP3	cyan	VSMC_M2
GO:0061138	0.02	0.99	18	147	morphogenesis of a branching epithelium	BP	0.44148	TCF21,GLI3,NRP1,SOCS3,WT1,SFRP2,SRC,TGM2,LEF1,WNT2B,BMP4,DLG5,EPHA2,SLIT2,AR,FOXC2,ABL1,PML	cyan	VSMC_M2
GO:0032330	0.02	1.00	8	46	regulation of chondrocyte differentiation	BP	0.44148	EFEMP1,GLI3,PKDCC,RARG,SOX5,LTBP3,ADAMTS7,BMP4	cyan	VSMC_M2
GO:0050806	0.02	0.99	14	104	positive regulation of synaptic transmission	BP	0.44148	FLOT1,APOE,TSHZ3,CHRNA7,ADCY1,ADORA2A,ARRB2,AKAP5,SERPINE2,NTRK1,CLSTN1,ABL1,SLC8A3,STX3	cyan	VSMC_M2
GO:0097435	0.02	0.99	58	622	supramolecular fiber organization	BP	0.44148	ADAMTS2,ARHGAP18,ELMO1,COBL,GSN,NRP1,RHOB,BAX,VIM,BIN1,APOE,TPPP2,ARAP1,RHOG,CLIP3,RHPN2,SFRP2,PRKCD,SRC,C15orf62,SORBS3,PHACTR1,CHRNA7,CAPN3,TJP1,CTTN,TPPP,SSH3,GAS2L1,FES,PRUNE1,FURIN,CTNNA3,WIPF1,ARPC5,LTBP3,B2M,ARHGEF10,RND2,ADD1,CAPZB,MAP1S,HDAC6,ARHGEF10L,DNAJB6,FKBP10,ALOX15,CGNL1,SLIT2,PPP1R9B,PDGFRB,FLII,DVL1,FOXC2,AIF1L,ABL1,KRT25,SDC4	cyan	VSMC_M2
GO:0016049	0.02	0.99	40	399	cell growth	BP	0.44279	CTDP1,COBL,NRP1,APOE,LTBP4,PAK4,DCLK1,TMEM108,RARG,IGF1,WT1,SFRP2,NDRG3,NDN,CTTN,SEMA3B,RGMA,LAMB2,SEMA4B,SEMA6C,RERG,RND2,HDAC6,SERPINE2,ERBB2,BRAT1,SLIT2,TP53,PPP1R9B,ADAM15,PTPRS,DVL1,CLSTN1,ABL1,OSGIN1,IST1,PML,GATA4,BST2,OGFR	cyan	VSMC_M2
GO:1903900	0.02	0.99	14	104	regulation of viral life cycle	BP	0.44279	TRIM14,GSN,TRIM13,TRIM21,CHMP3,PLSCR1,TRIM8,RNASEL,ADAR,ISG15,OAS2,TRIM26,PML,BST2	cyan	VSMC_M2
GO:1901699	0.02	0.99	49	508	cellular response to nitrogen compound	BP	0.44307	STAT6,FLOT1,EHMT2,DAXX,APPL2,RRAGC,IRF3,KLF15,VIM,ATG7,SOCS3,FOLR2,KAT2B,IGF1,TLR3,WT1,PRKCD,SRC,TGM2,GNAO1,MMP2,STAT1,CHRNA7,NFKB1,GNAI2,ERFE,LINC02210-CRHR1,HDAC5,STAT5A,PQBP1,ARRB2,JUP,PRKACA,ZFP36L1,SLIT2,TP53,PDK2,PPP1R9B,SHC1,GRIA1,ABCC1,AGRN,TSC2,FOXC2,ABL1,SLC2A8,SLC8A3,RGS8,RGS10	cyan	VSMC_M2
GO:0021782	0.02	0.99	12	86	glial cell development	BP	0.44307	VIM,TPPP,B4GALT5,LAMB2,ARHGEF10,ADORA2A,GRN,MYRF,MED12,ROR1,ASPA,ABCA2	cyan	VSMC_M2
GO:0051130	0.02	0.99	78	870	positive regulation of cellular component organization	BP	0.44307	FLOT1,PLXNB2,KCTD17,APPL2,P3H1,COBL,AP2A1,GSN,NRP1,BAX,FZD4,MARK4,BIN1,APOE,SLITRK6,CAMK1,DZIP1,TPPP2,ARAP1,TBC1D5,SMPD1,APBB1,CLIP3,SCN1B,IGF1,CAMKK2,NDRG4,EPHA3,SRC,LRP4,C15orf62,SORBS3,TIRAP,CTTN,TPPP,RGMA,NCKIPSD,FES,STK25,ARPC5,B2M,ARHGEF10,FYCO1,GRN,GPC2,RND2,ADD1,DLG5,ARHGEF10L,CROCC,ARRB2,ALOX15,EPHA2,PLEKHM2,NTRK1,SLIT2,AR,TP53,GBA,WARS,PDGFRB,ROR1,SH3GL1,DVL1,AGRN,ISG15,NPHP4,ENTR1,CLSTN1,ABL1,ATMIN,IST1,ZNF205,SERPINF1,PML,LRRC7,BMF,SDC4	cyan	VSMC_M2
GO:0022612	0.02	0.99	13	95	gland morphogenesis	BP	0.44307	STAT6,NFIB,GLI3,NRP1,BAX,RARG,SRC,TGM2,CAPN1,BMP4,EPHA2,AR,PML	cyan	VSMC_M2
GO:0006635	0.02	0.99	10	64	fatty acid beta-oxidation	BP	0.44361	ACAA1,ECH1,DECR1,ACADS,HADH,ECHS1,ACAT1,CPT2,ABCD1,CRAT	cyan	VSMC_M2
GO:0007266	0.02	0.99	15	116	Rho protein signal transduction	BP	0.44599	ARHGEF25,FLOT1,NRP1,RHOB,APOE,RHOG,ARHGAP1,C15orf62,ARHGEF12,HEG1,ARHGEF10,BCR,KANK2,PDGFRB,ABL1	cyan	VSMC_M2
GO:0061037	0.02	1.00	6	29	negative regulation of cartilage development	BP	0.44599	EFEMP1,RARG,CTSK,LTBP3,ADAMTS7,BMP4	cyan	VSMC_M2
GO:0034433	0.02	1.00	4	14	steroid esterification	BP	0.44599	APOE,ACAT1,LCAT,ABCA2	cyan	VSMC_M2
GO:0034434	0.02	1.00	4	14	sterol esterification	BP	0.44599	APOE,ACAT1,LCAT,ABCA2	cyan	VSMC_M2
GO:0034435	0.02	1.00	4	14	cholesterol esterification	BP	0.44599	APOE,ACAT1,LCAT,ABCA2	cyan	VSMC_M2
GO:1903170	0.02	1.00	6	29	negative regulation of calcium ion transmembrane transport	BP	0.44882	BIN1,CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:1904035	0.02	0.99	10	65	regulation of epithelial cell apoptotic process	BP	0.4492	HMOX1,GSN,ZFP36,PAK4,CAST,PLCG1,ARRB2,ZFP36L1,NUPR1,ABL1	cyan	VSMC_M2
GO:0051960	0.02	0.99	35	344	regulation of nervous system development	BP	0.4492	PLXNB2,KIAA1324L,APPL2,GLI3,NRP1,BIN1,SLITRK6,RARG,MAN2A1,TGM2,LRP4,SEMA3B,TPPP,RGMA,SEMA4B,PRUNE1,SEMA6C,STK25,ELL3,B2M,RND2,DLG5,MYRF,SERPINE2,NTRK1,SLIT2,TP53,TMEM98,PTPRS,ASPA,AGRN,CLSTN1,IL34,IST1,SERPINF1	cyan	VSMC_M2
GO:1902430	0.02	1.00	5	22	negative regulation of amyloid-beta formation	BP	0.4492	BIN1,APOE,IGF1,SPON1,CHRNA7	cyan	VSMC_M2
GO:0034614	0.02	0.99	16	124	cellular response to reactive oxygen species	BP	0.4492	STAT6,PTPRK,RHOB,AGAP3,CAMKK2,PRKCD,SRC,MMP2,CCS,STK25,HDAC6,PCGF2,PDK2,ABL1,ADPRHL2,MPV17	cyan	VSMC_M2
GO:0034204	0.02	1.00	7	39	lipid translocation	BP	0.4492	ATP10D,PLSCR1,PRKCD,PLSCR3,ATP8B2,ABCC1,ABCA2	cyan	VSMC_M2
GO:0072243	0.02	1.00	4	15	metanephric nephron epithelium development	BP	0.4492	WWTR1,STAT1,LAMB2,ACAT1	cyan	VSMC_M2
GO:0048880	0.02	0.99	30	286	sensory system development	BP	0.44976	EFEMP1,MEIS1,GLI3,SLC17A7,NRP1,BAX,MEIS3,FZD4,VIM,SLITRK6,RARG,MAN2A1,WT1,FOXF2,LAMB2,CLCN2,WNT2B,BMP4,NAGLU,CC2D2A,CPAMD8,EPHA2,SMOC1,PDGFRB,NPHP4,FOXC2,PBX3,SERPINF1,PYGO2,COL8A1	cyan	VSMC_M2
GO:0070372	0.02	0.99	24	211	regulation of ERK1 and ERK2 cascade	BP	0.44976	AKAP12,GPNMB,RRAS,NRP1,APOE,MAP3K12,IGF1,NDRG4,SRC,CHRNA7,TIRAP,GNAI2,LMO3,BMP4,ARRB2,ALOX15,EPHA2,ERBB2,NTRK1,SHC1,PDGFRB,TRAF7,ABL1,GATA4	cyan	VSMC_M2
GO:0072006	0.02	0.99	15	118	nephron development	BP	0.45312	TCF21,GLI3,KLF15,WT1,WWTR1,LZTS2,STAT1,LAMB2,WNT2B,ACAT1,WNK4,BMP4,PDGFRB,FOXC2,MPV17	cyan	VSMC_M2
GO:0006024	0.02	0.99	10	66	glycosaminoglycan biosynthetic process	BP	0.45315	ST3GAL1,AP2A1,CHST14,EXT2,NFKB1,B4GAT1,B3GAT3,XYLT2,PDGFRB,HS3ST3B1	cyan	VSMC_M2

GO:2000145	0.02	0.99	70	772	regulation of cell motility	BP	0.4532	AKAP12,PLXNB2,AFDN,PTPRK,ARHGAP18,CARD10,HMOX1,APPL2,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,APOE,TPPP2,RHOG,FGFR1,ADGRA2,ANGPT4,IGF1,SFRP2,NDRG4,SRC,PLCG1,BBS2,NISCH,PHACTR1,CD81,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,ECM1,SEMA4B,FES,SEMA6C,FAM89B,GRN,HDAC5,VEGFB,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,JUP,EPHA2,SERPINE2,MCC,IL27RA,SLIT2,ADAM15,PDGFRB,MAP2K3,PODN,TNFRSF14,PHPT1,FOXC2,ABL1,OSGIN1,IL34,SERPINF1,PLPP3,SDC4,BST2	cyan	VSMC_M2
GO:0022617	0.02	0.99	8	47	extracellular matrix disassembly	BP	0.45518	MMP19,FLOT1,MMP2,EXOC8,CTSK,FURIN,ADAM15,PBXIP1	cyan	VSMC_M2
GO:0060078	0.02	0.99	12	85	regulation of postsynaptic membrane potential	BP	0.45596	TMEM108,GLRB,CACNB3,CHRNA7,ADORA2A,CHRNE,ARRB2,GRIA1,SH3GL1,DVL1,SLC8A3,KCND2	cyan	VSMC_M2
GO:0051336	0.02	0.99	69	754	regulation of hydrolase activity	BP	0.45715	PPP6R2,PLXNB2,TBC1D22A,AFDN,MTCH1,TBC1D2,TBC1D17,GSN,BAX,BIN1,TIMP2,ARAP1,TBC1D5,RHOG,FGFR1,EFNA5,SERPING1,CAST,SFRP2,PRKCD,EPHA3,SRC,TGM2,GNAO1,PCSK6,CSTB,GNAI2,RGMA,SGSM1,SPA1L2,APH1A,ECM1,CASP10,FURIN,ARHGEF10,BCR,ADORA2A,GRN,PCOLCE,PSAP,CPAMD8,DNAJB6,ARRB2,EPHA2,SERPINE2,CASP9,ERBB2,NTRK1,PPP1R9B,PBXIP1,PDGFRB,SGSM2,AGRN,RENBP,TSC2,ABL1,CNN3,OAS2,ABCA2,SERPINF1,PML,SERPINB6,CALM3,CARD8,GCHFR,PSMB9,RGS8,RGS10,BST2	cyan	VSMC_M2
GO:0016331	0.02	0.99	16	127	morphogenesis of embryonic epithelium	BP	0.45728	PLXNB2,COBL,RARG,SFRP2,RGMA,VANGL2,WNT2B,BMP4,CC2D2A,PRKACA,AR,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0040013	0.02	0.99	28	261	negative regulation of locomotion	BP	0.46708	AFDN,PTPRK,CARD10,HMOX1,RRAS,NRP1,RHOB,APOE,ANGPT4,ARRDC3,SFRP2,NDRG4,NISCH,SEMA3B,SEMA4B,SEMA6C,ADORA2A,HDAC5,NBL1,DLG5,JUP,MCC,IL27RA,SLIT2,ADAM15,PODN,SERPINF1,BST2	cyan	VSMC_M2
GO:0065005	0.02	1.00	5	22	protein-lipid complex assembly	BP	0.4682	BIN1,APOE,PRKACA,LCAT,DGAT1	cyan	VSMC_M2
GO:0072202	0.02	1.00	5	22	cell differentiation involved in metanephros development	BP	0.47492	TCF21,WWTR1,STAT1,LAMB2,BMP4	cyan	VSMC_M2
GO:0003012	0.02	0.99	34	332	muscle system process	BP	0.47981	CTDP1,MYL6B,FBXO32,HMOX1,MLIP,GSN,KLF15,BIN1,EHD3,GAA,APBB1,HSPB6,SCN1B,IGF1,SNTA1,GNAO1,CTTN,TPCN2,GATA5,CTNNA3,KCND3,VEGFB,CHRNE,JUP,PRKACA,MAP2K3,EEF2,HSBP1,SLC8A3,GATA4,CALM3,CLIC2,CDK9,EMD	cyan	VSMC_M2
GO:0050877	0.02	0.99	62	678	nervous system process	BP	0.47981	EHMT2,RPS6KA2,TGFBI,NPTXR,TRPM3,EFEMP1,BBS9,FZD4,APOE,SLITRK6,GAA,NPTX1,EPYC,TMEM108,TPP1,SCN1B,CYP4V2,TSHZ3,HEXB,NDRG4,GLRB,SRC,CACNB3,BBS2,SFRP5,NDN,CHRNA7,TPPP,LEF1,RLBP1,LAMB2,ADCY1,PTCHD1,B2M,ADORA2A,RPGR,NYX,DGCR2,NR2F6,CHRNE,ARRB2,MYRF,SERPINE2,NTRK1,GBA,PPP1R9B,GRIA1,TMEM98,ROR1,PIEZO2,SH3GL1,RETREG1,EEF2,DVL1,ABL1,PBX3,SLC8A3,SERPINF1,KCND2,LRRN4,SERPINB6,EN1	cyan	VSMC_M2
GO:0032331	0.02	1.00	5	22	negative regulation of chondrocyte differentiation	BP	0.47981	EFEMP1,RARG,LTBP3,ADAMTS7,BMP4	cyan	VSMC_M2
GO:0046640	0.02	1.00	5	22	regulation of alpha-beta T cell proliferation	BP	0.47981	IRF1,MAPK8IP1,CD81,TNFRSF14,CD55	cyan	VSMC_M2
GO:0060993	0.02	0.99	11	77	kidney morphogenesis	BP	0.47981	TCF21,GCNT1,GLI3,WT1,WWTR1,LZTS2,STAT1,WNT2B,WNK4,BMP4,PDGFRB	cyan	VSMC_M2
GO:0034349	0.02	1.00	4	15	glial cell apoptotic process	BP	0.47981	AKAP12,PRKCD,CASP9,TP53	cyan	VSMC_M2
GO:0060047	0.02	0.99	20	172	heart contraction	BP	0.47981	RPS6KA2,GSN,BIN1,EHD3,GAA,SCN1B,SNTA1,GNAO1,EXT2,CTNNA3,KCND3,VEGFB,JUP,PRKACA,MAP2K3,SLC8A3,GATA4,CALM3,CLIC2,RNLS	cyan	VSMC_M2
GO:0003002	0.02	0.99	27	251	regionalization	BP	0.48217	TSHZ1,COBL,GLI3,NRP1,RARG,WT1,SFRP2,LRP4,PCSK6,LEF1,GATA5,WNT2B,BMP4,NBL1,PRKACA,PCGF2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,FOXC2,DNAAF1,PBX3,GATA4,EN1	cyan	VSMC_M2
GO:0072109	0.02	1.00	4	15	glomerular mesangium development	BP	0.48217	WT1,BMP4,PDGFRB,FOXC2	cyan	VSMC_M2
GO:0030198	0.02	0.99	27	250	extracellular matrix organization	BP	0.48217	MMP19,ADAMTS2,FLOT1,TGFBI,BCL3,MMP17,WT1,SFRP2,FOXF2,MMP2,EGFL6,LAMB2,EXOC8,CTSK,FURIN,OLFML2B,LTBP3,ADAMTS7,DNAJB6,FKBP10,SMOC1,ADAM15,PBXIP1,FOXC2,ABL1,COL8A1,MPV17	cyan	VSMC_M2
GO:0043330	0.02	1.00	6	30	response to exogenous dsRNA	BP	0.48228	FLOT1,IRF3,RFTN1,TLR3,NFKBIA,PQBP1	cyan	VSMC_M2
GO:0002115	0.02	1.00	4	15	store-operated calcium entry	BP	0.48228	CRACR2B,ORAI2,HOMER3,ORAI3	cyan	VSMC_M2
GO:0001838	0.02	0.99	14	107	embryonic epithelial tube formation	BP	0.48228	PLXNB2,COBL,RARG,SFRP2,RGMA,VANGL2,BMP4,CC2D2A,PRKACA,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0001574	0.02	1.00	4	15	ganglioside biosynthetic process	BP	0.48235	B3GALT4,ST3GAL1,B4GALT5,AL157935.2	cyan	VSMC_M2
GO:1900120	0.02	1.00	4	15	regulation of receptor binding	BP	0.48374	NRP1,RGMA,B2M,ADAM15	cyan	VSMC_M2
GO:0043010	0.02	0.99	26	242	camera-type eye development	BP	0.4845	EFEMP1,MEIS1,GLI3,SLC17A7,NRP1,BAX,FZD4,VIM,SLITRK6,RARG,MAN2A1,WT1,FOXF2,LAMB2,CLCN2,WNT2B,BMP4,NAGLU,CC2D2A,EPHA2,PDGFRB,NPHP4,FOXC2,SERPINF1,PYGO2,COL8A1	cyan	VSMC_M2
GO:0045165	0.02	0.99	20	172	cell fate commitment	BP	0.4845	STAT6,EHMT2,TEAD3,GLI3,NRP1,WT1,SFRP2,TM2D3,SOX5,GATA5,WNT2B,BMP4,AR,TP53,TCF3,FOXC2,GAS1,PML,GATA4,ZFPM1	cyan	VSMC_M2
GO:0010942	0.02	0.99	46	470	positive regulation of cell death	BP	0.4845	AKAP12,RPS6KA2,DAXX,MTCH1,HMOX1,STK17A,GSN,RHOB,BAX,TRIM13,MARK4,BIN1,ATG7,EFNB2,SMPD1,APBB1,CLIP3,RBCK1,RARG,TLR3,SFRP2,PRKCD,SRC,TGM2,PLCG1,PTGIS,ADORA2A,AIFM2,GRN,BMP4,HDAC6,ARRB2,CASP9,TP53BP2,NTRK1,SLIT2,TP53,NUPR1,PDGFRB,TRAF7,ABL1,OSGIN1,INCA1,PML,EEF1A2,BMF	cyan	VSMC_M2
GO:0095500	0.02	1.00	5	22	acetylcholine receptor signaling pathway	BP	0.48469	CHRNA7,GNAI2,AGRN,RGS8,RGS10	cyan	VSMC_M2
GO:0002253	0.02	0.99	22	191	activation of immune response	BP	0.48469	CFB,APPL2,COLEC11,BAX,RFTN1,RBCK1,SERPING1,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,CD81,C1R,C1S,PQBP1,PLD2,C6,PHPT1,ABL1,HEXIM1,CD55	cyan	VSMC_M2
GO:0099537	0.02	0.99	46	477	trans-synaptic signaling	BP	0.48469	AKAP12,FLOT1,RPS6KA2,PACSIN2,NPTXR,CADPS2,SLC17A7,APOE,NPTX1,TMEM108,RIMBP2,TSHZ3,GLRB,SRC,CACNB3,PLCG1,NISCH,CHRNA7,GNAI2,SV2A,ADCY1,ANXA9,PTCHD1,BCR,ADORA2A,CHRNE,ARRB2,AKAP5,DAGLA,GABARAP,SERPINE2,GIPC1,PRKACA,NTRK1,CPLX2,PPP1R9B,GRIA1,PTPRS,SH3GL1,DVL1,CLSTN1,ABL1,SLC8A3,KCND2,CALM3,STX3	cyan	VSMC_M2
GO:0006658	0.02	1.00	5	22	phosphatidylserine metabolic process	BP	0.48469	OSBPL10,LPCAT4,PLSCR1,PTDSS1,OSBPL5	cyan	VSMC_M2

GO:0006066	0.02	0.99	28	258	alcohol metabolic process	BP	0.48469	MOXD1,CYB5R3,ACSS1,APOE,PLB1,SMPD1,IGF1,ACSS2,SLC5A3,PNPLA2,OSBPL5,NFKB1,IP6K1,CLCN2,PCBD1,QDPR,STARD3,NPC2,GBA,DHRS13,IDH3G,INPP5E,H6PD,PLPP2,LCAT,ABCA2,DGAT1,PLPP3	cyan	VSMC_M2
GO:1905209	0.02	1.00	4	15	positive regulation of cardiocyte differentiation	BP	0.48469	EFNB2,BMP4,ARRB2,GATA4	cyan	VSMC_M2
GO:0048010	0.02	0.99	8	48	vascular endothelial growth factor receptor signaling pathway	BP	0.48575	NRP1,FZD4,HGS,SRC,VEGFD,VEGFB,EPN2,FOXC2	cyan	VSMC_M2
GO:0042176	0.02	0.99	35	342	regulation of protein catabolic process	BP	0.48575	EIF3H,GGA1,RNF144A,NOP53,APOE,ATRAID,ATG7,TIMP2,HGS,FOXF2,CTSA,CD81,RGMA,RHBDD3,FURIN,VPS11,ATG4B,MAGEF1,GABARAP,SERPINE2,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,SNX33,DVL1,ELOB,AXIN1,RHBDF1,CBFA2T3,ABCA2,PML,EEF1A2	cyan	VSMC_M2
GO:0031647	0.02	0.99	27	249	regulation of protein stability	BP	0.48588	FLOT1,P3H1,GSN,NOP53,TSPAN1,CMTM6,TRIM21,LAMP1,IGF1,PRKCD,SRC,CTSA,CD81,CAPN3,B4GALT5,VPS11,GRN,IFI30,HDAC6,WIZ,GIPC1,TP53,GLMP,SLC51B,WDR81,DVL1,PLPP3	cyan	VSMC_M2
GO:2001258	0.02	1.00	6	30	negative regulation of cation channel activity	BP	0.48801	SLC6A9,CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0045229	0.02	0.99	27	251	external encapsulating structure organization	BP	0.48818	MMP19,ADAMTS2,FLOT1,TGFBI,BCL3,MMP17,WT1,SFRP2,FOXF2,MMP2,EGFL6,LAMB2,EXOC8,CTSK,FURIN,OLFML2B,LTBP3,ADAMTS7,DNAJB6,FKBP10,SMOC1,ADAM15,PBXIP1,FOXC2,ABL1,COL8A1,MPV17	cyan	VSMC_M2
GO:0016064	0.02	0.99	12	85	immunoglobulin mediated immune response	BP	0.48818	STAT6,BCL3,SLC15A4,SERPING1,PRKCD,CD81,B2M,C1R,C1S,IL27RA,C6,CD55	cyan	VSMC_M2
GO:0030301	0.02	0.99	11	77	cholesterol transport	BP	0.48818	EEPD1,APOE,OSBPL5,TPCN2,NFKB1,FURIN,NFKBIA,STARD3,NPC2,LCAT,ABCA2	cyan	VSMC_M2
GO:0035567	0.02	0.99	10	68	non-canonical Wnt signaling pathway	BP	0.48818	FZD4,RNF213,PRICKLE2,SFRP2,SFRP5,VANGL2,MED12,ROR1,DVL1,ABL1	cyan	VSMC_M2
GO:0035264	0.02	0.99	14	108	multicellular organism growth	BP	0.49005	STK40,SLITRK6,GPAT4,PKDCC,RARG,IGF1,WWTR1,BBS2,HEG1,STAT5A,ZFP36L1,AR,TP53,EN1	cyan	VSMC_M2
GO:0051924	0.02	0.99	20	172	regulation of calcium ion transport	BP	0.49319	BAX,BIN1,EHD3,CACNB3,PLCG1,GNAO1,CRACR2B,CAPN3,GNAI2,LINC02210-CRHR1,ADORA2A,HOMER3,ARRB2,PRKACA,PDGFRB,ABL1,CBARP,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0030166	0.02	0.99	8	49	proteoglycan biosynthetic process	BP	0.49319	CANT1,IGF1,CHST14,EXT2,B3GAT3,XYLT2,CHST8,HS3ST3B1	cyan	VSMC_M2
GO:0035148	0.02	0.99	16	129	tube formation	BP	0.49319	PLXNB2,NFIB,COBL,RARG,SFRP2,TGM2,RGMA,VANGL2,BMP4,CC2D2A,PRKACA,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0048598	0.02	0.99	45	469	embryonic morphogenesis	BP	0.49488	TSHZ1,TCF21,PLXNB2,EFEMP1,COBL,GLI3,BAX,SLITRK6,SOCS3,RARG,SFRP2,NDRG4,LRP4,FOXF2,MMP2,EXT2,RGMA,LEF1,VANGL2,WNT2B,BMP4,NAGLU,CC2D2A,DNAJB6,EPHA2,ZBTB17,PRKACA,ZFP36L1,PCGF2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,DVL1,TSC2,FOXC2,ABL1,DNAAF1,HSBP1,GATA4,SDC4,COL8A1,EN1	cyan	VSMC_M2
GO:0043549	0.02	0.99	57	612	regulation of kinase activity	BP	0.49573	DEPTOR,DAXX,CARD10,AKT1S1,FZD4,CAB39L,APOE,SOCS3,CAMK1,HGS,KAT2B,FGFR1,SH3BP5,SMPD1,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,MAPK8IP1,CD81,TIRAP,HEG1,ADORA2A,BMP4,LDB2,EPHA2,ERBB2,NTRK1,GBA,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MAP2K3,ROR1,MLLT1,TRAF4,WDR81,DVL1,TSC2,AXIN1,ABL1,IL34,INCA1,SLC8A3,HEXIM1,EEF1A2,CALM3,SDC4	cyan	VSMC_M2
GO:0072012	0.02	1.00	5	23	glomerulus vasculature development	BP	0.49727	TCF21,WT1,BMP4,PDGFRB,FOXC2	cyan	VSMC_M2
GO:0044281	0.02	0.98	113	1301	small molecule metabolic process	BP	0.49843	ZADH2,MOXD1,DDAH2,CYB5R3,ST3GAL1,ACO1,APPL2,PLA2G7,IARS,BCKDHB,AASS,ACSS1,ME3,APOE,ACAA1,CYP2S1,COQ8B,PLB1,PNP,GAA,ECH1,GPAT4,KAT2B,DCXR,SMPD1,IGF1,CYP4V2,MAN2A1,GGT7,ACSS2,NEIL2,COQ9,SRC,DECR1,NISCH,SLC5A3,PNPLA2,ABHD14B,SLC45A3,OSBPL5,NADSYN1,ACADS,NFKB1,HADH,IP6K1,PTGIS,RLBP1,ADCY1,SCLY,ERFE,SLC16A9,CLCN2,FUCA1,UCKL1,NMNAT2,ECHS1,AIFM2,PCBD1,G6PC3,ACAT1,NUDT13,MACROD1,QDPR,STAT5A,ALOX15,EPHA2,DAGLA,BRAT1,STARD3,UBIAD1,MRI1,TP53,HSD3B7,NPC2,PDK2,GBA,NUPR1,SLC16A2,WARS,PPCDC,MAN2C1,ABCC1,NUDT14,DHRS13,CPT2,ABCD1,IDH3G,ASPA,RENBP,HAGH,UAP1L1,PTGDS,FAM3A,INPP5E,H6PD,PLPP2,GSTM4,CBFA2T3,CRAT,DPYD,LDHD,FPGS,LCAT,TK2,ABCA2,ACOT6,ZBTB7A,DGAT1,PLPP3,CA11,NAGK,MACROD2,PDXK	cyan	VSMC_M2
GO:0071360	0.02	1.00	4	15	cellular response to exogenous dsRNA	BP	0.49843	FLOT1,IRF3,TLR3,PQBP1	cyan	VSMC_M2
GO:0010959	0.02	0.99	28	263	regulation of metal ion transport	BP	0.49942	STOM,BAX,BIN1,SLC6A9,EHD3,SCN1B,SNTA1,CACNB3,PLCG1,GNAO1,CRACR2B,CAPN3,GNAI2,LINC02210-CRHR1,B2M,ADORA2A,HOMER3,WNK4,ARRB2,SERPINE2,PRKACA,MLLT6,PDGFRB,ABL1,CBARP,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0062207	0.02	0.99	11	77	regulation of pattern recognition receptor signaling pathway	BP	0.49942	FLOT1,IRF1,APPL2,NOP53,SLC15A4,TLR3,TIRAP,DHX58,ARRB2,PTPRS,NFKBIL1	cyan	VSMC_M2
GO:0034138	0.02	1.00	4	15	toll-like receptor 3 signaling pathway	BP	0.49996	FLOT1,RFTN1,TLR3,TIRAP	cyan	VSMC_M2
GO:0051926	0.02	0.99	7	39	negative regulation of calcium ion transport	BP	0.50049	BIN1,CACNB3,GNAO1,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0043410	0.02	0.99	36	356	positive regulation of MAPK cascade	BP	0.50655	AKAP12,GPNMB,NRP1,FZD4,APOE,TIMP2,FGFR1,MAP3K12,IGF1,TLR3,NDRG4,SRC,MAPK8IP1,SORBS3,CD81,CHRNA7,TIRAP,GNAI2,STK25,TMEM106A,BMP4,ARRB2,ALOX15,ERBB2,NTRK1,AR,SHC1,PDGFRB,MAP2K3,ROR1,TRAF4,TRAF7,AXIN1,ABL1,IL34,GATA4	cyan	VSMC_M2
GO:0002832	0.02	0.99	11	77	negative regulation of response to biotic stimulus	BP	0.50686	TRIM21,SERPING1,GRN,DHX58,ARRB2,ADAR,ISG15,FAM3A,RPS19,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0048147	0.02	1.00	5	23	negative regulation of fibroblast proliferation	BP	0.50686	BAX,IFI30,TP53,NUPR1,EMD	cyan	VSMC_M2
GO:0035023	0.02	0.99	10	69	regulation of Rho protein signal transduction	BP	0.50686	ARHGEF25,FLOT1,NRP1,APOE,HEG1,ARHGEF10,BCR,KANK2,PDGFRB,ABL1	cyan	VSMC_M2
GO:0070371	0.02	0.99	25	227	ERK1 and ERK2 cascade	BP	0.50686	AKAP12,GPNMB,RRAS,NRP1,APOE,MAP3K12,IGF1,NDRG4,SRC,CHRNA7,TIRAP,GNAI2,LMO3,BMP4,ARRB2,ALOX15,EPHA2,ERBB2,ZFP36L1,NTRK1,SHC1,PDGFRB,TRAF7,ABL1,GATA4	cyan	VSMC_M2

GO:0002433	0.02	1.00	5	23	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	BP	0.50686	APPL2,PRKCD,SRC,PLD2,ABL1	cyan	VSMC_M2
GO:0038096	0.02	1.00	5	23	Fc-gamma receptor signaling pathway involved in phagocytosis	BP	0.50686	APPL2,PRKCD,SRC,PLD2,ABL1	cyan	VSMC_M2
GO:0050778	0.02	0.99	32	306	positive regulation of immune response	BP	0.50686	STAT6,CFB,APPL2,COLEC11,IRF3,BAX,RFTN1,LAMP1,SLC15A4,RBCK1,SERPING1,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,CD81,IKBKE,TIRAP,B2M,GRN,C1R,C1S,PQBP1,PLD2,IL27RA,C6,PHPT1,ABL1,HEXIM1,CD55,RPS19	cyan	VSMC_M2
GO:0045926	0.02	0.99	22	195	negative regulation of growth	BP	0.50927	CTDP1,MEIS1,NRP1,WT1,SFRP2,NDRG3,BBS2,SEMA3B,RGMA,SEMA4B,SEMA6C,RERG,BMP4,SERPINE2,SLIT2,TP53,PPP1R9B,ADAM15,PTPRS,OSGIN1,PML,BST2	cyan	VSMC_M2
GO:0048011	0.02	1.00	5	23	neurotrophin TRK receptor signaling pathway	BP	0.51072	AKT1S1,TMEM108,SRC,NDN,NTRK1	cyan	VSMC_M2
GO:0006486	0.02	0.99	21	182	protein glycosylation	BP	0.51499	MGAT4B,B3GALT4,ST3GAL1,GCNT1,GALNT12,FKRP,MAN2A1,DPY19L3,GALNT18,EXT2,B4GALT4,B4GALT5,GCNT7,B4GAT1,VEGFB,B3GAT3,SLC51B,NUDT14,NAGPA,ABCA2,AL157935.2	cyan	VSMC_M2
GO:0043413	0.02	0.99	21	182	macromolecule glycosylation	BP	0.51499	MGAT4B,B3GALT4,ST3GAL1,GCNT1,GALNT12,FKRP,MAN2A1,DPY19L3,GALNT18,EXT2,B4GALT4,B4GALT5,GCNT7,B4GAT1,VEGFB,B3GAT3,SLC51B,NUDT14,NAGPA,ABCA2,AL157935.2	cyan	VSMC_M2
GO:0048534	0.02	0.99	60	649	hematopoietic or lymphoid organ development	BP	0.51591	STAT6,TCF21,IRF1,PTPRK,ST3GAL1,ITGB8,MEIS1,GLI3,RRAS,FLT3LG,BAX,LRRC17,TMEM176B,BCL3,PNP,ZFP36,RARG,TLR3,SFRP2,SRC,STAT1,CD81,TIRAP,TUSC2,LEF1,FES,NFKBIA,B2M,WNT2B,DPF2,HDAC5,BMP4,MAEA,EPHA2,CASP9,ERBB2,ZFP36L1,NTRK1,TP53,KAT8,HOXB4,GBA,ADAR,SIGLEC15,TMEM98,CRIP2,EEF2,ISG15,TCF3,SBNO2,CBFA2T3,ABL1,IL34,SLC8A3,ZBTB7A,PML,RPS19,JUNB,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0042325	0.02	0.98	85	967	regulation of phosphorylation	BP	0.51867	FLOT1,PLXNB2,DEPTOR,DAXX,CARD10,GPNMB,AKT1S1,NRP1,BAX,NOP53,FZD4,CAB39L,APOE,SOCS3,CAMK1,HGS,KAT2B,FGFR1,SH3BP5,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,LRP4,MAPK8IP1,PTPN13,MOB2,GFRA2,CD81,CHRNA7,TIRAP,VEGFD,HEG1,ADORA2A,VEGFB,BMP4,LDB2,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,NTRK1,SLIT2,AR,TP53,GBA,PPP1R9B,NUPR1,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MAP2K3,ROR1,MLLT1,TRAF4,WDR81,DVL1,TNFRSF14,TSC2,AXIN1,CBFA2T3,ABL1,IL34,INCA1,SLC8A3,HEXIM1,ZBTB7A,PML,PLPP3,EEF1A2,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0048670	0.02	1.00	4	16	regulation of collateral sprouting	BP	0.52503	RGMA,RND2,PTPRS,IST1	cyan	VSMC_M2
GO:0030029	0.02	0.98	60	662	actin filament-based process	BP	0.52605	MYL6B,PACSIN2,ARHGAP18,ELMO1,COBL,GSN,NRP1,RHOB,LURAP1,BIN1,ARAP1,RHOG,SCN1B,SNTA1,EFNA5,RHPN2,PRKCD,EPHA3,SRC,PDLIM2,C15orf62,SORBS3,NISCH,PHACTR1,CAPN3,TJP1,CTTN,SSH3,GAS2L1,FES,CTNNA3,WIPF1,ARPC5,KCND3,ARHGEF10,CDC42BPG,RND2,ADD1,CAPZB,ARHGEF10L,DNAJB6,JUP,ALOX15,CGNL1,SLIT2,PPP1R9B,SHC1,ARHGAP17,SIGLEC15,PDGFRB,FLII,LLGL1,NPHP4,PHPT1,AIF1L,ABL1,CNN3,GATA4,SDC4,BST2	cyan	VSMC_M2
GO:0014065	0.02	0.99	14	111	phosphatidylinositol 3-kinase signaling	BP	0.52791	NOP53,FGFR1,IGF1,SRC,PTPN13,PIK3C2B,SERPINE2,ERBB2,ZFP36L1,NTRK1,PDGFRB,ROR1,TSC2,INPP5E	cyan	VSMC_M2
GO:0010955	0.02	1.00	5	23	negative regulation of protein processing	BP	0.52791	CAST,SERPINE2,TMEM98,GAS1,CARD8	cyan	VSMC_M2
GO:1903318	0.02	1.00	5	23	negative regulation of protein maturation	BP	0.52791	CAST,SERPINE2,TMEM98,GAS1,CARD8	cyan	VSMC_M2
GO:0035850	0.02	0.99	7	41	epithelial cell differentiation involved in kidney development	BP	0.52791	KLF15,WT1,WWTR1,STAT1,LAMB2,BMP4,FOXC2	cyan	VSMC_M2
GO:0030030	0.02	0.98	104	1226	cell projection organization	BP	0.52931	FLOT1,PLXNB2,PACSIN2,PTPRK,CDC14C,KCTD17,NFIB,RSPH9,P3H1,BBS9,COBL,GLI3,AP2A1,GSN,NRP1,CCDC114,FZD4,MARK4,VIM,APOE,SLITRK6,CAMK1,EHD3,DZIP1,ARAP1,NPTX1,RHOG,EFNB2,POC1B,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,SFRP2,WWTR1,NDRG4,PRKCD,EPHA3,SRC,LRP4,BBS2,GNAO1,C15orf62,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,SEMA4B,NCKIPSD,ADCY1,FES,SEMA6C,VANGL2,KIF1A,STK25,ARPC5,MOV10,B2M,ADORA2A,RPGR,GRN,GPC2,RND2,NBL1,CAPZB,MAP1S,CC2D2A,DLG5,HDAC6,PQBP1,CROCC,EPHA2,ERBB2,NTRK1,SLIT2,PPP1R9B,NEO1,LLGL1,ROR1,PTPRS,ABCD1,DVL1,AGRN,WDR90,ENTR1,RERE,AIF1L,ABL1,DNAAF1,ATMIN,IST1,ATP6V0D1,SERPINF1,LRRC7,TMEM250,SDC4,STX3	cyan	VSMC_M2
GO:0061351	0.02	0.99	14	111	neural precursor cell proliferation	BP	0.53305	PLXNB2,TEAD3,APPL2,GLI3,GNAI2,LEF1,SOX5,KIF1A,ELL3,ZNF503,DAGLA,TP53,SLC16A2,RERE	cyan	VSMC_M2
GO:0070085	0.02	0.99	22	194	glycosylation	BP	0.53337	MGAT4B,B3GALT4,ST3GAL1,GCNT1,GALNT12,FKRP,MAN2A1,DPY19L3,GALNT18,EXT2,B4GALT4,B4GALT5,GCNT7,B4GAT1,VEGFB,B3GAT3,GBA,SLC51B,NUDT14,NAGPA,ABCA2,AL157935.2	cyan	VSMC_M2
GO:0019724	0.02	0.99	12	87	B cell mediated immunity	BP	0.53796	STAT6,BCL3,SLC15A4,SERPING1,PRKCD,CD81,B2M,C1R,C1S,IL27RA,C6,CD55	cyan	VSMC_M2
GO:0010648	0.02	0.98	91	1047	negative regulation of cell communication	BP	0.53796	TCF21,DEPTOR,GRINA,TLE1,HMOX1,CARD19,AKT1S1,GLI3,NRP1,BAX,NOP53,MEIS3,FZD4,APOE,BCL3,SOCS3,TIMP2,RNF213,HGS,RAB11FIP1,ADGRA2,SMPD1,IGF1,ARRDC3,SFRP2,WWTR1,NDRG4,PRKCD,SRC,LRP4,SFRP5,MAPK8IP1,LZTS2,STAT1,CTTN,GNAI2,HADH,KIF7,ECM1,VPS11,BCL9L,HEG1,LMO3,ELL3,NFKBIA,FAM89B,FRMD8,TMEM161A,HOMER3,TMBIM1,BMP4,NBL1,DLG5,DHX58,ARRB2,EPHA2,SERPINE2,MCC,CGNL1,PRKACA,UBQLN2,PCGF2,SLIT2,AR,TP53,GBA,ADAR,KANK2,GRIA1,ULK3,EPN2,MAP2K3,PTPRS,GLIS2,ISG15,TSC2,NPHP4,PHPT1,INPP5E,RAB11FIP3,AXIN1,NPRL3,ABL1,ZBTB7A,GATA4,CARD8,NFKBIL1,RGS19,RGS8,RGS10,EMD	cyan	VSMC_M2

GO:0007268	0.02	0.98	45	471	chemical synaptic transmission	BP	0.53878	AKAP12,FLOT1,RPS6KA2,PACSIN2,NPTXR,CADPS2,SLC17A7,APOE,NPTX1,TMEM108,RIMBP2,TSHZ3,GLRB,SRC,CACNB3,PLCG1,NISCH,CHRNA7,GNAI2,SV2A,ADCY1,ANXA9,PTCHD1,BCR,ADORA2A,CHRNE,ARRB2,AKAP5,GABARAP,SERPINE2,GIPC1,PRKACA,NTRK1,CPLX2,PPP1R9B,GRIA1,PTPRS,SH3GL1,DVL1,CLSTN1,ABL1,SLC8A3,KCND2,CALM3,STX3	cyan	VSMC_M2
GO:0098916	0.02	0.98	45	471	anterograde trans-synaptic signaling	BP	0.53878	AKAP12,FLOT1,RPS6KA2,PACSIN2,NPTXR,CADPS2,SLC17A7,APOE,NPTX1,TMEM108,RIMBP2,TSHZ3,GLRB,SRC,CACNB3,PLCG1,NISCH,CHRNA7,GNAI2,SV2A,ADCY1,ANXA9,PTCHD1,BCR,ADORA2A,CHRNE,ARRB2,AKAP5,GABARAP,SERPINE2,GIPC1,PRKACA,NTRK1,CPLX2,PPP1R9B,GRIA1,PTPRS,SH3GL1,DVL1,CLSTN1,ABL1,SLC8A3,KCND2,CALM3,STX3	cyan	VSMC_M2
GO:0010975	0.02	0.99	37	376	regulation of neuron projection development	BP	0.53878	PLXNB2,P3H1,COBL,AP2A1,NRP1,VIM,APOE,CAMK1,EFNB2,LZTS3,APBB1,SCN1B,SFRP2,NDRG4,EPHA3,LRP4,SEMA3B,RGMA,SEMA4B,NCKIPSD,FES,SEMA6C,KIF1A,STK25,B2M,GRN,GPC2,RND2,PQBP1,NTRK1,SLIT2,ROR1,PTPRS,DVL1,IST1,SERPINF1,LRRC7	cyan	VSMC_M2
GO:0015918	0.02	0.99	12	89	sterol transport	BP	0.53878	EEPD1,APOE,OSBPL10,OSBPL5,TPCN2,NFKB1,FURIN,NFKBIA,STARD3,NPC2,LCAT,ABCA2	cyan	VSMC_M2
GO:0031644	0.02	0.99	13	100	regulation of nervous system process	BP	0.53878	NPTXR,NPTX1,TMEM108,SRC,CACNB3,CHRNA7,TPPP,MYRF,GBA,TMEM98,SH3GL1,DVL1,SLC8A3	cyan	VSMC_M2
GO:0043094	0.02	0.99	5	23	cellular metabolic compound salvage	BP	0.53878	PNP,UCKL1,MRI1,TK2,PDXK	cyan	VSMC_M2
GO:0045862	0.02	0.99	31	297	positive regulation of proteolysis	BP	0.54238	MTCH1,RNF144A,GSN,BAX,NOP53,APOE,SPON1,SFRP2,SRC,CAPN3,RGMA,APH1A,CASP10,FURIN,MAGEF1,CLEC3B,GRN,PCOLCE,GABARAP,CASP9,UBQLN2,GBA,NUPR1,SNX33,DVL1,ELOB,AXIN1,CBFA2T3,IST1,PML,CARD8	cyan	VSMC_M2
GO:0023057	0.02	0.98	91	1048	negative regulation of signaling	BP	0.54247	TCF21,DEPTOR,GRINA,TLE1,HMOX1,CARD19,AKT1S1,GLI3,NRP1,BAX,NOP53,MEIS3,FZD4,APOE,BCL3,SOCS3,TIMP2,RNF213,HGS,RAB11FIP1,ADGRA2,SMPD1,IGF1,ARRDC3,SFRP2,WWTR1,NDRG4,PRKCD,SRC,LRP4,SFRP5,MAPK8IP1,LZTS2,STAT1,CTTN,GNAI2,HADH,KIF7,ECM1,VPS11,BCL9L,HEG1,LMO3,ELL3,NFKBIA,FAM89B,FRMD8,TMEM161A,HOMER3,TMBIM1,BMP4,NBL1,DLG5,DHX58,ARRB2,EPHA2,SERPINE2,MCC,CGNL1,PRKACA,UBQLN2,PCGF2,SLIT2,AR,TP53,GBA,ADAR,KANK2,GRIA1,ULK3,EPN2,MAP2K3,PTPRS,GLIS2,ISG15,TSC2,NPHP4,PHPT1,INPP5E,RAB11FIP3,AXIN1,NPRL3,ABL1,ZBTB7A,GATA4,CARD8,NFKBIL1,RGS19,RGS8,RGS10,EMD	cyan	VSMC_M2
GO:0032469	0.02	0.99	5	24	endoplasmic reticulum calcium ion homeostasis	BP	0.54247	GRINA,KCTD17,BAX,TGM2,PML	cyan	VSMC_M2
GO:0035556	0.02	0.98	168	2063	intracellular signal transduction	BP	0.54247	ARHGEF25,AKAP12,FLOT1,DDAH2,RPS6KA2,DEPTOR,ARHGAP18,TEAD3,GRINA,TLE1,CARD10,ARHGAP39,HMOX1,LRRC19,CARD19,TRIM14,GPNMB,RRAGC,ELMO1,STK40,AKT1S1,STK17A,IRF3,RRAS,NRP1,RHOB,BAX,NOP53,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,MARK4,APOE,BCL3,SOCS3,TIMP2,ZFP36,CANT1,PAK4,ARAP1,RHOG,FGFR1,SH3BP5,TRIM21,DCLK1,ACKR4,SMPD1,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,CAMKK2,SFRP2,WWTR1,NDRG4,PRKCD,SRC,TGM2,PLCG1,MMS19,ARHGAP1,SFRP5,C15orf62,MAPK8IP1,SORBS3,NISCH,PTPN13,PIK3C2B,STAT1,FAM13A,CD81,FIBIN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,TPCN2,NFKB1,GNAI2,ADGRB2,SIPA1L2,ARHGEF12,ECM1,RHBDD3,CASP10,ADCY1,HEG1,LMO3,RERG,STK25,MUS81,ELL3,RGL1,NFKBIA,ARHGEF10,BCR,PLCD3,CDC42BPG,TMEM161A,TMEM101,HOMER3,TMEM106A,RND2,WNK4,BMP4,DLG5,DHX58,ARHGEF10L,PLD2,ARRB2,ALOX15,EPHA2,AKAP5,GABARAP,SERPINE2,CGNL1,CASP9,ERBB2,TP53BP2,PRKACA,ZFP36L1,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,NUPR1,SHC1,KANK2,PRKCSH,DENND4B,ARHGAP17,DOCK6,TEX14,SLC44A2,GPRC5B,PDGFRB,MCOLN1,MAP2K3,ROR1,ZDHHC9,TRAF4,DVL1,TRAF7,TSC2,RHOT2,INPP5E,AXIN1,NPRL3,RALGDS,ABL1,IL34,RPS15,HEXIM1,PML,GATA4,CALM3,CARD8,CLIC2,NFKBIL1,RGS19,BST2	cyan	VSMC_M2
GO:0035094	0.02	0.99	6	32	response to nicotine	BP	0.54247	HMOX1,CHRNA7,NFKB1,B2M,NTRK1,PPP1R9B	cyan	VSMC_M2
GO:1902992	0.02	0.99	5	24	negative regulation of amyloid precursor protein catabolic process	BP	0.54247	BIN1,APOE,IGF1,SPON1,CHRNA7	cyan	VSMC_M2
GO:0060079	0.02	0.99	10	69	excitatory postsynaptic potential	BP	0.54311	TMEM108,GLRB,CACNB3,CHRNA7,ADORA2A,CHRNE,ARRB2,SH3GL1,DVL1,SLC8A3	cyan	VSMC_M2
GO:0045321	0.02	0.98	55	586	leukocyte activation	BP	0.54311	STAT6,ULBP2,IRF1,PTPRK,ST3GAL1,HMOX1,ITGB8,GPNMB,GLI3,GSN,BAX,BCL3,PNP,LAMP1,WDFY4,SLC15A4,LMO1,IGF1,TLR3,PLSCR1,PRKCD,SRC,BPI,MAPK8IP1,CD81,TIRAP,TUSC2,LEF1,RHBDD3,FES,B2M,ADORA2A,GRN,HDAC5,TMEM106A,BMP4,DLG5,ERBB2,ZFP36L1,IL27RA,NTRK1,TP53,CPLX2,GBA,TMEM98,TNFRSF14,TCF3,PTGDS,SBNO2,ABL1,ZBTB7A,CD55,SDC4,BST2,ZFPM1	cyan	VSMC_M2
GO:0006816	0.02	0.99	29	282	calcium ion transport	BP	0.54311	TRPM3,BAX,BIN1,EHD3,CACNB3,PLCG1,GNAO1,CRACR2B,CHRNA7,CAPN3,CACNA2D2,TPCN2,GNAI2,ANXA9,LINC02210-CRHR1,ORAI2,ADORA2A,HOMER3,ARRB2,PRKACA,ORAI3,PDGFRB,MCOLN1,ABL1,SLC8A3,CBARP,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0015914	0.02	0.99	10	70	phospholipid transport	BP	0.54351	ATP10D,APOE,OSBPL10,PLSCR1,PRKCD,OSBPL5,PLSCR3,NPC2,ATP8B2,ABCC1	cyan	VSMC_M2
GO:0002521	0.02	0.98	38	383	leukocyte differentiation	BP	0.55135	STAT6,IRF1,PTPRK,ST3GAL1,ITGB8,GLI3,RRAS,BAX,LRRC17,TMEM176B,BCL3,PNP,TLR3,SRC,CD81,TUSC2,LEF1,FES,B2M,HDAC5,BMP4,EPHA2,ERBB2,ZFP36L1,NTRK1,TP53,GBA,SIGLEC15,TMEM98,TCF3,SBNO2,CBFA2T3,ABL1,IL34,ZBTB7A,JUNB,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0007585	0.02	0.99	8	50	respiratory gaseous exchange by respiratory system	BP	0.5517	STK40,GAA,MAN2A1,TSHZ3,SLC5A3,NDN,TRAF4,PBX3	cyan	VSMC_M2

GO:0007389	0.02	0.98	33	329	pattern specification process	BP	0.55308	TSHZ1,MEIS1,COBL,GLI3,NRP1,MEIS3,RFNG,RARG,WT1,SFRP2,NDRG4,LRP4,PCSK6,LEF1,VANGL2,GATA5,WNT2B,BMP4,NBL1,CC2D2A,PRKACA,PCGF2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,FOXC2,DNAAF1,PBX3,GATA4,EN1	cyan	VSMC_M2
GO:0046519	0.02	1.00	4	16	sphingoid metabolic process	BP	0.55308	GBA,PLPP2,ABCA2,PLPP3	cyan	VSMC_M2
GO:0007411	0.02	0.99	20	181	axon guidance	BP	0.55447	PLXNB2,NFIB,GLI3,NRP1,RHOG,EFNB2,SCN1B,EFNA5,EPHA3,BOC,SEMA3B,LAMB2,SEMA4B,SEMA6C,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,DVL1	cyan	VSMC_M2
GO:0034613	0.02	0.98	122	1451	cellular protein localization	BP	0.55728	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,AFDN,PACSIN2,PTPRK,GGA1,CARD10,APPL2,TBC1D2,BBS9,RRAGC,TBC1D17,GLI3,AP2A1,GSN,STOM,NRP1,RHOB,BAX,NOP53,MARK4,APOE,BCL3,CAMK1,EHD3,DZIP1,HGS,TBC1D5,RFTN1,RHOG,DCLK1,LAMP1,PKDCC,TPP1,CLIP3,GNPTAB,CHMP4B,TP53INP2,EDEM2,WWTR1,GLRB,PRKCD,EPHA3,SRC,CACNB3,CPE,LRP4,BBS2,SLC5A3,CRACR2B,SYS1,LZTS2,CTSA,HPS6,CD81,TRIM8,CAPN3,CTTN,SGSM1,EXOC8,GAS2L1,VPS11,KIF1A,FAM53B,NFKBIA,M6PR,RPGR,HOMER3,GPC2,TMBIM1,BMP4,CC2D2A,HDAC6,B3GAT3,WDR45,CROCC,DNAJB6,JUP,EPHA2,AKAP5,GABARAP,GIPC1,ERBB2,PRKACA,AR,TP53,GLMP,PPP1R9B,SLC51B,SNX33,TMEM98,ZDHHC9,NAGPA,GLIS2,DVL1,SGSM2,AGRN,ISG15,TSC2,SLC9A3R2,NPHP4,INPP5E,RAB11FIP3,ENTR1,CLSTN1,MON1B,ABCA2,ZBTB7A,RAB43,GRASP,PML,CALM3,LRRC7,VPS26B,TMEM250,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0001570	0.02	0.99	10	71	vasculogenesis	BP	0.55774	ZFPM2,ITGB8,RRAS,FZD4,WT1,HEG1,EPHA2,ZFP36L1,PDGFRB,JUNB	cyan	VSMC_M2
GO:0038094	0.02	0.99	5	24	Fc-gamma receptor signaling pathway	BP	0.56013	APPL2,PRKCD,SRC,PLD2,ABL1	cyan	VSMC_M2
GO:0008406	0.03	0.99	19	166	gonad development	BP	0.5613	TCF21,ZFPM2,MEA1,BAX,FZD4,TLR3,WT1,SFRP2,SRC,REC8,WNT2B,ARRB2,NTRK1,SLIT2,AR,ADAM15,NUPR1,PDGFRB,GATA4	cyan	VSMC_M2
GO:0003156	0.03	0.99	5	24	regulation of animal organ formation	BP	0.5613	WT1,GATA5,WNT2B,BMP4,AR	cyan	VSMC_M2
GO:0050829	0.03	0.99	6	32	defense response to Gram-negative bacterium	BP	0.5613	GSDMD,BPI,TUSC2,TNFRSF14,RPS19,IL22RA1	cyan	VSMC_M2
GO:0010634	0.03	0.99	17	143	positive regulation of epithelial cell migration	BP	0.5613	HMOX1,RRAS,NRP1,RHOB,FGFR1,ADGRA2,ANGPT4,SRC,PLCG1,GRN,BMP4,STAT5A,HDAC6,MAP2K3,FOXC2,ABL1,PLPP3	cyan	VSMC_M2
GO:0150076	0.03	0.99	5	24	neuroinflammatory response	BP	0.5613	IGF1,ADCY1,GRN,DAGLA,NUPR1	cyan	VSMC_M2
GO:0006085	0.03	1.00	4	16	acetyl-CoA biosynthetic process	BP	0.5613	ACSS1,ACSS2,ACAT1,PDK2	cyan	VSMC_M2
GO:0001932	0.03	0.98	75	845	regulation of protein phosphorylation	BP	0.5613	FLOT1,PLXNB2,DEPTOR,DAXX,CARD10,GPNMB,AKT1S1,NRP1,BAX,NOP53,FZD4,CAB39L,APOE,SOCS3,CAMK1,HGS,KAT2B,FGFR1,SH3BP5,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,SRC,LRP4,MAPK8IP1,PTPN13,MOB2,GFRA2,CD81,CHRNA7,TIRAP,VEGFD,HEG1,ADORA2A,VEGFB,BMP4,HDAC6,ARRB2,ERBB2,BRAT1,NTRK1,SLIT2,TP53,GBA,PPP1R9B,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MAP2K3,MLLT1,TRAF4,DVL1,TNFRSF14,TSC2,AXIN1,ABL1,IL34,INCA1,SLC8A3,HEXIM1,PML,PLPP3,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0051338	0.03	0.98	64	706	regulation of transferase activity	BP	0.5613	DEPTOR,DAXX,CARD10,AKT1S1,FZD4,CAB39L,APOE,SOCS3,CAMK1,ZFP36,HGS,KAT2B,FGFR1,SH3BP5,SMPD1,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,ARRDC3,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,MAPK8IP1,CD81,CHRNA7,TIRAP,HEG1,ADORA2A,BMP4,RARRES3,LDB2,EPHA2,ERBB2,NTRK1,TP53,GBA,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MAP2K3,ROR1,MLLT1,TRAF4,WDR81,DVL1,TSC2,PHPT1,AXIN1,ABL1,IL34,INCA1,RPS15,SLC8A3,HEXIM1,EEF1A2,CALM3,SDC4	cyan	VSMC_M2
GO:0051604	0.03	0.99	25	230	protein maturation	BP	0.5619	ADAMTS2,RPS6KA2,GLI3,GSN,FKRP,KAT2B,CAST,SPON1,SRC,CPE,MMS19,PCSK6,APH1A,FURIN,CCS,MAGEF1,PHEX,CLEC3B,C1R,MYRF,SERPINE2,PRKACA,TMEM98,GAS1,CARD8	cyan	VSMC_M2
GO:0043603	0.03	0.98	80	897	cellular amide metabolic process	BP	0.5619	PYM1,NEU1,PLXNB2,EIF3H,B3GALT4,TAPBP,NAGA,ST3GAL1,OPLAH,ACO1,IARS,ITGB8,AASS,RPL18,ABTB1,ACSS1,VIM,BIN1,APOE,BCL3,ETHE1,MIF4GD,PNP,RPS16,ZFP36,SAMD4B,GPAT4,RPL15,EIF3K,SMPD1,TPP1,EIF3F,IGF1,PATL1,GGT7,ACSS2,HEXB,SPON1,PRKCD,CPE,CHRNA7,MRPL36,PCSK6,B4GALT5,APH1A,FURIN,NIT1,MOV10,ACAT1,RARRES3,ERBB2,ZFP36L1,TP53,PDK2,GBA,WARS,CERS4,EEF2,ABCD1,DPH7,RENBP,HAGH,INPP5E,PLPP2,GSTM4,RPL13,FPGS,ABCA2,RPS15,ACOT6,MEX3D,DGAT1,RPS19,PLPP3,EEF1A2,CLIC2,CLIC3,RPL36A,NAGK,AL157935.2	cyan	VSMC_M2
GO:0007213	0.03	1.00	4	16	G protein-coupled acetylcholine receptor signaling pathway	BP	0.56239	GNAI2,AGRN,RGS8,RGS10	cyan	VSMC_M2
GO:0006935	0.03	0.98	41	426	chemotaxis	BP	0.56239	PLXNB2,NFIB,PLA2G7,GPNMB,GLI3,NRP1,RHOG,FGFR1,EFNB2,ADGRA2,ACKR4,SCN1B,EFNA5,PRKCD,EPHA3,TIRAP,BOC,SEMA3B,LEF1,LAMB2,VEGFD,SEMA4B,FES,SEMA6C,VEGFB,BMP4,NBL1,ARRB2,EPHA2,ERBB2,NTRK1,SLIT2,HSD3B7,NEO1,ABCC1,PDGFRB,DVL1,TSC2,IL34,RPS19,STX3	cyan	VSMC_M2
GO:1905144	0.03	0.99	5	24	response to acetylcholine	BP	0.56375	CHRNA7,GNAI2,AGRN,RGS8,RGS10	cyan	VSMC_M2
GO:1905145	0.03	0.99	5	24	cellular response to acetylcholine	BP	0.56375	CHRNA7,GNAI2,AGRN,RGS8,RGS10	cyan	VSMC_M2
GO:0030323	0.03	0.99	17	145	respiratory tube development	BP	0.56522	TCF21,ADAMTS2,ZFPM2,NFIB,STK40,GLI3,PKDCC,MAN2A1,HEG1,PHEX,LTBP3,WNT2B,BMP4,DLG5,PDGFRB,TRAF4,DNAAF1	cyan	VSMC_M2
GO:0007405	0.03	0.99	7	42	neuroblast proliferation	BP	0.56522	PLXNB2,TEAD3,GLI3,LEF1,SOX5,DAGLA,TP53	cyan	VSMC_M2
GO:0010657	0.03	0.99	9	60	muscle cell apoptotic process	BP	0.56522	RPS6KA2,HMOX1,HSPB6,IGF1,SFRP2,ARRB2,TP53,NUPR1,GATA4	cyan	VSMC_M2
GO:0097485	0.03	0.99	20	182	neuron projection guidance	BP	0.56522	PLXNB2,NFIB,GLI3,NRP1,RHOG,EFNB2,SCN1B,EFNA5,EPHA3,BOC,SEMA3B,LAMB2,SEMA4B,SEMA6C,EPHA2,ERBB2,NTRK1,SLIT2,NEO1,DVL1	cyan	VSMC_M2
GO:0002861	0.03	0.99	5	24	regulation of inflammatory response to antigenic stimulus	BP	0.56522	RHBDF2,SRC,PLCG1,CD81,FURIN	cyan	VSMC_M2

GO:0071702	0.03	0.98	156	1891	organic substance transport	BP	0.56531	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,TAPBP,GGA1,APPL2,ATP10D,TBC1D2,P3H1,SLC44A1,BBS9,EEPD1,TBC1D17,GLI3,AP2A1,CADPS2,SLC17A7,STOM,KLF15,RHOB,BAX,DENND2A,FZD4,APOE,BCL3,SLC6A9,ATG7,EXOC7,RHBDF2,LTBP4,CAMK1,EHD3,CMTM6,OSBPL10,ZFP36,STARD10,SLC4A9,FOLR2,HGS,TBC1D5,RFTN1,RAB11FIP1,APBB1,PKDCC,CLIP3,SLC15A4,SLC7A2,GNPTAB,IGF1,EFNA5,CHMP4B,CHMP3,EDEM2,ARRDC3,PLSCR1,SLC38A7,PRKCD,SRC,CACNB3,BBS2,ARHGAP1,EXOC2,NISCH,SLC5A3,SYS1,CTSA,CD81,SLC45A3,OSBPL5,AGFG1,CTTN,TMEM115,TPCN2,NFKB1,LRP10,HADH,DISP1,SGSM1,SV2A,EXOC8,RHBDD3,FURIN,VPS11,ERFE,SLC16A9,KIF1A,FAM53B,TCN2,ATG4B,RNASEL,NFKBIA,LINC02210-CRHR1,M6PR,ADORA2A,RPGR,G6PC3,PSAP,HOMER3,BMP4,PORCN,USE1,HDAC6,B3GAT3,ARRB2,JUP,AKAP5,GABARAP,PLSCR3,GIPC1,ERBB2,STARD3,PRKACA,ZFP36L1,TP53,NPC2,SLC51B,SLC16A2,ATP8B2,SPNS1,SLC44A2,SNX33,RASL10B,ABCC1,MCOLN1,LLGL1,ZDHHC9,NAGPA,CPT2,MFSD12,ABCD1,SGSM2,TSC2,PHPT1,SLC10A3,RAB11FIP3,ENTR1,RHBDF1,CLSTN1,MON1B,SLC2A8,IST1,LCAT,APOL5,ABCA2,RAB43,GRASP,PML,SCAMP4,VPS26B,STX3,RAB11B,MCFD2,EMD,UBL5	cyan	VSMC_M2
GO:0042330	0.03	0.98	41	427	taxis	BP	0.56722	PLXNB2,NFIB,PLA2G7,GPNMB,GLI3,NRP1,RHOG,FGFR1,EFNB2,ADGRA2,ACKR4,SCN1B,EFNA5,PRKCD,EPHA3,TIRAP,BOC,SEMA3B,LEF1,LAMB2,VEGFD,SEMA4B,FES,SEMA6C,VEGFB,BMP4,NBL1,ARRB2,EPHA2,ERBB2,NTRK1,SLIT2,HSD3B7,NEO1,ABCC1,PDGFRB,DVL1,TSC2,IL34,RPS19,STX3	cyan	VSMC_M2
GO:0008152	0.03	0.98	634	8467	metabolic process	BP	0.56722	CTDP1,TSHZ1,ZADH2,MMP19,PYM1,PMEL,RBMS2,STAT6,MOXD1,TCF21,OS9,ADAMTS2,MGAT4B,GNS,AKAP12,FLOT1,CHKB,DDAH2,PPP6R2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,CFB,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,B3GALT4,CYB5R3,TAPBP,TCF20,DAXX,NAGA,FBXO32,HDDC2,TEF,PTPRK,ST3GAL1,IBA57,CDC14C,GSDMD,TEAD3,MTCH1,TLE1,GGA1,OPLAH,CARD10,KCTD17,NFIB,TRERF1,GCNT1,HMOX1,LRRC19,ACO1,CUL9,KLF9,APPL2,PLA2G7,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,ITGB8,P3H1,NAT14,TMEM150B,GPNMB,SLC44A1,BCKDHB,EFEMP1,TRIL,RRAGC,EEPD1,MEIS1,RNF144A,IAH1,STK40,TBC1D17,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,RPL18,PARP12,NOP53,ABTB1,BICRA,MEIS3,FKRP,UQCRH,LURAP1,TRIM13,ACSS1,FZD4,ME3,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,UROD,BCL3,ETHE1,MIF4GD,AGAP3,ATRAID,SLC6A9,ACAA1,ATG7,EXOC7,CYP2S1,COQ8B,LTBP4,CAPN5,PLB1,SOCS3,CAMK1,EHD3,PLD3,TEP1,OSBPL10,RNF170,PNP,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,GAA,PAK4,SGSH,ECH1,RNF213,ARAP1,GPAT4,RPL15,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,DCXR,FGFR1,IL5RA,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PGGHG,PKDCC,TPP1,MMP17,WDFY4,CLIP3,GTF3A,SLC15A4,ANGPT4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,GNPTAB,IGF1,CYP4V2,TLR3,SNTA1,MAN2A1,WT1,EFNA5,CHMP4B,CHMP3,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,GGCX,POU6F1,LPCAT4,SERPING1,CAST,LACTB2,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,STBD1,PRKCD,COQ9,EPHA3,SRC,CPE,TGM2,BPI,LRP4,DECR1,PLBD2,PLCG1,ZH	cyan	VSMC_M2
GO:0030182	0.03	0.98	91	1067	neuron differentiation	BP	0.56815	FLOT1,EHMT2,PLXNB2,PTPRK,MTCH1,NFIB,P3H1,MEIS1,COBL,GLI3,AP2A1,NRP1,FZD4,VIM,BIN1,APOE,SLITRK6,CAMK1,TIMP2,NPTX1,RHOG,FGFR1,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,SFRP2,NDRG4,EPHA3,LRP4,GNAO1,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,B4GALT5,LAMB2,VEGFD,SEMA4B,NCKIPSD,ADCY1,FES,SEMA6C,KIF1A,STK25,MOV10,B2M,WNT2B,ADORA2A,GRN,GPC2,RND2,BMP4,NAGLU,NBL1,MAP1S,NR2F6,DLG5,HDAC6,PQBP1,EPHA2,TCF12,ERBB2,NTRK1,SLIT2,GBA,PPP1R9B,NEO1,GPRC5B,LLGL1,ROR1,PTPRS,DVL1,AGRN,TCF3,NPHP4,RERE,ABL1,PBX3,IST1,SERPINF1,LRRC7,SDC4,STX3,EN1	cyan	VSMC_M2
GO:0046596	0.03	0.99	5	24	regulation of viral entry into host cell	BP	0.56815	TRIM14,GSN,TRIM21,TRIM8,TRIM26	cyan	VSMC_M2
GO:0006656	0.03	0.99	5	24	phosphatidylcholine biosynthetic process	BP	0.56815	CHKB,SLC44A1,GPAT4,SLC44A2,LCAT	cyan	VSMC_M2
GO:0070663	0.03	0.99	18	153	regulation of leukocyte proliferation	BP	0.56819	IRF1,GPNMB,PNP,IL5RA,LMO1,IGF1,MAPK8IP1,CD81,TIRAP,BMP4,DLG5,ERBB2,IL27RA,TNFRSF14,IL34,CD55,SDC4,BST2	cyan	VSMC_M2
GO:0048565	0.03	0.99	12	92	digestive tract development	BP	0.56819	TCF21,COBL,GLI3,PKDCC,SFRP2,SRC,FOXF2,SFRP5,GATA5,BMP4,DNAAF1,GATA4	cyan	VSMC_M2
GO:0007610	0.03	0.98	39	406	behavior	BP	0.57337	EHMT2,MEIS1,GLI3,FZD4,APOE,SLITRK6,GAA,ARRDC3,HEXB,NDRG4,GLRB,BBS2,GNAO1,CHRNA7,CSTB,ADCY1,PTCHD1,B2M,ADORA2A,ASTN1,NAGLU,ARRB2,NTRK1,TP53,GBA,PPP1R9B,GRIA1,MTA1,DVL1,NPHP4,PTGDS,PBX3,ABCA2,SLC8A3,SERPINF1,KCND2,LRRN4,SELENOP,EN1	cyan	VSMC_M2
GO:1900271	0.03	0.99	6	33	regulation of long-term synaptic potentiation	BP	0.57815	APOE,CHRNA7,ADCY1,ADORA2A,AKAP5,ABL1	cyan	VSMC_M2
GO:2000810	0.03	0.99	4	17	regulation of bicellular tight junction assembly	BP	0.5836	TJP1,EPHA2,PRKACA,NPHP4	cyan	VSMC_M2
GO:0046513	0.03	0.99	8	51	ceramide biosynthetic process	BP	0.5836	B3GALT4,ST3GAL1,SMPD1,PRKCD,B4GALT5,GBA,CERS4,AL157935.2	cyan	VSMC_M2
GO:0001775	0.03	0.98	63	692	cell activation	BP	0.5836	STAT6,ULBP2,AKAP12,IRF1,PTPRK,ST3GAL1,HMOX1,ITGB8,GPNMB,GLI3,GSN,BAX,APOE,BCL3,PNP,LAMP1,WDFY4,SLC15A4,LMO1,IGF1,TLR3,PLSCR1,PRKCD,SRC,BPI,MAPK8IP1,CD81,CAPN3,TIRAP,TUSC2,LEF1,RHBDD3,FES,FIBP,B2M,ADORA2A,GRN,HDAC5,TMEM106A,BMP4,DLG5,IL17RA,SERPINE2,ERBB2,ZFP36L1,IL27RA,NTRK1,TP53,CPLX2,GBA,ULK3,PDGFRB,TMEM98,TNFRSF14,TCF3,PTGDS,SBNO2,ABL1,ZBTB7A,CD55,SDC4,BST2,ZFPM1	cyan	VSMC_M2
GO:0097035	0.03	0.99	7	43	regulation of membrane lipid distribution	BP	0.5836	ATP10D,PLSCR1,PRKCD,PLSCR3,ATP8B2,ABCC1,ABCA2	cyan	VSMC_M2
GO:0051156	0.03	0.99	4	17	glucose 6-phosphate metabolic process	BP	0.58506	G6PC3,PGLS,TP53,H6PD	cyan	VSMC_M2

GO:0043065	0.03	0.98	40	410	positive regulation of apoptotic process	BP	0.58515	AKAP12,RPS6KA2,MTCH1,HMOX1,STK17A,GSN,RHOB,BAX,BIN1,ATG7,SMPD1,APBB1,CLIP3,RBCK1,RARG,TLR3,SFRP2,PRKCD,SRC,TGM2,PLCG1,PTGIS,ADORA2A,AIFM2,GRN,BMP4,ARRB2,CASP9,TP53BP2,SLIT2,TP53,NUPR1,PDGFRB,TRAF7,ABL1,OSGIN1,INCA1,PML,EEF1A2,BMF	cyan	VSMC_M2
GO:1903362	0.03	0.98	24	222	regulation of cellular protein catabolic process	BP	0.58529	EIF3H,RNF144A,NOP53,APOE,ATRAID,FOXF2,CD81,FURIN,VPS11,MAGEF1,GABARAP,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,DVL1,ELOB,AXIN1,RHBDF1,CBFA2T3,ABCA2,PML	cyan	VSMC_M2
GO:1901890	0.03	0.99	11	82	positive regulation of cell junction assembly	BP	0.58693	FLOT1,NRP1,SLITRK6,DLG5,EPHA2,NTRK1,AGRN,NPHP4,CLSTN1,ABL1,SDC4	cyan	VSMC_M2
GO:0006810	0.03	0.98	260	3300	transport	BP	0.58712	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,PACSIN2,TAPBP,GGA1,HMOX1,ACO1,TRPM3,APPL2,ATP10D,TBC1D2,P3H1,KCNQ5,SLC44A1,BBS9,EEPD1,ELMO1,TBC1D17,GLI3,AP2A1,CADPS2,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,BAX,DENND2A,UQCRH,FZD4,BIN1,APOE,BCL3,ABCB8,SLC6A9,ATG7,EXOC7,RHBDF2,LTBP4,CAMK1,EHD3,CMTM6,OSBPL10,ZFP36,LGALS3BP,SLC26A11,STARD10,GPAT4,SLC4A9,FOLR2,HGS,TBC1D5,RFTN1,RHOG,RAB11FIP1,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,PKDCC,CLIP3,SLC15A4,SLC7A2,ATP4A,SCN1B,GNPTAB,IGF1,REEP5,SNTA1,EFNA5,CHMP4B,CHMP3,EDEM2,ERGIC3,ARRDC3,PLSCR1,SLC38A7,NDRG4,GLRB,STBD1,PRKCD,EPHA3,SRC,CACNB3,TGM2,LRP4,PLCG1,BBS2,ARHGAP1,EXOC2,GNAO1,MAPK8IP1,NISCH,EXT2,SLC5A3,CRACR2B,SYS1,LZTS2,CTSA,CD81,SLC45A3,CHRNA7,OSBPL5,CAPN3,CACNA2D2,AGFG1,CTTN,PCSK6,TMEM115,TUSC2,TPCN2,NFKB1,GNAI2,LRP10,HADH,DISP1,SGSM1,SV2A,EXOC8,RHBDD3,NCKIPSD,ADCY1,FES,ANXA9,FURIN,VPS11,ERFE,SLC16A9,KIF1A,FAM53B,CLCN2,TCN2,TMEM50A,ATG4B,RNASEL,NFKBIA,LINC02210-CRHR1,B2M,KCND3,ORAI2,M6PR,ADORA2A,CAPN1,FYCO1,RPGR,GRN,G6PC3,PSAP,HOMER3,WNK4,BMP4,MAP1S,STAT5A,PORCN,USE1,HDAC6,B3GAT3,CHRNE,PLD2,ARRB2,JUP,ALOX15,AKAP5,GABARAP,SERPINE2,PLSCR3,GIPC1,ERBB2,STARD3,PRKACA,ZFP36L1,UBQLN2,CLCN6,MLLT6,TMEM175,TP53,CPLX2,ORAI3,ERGIC1,NPC2,SLC51B,SLC16A2,ATP8B2,C1orf43,STON2,SPNS1,SLC44A2,GRIA1,ATOX1,SNX33,RASL10B,ABCC1,EPN2,PDGFRB,MCOLN1,LLGL1,ZDHHC9,PIEZO2,UBXN6,SH3GL1,NAGPA,CPT2,MFSD12,WDR81,ABCD1,D	cyan	VSMC_M2
GO:0090090	0.03	0.99	14	113	negative regulation of canonical Wnt signaling pathway	BP	0.58712	TLE1,GLI3,FZD4,APOE,SFRP2,WWTR1,LRP4,SFRP5,LZTS2,FRMD8,MCC,NPHP4,AXIN1,EMD	cyan	VSMC_M2
GO:0043547	0.03	0.98	22	202	positive regulation of GTPase activity	BP	0.5877	TBC1D22A,AFDN,TBC1D2,TBC1D17,ARAP1,TBC1D5,RHOG,TGM2,GNAO1,RGMA,SGSM1,SIPA1L2,ARHGEF10,BCR,EPHA2,ERBB2,NTRK1,SGSM2,AGRN,TSC2,RGS8,RGS10	cyan	VSMC_M2
GO:0061035	0.03	0.99	9	61	regulation of cartilage development	BP	0.5877	EFEMP1,GLI3,PKDCC,RARG,SOX5,CTSK,LTBP3,ADAMTS7,BMP4	cyan	VSMC_M2
GO:0072210	0.03	0.99	6	34	metanephric nephron development	BP	0.58861	TCF21,WT1,STAT1,LAMB2,BMP4,PDGFRB	cyan	VSMC_M2
GO:0002443	0.03	0.98	24	221	leukocyte mediated immunity	BP	0.58861	STAT6,ULBP2,HMOX1,BCL3,RFTN1,LAMP1,SLC15A4,TLR3,SERPING1,PRKCD,CD81,TUSC2,FES,B2M,C1R,C1S,ARRB2,PLEKHM2,IL27RA,CPLX2,C6,PTGDS,CD55,BST2	cyan	VSMC_M2
GO:0006793	0.03	0.98	176	2169	phosphorus metabolic process	BP	0.58861	CTDP1,FLOT1,CHKB,PPP6R2,PLXNB2,RPS6KA2,DEPTOR,DAXX,HDDC2,PTPRK,ST3GAL1,CDC14C,CARD10,PLA2G7,GPNMB,SLC44A1,EFEMP1,STK40,AKT1S1,STK17A,AASS,NRP1,BAX,NOP53,ACSS1,FZD4,CAB39L,MARK4,APOE,PLB1,SOCS3,CAMK1,OSBPL10,PNP,PAK4,GPAT4,HGS,KAT2B,FGFR1,SH3BP5,DCLK1,SMPD1,PKDCC,CLIP3,ANGPT4,MAP3K12,GNPTAB,IGF1,TLR3,EFNA5,ACSS2,LPCAT4,NEIL2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,LRP4,PLBD2,PLCG1,MAPK8IP1,PTPN13,PTDSS1,PIK3C2B,ABHD14B,MOB2,GFRA2,CD81,PHKG1,CHRNA7,IKBKE,OSBPL5,NADSYN1,TIRAP,GNAI2,IP6K1,PTGIS,SSH3,VEGFD,GRK5,ADCY1,FES,TNS3,PRUNE1,HEG1,STK25,UCKL1,RNASEL,NMNAT2,PHEX,BCR,ADORA2A,PPA1,CDC42BPG,G6PC3,ACAT1,VEGFB,NUDT13,WNK4,BMP4,RARRES3,LDB2,PGLS,HDAC6,PLD2,ARRB2,ALOX15,EPHA2,PLSCR3,ERBB2,BRAT1,PRKACA,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,NUPR1,SHC1,ADAR,ACP5,TEX14,SLC44A2,WARS,ULK3,PPCDC,GPRC5B,PDGFRB,NUDT14,MAP2K3,ROR1,MLLT1,TRAF4,PTPRS,WDR81,ABCD1,DVL1,PNPLA7,TNFRSF14,TSC2,UAP1L1,PHPT1,PIGQ,INPP5E,AXIN1,H6PD,PLPP2,CBFA2T3,ABL1,DPYD,IL34,LCAT,TK2,INCA1,ABCA2,ACOT6,SLC8A3,HEXIM1,ZBTB7A,DGAT1,PML,PLPP3,EEF1A2,CALM3,CPPED1,CDK9,SDC4,NAGK,PDXK,GTF2H4	cyan	VSMC_M2
GO:2000738	0.03	0.99	4	17	positive regulation of stem cell differentiation	BP	0.58861	SOX5,LTBP3,HOXB4,GATA4	cyan	VSMC_M2
GO:0030510	0.03	0.99	10	74	regulation of BMP signaling pathway	BP	0.58861	KIAA1324L,SFRP2,SFRP5,PCSK6,RGMA,BMP4,NBL1,NEO1,ABL1,GATA4	cyan	VSMC_M2
GO:0086005	0.03	0.99	5	26	ventricular cardiac muscle cell action potential	BP	0.58861	BIN1,SNTA1,CTNNA3,KCND3,JUP	cyan	VSMC_M2
GO:0002221	0.03	0.99	16	134	pattern recognition receptor signaling pathway	BP	0.58861	FLOT1,IRF1,LRRC19,APPL2,TRIL,IRF3,NOP53,RFTN1,SLC15A4,TLR3,TIRAP,NFKBIA,DHX58,ARRB2,PTPRS,NFKBIL1	cyan	VSMC_M2
GO:0016048	0.03	0.99	4	17	detection of temperature stimulus	BP	0.58861	TRPM3,NR2F6,ARRB2,NTRK1	cyan	VSMC_M2
GO:0030879	0.03	0.99	14	114	mammary gland development	BP	0.58861	STAT6,GLI3,BAX,GPAT4,SRC,LEF1,CAPN1,BMP4,STAT5A,EPHA2,AR,OAS2,PML,PYGO2	cyan	VSMC_M2
GO:0072111	0.03	0.99	4	17	cell proliferation involved in kidney development	BP	0.58861	WT1,STAT1,BMP4,PDGFRB	cyan	VSMC_M2
GO:0034599	0.03	0.98	25	234	cellular response to oxidative stress	BP	0.58861	STAT6,PTPRK,HMOX1,RHOB,AGAP3,ATG7,CAMKK2,PRKCD,SRC,MMP2,CCS,STK25,AIFM2,TMEM161A,HDAC6,PCGF2,TP53,PDK2,ABCC1,ABCD1,ABL1,PML,GATA4,ADPRHL2,MPV17	cyan	VSMC_M2
GO:0002862	0.03	0.99	4	17	negative regulation of inflammatory response to antigenic stimulus	BP	0.5894	RHBDF2,SRC,PLCG1,FURIN	cyan	VSMC_M2
GO:0031349	0.03	0.98	20	177	positive regulation of defense response	BP	0.5902	PLA2G7,IRF3,LAMP1,SLC15A4,TLR3,PLSCR1,SRC,TGM2,CD81,IKBKE,TIRAP,NFKBIA,GRN,PQBP1,IL17RA,NUPR1,GPRC5B,ABCC1,HEXIM1,RPS19	cyan	VSMC_M2

GO:0031325	0.03	0.98	199	2483	positive regulation of cellular metabolic process	BP	0.5902	PYM1,STAT6,TCF21,FLOT1,DDAH2,PLXNB2,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,MTCH1,CARD10,NFIB,TRERF1,HMOX1,MLIP,TRIM14,NAT14,GPNMB,MEIS1,RNF144A,PTOV1,GLI3,IRF3,GSN,NRP1,KLF15,BAX,DBP,NOP53,BICRA,MEIS3,TRIM13,FZD4,CAB39L,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,ZFP36,SAMD4B,ARAP1,KAT2B,TBC1D5,RHOG,DCXR,FGFR1,TRIM21,SMPD1,APBB1,CLIP3,ANGPT4,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,EFNA5,TP53INP2,PATL1,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,EPHA3,SRC,LRP4,MMS19,FOXF2,SLC5A3,PNPLA2,STAT1,ABHD14B,MOB2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,CAPN3,TIRAP,ZNF496,NFKB1,GNAI2,RGMA,BCL9,LEF1,APH1A,VEGFD,CASP10,FURIN,VPS11,BCL9L,RFX5,GATA5,HELZ2,RNASEL,MAGEF1,ELL3,NFKBIA,MOV10,DPF2,FYCO1,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,VEGFB,BMP4,LDB2,TCEA2,HDAC6,PQBP1,ARRB2,JUP,WIZ,EPHA2,MYRF,GABARAP,ZBTB17,TCF12,CASP9,GIPC1,ERBB2,BRAT1,ZFP36L1,UBQLN2,NTRK1,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,GPRC5B,SNX33,PDGFRB,MTA1,MAP2K3,ROR1,TRAF4,MOSPD1,MPND,EEF2,GLIS2,ABCD1,DVL1,AGRN,ELOB,E4F1,TNFRSF14,TSC2,TCF3,SBNO2,EDF1,AXIN1,RERE,CBFA2T3,FOXC2,ABL1,ATMIN,IL34,PBX3,IST1,NFIA,ABCA2,MEX3D,ZNF205,PML,JUNB,EEF1A2,GATA4,CALM3,CARD8,CDK9,SDC4,ZFPM1,EN1	cyan	VSMC_M2
GO:0031579	0.03	0.99	4	17	membrane raft organization	BP	0.59074	FLOT1,PACSIN2,GSN,RFTN1	cyan	VSMC_M2
GO:0048017	0.03	0.99	16	137	inositol lipid-mediated signaling	BP	0.59074	NOP53,FGFR1,IGF1,SRC,PTPN13,PIK3C2B,PLCD3,PLD2,SERPINE2,ERBB2,ZFP36L1,NTRK1,PDGFRB,ROR1,TSC2,INPP5E	cyan	VSMC_M2
GO:0098815	0.03	0.99	6	34	modulation of excitatory postsynaptic potential	BP	0.59074	TMEM108,CACNB3,CHRNA7,SH3GL1,DVL1,SLC8A3	cyan	VSMC_M2
GO:0001569	0.03	0.99	5	25	branching involved in blood vessel morphogenesis	BP	0.59105	NRP1,SFRP2,LEF1,FOXC2,ABL1	cyan	VSMC_M2
GO:0045859	0.03	0.98	48	513	regulation of protein kinase activity	BP	0.59155	DEPTOR,DAXX,CARD10,AKT1S1,FZD4,CAB39L,APOE,CAMK1,HGS,KAT2B,FGFR1,SH3BP5,SMPD1,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,SRC,MAPK8IP1,TIRAP,HEG1,ADORA2A,BMP4,ERBB2,GBA,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MAP2K3,MLLT1,TRAF4,DVL1,TSC2,AXIN1,ABL1,IL34,INCA1,SLC8A3,HEXIM1,CALM3,SDC4	cyan	VSMC_M2
GO:0006749	0.03	0.99	7	42	glutathione metabolic process	BP	0.5916	OPLAH,ETHE1,GGT7,HAGH,GSTM4,CLIC2,CLIC3	cyan	VSMC_M2
GO:1905037	0.03	0.99	12	92	autophagosome organization	BP	0.5916	EHMT2,ATG7,CHMP4B,TP53INP2,WDR45,GABARAP,UBQLN2,GBA,NUPR1,ULK3,NPRL3,RAB43	cyan	VSMC_M2
GO:0046651	0.03	0.98	20	177	lymphocyte proliferation	BP	0.59256	IRF1,GPNMB,BAX,PNP,LMO1,IGF1,PRKCD,MAPK8IP1,CD81,TIRAP,LEF1,BMP4,DLG5,ERBB2,IL27RA,TP53,TNFRSF14,ABL1,CD55,SDC4	cyan	VSMC_M2
GO:0050951	0.03	0.99	4	17	sensory perception of temperature stimulus	BP	0.59256	TRPM3,NR2F6,ARRB2,NTRK1	cyan	VSMC_M2
GO:0061448	0.03	0.98	22	203	connective tissue development	BP	0.59256	TGFBI,NFIB,ITGB8,EFEMP1,GLI3,EPYC,PKDCC,RARG,WT1,ARRDC3,SFRP2,SOX5,ECM1,CTSK,LTBP3,WNT2B,ADAMTS7,ACAT1,BMP4,PBXIP1,PDGFRB,FOXC2	cyan	VSMC_M2
GO:0034312	0.03	0.99	4	17	diol biosynthetic process	BP	0.59277	PCBD1,QDPR,GBA,ABCA2	cyan	VSMC_M2
GO:0008015	0.03	0.98	36	369	blood circulation	BP	0.59669	AKAP12,RPS6KA2,CYB5R3,HMOX1,GSN,BIN1,APOE,EHD3,GAA,SCN1B,SNTA1,SERPING1,SRC,GNAO1,NISCH,EXT2,STAT1,TJP1,CTNNA3,KCND3,ADORA2A,VEGFB,JUP,PRKACA,SLIT2,AR,HOXB2,RASL10B,MAP2K3,RENBP,FOXC2,SLC8A3,GATA4,CALM3,CLIC2,RNLS	cyan	VSMC_M2
GO:0048286	0.03	0.99	6	35	lung alveolus development	BP	0.59689	TCF21,STK40,PKDCC,MAN2A1,LTBP3,BMP4	cyan	VSMC_M2
GO:0034308	0.03	0.99	9	61	primary alcohol metabolic process	BP	0.59689	ACSS1,PLB1,IGF1,ACSS2,PNPLA2,CLCN2,DHRS13,H6PD,DGAT1	cyan	VSMC_M2
GO:0046633	0.03	0.99	5	25	alpha-beta T cell proliferation	BP	0.59689	IRF1,MAPK8IP1,CD81,TNFRSF14,CD55	cyan	VSMC_M2
GO:0030902	0.03	0.99	14	116	hindbrain development	BP	0.60447	NFIB,FZD4,COQ8B,LEF1,NAGLU,SERPINE2,TP53,HOXB1,HOXB2,GBA,PTPRS,RERE,ABL1,EN1	cyan	VSMC_M2
GO:0090316	0.03	0.98	16	136	positive regulation of intracellular protein transport	BP	0.60468	GLI3,STOM,CAMK1,EDEM2,PRKCD,CACNB3,CD81,VPS11,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,EMD,UBL5	cyan	VSMC_M2
GO:1901020	0.03	0.99	5	25	negative regulation of calcium ion transmembrane transporter activity	BP	0.60539	CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0045137	0.03	0.98	19	170	development of primary sexual characteristics	BP	0.60539	TCF21,ZFPM2,MEA1,BAX,FZD4,TLR3,WT1,SFRP2,SRC,REC8,WNT2B,ARRB2,NTRK1,SLIT2,AR,ADAM15,NUPR1,PDGFRB,GATA4	cyan	VSMC_M2
GO:0042088	0.03	0.99	5	25	T-helper 1 type immune response	BP	0.60973	STAT6,BCL3,LEF1,IL27RA,TMEM98	cyan	VSMC_M2
GO:0022037	0.03	0.99	11	84	metencephalon development	BP	0.61228	FZD4,COQ8B,NAGLU,SERPINE2,TP53,HOXB1,GBA,PTPRS,RERE,ABL1,EN1	cyan	VSMC_M2

GO:0006796	0.03	0.97	174	2150	phosphate-containing compound metabolic process	BP	0.61484	CTDP1,FLOT1,CHKB,PPP6R2,PLXNB2,RPS6KA2,DEPTOR,DAXX,HDDC2,PTPRK,ST3GAL1,CDC14C,CARD10,PLA2G7,GPNMB,SLC44A1,EFEMP1,STK40,AKT1S1,STK17A,AASS,NRP1,BAX,NOP53,ACSS1,FZD4,CAB39L,MARK4,APOE,PLB1,SOCS3,CAMK1,OSBPL10,PNP,PAK4,GPAT4,HGS,KAT2B,FGFR1,SH3BP5,DCLK1,SMPD1,PKDCC,CLIP3,ANGPT4,MAP3K12,GNPTAB,IGF1,TLR3,EFNA5,ACSS2,LPCAT4,NEIL2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,LRP4,PLBD2,PLCG1,MAPK8IP1,PTPN13,PTDSS1,PIK3C2B,ABHD14B,MOB2,GFRA2,CD81,PHKG1,CHRNA7,IKBKE,OSBPL5,NADSYN1,TIRAP,GNAI2,IP6K1,PTGIS,SSH3,VEGFD,GRK5,ADCY1,FES,TNS3,PRUNE1,HEG1,STK25,UCKL1,RNASEL,NMNAT2,BCR,ADORA2A,PPA1,CDC42BPG,G6PC3,ACAT1,VEGFB,NUDT13,WNK4,BMP4,RARRES3,LDB2,PGLS,HDAC6,PLD2,ARRB2,ALOX15,EPHA2,PLSCR3,ERBB2,BRAT1,PRKACA,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,NUPR1,SHC1,ADAR,ACP5,TEX14,SLC44A2,WARS,ULK3,PPCDC,GPRC5B,PDGFRB,NUDT14,MAP2K3,ROR1,MLLT1,TRAF4,PTPRS,WDR81,ABCD1,DVL1,PNPLA7,TNFRSF14,TSC2,PHPT1,PIGQ,INPP5E,AXIN1,H6PD,PLPP2,CBFA2T3,ABL1,DPYD,IL34,LCAT,TK2,INCA1,ABCA2,ACOT6,SLC8A3,HEXIM1,ZBTB7A,DGAT1,PML,PLPP3,EEF1A2,CALM3,CPPED1,CDK9,SDC4,NAGK,PDXK,GTF2H4	cyan	VSMC_M2
GO:0052547	0.03	0.98	30	294	regulation of peptidase activity	BP	0.61653	MTCH1,GSN,BAX,BIN1,TIMP2,SERPING1,CAST,SFRP2,SRC,CSTB,APH1A,ECM1,CASP10,FURIN,ADORA2A,GRN,PCOLCE,CPAMD8,DNAJB6,ARRB2,SERPINE2,CASP9,RENBP,ABCA2,SERPINF1,PML,SERPINB6,CARD8,PSMB9,BST2	cyan	VSMC_M2
GO:0045332	0.03	0.99	6	35	phospholipid translocation	BP	0.61713	ATP10D,PLSCR1,PRKCD,PLSCR3,ATP8B2,ABCC1	cyan	VSMC_M2
GO:0032092	0.03	0.99	10	73	positive regulation of protein binding	BP	0.61713	FLOT1,NRP1,APOE,RFNG,TRIM21,SPON1,B2M,ADD1,BMP4,ABL1	cyan	VSMC_M2
GO:0048675	0.03	0.98	13	106	axon extension	BP	0.61769	NRP1,APOE,DCLK1,NDN,CTTN,SEMA3B,LAMB2,SEMA4B,SEMA6C,SLIT2,PTPRS,DVL1,ABL1	cyan	VSMC_M2
GO:0060444	0.03	0.99	4	18	branching involved in mammary gland duct morphogenesis	BP	0.61915	SRC,EPHA2,AR,PML	cyan	VSMC_M2
GO:0060216	0.03	0.99	4	18	definitive hemopoiesis	BP	0.62164	MEIS1,HOXB4,ADAR,ZFPM1	cyan	VSMC_M2
GO:0030334	0.03	0.98	65	735	regulation of cell migration	BP	0.62164	AKAP12,PLXNB2,AFDN,PTPRK,CARD10,HMOX1,APPL2,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,APOE,RHOG,FGFR1,ADGRA2,ANGPT4,IGF1,SFRP2,NDRG4,SRC,PLCG1,NISCH,PHACTR1,CD81,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,ECM1,SEMA4B,SEMA6C,FAM89B,GRN,HDAC5,VEGFB,BMP4,LDB2,NBL1,STAT5A,DLG5,HDAC6,JUP,EPHA2,SERPINE2,MCC,IL27RA,SLIT2,ADAM15,PDGFRB,MAP2K3,PODN,TNFRSF14,FOXC2,ABL1,OSGIN1,IL34,SERPINF1,PLPP3,SDC4,BST2	cyan	VSMC_M2
GO:0051641	0.03	0.97	184	2295	cellular localization	BP	0.62164	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,AFDN,PACSIN2,PTPRK,GGA1,CARD10,HMOX1,APPL2,TBC1D2,BBS9,RRAGC,TBC1D17,GLI3,AP2A1,CADPS2,GSN,SLC17A7,STOM,NRP1,RHOB,BAX,DENND2A,NOP53,MARK4,BIN1,APOE,BCL3,SLC6A9,CAMK1,EHD3,CMTM6,DZIP1,ZFP36,GAA,HGS,TBC1D5,RFTN1,RHOG,DCLK1,LAMP1,TMEM108,PKDCC,TPP1,CLIP3,SCN1B,GNPTAB,REEP5,SNTA1,EFNA5,CHMP4B,CHMP3,TP53INP2,EDEM2,ERGIC3,WWTR1,NDRG4,GLRB,STBD1,PRKCD,EPHA3,SRC,CACNB3,CPE,LRP4,PLCG1,BBS2,ARHGAP1,EXOC2,SLC5A3,CRACR2B,SYS1,LZTS2,CTSA,HPS6,CD81,TRIM8,OSBPL5,CAPN3,AGFG1,CTTN,TPCN2,SGSM1,SV2A,EXOC8,GAS2L1,ADCY1,FES,VPS11,KIF1A,FAM53B,TMEM50A,PARD3B,STK25,NFKBIA,KCND3,M6PR,ADORA2A,FYCO1,RPGR,PSAP,HOMER3,GPC2,TMBIM1,BMP4,MAP1S,CC2D2A,HDAC6,B3GAT3,WDR45,PLD2,CROCC,DNAJB6,JUP,EPHA2,AKAP5,GABARAP,PLEKHM2,GIPC1,ERBB2,BRAT1,STARD3,PRKACA,ZFP36L1,AR,TP53,CPLX2,ERGIC1,GLMP,NPC2,PPP1R9B,SLC51B,STON2,ANKFN1,SNX33,MCOLN1,LLGL1,TMEM98,ZDHHC9,UBXN6,SH3GL1,NAGPA,CPT2,GLIS2,WDR81,ABCD1,DVL1,SGSM2,AGRN,ISG15,TSC2,SLC9A3R2,NPHP4,PTGDS,PHPT1,RHOT2,INPP5E,RAB11FIP3,ENTR1,CLSTN1,ABL1,HSBP1,MON1B,ABCA2,RPS15,GAS1,MEX3D,SLC8A3,ZBTB7A,RAB43,GRASP,PML,CALM3,CLIC2,LRRC7,VPS26B,TMEM250,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0023056	0.03	0.97	106	1258	positive regulation of signaling	BP	0.62554	AKAP12,FLOT1,HMOX1,LRRC19,KIAA1324L,APPL2,TRIM14,GPNMB,RRAGC,IRF3,NRP1,BAX,MEIS3,LURAP1,TRIM13,FZD4,APOE,SHKBP1,TIMP2,CANT1,ARAP1,RFNG,FGFR1,TRIM21,ADGRA2,TMEM108,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,TSHZ3,SFRP2,NDRG4,PRKCD,SRC,CACNB3,TGM2,MAPK8IP1,SORBS3,CD81,CHRNA7,TRIM8,IKBKE,TIRAP,TM2D3,NFKB1,GNAI2,LEF1,PTGIS,MN1,KIF7,ECM1,CASP10,ADCY1,ERFE,LMO3,GATA5,FAM53B,STK25,ADORA2A,TMEM101,TMEM106A,BMP4,DLG5,DHX58,ARRB2,JUP,ALOX15,AKAP5,SERPINE2,GIPC1,ERBB2,NTRK1,AR,TP53,GBA,NUPR1,SHC1,PBXIP1,SLC44A2,NEO1,ULK3,GPRC5B,RASL10B,EPN2,PDGFRB,MAP2K3,ROR1,TRAF4,DVL1,TRAF7,PHPT1,AXIN1,CLSTN1,ABL1,IL34,INCA1,RPS15,SLC8A3,HEXIM1,PML,GATA4,STX3,OCIAD2,BST2	cyan	VSMC_M2
GO:0045732	0.03	0.98	22	203	positive regulation of protein catabolic process	BP	0.62682	GGA1,RNF144A,NOP53,APOE,ATG7,CD81,RGMA,RHBDD3,FURIN,VPS11,ATG4B,MAGEF1,GABARAP,UBQLN2,GBA,NUPR1,SNX33,DVL1,ELOB,AXIN1,CBFA2T3,ABCA2	cyan	VSMC_M2
GO:0072657	0.03	0.98	44	466	protein localization to membrane	BP	0.62682	FLOT1,AFDN,GGA1,GSN,STOM,BAX,APOE,EHD3,HGS,RFTN1,RHOG,PKDCC,CLIP3,CHMP4B,GLRB,EPHA3,CACNB3,CPE,LRP4,BBS2,SLC5A3,SYS1,HPS6,CD81,CAPN3,GPC2,TMBIM1,JUP,EPHA2,AKAP5,ERBB2,AR,PPP1R9B,SLC51B,ZDHHC9,DVL1,AGRN,SLC9A3R2,CLSTN1,GRASP,CALM3,LRRC7,STX3,RAB11B	cyan	VSMC_M2

GO:0031668	0.03	0.98	22	205	cellular response to extracellular stimulus	BP	0.62804	EHMT2,GSDMD,HMOX1,RRAGC,ATG7,FOLR2,SFRP2,CACNB3,MN1,GAS2L1,FES,PHEX,WNT2B,WDR45,GABARAP,TP53,PDK2,GBA,PPP1R9B,KANK2,NDOR1,NPRL3	cyan	VSMC_M2
GO:0032943	0.03	0.98	20	179	mononuclear cell proliferation	BP	0.63439	IRF1,GPNMB,BAX,PNP,LMO1,IGF1,PRKCD,MAPK8IP1,CD81,TIRAP,LEF1,BMP4,DLG5,ERBB2,IL27RA,TP53,TNFRSF14,ABL1,CD55,SDC4	cyan	VSMC_M2
GO:0030036	0.03	0.98	54	600	actin cytoskeleton organization	BP	0.63958	PACSIN2,ARHGAP18,ELMO1,COBL,GSN,NRP1,RHOB,LURAP1,BIN1,ARAP1,RHOG,EFNA5,RHPN2,PRKCD,EPHA3,SRC,PDLIM2,C15orf62,SORBS3,NISCH,PHACTR1,CAPN3,TJP1,CTTN,SSH3,GAS2L1,FES,CTNNA3,WIPF1,ARPC5,ARHGEF10,CDC42BPG,RND2,ADD1,CAPZB,ARHGEF10L,DNAJB6,ALOX15,CGNL1,SLIT2,PPP1R9B,SHC1,ARHGAP17,SIGLEC15,PDGFRB,FLII,LLGL1,NPHP4,PHPT1,AIF1L,ABL1,CNN3,SDC4,BST2	cyan	VSMC_M2
GO:0034205	0.03	0.99	7	44	amyloid-beta formation	BP	0.63958	BIN1,APOE,IGF1,SPON1,CHRNA7,APH1A,ABCA2	cyan	VSMC_M2
GO:1990000	0.03	0.99	5	26	amyloid fibril formation	BP	0.63958	GSN,APOE,CHRNA7,FURIN,B2M	cyan	VSMC_M2
GO:0072175	0.03	0.98	14	116	epithelial tube formation	BP	0.63968	PLXNB2,COBL,RARG,SFRP2,RGMA,VANGL2,BMP4,CC2D2A,PRKACA,MED12,DVL1,TSC2,ABL1,SDC4	cyan	VSMC_M2
GO:0035282	0.03	0.99	10	74	segmentation	BP	0.64343	COBL,NRP1,WT1,SFRP2,PCSK6,LEF1,BMP4,TP53,MED12,FOXC2	cyan	VSMC_M2
GO:1902003	0.03	0.99	6	35	regulation of amyloid-beta formation	BP	0.64692	BIN1,APOE,IGF1,SPON1,CHRNA7,ABCA2	cyan	VSMC_M2
GO:0050866	0.03	0.98	16	136	negative regulation of cell activation	BP	0.65454	IRF1,HMOX1,GPNMB,GLI3,APOE,PRKCD,BPI,RHBDD3,ADORA2A,GRN,BMP4,DLG5,SERPINE2,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0019082	0.04	0.99	5	26	viral protein processing	BP	0.65989	MGAT4B,ST3GAL1,MAN2A1,EDEM2,FURIN	cyan	VSMC_M2
GO:0072080	0.04	0.99	10	75	nephron tubule development	BP	0.6615	TCF21,GLI3,WT1,WWTR1,LZTS2,STAT1,WNT2B,ACAT1,WNK4,BMP4	cyan	VSMC_M2
GO:0060713	0.04	0.99	4	18	labyrinthine layer morphogenesis	BP	0.66195	SOCS3,LEF1,DNAJB6,ZFP36L1	cyan	VSMC_M2
GO:0030038	0.04	0.98	12	95	contractile actin filament bundle assembly	BP	0.66195	NRP1,ARAP1,RHPN2,SRC,SORBS3,PHACTR1,TJP1,ARHGEF10,ARHGEF10L,CGNL1,ABL1,SDC4	cyan	VSMC_M2
GO:0043149	0.04	0.98	12	95	stress fiber assembly	BP	0.66195	NRP1,ARAP1,RHPN2,SRC,SORBS3,PHACTR1,TJP1,ARHGEF10,ARHGEF10L,CGNL1,ABL1,SDC4	cyan	VSMC_M2
GO:0002718	0.04	0.99	9	63	regulation of cytokine production involved in immune response	BP	0.66219	HMOX1,TRIL,TLR3,CD81,B2M,GPRC5B,TNFRSF14,CD55,BST2	cyan	VSMC_M2
GO:0030148	0.04	0.98	11	83	sphingolipid biosynthetic process	BP	0.66219	B3GALT4,ST3GAL1,SMPD1,PRKCD,B4GALT5,GBA,CERS4,PLPP2,ABCA2,PLPP3,AL157935.2	cyan	VSMC_M2
GO:0000902	0.04	0.97	69	799	cell morphogenesis	BP	0.66219	FLOT1,PLXNB2,PACSIN2,ARHGAP18,NFIB,COBL,GLI3,NRP1,RHOB,FZD4,APOE,SLITRK6,ARAP1,NPTX1,RHOG,EFNB2,DCLK1,TMEM108,LZTS3,APBB1,SCN1B,EFNA5,HEXB,EPHA3,SRC,LRP4,C15orf62,PHACTR1,NDN,CHRNA7,CTTN,BOC,SEMA3B,RGMA,LEF1,B4GALT5,ATRNL1,LAMB2,SEMA4B,ADCY1,FES,BCL9L,SEMA6C,HEG1,KIF1A,STK25,MOV10,ADORA2A,RND2,NBL1,CAPZB,MAP1S,HDAC6,PQBP1,EPHA2,CASP9,ERBB2,NTRK1,SLIT2,AR,ZMYM3,NEO1,LLGL1,PTPRS,DVL1,RERE,ABL1,IST1,ZFPM1	cyan	VSMC_M2
GO:0031330	0.04	0.98	22	207	negative regulation of cellular catabolic process	BP	0.66501	EHMT2,EIF3H,HMOX1,NOP53,ATRAID,ATG7,TIMP2,ZFP36,CHMP4B,CTSA,IKBKE,TIRAP,WDR6,FURIN,GIPC1,TP53,UBQLN4,NUPR1,TSC2,PML,GATA4,BMF	cyan	VSMC_M2
GO:0002520	0.04	0.97	62	694	immune system development	BP	0.66526	STAT6,TCF21,IRF1,PTPRK,ST3GAL1,ITGB8,MEIS1,GLI3,RRAS,FLT3LG,BAX,LRRC17,TMEM176B,BCL3,PNP,ZFP36,SLC15A4,RARG,TLR3,SFRP2,SRC,STAT1,CD81,TIRAP,TUSC2,LEF1,FES,NFKBIA,B2M,WNT2B,DPF2,HDAC5,BMP4,MAEA,EPHA2,CASP9,ERBB2,ZFP36L1,IL27RA,NTRK1,TP53,KAT8,HOXB4,GBA,ADAR,SIGLEC15,TMEM98,CRIP2,EEF2,ISG15,TCF3,SBNO2,CBFA2T3,ABL1,IL34,SLC8A3,ZBTB7A,PML,RPS19,JUNB,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0099565	0.04	0.98	10	74	chemical synaptic transmission, postsynaptic	BP	0.66735	TMEM108,GLRB,CACNB3,CHRNA7,ADORA2A,CHRNE,ARRB2,SH3GL1,DVL1,SLC8A3	cyan	VSMC_M2
GO:0071825	0.04	0.99	6	35	protein-lipid complex subunit organization	BP	0.66735	PLA2G7,BIN1,APOE,PRKACA,LCAT,DGAT1	cyan	VSMC_M2
GO:0032729	0.04	0.99	6	35	positive regulation of interferon-gamma production	BP	0.66735	BCL3,TLR3,IL27RA,ISG15,ABL1,ZFPM1	cyan	VSMC_M2
GO:0019222	0.04	0.97	372	4858	regulation of metabolic process	BP	0.6692	CTDP1,TSHZ1,PYM1,STAT6,TCF21,AKAP12,FLOT1,DDAH2,PPP6R2,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,TAPBP,TCF20,DAXX,TEF,PTPRK,GSDMD,TEAD3,MTCH1,TLE1,GGA1,CARD10,NFIB,TRERF1,HMOX1,LRRC19,ACO1,KLF9,APPL2,MLIP,ZBTB45,ZSCAN18,TRIM14,ITGB8,P3H1,NAT14,GPNMB,EFEMP1,TRIL,RRAGC,MEIS1,RNF144A,STK40,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,EXOC7,LTBP4,SOCS3,CAMK1,PLD3,PNP,TIMP2,ZFP36,SAMD4B,ARAP1,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,DCXR,FGFR1,IL5RA,SH3BP5,TRIM21,SMPD1,APBB1,CLIP3,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,SNTA1,WT1,EFNA5,CHMP4B,TP53INP2,PATL1,TSHZ3,POU6F1,SERPING1,CAST,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,EPHA3,SRC,BPI,LRP4,DECR1,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTPN13,SLC5A3,PNPLA2,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,CSTB,TUSC2,ZNF496,TPCN2,NFKB1,GNAI2,SPOCD1,TPPP,HIST1H1C,PKNOX2,RGMA,BCL9,HADH,IP6K1,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,APH1A,EXOC8,MN1,VEGFD,WDR6,ECM1,RHBDD3,NELFCD,CASP10,ADCY1,FURIN,VPS11,ERFE,BCL9L,HEG1,RFX5,GATA5,CLCN2,HELZ2,ATG4B,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,FRMD8,B2M,DPF2,ADORA2A,CAPN1,FYCO1,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,PSAP,TSC22D4,HOMER3,VEGFB,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STA	cyan	VSMC_M2
GO:0032147	0.04	0.98	13	105	activation of protein kinase activity	BP	0.67103	DAXX,CARD10,ANGPT4,IGF1,TLR3,EFNA5,PRKCD,SRC,TIRAP,GPRC5B,TRAF4,AXIN1,ABL1	cyan	VSMC_M2
GO:0014066	0.04	0.98	11	86	regulation of phosphatidylinositol 3-kinase signaling	BP	0.67103	NOP53,FGFR1,IGF1,SRC,PTPN13,SERPINE2,NTRK1,PDGFRB,ROR1,TSC2,INPP5E	cyan	VSMC_M2
GO:0019369	0.04	0.99	5	26	arachidonic acid metabolic process	BP	0.67103	CYP2S1,PTGIS,ALOX15,DAGLA,PTGDS	cyan	VSMC_M2
GO:0097300	0.04	0.99	6	35	programmed necrotic cell death	BP	0.67103	IRF3,BAX,RBCK1,TLR3,TP53,NUPR1	cyan	VSMC_M2

GO:0032103	0.04	0.98	29	286	positive regulation of response to external stimulus	BP	0.67103	PLA2G7,IRF3,NRP1,FGFR1,LAMP1,SLC15A4,TLR3,PLSCR1,SRC,TGM2,CD81,IKBKE,TIRAP,VEGFD,NFKBIA,GRN,VEGFB,PQBP1,DHX58,IL17RA,SLIT2,NUPR1,GPRC5B,ABCC1,PDGFRB,IL34,HEXIM1,RPS19,STX3	cyan	VSMC_M2
GO:0010647	0.04	0.97	105	1251	positive regulation of cell communication	BP	0.67103	AKAP12,FLOT1,HMOX1,LRRC19,KIAA1324L,APPL2,TRIM14,GPNMB,RRAGC,IRF3,NRP1,BAX,MEIS3,LURAP1,TRIM13,FZD4,APOE,SHKBP1,TIMP2,CANT1,RFNG,FGFR1,TRIM21,ADGRA2,TMEM108,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,TSHZ3,SFRP2,NDRG4,PRKCD,SRC,CACNB3,TGM2,MAPK8IP1,SORBS3,CD81,CHRNA7,TRIM8,IKBKE,TIRAP,TM2D3,NFKB1,GNAI2,LEF1,PTGIS,MN1,KIF7,ECM1,CASP10,ADCY1,ERFE,LMO3,GATA5,FAM53B,STK25,ADORA2A,TMEM101,TMEM106A,BMP4,DLG5,DHX58,ARRB2,JUP,ALOX15,AKAP5,SERPINE2,GIPC1,ERBB2,NTRK1,AR,TP53,GBA,NUPR1,SHC1,PBXIP1,SLC44A2,NEO1,ULK3,GPRC5B,RASL10B,EPN2,PDGFRB,MAP2K3,ROR1,TRAF4,DVL1,TRAF7,PHPT1,AXIN1,CLSTN1,ABL1,IL34,INCA1,RPS15,SLC8A3,HEXIM1,PML,GATA4,STX3,OCIAD2,BST2	cyan	VSMC_M2
GO:0048546	0.04	0.99	6	36	digestive tract morphogenesis	BP	0.67103	TCF21,GLI3,SFRP2,SFRP5,BMP4,GATA4	cyan	VSMC_M2
GO:0007169	0.04	0.97	46	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	0.67103	STAT6,EFEMP1,AKT1S1,NRP1,FZD4,RHBDF2,SHKBP1,SOCS3,HGS,FGFR1,EFNB2,ADGRA2,TMEM108,ANGPT4,IGF1,EFNA5,NDRG4,PRKCD,EPHA3,SRC,PLCG1,MMP2,GFRA2,NDN,GNAI2,VEGFD,FES,ERFE,SAMD10,FIBP,BCR,VEGFB,STAT5A,EPHA2,ERBB2,NTRK1,AR,PDK2,SHC1,EPN2,PDGFRB,TSC2,RHBDF1,FOXC2,ABL1,SLC2A8	cyan	VSMC_M2
GO:0045935	0.04	0.97	123	1489	positive regulation of nucleobase-containing compound metabolic process	BP	0.67103	STAT6,TCF21,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,NFIB,TRERF1,MLIP,TRIM14,NAT14,MEIS1,PTOV1,GLI3,IRF3,KLF15,BAX,DBP,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,SAMD4B,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,MMS19,FOXF2,STAT1,ABHD14B,CD81,NDN,TRIM8,CAPN3,ZNF496,NFKB1,RGMA,BCL9,LEF1,BCL9L,RFX5,GATA5,HELZ2,RNASEL,ELL3,NFKBIA,MOV10,DPF2,PCBD1,HDAC5,TMEM161A,BMP4,LDB2,TCEA2,PQBP1,ARRB2,JUP,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,NUPR1,SHC1,PBXIP1,PDGFRB,MTA1,MAP2K3,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,EDF1,AXIN1,RERE,FOXC2,ABL1,ATMIN,PBX3,NFIA,MEX3D,PML,JUNB,GATA4,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0046661	0.04	0.98	15	128	male sex differentiation	BP	0.67103	TCF21,ZFPM2,MEA1,BAX,TLR3,WT1,SFRP2,REC8,WNT2B,NTRK1,AR,ADAM15,NUPR1,PDGFRB,GATA4	cyan	VSMC_M2
GO:0072028	0.04	0.99	9	65	nephron morphogenesis	BP	0.6716	TCF21,GLI3,WT1,LZTS2,STAT1,WNT2B,WNK4,BMP4,PDGFRB	cyan	VSMC_M2
GO:0048013	0.04	0.99	7	45	ephrin receptor signaling pathway	BP	0.67913	EFNB2,EFNA5,EPHA3,SRC,MMP2,EPHA2,NTRK1	cyan	VSMC_M2
GO:0042092	0.04	0.99	5	26	type 2 immune response	BP	0.67964	STAT6,BCL3,CD81,ECM1,IL27RA	cyan	VSMC_M2
GO:0006936	0.04	0.98	26	256	muscle contraction	BP	0.67964	MYL6B,GSN,BIN1,EHD3,GAA,APBB1,HSPB6,SCN1B,SNTA1,GNAO1,CTTN,TPCN2,CTNNA3,KCND3,VEGFB,CHRNE,JUP,PRKACA,MAP2K3,EEF2,HSBP1,SLC8A3,GATA4,CALM3,CLIC2,EMD	cyan	VSMC_M2
GO:0086003	0.04	0.99	8	57	cardiac muscle cell contraction	BP	0.68202	GSN,BIN1,SCN1B,SNTA1,CTNNA3,KCND3,JUP,GATA4	cyan	VSMC_M2
GO:0009311	0.04	0.99	7	44	oligosaccharide metabolic process	BP	0.68244	NEU1,B3GALT4,NAGA,GAA,HEXB,MAN2C1,AL157935.2	cyan	VSMC_M2
GO:0032870	0.04	0.97	42	450	cellular response to hormone stimulus	BP	0.68302	STAT6,TCF21,DAXX,FBXO32,TRERF1,KLF9,APPL2,SOCS3,ZFP36,KAT2B,RARG,WT1,CTSB,PRKCD,SRC,BBS2,STAT1,NFKB1,GNAI2,GAS2L1,VPS11,ERFE,LMO3,PHEX,LINC02210-CRHR1,HDAC5,BMP4,STAT5A,HDAC6,CASP9,PRKACA,ZFP36L1,SLIT2,AR,PDK2,SHC1,KANK2,TSC2,FOXC2,SLC2A8,SERPINF1,ZBTB7A	cyan	VSMC_M2
GO:0042110	0.04	0.98	31	310	T cell activation	BP	0.68341	STAT6,IRF1,PTPRK,GPNMB,GLI3,GSN,BAX,BCL3,PNP,WDFY4,LMO1,IGF1,SRC,MAPK8IP1,CD81,LEF1,B2M,ADORA2A,BMP4,DLG5,ERBB2,ZFP36L1,IL27RA,TP53,GBA,TMEM98,TNFRSF14,ABL1,CD55,SDC4,ZFPM1	cyan	VSMC_M2
GO:0046339	0.04	0.99	4	19	diacylglycerol metabolic process	BP	0.68896	GPAT4,PNPLA2,DAGLA,DGAT1	cyan	VSMC_M2
GO:0002042	0.04	0.99	8	55	cell migration involved in sprouting angiogenesis	BP	0.68896	CARD10,HMOX1,NRP1,EFNB2,HDAC5,SLIT2,FOXC2,ABL1	cyan	VSMC_M2
GO:0016197	0.04	0.98	22	209	endosomal transport	BP	0.68896	GGA1,TBC1D17,DENND2A,EHD3,CMTM6,HGS,TBC1D5,DCLK1,CHMP4B,CHMP3,NDRG4,ARHGAP1,TMEM50A,AKAP5,SNX33,UBXN6,SGSM2,RAB11FIP3,ENTR1,GRASP,VPS26B,RAB11B	cyan	VSMC_M2
GO:0030324	0.04	0.98	16	141	lung development	BP	0.69065	TCF21,ADAMTS2,ZFPM2,NFIB,STK40,GLI3,PKDCC,MAN2A1,HEG1,PHEX,LTBP3,WNT2B,BMP4,DLG5,PDGFRB,DNAAF1	cyan	VSMC_M2
GO:0002367	0.04	0.98	9	64	cytokine production involved in immune response	BP	0.69142	HMOX1,TRIL,TLR3,CD81,B2M,GPRC5B,TNFRSF14,CD55,BST2	cyan	VSMC_M2
GO:0033687	0.04	0.99	5	27	osteoblast proliferation	BP	0.69142	ATRAID,MN1,MUS81,ABL1,JUNB	cyan	VSMC_M2
GO:1900273	0.04	0.99	4	19	positive regulation of long-term synaptic potentiation	BP	0.69142	CHRNA7,ADCY1,ADORA2A,AKAP5	cyan	VSMC_M2
GO:0007178	0.04	0.98	27	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.69765	PTPRK,KIAA1324L,APPL2,ITGB8,VIM,LTBP4,SFRP2,WWTR1,SRC,SFRP5,PCSK6,RGMA,LEF1,FURIN,BCL9L,FAM89B,LTBP3,BMP4,NBL1,ARRB2,GIPC1,TP53,NEO1,ABL1,ZBTB7A,PML,GATA4	cyan	VSMC_M2
GO:0048771	0.04	0.98	15	129	tissue remodeling	BP	0.69847	GPNMB,BAX,TPP1,SRC,TGM2,MMP2,CTSK,LTBP3,CAPN1,TMBIM1,EPHA2,TP53,ACP5,SIGLEC15,FOXC2	cyan	VSMC_M2
GO:0006959	0.04	0.98	11	84	humoral immune response	BP	0.69974	CFB,COLEC11,BCL3,SERPING1,CD81,C1R,C1S,C6,FAM3A,CD55,RPS19	cyan	VSMC_M2
GO:0010659	0.04	0.99	6	36	cardiac muscle cell apoptotic process	BP	0.70722	RPS6KA2,HSPB6,SFRP2,TP53,NUPR1,GATA4	cyan	VSMC_M2
GO:0030282	0.04	0.98	12	97	bone mineralization	BP	0.70943	GPNMB,ATRAID,PKDCC,IGF1,ECM1,PHEX,LTBP3,CLEC3B,BMP4,ALOX15,ISG15,SBNO2	cyan	VSMC_M2
GO:0001523	0.04	0.99	7	45	retinoid metabolic process	BP	0.71035	CYP2S1,PLB1,CYP4V2,PNPLA2,RLBP1,DHRS13,DGAT1	cyan	VSMC_M2
GO:0006739	0.04	0.99	5	27	NADP metabolic process	BP	0.71035	DCXR,NUDT13,PGLS,TP53,H6PD	cyan	VSMC_M2

GO:0006509	0.04	0.99	6	36	membrane protein ectodomain proteolysis	BP	0.71255	APOE,TIMP2,RGMA,APH1A,FURIN,SNX33	cyan	VSMC_M2
GO:0042181	0.04	0.99	6	36	ketone biosynthetic process	BP	0.71531	COQ8B,COQ9,CLCN2,STARD3,UBIAD1,H6PD	cyan	VSMC_M2
GO:0051493	0.04	0.97	42	457	regulation of cytoskeleton organization	BP	0.71574	ARHGAP18,GSN,NRP1,RHOB,BIN1,ARAP1,KAT2B,RHOG,CLIP3,EFNA5,RHPN2,CHMP4B,PRKCD,EPHA3,C15orf62,SORBS3,TJP1,CTTN,TPPP,SSH3,GAS2L1,FES,PRUNE1,ARPC5,ARHGEF10,RND2,ADD1,CAPZB,MAP1S,HDAC6,ARHGEF10L,ALOX15,CGNL1,SLIT2,ARHGAP17,SIGLEC15,PDGFRB,FLII,PHPT1,ABL1,SDC4,BST2	cyan	VSMC_M2
GO:0046649	0.04	0.97	44	470	lymphocyte activation	BP	0.71625	STAT6,ULBP2,IRF1,PTPRK,ST3GAL1,GPNMB,GLI3,GSN,BAX,BCL3,PNP,LAMP1,WDFY4,SLC15A4,LMO1,IGF1,PRKCD,SRC,MAPK8IP1,CD81,TIRAP,TUSC2,LEF1,RHBDD3,B2M,ADORA2A,HDAC5,BMP4,DLG5,ERBB2,ZFP36L1,IL27RA,NTRK1,TP53,GBA,TMEM98,TNFRSF14,TCF3,ABL1,ZBTB7A,CD55,SDC4,BST2,ZFPM1	cyan	VSMC_M2
GO:0061326	0.04	0.98	10	77	renal tubule development	BP	0.71625	TCF21,GLI3,WT1,WWTR1,LZTS2,STAT1,WNT2B,ACAT1,WNK4,BMP4	cyan	VSMC_M2
GO:0009967	0.04	0.97	95	1127	positive regulation of signal transduction	BP	0.71625	AKAP12,FLOT1,HMOX1,LRRC19,KIAA1324L,APPL2,TRIM14,GPNMB,RRAGC,IRF3,NRP1,BAX,MEIS3,LURAP1,TRIM13,FZD4,APOE,SHKBP1,TIMP2,CANT1,RFNG,FGFR1,TRIM21,ADGRA2,TMEM108,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,SFRP2,NDRG4,PRKCD,SRC,CACNB3,TGM2,MAPK8IP1,SORBS3,CD81,CHRNA7,TRIM8,IKBKE,TIRAP,TM2D3,NFKB1,GNAI2,LEF1,PTGIS,MN1,KIF7,ECM1,CASP10,ERFE,LMO3,GATA5,FAM53B,STK25,ADORA2A,TMEM101,TMEM106A,BMP4,DLG5,DHX58,ARRB2,JUP,ALOX15,GIPC1,ERBB2,NTRK1,AR,TP53,NUPR1,SHC1,PBXIP1,SLC44A2,NEO1,ULK3,GPRC5B,EPN2,PDGFRB,MAP2K3,ROR1,TRAF4,DVL1,TRAF7,AXIN1,ABL1,IL34,INCA1,RPS15,HEXIM1,PML,GATA4,OCIAD2,BST2	cyan	VSMC_M2
GO:0021549	0.04	0.98	10	77	cerebellum development	BP	0.71641	FZD4,COQ8B,NAGLU,SERPINE2,TP53,GBA,PTPRS,RERE,ABL1,EN1	cyan	VSMC_M2
GO:0009725	0.04	0.97	58	652	response to hormone	BP	0.71644	STAT6,TCF21,DAXX,FBXO32,TRERF1,GCNT1,HMOX1,KLF9,APPL2,GLI3,KLF15,SOCS3,TIMP2,ZFP36,KAT2B,RARG,WT1,CTSB,PRKCD,SRC,BBS2,MMS19,STAT1,FIBIN,NFKB1,GNAI2,HADH,GAS2L1,VPS11,ERFE,LMO3,RERG,PHEX,LINC02210-CRHR1,HDAC5,ACAT1,BMP4,QDPR,STAT5A,HDAC6,CASP9,PRKACA,ZFP36L1,SLIT2,AR,PDK2,GBA,PPP1R9B,SHC1,KANK2,PDGFRB,TSC2,FOXC2,SLC2A8,ABCA2,SERPINF1,ZBTB7A,CALM3	cyan	VSMC_M2
GO:0051090	0.04	0.97	32	328	regulation of DNA-binding transcription factor activity	BP	0.71644	FLOT1,HMOX1,TRIM14,TRIM13,FZD4,BCL3,TRIM21,RBCK1,TLR3,SFRP5,NDN,TRIM8,IKBKE,CAPN3,TIRAP,PTGIS,ADCY1,NFKBIA,HDAC5,ARRB2,JUP,NTRK1,AR,NUPR1,ROR1,GLIS2,TCF3,ZBTB7A,TRIM26,PLPP3,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0034377	0.04	0.99	4	19	plasma lipoprotein particle assembly	BP	0.72067	APOE,PRKACA,LCAT,DGAT1	cyan	VSMC_M2
GO:0051234	0.04	0.96	267	3429	establishment of localization	BP	0.72196	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,AFDN,PACSIN2,TAPBP,GGA1,HMOX1,ACO1,TRPM3,APPL2,ATP10D,TBC1D2,P3H1,KCNQ5,SLC44A1,BBS9,EEPD1,ELMO1,TBC1D17,GLI3,AP2A1,CADPS2,GSN,SLC17A7,STOM,NRP1,KLF15,RHOB,BAX,DENND2A,UQCRH,FZD4,BIN1,APOE,BCL3,ABCB8,SLC6A9,ATG7,EXOC7,RHBDF2,LTBP4,CAMK1,EHD3,CMTM6,OSBPL10,DZIP1,ZFP36,LGALS3BP,SLC26A11,STARD10,GPAT4,SLC4A9,FOLR2,HGS,TBC1D5,RFTN1,RHOG,RAB11FIP1,DCLK1,LAMP1,ACKR4,SMPD1,TMEM108,APBB1,PKDCC,CLIP3,SLC15A4,SLC7A2,ATP4A,SCN1B,GNPTAB,IGF1,REEP5,SNTA1,EFNA5,CHMP4B,CHMP3,EDEM2,ERGIC3,ARRDC3,PLSCR1,SLC38A7,NDRG4,GLRB,STBD1,PRKCD,EPHA3,SRC,CACNB3,TGM2,LRP4,PLCG1,BBS2,ARHGAP1,EXOC2,GNAO1,MAPK8IP1,NISCH,EXT2,SLC5A3,CRACR2B,SYS1,LZTS2,CTSA,CD81,SLC45A3,CHRNA7,OSBPL5,CAPN3,CACNA2D2,AGFG1,CTTN,PCSK6,TMEM115,TUSC2,TPCN2,NFKB1,GNAI2,LRP10,HADH,DISP1,SGSM1,SV2A,EXOC8,RHBDD3,NCKIPSD,ADCY1,FES,ANXA9,FURIN,VPS11,ERFE,SLC16A9,KIF1A,FAM53B,CLCN2,TCN2,TMEM50A,PARD3B,STK25,ATG4B,RNASEL,NFKBIA,LINC02210-CRHR1,B2M,KCND3,ORAI2,M6PR,ADORA2A,CAPN1,FYCO1,RPGR,GRN,G6PC3,PSAP,HOMER3,WNK4,BMP4,MAP1S,STAT5A,PORCN,USE1,HDAC6,B3GAT3,CHRNE,PLD2,CROCC,ARRB2,JUP,ALOX15,AKAP5,GABARAP,SERPINE2,MCC,PLSCR3,GIPC1,ERBB2,STARD3,PRKACA,ZFP36L1,UBQLN2,CLCN6,MLLT6,TMEM175,TP53,CPLX2,ORAI3,ERGIC1,NPC2,SLC51B,SLC16A2,ATP8B2,C1orf43,STON2,SPNS1,ANKFN1,SLC44A2,GRIA1,ATOX1,SNX33,RASL10B,ABCC1,EPN2,PDGFRB,MCOLN1,LLGL	cyan	VSMC_M2
GO:0060322	0.04	0.97	55	624	head development	BP	0.72196	PLXNB2,NFIB,MEIS1,GLI3,RRAS,SLC17A7,NRP1,BAX,MEIS3,FZD4,COQ8B,DCLK1,TMEM108,RARG,POU6F1,SFRP2,NDRG4,SRC,BBS2,GNAO1,MMP2,PHACTR1,LEF1,ADCY1,TACC2,KIF1A,ARPC5,PTCHD1,B2M,WNT2B,CCDC141,ACAT1,BMP4,NAGLU,MAP1S,DLG5,ARRB2,SERPINE2,SLIT2,TP53,HOXB1,HOXB2,GBA,PPP1R9B,PTPRS,RERE,ABL1,FPGS,PBX3,ATP6V0D1,SLC8A3,SELENOP,CALM3,PYGO2,EN1	cyan	VSMC_M2
GO:0045761	0.04	0.99	4	20	regulation of adenylate cyclase activity	BP	0.72273	TIMP2,GNAI2,LINC02210-CRHR1,AKAP5	cyan	VSMC_M2
GO:0009651	0.04	0.99	4	19	response to salt stress	BP	0.72332	BAX,CAPN3,ZFP36L1,TP53	cyan	VSMC_M2
GO:1901655	0.04	0.98	10	77	cellular response to ketone	BP	0.72332	FBXO32,TRERF1,KLF9,SRC,ADCY1,CASP9,AR,ADAM15,NDOR1,SERPINF1	cyan	VSMC_M2
GO:0009395	0.04	0.99	6	36	phospholipid catabolic process	BP	0.72332	PLA2G7,SMPD1,PRKCD,PLBD2,PLCG1,PNPLA7	cyan	VSMC_M2
GO:0006893	0.04	0.98	8	56	Golgi to plasma membrane transport	BP	0.72332	GGA1,PKDCC,BBS2,EXOC2,SYS1,OSBPL5,EXOC8,LLGL1	cyan	VSMC_M2
GO:0007420	0.04	0.97	52	587	brain development	BP	0.72332	PLXNB2,NFIB,MEIS1,GLI3,SLC17A7,NRP1,BAX,MEIS3,FZD4,COQ8B,DCLK1,TMEM108,POU6F1,SFRP2,NDRG4,SRC,BBS2,GNAO1,PHACTR1,LEF1,ADCY1,TACC2,KIF1A,ARPC5,PTCHD1,B2M,WNT2B,CCDC141,ACAT1,BMP4,NAGLU,MAP1S,DLG5,ARRB2,SERPINE2,SLIT2,TP53,HOXB1,HOXB2,GBA,PPP1R9B,PTPRS,RERE,ABL1,FPGS,PBX3,ATP6V0D1,SLC8A3,SELENOP,CALM3,PYGO2,EN1	cyan	VSMC_M2

GO:0006644	0.04	0.97	31	314	phospholipid metabolic process	BP	0.72332	CHKB,PLA2G7,SLC44A1,PLB1,SOCS3,OSBPL10,GPAT4,SMPD1,LPCAT4,PLSCR1,HEXB,PRKCD,PLBD2,PLCG1,PTDSS1,PIK3C2B,OSBPL5,IP6K1,RARRES3,PLD2,ALOX15,PLSCR3,SLC44A2,PDGFRB,PNPLA7,PIGQ,INPP5E,PLPP2,LCAT,ABCA2,PLPP3	cyan	VSMC_M2
GO:0060485	0.04	0.97	24	235	mesenchyme development	BP	0.72758	TCF21,ZFPM2,NRP1,FGFR1,WT1,SFRP2,WWTR1,EPHA3,FOXF2,STAT1,SEMA3B,LEF1,SEMA4B,BCL9L,SEMA6C,GATA5,ELL3,BMP4,DLG5,ZFP36L1,ADAM15,PDGFRB,FOXC2,GATA4	cyan	VSMC_M2
GO:0006029	0.04	0.98	9	67	proteoglycan metabolic process	BP	0.73148	CANT1,SGSH,IGF1,CHST14,EXT2,B3GAT3,XYLT2,CHST8,HS3ST3B1	cyan	VSMC_M2
GO:0030178	0.04	0.98	16	142	negative regulation of Wnt signaling pathway	BP	0.73209	TLE1,GLI3,FZD4,APOE,RNF213,SFRP2,WWTR1,LRP4,SFRP5,LZTS2,FRMD8,MCC,TSC2,NPHP4,AXIN1,EMD	cyan	VSMC_M2
GO:0030850	0.04	0.99	6	37	prostate gland development	BP	0.73391	GLI3,RARG,PSAP,BMP4,AR,SERPINF1	cyan	VSMC_M2
GO:0032091	0.04	0.98	10	76	negative regulation of protein binding	BP	0.73658	BAX,CAMK1,PRKCD,RGMA,B2M,ARRB2,ADAM15,TEX14,DVL1,ZFPM1	cyan	VSMC_M2
GO:0055123	0.04	0.98	12	99	digestive system development	BP	0.73897	TCF21,COBL,GLI3,PKDCC,SFRP2,SRC,FOXF2,SFRP5,GATA5,BMP4,DNAAF1,GATA4	cyan	VSMC_M2
GO:0048015	0.04	0.98	15	133	phosphatidylinositol-mediated signaling	BP	0.73956	NOP53,FGFR1,IGF1,SRC,PTPN13,PIK3C2B,PLCD3,SERPINE2,ERBB2,ZFP36L1,NTRK1,PDGFRB,ROR1,TSC2,INPP5E	cyan	VSMC_M2
GO:0021955	0.04	0.99	5	29	central nervous system neuron axonogenesis	BP	0.74157	NFIB,DCLK1,SCN1B,B4GALT5,SLIT2	cyan	VSMC_M2
GO:0051099	0.04	0.98	16	141	positive regulation of binding	BP	0.74332	FLOT1,NRP1,APOE,RFNG,TRIM21,IGF1,SPON1,B2M,ADD1,BMP4,EDF1,ABL1,CALM3,CLIC2,CDK9,PYGO2	cyan	VSMC_M2
GO:0060711	0.05	0.99	6	37	labyrinthine layer development	BP	0.7456	SOCS3,LEF1,PLCD3,DNAJB6,ZFP36L1,JUNB	cyan	VSMC_M2
GO:0006897	0.05	0.97	41	444	endocytosis	BP	0.75261	RAB5B,FLOT1,PACSIN2,APPL2,ELMO1,AP2A1,GSN,SLC17A7,BIN1,APOE,EHD3,LGALS3BP,TBC1D5,RHOG,ACKR4,SMPD1,TMEM108,CLIP3,EPHA3,SRC,LRP4,CD81,CTTN,TPCN2,LRP10,NCKIPSD,B2M,M6PR,ARRB2,ALOX15,UBQLN2,STON2,GRIA1,SNX33,EPN2,SH3GL1,TSC2,ABL1,ABCA2,CALM3,OCIAD2	cyan	VSMC_M2
GO:0006743	0.05	0.99	4	19	ubiquinone metabolic process	BP	0.75261	COQ8B,COQ9,AIFM2,UBIAD1	cyan	VSMC_M2
GO:0051216	0.05	0.98	17	154	cartilage development	BP	0.75261	TGFBI,NFIB,ITGB8,EFEMP1,GLI3,EPYC,PKDCC,RARG,SFRP2,SOX5,ECM1,CTSK,LTBP3,WNT2B,ADAMTS7,BMP4,PBXIP1	cyan	VSMC_M2
GO:0080134	0.05	0.96	83	970	regulation of response to stress	BP	0.75424	IRF1,GRINA,LRRC19,APPL2,PLA2G7,MLIP,IRF3,BAX,APOE,ATG7,RHBDF2,SOCS3,ZFP36,TRIM21,LAMP1,APBB1,SLC15A4,IGF1,TLR3,GGT7,SERPING1,PLSCR1,SFRP2,PRKCD,SRC,TGM2,PLCG1,MMS19,MAPK8IP1,STAT1,CD81,IKBKE,TIRAP,NFKB1,RGMA,PTGIS,RHBDD3,FURIN,STK25,MAGEF1,ELL3,NFKBIA,B2M,ADORA2A,AIFM2,GRN,TMEM161A,BMP4,HDAC6,PQBP1,DHX58,DNAJB6,ARRB2,ALOX15,DAGLA,IL17RA,SERPINE2,CASP9,UBQLN2,TP53,UBQLN4,GBA,NUPR1,ADAR,ACP5,GPRC5B,ABCC1,TRAF4,PTPRS,ABCD1,ISG15,SBNO2,FAM3A,AXIN1,FOXC2,ABL1,HEXIM1,SERPINF1,PML,RPS19,PLPP3,GATA4,CDK9	cyan	VSMC_M2
GO:0006942	0.05	0.98	9	68	regulation of striated muscle contraction	BP	0.75424	BIN1,EHD3,CTNNA3,JUP,PRKACA,SLC8A3,GATA4,CALM3,CLIC2	cyan	VSMC_M2
GO:0043407	0.05	0.98	7	47	negative regulation of MAP kinase activity	BP	0.75424	APOE,SMPD1,SFRP2,PRKCD,MAPK8IP1,BMP4,GBA	cyan	VSMC_M2
GO:0051339	0.05	0.99	5	29	regulation of lyase activity	BP	0.7567	TIMP2,GNAI2,LINC02210-CRHR1,AKAP5,PHPT1	cyan	VSMC_M2
GO:0098900	0.05	0.98	6	39	regulation of action potential	BP	0.7567	BIN1,CACNB3,CTNNA3,JUP,GBA,CALM3	cyan	VSMC_M2
GO:0043403	0.05	0.99	5	28	skeletal muscle tissue regeneration	BP	0.75818	IGF1,CD81,CAPN3,BCL9,PTGFRN	cyan	VSMC_M2
GO:0021545	0.05	0.98	6	38	cranial nerve development	BP	0.7589	GLI3,NRP1,SLITRK6,NTRK1,HOXB1,HOXB2	cyan	VSMC_M2
GO:1902533	0.05	0.96	64	731	positive regulation of intracellular signal transduction	BP	0.7589	AKAP12,HMOX1,LRRC19,TRIM14,GPNMB,RRAGC,IRF3,NRP1,BAX,MEIS3,LURAP1,TRIM13,FZD4,APOE,TIMP2,CANT1,FGFR1,TRIM21,SLC15A4,MAP3K12,RBCK1,IGF1,TLR3,NDRG4,SRC,TGM2,MAPK8IP1,SORBS3,CD81,CHRNA7,TRIM8,IKBKE,TIRAP,GNAI2,ECM1,CASP10,STK25,TMEM101,TMEM106A,BMP4,DLG5,DHX58,ARRB2,ALOX15,ERBB2,NTRK1,AR,TP53,NUPR1,SHC1,SLC44A2,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,TRAF7,AXIN1,ABL1,IL34,RPS15,HEXIM1,GATA4,BST2	cyan	VSMC_M2
GO:0062149	0.05	0.99	4	20	detection of stimulus involved in sensory perception of pain	BP	0.7589	CACNB3,NR2F6,ARRB2,NTRK1	cyan	VSMC_M2
GO:0002573	0.05	0.97	17	154	myeloid leukocyte differentiation	BP	0.7589	ITGB8,LRRC17,TLR3,SRC,CD81,LEF1,FES,BMP4,EPHA2,ZFP36L1,GBA,SIGLEC15,SBNO2,CBFA2T3,IL34,JUNB,ZFPM1	cyan	VSMC_M2
GO:0055117	0.05	0.98	8	58	regulation of cardiac muscle contraction	BP	0.7589	BIN1,EHD3,CTNNA3,JUP,PRKACA,GATA4,CALM3,CLIC2	cyan	VSMC_M2
GO:0062197	0.05	0.97	28	282	cellular response to chemical stress	BP	0.7589	STAT6,PTPRK,HMOX1,RHOB,AGAP3,ATG7,CAMKK2,PRKCD,SRC,MMP2,CAPN3,CCS,STK25,AIFM2,TMEM161A,HDAC6,ZFP36L1,PCGF2,TP53,PDK2,ABCC1,ABCD1,ABL1,PML,SERPINB6,GATA4,ADPRHL2,MPV17	cyan	VSMC_M2
GO:0060071	0.05	0.98	7	48	Wnt signaling pathway, planar cell polarity pathway	BP	0.7589	PRICKLE2,SFRP2,VANGL2,MED12,ROR1,DVL1,ABL1	cyan	VSMC_M2
GO:1901385	0.05	0.99	5	28	regulation of voltage-gated calcium channel activity	BP	0.7589	EHD3,CACNB3,LINC02210-CRHR1,CBARP,CALM3	cyan	VSMC_M2
GO:0070252	0.05	0.98	9	70	actin-mediated cell contraction	BP	0.7589	MYL6B,GSN,BIN1,SCN1B,SNTA1,CTNNA3,KCND3,JUP,GATA4	cyan	VSMC_M2
GO:0001676	0.05	0.98	9	66	long-chain fatty acid metabolic process	BP	0.7589	ACAA1,CYP2S1,PTGIS,ALOX15,DAGLA,CPT2,ABCD1,PTGDS,GSTM4	cyan	VSMC_M2
GO:1903146	0.05	0.99	5	30	regulation of autophagy of mitochondrion	BP	0.7589	CAMKK2,CTTN,HDAC6,TP53,TSC2	cyan	VSMC_M2
GO:0040008	0.05	0.97	47	518	regulation of growth	BP	0.7589	CTDP1,ZFPM2,MEIS1,NRP1,APOE,LTBP4,SOCS3,PAK4,GPAT4,RFTN1,IGF1,WT1,SFRP2,NDRG3,BBS2,NDN,CAPN3,CTTN,SEMA3B,RGMA,SEMA4B,SEMA6C,RERG,RND2,BMP4,STAT5A,SERPINE2,ERBB2,BRAT1,SLIT2,AR,TP53,PPP1R9B,ADAM15,SHC1,PTPRS,AGRN,E4F1,CLSTN1,FOXC2,ABL1,OSGIN1,IST1,PML,SELENOP,BST2,OGFR	cyan	VSMC_M2
GO:0051016	0.05	0.99	4	20	barbed-end actin filament capping	BP	0.7589	GSN,ADD1,CAPZB,FLII	cyan	VSMC_M2
GO:0051281	0.05	0.99	5	29	positive regulation of release of sequestered calcium ion into cytosol	BP	0.7589	BAX,PLCG1,CAPN3,ABL1,CALM3	cyan	VSMC_M2
GO:0048008	0.05	0.98	7	48	platelet-derived growth factor receptor signaling pathway	BP	0.7589	NRP1,HGS,NDRG4,SRC,BCR,PDGFRB,ABL1	cyan	VSMC_M2
GO:0071305	0.05	0.99	4	20	cellular response to vitamin D	BP	0.7589	MN1,FES,PHEX,KANK2	cyan	VSMC_M2

GO:0045595	0.05	0.96	96	1153	regulation of cell differentiation	BP	0.7589	CTDP1,ZADH2,PLXNB2,ZFPM2,IRF1,APPL2,EFEMP1,MEIS1,GLI3,RRAS,NRP1,LRRC17,TMEM176B,BIN1,ATRAID,LTBP4,SOCS3,CAMK1,PNP,TIMP2,ZFP36,FGFR1,EFNB2,ADGRA2,PKDCC,RARG,IGF1,TLR3,MAN2A1,EFNA5,SFRP2,WWTR1,EPHA3,TGM2,LRP4,ZHX3,STAT1,SLC45A3,CAPN3,BOC,SEMA3B,NFKB1,RGMA,LEF1,SOX5,SEMA4B,FES,PRUNE1,BCL9L,SEMA6C,LMO3,GATA5,STK25,ELL3,NFKBIA,LTBP3,B2M,DPF2,ADAMTS7,GRN,HDAC5,RND2,ADD1,BMP4,RARRES3,NBL1,HDAC6,ARRB2,TCF12,SERPINE2,ERBB2,PRKACA,ZFP36L1,SMOC1,SLIT2,AR,TP53,HOXB4,SIGLEC15,GPRC5B,TMEM98,PTPRS,ASPA,ISG15,NELFB,TCF3,ABL1,IL34,IST1,SERPINF1,RPS19,JUNB,GATA4,CDK9,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0010596	0.05	0.98	7	48	negative regulation of endothelial cell migration	BP	0.7589	CARD10,APOE,ANGPT4,HDAC5,JUP,SLIT2,SERPINF1	cyan	VSMC_M2
GO:0010660	0.05	0.98	8	57	regulation of muscle cell apoptotic process	BP	0.7589	HMOX1,HSPB6,IGF1,SFRP2,ARRB2,TP53,NUPR1,GATA4	cyan	VSMC_M2
GO:0051173	0.05	0.96	185	2331	positive regulation of nitrogen compound metabolic process	BP	0.7589	PYM1,STAT6,TCF21,FLOT1,DDAH2,PLXNB2,ZFPM2,IRF1,TCF20,DAXX,TEF,TEAD3,MTCH1,GGA1,CARD10,NFIB,TRERF1,MLIP,TRIM14,NAT14,GPNMB,MEIS1,RNF144A,PTOV1,GLI3,IRF3,GSN,NRP1,KLF15,BAX,DBP,NOP53,BICRA,MEIS3,TRIM13,FZD4,CAB39L,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,ZFP36,SAMD4B,KAT2B,RHOG,FGFR1,TRIM21,SMPD1,APBB1,CLIP3,ANGPT4,LMO1,MAP3K12,RARG,IGF1,TLR3,WT1,EFNA5,TP53INP2,PATL1,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,LRP4,MMS19,FOXF2,STAT1,ABHD14B,MOB2,CD81,NDN,CHRNA7,TRIM8,CAPN3,TIRAP,ZNF496,NFKB1,RGMA,BCL9,LEF1,APH1A,VEGFD,RHBDD3,CASP10,FURIN,VPS11,BCL9L,RFX5,GATA5,HELZ2,ATG4B,RNASEL,MAGEF1,ELL3,NFKBIA,MOV10,DPF2,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,VEGFB,TMEM106A,BMP4,LDB2,TCEA2,HDAC6,PQBP1,ARRB2,JUP,MYRF,GABARAP,ZBTB17,TCF12,CASP9,ERBB2,BRAT1,ZFP36L1,UBQLN2,NTRK1,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,GPRC5B,SNX33,PDGFRB,MTA1,MAP2K3,TRAF4,MOSPD1,MPND,EEF2,GLIS2,DVL1,AGRN,ELOB,E4F1,TNFRSF14,TCF3,SBNO2,EDF1,AXIN1,RERE,CBFA2T3,FOXC2,ABL1,ATMIN,IL34,PBX3,IST1,NFIA,ABCA2,MEX3D,PML,JUNB,GATA4,CALM3,CARD8,CDK9,SDC4,ZFPM1,EN1	cyan	VSMC_M2
GO:0034340	0.05	0.98	7	47	response to type I interferon	BP	0.7589	IRF3,SMPD1,STAT1,IKBKE,ADAR,ISG15,OAS2	cyan	VSMC_M2
GO:0090287	0.05	0.97	23	230	regulation of cellular response to growth factor stimulus	BP	0.7589	KIAA1324L,FZD4,LTBP4,HGS,FGFR1,ADGRA2,TMEM108,SFRP2,SFRP5,PCSK6,RGMA,BCL9L,FAM89B,BMP4,NBL1,GIPC1,SLIT2,TP53,NEO1,EPN2,ABL1,ZBTB7A,GATA4	cyan	VSMC_M2
GO:0052548	0.05	0.97	27	270	regulation of endopeptidase activity	BP	0.7589	MTCH1,GSN,BAX,BIN1,TIMP2,SERPING1,CAST,SFRP2,SRC,CSTB,APH1A,CASP10,FURIN,ADORA2A,CPAMD8,DNAJB6,ARRB2,SERPINE2,CASP9,RENBP,ABCA2,SERPINF1,PML,SERPINB6,CARD8,PSMB9,BST2	cyan	VSMC_M2
GO:2001233	0.05	0.97	29	292	regulation of apoptotic signaling pathway	BP	0.7589	DEPTOR,GRINA,HMOX1,NRP1,BAX,MEIS3,FGFR1,RBCK1,IGF1,SFRP2,PRKCD,SRC,MAPK8IP1,CTTN,GNAI2,ELL3,ADORA2A,TMEM161A,TMBIM1,BMP4,ARRB2,PCGF2,AR,TP53,NUPR1,TRAF7,INCA1,PML,GATA4	cyan	VSMC_M2
GO:0086091	0.05	0.99	5	30	regulation of heart rate by cardiac conduction	BP	0.7589	BIN1,SCN1B,CTNNA3,KCND3,JUP	cyan	VSMC_M2
GO:0001759	0.05	0.99	4	20	organ induction	BP	0.7589	GATA5,WNT2B,BMP4,AR	cyan	VSMC_M2
GO:0032967	0.05	0.99	4	20	positive regulation of collagen biosynthetic process	BP	0.7589	VIM,BMP4,ARRB2,PDGFRB	cyan	VSMC_M2
GO:0032615	0.05	0.98	6	38	interleukin-12 production	BP	0.7589	IRF1,TLR3,TIRAP,NFKB1,ARRB2,ACP5	cyan	VSMC_M2
GO:0032655	0.05	0.98	6	38	regulation of interleukin-12 production	BP	0.7589	IRF1,TLR3,TIRAP,NFKB1,ARRB2,ACP5	cyan	VSMC_M2
GO:0007015	0.05	0.97	35	373	actin filament organization	BP	0.7589	ARHGAP18,ELMO1,COBL,GSN,NRP1,RHOB,BIN1,ARAP1,RHOG,RHPN2,PRKCD,SRC,C15orf62,SORBS3,PHACTR1,TJP1,CTTN,SSH3,GAS2L1,CTNNA3,WIPF1,ARPC5,ARHGEF10,RND2,ADD1,CAPZB,ARHGEF10L,ALOX15,CGNL1,SLIT2,PPP1R9B,FLII,AIF1L,ABL1,SDC4	cyan	VSMC_M2
GO:0010658	0.05	0.98	6	38	striated muscle cell apoptotic process	BP	0.7589	RPS6KA2,HSPB6,SFRP2,TP53,NUPR1,GATA4	cyan	VSMC_M2
GO:0030201	0.05	0.99	5	29	heparan sulfate proteoglycan metabolic process	BP	0.7589	SGSH,EXT2,B3GAT3,XYLT2,HS3ST3B1	cyan	VSMC_M2
GO:0035265	0.05	0.97	15	134	organ growth	BP	0.7589	CTDP1,EHMT2,ZFPM2,MEIS1,RARG,IGF1,WT1,NDRG4,ECM1,HEG1,PSAP,AR,PDGFRB,FOXC2,GATA4	cyan	VSMC_M2
GO:0050678	0.05	0.97	27	275	regulation of epithelial cell proliferation	BP	0.7589	PTPRK,NFIB,HMOX1,KLF9,NRP1,BAX,APOE,ZFP36,FGFR1,IGF1,SFRP2,PLCG1,STAT1,VEGFD,ECM1,B2M,GRN,VEGFB,BMP4,STAT5A,MCC,ERBB2,ZFP36L1,AR,NUPR1,SERPINF1,PYGO2	cyan	VSMC_M2
GO:0010954	0.05	0.99	4	20	positive regulation of protein processing	BP	0.7589	GSN,SPON1,SRC,CLEC3B	cyan	VSMC_M2
GO:0021675	0.05	0.98	8	59	nerve development	BP	0.7589	GLI3,NRP1,SLITRK6,NPTX1,SERPINE2,NTRK1,HOXB1,HOXB2	cyan	VSMC_M2
GO:0006468	0.05	0.96	101	1223	protein phosphorylation	BP	0.7589	FLOT1,PLXNB2,RPS6KA2,DEPTOR,DAXX,ST3GAL1,CARD10,GPNMB,EFEMP1,STK40,AKT1S1,STK17A,NRP1,BAX,NOP53,FZD4,CAB39L,MARK4,APOE,SOCS3,CAMK1,PAK4,HGS,KAT2B,FGFR1,SH3BP5,DCLK1,SMPD1,PKDCC,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,LRP4,MAPK8IP1,PTPN13,MOB2,GFRA2,CD81,PHKG1,CHRNA7,IKBKE,TIRAP,VEGFD,GRK5,FES,HEG1,STK25,RNASEL,BCR,ADORA2A,CDC42BPG,VEGFB,WNK4,BMP4,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,PRKACA,NTRK1,SLIT2,TP53,PDK2,GBA,PPP1R9B,SHC1,ADAR,TEX14,WARS,ULK3,GPRC5B,PDGFRB,MAP2K3,ROR1,MLLT1,TRAF4,DVL1,TNFRSF14,TSC2,AXIN1,ABL1,IL34,INCA1,SLC8A3,HEXIM1,PML,PLPP3,CALM3,CDK9,SDC4,GTF2H4	cyan	VSMC_M2

GO:1901566	0.05	0.96	110	1317	organonitrogen compound biosynthetic process	BP	0.7589	PYM1,MOXD1,MGAT4B,CHKB,PLXNB2,EIF3H,B3GALT4,ST3GAL1,IBA57,GCNT1,ACO1,IARS,GALNT12,SLC44A1,AASS,AP2A1,RPL18,ABTB1,FKRP,ACSS1,VIM,APOE,UROD,BCL3,MIF4GD,SLC6A9,ATG7,PNP,RPS16,ZFP36,CANT1,SAMD4B,GPAT4,RPL15,EIF3K,SMPD1,CLIP3,EIF3F,IGF1,MAN2A1,DPY19L3,PATL1,GGT7,ACSS2,GALNT18,PLSCR1,PRKCD,CHST14,PTDSS1,EXT2,NADSYN1,MRPL36,NFKB1,B4GALT4,PTGIS,B4GALT5,GCNT7,ADCY1,FURIN,B4GAT1,UCKL1,NMNAT2,MOV10,PCBD1,ACAT1,VEGFB,TMEM106A,QDPR,PORCN,B3GAT3,WDR45,ERBB2,ZFP36L1,MRI1,PDK2,GBA,XYLT2,SLC51B,SLC44A2,WARS,PPCDC,PDGFRB,NUDT14,CERS4,ZDHHC9,NAGPA,EEF2,DPH7,HAGH,PIGQ,INPP5E,PLPP2,RPL13,DPYD,FPGS,LCAT,TK2,ABCA2,RPS15,MEX3D,CHST8,NMT2,RPS19,PLPP3,EEF1A2,HS3ST3B1,SAT1,RPL36A,AL157935.2,PDXK	cyan	VSMC_M2
GO:0031032	0.05	0.97	18	172	actomyosin structure organization	BP	0.7589	NRP1,LURAP1,ARAP1,RHPN2,SRC,SORBS3,PHACTR1,CAPN3,TJP1,ARHGEF10,CDC42BPG,ARHGEF10L,CGNL1,PDGFRB,FLII,ABL1,CNN3,SDC4		
GO:0006084	0.05	0.98	5	29	acetyl-CoA metabolic process	BP	0.7589	AASS,ACSS1,ACSS2,ACAT1,PDK2	cyan	VSMC_M2
GO:0033619	0.05	0.98	7	48	membrane protein proteolysis	BP	0.7589	APOE,TIMP2,RGMA,APH1A,FURIN,SNX33,CLPP	cyan	VSMC_M2
GO:0010633	0.05	0.98	8	59	negative regulation of epithelial cell migration	BP	0.7589	CARD10,APOE,ANGPT4,HDAC5,JUP,MCC,SLIT2,SERPINF1	cyan	VSMC_M2
GO:0003016	0.05	0.98	5	29	respiratory system process	BP	0.7589	STK40,GAA,TSHZ3,NDN,PBX3	cyan	VSMC_M2
GO:0045912	0.05	0.98	6	39	negative regulation of carbohydrate metabolic process	BP	0.7589	AP2A1,ERFE,TP53,NUPR1,FAM3A,CBFA2T3	cyan	VSMC_M2
GO:0051492	0.05	0.98	10	80	regulation of stress fiber assembly	BP	0.7589	NRP1,ARAP1,RHPN2,SORBS3,TJP1,ARHGEF10,ARHGEF10L,CGNL1,ABL1,SDC4	cyan	VSMC_M2
GO:0051091	0.05	0.97	21	204	positive regulation of DNA-binding transcription factor activity	BP	0.7589	FLOT1,TRIM14,TRIM13,FZD4,TRIM21,RBCK1,TLR3,TRIM8,IKBKE,CAPN3,TIRAP,ADCY1,HDAC5,JUP,NTRK1,AR,ROR1,TCF3,ZBTB7A,TRIM26,PLPP3	cyan	VSMC_M2
GO:1903076	0.06	0.97	11	90	regulation of protein localization to plasma membrane	BP	0.7589	RHOG,PKDCC,CLIP3,EPHA3,TMBIM1,EPHA2,AKAP5,AR,PPP1R9B,GRASP,STX3	cyan	VSMC_M2
GO:1902106	0.06	0.98	9	69	negative regulation of leukocyte differentiation	BP	0.7589	IRF1,GLI3,LRRC17,TMEM176B,TLR3,BMP4,ERBB2,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0045892	0.06	0.96	80	943	negative regulation of transcription, DNA-templated	BP	0.7589	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,BCL3,ZFP36,APBB1,LMO1,RARG,WT1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,CAPN3,NFKB1,HIST1H1C,LEF1,TBL1Y,NELFCD,RFX5,MAGEF1,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,KANK2,MTA1,MOSPD1,GLIS2,E4F1,NELFB,TCF3,SBNO2,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,ZFPM1,EN1	cyan	VSMC_M2
GO:0038093	0.06	0.98	6	39	Fc receptor signaling pathway	BP	0.7589	APPL2,PRKCD,SRC,PLCG1,PLD2,ABL1	cyan	VSMC_M2
GO:1902991	0.06	0.98	6	39	regulation of amyloid precursor protein catabolic process	BP	0.7589	BIN1,APOE,IGF1,SPON1,CHRNA7,ABCA2	cyan	VSMC_M2
GO:0086002	0.06	0.98	6	41	cardiac muscle cell action potential involved in contraction	BP	0.7589	BIN1,SCN1B,SNTA1,CTNNA3,KCND3,JUP	cyan	VSMC_M2
GO:0030111	0.06	0.96	27	277	regulation of Wnt signaling pathway	BP	0.7589	TLE1,GLI3,KLF15,FZD4,APOE,RNF213,ADGRA2,SFRP2,WWTR1,SRC,LRP4,SFRP5,LZTS2,NFKB1,LEF1,FAM53B,FRMD8,JUP,MCC,PBXIP1,GPRC5B,TSC2,NPHP4,AXIN1,ABL1,PLPP3,EMD	cyan	VSMC_M2
GO:0098901	0.06	0.99	4	22	regulation of cardiac muscle cell action potential	BP	0.7589	BIN1,CTNNA3,JUP,CALM3	cyan	VSMC_M2
GO:0043114	0.06	0.98	6	40	regulation of vascular permeability	BP	0.7589	AKAP12,APOE,SRC,TJP1,ADORA2A,SLIT2	cyan	VSMC_M2
GO:0042445	0.06	0.97	15	133	hormone metabolic process	BP	0.7589	CYP2S1,PLB1,CTSB,PNPLA2,PCSK6,NFKB1,CTSK,FURIN,CLCN2,STARD3,SLC16A2,DHRS13,H6PD,CHST8,DGAT1	cyan	VSMC_M2
GO:0060425	0.06	0.98	6	39	lung morphogenesis	BP	0.7589	TCF21,NFIB,STK40,WNT2B,BMP4,DLG5	cyan	VSMC_M2
GO:0032607	0.06	0.99	4	21	interferon-alpha production	BP	0.7589	IRF3,TLR3,STAT1,PTPRS	cyan	VSMC_M2
GO:0032647	0.06	0.99	4	21	regulation of interferon-alpha production	BP	0.7589	IRF3,TLR3,STAT1,PTPRS	cyan	VSMC_M2
GO:0002833	0.06	0.97	12	101	positive regulation of response to biotic stimulus	BP	0.7589	IRF3,LAMP1,SLC15A4,PLSCR1,SRC,IKBKE,TIRAP,GRN,PQBP1,DHX58,HEXIM1,RPS19	cyan	VSMC_M2
GO:0009991	0.06	0.96	36	385	response to extracellular stimulus	BP	0.7589	EHMT2,GSDMD,HMOX1,APPL2,BCKDHB,RRAGC,APOE,ATG7,ZFP36,FOLR2,TBC1D5,SFRP2,SRC,CACNB3,BBS2,STAT1,GNAI2,MN1,GAS2L1,FES,PHEX,WNT2B,ACAT1,WDR45,GABARAP,NTRK1,TP53,PDK2,GBA,PPP1R9B,KANK2,EEF2,NDOR1,NPRL3,RPS19,GATA4	cyan	VSMC_M2
GO:0015748	0.06	0.97	12	102	organophosphate ester transport	BP	0.7589	ATP10D,APOE,OSBPL10,PLSCR1,PRKCD,OSBPL5,G6PC3,PLSCR3,NPC2,ATP8B2,ABCC1,ABCD1	cyan	VSMC_M2
GO:0032456	0.06	0.98	9	70	endocytic recycling	BP	0.7589	EHD3,CMTM6,NDRG4,ARHGAP1,AKAP5,RAB11FIP3,ENTR1,GRASP,RAB11B	cyan	VSMC_M2
GO:0060491	0.06	0.97	17	159	regulation of cell projection assembly	BP	0.7589	KCTD17,COBL,NRP1,MARK4,DZIP1,ARAP1,RHOG,PRKCD,SRC,C15orf62,CAPZB,CROCC,EPHA2,SLIT2,AGRN,ENTR1,ATMIN	cyan	VSMC_M2
GO:1902117	0.06	0.98	8	61	positive regulation of organelle assembly	BP	0.7589	KCTD17,MARK4,DZIP1,SRC,CROCC,ENTR1,ATMIN,SDC4	cyan	VSMC_M2
GO:0120034	0.06	0.97	11	92	positive regulation of plasma membrane bounded cell projection assembly	BP	0.7589	KCTD17,COBL,NRP1,MARK4,DZIP1,ARAP1,C15orf62,CROCC,AGRN,ENTR1,ATMIN	cyan	VSMC_M2
GO:0060669	0.06	0.99	4	21	embryonic placenta morphogenesis	BP	0.7589	SOCS3,LEF1,DNAJB6,ZFP36L1	cyan	VSMC_M2
GO:0008333	0.06	0.98	7	50	endosome to lysosome transport	BP	0.7589	RHOB,BIN1,CHMP3,TPCN2,VPS11,M6PR,UBXN6	cyan	VSMC_M2
GO:0031399	0.06	0.95	98	1182	regulation of protein modification process	BP	0.7589	FLOT1,PPP6R2,EHMT2,PLXNB2,DEPTOR,DAXX,CARD10,P3H1,GPNMB,AKT1S1,AASS,NRP1,KLF15,BAX,NOP53,FZD4,CAB39L,APOE,ATG7,SOCS3,CAMK1,HGS,KAT2B,FGFR1,SH3BP5,TRIM21,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,SNTA1,EFNA5,ARRDC3,CAMKK2,SFRP2,WWTR1,PRKCD,SRC,LRP4,FOXF2,MAPK8IP1,PTPN13,MOB2,GFRA2,CD81,NDN,CHRNA7,CAPN3,TIRAP,GNAI2,TPPP,VEGFD,HEG1,ADORA2A,VEGFB,BMP4,HDAC6,ARRB2,GABARAP,ERBB2,BRAT1,NTRK1,MLLT6,SLIT2,TP53,GBA,PPP1R9B,SLC51B,NUPR1,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MTA1,MAP2K3,MLLT1,TRAF4,DVL1,ISG15,TNFRSF14,TSC2,AXIN1,ABL1,IL34,INCA1,ABCA2,RPS15,SLC8A3,HEXIM1,PML,PLPP3,CALM3,CDK9,SDC4,PYGO2	cyan	VSMC_M2

GO:1903507	0.06	0.96	80	945	negative regulation of nucleic acid-templated transcription	BP	0.7589	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,BCL3,ZFP36,APBB1,LMO1,RARG,WT1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,CAPN3,NFKB1,HIST1H1C,LEF1,TBL1Y,NELFCD,RFX5,MAGEF1,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,KANK2,MTA1,MOSPD1,GLIS2,E4F1,NELFB,TCF3,SBNO2,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,ZFPM1,EN1	cyan	VSMC_M2
GO:0031669	0.06	0.97	19	182	cellular response to nutrient levels	BP	0.7589	EHMT2,HMOX1,RRAGC,ATG7,FOLR2,CACNB3,MN1,GAS2L1,FES,PHEX,WNT2B,WDR45,GABARAP,TP53,PDK2,GBA,KANK2,NDOR1,NPRL3	cyan	VSMC_M2
GO:0051898	0.06	0.98	5	30	negative regulation of protein kinase B signaling	BP	0.7589	NOP53,SFRP5,ARRB2,EPHA2,TSC2	cyan	VSMC_M2
GO:0034097	0.06	0.96	58	659	response to cytokine	BP	0.7589	STAT6,AKAP12,IRF1,APPL2,IRF3,FZD4,VIM,IL17RC,SOCS3,RPS16,TIMP2,ZFP36,IL5RA,TRIM21,ACKR4,SMPD1,RARG,TLR3,GGT7,PLSCR1,SRC,BBS2,GNAO1,STAT1,IKBKE,NFKB1,LEF1,PTGIS,ECM1,NFKBIA,ADAMTS7,STAT5A,ALOX15,IL17RA,GIPC1,PRKACA,ZFP36L1,IL27RA,SLIT2,TP53,GBA,ADAR,ACP5,TEX14,IL13RA1,ISG15,TNFRSF14,SBNO2,IL34,GBP6,OAS2,RAB43,PML,CARD8,VPS26B,CDK9,IL22RA1,BST2	cyan	VSMC_M2
GO:1902679	0.06	0.95	80	946	negative regulation of RNA biosynthetic process	BP	0.7589	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,BCL3,ZFP36,APBB1,LMO1,RARG,WT1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,CAPN3,NFKB1,HIST1H1C,LEF1,TBL1Y,NELFCD,RFX5,MAGEF1,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,KANK2,MTA1,MOSPD1,GLIS2,E4F1,NELFB,TCF3,SBNO2,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,ZFPM1,EN1	cyan	VSMC_M2
GO:0097066	0.06	0.99	4	21	response to thyroid hormone	BP	0.7589	KLF9,CTSB,GAS2L1,GBA	cyan	VSMC_M2
GO:0010714	0.06	0.99	4	21	positive regulation of collagen metabolic process	BP	0.7589	VIM,BMP4,ARRB2,PDGFRB	cyan	VSMC_M2
GO:0044089	0.06	0.96	40	441	positive regulation of cellular component biogenesis	BP	0.7589	FLOT1,KCTD17,COBL,GSN,NRP1,BAX,MARK4,BIN1,SLITRK6,DZIP1,TPPP2,ARAP1,HGS,SRC,C15orf62,SORBS3,TIRAP,CTTN,TPPP,FES,ARPC5,ARHGEF10,LDB2,DLG5,ARHGEF10L,CROCC,ALOX15,EPHA2,NTRK1,TP53,WARS,AGRN,ISG15,NPHP4,ENTR1,CLSTN1,ABL1,ATMIN,BMF,SDC4	cyan	VSMC_M2
GO:0048708	0.06	0.98	8	60	astrocyte differentiation	BP	0.7589	VIM,BIN1,LAMB2,ADORA2A,GRN,SERPINE2,ROR1,ABL1	cyan	VSMC_M2
GO:0001503	0.06	0.96	31	328	ossification	BP	0.7589	IARS,GPNMB,GLI3,ATRAID,PKDCC,IGF1,TP53INP2,SFRP2,WWTR1,LRP4,ZHX3,MMP2,EXT2,LEF1,MN1,ECM1,CTSK,PHEX,LTBP3,CLEC3B,BMP4,ALOX15,EPHA2,PRKACA,SMOC1,ADAR,ISG15,SBNO2,FOXC2,RPS15,JUNB	cyan	VSMC_M2
GO:0098926	0.06	0.98	5	30	postsynaptic signal transduction	BP	0.7589	CHRNA7,GNAI2,AGRN,RGS8,RGS10	cyan	VSMC_M2
GO:0031333	0.06	0.97	13	115	negative regulation of protein-containing complex assembly	BP	0.7589	GSN,NOP53,CLIP3,PRKCD,SRC,SSH3,ADD1,CAPZB,HDAC6,SLIT2,GBA,FLII,CARD8	cyan	VSMC_M2
GO:1902115	0.06	0.97	17	161	regulation of organelle assembly	BP	0.7589	EHMT2,KCTD17,GSN,MARK4,DZIP1,KAT2B,CHMP4B,SRC,VPS11,CROCC,UBQLN2,NUPR1,PTPRS,ENTR1,NPRL3,ATMIN,SDC4	cyan	VSMC_M2
GO:0060021	0.06	0.97	9	71	roof of mouth development	BP	0.7589	TSHZ1,TCF21,ITGB8,GLI3,PKDCC,FOXF2,LEF1,NPRL3,PYGO2	cyan	VSMC_M2
GO:0070588	0.06	0.96	21	211	calcium ion transmembrane transport	BP	0.7589	TRPM3,BAX,BIN1,EHD3,CACNB3,PLCG1,CHRNA7,CAPN3,CACNA2D2,TPCN2,ANXA9,LINC02210-CRHR1,ORAI2,PRKACA,ORAI3,MCOLN1,ABL1,SLC8A3,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0009790	0.06	0.95	71	841	embryo development	BP	0.7589	TSHZ1,TCF21,PLXNB2,ZFPM2,TEAD3,EFEMP1,MEIS1,COBL,GLI3,FLT3LG,NRP1,BAX,MEIS3,SLITRK6,SOCS3,FGFR1,PKDCC,RARG,IGF1,MAN2A1,WT1,SFRP2,NDRG4,LRP4,PLCG1,FOXF2,MMP2,EXT2,PCSK6,RGMA,LEF1,B4GALT5,FURIN,HEG1,VANGL2,WNT2B,PLCD3,BMP4,NAGLU,CC2D2A,DNAJB6,FKBP10,EPHA2,ZBTB17,PRKACA,ZFP36L1,PCGF2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,C6,CPT2,DVL1,E4F1,TSC2,RPL13,FOXC2,ABL1,DNAAF1,HSBP1,PBX3,JUNB,GATA4,LRRC7,SDC4,COL8A1,ZFPM1,EN1	cyan	VSMC_M2
GO:0045807	0.06	0.97	10	82	positive regulation of endocytosis	BP	0.7589	FLOT1,APPL2,AP2A1,APOE,TBC1D5,SMPD1,CLIP3,B2M,ARRB2,SH3GL1	cyan	VSMC_M2
GO:0032386	0.06	0.96	28	290	regulation of intracellular transport	BP	0.7589	OS9,GLI3,STOM,CAMK1,LAMP1,REEP5,CHMP3,EDEM2,NDRG4,PRKCD,SRC,CACNB3,ARHGAP1,CD81,VPS11,BMP4,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,ABCA2,GAS1,GRASP,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0051961	0.06	0.97	12	106	negative regulation of nervous system development	BP	0.7589	KIAA1324L,APPL2,NRP1,LRP4,SEMA3B,RGMA,SEMA4B,SEMA6C,B2M,TP53,TMEM98,PTPRS	cyan	VSMC_M2
GO:0090630	0.06	0.97	11	93	activation of GTPase activity	BP	0.7589	TBC1D22A,TBC1D2,TBC1D17,TBC1D5,RHOG,SGSM1,SIPA1L2,ARHGEF10,BCR,EPHA2,SGSM2	cyan	VSMC_M2
GO:0090199	0.06	0.98	6	39	regulation of release of cytochrome c from mitochondria	BP	0.7589	BAX,IGF1,ARRB2,PLSCR3,TP53,BMF	cyan	VSMC_M2
GO:0050673	0.06	0.96	30	316	epithelial cell proliferation	BP	0.7589	STAT6,PTPRK,NFIB,HMOX1,KLF9,NRP1,BAX,APOE,ZFP36,FGFR1,IGF1,SFRP2,PLCG1,STAT1,VEGFD,ECM1,B2M,GRN,VEGFB,BMP4,STAT5A,EPHA2,MCC,ERBB2,ZFP36L1,AR,NUPR1,SERPINF1,PYGO2,COL8A1	cyan	VSMC_M2
GO:0060402	0.06	0.97	12	107	calcium ion transport into cytosol	BP	0.7589	BAX,CACNB3,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,SLC8A3,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0043408	0.06	0.96	45	502	regulation of MAPK cascade	BP	0.7589	AKAP12,GPNMB,STK40,RRAS,NRP1,FZD4,APOE,TIMP2,PAK4,FGFR1,SMPD1,MAP3K12,IGF1,TLR3,SFRP2,NDRG4,PRKCD,SRC,MAPK8IP1,SORBS3,CD81,CHRNA7,TIRAP,GNAI2,LMO3,STK25,TMEM106A,BMP4,ARRB2,ALOX15,EPHA2,ERBB2,NTRK1,AR,GBA,SHC1,PDGFRB,MAP2K3,ROR1,TRAF4,TRAF7,AXIN1,ABL1,IL34,GATA4	cyan	VSMC_M2
GO:0002532	0.06	0.97	8	59	production of molecular mediator involved in inflammatory response	BP	0.7589	APPL2,PLD3,GRN,IL17RA,PBXIP1,ABCD1,MIR197,RPS19	cyan	VSMC_M2

GO:0050435	0.06	0.98	7	50	amyloid-beta metabolic process	BP	0.7589	BIN1,APOE,IGF1,SPON1,CHRNA7,APH1A,ABCA2	cyan	VSMC_M2
GO:0071704	0.06	0.95	601	8083	organic substance metabolic process	BP	0.7589	CTDP1,TSHZ1,ZADH2,MMP19,PYM1,PMEL,RBMS2,STAT6,MOXD1,TCF21,OS9,ADAMTS2,MGAT4B,GNS,AKAP12,FLOT1,CHKB,DDAH2,PPP6R2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,CFB,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,B3GALT4,CYB5R3,TAPBP,TCF20,DAXX,NAGA,FBXO32,TEF,PTPRK,ST3GAL1,IBA57,CDC14C,GSDMD,TEAD3,MTCH1,TLE1,GGA1,OPLAH,CARD10,KCTD17,NFIB,TRERF1,GCNT1,HMOX1,LRRC19,ACO1,CUL9,KLF9,APPL2,PLA2G7,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,ITGB8,P3H1,NAT14,GPNMB,SLC44A1,BCKDHB,EFEMP1,TRIL,RRAGC,EEPD1,MEIS1,RNF144A,IAH1,STK40,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,RPL18,PARP12,NOP53,ABTB1,BICRA,MEIS3,FKRP,LURAP1,TRIM13,ACSS1,FZD4,ME3,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,UROD,BCL3,ETHE1,MIF4GD,AGAP3,ATRAID,SLC6A9,ACAA1,ATG7,CYP2S1,COQ8B,LTBP4,CAPN5,PLB1,SOCS3,CAMK1,EHD3,PLD3,TEP1,OSBPL10,RNF170,PNP,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,GAA,PAK4,SGSH,ECH1,RNF213,ARAP1,GPAT4,RPL15,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,DCXR,FGFR1,IL5RA,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PGGHG,PKDCC,TPP1,MMP17,CLIP3,GTF3A,SLC15A4,ANGPT4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,GNPTAB,IGF1,CYP4V2,TLR3,SNTA1,MAN2A1,WT1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,GGCX,POU6F1,LPCAT4,SERPING1,CAST,LACTB2,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,STBD1,PRKCD,COQ9,EPHA3,SRC,CPE,TGM2,BPI,LRP4,DECR1,PLBD2,PLCG1,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,NISCH,AMN2,PTPN13,PTPDC1,EXT2,SLC6A3,PNPLA3,PIK3	cyan	VSMC_M2
GO:0002437	0.06	0.98	6	40	inflammatory response to antigenic stimulus	BP	0.7589	RHBDF2,IL5RA,SRC,PLCG1,CD81,FURIN	cyan	VSMC_M2
GO:0031532	0.06	0.97	11	94	actin cytoskeleton reorganization	BP	0.7589	GSN,NRP1,ARAP1,PHACTR1,TJP1,CTTN,FES,CDC42BPG,SHC1,PHPT1,ABL1	cyan	VSMC_M2
GO:0071496	0.06	0.96	26	267	cellular response to external stimulus	BP	0.7589	EHMT2,IRF1,GSDMD,HMOX1,RRAGC,ATG7,FOLR2,TLR3,SFRP2,CACNB3,NFKB1,MN1,GAS2L1,FES,PHEX,WNT2B,WDR45,GABARAP,TP53,PDK2,GBA,PPP1R9B,KANK2,PIEZO2,NDOR1,NPRL3	cyan	VSMC_M2
GO:0050865	0.06	0.96	36	385	regulation of cell activation	BP	0.7589	STAT6,IRF1,HMOX1,GPNMB,GLI3,APOE,PNP,LAMP1,SLC15A4,LMO1,IGF1,PLSCR1,PRKCD,SRC,BPI,MAPK8IP1,CD81,CAPN3,TIRAP,LEF1,RHBDD3,FES,B2M,ADORA2A,GRN,BMP4,DLG5,SERPINE2,ERBB2,ZFP36L1,IL27RA,PDGFRB,TNFRSF14,ABL1,CD55,SDC4	cyan	VSMC_M2
GO:0006622	0.06	0.98	4	22	protein targeting to lysosome	BP	0.7589	HGS,GNPTAB,M6PR,NAGPA	cyan	VSMC_M2
GO:0042130	0.06	0.98	6	40	negative regulation of T cell proliferation	BP	0.7589	GPNMB,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0002764	0.06	0.96	27	278	immune response-regulating signaling pathway	BP	0.7589	FLOT1,IRF1,LRRC19,APPL2,TRIL,IRF3,BAX,NOP53,RFTN1,SLC15A4,RBCK1,TLR3,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,CD81,TIRAP,NFKBIA,DHX58,PLD2,ARRB2,PTPRS,PHPT1,ABL1,NFKBIL1	cyan	VSMC_M2
GO:0097194	0.06	0.97	8	60	execution phase of apoptosis	BP	0.7589	COLEC11,BAX,PLSCR1,PTGIS,CASP10,CASP9,TP53BP2,TP53	cyan	VSMC_M2
GO:0090175	0.06	0.98	7	51	regulation of establishment of planar polarity	BP	0.7589	PRICKLE2,SFRP2,VANGL2,MED12,ROR1,DVL1,ABL1	cyan	VSMC_M2
GO:0000165	0.06	0.95	51	579	MAPK cascade	BP	0.7589	AKAP12,GPNMB,STK40,RRAS,NRP1,FZD4,APOE,TIMP2,ZFP36,PAK4,FGFR1,SMPD1,MAP3K12,IGF1,TLR3,CAMKK2,SFRP2,NDRG4,PRKCD,SRC,MAPK8IP1,SORBS3,CD81,CHRNA7,TIRAP,NFKB1,GNAI2,RHBDD3,LMO3,STK25,TMEM106A,BMP4,ARRB2,ALOX15,EPHA2,ERBB2,ZFP36L1,NTRK1,AR,GBA,SHC1,PDGFRB,MAP2K3,ROR1,ZDHHC9,TRAF4,TRAF7,AXIN1,ABL1,IL34,GATA4	cyan	VSMC_M2
GO:0051346	0.07	0.96	24	242	negative regulation of hydrolase activity	BP	0.7589	BIN1,TIMP2,SERPING1,CAST,SFRP2,SRC,CSTB,GNAI2,ECM1,FURIN,ADORA2A,CPAMD8,DNAJB6,ARRB2,SERPINE2,PPP1R9B,RENBP,ABL1,CNN3,SERPINF1,SERPINB6,CARD8,GCHFR,BST2	cyan	VSMC_M2
GO:0051051	0.07	0.96	30	314	negative regulation of transport	BP	0.7589	OS9,PACSIN2,HMOX1,APPL2,BIN1,APOE,SLC6A9,RHBDF2,RAB11FIP1,PKDCC,PLSCR1,EPHA3,CACNB3,ARHGAP1,GNAO1,NFKB1,GNAI2,HADH,LINC02210-CRHR1,WNK4,SERPINE2,UBQLN2,SNX33,RAB11FIP3,RHBDF1,ABCA2,CBARP,CALM3,CLIC2,BST2	cyan	VSMC_M2
GO:0060284	0.07	0.96	35	384	regulation of cell development	BP	0.7589	PLXNB2,APPL2,GLI3,NRP1,BIN1,ADGRA2,IGF1,MAN2A1,EFNA5,TGM2,LRP4,SEMA3B,RGMA,SEMA4B,PRUNE1,SEMA6C,STK25,ELL3,B2M,GRN,RND2,ADD1,BMP4,SERPINE2,SLIT2,TP53,SIGLEC15,TMEM98,PTPRS,ASPA,ABL1,IL34,IST1,SERPINF1,RPS19	cyan	VSMC_M2
GO:1900076	0.07	0.97	7	51	regulation of cellular response to insulin stimulus	BP	0.7589	APPL2,SOCS3,PRKCD,SRC,GNAI2,ERFE,TSC2	cyan	VSMC_M2
GO:0019220	0.07	0.95	89	1074	regulation of phosphate metabolic process	BP	0.7589	FLOT1,PPP6R2,PLXNB2,DEPTOR,DAXX,CARD10,GPNMB,AKT1S1,NRP1,BAX,NOP53,FZD4,CAB39L,APOE,SOCS3,CAMK1,HGS,KAT2B,FGFR1,SH3BP5,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,LRP4,MAPK8IP1,PTPN13,MOB2,GFRA2,CD81,CHRNA7,TIRAP,GNAI2,VEGFD,HEG1,ADORA2A,VEGFB,BMP4,LDB2,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,NUPR1,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MAP2K3,ROR1,MLLT1,TRAF4,WDR81,DVL1,TNFRSF14,TSC2,AXIN1,CBFA2T3,ABL1,IL34,INCA1,ABCA2,SLC8A3,HEXIM1,ZBTB7A,PML,PLPP3,EEF1A2,CALM3,CDK9,SDC4	cyan	VSMC_M2

GO:0051174	0.07	0.95	89	1074	regulation of phosphorus metabolic process	BP	0.7589	FLOT1,PPP6R2,PLXNB2,DEPTOR,DAXX,CARD10,GPNMB,AKT1S1,NRP1,BAX,NOP53,FZD4,CAB39L,APOE,SOCS3,CAMK1,HGS,KAT2B,FGFR1,SH3BP5,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,LRP4,MAPK8IP1,PTPN13,MOB2,GFRA2,CD81,CHRNA7,TIRAP,GNAI2,VEGFD,HEG1,ADORA2A,VEGFB,BMP4,LDB2,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,NUPR1,SHC1,ADAR,WARS,GPRC5B,PDGFRB,MAP2K3,ROR1,MLLT1,TRAF4,WDR81,DVL1,TNFRSF14,TSC2,AXIN1,CBFA2T3,ABL1,IL34,INCA1,ABCA2,SLC8A3,HEXIM1,ZBTB7A,PML,PLPP3,EEF1A2,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0090049	0.07	0.98	6	41	regulation of cell migration involved in sprouting angiogenesis	BP	0.7589	CARD10,HMOX1,NRP1,HDAC5,FOXC2,ABL1	cyan	VSMC_M2
GO:0001889	0.07	0.97	13	116	liver development	BP	0.7589	HMOX1,COBL,GLI3,DBP,RPS16,MAN2A1,RHBDD3,ACAT1,QDPR,PRKCSH,DNAAF1,FPGS,RPS15	cyan	VSMC_M2
GO:0071548	0.07	0.98	5	31	response to dexamethasone	BP	0.7589	FBXO32,FIBIN,CASP9,GBA,SERPINF1	cyan	VSMC_M2
GO:0016101	0.07	0.97	7	50	diterpenoid metabolic process	BP	0.7589	CYP2S1,PLB1,CYP4V2,PNPLA2,RLBP1,DHRS13,DGAT1	cyan	VSMC_M2
GO:0031323	0.07	0.94	334	4391	regulation of cellular metabolic process	BP	0.7589	CTDP1,TSHZ1,PYM1,STAT6,TCF21,FLOT1,DDAH2,PPP6R2,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,DEPTOR,TCF20,DAXX,TEF,PTPRK,TEAD3,MTCH1,TLE1,CARD10,NFIB,TRERF1,HMOX1,ACO1,KLF9,APPL2,MLIP,ZBTB45,ZSCAN18,TRIM14,P3H1,NAT14,GPNMB,EFEMP1,RRAGC,MEIS1,RNF144A,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,CAB39L,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,EXOC7,SOCS3,CAMK1,TIMP2,ZFP36,SAMD4B,ARAP1,HGS,KAT2B,TBC1D5,EIF3K,RHOG,DCXR,FGFR1,SH3BP5,TRIM21,SMPD1,APBB1,CLIP3,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,SNTA1,WT1,EFNA5,CHMP4B,TP53INP2,PATL1,TSHZ3,POU6F1,SERPING1,CAST,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,EPHA3,SRC,LRP4,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTPN13,SLC5A3,PNPLA2,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CTTN,CSTB,TUSC2,ZNF496,TPCN2,NFKB1,GNAI2,TPPP,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,APH1A,EXOC8,MN1,VEGFD,WDR6,ECM1,NELFCD,CASP10,ADCY1,FURIN,VPS11,ERFE,BCL9L,HEG1,RFX5,GATA5,CLCN2,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,CAPN1,FYCO1,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,PSAP,TSC22D4,VEGFB,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,CPAMD8,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,EPHA2,MYRF,GABARAP,ZBTB17,TCF12,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PRKACA,ZFP36L1,IL27RA,UBQLN2,RFX1,SPIN4,NTRK1	cyan	VSMC_M2
GO:0021952	0.07	0.98	4	23	central nervous system projection neuron axonogenesis	BP	0.7589	NFIB,DCLK1,SCN1B,SLIT2	cyan	VSMC_M2
GO:0002027	0.07	0.97	9	73	regulation of heart rate	BP	0.7589	BIN1,SCN1B,SNTA1,CTNNA3,KCND3,JUP,PRKACA,CALM3,RNLS	cyan	VSMC_M2
GO:0061462	0.07	0.98	6	41	protein localization to lysosome	BP	0.7589	HGS,GNPTAB,CD81,M6PR,GLMP,NAGPA	cyan	VSMC_M2
GO:0002449	0.07	0.96	17	159	lymphocyte mediated immunity	BP	0.7589	STAT6,ULBP2,BCL3,RFTN1,LAMP1,SLC15A4,SERPING1,PRKCD,CD81,B2M,C1R,C1S,ARRB2,PLEKHM2,IL27RA,C6,CD55	cyan	VSMC_M2
GO:0050670	0.07	0.96	15	137	regulation of lymphocyte proliferation	BP	0.7589	IRF1,GPNMB,PNP,LMO1,IGF1,MAPK8IP1,CD81,TIRAP,BMP4,DLG5,ERBB2,IL27RA,TNFRSF14,CD55,SDC4	cyan	VSMC_M2
GO:0072088	0.07	0.97	8	62	nephron epithelium morphogenesis	BP	0.7589	TCF21,GLI3,WT1,LZTS2,STAT1,WNT2B,WNK4,BMP4	cyan	VSMC_M2
GO:0061387	0.07	0.97	11	95	regulation of extent of cell growth	BP	0.7589	NRP1,APOE,CTTN,SEMA3B,RGMA,SEMA4B,SEMA6C,RND2,PTPRS,ABL1,IST1	cyan	VSMC_M2
GO:0016482	0.07	0.96	16	153	cytosolic transport	BP	0.7589	GGA1,TBC1D17,AP2A1,DENND2A,EHD3,TBC1D5,LAMP1,CHMP3,SRC,SYS1,TPCN2,VPS11,KIF1A,WDR81,SGSM2,VPS26B	cyan	VSMC_M2
GO:0007600	0.07	0.96	30	320	sensory perception	BP	0.7589	TGFBI,TRPM3,EFEMP1,BBS9,FZD4,SLITRK6,EPYC,CYP4V2,HEXB,GLRB,CACNB3,BBS2,SFRP5,NDN,CHRNA7,LEF1,RLBP1,LAMB2,ADORA2A,RPGR,NYX,NR2F6,ARRB2,SERPINE2,NTRK1,ROR1,PIEZO2,RETREG1,KCND2,SERPINB6	cyan	VSMC_M2
GO:0031099	0.07	0.96	16	150	regeneration	BP	0.7589	HMOX1,GLI3,RPS16,IGF1,CD81,CAPN3,RGMA,BCL9,LAMB2,GRN,ADAM15,PTPRS,FPGS,RPS15,PTGFRN,GATA4	cyan	VSMC_M2
GO:0050771	0.07	0.97	7	52	negative regulation of axonogenesis	BP	0.7589	NRP1,LRP4,SEMA3B,RGMA,SEMA4B,SEMA6C,PTPRS	cyan	VSMC_M2
GO:0031279	0.07	0.98	5	32	regulation of cyclase activity	BP	0.7589	TIMP2,GNAI2,LINC02210-CRHR1,AKAP5,CALM3	cyan	VSMC_M2
GO:0071383	0.07	0.96	17	163	cellular response to steroid hormone stimulus	BP	0.7589	TCF21,DAXX,FBXO32,TRERF1,KLF9,ZFP36,SRC,VPS11,LMO3,BMP4,HDAC6,CASP9,ZFP36L1,AR,KANK2,SERPINF1,ZBTB7A	cyan	VSMC_M2
GO:1903364	0.07	0.96	15	137	positive regulation of cellular protein catabolic process	BP	0.7589	RNF144A,NOP53,APOE,CD81,VPS11,MAGEF1,GABARAP,UBQLN2,GBA,NUPR1,DVL1,ELOB,AXIN1,CBFA2T3,ABCA2	cyan	VSMC_M2
GO:0030336	0.07	0.96	22	223	negative regulation of cell migration	BP	0.7589	AFDN,PTPRK,CARD10,HMOX1,RRAS,RHOB,APOE,ANGPT4,SFRP2,NDRG4,NISCH,HDAC5,NBL1,DLG5,JUP,MCC,IL27RA,SLIT2,ADAM15,PODN,SERPINF1,BST2	cyan	VSMC_M2

GO:0006355	0.07	0.94	189	2411	regulation of transcription, DNA-templated	BP	0.7589	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0043087	0.07	0.96	27	285	regulation of GTPase activity	BP	0.7589	PLXNB2,TBC1D22A,AFDN,TBC1D2,TBC1D17,ARAP1,TBC1D5,RHOG,EFNA5,EPHA3,TGM2,GNAO1,RGMA,SGSM1,SIPA1L2,ARHGEF10,BCR,ARRB2,EPHA2,ERBB2,NTRK1,PBXIP1,SGSM2,AGRN,TSC2,RGS8,RGS10	cyan	VSMC_M2
GO:0140352	0.07	0.95	54	618	export from cell	BP	0.7589	HMOX1,P3H1,CADPS2,FZD4,APOE,EXOC7,RHBDF2,LTBP4,HGS,RAB11FIP1,LAMP1,APBB1,ATP4A,GNPTAB,IGF1,EFNA5,EXOC2,NISCH,PCSK6,TPCN2,GNAI2,HADH,DISP1,SV2A,EXOC8,RHBDD3,ADCY1,FES,FURIN,VPS11,LINC02210-CRHR1,KCND3,M6PR,ADORA2A,PORCN,USE1,SERPINE2,GIPC1,CPLX2,RASL10B,ABCC1,LLGL1,NAGPA,DVL1,PTGDS,PHPT1,RAB11FIP3,RHBDF1,SLC8A3,CBARP,CALM3,SDC4,STX3,RAB11B	cyan	VSMC_M2
GO:1903506	0.07	0.94	189	2412	regulation of nucleic acid-templated transcription	BP	0.7589	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0030001	0.07	0.95	51	587	metal ion transport	BP	0.7589	TRPM3,KCNQ5,SLC17A7,STOM,BAX,BIN1,ABCB8,SLC6A9,EHD3,SLC4A9,ATP4A,SCN1B,SNTA1,SLC38A7,CACNB3,PLCG1,ARHGAP1,GNAO1,SLC5A3,CRACR2B,CHRNA7,CAPN3,CACNA2D2,TPCN2,GNAI2,ANXA9,TCN2,LINC02210-CRHR1,B2M,KCND3,ORAI2,ADORA2A,HOMER3,WNK4,ARRB2,SERPINE2,PRKACA,MLLT6,TMEM175,ORAI3,ATOX1,PDGFRB,MCOLN1,ABL1,SLC8A3,CBARP,KCND2,PML,CALM3,CLIC2,RAB11B	cyan	VSMC_M2
GO:1903707	0.07	0.97	9	72	negative regulation of hemopoiesis	BP	0.7589	IRF1,GLI3,LRRC17,TMEM176B,TLR3,BMP4,ERBB2,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0150077	0.07	0.98	4	22	regulation of neuroinflammatory response	BP	0.7589	IGF1,GRN,DAGLA,NUPR1	cyan	VSMC_M2
GO:0032886	0.07	0.96	20	202	regulation of microtubule-based process	BP	0.7589	MARK4,TPPP2,KAT2B,LAMP1,CLIP3,EFNA5,CHMP4B,CHMP3,EPHA3,BBS2,TPPP,GAS2L1,FES,PRUNE1,MAP1S,HDAC6,ERBB2,FBXW5,ABL1,DNAAF1	cyan	VSMC_M2
GO:1903319	0.07	0.98	4	22	positive regulation of protein maturation	BP	0.7589	GSN,SPON1,SRC,CLEC3B	cyan	VSMC_M2
GO:1901888	0.07	0.96	17	165	regulation of cell junction assembly	BP	0.7589	FLOT1,NRP1,SLITRK6,EFNA5,EPHA3,SRC,TJP1,DLG5,EPHA2,PRKACA,NTRK1,PTPRS,AGRN,NPHP4,CLSTN1,ABL1,SDC4	cyan	VSMC_M2
GO:0009268	0.07	0.98	5	31	response to pH	BP	0.7589	SRC,GBA,MCOLN1,SERPINF1,RAB11B	cyan	VSMC_M2
GO:0014002	0.07	0.98	5	32	astrocyte development	BP	0.7589	VIM,LAMB2,ADORA2A,GRN,ROR1	cyan	VSMC_M2
GO:0050729	0.07	0.97	11	93	positive regulation of inflammatory response	BP	0.7589	PLA2G7,TLR3,TGM2,CD81,NFKBIA,GRN,IL17RA,NUPR1,GPRC5B,ABCC1,RPS19	cyan	VSMC_M2
GO:0072525	0.07	0.98	4	22	pyridine-containing compound biosynthetic process	BP	0.7589	NADSYN1,PTGIS,NMNAT2,PDXK	cyan	VSMC_M2
GO:0032944	0.07	0.96	15	138	regulation of mononuclear cell proliferation	BP	0.7589	IRF1,GPNMB,PNP,LMO1,IGF1,MAPK8IP1,CD81,TIRAP,BMP4,DLG5,ERBB2,IL27RA,TNFRSF14,CD55,SDC4	cyan	VSMC_M2
GO:0060337	0.07	0.97	6	41	type I interferon signaling pathway	BP	0.7589	IRF3,STAT1,IKBKE,ADAR,ISG15,OAS2	cyan	VSMC_M2
GO:0030837	0.07	0.97	7	53	negative regulation of actin filament polymerization	BP	0.7589	GSN,PRKCD,SSH3,ADD1,CAPZB,SLIT2,FLII	cyan	VSMC_M2
GO:0045089	0.07	0.97	10	83	positive regulation of innate immune response	BP	0.7589	IRF3,LAMP1,SLC15A4,PLSCR1,SRC,IKBKE,TIRAP,PQBP1,HEXIM1,RPS19	cyan	VSMC_M2
GO:0072273	0.07	0.98	4	23	metanephric nephron morphogenesis	BP	0.7589	WT1,STAT1,BMP4,PDGFRB	cyan	VSMC_M2

GO:0010092	0.07	0.98	5	32	specification of animal organ identity	BP	0.7589	GLI3,GATA5,WNT2B,BMP4,AR	cyan	VSMC_M2
GO:0002828	0.07	0.98	4	22	regulation of type 2 immune response	BP	0.7589	STAT6,CD81,ECM1,IL27RA	cyan	VSMC_M2
GO:0007224	0.07	0.96	13	119	smoothened signaling pathway	BP	0.7589	GLI3,DZIP1,BOC,KIF7,PTCHD1,GPC2,CC2D2A,DLG5,SERPINE2,PRKACA,ULK3,GLIS2,GAS1	cyan	VSMC_M2
GO:2001141	0.07	0.94	189	2416	regulation of RNA biosynthetic process	BP	0.7589	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:1903078	0.07	0.97	7	52	positive regulation of protein localization to plasma membrane	BP	0.7589	RHOG,CLIP3,EPHA3,EPHA2,AKAP5,PPP1R9B,STX3	cyan	VSMC_M2
GO:0045646	0.07	0.97	6	42	regulation of erythrocyte differentiation	BP	0.7589	ZFP36,STAT1,B2M,ZFP36L1,ISG15,ZFPM1	cyan	VSMC_M2
GO:0016310	0.07	0.94	116	1440	phosphorylation	BP	0.7589	FLOT1,CHKB,PLXNB2,RPS6KA2,DEPTOR,DAXX,ST3GAL1,CARD10,GPNMB,EFEMP1,STK40,AKT1S1,STK17A,NRP1,BAX,NOP53,FZD4,CAB39L,MARK4,APOE,SOCS3,CAMK1,PAK4,HGS,KAT2B,FGFR1,SH3BP5,DCLK1,SMPD1,PKDCC,CLIP3,ANGPT4,MAP3K12,GNPTAB,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,LRP4,MAPK8IP1,PTPN13,PIK3C2B,MOB2,GFRA2,CD81,PHKG1,CHRNA7,IKBKE,TIRAP,IP6K1,VEGFD,GRK5,FES,HEG1,STK25,UCKL1,RNASEL,BCR,ADORA2A,CDC42BPG,VEGFB,WNK4,BMP4,LDB2,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,PRKACA,NTRK1,SLIT2,AR,TP53,PDK2,GBA,PPP1R9B,NUPR1,SHC1,ADAR,TEX14,WARS,ULK3,GPRC5B,PDGFRB,MAP2K3,ROR1,MLLT1,TRAF4,WDR81,DVL1,TNFRSF14,TSC2,AXIN1,CBFA2T3,ABL1,IL34,TK2,INCA1,SLC8A3,HEXIM1,ZBTB7A,PML,PLPP3,EEF1A2,CALM3,CDK9,SDC4,NAGK,PDXK,GTF2H4	cyan	VSMC_M2
GO:0072332	0.07	0.97	8	63	intrinsic apoptotic signaling pathway by p53 class mediator	BP	0.7589	BAX,BCL3,ELL3,TP53BP2,TP53,PDK2,NUPR1,PML	cyan	VSMC_M2
GO:0071407	0.07	0.95	40	448	cellular response to organic cyclic compound	BP	0.7589	TCF21,FLOT1,EHMT2,DAXX,FBXO32,TRERF1,KLF9,IRF3,ATG7,ZFP36,FOLR2,TLR3,WT1,SRC,TGM2,GNAO1,STAT1,NFKB1,MN1,ADCY1,FES,VPS11,LMO3,PHEX,BMP4,HDAC6,PQBP1,ARRB2,JUP,CASP9,PRKACA,ZFP36L1,AR,PPP1R9B,KANK2,ABL1,SLC8A3,SERPINF1,ZBTB7A,RGS8	cyan	VSMC_M2
GO:0051607	0.07	0.96	18	174	defense response to virus	BP	0.76061	IRF1,IRF3,NOP53,AGBL5,ATG7,TLR3,PLSCR1,STAT1,RNASEL,MOV10,PQBP1,DHX58,ADAR,ISG15,OAS2,PML,CARD8,BST2	cyan	VSMC_M2
GO:0140546	0.07	0.96	18	174	defense response to symbiont	BP	0.76061	IRF1,IRF3,NOP53,AGBL5,ATG7,TLR3,PLSCR1,STAT1,RNASEL,MOV10,PQBP1,DHX58,ADAR,ISG15,OAS2,PML,CARD8,BST2	cyan	VSMC_M2
GO:0042987	0.07	0.97	7	52	amyloid precursor protein catabolic process	BP	0.76223	BIN1,APOE,IGF1,SPON1,CHRNA7,APH1A,ABCA2	cyan	VSMC_M2
GO:0032801	0.07	0.98	4	23	receptor catabolic process	BP	0.76384	APOE,FURIN,CAPN1,ABCA2	cyan	VSMC_M2
GO:0110053	0.07	0.95	23	237	regulation of actin filament organization	BP	0.7648	ARHGAP18,GSN,NRP1,BIN1,ARAP1,RHPN2,PRKCD,C15orf62,SORBS3,TJP1,CTTN,SSH3,ARPC5,ARHGEF10,ADD1,CAPZB,ARHGEF10L,ALOX15,CGNL1,SLIT2,FLII,ABL1,SDC4	cyan	VSMC_M2
GO:0071827	0.07	0.98	5	32	plasma lipoprotein particle organization	BP	0.7648	PLA2G7,APOE,PRKACA,LCAT,DGAT1	cyan	VSMC_M2
GO:0033143	0.07	0.97	8	63	regulation of intracellular steroid hormone receptor signaling pathway	BP	0.76631	TCF21,SRC,VPS11,LMO3,HDAC6,AR,KANK2,ZBTB7A	cyan	VSMC_M2
GO:0060632	0.08	0.98	5	32	regulation of microtubule-based movement	BP	0.76755	TPPP2,LAMP1,BBS2,HDAC6,DNAAF1	cyan	VSMC_M2
GO:0061337	0.08	0.97	9	76	cardiac conduction	BP	0.76909	BIN1,EHD3,SCN1B,CTNNA3,KCND3,JUP,PRKACA,SLC8A3,CALM3	cyan	VSMC_M2
GO:0090050	0.08	0.98	4	23	positive regulation of cell migration involved in sprouting angiogenesis	BP	0.77085	HMOX1,NRP1,FOXC2,ABL1	cyan	VSMC_M2
GO:0021680	0.08	0.98	4	24	cerebellar Purkinje cell layer development	BP	0.77409	COQ8B,NAGLU,GBA,RERE	cyan	VSMC_M2

GO:0010468	0.08	0.93	263	3428	regulation of gene expression	BP	0.77544	CTDP1,TSHZ1,PYM1,STAT6,TCF21,AKAP12,FLOT1,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,AFDN,TAPBP,TCF20,DAXX,TEF,PTPRK,GSDMD,TEAD3,TLE1,NFIB,TRERF1,HMOX1,LRRC19,ACO1,KLF9,APPL2,MLIP,ZBTB45,ZSCAN18,TRIM14,ITGB8,NAT14,GPNMB,EFEMP1,TRIL,MEIS1,STK40,PTOV1,AASS,GLI3,SIM1,IRF3,GSN,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,LURAP1,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,ATRAID,CAMK1,PLD3,PNP,ZFP36,SAMD4B,HGS,KAT2B,EIF3K,RFTN1,RHOG,IL5RA,TRIM21,APBB1,SLC15A4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,CAST,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,BPI,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,TUSC2,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,FURIN,BCL9L,HEG1,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,FRMD8,B2M,DPF2,ADORA2A,CLEC3B,PCBD1,HDAC5,TSC22D4,HOMER3,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DHX58,DNAJB6,ARRB2,JUP,WIZ,EPHA2,MYRF,IL17RA,ZBTB17,TCF12,SERPINE2,ERBB2,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,GBA,NUPR1,SHC1,PBXIP1,ADAR,ACP5,KANK2,WARS,CENPV,GPRC5B,TMEM98,MTA1,MAP2K3,ROR1,MLLT1,PTPRS,MOSPD1,MPND,EEF2,GLIS2,ABCD1,DVL1,AGRN,ISG15,E4F1,DPH7,TNFRSF14,NELFB,TCF3,SBNO2,EDF1,INPP5E,AXIN1,RERE,TCF25,BRD3,CBFA2T	cyan	VSMC_M2
GO:0001578	0.08	0.96	10	86	microtubule bundle formation	BP	0.77576	RSPH9,CCDC114,MARK4,BBS2,TPPP,GAS2L1,FES,MAP1S,CC2D2A,DNAAF1	cyan	VSMC_M2
GO:0000423	0.08	0.98	4	24	mitophagy	BP	0.77758	HDAC6,TP53,RETREG1,TSC2	cyan	VSMC_M2
GO:0061008	0.08	0.96	13	119	hepaticobiliary system development	BP	0.77918	HMOX1,COBL,GLI3,DBP,RPS16,MAN2A1,RHBDD3,ACAT1,QDPR,PRKCSH,DNAAF1,FPGS,RPS15	cyan	VSMC_M2
GO:0070861	0.08	0.98	4	23	regulation of protein exit from endoplasmic reticulum	BP	0.7822	OS9,EDEM2,CD81,SLC51B	cyan	VSMC_M2
GO:0006690	0.08	0.97	8	62	icosanoid metabolic process	BP	0.78432	ZADH2,CYP2S1,GGT7,PTGIS,ALOX15,DAGLA,ABCC1,PTGDS	cyan	VSMC_M2
GO:0046632	0.08	0.96	9	74	alpha-beta T cell differentiation	BP	0.78503	STAT6,IRF1,GLI3,BCL3,PNP,LEF1,TMEM98,ABL1,ZFPM1	cyan	VSMC_M2
GO:0110020	0.08	0.96	10	86	regulation of actomyosin structure organization	BP	0.78552	NRP1,ARAP1,RHPN2,SORBS3,TJP1,ARHGEF10,ARHGEF10L,CGNL1,ABL1,SDC4	cyan	VSMC_M2
GO:0050680	0.08	0.96	12	108	negative regulation of epithelial cell proliferation	BP	0.78552	PTPRK,NFIB,KLF9,APOE,SFRP2,STAT1,B2M,BMP4,MCC,AR,NUPR1,SERPINF1	cyan	VSMC_M2
GO:0001736	0.08	0.97	8	64	establishment of planar polarity	BP	0.78552	PRICKLE2,SFRP2,FOXF2,VANGL2,MED12,ROR1,DVL1,ABL1	cyan	VSMC_M2
GO:0007164	0.08	0.97	8	64	establishment of tissue polarity	BP	0.78552	PRICKLE2,SFRP2,FOXF2,VANGL2,MED12,ROR1,DVL1,ABL1	cyan	VSMC_M2
GO:0010035	0.08	0.94	39	435	response to inorganic substance	BP	0.78552	STAT6,DAXX,CUTA,HMOX1,ACO1,RHOB,SELENOW,ATG7,SMPD1,APBB1,PLSCR1,PRKCD,SRC,GNAO1,STAT1,FIBIN,CAPN3,ADCY1,CCS,STK25,PHEX,B2M,ADD1,QDPR,HDAC6,ALOX15,CASP9,NTRK1,PCGF2,GRIA1,PDGFRB,MCOLN1,EEF2,ABL1,SERPINF1,JUNB,EEF1A2,CALM3,ADPRHL2	cyan	VSMC_M2
GO:0032611	0.08	0.97	7	52	interleukin-1 beta production	BP	0.78552	GSDMD,IGF1,TMEM106A,ARRB2,ACP5,PML,CARD8	cyan	VSMC_M2
GO:0032651	0.08	0.97	7	52	regulation of interleukin-1 beta production	BP	0.78552	GSDMD,IGF1,TMEM106A,ARRB2,ACP5,PML,CARD8	cyan	VSMC_M2
GO:0045747	0.08	0.97	5	33	positive regulation of Notch signaling pathway	BP	0.78854	RFNG,SRC,TM2D3,GATA5,EPN2	cyan	VSMC_M2
GO:0043537	0.08	0.97	5	33	negative regulation of blood vessel endothelial cell migration	BP	0.78854	CARD10,APOE,ANGPT4,HDAC5,JUP	cyan	VSMC_M2
GO:1904375	0.08	0.96	12	107	regulation of protein localization to cell periphery	BP	0.78997	RHOG,PKDCC,CLIP3,EPHA3,TMBIM1,EPHA2,AKAP5,AR,PPP1R9B,ABCA2,GRASP,STX3	cyan	VSMC_M2
GO:1904019	0.08	0.96	10	86	epithelial cell apoptotic process	BP	0.78997	HMOX1,GSN,ZFP36,PAK4,CAST,PLCG1,ARRB2,ZFP36L1,NUPR1,ABL1	cyan	VSMC_M2
GO:0007423	0.08	0.94	37	415	sensory organ development	BP	0.78997	TSHZ1,EFEMP1,MEIS1,GLI3,SLC17A7,NRP1,BAX,MEIS3,FZD4,VIM,SLITRK6,RARG,MAN2A1,WT1,FOXF2,LRP10,LEF1,LAMB2,CLCN2,WNT2B,BMP4,NAGLU,CC2D2A,CPAMD8,EPHA2,SMOC1,PDGFRB,ROR1,DVL1,NPHP4,FOXC2,PBX3,SERPINF1,SDC4,PYGO2,COL8A1,MPV17	cyan	VSMC_M2
GO:0042552	0.08	0.96	12	109	myelination	BP	0.79029	RARG,HEXB,TPPP,B4GALT5,ARHGEF10,MYRF,ERBB2,TMEM98,ABCD1,ASPA,ABCA2,SLC8A3	cyan	VSMC_M2
GO:0021761	0.08	0.96	9	75	limbic system development	BP	0.79093	GLI3,NRP1,BAX,TMEM108,BBS2,LEF1,ARPC5,PPP1R9B,PTPRS	cyan	VSMC_M2
GO:0071357	0.08	0.97	6	42	cellular response to type I interferon	BP	0.79093	IRF3,STAT1,IKBKE,ADAR,ISG15,OAS2	cyan	VSMC_M2
GO:0043153	0.08	0.98	4	23	entrainment of circadian clock by photoperiod	BP	0.79093	NR2F6,TP53,MTA1,PML	cyan	VSMC_M2
GO:0002700	0.08	0.96	12	106	regulation of production of molecular mediator of immune response	BP	0.79093	STAT6,HMOX1,TRIL,SLC15A4,TLR3,CD81,B2M,IL27RA,GPRC5B,TNFRSF14,CD55,BST2	cyan	VSMC_M2
GO:0033598	0.08	0.98	4	24	mammary gland epithelial cell proliferation	BP	0.79126	STAT6,BAX,EPHA2,PYGO2	cyan	VSMC_M2
GO:0044088	0.08	0.97	6	42	regulation of vacuole organization	BP	0.79126	EHMT2,CHMP4B,GRN,UBQLN2,NUPR1,NPRL3	cyan	VSMC_M2
GO:0043254	0.08	0.95	33	361	regulation of protein-containing complex assembly	BP	0.79126	ARHGAP18,GSN,BAX,NOP53,BIN1,APOE,TPPP2,CLIP3,PRKCD,SRC,C15orf62,IKBKE,TIRAP,CTTN,TPPP,SSH3,FES,PRUNE1,ARPC5,ADD1,CAPZB,HDAC6,ALOX15,SLIT2,TP53,GBA,WARS,FLII,ISG15,ABL1,LCAT,CARD8,BMF	cyan	VSMC_M2
GO:0001707	0.08	0.97	7	53	mesoderm formation	BP	0.79211	SFRP2,EXT2,LEF1,BMP4,EPHA2,PRKACA,FOXC2	cyan	VSMC_M2
GO:1902903	0.08	0.95	30	327	regulation of supramolecular fiber organization	BP	0.79252	ARHGAP18,GSN,NRP1,BIN1,APOE,ARAP1,CLIP3,RHPN2,PRKCD,C15orf62,SORBS3,CHRNA7,TJP1,CTTN,SSH3,FES,PRUNE1,ARPC5,ARHGEF10,ADD1,CAPZB,MAP1S,HDAC6,ARHGEF10L,ALOX15,CGNL1,SLIT2,FLII,ABL1,SDC4	cyan	VSMC_M2
GO:1903131	0.08	0.95	28	297	mononuclear cell differentiation	BP	0.79273	STAT6,IRF1,PTPRK,ST3GAL1,ITGB8,GLI3,BAX,TMEM176B,BCL3,PNP,TUSC2,LEF1,FES,B2M,HDAC5,BMP4,ERBB2,ZFP36L1,NTRK1,TP53,GBA,TMEM98,TCF3,ABL1,IL34,ZBTB7A,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0050808	0.08	0.95	30	329	synapse organization	BP	0.79623	PLXNB2,ARHGAP39,NRP1,APOE,SLITRK6,CAMK1,EFNB2,TMEM108,LZTS3,PPFIBP2,SNTA1,CAST,GLRB,CACNB3,LRP4,CHRNA7,CTTN,LAMB2,KIF1A,DLG5,HDAC6,ERBB2,NTRK1,PTPRS,DVL1,AGRN,CLSTN1,ABL1,NFIA,SLC8A3	cyan	VSMC_M2
GO:0034123	0.08	0.98	4	23	positive regulation of toll-like receptor signaling pathway	BP	0.7991	FLOT1,SLC15A4,TLR3,TIRAP	cyan	VSMC_M2

GO:0042158	0.08	0.96	10	84	lipoprotein biosynthetic process	BP	0.7991	APOE,ATG7,CLIP3,PORCN,WDR45,GBA,ZDHHC9,PIGQ,LCAT,NMT2	cyan	VSMC_M2
GO:2000242	0.08	0.97	6	42	negative regulation of reproductive process	BP	0.7991	ZFPM2,RPS6KA2,IGF1,WT1,BMP4,SERPINF1	cyan	VSMC_M2
GO:0048846	0.08	0.97	5	34	axon extension involved in axon guidance	BP	0.7991	NRP1,SEMA3B,SEMA4B,SEMA6C,SLIT2	cyan	VSMC_M2
GO:1902284	0.08	0.97	5	34	neuron projection extension involved in neuron projection guidance	BP	0.7991	NRP1,SEMA3B,SEMA4B,SEMA6C,SLIT2	cyan	VSMC_M2
GO:0044267	0.08	0.93	285	3725	cellular protein metabolic process	BP	0.7991	CTDP1,PYM1,OS9,MGAT4B,FLOT1,PPP6R2,EHMT2,PLXNB2,EIF3H,RPS6KA2,DEPTOR,B3GALT4,DAXX,FBXO32,PTPRK,ST3GAL1,CDC14C,MTCH1,CARD10,KCTD17,TRERF1,GCNT1,ACO1,CUL9,IARS,TRIM14,GALNT12,P3H1,GPNMB,EFEMP1,RNF144A,STK40,AKT1S1,STK17A,AASS,GSN,NRP1,KLF15,BAX,RPL18,PARP12,NOP53,ABTB1,FKRP,TRIM13,FZD4,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,BCL3,MIF4GD,AGAP3,ATRAID,ATG7,SOCS3,CAMK1,RNF170,RPS16,TIMP2,ZFP36,SAMD4B,PAK4,RNF213,RPL15,HGS,KAT2B,EIF3K,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,TPP1,CLIP3,ANGPT4,EIF3F,MAP3K12,RBCK1,IGF1,TLR3,SNTA1,MAN2A1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,GGT7,GALNT18,GGCX,SERPING1,CAST,EDEM2,CTSB,ARRDC3,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,RIOX2,FOXF2,MAPK8IP1,MMP2,PTPN13,EXT2,MOB2,GFRA2,CD81,NDN,PHKG1,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,MRPL36,CSTB,NFKB1,GNAI2,TPPP,B4GALT4,HIST1H1C,RGMA,UBA7,LEF1,TBL1Y,B4GALT5,SSH3,APH1A,DCAF11,VEGFD,GCNT7,ECM1,CTSK,GRK5,CASP10,FES,MINDY1,FURIN,VPS11,HEG1,B4GAT1,STK25,ATG4B,RNASEL,MAGEF1,PHEX,NFKBIA,MOV10,DTX2,BCR,ADORA2A,CLEC3B,ADAMTS7,CDC42BPG,GRN,PCOLCE,HDAC5,VEGFB,MACROD1,WNK4,BMP4,MAEA,PORCN,CPAMD8,HDAC6,B3GAT3,WDR45,DNAJB6,FKBP10,ARRB2,EPHA2,GABARAP,FNTB,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PRKACA,ZFP36L1,UBQLN2,NTRK1,PCGF2,MLLT6,SLIT2,TP53,KAT8,ELMSAN1,UBQLN4,PDK2,MED12,GBA,PPP1R9B,SLC51B,NUPR1,SHC1,PBXIP1,ADAR,TEX14,WARS,ULK3,GPRC5B,SNX33,PDGFRB,TMEM98,NUDT14,MTA1,MARBX2,PDP1,MLLT1,CLPP,TBL1XR1,TRAF4,NTRK3,K	cyan	VSMC_M2
GO:0072329	0.08	0.96	11	95	monocarboxylic acid catabolic process	BP	0.7991	ACAA1,ECH1,DECR1,ACADS,HADH,ECHS1,ACAT1,CPT2,ABCD1,CRAT,LDHD	cyan	VSMC_M2
GO:0008016	0.08	0.95	15	144	regulation of heart contraction	BP	0.7991	BIN1,EHD3,GAA,SCN1B,SNTA1,GNAO1,CTNNA3,KCND3,JUP,PRKACA,SLC8A3,GATA4,CALM3,CLIC2,RNLS	cyan	VSMC_M2
GO:0008045	0.08	0.98	4	24	motor neuron axon guidance	BP	0.7991	NRP1,RHOG,ERBB2,SLIT2	cyan	VSMC_M2
GO:0060255	0.08	0.93	338	4468	regulation of macromolecule metabolic process	BP	0.7991	CTDP1,TSHZ1,PYM1,STAT6,TCF21,AKAP12,FLOT1,PPP6R2,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,TAPBP,TCF20,DAXX,TEF,PTPRK,GSDMD,TEAD3,MTCH1,TLE1,GGA1,CARD10,NFIB,TRERF1,HMOX1,LRRC19,ACO1,KLF9,APPL2,MLIP,ZBTB45,ZSCAN18,TRIM14,ITGB8,P3H1,NAT14,GPNMB,EFEMP1,TRIL,MEIS1,RNF144A,STK40,AKT1S1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,LURAP1,TRIM13,FZD4,CAB39L,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,LTBP4,SOCS3,CAMK1,PLD3,PNP,TIMP2,ZFP36,SAMD4B,ARAP1,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,FGFR1,IL5RA,SH3BP5,TRIM21,SMPD1,APBB1,CLIP3,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,SNTA1,WT1,EFNA5,TP53INP2,PATL1,TSHZ3,POU6F1,SERPING1,CAST,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,BPI,LRP4,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTPN13,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CSTB,TUSC2,ZNF496,NFKB1,GNAI2,SPOCD1,TPPP,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,APH1A,MN1,VEGFD,ECM1,RHBDD3,NELFCD,CASP10,ADCY1,FURIN,VPS11,BCL9L,HEG1,RFX5,GATA5,HELZ2,ATG4B,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,FRMD8,B2M,DPF2,ADORA2A,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,TSC22D4,HOMER3,VEGFB,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,CPAMD8,HDAC6,ZBTB3,PQBP1,DHX58,DNAJB6,ARRB2,JUP,WIZ,EPHA2,MYRF,IL17RA,GABARAP,ZBTB17,TCF12,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PR	cyan	VSMC_M2
GO:2001234	0.08	0.95	19	187	negative regulation of apoptotic signaling pathway	BP	0.7991	GRINA,HMOX1,NRP1,BAX,MEIS3,IGF1,SFRP2,SRC,MAPK8IP1,CTTN,GNAI2,ELL3,TMEM161A,TMBIM1,BMP4,ARRB2,PCGF2,AR,GATA4	cyan	VSMC_M2
GO:2000027	0.08	0.96	12	108	regulation of animal organ morphogenesis	BP	0.7991	PRICKLE2,WT1,SFRP2,VANGL2,GATA5,WNT2B,BMP4,AR,MED12,ROR1,DVL1,ABL1	cyan	VSMC_M2
GO:0032940	0.08	0.94	50	574	secretion by cell	BP	0.7991	HMOX1,P3H1,CADPS2,FZD4,APOE,EXOC7,RHBDF2,LTBP4,HGS,RAB11FIP1,LAMP1,APBB1,GNPTAB,IGF1,EFNA5,EXOC2,NISCH,PCSK6,TPCN2,GNAI2,HADH,DISP1,SV2A,EXOC8,RHBDD3,ADCY1,FES,FURIN,VPS11,LINC02210-CRHR1,M6PR,ADORA2A,PORCN,USE1,SERPINE2,GIPC1,CPLX2,RASL10B,LLGL1,NAGPA,DVL1,PTGDS,PHPT1,RAB11FIP3,RHBDF1,CBARP,CALM3,SDC4,STX3,RAB11B	cyan	VSMC_M2
GO:0019362	0.08	0.98	4	23	pyridine nucleotide metabolic process	BP	0.7991	NADSYN1,PTGIS,NMNAT2,NUDT13	cyan	VSMC_M2
GO:0046496	0.08	0.98	4	23	nicotinamide nucleotide metabolic process	BP	0.7991	NADSYN1,PTGIS,NMNAT2,NUDT13	cyan	VSMC_M2
GO:0046634	0.08	0.96	8	63	regulation of alpha-beta T cell activation	BP	0.7991	IRF1,GLI3,PNP,MAPK8IP1,CD81,ADORA2A,TNFRSF14,CD55	cyan	VSMC_M2
GO:0010667	0.08	0.98	4	23	negative regulation of cardiac muscle cell apoptotic process	BP	0.79925	HSPB6,SFRP2,NUPR1,GATA4	cyan	VSMC_M2
GO:0071385	0.08	0.97	6	43	cellular response to glucocorticoid stimulus	BP	0.80013	FBXO32,KLF9,ZFP36,CASP9,ZFP36L1,SERPINF1	cyan	VSMC_M2
GO:0042542	0.08	0.96	13	118	response to hydrogen peroxide	BP	0.80043	STAT6,HMOX1,RHOB,PRKCD,SRC,GNAO1,STAT1,STK25,HDAC6,PCGF2,PDGFRB,EEF2,ABL1	cyan	VSMC_M2
GO:0002695	0.08	0.96	13	118	negative regulation of leukocyte activation	BP	0.80324	IRF1,HMOX1,GPNMB,GLI3,BPI,RHBDD3,ADORA2A,GRN,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0001975	0.08	0.98	4	23	response to amphetamine	BP	0.80378	ADORA2A,PPP1R9B,CALM3,RGS10	cyan	VSMC_M2

GO:0051171	0.08	0.93	310	4082	regulation of nitrogen compound metabolic process	BP	0.80684	CTDP1,TSHZ1,PYM1,STAT6,TCF21,FLOT1,DDAH2,PPP6R2,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,DEPTOR,TCF20,DAXX,TEF,PTPRK,TEAD3,MTCH1,TLE1,GGA1,CARD10,NFIB,TRERF1,HMOX1,ACO1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,P3H1,NAT14,GPNMB,EFEMP1,MEIS1,RNF144A,AKT1S1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,CAB39L,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,LTBP4,SOCS3,CAMK1,TIMP2,ZFP36,SAMD4B,HGS,KAT2B,EIF3K,RHOG,FGFR1,SH3BP5,TRIM21,SMPD1,APBB1,CLIP3,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,SNTA1,WT1,EFNA5,TP53INP2,PATL1,TSHZ3,POU6F1,SERPING1,CAST,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,LRP4,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTPN13,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CSTB,ZNF496,NFKB1,GNAI2,TPPP,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,APH1A,MN1,VEGFD,ECM1,RHBDD3,NELFCD,CASP10,ADCY1,FURIN,VPS11,BCL9L,HEG1,RFX5,GATA5,HELZ2,ATG4B,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,TSC22D4,VEGFB,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,CPAMD8,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,GABARAP,ZBTB17,TCF12,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PRKACA,ZFP36L1,IL27RA,UBQLN2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,SLIT2,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,PDK2,MED12,GBA	cyan	VSMC_M2
GO:0016054	0.08	0.95	19	186	organic acid catabolic process	BP	0.80734	DDAH2,BCKDHB,AASS,ACAA1,ECH1,DECR1,ACADS,HADH,SCLY,ECHS1,ACAT1,QDPR,CPT2,ABCD1,ASPA,RENBP,CRAT,LDHD,NAGK	cyan	VSMC_M2
GO:0042771	0.08	0.97	5	34	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	BP	0.80867	BCL3,ELL3,TP53,NUPR1,PML	cyan	VSMC_M2
GO:0062208	0.08	0.97	5	33	positive regulation of pattern recognition receptor signaling pathway	BP	0.80906	FLOT1,SLC15A4,TLR3,TIRAP,DHX58	cyan	VSMC_M2
GO:0007272	0.08	0.96	12	110	ensheathment of neurons	BP	0.80906	RARG,HEXB,TPPP,B4GALT5,ARHGEF10,MYRF,ERBB2,TMEM98,ABCD1,ASPA,ABCA2,SLC8A3	cyan	VSMC_M2
GO:0008366	0.08	0.96	12	110	axon ensheathment	BP	0.80906	RARG,HEXB,TPPP,B4GALT5,ARHGEF10,MYRF,ERBB2,TMEM98,ABCD1,ASPA,ABCA2,SLC8A3	cyan	VSMC_M2
GO:0045055	0.08	0.95	17	167	regulated exocytosis	BP	0.80906	HMOX1,CADPS2,RAB11FIP1,LAMP1,GNAI2,SV2A,ADCY1,FES,ADORA2A,GIPC1,CPLX2,DVL1,PTGDS,CBARP,CALM3,STX3,RAB11B	cyan	VSMC_M2
GO:0010665	0.08	0.97	5	33	regulation of cardiac muscle cell apoptotic process	BP	0.80906	HSPB6,SFRP2,TP53,NUPR1,GATA4	cyan	VSMC_M2
GO:0071345	0.08	0.94	50	574	cellular response to cytokine stimulus	BP	0.80972	STAT6,AKAP12,IRF1,APPL2,IRF3,FZD4,VIM,IL17RC,SOCS3,RPS16,ZFP36,IL5RA,ACKR4,RARG,TLR3,SRC,BBS2,STAT1,IKBKE,NFKB1,LEF1,PTGIS,ECM1,NFKBIA,ADAMTS7,STAT5A,ALOX15,IL17RA,GIPC1,PRKACA,ZFP36L1,IL27RA,SLIT2,TP53,GBA,ADAR,TEX14,IL13RA1,ISG15,TNFRSF14,SBNO2,IL34,GBP6,OAS2,RAB43,PML,CARD8,VPS26B,CDK9,IL22RA1	cyan	VSMC_M2
GO:0001945	0.08	0.98	4	25	lymph vessel development	BP	0.80972	LGALS8,HEG1,EPHA2,FOXC2	cyan	VSMC_M2
GO:0006892	0.08	0.96	11	99	post-Golgi vesicle-mediated transport	BP	0.80972	GGA1,AP2A1,EHD3,LAMP1,PKDCC,BBS2,EXOC2,SYS1,OSBPL5,EXOC8,LLGL1	cyan	VSMC_M2
GO:0042246	0.08	0.97	7	53	tissue regeneration	BP	0.80972	IGF1,CD81,CAPN3,BCL9,ADAM15,PTGFRN,GATA4	cyan	VSMC_M2
GO:0048843	0.08	0.98	4	24	negative regulation of axon extension involved in axon guidance	BP	0.80972	NRP1,SEMA3B,SEMA4B,SEMA6C	cyan	VSMC_M2
GO:0051092	0.08	0.95	13	119	positive regulation of NF-kappaB transcription factor activity	BP	0.80972	FLOT1,TRIM14,TRIM13,TRIM21,RBCK1,TLR3,TRIM8,CAPN3,TIRAP,NTRK1,AR,ROR1,ZBTB7A	cyan	VSMC_M2
GO:0006623	0.08	0.97	5	35	protein targeting to vacuole	BP	0.80972	HGS,GNPTAB,M6PR,NAGPA,MON1B	cyan	VSMC_M2
GO:0000768	0.08	0.97	5	34	syncytium formation by plasma membrane fusion	BP	0.80972	FLOT1,CAMK1,CD81,SBNO2,PTGFRN	cyan	VSMC_M2
GO:0140253	0.08	0.97	5	34	cell-cell fusion	BP	0.80972	FLOT1,CAMK1,CD81,SBNO2,PTGFRN	cyan	VSMC_M2
GO:0044458	0.08	0.97	5	33	motile cilium assembly	BP	0.81321	RSPH9,BBS2,CC2D2A,DNAAF1,ATMIN	cyan	VSMC_M2
GO:0006631	0.09	0.94	26	271	fatty acid metabolic process	BP	0.81438	ZADH2,APPL2,ACSS1,ACAA1,CYP2S1,ECH1,GPAT4,CYP4V2,ACSS2,DECR1,SLC45A3,ACADS,HADH,PTGIS,ERFE,ECHS1,ACAT1,ALOX15,DAGLA,PDK2,CPT2,ABCD1,PTGDS,GSTM4,CRAT,ACOT6	cyan	VSMC_M2
GO:0031667	0.09	0.94	33	362	response to nutrient levels	BP	0.81438	EHMT2,HMOX1,APPL2,BCKDHB,RRAGC,APOE,ATG7,ZFP36,FOLR2,TBC1D5,SFRP2,SRC,CACNB3,BBS2,STAT1,GNAI2,MN1,GAS2L1,FES,PHEX,WNT2B,ACAT1,WDR45,GABARAP,NTRK1,TP53,PDK2,GBA,KANK2,EEF2,NDOR1,NPRL3,GATA4	cyan	VSMC_M2
GO:0033043	0.09	0.93	78	950	regulation of organelle organization	BP	0.81438	EHMT2,RPS6KA2,ARHGAP18,KCTD17,CUL9,GSN,NRP1,RHOB,BAX,MARK4,BIN1,EHD3,DZIP1,ARAP1,KAT2B,RHOG,CLIP3,IGF1,EFNA5,RHPN2,CHMP4B,CAMKK2,PRKCD,EPHA3,SRC,C15orf62,SORBS3,TJP1,CTTN,TPPP,SSH3,GAS2L1,FES,PRUNE1,VPS11,ARPC5,ARHGEF10,FYCO1,GRN,RND2,VAT1,ADD1,BMP4,CAPZB,MAP1S,HDAC6,ARHGEF10L,CROCC,ARRB2,ALOX15,CGNL1,PLSCR3,UBQLN2,SLIT2,TP53,CPLX2,UBQLN4,NUPR1,ARHGAP17,TEX14,SIGLEC15,CENPV,PDGFRB,FLII,PTPRS,TSC2,FBXW5,PHPT1,RHOT2,ENTR1,NPRL3,ABL1,ATMIN,ZNF205,PML,BMF,SDC4,BST2	cyan	VSMC_M2
GO:0051271	0.09	0.95	23	241	negative regulation of cellular component movement	BP	0.81438	AFDN,PTPRK,CARD10,HMOX1,RRAS,RHOB,BIN1,APOE,ANGPT4,SFRP2,NDRG4,NISCH,HDAC5,NBL1,DLG5,JUP,MCC,IL27RA,SLIT2,ADAM15,PODN,SERPINF1,BST2	cyan	VSMC_M2
GO:0015012	0.09	0.98	4	24	heparan sulfate proteoglycan biosynthetic process	BP	0.81438	EXT2,B3GAT3,XYLT2,HS3ST3B1	cyan	VSMC_M2
GO:0034643	0.09	0.98	4	24	establishment of mitochondrion localization, microtubule-mediated	BP	0.81438	MAP1S,HDAC6,RHOT2,HSBP1	cyan	VSMC_M2
GO:0047497	0.09	0.98	4	24	mitochondrion transport along microtubule	BP	0.81438	MAP1S,HDAC6,RHOT2,HSBP1	cyan	VSMC_M2
GO:1901214	0.09	0.94	24	251	regulation of neuron death	BP	0.81696	DAXX,HMOX1,GPNMB,AKT1S1,NRP1,BAX,APOE,ATG7,EFNB2,CHMP4B,CHRNA7,ADORA2A,GRN,ARRB2,CASP9,TP53BP2,NTRK1,TP53,GBA,NUPR1,RETREG1,ABL1,SERPINF1,EN1	cyan	VSMC_M2
GO:0044091	0.09	0.97	6	44	membrane biogenesis	BP	0.81842	FLOT1,PACSIN2,RFTN1,CLIP3,CHMP4B,LRP4	cyan	VSMC_M2
GO:0038179	0.09	0.97	5	34	neurotrophin signaling pathway	BP	0.81842	AKT1S1,TMEM108,SRC,NDN,NTRK1	cyan	VSMC_M2

GO:0001558	0.09	0.94	31	339	regulation of cell growth	BP	0.81842	CTDP1,NRP1,APOE,LTBP4,PAK4,IGF1,WT1,SFRP2,NDRG3,CTTN,SEMA3B,RGMA,SEMA4B,SEMA6C,RERG,RND2,SERPINE2,ERBB2,BRAT1,SLIT2,TP53,PPP1R9B,ADAM15,PTPRS,CLSTN1,ABL1,OSGIN1,IST1,PML,BST2,OGFR	cyan	VSMC_M2
GO:0010324	0.09	0.96	7	54	membrane invagination	BP	0.81842	APPL2,ELMO1,GSN,HGS,RHOG,ALOX15,SNX33	cyan	VSMC_M2
GO:0021602	0.09	0.98	4	24	cranial nerve morphogenesis	BP	0.81842	GLI3,NRP1,HOXB1,HOXB2	cyan	VSMC_M2
GO:0042440	0.09	0.96	8	65	pigment metabolic process	BP	0.81842	PMEL,IBA57,HMOX1,UROD,SLC6A9,GIPC1,ABCC1,MFSD12	cyan	VSMC_M2
GO:0030522	0.09	0.95	21	217	intracellular receptor signaling pathway	BP	0.81842	TCF21,DAXX,TRERF1,IRF3,NOP53,SLC15A4,RARG,SRC,PTGIS,MN1,VPS11,LMO3,NFKBIA,NR2F6,HDAC6,DHX58,ALOX15,AR,KANK2,ZBTB7A,PML	cyan	VSMC_M2
GO:0032272	0.09	0.96	8	66	negative regulation of protein polymerization	BP	0.81842	GSN,CLIP3,PRKCD,SSH3,ADD1,CAPZB,SLIT2,FLII	cyan	VSMC_M2
GO:0019915	0.09	0.96	8	65	lipid storage	BP	0.81842	APOE,HEXB,PNPLA2,IKBKE,NFKB1,NFKBIA,GBA,DGAT1	cyan	VSMC_M2
GO:1903169	0.09	0.95	12	110	regulation of calcium ion transmembrane transport	BP	0.81842	BAX,BIN1,EHD3,CACNB3,PLCG1,CAPN3,LINC02210-CRHR1,PRKACA,ABL1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:2000058	0.09	0.95	15	143	regulation of ubiquitin-dependent protein catabolic process	BP	0.81842	EIF3H,RNF144A,NOP53,FOXF2,MAGEF1,GABARAP,GIPC1,UBQLN2,UBQLN4,GBA,DVL1,ELOB,AXIN1,CBFA2T3,PML	cyan	VSMC_M2
GO:2000249	0.09	0.97	5	34	regulation of actin cytoskeleton reorganization	BP	0.81842	NRP1,TJP1,FES,PHPT1,ABL1	cyan	VSMC_M2
GO:0015850	0.09	0.95	18	179	organic hydroxy compound transport	BP	0.81842	EEPD1,APOE,OSBPL10,NISCH,SLC5A3,OSBPL5,TPCN2,NFKB1,FURIN,NFKBIA,LINC02210-CRHR1,ADORA2A,STARD3,NPC2,SLC51B,SLC10A3,LCAT,ABCA2	cyan	VSMC_M2
GO:0043124	0.09	0.97	5	34	negative regulation of I-kappaB kinase/NF-kappaB signaling	BP	0.82134	TLE1,CARD19,STAT1,ABL1,CARD8	cyan	VSMC_M2
GO:2000377	0.09	0.95	13	120	regulation of reactive oxygen species metabolic process	BP	0.82182	STK17A,DCXR,PRKCD,SLC5A3,TUSC2,GNAI2,HDAC6,TP53,ACP5,PDGFRB,ABCD1,ZNF205,MPV17	cyan	VSMC_M2
GO:0006688	0.09	0.97	4	24	glycosphingolipid biosynthetic process	BP	0.82184	B3GALT4,ST3GAL1,B4GALT5,AL157935.2	cyan	VSMC_M2
GO:0009895	0.09	0.94	24	254	negative regulation of catabolic process	BP	0.82225	EHMT2,EIF3H,HMOX1,NOP53,ATRAID,ATG7,TIMP2,ZFP36,CHMP4B,CTSA,IKBKE,TIRAP,WDR6,FURIN,SERPINE2,GIPC1,TP53,UBQLN4,NUPR1,TSC2,CBFA2T3,PML,GATA4,BMF	cyan	VSMC_M2
GO:1904427	0.09	0.96	7	55	positive regulation of calcium ion transmembrane transport	BP	0.82685	BAX,EHD3,CACNB3,PLCG1,CAPN3,ABL1,CALM3	cyan	VSMC_M2
GO:2001236	0.09	0.95	13	121	regulation of extrinsic apoptotic signaling pathway	BP	0.82685	DEPTOR,HMOX1,NRP1,FGFR1,RBCK1,IGF1,SFRP2,SRC,CTTN,TMBIM1,BMP4,AR,PML	cyan	VSMC_M2
GO:0007548	0.09	0.94	20	206	sex differentiation	BP	0.83089	TCF21,ZFPM2,MEA1,BAX,FZD4,TLR3,WT1,SFRP2,SRC,FOXF2,REC8,WNT2B,ARRB2,NTRK1,SLIT2,AR,ADAM15,NUPR1,PDGFRB,GATA4	cyan	VSMC_M2
GO:0009062	0.09	0.96	10	86	fatty acid catabolic process	BP	0.83246	ACAA1,ECH1,DECR1,ACADS,HADH,ECHS1,ACAT1,CPT2,ABCD1,CRAT	cyan	VSMC_M2
GO:0033559	0.09	0.96	8	64	unsaturated fatty acid metabolic process	BP	0.83246	ZADH2,ACAA1,CYP2S1,PTGIS,ALOX15,DAGLA,ABCD1,PTGDS	cyan	VSMC_M2
GO:0060419	0.09	0.96	9	77	heart growth	BP	0.83246	CTDP1,ZFPM2,MEIS1,IGF1,WT1,NDRG4,HEG1,FOXC2,GATA4	cyan	VSMC_M2
GO:1902017	0.09	0.96	6	45	regulation of cilium assembly	BP	0.834	KCTD17,MARK4,DZIP1,CROCC,ENTR1,ATMIN	cyan	VSMC_M2
GO:0006887	0.09	0.94	25	266	exocytosis	BP	0.8359	HMOX1,CADPS2,EXOC7,HGS,RAB11FIP1,LAMP1,EXOC2,TPCN2,GNAI2,SV2A,EXOC8,ADCY1,FES,VPS11,ADORA2A,GIPC1,CPLX2,LLGL1,DVL1,PTGDS,CBARP,CALM3,SDC4,STX3,RAB11B	cyan	VSMC_M2
GO:0051235	0.09	0.94	23	248	maintenance of location	BP	0.83794	OS9,GSN,BAX,APOE,DZIP1,GAA,HEXB,PLCG1,PNPLA2,IKBKE,CAPN3,TPCN2,NFKB1,NFKBIA,NBL1,PRKACA,GBA,MCOLN1,ABL1,DGAT1,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:1904036	0.09	0.97	5	34	negative regulation of epithelial cell apoptotic process	BP	0.83834	HMOX1,PAK4,CAST,NUPR1,ABL1	cyan	VSMC_M2
GO:0048332	0.09	0.96	7	55	mesoderm morphogenesis	BP	0.83834	SFRP2,EXT2,LEF1,BMP4,EPHA2,PRKACA,FOXC2	cyan	VSMC_M2
GO:0009791	0.09	0.96	8	68	post-embryonic development	BP	0.83906	ACO1,EFEMP1,BAX,NDN,HEG1,BMP4,ABL1,SELENOP	cyan	VSMC_M2
GO:0055078	0.09	0.97	5	34	sodium ion homeostasis	BP	0.83906	ATP4A,EXT2,GNAI2,ADORA2A,MLLT6	cyan	VSMC_M2
GO:0003206	0.09	0.95	11	101	cardiac chamber morphogenesis	BP	0.83906	ZFPM2,NRP1,SFRP2,CPE,HEG1,BMP4,SLIT2,TP53,FOXC2,GATA4,ZFPM1	cyan	VSMC_M2
GO:0120032	0.09	0.95	16	158	regulation of plasma membrane bounded cell projection assembly	BP	0.84406	KCTD17,COBL,NRP1,MARK4,DZIP1,ARAP1,RHOG,PRKCD,C15orf62,CAPZB,CROCC,EPHA2,SLIT2,AGRN,ENTR1,ATMIN	cyan	VSMC_M2
GO:0002262	0.09	0.95	14	134	myeloid cell homeostasis	BP	0.84406	HMOX1,BAX,ZFP36,SLC15A4,STAT1,B2M,BMP4,MAEA,ZFP36L1,ADAR,ISG15,ZBTB7A,RPS19,ZFPM1	cyan	VSMC_M2
GO:0034101	0.09	0.95	12	111	erythrocyte homeostasis	BP	0.84441	HMOX1,ZFP36,STAT1,B2M,BMP4,MAEA,ZFP36L1,ADAR,ISG15,ZBTB7A,RPS19,ZFPM1	cyan	VSMC_M2
GO:0043069	0.09	0.93	58	681	negative regulation of programmed cell death	BP	0.84492	DDAH2,ST3GAL1,GRINA,TLE1,HMOX1,HIGD2A,STK40,GLI3,NRP1,BAX,MEIS3,APOE,BCL3,SOCS3,PAK4,HSPB6,ANGPT4,RBCK1,IGF1,WT1,CAST,SFRP2,PRKCD,SRC,MAPK8IP1,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,GRK5,ELL3,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,DNAJB6,ARRB2,NTRK1,PCGF2,AR,TP53,GBA,NUPR1,SHC1,ADAR,KANK2,ATOX1,PDGFRB,RETREG1,FOXC2,ABL1,GATA4,EN1	cyan	VSMC_M2
GO:0019637	0.09	0.93	63	743	organophosphate metabolic process	BP	0.8479	CHKB,PLA2G7,SLC44A1,AASS,ACSS1,PLB1,SOCS3,OSBPL10,PNP,GPAT4,SMPD1,IGF1,ACSS2,LPCAT4,NEIL2,PLSCR1,HEXB,PRKCD,PLBD2,PLCG1,PTDSS1,PIK3C2B,ABHD14B,OSBPL5,NADSYN1,IP6K1,PTGIS,ADCY1,UCKL1,NMNAT2,PHEX,G6PC3,ACAT1,NUDT13,RARRES3,PGLS,PLD2,ALOX15,EPHA2,PLSCR3,TP53,PDK2,NUPR1,SLC44A2,PPCDC,PDGFRB,NUDT14,ABCD1,PNPLA7,PIGQ,INPP5E,H6PD,PLPP2,CBFA2T3,DPYD,LCAT,TK2,ABCA2,ACOT6,ZBTB7A,DGAT1,PLPP3,PDXK	cyan	VSMC_M2
GO:0048638	0.09	0.94	24	257	regulation of developmental growth	BP	0.8479	CTDP1,ZFPM2,MEIS1,NRP1,APOE,GPAT4,IGF1,WT1,BBS2,CAPN3,CTTN,SEMA3B,RGMA,SEMA4B,SEMA6C,RND2,BMP4,STAT5A,AR,PTPRS,AGRN,FOXC2,ABL1,IST1	cyan	VSMC_M2
GO:0050768	0.09	0.95	11	102	negative regulation of neurogenesis	BP	0.8479	APPL2,NRP1,LRP4,SEMA3B,RGMA,SEMA4B,SEMA6C,B2M,TP53,TMEM98,PTPRS	cyan	VSMC_M2
GO:0006949	0.09	0.97	5	35	syncytium formation	BP	0.8479	FLOT1,CAMK1,CD81,SBNO2,PTGFRN	cyan	VSMC_M2
GO:0043405	0.09	0.95	15	146	regulation of MAP kinase activity	BP	0.8479	FZD4,APOE,HGS,FGFR1,SMPD1,MAP3K12,SFRP2,PRKCD,SRC,MAPK8IP1,BMP4,ERBB2,GBA,PDGFRB,IL34	cyan	VSMC_M2

GO:1903050	0.09	0.94	19	192	regulation of proteolysis involved in cellular protein catabolic process	BP	0.8479	EIF3H,RNF144A,NOP53,APOE,FOXF2,MAGEF1,GABARAP,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,DVL1,ELOB,AXIN1,RHBDF1,CBFA2T3,PML	cyan	VSMC_M2
GO:0010828	0.09	0.97	5	35	positive regulation of glucose transmembrane transport	BP	0.85032	KLF15,CLIP3,IGF1,ERFE,RNASEL	cyan	VSMC_M2
GO:0031663	0.09	0.96	6	44	lipopolysaccharide-mediated signaling pathway	BP	0.85032	IRF3,BPI,NFKBIA,CD55,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0051093	0.09	0.93	57	676	negative regulation of developmental process	BP	0.85032	CTDP1,ZADH2,ZFPM2,IRF1,NFIB,KIAA1324L,APPL2,EFEMP1,MEIS1,GLI3,NRP1,LRRC17,TMEM176B,ZFP36,HGS,ANGPT4,RARG,IGF1,TLR3,WT1,EFNA5,SFRP2,WWTR1,LRP4,BBS2,SFRP5,STAT1,SEMA3B,ADGRB2,RGMA,LEF1,ECM1,SEMA4B,CTSK,SEMA6C,NFKBIA,LTBP3,B2M,DPF2,ADAMTS7,HDAC5,VAT1,BMP4,EPHA2,ERBB2,ZFP36L1,TP53,EPN2,TMEM98,PTPRS,NELFB,FOXC2,ABL1,SERPINF1,PML,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0048144	0.09	0.96	8	66	fibroblast proliferation	BP	0.85032	BAX,IGF1,IFI30,TP53,NUPR1,PDGFRB,PML,EMD	cyan	VSMC_M2
GO:0048145	0.09	0.96	8	66	regulation of fibroblast proliferation	BP	0.85032	BAX,IGF1,IFI30,TP53,NUPR1,PDGFRB,PML,EMD	cyan	VSMC_M2
GO:0050868	0.09	0.95	9	76	negative regulation of T cell activation	BP	0.85146	IRF1,GPNMB,GLI3,ADORA2A,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0071772	0.10	0.95	13	126	response to BMP	BP	0.85457	KIAA1324L,SFRP2,SFRP5,PCSK6,RGMA,LEF1,GATA5,ADAMTS7,BMP4,NBL1,NEO1,ABL1,GATA4	cyan	VSMC_M2
GO:0071773	0.10	0.95	13	126	cellular response to BMP stimulus	BP	0.85457	KIAA1324L,SFRP2,SFRP5,PCSK6,RGMA,LEF1,GATA5,ADAMTS7,BMP4,NBL1,NEO1,ABL1,GATA4	cyan	VSMC_M2
GO:0000045	0.10	0.95	10	88	autophagosome assembly	BP	0.85457	EHMT2,ATG7,CHMP4B,TP53INP2,WDR45,GABARAP,UBQLN2,NUPR1,NPRL3,RAB43	cyan	VSMC_M2
GO:0061951	0.10	0.96	7	55	establishment of protein localization to plasma membrane	BP	0.85457	AFDN,GGA1,PKDCC,BBS2,SYS1,AKAP5,GRASP	cyan	VSMC_M2
GO:0034644	0.10	0.95	9	77	cellular response to UV	BP	0.85587	PTPRK,BAX,SMPD1,PRKCD,MMP2,TMEM161A,CASP9,TP53,BMF	cyan	VSMC_M2
GO:0061036	0.10	0.97	4	25	positive regulation of cartilage development	BP	0.85599	GLI3,PKDCC,SOX5,BMP4	cyan	VSMC_M2
GO:0046578	0.10	0.94	16	161	regulation of Ras protein signal transduction	BP	0.85679	ARHGEF25,FLOT1,NRP1,APOE,TIMP2,IGF1,HEG1,ARHGEF10,BCR,GABARAP,NTRK1,KANK2,DENND4B,ARHGAP17,PDGFRB,ABL1	cyan	VSMC_M2
GO:0002366	0.10	0.94	18	181	leukocyte activation involved in immune response	BP	0.85978	STAT6,ST3GAL1,HMOX1,BCL3,LAMP1,SLC15A4,CD81,LEF1,FES,GRN,IL27RA,TP53,CPLX2,TMEM98,PTGDS,SBNO2,ABL1,ZFPM1	cyan	VSMC_M2
GO:1903008	0.10	0.95	11	101	organelle disassembly	BP	0.86179	ATG7,CAMKK2,CTTN,CTSK,HDAC6,WDR45,GABARAP,TP53,GBA,RETREG1,TSC2	cyan	VSMC_M2
GO:0048844	0.10	0.96	7	57	artery morphogenesis	BP	0.86255	NRP1,APOE,BMP4,FKBP10,PDGFRB,NPRL3,FOXC2	cyan	VSMC_M2
GO:0050767	0.10	0.94	26	285	regulation of neurogenesis	BP	0.86255	PLXNB2,APPL2,GLI3,NRP1,BIN1,MAN2A1,TGM2,LRP4,SEMA3B,RGMA,SEMA4B,PRUNE1,SEMA6C,STK25,ELL3,B2M,RND2,SERPINE2,SLIT2,TP53,TMEM98,PTPRS,ASPA,IL34,IST1,SERPINF1	cyan	VSMC_M2
GO:0001938	0.10	0.95	9	78	positive regulation of endothelial cell proliferation	BP	0.86258	HMOX1,NRP1,FGFR1,PLCG1,VEGFD,ECM1,VEGFB,BMP4,STAT5A	cyan	VSMC_M2
GO:0045669	0.10	0.96	7	56	positive regulation of osteoblast differentiation	BP	0.86281	GLI3,ATRAID,IGF1,SFRP2,WWTR1,ZHX3,BMP4	cyan	VSMC_M2
GO:0051494	0.10	0.95	14	138	negative regulation of cytoskeleton organization	BP	0.86281	GSN,ARAP1,KAT2B,CLIP3,RHPN2,PRKCD,TJP1,SSH3,ADD1,CAPZB,HDAC6,CGNL1,SLIT2,FLII	cyan	VSMC_M2
GO:0006890	0.10	0.96	6	45	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	BP	0.86281	TAPBP,ERGIC3,TMEM115,USE1,ERGIC1,PLPP3	cyan	VSMC_M2
GO:1901698	0.10	0.92	70	845	response to nitrogen compound	BP	0.86575	STAT6,OS9,FLOT1,EHMT2,DAXX,GCNT1,APPL2,RRAGC,IRF3,KLF15,TRIM13,VIM,APOE,ATG7,SOCS3,FOLR2,KAT2B,RFTN1,SMPD1,IGF1,TLR3,WT1,EDEM2,GLRB,PRKCD,SRC,TGM2,GNAO1,MMP2,STAT1,CD81,CHRNA7,NFKB1,GNAI2,HADH,ERFE,PHEX,NFKBIA,LINC02210-CRHR1,ADORA2A,HDAC5,QDPR,STAT5A,PQBP1,ARRB2,JUP,PRKACA,ZFP36L1,UBQLN2,SLIT2,TP53,PDK2,PPP1R9B,SHC1,GRIA1,ABCC1,UBXN6,EEF2,AGRN,TSC2,FOXC2,ABL1,SLC2A8,SLC8A3,SERPINF1,CALM3,RNLS,RGS8,RGS10,EN1	cyan	VSMC_M2
GO:0035307	0.10	0.97	5	35	positive regulation of protein dephosphorylation	BP	0.86946	SMPD1,PRKCD,GBA,PDGFRB,CALM3	cyan	VSMC_M2
GO:0086001	0.10	0.96	7	58	cardiac muscle cell action potential	BP	0.86946	BIN1,SCN1B,SNTA1,CTNNA3,KCND3,JUP,CALM3	cyan	VSMC_M2
GO:0048566	0.10	0.97	4	25	embryonic digestive tract development	BP	0.87033	TCF21,GLI3,PKDCC,FOXF2	cyan	VSMC_M2
GO:0032365	0.10	0.97	5	35	intracellular lipid transport	BP	0.87033	TPCN2,NPC2,CPT2,ABCD1,ABCA2	cyan	VSMC_M2
GO:0006082	0.10	0.92	59	689	organic acid metabolic process	BP	0.87443	ZADH2,DDAH2,ST3GAL1,ACO1,APPL2,IARS,BCKDHB,AASS,ACSS1,ME3,ACAA1,CYP2S1,PNP,ECH1,GPAT4,IGF1,CYP4V2,GGT7,ACSS2,DECR1,ABHD14B,SLC45A3,ACADS,HADH,PTGIS,SCLY,ERFE,SLC16A9,ECHS1,PCBD1,ACAT1,QDPR,STAT5A,ALOX15,DAGLA,MRI1,TP53,HSD3B7,PDK2,NUPR1,SLC16A2,WARS,ABCC1,CPT2,ABCD1,IDH3G,ASPA,RENBP,HAGH,PTGDS,GSTM4,CBFA2T3,CRAT,DPYD,LDHD,FPGS,ACOT6,ZBTB7A,NAGK	cyan	VSMC_M2
GO:0001657	0.10	0.95	9	78	ureteric bud development	BP	0.87527	TCF21,GLI3,WT1,LZTS2,WNT2B,BMP4,SLIT2,FOXC2,SDC4	cyan	VSMC_M2
GO:0071219	0.10	0.94	14	133	cellular response to molecule of bacterial origin	BP	0.87732	IRF3,VIM,ZFP36,SRC,BPI,TIRAP,NFKB1,NFKBIA,PLSCR3,SBNO2,ABL1,CD55,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0071216	0.10	0.94	16	157	cellular response to biotic stimulus	BP	0.88367	IRF3,VIM,ZFP36,SRC,BPI,TIRAP,NFKB1,MUS81,NFKBIA,PLSCR3,TP53,SBNO2,ABL1,CD55,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0010628	0.10	0.92	67	803	positive regulation of gene expression	BP	0.88723	PYM1,STAT6,AKAP12,FLOT1,PLXNB2,RPS6KA2,IRF1,AFDN,GSDMD,TLE1,HMOX1,ITGB8,IRF3,GSN,LURAP1,VIM,BCL3,MIF4GD,PNP,ZFP36,HGS,KAT2B,RFTN1,RARG,IGF1,TLR3,WT1,PLSCR1,SPON1,SRC,STAT1,CD81,IKBKE,TIRAP,TUSC2,LEF1,FURIN,HEG1,GATA5,FRMD8,B2M,CLEC3B,TMEM106A,BMP4,PQBP1,DHX58,ARRB2,IL17RA,TCF12,ERBB2,IL27RA,AR,TP53,ADAR,WARS,GPRC5B,EEF2,ISG15,TNFRSF14,ABL1,ATMIN,IL34,OAS2,CD55,GATA4,CARD8,ZFPM1	cyan	VSMC_M2
GO:0050905	0.10	0.95	11	103	neuromuscular process	BP	0.88883	SLITRK6,GAA,TPP1,HEXB,GLRB,ADORA2A,GBA,EEF2,DVL1,ABL1,SLC8A3	cyan	VSMC_M2
GO:0045071	0.10	0.96	5	35	negative regulation of viral genome replication	BP	0.89249	PLSCR1,RNASEL,ISG15,OAS2,BST2	cyan	VSMC_M2
GO:1901653	0.10	0.93	25	270	cellular response to peptide	BP	0.89321	STAT6,APPL2,KLF15,VIM,SOCS3,KAT2B,IGF1,PRKCD,SRC,STAT1,NFKB1,GNAI2,ERFE,LINC02210-CRHR1,HDAC5,STAT5A,ZFP36L1,TP53,PDK2,PPP1R9B,SHC1,ABCC1,TSC2,FOXC2,SLC2A8	cyan	VSMC_M2
GO:0009648	0.10	0.97	4	25	photoperiodism	BP	0.89321	NR2F6,TP53,MTA1,PML	cyan	VSMC_M2

GO:0032270	0.10	0.92	87	1066	positive regulation of cellular protein metabolic process	BP	0.89558	PYM1,FLOT1,PLXNB2,DAXX,MTCH1,CARD10,GPNMB,RNF144A,GSN,NRP1,BAX,NOP53,FZD4,CAB39L,VIM,APOE,BCL3,MIF4GD,ATG7,CAMK1,FGFR1,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,ARRDC3,CAMKK2,SPON1,SFRP2,PRKCD,SRC,LRP4,MOB2,CD81,NDN,CHRNA7,CAPN3,TIRAP,RGMA,APH1A,VEGFD,CASP10,FURIN,VPS11,MAGEF1,NFKBIA,CLEC3B,GRN,PCOLCE,VEGFB,BMP4,HDAC6,ARRB2,GABARAP,CASP9,ERBB2,BRAT1,UBQLN2,NTRK1,TP53,GBA,SLC51B,NUPR1,GPRC5B,SNX33,PDGFRB,MTA1,MAP2K3,TRAF4,EEF2,DVL1,ELOB,TNFRSF14,AXIN1,CBFA2T3,ABL1,IL34,IST1,ABCA2,PML,CALM3,CARD8,CDK9,SDC4	cyan	VSMC_M2
GO:0045597	0.10	0.92	54	639	positive regulation of cell differentiation	BP	0.89591	PLXNB2,GLI3,RRAS,NRP1,BIN1,ATRAID,SOCS3,CAMK1,PNP,TIMP2,ZFP36,FGFR1,EFNB2,PKDCC,IGF1,MAN2A1,SFRP2,WWTR1,TGM2,ZHX3,STAT1,BOC,NFKB1,LEF1,SOX5,FES,BCL9L,LMO3,GATA5,STK25,ELL3,LTBP3,RND2,ADD1,BMP4,RARRES3,NBL1,ARRB2,TCF12,SERPINE2,ZFP36L1,SLIT2,AR,HOXB4,GPRC5B,ASPA,ISG15,TCF3,ABL1,IL34,IST1,SERPINF1,JUNB,GATA4	cyan	VSMC_M2
GO:0072163	0.10	0.95	9	79	mesonephric epithelium development	BP	0.89591	TCF21,GLI3,WT1,LZTS2,WNT2B,BMP4,SLIT2,FOXC2,SDC4	cyan	VSMC_M2
GO:0072164	0.10	0.95	9	79	mesonephric tubule development	BP	0.89591	TCF21,GLI3,WT1,LZTS2,WNT2B,BMP4,SLIT2,FOXC2,SDC4	cyan	VSMC_M2
GO:0050922	0.10	0.96	6	46	negative regulation of chemotaxis	BP	0.89591	NRP1,SEMA3B,SEMA4B,SEMA6C,NBL1,SLIT2	cyan	VSMC_M2
GO:0032088	0.10	0.95	8	67	negative regulation of NF-kappaB transcription factor activity	BP	0.89591	BCL3,TRIM21,RBCK1,PTGIS,NFKBIA,ARRB2,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0017157	0.10	0.94	15	147	regulation of exocytosis	BP	0.89591	HMOX1,CADPS2,HGS,LAMP1,TPCN2,GNAI2,ADCY1,FES,ADORA2A,GIPC1,CPLX2,DVL1,CBARP,CALM3,SDC4	cyan	VSMC_M2
GO:0060674	0.10	0.97	4	26	placenta blood vessel development	BP	0.89591	ITGB8,SOCS3,PLCD3,JUNB	cyan	VSMC_M2
GO:0010662	0.10	0.96	5	35	regulation of striated muscle cell apoptotic process	BP	0.89591	HSPB6,SFRP2,TP53,NUPR1,GATA4	cyan	VSMC_M2
GO:0048640	0.10	0.95	10	90	negative regulation of developmental growth	BP	0.89591	CTDP1,MEIS1,NRP1,BBS2,SEMA3B,RGMA,SEMA4B,SEMA6C,BMP4,PTPRS	cyan	VSMC_M2
GO:0051209	0.10	0.95	9	82	release of sequestered calcium ion into cytosol	BP	0.89591	BAX,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,CALM3,CLIC2	cyan	VSMC_M2
GO:0022411	0.10	0.93	33	375	cellular component disassembly	BP	0.89591	MMP19,PYM1,FLOT1,GSN,BAX,ATG7,CHMP3,CAMKK2,MMP2,CTTN,EXOC8,CTSK,FURIN,FYCO1,ADD1,CAPZB,MAP1S,TECPR1,HDAC6,WDR45,GABARAP,TP53,UBQLN4,GBA,PPP1R9B,ADAM15,PBXIP1,MCOLN1,FLII,SH3GL1,RETREG1,TSC2,IST1	cyan	VSMC_M2
GO:1902904	0.10	0.94	14	139	negative regulation of supramolecular fiber organization	BP	0.89591	GSN,APOE,ARAP1,CLIP3,RHPN2,PRKCD,TJP1,SSH3,ADD1,CAPZB,HDAC6,CGNL1,SLIT2,FLII	cyan	VSMC_M2
GO:2000146	0.10	0.93	22	234	negative regulation of cell motility	BP	0.89591	AFDN,PTPRK,CARD10,HMOX1,RRAS,RHOB,APOE,ANGPT4,SFRP2,NDRG4,NISCH,HDAC5,NBL1,DLG5,JUP,MCC,IL27RA,SLIT2,ADAM15,PODN,SERPINF1,BST2	cyan	VSMC_M2
GO:0060603	0.10	0.97	4	26	mammary gland duct morphogenesis	BP	0.89591	SRC,EPHA2,AR,PML	cyan	VSMC_M2
GO:0050974	0.10	0.97	4	26	detection of mechanical stimulus involved in sensory perception	BP	0.89591	CACNB3,SERPINE2,NTRK1,PIEZO2	cyan	VSMC_M2
GO:0051279	0.10	0.96	7	58	regulation of release of sequestered calcium ion into cytosol	BP	0.89612	BAX,PLCG1,CAPN3,PRKACA,ABL1,CALM3,CLIC2	cyan	VSMC_M2
GO:0060828	0.10	0.93	20	210	regulation of canonical Wnt signaling pathway	BP	0.89749	TLE1,GLI3,FZD4,APOE,ADGRA2,SFRP2,WWTR1,SRC,LRP4,SFRP5,LZTS2,NFKB1,FAM53B,FRMD8,JUP,MCC,GPRC5B,NPHP4,AXIN1,EMD	cyan	VSMC_M2
GO:0051497	0.10	0.97	4	26	negative regulation of stress fiber assembly	BP	0.89749	ARAP1,RHPN2,TJP1,CGNL1	cyan	VSMC_M2
GO:0070265	0.10	0.96	6	45	necrotic cell death	BP	0.89749	IRF3,BAX,RBCK1,TLR3,TP53,NUPR1	cyan	VSMC_M2
GO:0010821	0.10	0.94	13	124	regulation of mitochondrion organization	BP	0.89749	BAX,IGF1,CAMKK2,CTTN,VAT1,HDAC6,ARRB2,PLSCR3,TP53,TSC2,RHOT2,ZNF205,BMF	cyan	VSMC_M2
GO:0034504	0.10	0.93	23	244	protein localization to nucleus	BP	0.89765	CARD10,APPL2,GLI3,NOP53,BCL3,DCLK1,WWTR1,PRKCD,SRC,LZTS2,TRIM8,FAM53B,NFKBIA,BMP4,DNAJB6,JUP,TP53,TMEM98,GLIS2,DVL1,TSC2,ZBTB7A,PML	cyan	VSMC_M2
GO:0002697	0.10	0.93	20	206	regulation of immune effector process	BP	0.89765	STAT6,HMOX1,APPL2,TRIL,LAMP1,SLC15A4,TLR3,SERPING1,CD81,FES,B2M,GRN,DHX58,ARRB2,IL27RA,GPRC5B,TNFRSF14,CD55,RPS19,BST2	cyan	VSMC_M2
GO:1901216	0.10	0.95	9	78	positive regulation of neuron death	BP	0.89765	DAXX,BAX,EFNB2,GRN,CASP9,TP53BP2,TP53,NUPR1,ABL1	cyan	VSMC_M2
GO:0030517	0.10	0.96	5	36	negative regulation of axon extension	BP	0.89765	NRP1,SEMA3B,SEMA4B,SEMA6C,PTPRS	cyan	VSMC_M2
GO:0007492	0.10	0.95	7	59	endoderm development	BP	0.89765	MMP2,BMP4,ZFP36L1,MED12,HSBP1,GATA4,COL8A1	cyan	VSMC_M2
GO:0032371	0.10	0.96	6	46	regulation of sterol transport	BP	0.89765	EEPD1,APOE,NFKB1,FURIN,NFKBIA,ABCA2	cyan	VSMC_M2
GO:0032374	0.10	0.96	6	46	regulation of cholesterol transport	BP	0.89765	EEPD1,APOE,NFKB1,FURIN,NFKBIA,ABCA2	cyan	VSMC_M2
GO:0036258	0.10	0.97	4	25	multivesicular body assembly	BP	0.89765	HGS,CHMP4B,CHMP3,IST1	cyan	VSMC_M2
GO:0030513	0.10	0.97	4	27	positive regulation of BMP signaling pathway	BP	0.89803	KIAA1324L,BMP4,NEO1,GATA4	cyan	VSMC_M2
GO:0043085	0.10	0.92	72	875	positive regulation of catalytic activity	BP	0.89803	TBC1D22A,AFDN,DAXX,MTCH1,CARD10,TBC1D2,TBC1D17,GSN,BAX,FZD4,CAB39L,APOE,CAMK1,TIMP2,ARAP1,TBC1D5,RHOG,FGFR1,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,ARRDC3,PLSCR1,SFRP2,PRKCD,EPHA3,SRC,TGM2,GNAO1,SLC5A3,CD81,CHRNA7,TIRAP,GNAI2,RGMA,SGSM1,SIPA1L2,APH1A,CASP10,CCS,ARHGEF10,BCR,GRN,PCOLCE,PSAP,RARRES3,B3GAT3,EPHA2,AKAP5,CASP9,ERBB2,NTRK1,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,SGSM2,AGRN,TSC2,AXIN1,ABL1,IL34,PML,EEF1A2,CALM3,CARD8,SDC4,RGS8,RGS10	cyan	VSMC_M2
GO:0016079	0.10	0.95	9	79	synaptic vesicle exocytosis	BP	0.89803	CADPS2,SV2A,ADCY1,ADORA2A,GIPC1,CPLX2,DVL1,CALM3,STX3	cyan	VSMC_M2
GO:0044283	0.10	0.92	37	414	small molecule biosynthetic process	BP	0.89803	MOXD1,CYB5R3,AASS,ACSS1,APOE,COQ8B,PNP,KAT2B,GGT7,ACSS2,COQ9,SLC45A3,NFKB1,IP6K1,PTGIS,ERFE,CLCN2,UCKL1,PCBD1,G6PC3,QDPR,ALOX15,STARD3,UBIAD1,MRI1,HSD3B7,PDK2,GBA,ABCD1,PTGDS,FAM3A,H6PD,GSTM4,DPYD,TK2,ABCA2,PDXK	cyan	VSMC_M2
GO:0030218	0.11	0.94	11	102	erythrocyte differentiation	BP	0.8998	ZFP36,STAT1,B2M,BMP4,MAEA,ZFP36L1,ADAR,ISG15,ZBTB7A,RPS19,ZFPM1	cyan	VSMC_M2

GO:0002684	0.11	0.92	47	542	positive regulation of immune system process	BP	0.902	STAT6,CFB,HMOX1,APPL2,PLA2G7,COLEC11,GLI3,IRF3,BAX,PNP,RFTN1,LAMP1,SLC15A4,RBCK1,IGF1,SERPING1,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,CD81,IKBKE,TIRAP,XG,LEF1,VEGFD,FES,B2M,GRN,C1R,C1S,VEGFB,PQBP1,DHX58,PLD2,ZFP36L1,IL27RA,GPRC5B,C6,TNFRSF14,PHPT1,ABL1,IL34,HEXIM1,CD55,RPS19	cyan	VSMC_M2
GO:0030316	0.11	0.95	8	68	osteoclast differentiation	BP	0.902	LRRC17,TLR3,SRC,CD81,EPHA2,SIGLEC15,SBNO2,JUNB	cyan	VSMC_M2
GO:0044273	0.11	0.97	4	25	sulfur compound catabolic process	BP	0.902	GNS,GGT7,ACAT1,ABCD1	cyan	VSMC_M2
GO:0002181	0.11	0.94	12	111	cytoplasmic translation	BP	0.902	EIF3H,RPL18,RPS16,RPL15,EIF3K,EIF3F,EEF2,DPH7,RPL13,RPS15,RPS19,RPL36A	cyan	VSMC_M2
GO:0048762	0.11	0.93	19	198	mesenchymal cell differentiation	BP	0.902	TCF21,NRP1,FGFR1,SFRP2,WWTR1,EPHA3,FOXF2,STAT1,SEMA3B,LEF1,SEMA4B,BCL9L,SEMA6C,GATA5,ELL3,BMP4,DLG5,ADAM15,FOXC2	cyan	VSMC_M2
GO:0071384	0.11	0.96	6	46	cellular response to corticosteroid stimulus	BP	0.90239	FBXO32,KLF9,ZFP36,CASP9,ZFP36L1,SERPINF1	cyan	VSMC_M2
GO:0071396	0.11	0.92	37	422	cellular response to lipid	BP	0.90244	TCF21,DAXX,FBXO32,TRERF1,KLF9,IRF3,FZD4,VIM,ZFP36,RARG,EPHA3,SRC,BPI,NFKB1,MN1,ADCY1,FES,VPS11,LMO3,PHEX,NFKBIA,BMP4,HDAC6,CASP9,PLSCR3,ZFP36L1,AR,PPP1R9B,ADAM15,KANK2,SBNO2,ABL1,SERPINF1,ZBTB7A,CD55,CARD8,NFKBIL1	cyan	VSMC_M2
GO:2001237	0.11	0.95	9	79	negative regulation of extrinsic apoptotic signaling pathway	BP	0.90244	HMOX1,NRP1,IGF1,SFRP2,SRC,CTTN,TMBIM1,BMP4,AR	cyan	VSMC_M2
GO:0080090	0.11	0.91	317	4206	regulation of primary metabolic process	BP	0.90546	CTDP1,TSHZ1,PYM1,STAT6,TCF21,FLOT1,PPP6R2,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,DEPTOR,TCF20,DAXX,TEF,PTPRK,TEAD3,MTCH1,TLE1,GGA1,CARD10,NFIB,TRERF1,HMOX1,ACO1,KLF9,APPL2,MLIP,ZBTB45,ZSCAN18,TRIM14,P3H1,NAT14,GPNMB,EFEMP1,MEIS1,RNF144A,AKT1S1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,CAB39L,VIM,BIN1,APOE,BCL3,MIF4GD,ATRAID,SLC6A9,ATG7,LTBP4,SOCS3,CAMK1,TIMP2,ZFP36,SAMD4B,HGS,KAT2B,EIF3K,RHOG,FGFR1,SH3BP5,TRIM21,SMPD1,APBB1,CLIP3,SLC15A4,ANGPT4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,SNTA1,WT1,EFNA5,TP53INP2,PATL1,TSHZ3,POU6F1,SERPING1,CAST,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,LRP4,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTPN13,PNPLA2,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,SLC45A3,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,CSTB,ZNF496,NFKB1,GNAI2,TPPP,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,APH1A,MN1,VEGFD,ECM1,RHBDD3,NELFCD,CASP10,ADCY1,FURIN,VPS11,ERFE,BCL9L,HEG1,RFX5,GATA5,CLCN2,HELZ2,ATG4B,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,CLEC3B,PCBD1,GRN,PCOLCE,HDAC5,TMEM161A,PSAP,TSC22D4,VEGFB,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,CPAMD8,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,GABARAP,ZBTB17,TCF12,SERPINE2,CASP9,GIPC1,ERBB2,BRAT1,PRKACA,ZFP36L1,IL27RA,UBQLN2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,SLIT2,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQ	cyan	VSMC_M2
GO:0009880	0.11	0.96	6	47	embryonic pattern specification	BP	0.90753	MEIS1,COBL,NRP1,MEIS3,WT1,PCSK6	cyan	VSMC_M2
GO:0006721	0.11	0.95	7	56	terpenoid metabolic process	BP	0.90753	CYP2S1,PLB1,CYP4V2,PNPLA2,RLBP1,DHRS13,DGAT1	cyan	VSMC_M2
GO:0033157	0.11	0.93	19	196	regulation of intracellular protein transport	BP	0.90758	OS9,GLI3,STOM,CAMK1,EDEM2,PRKCD,CACNB3,CD81,VPS11,BMP4,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,GRASP,EMD,UBL5	cyan	VSMC_M2
GO:0051253	0.11	0.91	84	1032	negative regulation of RNA metabolic process	BP	0.9077	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,BCL3,ZFP36,KAT2B,APBB1,LMO1,RARG,WT1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,IKBKE,CAPN3,TIRAP,NFKB1,HIST1H1C,LEF1,TBL1Y,NELFCD,RFX5,MAGEF1,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,KANK2,MTA1,MOSPD1,GLIS2,E4F1,NELFB,TCF3,SBNO2,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,CDK9,ZFPM1,EN1	cyan	VSMC_M2
GO:0051180	0.11	0.97	4	26	vitamin transport	BP	0.90837	FOLR2,TCN2,ABCC1,SLC2A8	cyan	VSMC_M2
GO:0009116	0.11	0.96	6	45	nucleoside metabolic process	BP	0.90837	PNP,UCKL1,MACROD1,DPYD,TK2,MACROD2	cyan	VSMC_M2
GO:0044249	0.11	0.90	323	4271	cellular biosynthetic process	BP	0.90848	CTDP1,TSHZ1,PYM1,PMEL,STAT6,MOXD1,TCF21,MGAT4B,FLOT1,CHKB,DDAH2,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,B3GALT4,CYB5R3,TCF20,DAXX,TEF,PTPRK,ST3GAL1,IBA57,TEAD3,TLE1,NFIB,TRERF1,GCNT1,HMOX1,ACO1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,NAT14,SLC44A1,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,ACSS1,FZD4,VIM,APOE,UROD,BCL3,MIF4GD,SLC6A9,ATG7,COQ8B,SOCS3,CAMK1,TEP1,PNP,RPS16,ZFP36,CANT1,SAMD4B,GPAT4,RPL15,KAT2B,EIF3K,RHOG,TRIM21,SMPD1,APBB1,CLIP3,GTF3A,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,MAN2A1,WT1,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,POU6F1,LPCAT4,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,COQ9,SRC,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTDSS1,EXT2,PNPLA2,PIK3C2B,STAT1,ABHD14B,CD81,NDN,SLC45A3,PHKG1,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,MRPL36,ZNF496,NFKB1,SPOCD1,B4GALT4,HIST1H1C,PKNOX2,RGMA,BCL9,IP6K1,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,MN1,GCNT7,ECM1,NELFCD,ADCY1,FURIN,ERFE,BCL9L,RFX5,GATA5,CLCN2,B4GAT1,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,ACAT1,VEGFB,TMEM106A,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,PORCN,NR2F6,HDAC6,ZBTB3,PQBP1,B3GAT3,WDR45,PLD2,DNAJB6,ARRB2,JUP,ALOX15,WIZ,MYRF,DAGLA,ZBTB17,TCF12,PLSCR3,GIPC1,ERBB2,STARD3,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,UBIAD1,MLLT6,MRI1,AR,TP53,HSD3B7,GLMP,KAT8,H	cyan	VSMC_M2

GO:0016052	0.11	0.94	12	113	carbohydrate catabolic process	BP	0.90848	NEU1,NAGA,GAA,IGF1,HEXB,STBD1,GUSB,TP53,NUPR1,MAN2C1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0061180	0.11	0.95	7	58	mammary gland epithelium development	BP	0.90858	STAT6,BAX,SRC,EPHA2,AR,PML,PYGO2	cyan	VSMC_M2
GO:0006650	0.11	0.93	24	257	glycerophospholipid metabolic process	BP	0.90935	CHKB,PLA2G7,SLC44A1,PLB1,SOCS3,OSBPL10,GPAT4,LPCAT4,PLSCR1,PLCG1,PTDSS1,PIK3C2B,OSBPL5,IP6K1,RARRES3,PLD2,ALOX15,PLSCR3,SLC44A2,PDGFRB,PNPLA7,PIGQ,INPP5E,LCAT	cyan	VSMC_M2
GO:0060548	0.11	0.92	63	754	negative regulation of cell death	BP	0.9094	DDAH2,ZFPM2,ST3GAL1,GRINA,TLE1,HMOX1,HIGD2A,GPNMB,STK40,GLI3,NRP1,BAX,MEIS3,APOE,BCL3,ATG7,SOCS3,PAK4,HSPB6,ANGPT4,RBCK1,IGF1,WT1,CHMP4B,CAST,SFRP2,PRKCD,SRC,MAPK8IP1,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,GRK5,ELL3,ADORA2A,AIFM2,GRN,TMEM161A,TMBIM1,BMP4,MAEA,DNAJB6,ARRB2,NTRK1,PCGF2,AR,TP53,GBA,NUPR1,SHC1,ADAR,KANK2,ATOX1,PDGFRB,RETREG1,FOXC2,ABL1,SERPINF1,GATA4,EN1	cyan	VSMC_M2
GO:0050863	0.11	0.93	20	206	regulation of T cell activation	BP	0.9094	IRF1,GPNMB,GLI3,PNP,LMO1,IGF1,SRC,MAPK8IP1,CD81,LEF1,B2M,ADORA2A,BMP4,DLG5,ERBB2,IL27RA,TNFRSF14,ABL1,CD55,SDC4	cyan	VSMC_M2
GO:0006637	0.11	0.95	9	78	acyl-CoA metabolic process	BP	0.9094	AASS,ACSS1,GPAT4,ACSS2,ACAT1,PDK2,ABCD1,ACOT6,DGAT1	cyan	VSMC_M2
GO:0035383	0.11	0.95	9	78	thioester metabolic process	BP	0.9094	AASS,ACSS1,GPAT4,ACSS2,ACAT1,PDK2,ABCD1,ACOT6,DGAT1	cyan	VSMC_M2
GO:2000379	0.11	0.95	7	57	positive regulation of reactive oxygen species metabolic process	BP	0.90948	DCXR,PRKCD,SLC5A3,GNAI2,TP53,PDGFRB,ZNF205	cyan	VSMC_M2
GO:0051283	0.11	0.95	9	83	negative regulation of sequestering of calcium ion	BP	0.91034	BAX,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,CALM3,CLIC2	cyan	VSMC_M2
GO:0035306	0.11	0.96	6	47	positive regulation of dephosphorylation	BP	0.91184	SMPD1,PRKCD,SRC,GBA,PDGFRB,CALM3	cyan	VSMC_M2
GO:0019221	0.11	0.92	28	306	cytokine-mediated signaling pathway	BP	0.91184	STAT6,IRF1,APPL2,IRF3,FZD4,IL17RC,IL5RA,ACKR4,SRC,BBS2,STAT1,IKBKE,ECM1,NFKBIA,STAT5A,IL17RA,PRKACA,IL27RA,SLIT2,TP53,ADAR,IL13RA1,ISG15,TNFRSF14,IL34,OAS2,CARD8,IL22RA1	cyan	VSMC_M2
GO:0060411	0.11	0.95	7	59	cardiac septum morphogenesis	BP	0.91361	ZFPM2,NRP1,BMP4,SLIT2,TP53,GATA4,ZFPM1	cyan	VSMC_M2
GO:0006950	0.11	0.90	209	2715	response to stress	BP	0.91361	STAT6,OS9,ULBP2,FLOT1,MSH5,EHMT2,CFB,IRF1,DAXX,PTPRK,GSDMD,GRINA,HMOX1,LRRC19,CNPY3,APPL2,PLA2G7,MLIP,TRIM14,TRIL,RRAGC,EEPD1,COLEC11,GLI3,IRF3,NRP1,KLF15,RHOB,BAX,NOP53,TRIM13,VIM,AGBL5,APOE,BCL3,AGAP3,ATG7,RHBDF2,IL17RC,SOCS3,PLD3,ZFP36,LGALS3BP,FOLR2,TBC1D5,IL5RA,TRIM21,LAMP1,SMPD1,APBB1,SLC15A4,ANGPT4,MAP3K12,IGF1,TLR3,GGT7,GGCX,SERPING1,EDEM2,NEIL2,PLSCR1,CAMKK2,SFRP2,PRKCD,SRC,TGM2,BPI,PLCG1,MMS19,GNAO1,MAPK8IP1,MMP2,STAT1,HPS6,CD81,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,TUSC2,NFKB1,LGALS8,RGMA,UBA7,PTGIS,LAMB2,VEGFD,ECM1,REC8,RHBDD3,GAS2L1,ADCY1,FES,FURIN,CCS,STK25,RNASEL,FIBP,MAGEF1,MUS81,ELL3,NFKBIA,MOV10,B2M,WNT2B,ADORA2A,AIFM2,GRN,C1R,HDAC5,C1S,TMEM161A,TSC22D4,ACAT1,VEGFB,TMEM106A,MACROD1,BMP4,STAT5A,HDAC6,PQBP1,DHX58,ARHGEF10L,WDR45,DNAJB6,FKBP10,ARRB2,ALOX15,EPHA2,DAGLA,IL17RA,GABARAP,PLEKHM2,SERPINE2,CASP9,ERBB2,BRAT1,PRKACA,ZFP36L1,IL27RA,UBQLN2,NTRK1,PCGF2,TP53,UBQLN4,PDK2,GBA,PPP1R9B,ADAM15,NUPR1,SHC1,PBXIP1,ADAR,ACP5,ULK3,GPRC5B,ABCC1,PDGFRB,MTA1,MAP2K3,C6,TRAF4,PTPRS,UBXN6,EEF2,ABCD1,ISG15,TNFRSF14,SBNO2,FAM3A,AXIN1,NPRL3,CBFA2T3,RNF166,FOXC2,ABL1,HSBP1,ATMIN,SLC2A8,IL34,GBP6,MIR197,OAS2,SLC8A3,HEXIM1,SERPINF1,KCND2,ZBTB7A,CD55,TRIM26,RAB43,PML,SERPINB6,RPS19,SELENOP,PLPP3,GATA4,CARD8,VPS26B,CDK9,SDC4,ADPRHL2,IL22RA1,RNLS,MACROD2,BST2,GTF2H4,MPV17	cyan	VSMC_M2
GO:0090314	0.11	0.97	4	26	positive regulation of protein targeting to membrane	BP	0.91361	STOM,CACNB3,ERBB2,SLC51B	cyan	VSMC_M2
GO:0032509	0.11	0.97	4	26	endosome transport via multivesicular body sorting pathway	BP	0.91361	CHMP4B,CHMP3,TMEM50A,UBXN6	cyan	VSMC_M2
GO:0032271	0.11	0.93	19	199	regulation of protein polymerization	BP	0.91361	ARHGAP18,GSN,BIN1,TPPP2,CLIP3,PRKCD,C15orf62,CTTN,TPPP,SSH3,FES,PRUNE1,ARPC5,ADD1,CAPZB,ALOX15,SLIT2,FLII,ABL1	cyan	VSMC_M2
GO:0071417	0.11	0.92	40	466	cellular response to organonitrogen compound	BP	0.91361	STAT6,EHMT2,APPL2,RRAGC,KLF15,VIM,ATG7,SOCS3,FOLR2,KAT2B,IGF1,WT1,PRKCD,SRC,TGM2,GNAO1,MMP2,STAT1,NFKB1,GNAI2,ERFE,LINC02210-CRHR1,HDAC5,STAT5A,ARRB2,JUP,PRKACA,ZFP36L1,SLIT2,TP53,PDK2,PPP1R9B,SHC1,ABCC1,TSC2,FOXC2,ABL1,SLC2A8,SLC8A3,RGS8	cyan	VSMC_M2
GO:0051602	0.11	0.97	4	26	response to electrical stimulus	BP	0.91361	AKAP12,SRC,NTRK1,EEF1A2	cyan	VSMC_M2
GO:0097553	0.11	0.94	10	95	calcium ion transmembrane import into cytosol	BP	0.91361	BAX,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,SLC8A3,CALM3,CLIC2	cyan	VSMC_M2
GO:0002263	0.11	0.93	18	185	cell activation involved in immune response	BP	0.91361	STAT6,ST3GAL1,HMOX1,BCL3,LAMP1,SLC15A4,CD81,LEF1,FES,GRN,IL27RA,TP53,CPLX2,TMEM98,PTGDS,SBNO2,ABL1,ZFPM1	cyan	VSMC_M2
GO:0008286	0.11	0.94	10	93	insulin receptor signaling pathway	BP	0.91361	SOCS3,PRKCD,SRC,GNAI2,ERFE,PDK2,SHC1,TSC2,FOXC2,SLC2A8	cyan	VSMC_M2
GO:0097191	0.11	0.93	17	173	extrinsic apoptotic signaling pathway	BP	0.91361	DEPTOR,DAXX,HMOX1,NRP1,BAX,FGFR1,RBCK1,IGF1,TLR3,SFRP2,SRC,CTTN,TMBIM1,BMP4,GABARAP,AR,PML	cyan	VSMC_M2

GO:0006351	0.11	0.90	194	2521	transcription, DNA-templated	BP	0.91361	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0046395	0.11	0.93	18	182	carboxylic acid catabolic process	BP	0.91361	DDAH2,BCKDHB,AASS,ACAA1,ECH1,DECR1,ACADS,HADH,ECHS1,ACAT1,QDPR,CPT2,ABCD1,ASPA,RENBP,CRAT,LDHD,NAGK	cyan	VSMC_M2
GO:0032231	0.11	0.94	10	92	regulation of actin filament bundle assembly	BP	0.91361	NRP1,ARAP1,RHPN2,SORBS3,TJP1,ARHGEF10,ARHGEF10L,CGNL1,ABL1,SDC4	cyan	VSMC_M2
GO:0048041	0.11	0.94	9	81	focal adhesion assembly	BP	0.91361	PTPRK,NRP1,EFNA5,EPHA3,SRC,CTTN,BCR,ABL1,SDC4	cyan	VSMC_M2
GO:0010458	0.11	0.96	4	26	exit from mitosis	BP	0.91361	CTDP1,CDC14C,CHMP4B,PPP1R9B	cyan	VSMC_M2
GO:0051129	0.11	0.91	48	569	negative regulation of cellular component organization	BP	0.91361	EHMT2,RPS6KA2,PACSIN2,GSN,NRP1,NOP53,VIM,APOE,ARAP1,KAT2B,EFNB2,CLIP3,IGF1,RHPN2,CHMP4B,PRKCD,EPHA3,SRC,LRP4,TJP1,SEMA3B,RGMA,SSH3,SEMA4B,SEMA6C,B2M,VAT1,ADD1,BMP4,CAPZB,HDAC6,DNAJB6,ARRB2,CGNL1,UBQLN2,SLIT2,AR,TP53,UBQLN4,GBA,NUPR1,TEX14,SNX33,FLII,PTPRS,TSC2,ABCA2,CARD8	cyan	VSMC_M2
GO:0016601	0.11	0.96	5	36	Rac protein signal transduction	BP	0.91361	ELMO1,RHOG,NISCH,GABARAP,ARHGAP17	cyan	VSMC_M2
GO:0043433	0.11	0.94	13	126	negative regulation of DNA-binding transcription factor activity	BP	0.91361	HMOX1,BCL3,TRIM21,RBCK1,SFRP5,NDN,PTGIS,NFKBIA,ARRB2,NUPR1,GLIS2,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0050918	0.11	0.95	6	47	positive chemotaxis	BP	0.91361	GPNMB,NRP1,VEGFD,VEGFB,BMP4,TSC2	cyan	VSMC_M2
GO:0009649	0.11	0.96	4	26	entrainment of circadian clock	BP	0.91361	NR2F6,TP53,MTA1,PML	cyan	VSMC_M2
GO:0007584	0.11	0.93	14	137	response to nutrient	BP	0.91361	HMOX1,BCKDHB,FOLR2,SFRP2,STAT1,GNAI2,MN1,FES,PHEX,PDK2,KANK2,EEF2,NDOR1,GATA4	cyan	VSMC_M2
GO:0150104	0.11	0.95	8	70	transport across blood-brain barrier	BP	0.91361	SLC44A1,APOE,SLC6A9,SLC7A2,SLC5A3,SLC16A2,ABCC1,ABCA2	cyan	VSMC_M2
GO:0097659	0.11	0.90	194	2522	nucleic acid-templated transcription	BP	0.91361	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:1904377	0.11	0.95	7	58	positive regulation of protein localization to cell periphery	BP	0.91361	RHOG,CLIP3,EPHA3,EPHA2,AKAP5,PPP1R9B,STX3	cyan	VSMC_M2
GO:0048562	0.11	0.93	21	225	embryonic organ morphogenesis	BP	0.91361	TSHZ1,TCF21,EFEMP1,GLI3,SLITRK6,RARG,NDRG4,FOXF2,VANGL2,BMP4,NAGLU,EPHA2,PCGF2,HOXB1,HOXB2,HOXB4,MED12,DVL1,FOXC2,DNAAF1,GATA4	cyan	VSMC_M2
GO:0010039	0.11	0.96	4	26	response to iron ion	BP	0.91361	HMOX1,ACO1,APBB1,B2M	cyan	VSMC_M2
GO:0009057	0.11	0.91	89	1102	macromolecule catabolic process	BP	0.91361	PYM1,OS9,GNS,EIF3H,GGA1,KCTD17,CUL9,RNF144A,BAX,NOP53,TRIM13,VIM,APOE,AGAP3,ATRAID,ATG7,TIMP2,ZFP36,SAMD4B,GAA,SGSH,RNF213,HGS,TPP1,RBCK1,CHMP4B,TP53INP2,PATL1,EDEM2,CTSB,WWTR1,STBD1,PRKCD,FOXF2,CTSA,CD81,GUSB,IKBKE,CAPN3,TIRAP,RGMA,UBA7,DCAF11,CTSK,RHBDD3,FURIN,VPS11,HELZ2,ATG4B,FUCA1,RNASEL,MAGEF1,MUS81,MOV10,CAPN1,ADAMTS7,NAGLU,MAEA,USE1,HDAC6,ARRB2,GABARAP,SERPINE2,GIPC1,PRKACA,ZFP36L1,UBQLN2,UBQLN4,GBA,NUPR1,SNX33,MTA1,CLPP,UBXN6,WDR81,DVL1,ISG15,ELOB,FBXW5,AXIN1,RHBDF1,CBFA2T3,RNF166,OAS2,ABCA2,MEX3D,PML,EEF1A2,PSMB9	cyan	VSMC_M2

GO:1901652	0.11	0.92	33	375	response to peptide	BP	0.91361	STAT6,GCNT1,APPL2,KLF15,VIM,SOCS3,KAT2B,IGF1,PRKCD,SRC,MMP2,STAT1,CHRNA7,NFKB1,GNAI2,HADH,ERFE,PHEX,NFKBIA,LINC02210-CRHR1,HDAC5,QDPR,STAT5A,ZFP36L1,TP53,PDK2,PPP1R9B,SHC1,ABCC1,TSC2,FOXC2,SLC2A8,SERPINF1	cyan	VSMC_M2
GO:0001756	0.11	0.95	6	48	somitogenesis	BP	0.91361	COBL,SFRP2,LEF1,TP53,MED12,FOXC2	cyan	VSMC_M2
GO:0006979	0.11	0.92	32	357	response to oxidative stress	BP	0.91361	STAT6,PTPRK,HMOX1,RHOB,APOE,AGAP3,ATG7,GGT7,CAMKK2,PRKCD,SRC,GNAO1,MMP2,STAT1,CCS,STK25,AIFM2,TMEM161A,HDAC6,PCGF2,TP53,PDK2,ABCC1,PDGFRB,EEF2,ABCD1,ABL1,PML,SELENOP,GATA4,ADPRHL2,MPV17	cyan	VSMC_M2
GO:0001823	0.12	0.94	9	81	mesonephros development	BP	0.91361	TCF21,GLI3,WT1,LZTS2,WNT2B,BMP4,SLIT2,FOXC2,SDC4	cyan	VSMC_M2
GO:0071526	0.12	0.96	5	38	semaphorin-plexin signaling pathway	BP	0.91361	PLXNB2,NRP1,SEMA3B,SEMA4B,SEMA6C	cyan	VSMC_M2
GO:0048592	0.12	0.94	12	118	eye morphogenesis	BP	0.91361	EFEMP1,MEIS1,GLI3,BAX,RARG,MAN2A1,FOXF2,WNT2B,BMP4,NAGLU,EPHA2,COL8A1	cyan	VSMC_M2
GO:0048713	0.12	0.96	4	27	regulation of oligodendrocyte differentiation	BP	0.91361	SLC45A3,TMEM98,ASPA,IL34	cyan	VSMC_M2
GO:0051282	0.12	0.94	9	84	regulation of sequestering of calcium ion	BP	0.91361	BAX,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,CALM3,CLIC2	cyan	VSMC_M2
GO:0001704	0.12	0.94	10	93	formation of primary germ layer	BP	0.91361	SFRP2,MMP2,EXT2,LEF1,BMP4,EPHA2,PRKACA,FOXC2,HSBP1,COL8A1	cyan	VSMC_M2
GO:0099024	0.12	0.95	6	47	plasma membrane invagination	BP	0.91361	APPL2,ELMO1,GSN,RHOG,ALOX15,SNX33	cyan	VSMC_M2
GO:0010664	0.12	0.96	4	26	negative regulation of striated muscle cell apoptotic process	BP	0.91361	HSPB6,SFRP2,NUPR1,GATA4	cyan	VSMC_M2
GO:0003338	0.12	0.96	4	27	metanephros morphogenesis	BP	0.91361	WT1,STAT1,BMP4,PDGFRB	cyan	VSMC_M2
GO:0051496	0.12	0.95	6	47	positive regulation of stress fiber assembly	BP	0.91361	NRP1,SORBS3,ARHGEF10,ARHGEF10L,ABL1,SDC4	cyan	VSMC_M2
GO:1901654	0.12	0.93	15	151	response to ketone	BP	0.91361	FBXO32,TRERF1,KLF9,SRC,FIBIN,ADCY1,CASP9,SLIT2,AR,GBA,PPP1R9B,ADAM15,NDOR1,SERPINF1,CALM3	cyan	VSMC_M2
GO:0070231	0.12	0.96	5	36	T cell apoptotic process	BP	0.91361	ST3GAL1,GLI3,BAX,BMP4,TP53	cyan	VSMC_M2
GO:0036257	0.12	0.96	4	26	multivesicular body organization	BP	0.91361	HGS,CHMP4B,CHMP3,IST1	cyan	VSMC_M2
GO:0007507	0.12	0.91	40	474	heart development	BP	0.91361	CTDP1,ZFPM2,RPS6KA2,MEIS1,GLI3,NRP1,GAA,KAT2B,EFNB2,IGF1,WT1,POU6F1,SFRP2,NDRG4,CPE,PDLIM2,HEG1,VANGL2,GATA5,VEGFB,BMP4,CC2D2A,ARRB2,ERBB2,ZFP36L1,SLIT2,TP53,MED12,ADAM15,SHC1,PDGFRB,DVL1,TSC2,NPRL3,TCF25,FOXC2,DNAAF1,HEXIM1,GATA4,ZFPM1	cyan	VSMC_M2
GO:0007219	0.12	0.93	14	138	Notch signaling pathway	BP	0.91361	RFNG,ANGPT4,SRC,TM2D3,APH1A,GATA5,NFKBIA,DTX2,EPN2,LLGL1,TRAF7,FOXC2,DTX3,ZBTB7A	cyan	VSMC_M2
GO:0051017	0.12	0.93	14	139	actin filament bundle assembly	BP	0.91361	NRP1,ARAP1,RHPN2,SRC,SORBS3,PHACTR1,TJP1,ARHGEF10,ADD1,ARHGEF10L,CGNL1,AIF1L,ABL1,SDC4	cyan	VSMC_M2
GO:0006368	0.12	0.95	7	58	transcription elongation from RNA polymerase II promoter	BP	0.91361	CTDP1,NELFCD,ELL3,ELOB,NELFB,HEXIM1,CDK9	cyan	VSMC_M2
GO:0010524	0.12	0.96	5	37	positive regulation of calcium ion transport into cytosol	BP	0.91361	BAX,PLCG1,CAPN3,ABL1,CALM3	cyan	VSMC_M2
GO:1905207	0.12	0.96	4	27	regulation of cardiocyte differentiation	BP	0.91361	EFNB2,BMP4,ARRB2,GATA4	cyan	VSMC_M2
GO:0033865	0.12	0.94	11	102	nucleoside bisphosphate metabolic process	BP	0.91361	AASS,ACSS1,GPAT4,ACSS2,ABHD14B,ACAT1,PDK2,PPCDC,ABCD1,ACOT6,DGAT1	cyan	VSMC_M2
GO:0033875	0.12	0.94	11	102	ribonucleoside bisphosphate metabolic process	BP	0.91361	AASS,ACSS1,GPAT4,ACSS2,ABHD14B,ACAT1,PDK2,PPCDC,ABCD1,ACOT6,DGAT1	cyan	VSMC_M2
GO:0034032	0.12	0.94	11	102	purine nucleoside bisphosphate metabolic process	BP	0.91361	AASS,ACSS1,GPAT4,ACSS2,ABHD14B,ACAT1,PDK2,PPCDC,ABCD1,ACOT6,DGAT1	cyan	VSMC_M2
GO:0000910	0.12	0.93	14	141	cytokinesis	BP	0.91361	CDC14C,RHOB,CHMP4B,CHMP3,LZTS2,GIPC1,TEX14,CENPV,SNX33,RAB11FIP3,ENTR1,IST1,CALM3,TMEM250	cyan	VSMC_M2
GO:0010721	0.12	0.93	13	130	negative regulation of cell development	BP	0.91361	APPL2,NRP1,IGF1,EFNA5,LRP4,SEMA3B,RGMA,SEMA4B,SEMA6C,B2M,TP53,TMEM98,PTPRS	cyan	VSMC_M2
GO:0003281	0.12	0.95	7	60	ventricular septum development	BP	0.91361	ZFPM2,HEG1,BMP4,SLIT2,NPRL3,GATA4,ZFPM1	cyan	VSMC_M2
GO:0042168	0.12	0.96	5	37	heme metabolic process	BP	0.91361	IBA57,HMOX1,UROD,SLC6A9,ABCC1	cyan	VSMC_M2
GO:0007431	0.12	0.96	4	27	salivary gland development	BP	0.91361	NFIB,NRP1,TGM2,CLCN2	cyan	VSMC_M2
GO:0032467	0.12	0.96	4	27	positive regulation of cytokinesis	BP	0.91361	CDC14C,CHMP3,GIPC1,CENPV	cyan	VSMC_M2
GO:0071705	0.12	0.90	127	1609	nitrogen compound transport	BP	0.91361	RAB5B,OS9,FLOT1,RABL2A,TBC1D22A,TAPBP,GGA1,APPL2,TBC1D2,P3H1,SLC44A1,BBS9,TBC1D17,GLI3,AP2A1,CADPS2,SLC17A7,STOM,RHOB,BAX,DENND2A,APOE,BCL3,SLC6A9,ATG7,EXOC7,RHBDF2,LTBP4,CAMK1,EHD3,CMTM6,ZFP36,FOLR2,HGS,TBC1D5,RFTN1,RAB11FIP1,APBB1,PKDCC,CLIP3,SLC15A4,SLC7A2,GNPTAB,IGF1,EFNA5,CHMP4B,CHMP3,EDEM2,ARRDC3,SLC38A7,PRKCD,SRC,CACNB3,BBS2,ARHGAP1,EXOC2,NISCH,SYS1,CTSA,CD81,AGFG1,CTTN,TMEM115,HADH,DISP1,SGSM1,SV2A,EXOC8,RHBDD3,VPS11,KIF1A,FAM53B,TCN2,ATG4B,NFKBIA,LINC02210-CRHR1,M6PR,ADORA2A,RPGR,PSAP,HOMER3,BMP4,PORCN,USE1,HDAC6,B3GAT3,ARRB2,JUP,AKAP5,GABARAP,GIPC1,ERBB2,PRKACA,ZFP36L1,TP53,SLC51B,SLC16A2,SLC44A2,SNX33,RASL10B,ABCC1,MCOLN1,LLGL1,ZDHHC9,NAGPA,MFSD12,ABCD1,SGSM2,TSC2,PHPT1,RAB11FIP3,ENTR1,RHBDF1,CLSTN1,MON1B,IST1,ABCA2,RAB43,GRASP,PML,SCAMP4,VPS26B,STX3,RAB11B,MCFD2,EMD,UBL5	cyan	VSMC_M2
GO:0030855	0.12	0.91	37	430	epithelial cell differentiation	BP	0.91361	TCF21,AFDN,NFIB,NRP1,KLF15,VIM,SLITRK6,ZFP36,GPAT4,TPP1,RARG,WT1,CTSB,WWTR1,SRC,STAT1,TJP1,LAMB2,HEG1,GATA5,BCR,PSAP,ADD1,BMP4,RARRES3,DLG5,EPHA2,KAZN,ZFP36L1,NTRK1,AR,PTPRS,EDF1,FOXC2,ABL1,CNN3,GATA4	cyan	VSMC_M2
GO:0046434	0.12	0.93	13	126	organophosphate catabolic process	BP	0.91361	PLA2G7,PNP,SMPD1,NEIL2,PRKCD,PLBD2,PLCG1,ACAT1,NUDT13,ABCD1,PNPLA7,INPP5E,DPYD	cyan	VSMC_M2
GO:1900077	0.12	0.96	4	27	negative regulation of cellular response to insulin stimulus	BP	0.91361	APPL2,SOCS3,PRKCD,TSC2	cyan	VSMC_M2
GO:0030521	0.12	0.96	5	37	androgen receptor signaling pathway	BP	0.91361	TCF21,DAXX,HDAC6,AR,ZBTB7A	cyan	VSMC_M2
GO:0010522	0.12	0.94	8	71	regulation of calcium ion transport into cytosol	BP	0.91361	BAX,PLCG1,CAPN3,PRKACA,ABL1,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0097352	0.12	0.96	5	37	autophagosome maturation	BP	0.91361	CHMP3,FYCO1,TECPR1,UBQLN4,MCOLN1	cyan	VSMC_M2
GO:0030048	0.12	0.94	10	97	actin filament-based movement	BP	0.91361	MYL6B,GSN,BIN1,SCN1B,SNTA1,CTNNA3,WIPF1,KCND3,JUP,GATA4	cyan	VSMC_M2
GO:0008589	0.12	0.94	8	71	regulation of smoothened signaling pathway	BP	0.91361	GLI3,KIF7,DLG5,SERPINE2,PRKACA,ULK3,GLIS2,GAS1	cyan	VSMC_M2

GO:0010232	0.12	0.94	8	71	vascular transport	BP	0.91361	SLC44A1,APOE,SLC6A9,SLC7A2,SLC5A3,SLC16A2,ABCC1,ABCA2	cyan	VSMC_M2
GO:0051654	0.12	0.96	4	27	establishment of mitochondrion localization	BP	0.91361	MAP1S,HDAC6,RHOT2,HSBP1	cyan	VSMC_M2
GO:0051223	0.12	0.91	36	412	regulation of protein transport	BP	0.91361	OS9,P3H1,GLI3,STOM,APOE,RHBDF2,CAMK1,RAB11FIP1,APBB1,PKDCC,IGF1,EFNA5,EDEM2,PRKCD,SRC,CACNB3,CD81,HADH,DISP1,RHBDD3,VPS11,ADORA2A,BMP4,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,LLGL1,PHPT1,RAB11FIP3,RHBDF1,GRASP,EMD,UBL5	cyan	VSMC_M2
GO:0051962	0.12	0.92	20	216	positive regulation of nervous system development	BP	0.91361	PLXNB2,GLI3,NRP1,BIN1,SLITRK6,MAN2A1,TGM2,ST K25,ELL3,RND2,DLG5,SERPINE2,NTRK1,SLIT2,ASPA,AGRN,CLSTN1,IL34,IST1,SERPINF1	cyan	VSMC_M2
GO:0060986	0.12	0.96	4	27	endocrine hormone secretion	BP	0.91361	FZD4,RAB11FIP1,LINC02210-CRHR1,RAB11FIP3	cyan	VSMC_M2
GO:0072665	0.12	0.95	7	60	protein localization to vacuole	BP	0.91361	HGS,GNPTAB,CD81,M6PR,GLMP,NAGPA,MON1B	cyan	VSMC_M2
GO:0030031	0.12	0.91	38	443	cell projection assembly	BP	0.91361	CDC14C,KCTD17,RSPH9,BBS9,COBL,GSN,NRP1,CCDC114,MARK4,EHD3,DZIP1,ARAP1,RHOG,POC1B,WWTR1,PRKCD,SRC,BBS2,C15orf62,CTTN,VANGL2,RPGR,CAPZB,CC2D2A,HDAC6,CROCC,EPHA2,SLIT2,PPP1R9B,AGRN,WDR90,ENTR1,AIF1L,ABL1,DNAAF1,ATMIN,ATP6V0D1,TMEM250	cyan	VSMC_M2
GO:0034330	0.12	0.91	45	541	cell junction organization	BP	0.91361	FLOT1,PLXNB2,AFDN,PTPRK,ARHGAP39,NRP1,APOE,SLITRK6,CAMK1,EFNB2,TMEM108,LZTS3,PPFIBP2,SNTA1,EFNA5,CAST,GLRB,EPHA3,SRC,CACNB3,LRP4,CHRNA7,TJP1,CTTN,LAMB2,HEG1,KIF1A,BCR,ADD1,DLG5,HDAC6,JUP,EPHA2,ERBB2,PRKACA,NTRK1,PTPRS,DVL1,AGRN,NPHP4,CLSTN1,ABL1,NFIA,SLC8A3,SDC4	cyan	VSMC_M2
GO:0071222	0.12	0.93	13	126	cellular response to lipopolysaccharide	BP	0.91361	IRF3,VIM,ZFP36,SRC,BPI,NFKB1,NFKBIA,PLSCR3,SBNO2,ABL1,CD55,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0042391	0.12	0.92	27	302	regulation of membrane potential	BP	0.91361	BAX,BIN1,EHD3,TMEM108,SCN1B,SNTA1,GLRB,SRC,CACNB3,CHRNA7,TUSC2,CTNNA3,KCND3,ADORA2A,CHRNE,ARRB2,JUP,GBA,GRIA1,PIEZO2,SH3GL1,ABCD1,DVL1,ABL1,SLC8A3,KCND2,CALM3	cyan	VSMC_M2
GO:0051345	0.12	0.91	38	440	positive regulation of hydrolase activity	BP	0.91361	TBC1D22A,AFDN,MTCH1,TBC1D2,TBC1D17,GSN,BAX,ARAP1,TBC1D5,RHOG,FGFR1,SFRP2,PRKCD,TGM2,GNAO1,RGMA,SGSM1,SIPA1L2,APH1A,CASP10,ARHGEF10,BCR,GRN,PCOLCE,PSAP,EPHA2,CASP9,ERBB2,NTRK1,PDGFRB,SGSM2,AGRN,TSC2,PML,CALM3,CARD8,RGS8,RGS10	cyan	VSMC_M2
GO:0007188	0.12	0.93	13	129	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	BP	0.91361	AKAP12,ADGRD1,ARRDC3,GNAO1,GNAI2,ADGRB2,GRK5,ADCY1,LINC02210-CRHR1,GNAZ,ADORA2A,PSAP,AKAP5	cyan	VSMC_M2
GO:2000785	0.12	0.95	5	37	regulation of autophagosome assembly	BP	0.91361	EHMT2,CHMP4B,UBQLN2,NUPR1,NPRL3	cyan	VSMC_M2
GO:0001738	0.12	0.94	9	84	morphogenesis of a polarized epithelium	BP	0.91361	PRICKLE2,SFRP2,FOXF2,VANGL2,DLG5,MED12,ROR1,DVL1,ABL1	cyan	VSMC_M2
GO:0043271	0.13	0.93	10	93	negative regulation of ion transport	BP	0.91361	BIN1,SLC6A9,CACNB3,GNAO1,LINC02210-CRHR1,WNK4,SERPINE2,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0032945	0.13	0.95	6	48	negative regulation of mononuclear cell proliferation	BP	0.91361	GPNMB,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0050672	0.13	0.95	6	48	negative regulation of lymphocyte proliferation	BP	0.91361	GPNMB,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0072078	0.13	0.94	7	60	nephron tubule morphogenesis	BP	0.91361	TCF21,GLI3,WT1,LZTS2,WNT2B,WNK4,BMP4	cyan	VSMC_M2
GO:0086004	0.13	0.96	4	29	regulation of cardiac muscle cell contraction	BP	0.91361	BIN1,CTNNA3,JUP,GATA4	cyan	VSMC_M2
GO:1903510	0.13	0.94	8	71	mucopolysaccharide metabolic process	BP	0.91361	GNS,ST3GAL1,AP2A1,CHST14,EXT2,NFKB1,B4GAT1,XYLT2	cyan	VSMC_M2
GO:0031128	0.13	0.96	4	28	developmental induction	BP	0.91361	GATA5,WNT2B,BMP4,AR	cyan	VSMC_M2
GO:0090183	0.13	0.96	4	27	regulation of kidney development	BP	0.91361	WT1,STAT1,WNT2B,BMP4	cyan	VSMC_M2
GO:0032465	0.13	0.94	8	72	regulation of cytokinesis	BP	0.91361	CDC14C,CHMP3,GIPC1,TEX14,CENPV,RAB11FIP3,ENTR1,CALM3	cyan	VSMC_M2
GO:0042398	0.13	0.95	5	37	cellular modified amino acid biosynthetic process	BP	0.91361	GGT7,PLSCR1,PTDSS1,HAGH,FPGS	cyan	VSMC_M2
GO:0061572	0.13	0.92	14	141	actin filament bundle organization	BP	0.91361	NRP1,ARAP1,RHPN2,SRC,SORBS3,PHACTR1,TJP1,ARHGEF10,ADD1,ARHGEF10L,CGNL1,AIF1L,ABL1,SDC4	cyan	VSMC_M2
GO:0009755	0.13	0.92	14	142	hormone-mediated signaling pathway	BP	0.91361	TCF21,DAXX,TRERF1,APPL2,RARG,SRC,VPS11,LMO3,LINC02210-CRHR1,BMP4,HDAC6,AR,KANK2,ZBTB7A	cyan	VSMC_M2
GO:0032774	0.13	0.89	194	2534	RNA biosynthetic process	BP	0.91361	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,APOE,BCL3,CAMK1,ZFP36,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0060041	0.13	0.93	11	108	retina development in camera-type eye	BP	0.91361	SLC17A7,NRP1,BAX,FZD4,MAN2A1,LAMB2,CLCN2,NAGLU,PDGFRB,NPHP4,SERPINF1	cyan	VSMC_M2
GO:1900180	0.13	0.93	12	116	regulation of protein localization to nucleus	BP	0.91361	CARD10,GLI3,DCLK1,WWTR1,PRKCD,SRC,LZTS2,TRIM8,BMP4,JUP,TMEM98,GLIS2	cyan	VSMC_M2

GO:0043269	0.13	0.90	38	444	regulation of ion transport	BP	0.91361	KCNQ5,STOM,BAX,BIN1,SLC6A9,EHD3,SCN1B,SNTA1,CACNB3,PLCG1,GNAO1,CRACR2B,CAPN3,CACNA2D2,TPCN2,GNAI2,SV2A,CLCN2,LINC02210-CRHR1,B2M,KCND3,ADORA2A,CAPN1,HOMER3,WNK4,ARRB2,SERPINE2,PRKACA,MLLT6,PDGFRB,ABL1,CBARP,KCND2,PML,CALM3,CLIC2,CLIC3,RAB11B	cyan	VSMC_M2
GO:0008645	0.13	0.93	9	83	hexose transmembrane transport	BP	0.91361	APPL2,KLF15,CLIP3,IGF1,SLC5A3,SLC45A3,ERFE,RNASEL,SLC2A8	cyan	VSMC_M2
GO:0071364	0.13	0.95	5	38	cellular response to epidermal growth factor stimulus	BP	0.91361	ZFP36,PLCG1,ERBB2,ZFP36L1,PPP1R9B	cyan	VSMC_M2
GO:0090257	0.13	0.92	17	179	regulation of muscle system process	BP	0.91361	CTDP1,FBXO32,MLIP,BIN1,EHD3,HSPB6,IGF1,CTTN,GATA5,CTNNA3,JUP,PRKACA,SLC8A3,GATA4,CALM3,CLIC2,CDK9	cyan	VSMC_M2
GO:0009582	0.13	0.93	9	83	detection of abiotic stimulus	BP	0.91361	TRPM3,CACNB3,NR2F6,ARRB2,JUP,SERPINE2,NTRK1,PIEZO2,NMT2	cyan	VSMC_M2
GO:0021695	0.13	0.95	5	39	cerebellar cortex development	BP	0.91361	COQ8B,NAGLU,SERPINE2,GBA,RERE	cyan	VSMC_M2
GO:0042572	0.13	0.96	4	27	retinol metabolic process	BP	0.91361	PLB1,PNPLA2,DHRS13,DGAT1	cyan	VSMC_M2
GO:0010837	0.13	0.96	4	28	regulation of keratinocyte proliferation	BP	0.91361	PTPRK,KLF9,ZFP36,ZFP36L1	cyan	VSMC_M2
GO:0005976	0.13	0.93	9	83	polysaccharide metabolic process	BP	0.91361	STK40,AP2A1,GAA,IGF1,STBD1,EXT2,PHKG1,NFKB1,B4GALT5	cyan	VSMC_M2
GO:1905039	0.13	0.93	11	105	carboxylic acid transmembrane transport	BP	0.91361	SLC17A7,SLC6A9,FOLR2,SLC15A4,SLC7A2,SLC38A7,SLC16A2,ABCC1,CPT2,MFSD12,ABCD1	cyan	VSMC_M2
GO:0008585	0.13	0.94	8	72	female gonad development	BP	0.91361	ZFPM2,BAX,FZD4,WT1,SRC,ARRB2,SLIT2,NUPR1	cyan	VSMC_M2
GO:0030224	0.13	0.96	4	28	monocyte differentiation	BP	0.91361	FES,BMP4,ZFP36L1,IL34	cyan	VSMC_M2
GO:0009953	0.13	0.94	7	60	dorsal/ventral pattern formation	BP	0.91361	GLI3,LRP4,BMP4,NBL1,PRKACA,HOXB2,EN1	cyan	VSMC_M2
GO:0071312	0.13	0.96	4	29	cellular response to alkaloid	BP	0.91361	EHMT2,ATG7,TGM2,PPP1R9B	cyan	VSMC_M2
GO:0051100	0.13	0.92	13	129	negative regulation of binding	BP	0.91361	HMOX1,BAX,CAMK1,PRKCD,RGMA,LEF1,NFKBIA,B2M,ARRB2,ADAM15,TEX14,DVL1,ZFPM1	cyan	VSMC_M2
GO:0071482	0.13	0.93	10	94	cellular response to light stimulus	BP	0.91361	PTPRK,BAX,SMPD1,PRKCD,MMP2,TMEM161A,CASP9,TP53,NMT2,BMF	cyan	VSMC_M2
GO:0055017	0.13	0.93	8	72	cardiac muscle tissue growth	BP	0.91361	CTDP1,ZFPM2,MEIS1,IGF1,NDRG4,HEG1,FOXC2,GATA4	cyan	VSMC_M2
GO:0048593	0.13	0.93	10	96	camera-type eye morphogenesis	BP	0.91361	MEIS1,GLI3,BAX,MAN2A1,FOXF2,WNT2B,BMP4,NAGLU,EPHA2,COL8A1	cyan	VSMC_M2
GO:0001836	0.13	0.94	6	48	release of cytochrome c from mitochondria	BP	0.91361	BAX,IGF1,ARRB2,PLSCR3,TP53,BMF	cyan	VSMC_M2
GO:0043112	0.13	0.92	13	131	receptor metabolic process	BP	0.91361	FLOT1,APOE,EHD3,ARAP1,TBC1D5,CD81,FURIN,CAPN1,ARRB2,UBQLN2,GRIA1,ABCA2,RAB11B	cyan	VSMC_M2
GO:0030518	0.13	0.93	10	96	intracellular steroid hormone receptor signaling pathway	BP	0.91361	TCF21,DAXX,TRERF1,SRC,VPS11,LMO3,HDAC6,AR,KANK2,ZBTB7A	cyan	VSMC_M2
GO:0009890	0.13	0.89	97	1222	negative regulation of biosynthetic process	BP	0.91361	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,AP2A1,IRF3,NOP53,APOE,BCL3,ATG7,ZFP36,SAMD4B,APBB1,LMO1,RARG,WT1,PATL1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,CAPN3,NFKB1,HIST1H1C,LEF1,TBL1Y,PTGIS,NELFCD,ERFE,RFX5,MAGEF1,MOV10,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,ZFP36L1,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,ACP5,KANK2,MTA1,MOSPD1,MFSD12,GLIS2,ABCD1,E4F1,NELFB,TCF3,SBNO2,FAM3A,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,GCHFR,ZFPM1,EN1	cyan	VSMC_M2
GO:1902532	0.13	0.90	35	407	negative regulation of intracellular signal transduction	BP	0.91361	DEPTOR,GRINA,TLE1,CARD19,AKT1S1,NOP53,APOE,TIMP2,SMPD1,SFRP2,PRKCD,SRC,SFRP5,MAPK8IP1,STAT1,HEG1,LMO3,ELL3,TMEM161A,HOMER3,BMP4,DLG5,DHX58,ARRB2,EPHA2,SERPINE2,CGNL1,SLIT2,GBA,MAP2K3,TSC2,INPP5E,NPRL3,ABL1,CARD8	cyan	VSMC_M2
GO:0051249	0.13	0.91	26	287	regulation of lymphocyte activation	BP	0.91361	STAT6,IRF1,GPNMB,GLI3,PNP,LAMP1,SLC15A4,LMO1,IGF1,SRC,MAPK8IP1,CD81,TIRAP,LEF1,RHBDD3,B2M,ADORA2A,BMP4,DLG5,ERBB2,ZFP36L1,IL27RA,TNFRSF14,ABL1,CD55,SDC4	cyan	VSMC_M2
GO:0050821	0.13	0.92	15	154	protein stabilization	BP	0.91361	FLOT1,P3H1,NOP53,TSPAN1,LAMP1,IGF1,PRKCD,GRN,IFI30,WIZ,TP53,GLMP,WDR81,DVL1,PLPP3	cyan	VSMC_M2
GO:0032413	0.13	0.94	6	49	negative regulation of ion transmembrane transporter activity	BP	0.91361	SLC6A9,CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0071709	0.14	0.95	5	39	membrane assembly	BP	0.91361	FLOT1,PACSIN2,RFTN1,CHMP4B,LRP4	cyan	VSMC_M2
GO:0015749	0.14	0.93	9	84	monosaccharide transmembrane transport	BP	0.91361	APPL2,KLF15,CLIP3,IGF1,SLC5A3,SLC45A3,ERFE,RNASEL,SLC2A8	cyan	VSMC_M2
GO:2000241	0.14	0.92	11	105	regulation of reproductive process	BP	0.91361	ZFPM2,RPS6KA2,PLB1,TPPP2,IGF1,WT1,SRC,BMP4,AR,NUPR1,SERPINF1	cyan	VSMC_M2
GO:0071277	0.14	0.94	7	63	cellular response to calcium ion	BP	0.91361	SMPD1,CAPN3,ADCY1,ADD1,ALOX15,MCOLN1,JUNB	cyan	VSMC_M2
GO:0120031	0.14	0.90	37	435	plasma membrane bounded cell projection assembly	BP	0.91361	CDC14C,KCTD17,RSPH9,BBS9,COBL,GSN,NRP1,CCDC114,MARK4,EHD3,DZIP1,ARAP1,RHOG,POC1B,WWTR1,PRKCD,BBS2,C15orf62,CTTN,VANGL2,RPGR,CAPZB,CC2D2A,HDAC6,CROCC,EPHA2,SLIT2,PPP1R9B,AGRN,WDR90,ENTR1,AIF1L,ABL1,DNAAF1,ATMIN,ATP6V0D1,TMEM250	cyan	VSMC_M2
GO:0051208	0.14	0.93	9	87	sequestering of calcium ion	BP	0.91361	BAX,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,CALM3,CLIC2	cyan	VSMC_M2
GO:0043066	0.14	0.89	55	662	negative regulation of apoptotic process	BP	0.91361	DDAH2,ST3GAL1,GRINA,TLE1,HMOX1,HIGD2A,STK40,GLI3,NRP1,BAX,MEIS3,APOE,BCL3,SOCS3,PAK4,HSPB6,ANGPT4,IGF1,WT1,CAST,SFRP2,PRKCD,SRC,MAPK8IP1,CAPN3,TJP1,CTTN,NFKB1,GNAI2,LEF1,GRK5,ELL3,ADORA2A,GRN,TMEM161A,TMBIM1,BMP4,MAEA,DNAJB6,ARRB2,NTRK1,PCGF2,AR,TP53,GBA,NUPR1,SHC1,ADAR,ATOX1,PDGFRB,RETREG1,FOXC2,ABL1,GATA4,EN1	cyan	VSMC_M2
GO:0050886	0.14	0.94	6	49	endocrine process	BP	0.91361	RPS6KA2,FZD4,RAB11FIP1,LINC02210-CRHR1,RASL10B,RAB11FIP3	cyan	VSMC_M2
GO:0001508	0.14	0.93	10	99	action potential	BP	0.91361	BIN1,SCN1B,SNTA1,CACNB3,CTNNA3,KCND3,JUP,GBA,KCND2,CALM3	cyan	VSMC_M2
GO:0007613	0.14	0.93	9	86	memory	BP	0.91361	EHMT2,APOE,CHRNA7,ADCY1,PTCHD1,GRIA1,SLC8A3,SERPINF1,LRRN4	cyan	VSMC_M2

GO:0051247	0.14	0.89	91	1140	positive regulation of protein metabolic process	BP	0.91361	PYM1,FLOT1,PLXNB2,DAXX,MTCH1,GGA1,CARD10,GPNMB,RNF144A,GSN,NRP1,BAX,NOP53,FZD4,CAB39L,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,FGFR1,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,ARRDC3,CAMKK2,SPON1,SFRP2,PRKCD,SRC,LRP4,MOB2,CD81,NDN,CHRNA7,CAPN3,TIRAP,RGMA,APH1A,VEGFD,RHBDD3,CASP10,FURIN,VPS11,ATG4B,MAGEF1,NFKBIA,CLEC3B,GRN,PCOLCE,VEGFB,BMP4,HDAC6,ARRB2,GABARAP,CASP9,ERBB2,BRAT1,UBQLN2,NTRK1,TP53,GBA,SLC51B,NUPR1,GPRC5B,SNX33,PDGFRB,MTA1,MAP2K3,TRAF4,EEF2,DVL1,ELOB,TNFRSF14,AXIN1,CBFA2T3,ABL1,IL34,IST1,ABCA2,PML,CALM3,CARD8,CDK9,SDC4	cyan	VSMC_M2
GO:0048841	0.14	0.95	4	29	regulation of axon extension involved in axon guidance	BP	0.91361	NRP1,SEMA3B,SEMA4B,SEMA6C	cyan	VSMC_M2
GO:0009581	0.14	0.93	9	84	detection of external stimulus	BP	0.91361	TRPM3,CACNB3,NR2F6,ARRB2,JUP,SERPINE2,NTRK1,PIEZO2,NMT2	cyan	VSMC_M2
GO:1903825	0.14	0.92	11	106	organic acid transmembrane transport	BP	0.91361	SLC17A7,SLC6A9,FOLR2,SLC15A4,SLC7A2,SLC38A7,SLC16A2,ABCC1,CPT2,MFSD12,ABCD1	cyan	VSMC_M2
GO:0015031	0.14	0.88	103	1301	protein transport	BP	0.91361	RAB5B,OS9,RABL2A,TBC1D22A,GGA1,APPL2,TBC1D2,P3H1,BBS9,TBC1D17,GLI3,AP2A1,CADPS2,STOM,RHOB,BAX,DENND2A,APOE,BCL3,ATG7,EXOC7,RHBDF2,CAMK1,EHD3,CMTM6,HGS,TBC1D5,RFTN1,RAB11FIP1,APBB1,PKDCC,CLIP3,SLC15A4,GNPTAB,IGF1,EFNA5,CHMP4B,CHMP3,EDEM2,ARRDC3,PRKCD,SRC,CACNB3,BBS2,ARHGAP1,EXOC2,SYS1,CTSA,CD81,CTTN,TMEM115,HADH,DISP1,SGSM1,EXOC8,RHBDD3,VPS11,KIF1A,FAM53B,ATG4B,NFKBIA,M6PR,ADORA2A,RPGR,HOMER3,BMP4,PORCN,USE1,HDAC6,B3GAT3,ARRB2,JUP,AKAP5,GABARAP,GIPC1,ERBB2,PRKACA,TP53,SLC51B,SNX33,MCOLN1,LLGL1,ZDHHC9,NAGPA,SGSM2,TSC2,PHPT1,RAB11FIP3,ENTR1,RHBDF1,CLSTN1,MON1B,IST1,RAB43,GRASP,PML,SCAMP4,VPS26B,STX3,RAB11B,MCFD2,EMD,UBL5	cyan	VSMC_M2
GO:2000736	0.14	0.94	6	50	regulation of stem cell differentiation	BP	0.91361	SOX5,LTBP3,HOXB4,NELFB,ABL1,GATA4	cyan	VSMC_M2
GO:0050920	0.14	0.91	16	167	regulation of chemotaxis	BP	0.91361	PLA2G7,NRP1,FGFR1,EFNB2,ADGRA2,TIRAP,SEMA3B,VEGFD,SEMA4B,SEMA6C,VEGFB,NBL1,SLIT2,PDGFRB,IL34,STX3	cyan	VSMC_M2
GO:1903305	0.14	0.93	10	95	regulation of regulated secretory pathway	BP	0.91361	HMOX1,LAMP1,GNAI2,ADCY1,FES,ADORA2A,GIPC1,DVL1,CBARP,CALM3	cyan	VSMC_M2
GO:0046626	0.14	0.94	6	50	regulation of insulin receptor signaling pathway	BP	0.91361	SOCS3,PRKCD,SRC,GNAI2,ERFE,TSC2	cyan	VSMC_M2
GO:0050982	0.14	0.95	5	40	detection of mechanical stimulus	BP	0.91361	CACNB3,JUP,SERPINE2,NTRK1,PIEZO2	cyan	VSMC_M2
GO:0061136	0.14	0.91	16	166	regulation of proteasomal protein catabolic process	BP	0.91361	EIF3H,RNF144A,NOP53,APOE,FOXF2,GABARAP,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,DVL1,ELOB,RHBDF1,CBFA2T3	cyan	VSMC_M2
GO:0097421	0.14	0.95	4	28	liver regeneration	BP	0.91361	HMOX1,GLI3,RPS16,RPS15	cyan	VSMC_M2
GO:0002065	0.14	0.94	7	61	columnar/cuboidal epithelial cell differentiation	BP	0.91361	GPAT4,RARG,SRC,GATA5,BMP4,ABL1,GATA4	cyan	VSMC_M2
GO:0021532	0.14	0.95	4	28	neural tube patterning	BP	0.91361	GLI3,BMP4,PRKACA,EN1	cyan	VSMC_M2
GO:0008610	0.14	0.89	46	544	lipid biosynthetic process	BP	0.91361	CHKB,B3GALT4,CYB5R3,ST3GAL1,SLC44A1,ACSS1,APOE,SOCS3,GPAT4,SMPD1,ACSS2,LPCAT4,PLSCR1,HEXB,PRKCD,PTDSS1,PNPLA2,PIK3C2B,SLC45A3,NFKB1,IP6K1,PTGIS,B4GALT5,CLCN2,ACAT1,PLD2,ALOX15,PLSCR3,STARD3,HSD3B7,GBA,SLC44A2,CERS4,ABCD1,PTGDS,FAM3A,PIGQ,INPP5E,H6PD,PLPP2,GSTM4,LCAT,ABCA2,DGAT1,PLPP3,AL157935.2	cyan	VSMC_M2
GO:0032232	0.14	0.95	4	29	negative regulation of actin filament bundle assembly	BP	0.91361	ARAP1,RHPN2,TJP1,CGNL1	cyan	VSMC_M2
GO:0044237	0.14	0.88	583	7918	cellular metabolic process	BP	0.91361	CTDP1,TSHZ1,ZADH2,PYM1,PMEL,RBMS2,STAT6,MOXD1,TCF21,OS9,MGAT4B,GNS,FLOT1,CHKB,DDAH2,PPP6R2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,DEPTOR,B3GALT4,CYB5R3,TAPBP,TCF20,DAXX,NAGA,FBXO32,HDDC2,TEF,PTPRK,ST3GAL1,IBA57,CDC14C,TEAD3,MTCH1,TLE1,OPLAH,CARD10,KCTD17,NFIB,TRERF1,GCNT1,HMOX1,ACO1,CUL9,KLF9,APPL2,PLA2G7,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,ITGB8,P3H1,NAT14,TMEM150B,GPNMB,SLC44A1,BCKDHB,EFEMP1,RRAGC,EEPD1,MEIS1,RNF144A,STK40,TBC1D17,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,RPL18,PARP12,NOP53,ABTB1,BICRA,MEIS3,FKRP,UQCRH,TRIM13,ACSS1,FZD4,ME3,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,UROD,BCL3,ETHE1,MIF4GD,AGAP3,ATRAID,SLC6A9,ACAA1,ATG7,EXOC7,CYP2S1,COQ8B,PLB1,SOCS3,CAMK1,EHD3,PLD3,TEP1,OSBPL10,RNF170,PNP,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,GAA,PAK4,SGSH,ECH1,RNF213,ARAP1,GPAT4,RPL15,HGS,KAT2B,TBC1D5,EIF3K,RHOG,DCXR,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,TPP1,WDFY4,CLIP3,GTF3A,SLC15A4,ANGPT4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,GNPTAB,IGF1,CYP4V2,TLR3,SNTA1,MAN2A1,WT1,EFNA5,CHMP4B,CHMP3,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,GGCX,POU6F1,LPCAT4,SERPING1,CAST,LACTB2,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,STBD1,PRKCD,COQ9,EPHA3,SRC,CPE,TGM2,LRP4,DECR1,PLBD2,PLCG1,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,MMP2,PTPN13,PTDSS1,EXT2,SLC5A3,PNPLA2,PIK3C2B,STAT1,CTSA,ABHD14B,	cyan	VSMC_M2
GO:0008361	0.14	0.91	15	157	regulation of cell size	BP	0.91361	DEPTOR,AKT1S1,NRP1,APOE,RARG,CTTN,SEMA3B,RGMA,SEMA4B,SEMA6C,RND2,CLCN6,PTPRS,ABL1,IST1	cyan	VSMC_M2
GO:0040017	0.14	0.90	39	462	positive regulation of locomotion	BP	0.91361	AKAP12,HMOX1,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,FGFR1,ADGRA2,ANGPT4,IGF1,SRC,PLCG1,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,SEMA4B,SEMA6C,FAM89B,GRN,VEGFB,BMP4,STAT5A,HDAC6,SLIT2,PDGFRB,MAP2K3,TNFRSF14,PHPT1,FOXC2,ABL1,IL34,PLPP3,STX3	cyan	VSMC_M2
GO:2000300	0.14	0.94	5	39	regulation of synaptic vesicle exocytosis	BP	0.91361	ADCY1,ADORA2A,GIPC1,DVL1,CALM3	cyan	VSMC_M2
GO:0044262	0.14	0.91	21	229	cellular carbohydrate metabolic process	BP	0.91361	STK40,GAA,KAT2B,GNPTAB,IGF1,STBD1,SRC,EXT2,SLC5A3,SLC45A3,PHKG1,GUSB,B4GALT5,ERFE,TP53,PDK2,NUPR1,FAM3A,INPP5E,CBFA2T3,NAGK	cyan	VSMC_M2
GO:0045666	0.14	0.93	7	61	positive regulation of neuron differentiation	BP	0.91361	TIMP2,FGFR1,BMP4,NBL1,TCF12,GPRC5B,TCF3	cyan	VSMC_M2

GO:1901617	0.14	0.91	17	178	organic hydroxy compound biosynthetic process	BP	0.91361	PMEL,MOXD1,CYB5R3,APOE,NFKB1,IP6K1,CLCN2,PCBD1,QDPR,ALOX15,GIPC1,HSD3B7,GBA,MFSD12,H6PD,ABCA2,PDXK	cyan	VSMC_M2
GO:0060249	0.14	0.91	20	218	anatomical structure homeostasis	BP	0.91361	BAX,GAA,POC1B,TPP1,CHMP4B,TP53INP2,WWTR1,SRC,BBS2,CAPN3,TJP1,CTSK,LTBP3,B2M,LDB2,CROCC,TMEM175,ACP5,SIGLEC15,NPHP4	cyan	VSMC_M2
GO:0061912	0.14	0.93	7	63	selective autophagy	BP	0.91361	STBD1,LGALS8,HDAC6,TP53,RETREG1,WDR81,TSC2	cyan	VSMC_M2
GO:1990138	0.14	0.91	14	147	neuron projection extension	BP	0.91361	NRP1,APOE,DCLK1,TMEM108,NDN,CTTN,SEMA3B,LAMB2,SEMA4B,SEMA6C,SLIT2,PTPRS,DVL1,ABL1	cyan	VSMC_M2
GO:0002694	0.14	0.90	31	352	regulation of leukocyte activation	BP	0.91451	STAT6,IRF1,HMOX1,GPNMB,GLI3,PNP,LAMP1,SLC15A4,LMO1,IGF1,PLSCR1,SRC,BPI,MAPK8IP1,CD81,TIRAP,LEF1,RHBDD3,FES,B2M,ADORA2A,GRN,BMP4,DLG5,ERBB2,ZFP36L1,IL27RA,TNFRSF14,ABL1,CD55,SDC4	cyan	VSMC_M2
GO:0006911	0.14	0.94	5	39	phagocytosis, engulfment	BP	0.91655	APPL2,ELMO1,GSN,RHOG,ALOX15	cyan	VSMC_M2
GO:2000117	0.14	0.93	7	60	negative regulation of cysteine-type endopeptidase activity	BP	0.91655	CAST,SFRP2,SRC,ADORA2A,DNAJB6,ARRB2,CARD8	cyan	VSMC_M2
GO:0002064	0.14	0.91	16	173	epithelial cell development	BP	0.91804	AFDN,VIM,SLITRK6,GPAT4,RARG,SRC,TJP1,LAMB2,HEG1,ADD1,BMP4,EPHA2,NTRK1,AR,PTPRS,FOXC2	cyan	VSMC_M2
GO:0046486	0.14	0.90	28	317	glycerolipid metabolic process	BP	0.91856	CHKB,PLA2G7,SLC44A1,APOE,PLB1,SOCS3,OSBPL10,GPAT4,LPCAT4,PLSCR1,PLCG1,PTDSS1,PNPLA2,PIK3C2B,OSBPL5,IP6K1,RARRES3,PLD2,ALOX15,DAGLA,PLSCR3,SLC44A2,PDGFRB,PNPLA7,PIGQ,INPP5E,LCAT,DGAT1	cyan	VSMC_M2
GO:0016051	0.14	0.91	15	155	carbohydrate biosynthetic process	BP	0.92033	B3GALT4,AP2A1,KAT2B,IGF1,CHST14,EXT2,PHKG1,NFKB1,B4GALT5,ERFE,G6PC3,PDK2,FAM3A,CHST8,AL157935.2	cyan	VSMC_M2
GO:0035924	0.14	0.93	7	62	cellular response to vascular endothelial growth factor stimulus	BP	0.92136	NRP1,ADGRA2,VEGFD,VEGFB,PDGFRB,MAP2K3,GAS1	cyan	VSMC_M2
GO:1903715	0.14	0.95	4	28	regulation of aerobic respiration	BP	0.92148	NOP53,NUPR1,ABCD1,CBFA2T3	cyan	VSMC_M2
GO:0007265	0.14	0.90	26	296	Ras protein signal transduction	BP	0.92207	ARHGEF25,FLOT1,ELMO1,RRAS,NRP1,RHOB,APOE,TIMP2,RHOG,IGF1,ARHGAP1,C15orf62,NISCH,ARHGEF12,HEG1,RERG,ARHGEF10,BCR,GABARAP,NTRK1,TP53,KANK2,DENND4B,ARHGAP17,PDGFRB,ABL1	cyan	VSMC_M2
GO:0045785	0.14	0.90	27	306	positive regulation of cell adhesion	BP	0.9236	FLOT1,AFDN,GLI3,RRAS,NRP1,PNP,IGF1,SFRP2,SRC,TGM2,CD81,TJP1,LEF1,EGFL6,B2M,JUP,ALOX15,ERBB2,IL27RA,TNFRSF14,FOXC2,ABL1,CD55,PLPP3,SDC4,STX3,COL8A1	cyan	VSMC_M2
GO:0010639	0.14	0.90	26	297	negative regulation of organelle organization	BP	0.92531	EHMT2,RPS6KA2,GSN,ARAP1,KAT2B,CLIP3,IGF1,RHPN2,CHMP4B,PRKCD,SRC,TJP1,SSH3,VAT1,ADD1,BMP4,CAPZB,HDAC6,ARRB2,CGNL1,SLIT2,TP53,NUPR1,TEX14,FLII,TSC2	cyan	VSMC_M2
GO:0003180	0.14	0.95	4	29	aortic valve morphogenesis	BP	0.92751	GATA5,BMP4,SLIT2,GATA4	cyan	VSMC_M2
GO:0055072	0.14	0.93	8	72	iron ion homeostasis	BP	0.92861	HMOX1,ACO1,SLC6A9,ERFE,CYB561,B2M,NEO1,ATP6V0D1	cyan	VSMC_M2
GO:1901661	0.15	0.95	4	28	quinone metabolic process	BP	0.92902	COQ8B,COQ9,AIFM2,UBIAD1	cyan	VSMC_M2
GO:0022407	0.15	0.90	26	293	regulation of cell-cell adhesion	BP	0.92902	FLOT1,IRF1,AFDN,GPNMB,GLI3,PNP,IGF1,EFNA5,PRKCD,SRC,CD81,TJP1,LEF1,B2M,ADORA2A,BMP4,DLG5,ALOX15,SERPINE2,ERBB2,IL27RA,TNFRSF14,ABL1,CD55,PLPP3,SDC4	cyan	VSMC_M2
GO:0034341	0.15	0.92	10	95	response to interferon-gamma	BP	0.93195	IRF1,VIM,TRIM21,TLR3,STAT1,TP53,GBP6,RAB43,VPS26B,BST2	cyan	VSMC_M2
GO:0045453	0.15	0.94	6	50	bone resorption	BP	0.93235	TPP1,SRC,CTSK,LTBP3,ACP5,SIGLEC15	cyan	VSMC_M2
GO:2000060	0.15	0.92	10	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	0.93235	RNF144A,NOP53,MAGEF1,GABARAP,UBQLN2,GBA,DVL1,ELOB,AXIN1,CBFA2T3	cyan	VSMC_M2
GO:0019730	0.15	0.95	4	28	antimicrobial humoral response	BP	0.93235	COLEC11,BCL3,FAM3A,RPS19	cyan	VSMC_M2
GO:1901137	0.15	0.89	42	494	carbohydrate derivative biosynthetic process	BP	0.93235	MGAT4B,B3GALT4,ST3GAL1,GCNT1,GALNT12,AP2A1,FKRP,ACSS1,PNP,CANT1,IGF1,MAN2A1,DPY19L3,ACSS2,GALNT18,CHST14,EXT2,NFKB1,B4GALT4,B4GALT5,GCNT7,ADCY1,B4GAT1,UCKL1,ACAT1,VEGFB,TMEM106A,B3GAT3,PDK2,XYLT2,SLC51B,PPCDC,PDGFRB,NUDT14,NAGPA,UAP1L1,PIGQ,TK2,ABCA2,CHST8,HS3ST3B1,AL157935.2	cyan	VSMC_M2
GO:0030183	0.15	0.92	10	96	B cell differentiation	BP	0.93638	ST3GAL1,BAX,BCL3,HDAC5,ZFP36L1,NTRK1,TP53,TCF3,ABL1,ZBTB7A	cyan	VSMC_M2
GO:0033077	0.15	0.93	7	61	T cell differentiation in thymus	BP	0.93769	GLI3,B2M,BMP4,ERBB2,ZFP36L1,TP53,GBA	cyan	VSMC_M2
GO:0051050	0.15	0.88	54	660	positive regulation of transport	BP	0.93769	FLOT1,APPL2,EEPD1,GLI3,AP2A1,CADPS2,STOM,KLF15,BAX,APOE,SLC6A9,CAMK1,EHD3,HGS,TBC1D5,LAMP1,SMPD1,APBB1,CLIP3,SCN1B,IGF1,EDEM2,PRKCD,SRC,CACNB3,PLCG1,CD81,CAPN3,GNAI2,VPS11,ERFE,RNASEL,NFKBIA,B2M,ADORA2A,WNK4,B3GAT3,ARRB2,JUP,AKAP5,ERBB2,PRKACA,MLLT6,SLC51B,RASL10B,PDGFRB,SH3GL1,PHPT1,ABL1,ZNF205,CALM3,SDC4,EMD,UBL5	cyan	VSMC_M2
GO:0070839	0.15	0.94	5	40	metal ion export	BP	0.93803	ATP4A,KCND3,ATOX1,SLC8A3,CALM3	cyan	VSMC_M2
GO:0002088	0.15	0.93	7	63	lens development in camera-type eye	BP	0.93891	MEIS1,VIM,SLITRK6,WNT2B,BMP4,EPHA2,PYGO2	cyan	VSMC_M2
GO:0019752	0.15	0.88	55	659	carboxylic acid metabolic process	BP	0.94316	ZADH2,DDAH2,ST3GAL1,ACO1,APPL2,IARS,BCKDHB,AASS,ACSS1,ME3,ACAA1,CYP2S1,ECH1,GPAT4,IGF1,CYP4V2,GGT7,ACSS2,DECR1,SLC45A3,ACADS,HADH,PTGIS,SCLY,ERFE,ECHS1,PCBD1,ACAT1,QDPR,ALOX15,DAGLA,MRI1,TP53,HSD3B7,PDK2,NUPR1,SLC16A2,WARS,ABCC1,CPT2,ABCD1,IDH3G,ASPA,RENBP,HAGH,PTGDS,GSTM4,CBFA2T3,CRAT,DPYD,LDHD,FPGS,ACOT6,ZBTB7A,NAGK	cyan	VSMC_M2
GO:0035304	0.15	0.92	8	74	regulation of protein dephosphorylation	BP	0.9446	PPP6R2,SMPD1,PRKCD,GNAI2,GBA,PPP1R9B,PDGFRB,CALM3	cyan	VSMC_M2
GO:0050730	0.15	0.90	18	193	regulation of peptidyl-tyrosine phosphorylation	BP	0.9446	NRP1,SOCS3,SH3BP5,ANGPT4,IGF1,EFNA5,SFRP2,PRKCD,SRC,LRP4,CD81,ARRB2,TP53,SHC1,GPRC5B,TNFRSF14,ABL1,IL34	cyan	VSMC_M2
GO:0061333	0.15	0.93	7	63	renal tubule morphogenesis	BP	0.9471	TCF21,GLI3,WT1,LZTS2,WNT2B,WNK4,BMP4	cyan	VSMC_M2
GO:0060326	0.15	0.90	19	206	cell chemotaxis	BP	0.94762	PLA2G7,NRP1,RHOG,FGFR1,ACKR4,PRKCD,TIRAP,LEF1,VEGFD,VEGFB,NBL1,ARRB2,EPHA2,SLIT2,HSD3B7,ABCC1,PDGFRB,IL34,RPS19	cyan	VSMC_M2
GO:0046189	0.15	0.95	4	29	phenol-containing compound biosynthetic process	BP	0.94762	PMEL,MOXD1,GIPC1,MFSD12	cyan	VSMC_M2
GO:0098751	0.15	0.95	4	30	bone cell development	BP	0.94762	MEIS1,SRC,SIGLEC15,ZFPM1	cyan	VSMC_M2
GO:0046165	0.15	0.92	11	108	alcohol biosynthetic process	BP	0.94762	MOXD1,CYB5R3,APOE,NFKB1,IP6K1,CLCN2,PCBD1,QDPR,GBA,H6PD,ABCA2	cyan	VSMC_M2

GO:0042113	0.15	0.90	18	193	B cell activation	BP	0.94762	STAT6,ST3GAL1,BAX,BCL3,SLC15A4,PRKCD,CD81,TIRAP,LEF1,HDAC5,ZFP36L1,IL27RA,NTRK1,TP53,TCF3,ABL1,ZBTB7A,BST2	cyan	VSMC_M2
GO:0090313	0.15	0.95	4	29	regulation of protein targeting to membrane	BP	0.94765	STOM,CACNB3,ERBB2,SLC51B	cyan	VSMC_M2
GO:0048511	0.15	0.90	20	223	rhythmic process	BP	0.95211	TEF,KLF9,DBP,FZD4,ATG7,KAT2B,SRC,ADCY1,ADORA2A,NAGLU,NR2F6,ARRB2,NTRK1,SLIT2,TP53,MTA1,PTGDS,SERPINF1,KCND2,PML	cyan	VSMC_M2
GO:0062014	0.15	0.92	8	73	negative regulation of small molecule metabolic process	BP	0.95211	APPL2,APOE,NFKB1,ERFE,TP53,NUPR1,FAM3A,CBFA2T3	cyan	VSMC_M2
GO:0034219	0.15	0.92	9	86	carbohydrate transmembrane transport	BP	0.95211	APPL2,KLF15,CLIP3,IGF1,SLC5A3,SLC45A3,ERFE,RNASEL,SLC2A8	cyan	VSMC_M2
GO:0035637	0.15	0.91	11	114	multicellular organismal signaling	BP	0.95211	BIN1,EHD3,SCN1B,CTNNA3,KCND3,JUP,PRKACA,GBA,SLC8A3,KCND2,CALM3	cyan	VSMC_M2
GO:0032787	0.15	0.89	35	404	monocarboxylic acid metabolic process	BP	0.95211	ZADH2,APPL2,ACSS1,ME3,ACAA1,CYP2S1,ECH1,GPAT4,IGF1,CYP4V2,ACSS2,DECR1,SLC45A3,ACADS,HADH,PTGIS,ERFE,ECHS1,ACAT1,ALOX15,DAGLA,TP53,HSD3B7,PDK2,NUPR1,CPT2,ABCD1,HAGH,PTGDS,GSTM4,CBFA2T3,CRAT,LDHD,ACOT6,ZBTB7A	cyan	VSMC_M2
GO:0051928	0.15	0.92	9	86	positive regulation of calcium ion transport	BP	0.95255	BAX,EHD3,CACNB3,PLCG1,CAPN3,ARRB2,PDGFRB,ABL1,CALM3	cyan	VSMC_M2
GO:0030163	0.15	0.88	66	815	protein catabolic process	BP	0.95255	OS9,EIF3H,GGA1,KCTD17,CUL9,RNF144A,NOP53,TRIM13,APOE,AGAP3,ATRAID,ATG7,TIMP2,SGSH,RNF213,HGS,TPP1,RBCK1,CHMP4B,TP53INP2,EDEM2,CTSB,WWTR1,FOXF2,CTSA,CD81,CAPN3,RGMA,UBA7,DCAF11,CTSK,RHBDD3,FURIN,VPS11,ATG4B,MAGEF1,ADAMTS7,MAEA,USE1,HDAC6,ARRB2,GABARAP,SERPINE2,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,SNX33,MTA1,CLPP,UBXN6,WDR81,DVL1,ISG15,ELOB,FBXW5,AXIN1,RHBDF1,CBFA2T3,RNF166,ABCA2,PML,EEF1A2,PSMB9	cyan	VSMC_M2
GO:0006778	0.15	0.94	5	40	porphyrin-containing compound metabolic process	BP	0.95531	IBA57,HMOX1,UROD,SLC6A9,ABCC1	cyan	VSMC_M2
GO:0003279	0.15	0.92	9	88	cardiac septum development	BP	0.95742	ZFPM2,NRP1,HEG1,BMP4,SLIT2,TP53,NPRL3,GATA4,ZFPM1	cyan	VSMC_M2
GO:0019882	0.15	0.93	7	61	antigen processing and presentation	BP	0.95771	RAB5B,TAPBP,RFTN1,WDFY4,B2M,IFI30,GBA	cyan	VSMC_M2
GO:0006692	0.15	0.95	4	29	prostanoid metabolic process	BP	0.95848	ZADH2,CYP2S1,PTGIS,PTGDS	cyan	VSMC_M2
GO:0006693	0.15	0.95	4	29	prostaglandin metabolic process	BP	0.95848	ZADH2,CYP2S1,PTGIS,PTGDS	cyan	VSMC_M2
GO:0032965	0.15	0.95	4	29	regulation of collagen biosynthetic process	BP	0.95869	VIM,BMP4,ARRB2,PDGFRB	cyan	VSMC_M2
GO:0048545	0.15	0.89	23	258	response to steroid hormone	BP	0.95869	TCF21,DAXX,FBXO32,TRERF1,KLF9,ZFP36,SRC,FIBIN,VPS11,LMO3,BMP4,HDAC6,CASP9,ZFP36L1,SLIT2,AR,GBA,PPP1R9B,KANK2,ABCA2,SERPINF1,ZBTB7A,CALM3	cyan	VSMC_M2
GO:0043473	0.15	0.92	8	75	pigmentation	BP	0.96017	PMEL,GLI3,BAX,BBS2,HPS6,MFSD12,RAB11B,EN1	cyan	VSMC_M2
GO:0032418	0.15	0.93	7	62	lysosome localization	BP	0.96095	HMOX1,HPS6,FES,HDAC6,PLEKHM2,CPLX2,PTGDS	cyan	VSMC_M2
GO:0021987	0.15	0.92	9	87	cerebral cortex development	BP	0.96127	GLI3,BAX,BBS2,PHACTR1,TACC2,CCDC141,SLIT2,PPP1R9B,PTPRS	cyan	VSMC_M2
GO:0003014	0.15	0.92	8	74	renal system process	BP	0.96195	GSN,RHPN2,GNAI2,ADORA2A,WNK4,BMP4,PRKACA,MLLT6	cyan	VSMC_M2
GO:0010874	0.15	0.95	4	30	regulation of cholesterol efflux	BP	0.96195	EEPD1,APOE,NFKBIA,ABCA2	cyan	VSMC_M2
GO:0043470	0.15	0.94	5	41	regulation of carbohydrate catabolic process	BP	0.96288	IGF1,TP53,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:1904063	0.15	0.93	7	62	negative regulation of cation transmembrane transport	BP	0.96402	BIN1,SLC6A9,CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0070201	0.16	0.88	37	436	regulation of establishment of protein localization	BP	0.96402	OS9,P3H1,GLI3,STOM,APOE,RHBDF2,CAMK1,RAB11FIP1,APBB1,PKDCC,IGF1,EFNA5,EDEM2,PRKCD,SRC,CACNB3,CD81,HADH,DISP1,RHBDD3,VPS11,ADORA2A,BMP4,HDAC6,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,LLGL1,PHPT1,RAB11FIP3,RHBDF1,GRASP,EMD,UBL5	cyan	VSMC_M2
GO:0043401	0.16	0.91	11	111	steroid hormone mediated signaling pathway	BP	0.96402	TCF21,DAXX,TRERF1,SRC,VPS11,LMO3,BMP4,HDAC6,AR,KANK2,ZBTB7A	cyan	VSMC_M2
GO:0002698	0.16	0.93	7	62	negative regulation of immune effector process	BP	0.96402	HMOX1,SERPING1,GRN,ARRB2,CD55,RPS19,BST2	cyan	VSMC_M2
GO:0046545	0.16	0.92	8	75	development of primary female sexual characteristics	BP	0.96498	ZFPM2,BAX,FZD4,WT1,SRC,ARRB2,SLIT2,NUPR1	cyan	VSMC_M2
GO:0007044	0.16	0.92	9	89	cell-substrate junction assembly	BP	0.96618	PTPRK,NRP1,EFNA5,EPHA3,SRC,CTTN,BCR,ABL1,SDC4	cyan	VSMC_M2
GO:0050709	0.16	0.93	6	51	negative regulation of protein secretion	BP	0.96759	APOE,RHBDF2,RAB11FIP1,HADH,RAB11FIP3,RHBDF1	cyan	VSMC_M2
GO:0038084	0.16	0.94	5	41	vascular endothelial growth factor signaling pathway	BP	0.9676	NRP1,ADGRA2,VEGFD,VEGFB,PDGFRB	cyan	VSMC_M2
GO:0006493	0.16	0.92	8	74	protein O-linked glycosylation	BP	0.9676	ST3GAL1,GCNT1,GALNT12,FKRP,GALNT18,B4GALT5,B4GAT1,VEGFB	cyan	VSMC_M2
GO:0045103	0.16	0.94	4	31	intermediate filament-based process	BP	0.96776	VIM,SYNC,DNAJB6,KRT25	cyan	VSMC_M2
GO:0032612	0.16	0.92	7	62	interleukin-1 production	BP	0.96776	GSDMD,IGF1,TMEM106A,ARRB2,ACP5,PML,CARD8	cyan	VSMC_M2
GO:0032652	0.16	0.92	7	62	regulation of interleukin-1 production	BP	0.96776	GSDMD,IGF1,TMEM106A,ARRB2,ACP5,PML,CARD8	cyan	VSMC_M2
GO:0006720	0.16	0.92	8	73	isoprenoid metabolic process	BP	0.96776	CYP2S1,PLB1,CYP4V2,PNPLA2,RLBP1,NPC2,DHRS13,DGAT1	cyan	VSMC_M2
GO:0043276	0.16	0.94	4	30	anoikis	BP	0.96776	TLE1,SRC,TSC2,BMF	cyan	VSMC_M2
GO:0046467	0.16	0.91	12	120	membrane lipid biosynthetic process	BP	0.96894	B3GALT4,ST3GAL1,SMPD1,PRKCD,B4GALT5,GBA,CERS4,PIGQ,PLPP2,ABCA2,PLPP3,AL157935.2	cyan	VSMC_M2
GO:0072666	0.16	0.94	5	42	establishment of protein localization to vacuole	BP	0.96894	HGS,GNPTAB,M6PR,NAGPA,MON1B	cyan	VSMC_M2
GO:0034329	0.16	0.89	27	318	cell junction assembly	BP	0.97085	FLOT1,PLXNB2,AFDN,PTPRK,NRP1,SLITRK6,EFNB2,EFNA5,EPHA3,SRC,LRP4,TJP1,CTTN,HEG1,BCR,DLG5,JUP,EPHA2,PRKACA,NTRK1,PTPRS,DVL1,AGRN,NPHP4,CLSTN1,ABL1,SDC4	cyan	VSMC_M2
GO:0043297	0.16	0.93	6	52	apical junction assembly	BP	0.97085	AFDN,TJP1,DLG5,EPHA2,PRKACA,NPHP4	cyan	VSMC_M2
GO:0032535	0.16	0.89	28	325	regulation of cellular component size	BP	0.97085	DEPTOR,ARHGAP18,AKT1S1,GSN,NRP1,BIN1,APOE,RARG,CHMP3,PRKCD,C15orf62,CTTN,SEMA3B,RGMA,SSH3,SEMA4B,SEMA6C,ARPC5,RND2,ADD1,CAPZB,ALOX15,CLCN6,SLIT2,FLII,PTPRS,ABL1,IST1	cyan	VSMC_M2
GO:0060675	0.16	0.93	6	52	ureteric bud morphogenesis	BP	0.97138	TCF21,GLI3,WT1,LZTS2,WNT2B,BMP4	cyan	VSMC_M2
GO:0007601	0.16	0.91	12	123	visual perception	BP	0.97157	TGFBI,EFEMP1,BBS9,SLITRK6,CYP4V2,GLRB,BBS2,SFRP5,RLBP1,LAMB2,RPGR,NYX	cyan	VSMC_M2
GO:0001936	0.16	0.91	11	111	regulation of endothelial cell proliferation	BP	0.97157	HMOX1,NRP1,APOE,FGFR1,PLCG1,STAT1,VEGFD,ECM1,VEGFB,BMP4,STAT5A	cyan	VSMC_M2
GO:0060401	0.16	0.91	12	126	cytosolic calcium ion transport	BP	0.97173	BAX,CACNB3,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,SLC8A3,PML,CALM3,CLIC2	cyan	VSMC_M2

GO:0045184	0.16	0.87	109	1395	establishment of protein localization	BP	0.97173	RAB5B,OS9,RABL2A,TBC1D22A,AFDN,GGA1,APPL2,TBC1D2,P3H1,BBS9,TBC1D17,GLI3,AP2A1,CADPS2,STOM,RHOB,BAX,DENND2A,APOE,BCL3,ATG7,EXOC7,RHBDF2,CAMK1,EHD3,CMTM6,DZIP1,HGS,TBC1D5,RFTN1,RAB11FIP1,LAMP1,APBB1,PKDCC,CLIP3,SLC15A4,GNPTAB,IGF1,EFNA5,CHMP4B,CHMP3,EDEM2,ARRDC3,PRKCD,SRC,CACNB3,BBS2,ARHGAP1,EXOC2,SYS1,CTSA,CD81,CTTN,TMEM115,HADH,DISP1,SGSM1,EXOC8,RHBDD3,VPS11,KIF1A,FAM53B,ATG4B,NFKBIA,M6PR,ADORA2A,RPGR,HOMER3,BMP4,PORCN,USE1,HDAC6,B3GAT3,ARRB2,JUP,AKAP5,GABARAP,MCC,GIPC1,ERBB2,PRKACA,TP53,SLC51B,SNX33,MCOLN1,LLGL1,ZDHHC9,NAGPA,SGSM2,TSC2,PHPT1,RAB11FIP3,ENTR1,RHBDF1,CLSTN1,ABL1,MON1B,IST1,RAB43,GRASP,PML,CALM3,SCAMP4,VPS26B,STX3,RAB11B,MCFD2,EMD,UBL5	cyan	VSMC_M2
GO:0032434	0.16	0.91	12	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	0.97446	EIF3H,RNF144A,NOP53,FOXF2,GABARAP,GIPC1,UBQLN2,UBQLN4,GBA,DVL1,ELOB,CBFA2T3	cyan	VSMC_M2
GO:0046903	0.16	0.87	55	673	secretion	BP	0.97616	HMOX1,P3H1,CADPS2,FZD4,APOE,EXOC7,RHBDF2,LTBP4,GPAT4,HGS,RAB11FIP1,LAMP1,APBB1,GNPTAB,IGF1,EFNA5,EXOC2,NISCH,PCSK6,TPCN2,GNAI2,HADH,DISP1,SV2A,EXOC8,RHBDD3,ADCY1,FES,FURIN,VPS11,LINC02210-CRHR1,M6PR,ADORA2A,WNK4,STAT5A,PORCN,USE1,SERPINE2,GIPC1,CPLX2,SLC51B,RASL10B,LLGL1,NAGPA,DVL1,PTGDS,PHPT1,RAB11FIP3,RHBDF1,OAS2,CBARP,CALM3,SDC4,STX3,RAB11B	cyan	VSMC_M2
GO:0002534	0.16	0.93	5	40	cytokine production involved in inflammatory response	BP	0.9768	APPL2,PLD3,IL17RA,ABCD1,MIR197	cyan	VSMC_M2
GO:1900015	0.16	0.93	5	40	regulation of cytokine production involved in inflammatory response	BP	0.9768	APPL2,PLD3,IL17RA,ABCD1,MIR197	cyan	VSMC_M2
GO:0001935	0.16	0.90	12	123	endothelial cell proliferation	BP	0.97708	HMOX1,NRP1,APOE,FGFR1,PLCG1,STAT1,VEGFD,ECM1,VEGFB,BMP4,STAT5A,EPHA2	cyan	VSMC_M2
GO:0019233	0.16	0.92	7	63	sensory perception of pain	BP	0.9771	CACNB3,NDN,NR2F6,ARRB2,NTRK1,RETREG1,KCND2	cyan	VSMC_M2
GO:0001934	0.16	0.88	45	543	positive regulation of protein phosphorylation	BP	0.9771	FLOT1,DAXX,CARD10,GPNMB,NRP1,FZD4,CAB39L,CAMK1,FGFR1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,PRKCD,SRC,LRP4,MOB2,CD81,CHRNA7,TIRAP,VEGFD,VEGFB,BMP4,HDAC6,ARRB2,ERBB2,BRAT1,NTRK1,TP53,GPRC5B,PDGFRB,MAP2K3,TRAF4,DVL1,TNFRSF14,AXIN1,ABL1,IL34,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0003231	0.16	0.91	10	101	cardiac ventricle development	BP	0.97714	ZFPM2,SFRP2,CPE,HEG1,BMP4,SLIT2,NPRL3,FOXC2,GATA4,ZFPM1	cyan	VSMC_M2
GO:0044275	0.16	0.94	4	30	cellular carbohydrate catabolic process	BP	0.9776	GAA,STBD1,GUSB,TP53	cyan	VSMC_M2
GO:0033280	0.16	0.94	4	30	response to vitamin D	BP	0.97937	MN1,FES,PHEX,KANK2	cyan	VSMC_M2
GO:0032869	0.16	0.90	15	161	cellular response to insulin stimulus	BP	0.97937	APPL2,SOCS3,KAT2B,PRKCD,SRC,STAT1,GNAI2,ERFE,HDAC5,ZFP36L1,PDK2,SHC1,TSC2,FOXC2,SLC2A8	cyan	VSMC_M2
GO:0043436	0.16	0.87	56	677	oxoacid metabolic process	BP	0.97937	ZADH2,DDAH2,ST3GAL1,ACO1,APPL2,IARS,BCKDHB,AASS,ACSS1,ME3,ACAA1,CYP2S1,ECH1,GPAT4,IGF1,CYP4V2,GGT7,ACSS2,DECR1,ABHD14B,SLC45A3,ACADS,HADH,PTGIS,SCLY,ERFE,ECHS1,PCBD1,ACAT1,QDPR,ALOX15,DAGLA,MRI1,TP53,HSD3B7,PDK2,NUPR1,SLC16A2,WARS,ABCC1,CPT2,ABCD1,IDH3G,ASPA,RENBP,HAGH,PTGDS,GSTM4,CBFA2T3,CRAT,DPYD,LDHD,FPGS,ACOT6,ZBTB7A,NAGK	cyan	VSMC_M2
GO:0050906	0.16	0.93	6	52	detection of stimulus involved in sensory perception	BP	0.98273	CACNB3,NR2F6,ARRB2,SERPINE2,NTRK1,PIEZO2	cyan	VSMC_M2
GO:0046148	0.16	0.93	6	52	pigment biosynthetic process	BP	0.98339	PMEL,IBA57,UROD,SLC6A9,GIPC1,MFSD12	cyan	VSMC_M2
GO:0099173	0.16	0.90	13	137	postsynapse organization	BP	0.98353	ARHGAP39,NRP1,APOE,TMEM108,LZTS3,GLRB,LRP4,CHRNA7,CTTN,KIF1A,HDAC6,PTPRS,DVL1	cyan	VSMC_M2
GO:0032388	0.16	0.90	16	173	positive regulation of intracellular transport	BP	0.98456	GLI3,STOM,CAMK1,EDEM2,PRKCD,CACNB3,CD81,VPS11,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,EMD,UBL5	cyan	VSMC_M2
GO:0070849	0.16	0.93	5	41	response to epidermal growth factor	BP	0.98472	ZFP36,PLCG1,ERBB2,ZFP36L1,PPP1R9B	cyan	VSMC_M2
GO:0033273	0.16	0.91	8	75	response to vitamin	BP	0.98925	FOLR2,MN1,FES,PHEX,KANK2,EEF2,NDOR1,GATA4	cyan	VSMC_M2
GO:0030098	0.16	0.89	23	259	lymphocyte differentiation	BP	0.98944	STAT6,IRF1,PTPRK,ST3GAL1,GLI3,BAX,BCL3,PNP,TUSC2,LEF1,B2M,HDAC5,BMP4,ERBB2,ZFP36L1,NTRK1,TP53,GBA,TMEM98,TCF3,ABL1,ZBTB7A,ZFPM1	cyan	VSMC_M2
GO:0006476	0.17	0.91	9	88	protein deacetylation	BP	0.98944	TRERF1,NDN,TPPP,TBL1Y,HDAC5,HDAC6,TP53,ELMSAN1,MTA1	cyan	VSMC_M2
GO:0110110	0.17	0.94	4	30	positive regulation of animal organ morphogenesis	BP	0.99108	GATA5,WNT2B,BMP4,AR	cyan	VSMC_M2
GO:0042327	0.17	0.87	50	612	positive regulation of phosphorylation	BP	0.99146	FLOT1,DAXX,CARD10,GPNMB,NRP1,FZD4,CAB39L,CAMK1,FGFR1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,PRKCD,EPHA3,SRC,LRP4,MOB2,CD81,CHRNA7,TIRAP,VEGFD,VEGFB,BMP4,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,NTRK1,AR,TP53,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,DVL1,TNFRSF14,AXIN1,ABL1,IL34,EEF1A2,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0046326	0.17	0.94	4	31	positive regulation of glucose import	BP	0.99491	KLF15,IGF1,ERFE,RNASEL	cyan	VSMC_M2
GO:0032715	0.17	0.94	4	30	negative regulation of interleukin-6 production	BP	0.99799	BPI,ARRB2,IL27RA,GBA	cyan	VSMC_M2
GO:1903115	0.17	0.94	4	32	regulation of actin filament-based movement	BP	0.99976	BIN1,CTNNA3,JUP,GATA4	cyan	VSMC_M2

GO:0009058	0.17	0.85	328	4393	biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,PMEL,STAT6,MOXD1,TCF21,MGAT4B,AKAP12,FLOT1,CHKB,DDAH2,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,B3GALT4,CYB5R3,TCF20,DAXX,TEF,PTPRK,ST3GAL1,IBA57,TEAD3,TLE1,NFIB,TRERF1,GCNT1,HMOX1,ACO1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,NAT14,SLC44A1,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,KLF15,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,ACSS1,FZD4,VIM,APOE,UROD,BCL3,MIF4GD,SLC6A9,ATG7,COQ8B,SOCS3,CAMK1,TEP1,PNP,RPS16,ZFP36,CANT1,SAMD4B,GPAT4,RPL15,KAT2B,EIF3K,RHOG,TRIM21,SMPD1,APBB1,CLIP3,GTF3A,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,MAN2A1,WT1,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,POU6F1,LPCAT4,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,COQ9,SRC,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTDSS1,EXT2,SLC5A3,PNPLA2,PIK3C2B,STAT1,ABHD14B,CD81,NDN,SLC45A3,PHKG1,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,MRPL36,ZNF496,NFKB1,SPOCD1,B4GALT4,HIST1H1C,PKNOX2,RGMA,BCL9,IP6K1,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,MN1,GCNT7,ECM1,NELFCD,ADCY1,FURIN,ERFE,BCL9L,RFX5,GATA5,CLCN2,B4GAT1,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,G6PC3,TSC22D4,ACAT1,VEGFB,TMEM106A,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,PORCN,NR2F6,GMPPA,HDAC6,ZBTB3,PQBP1,B3GAT3,WDR45,PLD2,DNAJB6,ARRB2,JUP,ALOX15,WIZ,MYRF,DAGLA,ZBTB17,TCF12,PLSCR3,GIPC1,ERBB2,STARD3,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,UBIAD1,MLLT6,	cyan	VSMC_M2
GO:0090218	0.17	0.94	4	31	positive regulation of lipid kinase activity	BP	1	SRC,CD81,PDGFRB,EEF1A2	cyan	VSMC_M2
GO:0007369	0.17	0.90	13	138	gastrulation	BP	1	SFRP2,MMP2,EXT2,LEF1,BMP4,EPHA2,ZBTB17,PRKACA,TP53,DVL1,FOXC2,HSBP1,COL8A1	cyan	VSMC_M2
GO:0034142	0.17	0.94	4	30	toll-like receptor 4 signaling pathway	BP	1	APPL2,TRIL,TIRAP,NFKBIA	cyan	VSMC_M2
GO:0019318	0.17	0.89	17	185	hexose metabolic process	BP	1	GAA,KAT2B,DCXR,IGF1,MAN2A1,SRC,NISCH,SLC45A3,ERFE,FUCA1,G6PC3,BRAT1,TP53,PDK2,MAN2C1,FAM3A,H6PD	cyan	VSMC_M2
GO:0045638	0.17	0.92	7	64	negative regulation of myeloid cell differentiation	BP	1	MEIS1,LRRC17,ZFP36,TLR3,NFKBIA,ZFP36L1,ZFPM1	cyan	VSMC_M2
GO:0072348	0.17	0.93	5	41	sulfur compound transport	BP	1	SLC26A11,SLC38A7,ABCC1,MFSD12,ABCD1	cyan	VSMC_M2
GO:0043500	0.17	0.91	9	88	muscle adaptation	BP	1	CTDP1,FBXO32,HMOX1,MLIP,GSN,KLF15,IGF1,GATA5,CDK9	cyan	VSMC_M2
GO:0072171	0.17	0.92	6	53	mesonephric tubule morphogenesis	BP	1	TCF21,GLI3,WT1,LZTS2,WNT2B,BMP4	cyan	VSMC_M2
GO:0045806	0.17	0.93	5	41	negative regulation of endocytosis	BP	1	PACSIN2,EPHA3,UBQLN2,SNX33,ABCA2	cyan	VSMC_M2
GO:0033344	0.17	0.93	5	42	cholesterol efflux	BP	1	EEPD1,APOE,NFKBIA,NPC2,ABCA2	cyan	VSMC_M2
GO:0006811	0.17	0.86	81	1026	ion transport	BP	1	TRPM3,ATP10D,KCNQ5,SLC44A1,SLC17A7,STOM,BAX,UQCRH,BIN1,ABCB8,SLC6A9,EHD3,SLC26A11,SLC4A9,FOLR2,SLC15A4,SLC7A2,ATP4A,SCN1B,SNTA1,SLC38A7,GLRB,CACNB3,PLCG1,ARHGAP1,GNAO1,SLC5A3,CRACR2B,CHRNA7,CAPN3,CACNA2D2,TPCN2,GNAI2,SV2A,ANXA9,SLC16A9,CLCN2,TCN2,LINC02210-CRHR1,B2M,KCND3,ORAI2,ADORA2A,CAPN1,PSAP,HOMER3,WNK4,CHRNE,ARRB2,SERPINE2,GIPC1,PRKACA,CLCN6,MLLT6,TMEM175,ORAI3,SLC51B,SLC16A2,ATP8B2,SLC44A2,GRIA1,ATOX1,ABCC1,PDGFRB,MCOLN1,PIEZO2,MFSD12,SLC10A3,ABL1,SLC2A8,ATP6V0D1,CNNM3,SLC8A3,CBARP,KCND2,PML,CALM3,CLIC2,LASP1,CLIC3,RAB11B	cyan	VSMC_M2
GO:0007155	0.17	0.86	81	1044	cell adhesion	BP	1	FLOT1,PLXNB2,IRF1,AFDN,TGFBI,PTPRK,GCNT1,ITGB8,GPNMB,GLI3,RRAS,NRP1,RHOB,FZD4,PNP,LGALS3BP,PAK4,FOLR2,ITGBL1,EFNB2,SCN1B,IGF1,EFNA5,SPON1,SFRP2,PRKCD,EPHA3,SRC,TGM2,SORBS3,CD81,TJP1,CTTN,BOC,XG,LEF1,ATRNL1,EGFL6,LAMB2,FES,ANXA9,GATA5,PARD3B,FIBP,CTNNA3,B2M,BCR,ADORA2A,ASTN1,DGCR2,BMP4,MAEA,DLG5,DNAJB6,JUP,ALOX15,EPHA2,SERPINE2,ERBB2,ZFP36L1,IL27RA,ADAM15,SHC1,PBXIP1,NEO1,ICAM4,PTPRS,TNFRSF14,NPHP4,CLSTN1,FOXC2,ABL1,CERCAM,CNN3,CD55,PML,PLPP3,LRRC7,SDC4,STX3,COL8A1	cyan	VSMC_M2
GO:1901215	0.17	0.89	15	161	negative regulation of neuron death	BP	1	HMOX1,GPNMB,NRP1,BAX,APOE,ATG7,CHMP4B,ADORA2A,GRN,ARRB2,NTRK1,GBA,RETREG1,SERPINF1,EN1	cyan	VSMC_M2
GO:0045687	0.17	0.94	4	31	positive regulation of glial cell differentiation	BP	1	BIN1,SERPINE2,ASPA,IL34	cyan	VSMC_M2
GO:0050731	0.17	0.89	13	136	positive regulation of peptidyl-tyrosine phosphorylation	BP	1	NRP1,ANGPT4,IGF1,EFNA5,SRC,LRP4,CD81,ARRB2,TP53,GPRC5B,TNFRSF14,ABL1,IL34	cyan	VSMC_M2
GO:0051258	0.17	0.88	22	250	protein polymerization	BP	1	ARHGAP18,COBL,GSN,BIN1,TPPP2,CLIP3,CHMP4B,CHMP3,PRKCD,C15orf62,CTTN,TPPP,SSH3,FES,PRUNE1,ARPC5,ADD1,CAPZB,ALOX15,SLIT2,FLII,ABL1	cyan	VSMC_M2
GO:0071985	0.17	0.94	4	31	multivesicular body sorting pathway	BP	1	CHMP4B,CHMP3,TMEM50A,UBXN6	cyan	VSMC_M2
GO:1903038	0.17	0.91	9	87	negative regulation of leukocyte cell-cell adhesion	BP	1	IRF1,GPNMB,GLI3,ADORA2A,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0002704	0.17	0.94	4	30	negative regulation of leukocyte mediated immunity	BP	1	HMOX1,ARRB2,CD55,BST2	cyan	VSMC_M2
GO:0006865	0.17	0.90	10	99	amino acid transport	BP	1	SLC17A7,SLC6A9,SLC15A4,SLC7A2,SLC38A7,SV2A,ADORA2A,GIPC1,SLC16A2,MFSD12	cyan	VSMC_M2
GO:0046605	0.17	0.93	5	42	regulation of centrosome cycle	BP	1	MARK4,KAT2B,CHMP4B,CHMP3,FBXW5	cyan	VSMC_M2
GO:0106027	0.17	0.91	8	78	neuron projection organization	BP	1	APOE,LZTS3,CHRNA7,CTTN,KIF1A,HDAC6,ABCD1,DVL1	cyan	VSMC_M2
GO:0033144	0.17	0.94	4	31	negative regulation of intracellular steroid hormone receptor signaling pathway	BP	1	TCF21,VPS11,KANK2,ZBTB7A	cyan	VSMC_M2

GO:0044271	0.17	0.84	258	3436	cellular nitrogen compound biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,MOXD1,TCF21,FLOT1,DDAH2,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,B3GALT4,CYB5R3,TCF20,DAXX,TEF,PTPRK,ST3GAL1,IBA57,TEAD3,TLE1,NFIB,TRERF1,HMOX1,ACO1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,TRIM13,ACSS1,FZD4,VIM,APOE,UROD,BCL3,MIF4GD,SLC6A9,CAMK1,TEP1,PNP,RPS16,ZFP36,SAMD4B,RPL15,KAT2B,EIF3K,RHOG,TRIM21,SMPD1,APBB1,GTF3A,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,MRPL36,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,MN1,ECM1,NELFCD,ADCY1,FURIN,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,ACAT1,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12,GBA,NUPR1,SHC1,PBXIP1,ACP5,KANK2,WARS,PPCDC,PDGFRB,MTA1,CERS4,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,EEF2,GLIS2,DVL1,AGRN,ELOB,E4F1,DPH7,NELFB,TCF3,HAGH,UAP1L1,SBNO2,EDF1,INPP5E,AXIN1,RERE,POLRMT,TCF25,BRD3,RPL13,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,FPGS,PBX3,TK2,NFIA,ABCA	cyan	VSMC_M2
GO:0031648	0.17	0.93	5	42	protein destabilization	BP	1	GSN,TRIM21,SRC,CAPN3,HDAC6	cyan	VSMC_M2
GO:0051250	0.17	0.90	10	99	negative regulation of lymphocyte activation	BP	1	IRF1,GPNMB,GLI3,RHBDD3,ADORA2A,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:0008593	0.17	0.91	8	76	regulation of Notch signaling pathway	BP	1	RFNG,SRC,TM2D3,GATA5,NFKBIA,EPN2,LLGL1,ZBTB7A	cyan	VSMC_M2
GO:0030509	0.17	0.90	11	116	BMP signaling pathway	BP	1	KIAA1324L,SFRP2,SFRP5,PCSK6,RGMA,LEF1,BMP4,NBL1,NEO1,ABL1,GATA4	cyan	VSMC_M2
GO:0099504	0.18	0.89	13	138	synaptic vesicle cycle	BP	1	CADPS2,SLC17A7,SV2A,ADCY1,ADORA2A,PLD2,GIPC1,CPLX2,STON2,SH3GL1,DVL1,CALM3,STX3	cyan	VSMC_M2
GO:0042157	0.18	0.90	11	111	lipoprotein metabolic process	BP	1	APOE,ATG7,CLIP3,PORCN,WDR45,GBA,ZDHHC9,PIGQ,LCAT,APOL5,NMT2	cyan	VSMC_M2
GO:0048536	0.18	0.93	4	31	spleen development	BP	1	TCF21,BCL3,HOXB4,ABL1	cyan	VSMC_M2
GO:0019751	0.18	0.90	9	88	polyol metabolic process	BP	1	SLC5A3,IP6K1,PCBD1,QDPR,GBA,INPP5E,PLPP2,ABCA2,PLPP3	cyan	VSMC_M2
GO:0031345	0.18	0.89	14	150	negative regulation of cell projection organization	BP	1	NRP1,VIM,APOE,EFNB2,PRKCD,LRP4,SEMA3B,RGMA,SEMA4B,SEMA6C,B2M,CAPZB,SLIT2,PTPRS	cyan	VSMC_M2
GO:0070664	0.18	0.92	6	53	negative regulation of leukocyte proliferation	BP	1	GPNMB,BMP4,DLG5,ERBB2,TNFRSF14,SDC4	cyan	VSMC_M2
GO:1900182	0.18	0.91	8	76	positive regulation of protein localization to nucleus	BP	1	CARD10,GLI3,WWTR1,PRKCD,SRC,TRIM8,JUP,GLIS2	cyan	VSMC_M2
GO:0070997	0.18	0.87	25	288	neuron death	BP	1	DAXX,HMOX1,GPNMB,AKT1S1,NRP1,BAX,APOE,ATG7,EFNB2,CHMP4B,CHRNA7,ADORA2A,GRN,ARRB2,CASP9,TP53BP2,NTRK1,TP53,GBA,NUPR1,RETREG1,ABL1,SERPINF1,ATN1,EN1	cyan	VSMC_M2
GO:0007186	0.18	0.86	38	458	G protein-coupled receptor signaling pathway	BP	1	AKAP12,FZD4,APOE,ADGRA2,ACKR4,ADGRD1,ARRDC3,GLRB,SRC,CPE,TGM2,GNAO1,MRGPRF,GNAI2,ADGRB2,ATRNL1,ARHGEF12,GRK5,ADCY1,LINC02210-CRHR1,GNAZ,ADORA2A,PSAP,HOMER3,ARRB2,AKAP5,DAGLA,GIPC1,UBQLN2,PPP1R9B,GPRC5B,PDGFRB,AGRN,NMT2,CALM3,RGS19,RGS8,RGS10	cyan	VSMC_M2
GO:0099003	0.18	0.89	14	151	vesicle-mediated transport in synapse	BP	1	CADPS2,SLC17A7,SV2A,ADCY1,ADORA2A,PLD2,GIPC1,CPLX2,STON2,SH3GL1,DVL1,CLSTN1,CALM3,STX3	cyan	VSMC_M2
GO:0022602	0.18	0.93	4	32	ovulation cycle process	BP	1	FZD4,SRC,ARRB2,SLIT2	cyan	VSMC_M2
GO:0046942	0.18	0.88	16	173	carboxylic acid transport	BP	1	SLC17A7,SLC6A9,FOLR2,SLC15A4,SLC7A2,SLC38A7,SV2A,SLC16A9,ADORA2A,PSAP,GIPC1,SLC51B,SLC16A2,ABCC1,MFSD12,SLC10A3	cyan	VSMC_M2
GO:0002286	0.18	0.91	7	65	T cell activation involved in immune response	BP	1	STAT6,BCL3,CD81,LEF1,TP53,TMEM98,ZFPM1	cyan	VSMC_M2
GO:0072659	0.18	0.88	21	239	protein localization to plasma membrane	BP	1	FLOT1,AFDN,GGA1,EHD3,RHOG,PKDCC,CLIP3,EPHA3,CACNB3,BBS2,SYS1,CD81,TMBIM1,JUP,EPHA2,AKAP5,AR,PPP1R9B,SLC9A3R2,GRASP,STX3	cyan	VSMC_M2
GO:0045685	0.18	0.92	6	54	regulation of glial cell differentiation	BP	1	BIN1,SLC45A3,SERPINE2,TMEM98,ASPA,IL34	cyan	VSMC_M2
GO:0031214	0.18	0.89	12	126	biomineral tissue development	BP	1	GPNMB,ATRAID,PKDCC,IGF1,ECM1,PHEX,LTBP3,CLEC3B,BMP4,ALOX15,ISG15,SBNO2	cyan	VSMC_M2
GO:0050953	0.18	0.89	12	126	sensory perception of light stimulus	BP	1	TGFBI,EFEMP1,BBS9,SLITRK6,CYP4V2,GLRB,BBS2,SFRP5,RLBP1,LAMB2,RPGR,NYX	cyan	VSMC_M2
GO:0035710	0.18	0.91	7	65	CD4-positive, alpha-beta T cell activation	BP	1	STAT6,BCL3,CD81,LEF1,TMEM98,CD55,ZFPM1	cyan	VSMC_M2
GO:0097006	0.18	0.92	6	53	regulation of plasma lipoprotein particle levels	BP	1	HMOX1,PLA2G7,APOE,PRKACA,LCAT,DGAT1	cyan	VSMC_M2
GO:0044282	0.18	0.87	25	284	small molecule catabolic process	BP	1	DDAH2,BCKDHB,AASS,APOE,ACAA1,PNP,ECH1,DECR1,ACADS,HADH,SCLY,ECHS1,ACAT1,QDPR,TP53,CPT2,ABCD1,ASPA,RENBP,HAGH,INPP5E,CRAT,DPYD,LDHD,NAGK	cyan	VSMC_M2
GO:0060271	0.18	0.87	23	266	cilium assembly	BP	1	CDC14C,KCTD17,RSPH9,BBS9,GSN,CCDC114,MARK4,EHD3,DZIP1,POC1B,WWTR1,BBS2,VANGL2,RPGR,CC2D2A,HDAC6,CROCC,WDR90,ENTR1,DNAAF1,ATMIN,ATP6V0D1,TMEM250	cyan	VSMC_M2
GO:0016358	0.18	0.88	18	204	dendrite development	BP	1	COBL,NRP1,APOE,CAMK1,DCLK1,LZTS3,LRP4,PHACTR1,CHRNA7,KIF1A,MAP1S,DLG5,HDAC6,PQBP1,PPP1R9B,PTPRS,DVL1,RERE	cyan	VSMC_M2
GO:0008637	0.18	0.90	9	87	apoptotic mitochondrial changes	BP	1	BAX,IGF1,AIFM2,ARRB2,PLSCR3,TP53,RHOT2,ZNF205,BMF	cyan	VSMC_M2
GO:0090150	0.18	0.88	19	210	establishment of protein localization to membrane	BP	1	AFDN,GGA1,STOM,BAX,RFTN1,PKDCC,CHMP4B,CACNB3,BBS2,SYS1,AKAP5,ERBB2,SLC51B,ZDHHC9,CLSTN1,GRASP,CALM3,STX3,RAB11B	cyan	VSMC_M2
GO:0033146	0.18	0.93	4	32	regulation of intracellular estrogen receptor signaling pathway	BP	1	SRC,VPS11,AR,KANK2	cyan	VSMC_M2

GO:0009889	0.18	0.84	226	3010	regulation of biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,TCF21,AKAP12,FLOT1,DDAH2,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,ACO1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,ZFP36,SAMD4B,KAT2B,EIF3K,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,SLC5A3,STAT1,ABHD14B,CD81,NDN,SLC45A3,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,ERFE,BCL9L,RFX5,GATA5,CLCN2,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,ACP5,KANK2,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,EEF2,MFSD12,GLIS2,ABCD1,DVL1,AGRN,E4F1,DPH7,NELFB,TCF3,SBNO2,EDF1,FAM3A,INPP5E,AXIN1,RERE,H6PD,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,GCHFR,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0010907	0.18	0.93	4	32	positive regulation of glucose metabolic process	BP	1	KAT2B,IGF1,SRC,SLC45A3	cyan	VSMC_M2
GO:0018958	0.18	0.91	7	65	phenol-containing compound metabolic process	BP	1	PMEL,MOXD1,CTSB,CTSK,GIPC1,SLC16A2,MFSD12	cyan	VSMC_M2
GO:0042982	0.18	0.91	7	65	amyloid precursor protein metabolic process	BP	1	BIN1,APOE,IGF1,SPON1,CHRNA7,APH1A,ABCA2	cyan	VSMC_M2
GO:0007498	0.18	0.90	9	89	mesoderm development	BP	1	ZFPM2,SFRP2,EXT2,LEF1,BMP4,EPHA2,PRKACA,ZFP36L1,FOXC2	cyan	VSMC_M2
GO:0046824	0.18	0.91	6	54	positive regulation of nucleocytoplasmic transport	BP	1	GLI3,CAMK1,PRKCD,JUP,PRKACA,EMD	cyan	VSMC_M2
GO:0002720	0.18	0.92	5	42	positive regulation of cytokine production involved in immune response	BP	1	CD81,B2M,GPRC5B,TNFRSF14,CD55	cyan	VSMC_M2
GO:0019068	0.18	0.93	4	31	virion assembly	BP	1	APOE,CHMP4B,CHMP3,RAB43	cyan	VSMC_M2
GO:0009410	0.18	0.87	27	314	response to xenobiotic stimulus	BP	1	EHMT2,HMOX1,ACAA1,CYP2S1,PNP,TIMP2,SMPD1,TLR3,SFRP2,SRC,GNAO1,STAT1,HADH,RHBDD3,ADCY1,B2M,ADORA2A,VEGFB,QDPR,NTRK1,PPP1R9B,ABCC1,EEF2,GSTM4,ABCA2,GATA4,CDK9	cyan	VSMC_M2
GO:0022610	0.19	0.85	81	1050	biological adhesion	BP	1	FLOT1,PLXNB2,IRF1,AFDN,TGFBI,PTPRK,GCNT1,ITGB8,GPNMB,GLI3,RRAS,NRP1,RHOB,FZD4,PNP,LGALS3BP,PAK4,FOLR2,ITGBL1,EFNB2,SCN1B,IGF1,EFNA5,SPON1,SFRP2,PRKCD,EPHA3,SRC,TGM2,SORBS3,CD81,TJP1,CTTN,BOC,XG,LEF1,ATRNL1,EGFL6,LAMB2,FES,ANXA9,GATA5,PARD3B,FIBP,CTNNA3,B2M,BCR,ADORA2A,ASTN1,DGCR2,BMP4,MAEA,DLG5,DNAJB6,JUP,ALOX15,EPHA2,SERPINE2,ERBB2,ZFP36L1,IL27RA,ADAM15,SHC1,PBXIP1,NEO1,ICAM4,PTPRS,TNFRSF14,NPHP4,CLSTN1,FOXC2,ABL1,CERCAM,CNN3,CD55,PML,PLPP3,LRRC7,SDC4,STX3,COL8A1	cyan	VSMC_M2
GO:0006109	0.19	0.88	13	139	regulation of carbohydrate metabolic process	BP	1	AP2A1,KAT2B,IGF1,SRC,SLC45A3,NFKB1,ERFE,TP53,PDK2,NUPR1,FAM3A,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0050801	0.19	0.86	44	542	ion homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,BAX,APOE,SLC6A9,SLC4A9,ACKR4,ATP4A,SCN1B,HEXB,SRC,CACNB3,TGM2,PLCG1,EXT2,CHRNA7,CAPN3,TPCN2,GNAI2,SV2A,ERFE,CYB561,B2M,ADORA2A,GRN,WNK4,PRKACA,MLLT6,TMEM175,PDK2,GRIA1,NEO1,MCOLN1,ABCD1,ABL1,ATP6V0D1,CNNM3,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0001894	0.19	0.88	17	189	tissue homeostasis	BP	1	BAX,POC1B,TPP1,CHMP4B,TP53INP2,WWTR1,SRC,BBS2,TJP1,CTSK,LTBP3,B2M,LDB2,CROCC,ACP5,SIGLEC15,NPHP4	cyan	VSMC_M2
GO:0001895	0.19	0.92	5	43	retina homeostasis	BP	1	POC1B,BBS2,B2M,CROCC,NPHP4	cyan	VSMC_M2
GO:0110148	0.19	0.89	12	127	biomineralization	BP	1	GPNMB,ATRAID,PKDCC,IGF1,ECM1,PHEX,LTBP3,CLEC3B,BMP4,ALOX15,ISG15,SBNO2	cyan	VSMC_M2
GO:1902742	0.19	0.93	4	32	apoptotic process involved in development	BP	1	BAX,LEF1,SLIT2,FOXC2	cyan	VSMC_M2
GO:1901576	0.19	0.83	322	4324	organic substance biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,PMEL,STAT6,MOXD1,TCF21,MGAT4B,AKAP12,FLOT1,CHKB,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,B3GALT4,CYB5R3,TCF20,DAXX,TEF,PTPRK,ST3GAL1,IBA57,TEAD3,TLE1,NFIB,TRERF1,GCNT1,HMOX1,ACO1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,NAT14,SLC44A1,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,KLF15,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,ACSS1,FZD4,VIM,APOE,UROD,BCL3,MIF4GD,SLC6A9,ATG7,COQ8B,SOCS3,CAMK1,TEP1,PNP,RPS16,ZFP36,CANT1,SAMD4B,GPAT4,RPL15,KAT2B,EIF3K,RHOG,TRIM21,SMPD1,APBB1,CLIP3,GTF3A,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,MAN2A1,WT1,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,POU6F1,LPCAT4,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,COQ9,SRC,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,PTDSS1,EXT2,PNPLA2,PIK3C2B,STAT1,ABHD14B,CD81,NDN,SLC45A3,PHKG1,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,MRPL36,ZNF496,NFKB1,SPOCD1,B4GALT4,HIST1H1C,PKNOX2,RGMA,BCL9,IP6K1,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,MN1,GCNT7,ECM1,NELFCD,ADCY1,FURIN,ERFE,BCL9L,RFX5,GATA5,CLCN2,B4GAT1,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,G6PC3,TSC22D4,ACAT1,VEGFB,TMEM106A,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,PORCN,NR2F6,HDAC6,ZBTB3,PQBP1,B3GAT3,WDR45,PLD2,DNAJB6,ARRB2,JUP,ALOX15,WIZ,MYRF,ZBTB17,TCF12,PLSCR3,GIPC1,ERBB2,STARD3,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,UBIAD1,MLLT6,MRI1,AR,TP53,HSD3B7,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12	cyan	VSMC_M2

GO:0006909	0.19	0.88	15	163	phagocytosis	BP	1	APPL2,ELMO1,GSN,RHOG,PLSCR1,PRKCD,SRC,TGM2,TUSC2,ADORA2A,PLD2,ALOX15,TMEM175,C1orf43,ABL1	cyan	VSMC_M2
GO:0014909	0.19	0.90	7	67	smooth muscle cell migration	BP	1	NRP1,IGF1,NDRG4,SRC,ARPC5,SLIT2,PDGFRB	cyan	VSMC_M2
GO:0007229	0.19	0.89	9	92	integrin-mediated signaling pathway	BP	1	ITGB8,NRP1,ITGBL1,SRC,ADAM11,ADAM15,ISG15,ABL1,PLPP3	cyan	VSMC_M2
GO:0001649	0.19	0.87	17	190	osteoblast differentiation	BP	1	IARS,GPNMB,GLI3,ATRAID,IGF1,TP53INP2,SFRP2,WWTR1,ZHX3,LEF1,BMP4,EPHA2,PRKACA,SMOC1,ADAR,RPS15,JUNB	cyan	VSMC_M2
GO:0050795	0.19	0.93	4	33	regulation of behavior	BP	1	APOE,ARRDC3,ADORA2A,PTGDS	cyan	VSMC_M2
GO:1901019	0.19	0.90	7	67	regulation of calcium ion transmembrane transporter activity	BP	1	EHD3,CACNB3,LINC02210-CRHR1,PRKACA,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0051489	0.19	0.92	5	44	regulation of filopodium assembly	BP	1	NRP1,ARAP1,PRKCD,CAPZB,AGRN	cyan	VSMC_M2
GO:0007179	0.19	0.88	14	156	transforming growth factor beta receptor signaling pathway	BP	1	PTPRK,APPL2,ITGB8,LTBP4,SRC,FURIN,BCL9L,FAM89B,LTBP3,ARRB2,GIPC1,TP53,ZBTB7A,PML	cyan	VSMC_M2
GO:0046324	0.19	0.92	5	44	regulation of glucose import	BP	1	APPL2,KLF15,IGF1,ERFE,RNASEL	cyan	VSMC_M2
GO:0021587	0.19	0.92	4	33	cerebellum morphogenesis	BP	1	COQ8B,SERPINE2,GBA,ABL1	cyan	VSMC_M2
GO:0086009	0.19	0.92	4	33	membrane repolarization	BP	1	SCN1B,SNTA1,CACNB3,KCND3	cyan	VSMC_M2
GO:0010823	0.19	0.91	5	43	negative regulation of mitochondrion organization	BP	1	IGF1,VAT1,ARRB2,TP53,TSC2	cyan	VSMC_M2
GO:0048661	0.19	0.90	8	78	positive regulation of smooth muscle cell proliferation	BP	1	HMOX1,IGF1,TGM2,MMP2,STAT1,GNAI2,BMP4,PDGFRB	cyan	VSMC_M2
GO:0003333	0.19	0.90	7	66	amino acid transmembrane transport	BP	1	SLC17A7,SLC6A9,SLC15A4,SLC7A2,SLC38A7,SLC16A2,MFSD12	cyan	VSMC_M2
GO:0002440	0.19	0.88	13	138	production of molecular mediator of immune response	BP	1	STAT6,HMOX1,TRIL,SLC15A4,TLR3,CD81,B2M,IL27RA,GPRC5B,TNFRSF14,TCF3,CD55,BST2	cyan	VSMC_M2
GO:0006040	0.19	0.92	4	32	amino sugar metabolic process	BP	1	ST3GAL1,RENBP,UAP1L1,NAGK	cyan	VSMC_M2
GO:0060840	0.20	0.89	8	81	artery development	BP	1	GLI3,NRP1,APOE,BMP4,FKBP10,PDGFRB,NPRL3,FOXC2	cyan	VSMC_M2
GO:0055065	0.20	0.85	36	438	metal ion homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,BAX,APOE,SLC6A9,ACKR4,ATP4A,HEXB,CACNB3,TGM2,PLCG1,EXT2,CHRNA7,CAPN3,TPCN2,GNAI2,SV2A,ERFE,CYB561,B2M,ADORA2A,PRKACA,MLLT6,GRIA1,NEO1,MCOLN1,ABL1,ATP6V0D1,CNNM3,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0099601	0.20	0.91	5	44	regulation of neurotransmitter receptor activity	BP	1	NPTXR,SLC6A9,NPTX1,SRC,CAPN1	cyan	VSMC_M2
GO:0002285	0.20	0.88	12	127	lymphocyte activation involved in immune response	BP	1	STAT6,ST3GAL1,BCL3,LAMP1,SLC15A4,CD81,LEF1,IL27RA,TP53,TMEM98,ABL1,ZFPM1	cyan	VSMC_M2
GO:0045581	0.20	0.92	4	32	negative regulation of T cell differentiation	BP	1	IRF1,GLI3,BMP4,ERBB2	cyan	VSMC_M2
GO:0051222	0.20	0.86	21	241	positive regulation of protein transport	BP	1	GLI3,STOM,CAMK1,APBB1,IGF1,EDEM2,PRKCD,SRC,CACNB3,CD81,VPS11,ADORA2A,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,PHPT1,EMD,UBL5	cyan	VSMC_M2
GO:0070830	0.20	0.91	5	44	bicellular tight junction assembly	BP	1	AFDN,TJP1,EPHA2,PRKACA,NPHP4	cyan	VSMC_M2
GO:0032007	0.20	0.92	4	33	negative regulation of TOR signaling	BP	1	DEPTOR,AKT1S1,TSC2,NPRL3	cyan	VSMC_M2
GO:0046847	0.20	0.91	6	56	filopodium assembly	BP	1	NRP1,ARAP1,PRKCD,CAPZB,PPP1R9B,AGRN	cyan	VSMC_M2
GO:0031327	0.20	0.83	93	1198	negative regulation of cellular biosynthetic process	BP	1	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,BCL3,ATG7,ZFP36,SAMD4B,APBB1,LMO1,RARG,WT1,PATL1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,CAPN3,NFKB1,HIST1H1C,LEF1,TBL1Y,PTGIS,NELFCD,ERFE,RFX5,MAGEF1,MOV10,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,ZFP36L1,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,ACP5,KANK2,MTA1,MOSPD1,MFSD12,GLIS2,E4F1,NELFB,TCF3,SBNO2,FAM3A,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,ZFPM1,EN1	cyan	VSMC_M2
GO:0010977	0.20	0.88	11	116	negative regulation of neuron projection development	BP	1	NRP1,VIM,APOE,EFNB2,LRP4,SEMA3B,RGMA,SEMA4B,SEMA6C,B2M,PTPRS	cyan	VSMC_M2
GO:0003208	0.20	0.90	6	57	cardiac ventricle morphogenesis	BP	1	ZFPM2,SFRP2,CPE,HEG1,FOXC2,GATA4	cyan	VSMC_M2
GO:0042093	0.20	0.91	5	44	T-helper cell differentiation	BP	1	STAT6,BCL3,LEF1,TMEM98,ZFPM1	cyan	VSMC_M2
GO:0043524	0.20	0.88	11	115	negative regulation of neuron apoptotic process	BP	1	HMOX1,NRP1,BAX,APOE,ADORA2A,GRN,ARRB2,NTRK1,GBA,RETREG1,EN1	cyan	VSMC_M2
GO:0006886	0.20	0.84	59	739	intracellular protein transport	BP	1	RAB5B,OS9,RABL2A,TBC1D22A,GGA1,APPL2,TBC1D2,TBC1D17,GLI3,AP2A1,STOM,RHOB,BAX,BCL3,CAMK1,HGS,TBC1D5,RFTN1,CLIP3,GNPTAB,CHMP4B,EDEM2,PRKCD,CACNB3,CTSA,CD81,CTTN,SGSM1,VPS11,KIF1A,FAM53B,NFKBIA,M6PR,RPGR,HOMER3,BMP4,HDAC6,B3GAT3,JUP,AKAP5,GABARAP,GIPC1,ERBB2,PRKACA,TP53,SLC51B,SNX33,ZDHHC9,NAGPA,SGSM2,TSC2,MON1B,RAB43,GRASP,PML,VPS26B,STX3,EMD,UBL5	cyan	VSMC_M2
GO:0001906	0.20	0.89	8	78	cell killing	BP	1	ULBP2,LAMP1,TUSC2,B2M,ARRB2,PLEKHM2,CD55,RPS19	cyan	VSMC_M2
GO:0048469	0.20	0.88	11	116	cell maturation	BP	1	RPS6KA2,MTCH1,GPAT4,TUSC2,B4GALT5,REC8,MAEA,PRKACA,GBA,AGRN,ZBTB7A	cyan	VSMC_M2
GO:0044272	0.20	0.88	12	127	sulfur compound biosynthetic process	BP	1	ST3GAL1,ACSS1,GGT7,ACSS2,CHST14,EXT2,B4GAT1,ACAT1,MRI1,PDK2,XYLT2,HAGH	cyan	VSMC_M2
GO:0045637	0.20	0.87	14	152	regulation of myeloid cell differentiation	BP	1	MEIS1,LRRC17,ZFP36,RARG,TLR3,STAT1,LEF1,FES,NFKBIA,B2M,ZFP36L1,ISG15,IL34,ZFPM1	cyan	VSMC_M2
GO:0051693	0.20	0.92	4	34	actin filament capping	BP	1	GSN,ADD1,CAPZB,FLII	cyan	VSMC_M2
GO:0051272	0.20	0.85	38	466	positive regulation of cellular component movement	BP	1	AKAP12,HMOX1,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,FGFR1,ADGRA2,ANGPT4,IGF1,SRC,PLCG1,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,SEMA4B,SEMA6C,FAM89B,GRN,VEGFB,BMP4,STAT5A,HDAC6,PDGFRB,MAP2K3,TNFRSF14,PHPT1,FOXC2,ABL1,IL34,RPS19,PLPP3	cyan	VSMC_M2
GO:2001257	0.20	0.88	11	116	regulation of cation channel activity	BP	1	STOM,SLC6A9,EHD3,SCN1B,CACNB3,LINC02210-CRHR1,CAPN1,PRKACA,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:1904659	0.20	0.89	8	80	glucose transmembrane transport	BP	1	APPL2,KLF15,CLIP3,IGF1,SLC5A3,ERFE,RNASEL,SLC2A8	cyan	VSMC_M2
GO:0071354	0.20	0.92	4	33	cellular response to interleukin-6	BP	1	SRC,NFKB1,PTGIS,SBNO2	cyan	VSMC_M2
GO:0008344	0.20	0.90	6	56	adult locomotory behavior	BP	1	SLITRK6,GLRB,CSTB,ARRB2,PBX3,EN1	cyan	VSMC_M2
GO:0010508	0.20	0.88	10	105	positive regulation of autophagy	BP	1	HMOX1,TRIM14,TRIM13,ATG7,TRIM21,TP53INP2,CAMKK2,TRIM8,FYCO1,TSC2	cyan	VSMC_M2
GO:1902116	0.20	0.92	4	33	negative regulation of organelle assembly	BP	1	EHMT2,KAT2B,CHMP4B,NUPR1	cyan	VSMC_M2
GO:0048872	0.20	0.86	20	229	homeostasis of number of cells	BP	1	HMOX1,LRRC19,BAX,ZFP36,SLC15A4,LMO1,STAT1,B2M,BMP4,MAEA,ZFP36L1,GBA,ADAR,GLIS2,ISG15,ABL1,ZBTB7A,RPS19,OCIAD2,ZFPM1	cyan	VSMC_M2

GO:0050770	0.20	0.87	12	132	regulation of axonogenesis	BP	1	PLXNB2,NRP1,LRP4,SEMA3B,RGMA,SEMA4B,SEMA6C,STK25,RND2,SLIT2,PTPRS,IST1	cyan	VSMC_M2
GO:0086065	0.20	0.91	5	46	cell communication involved in cardiac conduction	BP	1	SCN1B,CTNNA3,JUP,PRKACA,CALM3	cyan	VSMC_M2
GO:0007010	0.20	0.83	90	1177	cytoskeleton organization	BP	1	PACSIN2,ARHGAP18,CDC14C,KIFC2,CUL9,RSPH9,ELMO1,COBL,GSN,NRP1,RHOB,CCDC114,LURAP1,MARK4,VIM,BIN1,APOE,TPPP2,PAK4,ARAP1,KAT2B,RHOG,POC1B,CLIP3,EFNA5,RHPN2,CHMP4B,CHMP3,PRKCD,EPHA3,SRC,BBS2,PDLIM2,C15orf62,SORBS3,NISCH,LZTS2,PHACTR1,CAPN3,TJP1,CTTN,TPPP,SSH3,NCKIPSD,GAS2L1,FES,PRUNE1,TACC2,PARD3B,CTNNA3,WIPF1,ARPC5,ARHGEF10,CDC42BPG,RND2,ADD1,MAEA,CAPZB,MAP1S,CC2D2A,HDAC6,ARHGEF10L,PLD2,CROCC,DNAJB6,ALOX15,GABARAP,CGNL1,SLIT2,PPP1R9B,ZMYM3,SHC1,ANKFN1,ARHGAP17,SIGLEC15,PDGFRB,FLII,LLGL1,DVL1,AGRN,NPHP4,FBXW5,PHPT1,AIF1L,ABL1,DNAAF1,CNN3,KRT25,SDC4,BST2	cyan	VSMC_M2
GO:0032868	0.20	0.86	18	206	response to insulin	BP	1	GCNT1,APPL2,KLF15,SOCS3,KAT2B,PRKCD,SRC,STAT1,GNAI2,HADH,ERFE,HDAC5,ZFP36L1,PDK2,SHC1,TSC2,FOXC2,SLC2A8	cyan	VSMC_M2
GO:0010556	0.20	0.82	213	2846	regulation of macromolecule biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,TCF21,AKAP12,FLOT1,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,ACO1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,ZFP36,SAMD4B,KAT2B,EIF3K,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,KANK2,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,EEF2,GLIS2,DVL1,AGRN,E4F1,DPH7,NELFB,TCF3,SBNO2,EDF1,INPP5E,AXIN1,RERE,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0060412	0.20	0.92	4	34	ventricular septum morphogenesis	BP	1	ZFPM2,BMP4,SLIT2,ZFPM1	cyan	VSMC_M2
GO:0009059	0.20	0.82	266	3569	macromolecule biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,TCF21,MGAT4B,AKAP12,FLOT1,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,B3GALT4,TCF20,DAXX,TEF,PTPRK,ST3GAL1,TEAD3,TLE1,NFIB,TRERF1,GCNT1,HMOX1,ACO1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,KLF15,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,TEP1,RPS16,ZFP36,CANT1,SAMD4B,RPL15,KAT2B,EIF3K,RHOG,TRIM21,APBB1,CLIP3,GTF3A,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,MAN2A1,WT1,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,GALNT18,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,EXT2,STAT1,ABHD14B,CD81,NDN,PHKG1,TRIM8,IKBKE,CAPN3,TIRAP,MRPL36,ZNF496,NFKB1,SPOCD1,B4GALT4,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,MN1,GCNT7,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,B4GAT1,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,VEGFB,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,PORCN,NR2F6,HDAC6,ZBTB3,PQBP1,B3GAT3,WDR45,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,GBA,XYLT2,SLC51B,NUPR1,SHC1,PBXIP1,KANK2,WARS,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,ZDHHC9,MOSPD1,MPND,NAGPA,EEF2,GLIS2,DVL1,AGRN,ELOB,E4F1,DPH7,NELFB,TCF3,SBNO2,EDF1,PIGQ,INPP5E,AXIN1,RERE,POLRMT,TC	cyan	VSMC_M2
GO:0034764	0.20	0.87	14	155	positive regulation of transmembrane transport	BP	1	KLF15,BAX,SLC6A9,EHD3,CLIP3,IGF1,CACNB3,PLCG1,CAPN3,ERFE,RNASEL,WNK4,ABL1,CALM3	cyan	VSMC_M2

GO:0031326	0.20	0.82	221	2955	regulation of cellular biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,TCF21,FLOT1,DDAH2,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,ACO1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,ZFP36,SAMD4B,KAT2B,EIF3K,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,SLC45A3,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,ERFE,BCL9L,RFX5,GATA5,CLCN2,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,ACP5,KANK2,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,EEF2,MFSD12,GLS2,ABCD1,DVL1,AGRN,E4F1,DPH7,NELFB,TCF3,SBNO2,EDF1,FAM3A,INPP5E,AXIN1,RERE,H6PD,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0071375	0.20	0.86	19	219	cellular response to peptide hormone stimulus	BP	1	STAT6,APPL2,SOCS3,KAT2B,PRKCD,SRC,STAT1,NFKB1,GNAI2,ERFE,LINC02210-CRHR1,HDAC5,STAT5A,ZFP36L1,PDK2,SHC1,TSC2,FOXC2,SLC2A8	cyan	VSMC_M2
GO:0150115	0.21	0.88	9	95	cell-substrate junction organization	BP	1	PTPRK,NRP1,EFNA5,EPHA3,SRC,CTTN,BCR,ABL1,SDC4	cyan	VSMC_M2
GO:0032233	0.21	0.90	6	56	positive regulation of actin filament bundle assembly	BP	1	NRP1,SORBS3,ARHGEF10,ARHGEF10L,ABL1,SDC4	cyan	VSMC_M2
GO:0042100	0.21	0.90	6	56	B cell proliferation	BP	1	BAX,PRKCD,CD81,TIRAP,LEF1,ABL1	cyan	VSMC_M2
GO:0048645	0.21	0.90	6	56	animal organ formation	BP	1	GLI3,WT1,GATA5,WNT2B,BMP4,AR	cyan	VSMC_M2
GO:0021575	0.21	0.92	4	34	hindbrain morphogenesis	BP	1	COQ8B,SERPINE2,GBA,ABL1	cyan	VSMC_M2
GO:0006110	0.21	0.92	4	34	regulation of glycolytic process	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0070301	0.21	0.89	8	79	cellular response to hydrogen peroxide	BP	1	STAT6,RHOB,PRKCD,SRC,STK25,HDAC6,PCGF2,ABL1	cyan	VSMC_M2
GO:0050885	0.21	0.92	4	34	neuromuscular process controlling balance	BP	1	GAA,TPP1,HEXB,ABL1	cyan	VSMC_M2
GO:0048806	0.21	0.92	4	34	genitalia development	BP	1	BAX,WT1,FOXF2,AR	cyan	VSMC_M2
GO:0042267	0.21	0.92	4	33	natural killer cell mediated cytotoxicity	BP	1	ULBP2,LAMP1,ARRB2,PLEKHM2	cyan	VSMC_M2
GO:0001974	0.21	0.92	4	34	blood vessel remodeling	BP	1	BAX,TGM2,TMBIM1,FOXC2	cyan	VSMC_M2
GO:0051341	0.21	0.89	8	79	regulation of oxidoreductase activity	BP	1	DDAH2,APOE,NFKB1,GNAI2,CCS,HDAC6,ABL1,CALM3	cyan	VSMC_M2
GO:0055080	0.21	0.84	40	494	cation homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,BAX,APOE,SLC6A9,SLC4A9,ACKR4,ATP4A,HEXB,CACNB3,TGM2,PLCG1,EXT2,CHRNA7,CAPN3,TPCN2,GNAI2,SV2A,ERFE,CYB561,B2M,ADORA2A,GRN,PRKACA,MLLT6,TMEM175,PDK2,GRIA1,NEO1,MCOLN1,ABL1,ATP6V0D1,CNNM3,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:2000147	0.21	0.84	37	455	positive regulation of cell motility	BP	1	AKAP12,HMOX1,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,FGFR1,ADGRA2,ANGPT4,IGF1,SRC,PLCG1,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,SEMA4B,SEMA6C,FAM89B,GRN,VEGFB,BMP4,STAT5A,HDAC6,PDGFRB,MAP2K3,TNFRSF14,PHPT1,FOXC2,ABL1,IL34,PLPP3	cyan	VSMC_M2
GO:0016266	0.21	0.92	4	33	O-glycan processing	BP	1	ST3GAL1,GCNT1,GALNT12,B4GALT5	cyan	VSMC_M2
GO:0048167	0.21	0.87	13	143	regulation of synaptic plasticity	BP	1	APOE,TSHZ3,CHRNA7,ADCY1,ADORA2A,AKAP5,SERPINE2,GIPC1,CPLX2,GRIA1,ABL1,SLC8A3,STX3	cyan	VSMC_M2
GO:0015849	0.21	0.86	18	203	organic acid transport	BP	1	SLC17A7,APOE,SLC6A9,FOLR2,SLC15A4,SLC7A2,SLC38A7,SV2A,ERFE,ADORA2A,GIPC1,SLC51B,SLC16A2,ABCC1,CPT2,MFSD12,ABCD1,SLC10A3	cyan	VSMC_M2
GO:0051384	0.21	0.88	10	104	response to glucocorticoid	BP	1	FBXO32,KLF9,ZFP36,FIBIN,CASP9,ZFP36L1,SLIT2,GBA,SERPINF1,CALM3	cyan	VSMC_M2
GO:0002294	0.21	0.90	5	45	CD4-positive, alpha-beta T cell differentiation involved in immune response	BP	1	STAT6,BCL3,LEF1,TMEM98,ZFPM1	cyan	VSMC_M2
GO:2000008	0.21	0.91	4	34	regulation of protein localization to cell surface	BP	1	SNX33,ABCA2,STX3,RAB11B	cyan	VSMC_M2
GO:0030217	0.21	0.86	16	179	T cell differentiation	BP	1	STAT6,IRF1,PTPRK,GLI3,BCL3,PNP,LEF1,B2M,BMP4,ERRBB2,ZFP36L1,TP53,GBA,TMEM98,ABL1,ZFPM1	cyan	VSMC_M2
GO:0002685	0.21	0.86	14	152	regulation of leukocyte migration	BP	1	HMOX1,PLA2G7,RHOG,CD81,TIRAP,XG,VEGFD,ECM1,VEGFB,NBL1,IL27RA,SLIT2,TNFRSF14,IL34	cyan	VSMC_M2
GO:0006006	0.21	0.86	14	155	glucose metabolic process	BP	1	GAA,KAT2B,DCXR,IGF1,SRC,NISCH,SLC45A3,ERFE,G6PC3,BRAT1,TP53,PDK2,FAM3A,H6PD	cyan	VSMC_M2
GO:0030335	0.21	0.84	36	443	positive regulation of cell migration	BP	1	AKAP12,HMOX1,PLA2G7,GPNMB,RRAS,NRP1,RHOB,FZD4,FGFR1,ADGRA2,ANGPT4,IGF1,SRC,PLCG1,TJP1,TIRAP,SEMA3B,GNAI2,XG,LEF1,VEGFD,SEMA4B,SEMA6C,FAM89B,GRN,VEGFB,BMP4,STAT5A,HDAC6,PDGFRB,MAP2K3,TNFRSF14,FOXC2,ABL1,IL34,PLPP3	cyan	VSMC_M2
GO:1905952	0.21	0.87	11	118	regulation of lipid localization	BP	1	EEPD1,APOE,PRKCD,PNPLA2,IKBKE,NFKB1,FURIN,ERFE,NFKBIA,LINC02210-CRHR1,ABCA2	cyan	VSMC_M2
GO:0001941	0.21	0.91	4	34	postsynaptic membrane organization	BP	1	APOE,GLRB,LRP4,DVL1	cyan	VSMC_M2

GO:0019438	0.21	0.81	217	2902	aromatic compound biosynthetic process	BP	1	CTDP1,TSHZ1,PMEL,STAT6,MOXD1,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,IBA57,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,APOE,UROD,BCL3,SLC6A9,CAMK1,TEP1,PNP,ZFP36,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,ACSS2,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,ACAT1,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12,NUPR1,SHC1,PBXIP1,KANK2,PPCDC,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,MFSD12,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,UAP1L1,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,FPGS,PBX3,TK2,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,PDXK,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0097061	0.21	0.89	7	70	dendritic spine organization	BP	1	APOE,LZTS3,CHRNA7,CTTN,KIF1A,HDAC6,DVL1	cyan	VSMC_M2
GO:0043279	0.21	0.88	8	81	response to alkaloid	BP	1	EHMT2,ATG7,SMPD1,TGM2,GNAO1,ADORA2A,PPP1R9B,EN1	cyan	VSMC_M2
GO:0034645	0.21	0.81	263	3533	cellular macromolecule biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,TCF21,MGAT4B,FLOT1,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,B3GALT4,TCF20,DAXX,TEF,PTPRK,ST3GAL1,TEAD3,TLE1,NFIB,TRERF1,GCNT1,HMOX1,ACO1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,TEP1,RPS16,ZFP36,CANT1,SAMD4B,RPL15,KAT2B,EIF3K,RHOG,TRIM21,APBB1,CLIP3,GTF3A,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,MAN2A1,WT1,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,GALNT18,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,EXT2,STAT1,ABHD14B,CD81,NDN,PHKG1,TRIM8,IKBKE,CAPN3,TIRAP,MRPL36,ZNF496,NFKB1,SPOCD1,B4GALT4,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,MN1,GCNT7,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,B4GAT1,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,VEGFB,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,PORCN,NR2F6,HDAC6,ZBTB3,PQBP1,B3GAT3,WDR45,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,GBA,XYLT2,SLC51B,NUPR1,SHC1,PBXIP1,KANK2,WARS,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,ZDHHC9,MOSPD1,MPND,NAGPA,EEF2,GLIS2,DVL1,AGRN,ELOB,E4F1,DPH7,NELFB,TCF3,SBNO2,EDF1,PIGQ,INPP5E,AXIN1,RERE,POLRMT,TCF25,BRD3,RPL13,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,MGAT3,TK2,NFIA,AB	cyan	VSMC_M2
GO:0003007	0.21	0.86	17	197	heart morphogenesis	BP	1	ZFPM2,NRP1,GAA,SFRP2,NDRG4,CPE,HEG1,VANGL2,GATA5,BMP4,SLIT2,TP53,ADAM15,FOXC2,DNAAF1,GATA4,ZFPM1	cyan	VSMC_M2
GO:0006879	0.21	0.89	6	56	cellular iron ion homeostasis	BP	1	HMOX1,ACO1,SLC6A9,ERFE,CYB561,ATP6V0D1	cyan	VSMC_M2
GO:0035329	0.21	0.91	4	35	hippo signaling	BP	1	TEAD3,WWTR1,DLG5,MAP2K3	cyan	VSMC_M2
GO:1902414	0.21	0.88	8	82	protein localization to cell junction	BP	1	TJP1,HEG1,DLG5,CGNL1,DVL1,CLSTN1,GRASP,STX3	cyan	VSMC_M2
GO:0031960	0.21	0.87	11	117	response to corticosteroid	BP	1	FBXO32,KLF9,ZFP36,SRC,FIBIN,CASP9,ZFP36L1,SLIT2,GBA,SERPINF1,CALM3	cyan	VSMC_M2
GO:0002820	0.21	0.91	4	33	negative regulation of adaptive immune response	BP	1	ALOX15,IL27RA,TNFRSF14,CD55	cyan	VSMC_M2
GO:0090398	0.21	0.89	7	68	cellular senescence	BP	1	PRKCD,B2M,TP53,ULK3,MAP2K3,ABL1,PML	cyan	VSMC_M2
GO:0042698	0.21	0.90	5	46	ovulation cycle	BP	1	FZD4,SRC,ARRB2,SLIT2,SERPINF1	cyan	VSMC_M2
GO:0003176	0.21	0.91	4	34	aortic valve development	BP	1	GATA5,BMP4,SLIT2,GATA4	cyan	VSMC_M2
GO:0003158	0.21	0.87	10	107	endothelium development	BP	1	AFDN,NRP1,RHOB,TJP1,HEG1,ADD1,BMP4,PTPRS,EDF1,FOXC2	cyan	VSMC_M2
GO:0034766	0.21	0.89	7	68	negative regulation of ion transmembrane transport	BP	1	BIN1,SLC6A9,CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0071346	0.22	0.88	8	80	cellular response to interferon-gamma	BP	1	IRF1,VIM,TLR3,STAT1,TP53,GBP6,RAB43,VPS26B	cyan	VSMC_M2
GO:0006354	0.22	0.88	8	80	DNA-templated transcription, elongation	BP	1	CTDP1,NELFCD,ELL3,TCEA2,ELOB,NELFB,HEXIM1,CDK9	cyan	VSMC_M2
GO:0070741	0.22	0.91	4	34	response to interleukin-6	BP	1	SRC,NFKB1,PTGIS,SBNO2	cyan	VSMC_M2
GO:0051965	0.22	0.90	5	46	positive regulation of synapse assembly	BP	1	SLITRK6,DLG5,NTRK1,AGRN,CLSTN1	cyan	VSMC_M2
GO:0002686	0.22	0.91	4	33	negative regulation of leukocyte migration	BP	1	HMOX1,NBL1,IL27RA,SLIT2	cyan	VSMC_M2
GO:1902475	0.22	0.90	5	45	L-alpha-amino acid transmembrane transport	BP	1	SLC17A7,SLC6A9,SLC15A4,SLC7A2,SLC38A7	cyan	VSMC_M2
GO:0035272	0.22	0.91	4	34	exocrine system development	BP	1	NFIB,NRP1,TGM2,CLCN2	cyan	VSMC_M2
GO:0071867	0.22	0.88	7	69	response to monoamine	BP	1	TGM2,GNAO1,ARRB2,PRKACA,ABL1,RNLS,RGS8	cyan	VSMC_M2
GO:0071869	0.22	0.88	7	69	response to catecholamine	BP	1	TGM2,GNAO1,ARRB2,PRKACA,ABL1,RNLS,RGS8	cyan	VSMC_M2
GO:0022408	0.22	0.86	12	130	negative regulation of cell-cell adhesion	BP	1	IRF1,GPNMB,GLI3,PRKCD,ADORA2A,BMP4,DLG5,SERPINE2,ERBB2,TNFRSF14,ABL1,SDC4	cyan	VSMC_M2
GO:0010677	0.22	0.91	4	34	negative regulation of cellular carbohydrate metabolic process	BP	1	ERFE,NUPR1,FAM3A,CBFA2T3	cyan	VSMC_M2
GO:0048738	0.22	0.85	16	186	cardiac muscle tissue development	BP	1	CTDP1,ZFPM2,MEIS1,EFNB2,IGF1,WT1,NDRG4,HEG1,GATA5,BMP4,ARRB2,PDGFRB,NPRL3,FOXC2,GATA4,ZFPM1	cyan	VSMC_M2
GO:0007193	0.22	0.90	5	45	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	BP	1	AKAP12,GNAI2,GNAZ,PSAP,AKAP5	cyan	VSMC_M2

GO:0042592	0.22	0.81	99	1295	homeostatic process	BP	1	STAT6,GRINA,KCTD17,HMOX1,LRRC19,ACO1,APPL2,KLF15,BAX,APOE,SLC6A9,ZFP36,GAA,SLC4A9,POC1B,ACKR4,TPP1,SLC15A4,LMO1,ATP4A,SCN1B,EFNA5,CHMP4B,TP53INP2,ARRDC3,HEXB,WWTR1,SRC,CACNB3,TGM2,DECR1,PLCG1,BBS2,EXT2,PNPLA2,STAT1,NDN,CHRNA7,CAPN3,TJP1,TPCN2,GNAI2,HADH,IP6K1,SV2A,CTSK,ERFE,CYB561,LTBP3,B2M,ADORA2A,GRN,WNK4,BMP4,MAEA,LDB2,CROCC,PLSCR3,PRKACA,ZFP36L1,CLCN6,MLLT6,TMEM175,NPC2,PDK2,GBA,ADAR,ACP5,SIGLEC15,GRIA1,NEO1,MCOLN1,CPT2,GLIS2,ABCD1,ISG15,NPHP4,PHPT1,RHOT2,FOXC2,ABL1,LCAT,ATP6V0D1,ABCA2,CNNM3,SLC8A3,SERPINF1,ZBTB7A,CD55,DGAT1,PML,RPS19,GATA4,CALM3,CLIC2,OCIAD2,RAB11B,MPV17,ZFPM1	cyan	VSMC_M2
GO:0099054	0.22	0.91	4	35	presynapse assembly	BP	1	SLITRK6,EFNB2,LRP4,DVL1	cyan	VSMC_M2
GO:0034103	0.22	0.89	6	57	regulation of tissue remodeling	BP	1	GPNMB,SRC,LTBP3,TMBIM1,TP53,SIGLEC15	cyan	VSMC_M2
GO:0030155	0.22	0.82	43	541	regulation of cell adhesion	BP	1	FLOT1,PLXNB2,IRF1,AFDN,TGFBI,GPNMB,GLI3,RRAS,NRP1,FZD4,PNP,IGF1,EFNA5,SFRP2,PRKCD,EPHA3,SRC,TGM2,CD81,TJP1,LEF1,EGFL6,FES,B2M,ADORA2A,BMP4,DLG5,JUP,ALOX15,EPHA2,SERPINE2,ERBB2,IL27RA,ADAM15,TNFRSF14,FOXC2,ABL1,CD55,PML,PLPP3,SDC4,STX3,COL8A1	cyan	VSMC_M2
GO:0071560	0.22	0.85	17	199	cellular response to transforming growth factor beta stimulus	BP	1	PTPRK,APPL2,ITGB8,LTBP4,SRC,SOX5,FURIN,BCL9L,FAM89B,LTBP3,CLEC3B,ARRB2,GIPC1,ZFP36L1,TP53,ZBTB7A,PML	cyan	VSMC_M2
GO:0046849	0.22	0.88	7	69	bone remodeling	BP	1	TPP1,SRC,CTSK,LTBP3,EPHA2,ACP5,SIGLEC15	cyan	VSMC_M2
GO:0000271	0.22	0.89	6	58	polysaccharide biosynthetic process	BP	1	AP2A1,IGF1,EXT2,PHKG1,NFKB1,B4GALT5	cyan	VSMC_M2
GO:0051649	0.22	0.81	127	1679	establishment of localization in cell	BP	1	RAB5B,OS9,RABL2A,TBC1D22A,GGA1,HMOX1,APPL2,TBC1D2,TBC1D17,GLI3,AP2A1,CADPS2,SLC17A7,STOM,RHOB,BAX,DENND2A,BIN1,APOE,BCL3,SLC6A9,CAMK1,EHD3,CMTM6,HGS,TBC1D5,RFTN1,DCLK1,LAMP1,TMEM108,CLIP3,SCN1B,GNPTAB,REEP5,SNTA1,EFNA5,CHMP4B,CHMP3,EDEM2,ERGIC3,NDRG4,STBD1,PRKCD,SRC,CACNB3,PLCG1,BBS2,ARHGAP1,SYS1,LZTS2,CTSA,CD81,CAPN3,AGFG1,CTTN,TPCN2,SGSM1,SV2A,ADCY1,FES,VPS11,KIF1A,FAM53B,TMEM50A,PARD3B,STK25,NFKBIA,KCND3,M6PR,ADORA2A,FYCO1,RPGR,HOMER3,BMP4,MAP1S,HDAC6,B3GAT3,PLD2,JUP,AKAP5,GABARAP,GIPC1,ERBB2,STARD3,PRKACA,TP53,CPLX2,ERGIC1,NPC2,SLC51B,STON2,ANKFN1,SNX33,MCOLN1,LLGL1,ZDHHC9,UBXN6,SH3GL1,NAGPA,CPT2,WDR81,ABCD1,DVL1,SGSM2,TSC2,PTGDS,PHPT1,RHOT2,RAB11FIP3,ENTR1,ABL1,HSBP1,MON1B,ABCA2,RPS15,GAS1,SLC8A3,RAB43,GRASP,PML,CALM3,CLIC2,VPS26B,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0002228	0.22	0.91	4	34	natural killer cell mediated immunity	BP	1	ULBP2,LAMP1,ARRB2,PLEKHM2	cyan	VSMC_M2
GO:0032410	0.22	0.89	6	57	negative regulation of transporter activity	BP	1	SLC6A9,CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0003151	0.22	0.89	6	59	outflow tract morphogenesis	BP	1	ZFPM2,NRP1,SFRP2,BMP4,FOXC2,ZFPM1	cyan	VSMC_M2
GO:0010827	0.22	0.89	6	58	regulation of glucose transmembrane transport	BP	1	APPL2,KLF15,CLIP3,IGF1,ERFE,RNASEL	cyan	VSMC_M2
GO:0006919	0.22	0.89	6	57	activation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MTCH1,BAX,CASP10,CASP9,PML,CARD8	cyan	VSMC_M2
GO:0030516	0.22	0.87	8	83	regulation of axon extension	BP	1	NRP1,APOE,CTTN,SEMA3B,SEMA4B,SEMA6C,PTPRS,ABL1	cyan	VSMC_M2
GO:0002287	0.22	0.90	5	46	alpha-beta T cell activation involved in immune response	BP	1	STAT6,BCL3,LEF1,TMEM98,ZFPM1	cyan	VSMC_M2
GO:0002293	0.22	0.90	5	46	alpha-beta T cell differentiation involved in immune response	BP	1	STAT6,BCL3,LEF1,TMEM98,ZFPM1	cyan	VSMC_M2
GO:0043550	0.22	0.89	6	58	regulation of lipid kinase activity	BP	1	SOCS3,SRC,CD81,PDGFRB,WDR81,EEF1A2	cyan	VSMC_M2
GO:0008154	0.23	0.85	16	183	actin polymerization or depolymerization	BP	1	ARHGAP18,COBL,GSN,BIN1,PRKCD,C15orf62,CTTN,SSH3,WIPF1,ARPC5,ADD1,CAPZB,ALOX15,SLIT2,PPP1R9B,FLII	cyan	VSMC_M2
GO:0010243	0.23	0.81	62	793	response to organonitrogen compound	BP	1	STAT6,OS9,EHMT2,GCNT1,APPL2,RRAGC,KLF15,TRIM13,VIM,APOE,ATG7,SOCS3,FOLR2,KAT2B,SMPD1,IGF1,WT1,EDEM2,GLRB,PRKCD,SRC,TGM2,GNAO1,MMP2,STAT1,CD81,CHRNA7,NFKB1,GNAI2,HADH,ERFE,PHEX,NFKBIA,LINC02210-CRHR1,ADORA2A,HDAC5,QDPR,STAT5A,ARRB2,JUP,PRKACA,ZFP36L1,UBQLN2,SLIT2,TP53,PDK2,PPP1R9B,SHC1,ABCC1,UBXN6,EEF2,TSC2,FOXC2,ABL1,SLC2A8,SLC8A3,SERPINF1,CALM3,RNLS,RGS8,RGS10,EN1	cyan	VSMC_M2
GO:0016525	0.23	0.87	8	82	negative regulation of angiogenesis	BP	1	HGS,ANGPT4,STAT1,ADGRB2,EPHA2,EPN2,SERPINF1,PML	cyan	VSMC_M2
GO:0043523	0.23	0.85	15	169	regulation of neuron apoptotic process	BP	1	HMOX1,AKT1S1,NRP1,BAX,APOE,ADORA2A,GRN,ARRB2,CASP9,NTRK1,TP53,GBA,NUPR1,RETREG1,EN1	cyan	VSMC_M2
GO:0014911	0.23	0.91	4	35	positive regulation of smooth muscle cell migration	BP	1	NRP1,IGF1,SRC,PDGFRB	cyan	VSMC_M2
GO:0070665	0.23	0.87	9	93	positive regulation of leukocyte proliferation	BP	1	PNP,IL5RA,IGF1,CD81,TIRAP,IL27RA,IL34,CD55,BST2	cyan	VSMC_M2
GO:0060338	0.23	0.91	4	34	regulation of type I interferon-mediated signaling pathway	BP	1	IRF3,IKBKE,ADAR,ISG15	cyan	VSMC_M2
GO:0002066	0.23	0.91	4	35	columnar/cuboidal epithelial cell development	BP	1	GPAT4,RARG,SRC,BMP4	cyan	VSMC_M2
GO:0045934	0.23	0.81	86	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,BCL3,ZFP36,KAT2B,APBB1,LMO1,RARG,WT1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,IKBKE,CAPN3,TIRAP,NFKB1,HIST1H1C,LEF1,TBL1Y,NELFCD,RFX5,MAGEF1,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,UBQLN4,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MOSPD1,GLIS2,E4F1,NELFB,TCF3,SBNO2,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,CDK9,ZFPM1,EN1	cyan	VSMC_M2

GO:0051252	0.23	0.80	198	2654	regulation of RNA metabolic process	BP	1	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,CAMK1,ZFP36,SAMD4B,KAT2B,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,NUPR1,SHC1,PBXIP1,KANK2,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,OAS2,NFIA,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,AHNAK2,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0042733	0.23	0.89	5	47	embryonic digit morphogenesis	BP	1	GLI3,BAX,SFRP2,LRP4,BMP4	cyan	VSMC_M2
GO:0051646	0.23	0.89	5	46	mitochondrion localization	BP	1	MAP1S,HDAC6,BRAT1,RHOT2,HSBP1	cyan	VSMC_M2
GO:0043525	0.23	0.89	5	46	positive regulation of neuron apoptotic process	BP	1	BAX,GRN,CASP9,TP53,NUPR1	cyan	VSMC_M2
GO:0021766	0.23	0.88	6	59	hippocampus development	BP	1	GLI3,TMEM108,BBS2,LEF1,PPP1R9B,PTPRS	cyan	VSMC_M2
GO:0010712	0.23	0.90	4	34	regulation of collagen metabolic process	BP	1	VIM,BMP4,ARRB2,PDGFRB	cyan	VSMC_M2
GO:0032368	0.23	0.87	9	95	regulation of lipid transport	BP	1	EEPD1,APOE,PRKCD,NFKB1,FURIN,ERFE,NFKBIA,LINC02210-CRHR1,ABCA2	cyan	VSMC_M2
GO:1905332	0.23	0.90	4	34	positive regulation of morphogenesis of an epithelium	BP	1	WNT2B,BMP4,AR,ABL1	cyan	VSMC_M2
GO:0003205	0.23	0.85	12	135	cardiac chamber development	BP	1	ZFPM2,NRP1,SFRP2,CPE,HEG1,BMP4,SLIT2,TP53,NPRL3,FOXC2,GATA4,ZFPM1	cyan	VSMC_M2
GO:0034109	0.23	0.88	7	71	homotypic cell-cell adhesion	BP	1	PRKCD,XG,FIBP,CTNNA3,JUP,SERPINE2,PLPP3	cyan	VSMC_M2
GO:0043616	0.23	0.90	4	35	keratinocyte proliferation	BP	1	PTPRK,KLF9,ZFP36,ZFP36L1	cyan	VSMC_M2
GO:0030833	0.23	0.85	13	145	regulation of actin filament polymerization	BP	1	ARHGAP18,GSN,BIN1,PRKCD,C15orf62,CTTN,SSH3,ARPC5,ADD1,CAPZB,ALOX15,SLIT2,FLII	cyan	VSMC_M2
GO:1903706	0.23	0.83	22	258	regulation of hemopoiesis	BP	1	IRF1,MEIS1,GLI3,LRRC17,TMEM176B,PNP,ZFP36,RARG,TLR3,STAT1,LEF1,FES,NFKBIA,B2M,BMP4,ERBB2,ZFP36L1,ISG15,ABL1,IL34,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:1903052	0.23	0.86	11	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	RNF144A,NOP53,MAGEF1,GABARAP,UBQLN2,GBA,NUPR1,DVL1,ELOB,AXIN1,CBFA2T3	cyan	VSMC_M2
GO:0051651	0.23	0.85	14	163	maintenance of location in cell	BP	1	OS9,GSN,BAX,APOE,GAA,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0034394	0.23	0.88	6	59	protein localization to cell surface	BP	1	PTPRK,GGA1,SNX33,ABCA2,STX3,RAB11B	cyan	VSMC_M2
GO:0043666	0.23	0.89	5	47	regulation of phosphoprotein phosphatase activity	BP	1	PPP6R2,GNAI2,PPP1R9B,PDGFRB,CALM3	cyan	VSMC_M2
GO:0045596	0.23	0.82	39	489	negative regulation of cell differentiation	BP	1	CTDP1,ZADH2,ZFPM2,IRF1,APPL2,EFEMP1,MEIS1,GLI3,NRP1,LRRC17,TMEM176B,ZFP36,RARG,IGF1,TLR3,EFNA5,SFRP2,WWTR1,LRP4,STAT1,SEMA3B,RGMA,SEMA4B,SEMA6C,NFKBIA,LTBP3,B2M,DPF2,ADAMTS7,HDAC5,BMP4,ERBB2,ZFP36L1,TP53,TMEM98,PTPRS,NELFB,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0006497	0.23	0.87	8	81	protein lipidation	BP	1	ATG7,CLIP3,PORCN,WDR45,GBA,ZDHHC9,PIGQ,NMT2	cyan	VSMC_M2
GO:1902622	0.23	0.90	4	34	regulation of neutrophil migration	BP	1	RHOG,TIRAP,XG,SLIT2	cyan	VSMC_M2
GO:0006812	0.23	0.81	62	796	cation transport	BP	1	TRPM3,ATP10D,KCNQ5,SLC44A1,SLC17A7,STOM,BAX,UQCRH,BIN1,ABCB8,SLC6A9,EHD3,SLC4A9,SLC15A4,SLC7A2,ATP4A,SCN1B,SNTA1,SLC38A7,CACNB3,PLCG1,ARHGAP1,GNAO1,SLC5A3,CRACR2B,CHRNA7,CAPN3,CACNA2D2,TPCN2,GNAI2,ANXA9,TCN2,LINC02210-CRHR1,B2M,KCND3,ORAI2,ADORA2A,CAPN1,HOMER3,WNK4,CHRNE,ARRB2,SERPINE2,PRKACA,MLLT6,TMEM175,ORAI3,SLC44A2,ATOX1,PDGFRB,MCOLN1,PIEZO2,MFSD12,ABL1,ATP6V0D1,SLC8A3,CBARP,KCND2,PML,CALM3,CLIC2,RAB11B	cyan	VSMC_M2
GO:0048704	0.23	0.87	8	83	embryonic skeletal system morphogenesis	BP	1	GLI3,BMP4,PCGF2,HOXB1,HOXB2,HOXB4,MED12,FOXC2	cyan	VSMC_M2
GO:0006814	0.23	0.85	14	161	sodium ion transport	BP	1	SLC17A7,STOM,SLC6A9,SLC4A9,ATP4A,SCN1B,SNTA1,SLC38A7,SLC5A3,TPCN2,WNK4,SERPINE2,MLLT6,SLC8A3	cyan	VSMC_M2
GO:1902108	0.23	0.90	4	34	regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	BAX,TP53,RHOT2,ZNF205	cyan	VSMC_M2
GO:0019722	0.24	0.85	13	147	calcium-mediated signaling	BP	1	ACKR4,IGF1,CAMKK2,PLCG1,TPCN2,ADGRB2,HOMER3,PRKACA,PDK2,PPP1R9B,MCOLN1,CALM3,CLIC2	cyan	VSMC_M2
GO:0001658	0.24	0.89	5	47	branching involved in ureteric bud morphogenesis	BP	1	TCF21,GLI3,WT1,WNT2B,BMP4	cyan	VSMC_M2
GO:0001755	0.24	0.89	5	47	neural crest cell migration	BP	1	NRP1,SEMA3B,SEMA4B,SEMA6C,BMP4	cyan	VSMC_M2
GO:0035794	0.24	0.90	4	34	positive regulation of mitochondrial membrane permeability	BP	1	BAX,TP53,RHOT2,ZNF205	cyan	VSMC_M2
GO:0006970	0.24	0.87	7	71	response to osmotic stress	BP	1	BAX,TLR3,CAPN3,TSC22D4,ZFP36L1,TP53,SERPINB6	cyan	VSMC_M2
GO:0006937	0.24	0.85	11	121	regulation of muscle contraction	BP	1	BIN1,EHD3,HSPB6,CTTN,CTNNA3,JUP,PRKACA,SLC8A3,GATA4,CALM3,CLIC2	cyan	VSMC_M2
GO:0021872	0.24	0.90	4	35	forebrain generation of neurons	BP	1	GLI3,NRP1,LEF1,B2M	cyan	VSMC_M2
GO:2000181	0.24	0.87	8	83	negative regulation of blood vessel morphogenesis	BP	1	HGS,ANGPT4,STAT1,ADGRB2,EPHA2,EPN2,SERPINF1,PML	cyan	VSMC_M2

GO:0098771	0.24	0.81	40	502	inorganic ion homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,BAX,APOE,SLC6A9,SLC4A9,ACKR4,ATP4A,HEXB,CACNB3,TGM2,PLCG1,EXT2,CHRNA7,CAPN3,TPCN2,GNAI2,SV2A,ERFE,CYB561,B2M,ADORA2A,GRN,PRKACA,MLLT6,TMEM175,PDK2,GRIA1,NEO1,MCOLN1,ABL1,ATP6V0D1,CNNM3,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0061515	0.24	0.88	6	59	myeloid cell development	BP	1	MEIS1,SRC,MAEA,SIGLEC15,ZBTB7A,ZFPM1	cyan	VSMC_M2
GO:0030900	0.24	0.83	23	282	forebrain development	BP	1	NFIB,GLI3,NRP1,BAX,DCLK1,TMEM108,SRC,BBS2,GNAO1,PHACTR1,LEF1,TACC2,KIF1A,ARPC5,PTCHD1,B2M,WNT2B,CCDC141,BMP4,SLIT2,PPP1R9B,PTPRS,SLC8A3	cyan	VSMC_M2
GO:0014070	0.24	0.80	55	703	response to organic cyclic compound	BP	1	TCF21,FLOT1,EHMT2,DAXX,FBXO32,TRERF1,KLF9,IRF3,ATG7,ZFP36,FOLR2,RFTN1,SMPD1,TLR3,WT1,GGT7,SRC,TGM2,GNAO1,STAT1,FIBIN,NFKB1,MN1,ADCY1,FES,VPS11,LMO3,PHEX,NFKBIA,ADORA2A,ACAT1,BMP4,HDAC6,PQBP1,ARRB2,JUP,CASP9,PRKACA,ZFP36L1,SLIT2,AR,GBA,PPP1R9B,KANK2,PDGFRB,EEF2,ABL1,ABCA2,SLC8A3,SERPINF1,ZBTB7A,CALM3,RNLS,RGS8,EN1	cyan	VSMC_M2
GO:0055067	0.24	0.85	10	108	monovalent inorganic cation homeostasis	BP	1	SLC4A9,ATP4A,EXT2,GNAI2,ADORA2A,GRN,MLLT6,TMEM175,PDK2,ATP6V0D1	cyan	VSMC_M2
GO:0007032	0.24	0.87	7	71	endosome organization	BP	1	HGS,CHMP4B,CHMP3,EXOC8,VPS11,SNX33,IST1	cyan	VSMC_M2
GO:0016575	0.24	0.87	7	71	histone deacetylation	BP	1	TRERF1,TBL1Y,HDAC5,HDAC6,TP53,ELMSAN1,MTA1	cyan	VSMC_M2
GO:0014910	0.24	0.88	6	60	regulation of smooth muscle cell migration	BP	1	NRP1,IGF1,NDRG4,SRC,SLIT2,PDGFRB	cyan	VSMC_M2
GO:0042220	0.24	0.90	4	35	response to cocaine	BP	1	EHMT2,SMPD1,TGM2,EN1	cyan	VSMC_M2
GO:0051893	0.24	0.88	6	60	regulation of focal adhesion assembly	BP	1	NRP1,EFNA5,EPHA3,SRC,ABL1,SDC4	cyan	VSMC_M2
GO:0090109	0.24	0.88	6	60	regulation of cell-substrate junction assembly	BP	1	NRP1,EFNA5,EPHA3,SRC,ABL1,SDC4	cyan	VSMC_M2
GO:0042446	0.24	0.89	5	47	hormone biosynthetic process	BP	1	NFKB1,CLCN2,STARD3,H6PD,CHST8	cyan	VSMC_M2
GO:0048705	0.24	0.83	16	186	skeletal system morphogenesis	BP	1	GLI3,FGFR1,RARG,SFRP2,MMP2,EXT2,SOX5,LTBP3,BMP4,PCGF2,HOXB1,HOXB2,HOXB4,MED12,ACP5,FOXC2	cyan	VSMC_M2
GO:0043491	0.24	0.84	13	147	protein kinase B signaling	BP	1	RRAS,NOP53,MEIS3,FGFR1,IGF1,SRC,SFRP5,ARRB2,EPHA2,ZFP36L1,NTRK1,TSC2,GATA4	cyan	VSMC_M2
GO:0030195	0.24	0.90	4	35	negative regulation of blood coagulation	BP	1	APOE,SERPING1,PRKCD,SERPINE2	cyan	VSMC_M2
GO:0009628	0.24	0.79	69	891	response to abiotic stimulus	BP	1	AKAP12,IRF1,DAXX,PTPRK,HMOX1,TRPM3,APPL2,GSN,RHOB,BAX,NOP53,TRIM13,BCL3,ATG7,SLITRK6,SMPD1,ANGPT4,IGF1,TLR3,SFRP2,NDRG4,PRKCD,SRC,CACNB3,MMP2,STAT1,CHRNA7,CAPN3,NFKB1,PTGIS,VEGFD,NFKBIA,TMEM161A,TSC22D4,VEGFB,NR2F6,DNAJB6,ARRB2,JUP,SERPINE2,CASP9,BRAT1,PRKACA,ZFP36L1,NTRK1,CLCN6,TP53,GBA,ADAM15,PDGFRB,MCOLN1,MTA1,PIEZO2,NPHP4,CBFA2T3,HSBP1,SLC2A8,ATP6V0D1,SLC8A3,SERPINF1,KCND2,NMT2,LRRN4,PML,SERPINB6,EEF1A2,GATA4,BMF,RAB11B	cyan	VSMC_M2
GO:0010558	0.24	0.79	88	1150	negative regulation of macromolecule biosynthetic process	BP	1	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,AP2A1,IRF3,NOP53,BCL3,ATG7,ZFP36,SAMD4B,APBB1,LMO1,RARG,WT1,PATL1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,CAPN3,NFKB1,HIST1H1C,LEF1,TBL1Y,NELFCD,RFX5,MAGEF1,MOV10,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,ZFP36L1,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,KANK2,MTA1,MOSPD1,GLIS2,E4F1,NELFB,TCF3,SBNO2,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,MEX3D,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,ZFPM1,EN1	cyan	VSMC_M2
GO:0031641	0.24	0.89	4	36	regulation of myelination	BP	1	RARG,TPPP,MYRF,TMEM98	cyan	VSMC_M2
GO:0033627	0.25	0.87	6	60	cell adhesion mediated by integrin	BP	1	ITGB8,ITGBL1,SFRP2,EPHA2,FOXC2,PLPP3	cyan	VSMC_M2
GO:0030041	0.25	0.84	14	160	actin filament polymerization	BP	1	ARHGAP18,COBL,GSN,BIN1,PRKCD,C15orf62,CTTN,SSH3,ARPC5,ADD1,CAPZB,ALOX15,SLIT2,FLII	cyan	VSMC_M2
GO:0120192	0.25	0.88	5	48	tight junction assembly	BP	1	AFDN,TJP1,EPHA2,PRKACA,NPHP4	cyan	VSMC_M2
GO:0007588	0.25	0.89	4	36	excretion	BP	1	HMOX1,GNAI2,ADORA2A,MLLT6	cyan	VSMC_M2
GO:1901343	0.25	0.86	8	84	negative regulation of vasculature development	BP	1	HGS,ANGPT4,STAT1,ADGRB2,EPHA2,EPN2,SERPINF1,PML	cyan	VSMC_M2
GO:0046474	0.25	0.83	16	185	glycerophospholipid biosynthetic process	BP	1	CHKB,SLC44A1,SOCS3,GPAT4,LPCAT4,PLSCR1,PTDSS1,PIK3C2B,IP6K1,PLD2,ALOX15,PLSCR3,SLC44A2,PIGQ,INPP5E,LCAT	cyan	VSMC_M2
GO:1903363	0.25	0.87	6	60	negative regulation of cellular protein catabolic process	BP	1	EIF3H,NOP53,ATRAID,FURIN,GIPC1,PML	cyan	VSMC_M2
GO:0021954	0.25	0.87	6	61	central nervous system neuron development	BP	1	NFIB,NRP1,DCLK1,SCN1B,B4GALT5,SLIT2	cyan	VSMC_M2
GO:0001505	0.25	0.84	13	147	regulation of neurotransmitter levels	BP	1	MOXD1,FLOT1,CADPS2,SV2A,ADCY1,ADORA2A,DAGLA,GIPC1,CPLX2,DVL1,CALM3,GCHFR,STX3	cyan	VSMC_M2
GO:0032436	0.25	0.86	8	83	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	RNF144A,NOP53,GABARAP,UBQLN2,GBA,DVL1,ELOB,CBFA2T3	cyan	VSMC_M2
GO:2000243	0.25	0.88	5	47	positive regulation of reproductive process	BP	1	ZFPM2,PLB1,WT1,SRC,AR	cyan	VSMC_M2
GO:1905954	0.25	0.86	7	73	positive regulation of lipid localization	BP	1	EEPD1,APOE,PRKCD,IKBKE,NFKB1,ERFE,NFKBIA	cyan	VSMC_M2
GO:0032609	0.25	0.87	6	59	interferon-gamma production	BP	1	BCL3,TLR3,IL27RA,ISG15,ABL1,ZFPM1	cyan	VSMC_M2
GO:0032649	0.25	0.87	6	59	regulation of interferon-gamma production	BP	1	BCL3,TLR3,IL27RA,ISG15,ABL1,ZFPM1	cyan	VSMC_M2
GO:0034113	0.25	0.89	4	36	heterotypic cell-cell adhesion	BP	1	FLOT1,CTNNA3,JUP,ALOX15	cyan	VSMC_M2
GO:0050921	0.25	0.84	10	109	positive regulation of chemotaxis	BP	1	PLA2G7,NRP1,FGFR1,TIRAP,VEGFD,VEGFB,SLIT2,PDGFRB,IL34,STX3	cyan	VSMC_M2
GO:0006821	0.25	0.87	6	60	chloride transport	BP	1	GLRB,CLCN2,WNK4,CLCN6,CLIC2,CLIC3	cyan	VSMC_M2
GO:0030501	0.25	0.89	4	37	positive regulation of bone mineralization	BP	1	ATRAID,PKDCC,BMP4,ISG15	cyan	VSMC_M2
GO:0099172	0.25	0.89	4	37	presynapse organization	BP	1	SLITRK6,EFNB2,LRP4,DVL1	cyan	VSMC_M2
GO:0098609	0.25	0.80	46	592	cell-cell adhesion	BP	1	FLOT1,PLXNB2,IRF1,AFDN,GCNT1,GPNMB,GLI3,PNP,PAK4,IGF1,EFNA5,PRKCD,SRC,CD81,TJP1,XG,LEF1,ANXA9,GATA5,FIBP,CTNNA3,B2M,ADORA2A,ASTN1,BMP4,DLG5,DNAJB6,JUP,ALOX15,SERPINE2,ERBB2,ZFP36L1,IL27RA,SHC1,ICAM4,PTPRS,TNFRSF14,NPHP4,CLSTN1,ABL1,CERCAM,CNN3,CD55,PLPP3,LRRC7,SDC4	cyan	VSMC_M2
GO:0071559	0.25	0.82	17	205	response to transforming growth factor beta	BP	1	PTPRK,APPL2,ITGB8,LTBP4,SRC,SOX5,FURIN,BCL9L,FAM89B,LTBP3,CLEC3B,ARRB2,GIPC1,ZFP36L1,TP53,ZBTB7A,PML	cyan	VSMC_M2
GO:0046209	0.25	0.87	6	60	nitric oxide metabolic process	BP	1	DDAH2,CYB5R3,PTGIS,TMEM106A,ACP5,GCHFR	cyan	VSMC_M2
GO:0048483	0.25	0.89	4	37	autonomic nervous system development	BP	1	NRP1,NTRK1,HOXB1,HOXB2	cyan	VSMC_M2
GO:0005996	0.25	0.82	17	199	monosaccharide metabolic process	BP	1	GAA,KAT2B,DCXR,IGF1,MAN2A1,SRC,NISCH,SLC45A3,ERFE,FUCA1,G6PC3,BRAT1,TP53,PDK2,MAN2C1,FAM3A,H6PD	cyan	VSMC_M2

GO:1990778	0.26	0.81	23	279	protein localization to cell periphery	BP	1	FLOT1,AFDN,GGA1,EHD3,RHOG,PKDCC,CLIP3,EPHA3,CACNB3,BBS2,SYS1,CD81,TMBIM1,JUP,EPHA2,AKAP5,AR,PPP1R9B,SLC9A3R2,CLSTN1,ABCA2,GRASP,STX3	cyan	VSMC_M2
GO:0030835	0.26	0.89	4	38	negative regulation of actin filament depolymerization	BP	1	GSN,ADD1,CAPZB,FLII	cyan	VSMC_M2
GO:0006826	0.26	0.87	5	48	iron ion transport	BP	1	SLC6A9,ARHGAP1,B2M,MCOLN1,RAB11B	cyan	VSMC_M2
GO:0033674	0.26	0.80	30	373	positive regulation of kinase activity	BP	1	DAXX,CARD10,FZD4,CAB39L,CAMK1,FGFR1,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,PRKCD,EPHA3,SRC,CD81,TIRAP,EPHA2,ERBB2,NTRK1,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,AXIN1,ABL1,IL34,EEF1A2,CALM3,SDC4	cyan	VSMC_M2
GO:2000112	0.26	0.77	209	2822	regulation of cellular macromolecule biosynthetic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,TCF21,FLOT1,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,ACO1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,SLC6A9,ATG7,CAMK1,ZFP36,SAMD4B,KAT2B,EIF3K,RHOG,TRIM21,APBB1,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,GBA,SLC51B,NUPR1,SHC1,PBXIP1,KANK2,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,EEF2,GLIS2,DVL1,AGRN,E4F1,DPH7,NELFB,TCF3,SBNO2,EDF1,INPP5E,AXIN1,RERE,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0045620	0.26	0.89	4	36	negative regulation of lymphocyte differentiation	BP	1	IRF1,GLI3,BMP4,ERBB2	cyan	VSMC_M2
GO:0045576	0.26	0.87	5	48	mast cell activation	BP	1	HMOX1,PLSCR1,FES,CPLX2,PTGDS	cyan	VSMC_M2
GO:0071695	0.26	0.82	14	163	anatomical structure maturation	BP	1	RPS6KA2,MTCH1,GPAT4,IGF1,MMP2,TUSC2,B4GALT5,REC8,MAEA,PRKACA,GBA,AGRN,RERE,ZBTB7A	cyan	VSMC_M2
GO:1905314	0.26	0.89	4	37	semi-lunar valve development	BP	1	GATA5,BMP4,SLIT2,GATA4	cyan	VSMC_M2
GO:0009612	0.26	0.82	15	176	response to mechanical stimulus	BP	1	IRF1,GSN,SLITRK6,TLR3,SRC,CACNB3,STAT1,NFKB1,NFKBIA,JUP,SERPINE2,NTRK1,CLCN6,PIEZO2,GATA4	cyan	VSMC_M2
GO:1900047	0.26	0.89	4	36	negative regulation of hemostasis	BP	1	APOE,SERPING1,PRKCD,SERPINE2	cyan	VSMC_M2
GO:0031952	0.26	0.88	4	37	regulation of protein autophosphorylation	BP	1	GPNMB,SRC,GFRA2,CALM3	cyan	VSMC_M2
GO:0048813	0.26	0.83	11	126	dendrite morphogenesis	BP	1	NRP1,DCLK1,LZTS3,LRP4,PHACTR1,CHRNA7,KIF1A,HDAC6,PQBP1,DVL1,RERE	cyan	VSMC_M2
GO:0045022	0.26	0.88	4	37	early endosome to late endosome transport	BP	1	CHMP3,SRC,VPS11,WDR81	cyan	VSMC_M2
GO:0060996	0.26	0.85	8	87	dendritic spine development	BP	1	APOE,CAMK1,LZTS3,KIF1A,DLG5,HDAC6,PTPRS,DVL1	cyan	VSMC_M2
GO:0043009	0.26	0.79	41	522	chordate embryonic development	BP	1	PLXNB2,ZFPM2,COBL,GLI3,SOCS3,FGFR1,RARG,IGF1,MAN2A1,SFRP2,PLCG1,RGMA,LEF1,FURIN,HEG1,VANGL2,PLCD3,BMP4,CC2D2A,DNAJB6,FKBP10,EPHA2,PRKACA,ZFP36L1,PCGF2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,C6,CPT2,DVL1,TSC2,RPL13,FOXC2,ABL1,JUNB,SDC4,EN1	cyan	VSMC_M2
GO:0002460	0.26	0.82	15	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	STAT6,BCL3,RFTN1,SLC15A4,SERPING1,PRKCD,CD81,LEF1,B2M,C1R,C1S,IL27RA,TMEM98,C6,CD55	cyan	VSMC_M2
GO:0014075	0.26	0.88	4	36	response to amine	BP	1	ADORA2A,PPP1R9B,CALM3,RGS10	cyan	VSMC_M2
GO:0001954	0.26	0.87	5	49	positive regulation of cell-matrix adhesion	BP	1	RRAS,NRP1,JUP,ABL1,SDC4	cyan	VSMC_M2
GO:0002429	0.26	0.82	13	148	immune response-activating cell surface receptor signaling pathway	BP	1	APPL2,BAX,RFTN1,RBCK1,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,CD81,PLD2,PHPT1,ABL1	cyan	VSMC_M2
GO:0002757	0.26	0.82	13	148	immune response-activating signal transduction	BP	1	APPL2,BAX,RFTN1,RBCK1,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,CD81,PLD2,PHPT1,ABL1	cyan	VSMC_M2
GO:0010562	0.26	0.78	52	669	positive regulation of phosphorus metabolic process	BP	1	FLOT1,DAXX,CARD10,GPNMB,NRP1,FZD4,CAB39L,CAMK1,FGFR1,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,PRKCD,EPHA3,SRC,LRP4,MOB2,CD81,CHRNA7,TIRAP,VEGFD,VEGFB,BMP4,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,NTRK1,AR,TP53,GBA,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,DVL1,TNFRSF14,AXIN1,ABL1,IL34,EEF1A2,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0045937	0.26	0.78	52	669	positive regulation of phosphate metabolic process	BP	1	FLOT1,DAXX,CARD10,GPNMB,NRP1,FZD4,CAB39L,CAMK1,FGFR1,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,CAMKK2,SFRP2,PRKCD,EPHA3,SRC,LRP4,MOB2,CD81,CHRNA7,TIRAP,VEGFD,VEGFB,BMP4,HDAC6,ARRB2,EPHA2,ERBB2,BRAT1,NTRK1,AR,TP53,GBA,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,DVL1,TNFRSF14,AXIN1,ABL1,IL34,EEF1A2,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0090092	0.26	0.82	16	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	KIAA1324L,LTBP4,SFRP2,SFRP5,PCSK6,RGMA,BCL9L,FAM89B,BMP4,NBL1,GIPC1,TP53,NEO1,ABL1,ZBTB7A,GATA4	cyan	VSMC_M2
GO:0035601	0.26	0.84	9	99	protein deacylation	BP	1	TRERF1,NDN,TPPP,TBL1Y,HDAC5,HDAC6,TP53,ELMSAN1,MTA1	cyan	VSMC_M2
GO:0051048	0.26	0.83	10	110	negative regulation of secretion	BP	1	HMOX1,APOE,RHBDF2,RAB11FIP1,GNAI2,HADH,WNK4,RAB11FIP3,RHBDF1,CBARP	cyan	VSMC_M2
GO:0030500	0.26	0.86	6	62	regulation of bone mineralization	BP	1	ATRAID,PKDCC,ECM1,LTBP3,BMP4,ISG15	cyan	VSMC_M2
GO:0051588	0.26	0.85	7	73	regulation of neurotransmitter transport	BP	1	FLOT1,ADCY1,ADORA2A,GIPC1,CPLX2,DVL1,CALM3	cyan	VSMC_M2
GO:0007162	0.27	0.81	18	215	negative regulation of cell adhesion	BP	1	PLXNB2,IRF1,TGFBI,GPNMB,GLI3,FZD4,EFNA5,PRKCD,SRC,ADORA2A,BMP4,DLG5,SERPINE2,ERBB2,ADAM15,TNFRSF14,ABL1,SDC4	cyan	VSMC_M2

GO:0046777	0.27	0.81	17	204	protein autophosphorylation	BP	1	GPNMB,FGFR1,MAP3K12,CAMKK2,SRC,GFRA2,GRK5,FES,STK25,BCR,ERBB2,PRKACA,NTRK1,ULK3,PDGFRB,ABL1,CALM3	cyan	VSMC_M2
GO:0051702	0.27	0.86	6	61	biological process involved in interaction with symbiont	BP	1	CTDP1,LRRC19,STOM,APOE,TUSC2,LEF1	cyan	VSMC_M2
GO:2000113	0.27	0.77	87	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	STAT6,TCF21,EHMT2,ZFPM2,IRF1,DAXX,PTPRK,TLE1,NFIB,TRERF1,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,BCL3,ATG7,ZFP36,SAMD4B,APBB1,LMO1,RARG,WT1,PATL1,TSHZ3,POU6F1,SFRP2,WWTR1,SRC,ZHX3,RIOX2,FOXF2,SORBS3,STAT1,NDN,CAPN3,NFKB1,HIST1H1C,LEF1,TBL1Y,NELFCD,RFX5,MAGEF1,MOV10,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,ZNF503,NR2F6,HDAC6,DNAJB6,ZBTB17,ZFP36L1,PCGF2,AR,TP53,KAT8,HOXB4,ELMSAN1,SHC1,PBXIP1,KANK2,MTA1,MOSPD1,GLIS2,E4F1,NELFB,TCF3,SBNO2,INPP5E,RERE,TCF25,CBFA2T3,FOXC2,HSBP1,MEX3D,ZNF205,HEXIM1,ZBTB7A,ATN1,PML,ZFPM1,EN1	cyan	VSMC_M2
GO:2001057	0.27	0.86	6	61	reactive nitrogen species metabolic process	BP	1	DDAH2,CYB5R3,PTGIS,TMEM106A,ACP5,GCHFR	cyan	VSMC_M2
GO:0006636	0.27	0.88	4	36	unsaturated fatty acid biosynthetic process	BP	1	PTGIS,ALOX15,ABCD1,PTGDS	cyan	VSMC_M2
GO:0002200	0.27	0.86	6	61	somatic diversification of immune receptors	BP	1	STAT6,SLC15A4,LEF1,IL27RA,ADAR,TCF3	cyan	VSMC_M2
GO:0140115	0.27	0.87	5	49	export across plasma membrane	BP	1	ATP4A,KCND3,ABCC1,SLC8A3,CALM3	cyan	VSMC_M2
GO:0003179	0.27	0.87	5	50	heart valve morphogenesis	BP	1	GATA5,BMP4,SLIT2,GATA4,ZFPM1	cyan	VSMC_M2
GO:0060976	0.27	0.88	4	39	coronary vasculature development	BP	1	NRP1,VEGFB,BMP4,PDGFRB	cyan	VSMC_M2
GO:0033013	0.27	0.87	5	49	tetrapyrrole metabolic process	BP	1	IBA57,HMOX1,UROD,SLC6A9,ABCC1	cyan	VSMC_M2
GO:1905710	0.27	0.88	4	36	positive regulation of membrane permeability	BP	1	BAX,TP53,RHOT2,ZNF205	cyan	VSMC_M2
GO:0061028	0.27	0.88	4	38	establishment of endothelial barrier	BP	1	AFDN,TJP1,ADD1,PTPRS	cyan	VSMC_M2
GO:0045017	0.27	0.81	18	214	glycerolipid biosynthetic process	BP	1	CHKB,SLC44A1,SOCS3,GPAT4,LPCAT4,PLSCR1,PTDSS1,PNPLA2,PIK3C2B,IP6K1,PLD2,ALOX15,PLSCR3,SLC44A2,PIGQ,INPP5E,LCAT,DGAT1	cyan	VSMC_M2
GO:0043001	0.27	0.88	4	37	Golgi to plasma membrane protein transport	BP	1	GGA1,PKDCC,BBS2,SYS1	cyan	VSMC_M2
GO:0051896	0.27	0.83	11	125	regulation of protein kinase B signaling	BP	1	RRAS,NOP53,MEIS3,FGFR1,SRC,SFRP5,ARRB2,EPHA2,NTRK1,TSC2,GATA4	cyan	VSMC_M2
GO:0051155	0.27	0.88	4	37	positive regulation of striated muscle cell differentiation	BP	1	EFNB2,IGF1,BMP4,ARRB2	cyan	VSMC_M2
GO:1902930	0.27	0.88	4	37	regulation of alcohol biosynthetic process	BP	1	APOE,NFKB1,CLCN2,H6PD	cyan	VSMC_M2
GO:0003300	0.27	0.85	7	75	cardiac muscle hypertrophy	BP	1	CTDP1,MLIP,KLF15,IGF1,GATA5,GATA4,CDK9	cyan	VSMC_M2
GO:0045744	0.27	0.88	4	37	negative regulation of G protein-coupled receptor signaling pathway	BP	1	ARRDC3,GNAI2,ARRB2,UBQLN2	cyan	VSMC_M2
GO:0030042	0.27	0.86	5	51	actin filament depolymerization	BP	1	GSN,ADD1,CAPZB,PPP1R9B,FLII	cyan	VSMC_M2
GO:2000378	0.27	0.88	4	37	negative regulation of reactive oxygen species metabolic process	BP	1	HDAC6,TP53,ACP5,ABCD1	cyan	VSMC_M2
GO:1905953	0.27	0.88	4	37	negative regulation of lipid localization	BP	1	PNPLA2,NFKB1,NFKBIA,ABCA2	cyan	VSMC_M2
GO:2000177	0.27	0.85	6	62	regulation of neural precursor cell proliferation	BP	1	APPL2,GLI3,GNAI2,ELL3,TP53,SLC16A2	cyan	VSMC_M2
GO:0033993	0.27	0.77	51	657	response to lipid	BP	1	TCF21,AKAP12,DAXX,FBXO32,TRERF1,KLF9,IRF3,FZD4,VIM,ZFP36,RARG,GGT7,EPHA3,SRC,BPI,FIBIN,TIRAP,NFKB1,MN1,ADCY1,FES,VPS11,LMO3,PHEX,NFKBIA,TMEM161A,BMP4,HDAC6,CASP9,PLSCR3,ZFP36L1,SLIT2,AR,GBA,PPP1R9B,ADAM15,ACP5,KANK2,PDGFRB,EEF2,SBNO2,SLC10A3,ABL1,ABCA2,SERPINF1,ZBTB7A,CD55,GATA4,CALM3,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0009166	0.27	0.85	6	61	nucleotide catabolic process	BP	1	PNP,NEIL2,ACAT1,NUDT13,ABCD1,DPYD	cyan	VSMC_M2
GO:0038061	0.27	0.83	9	99	NIK/NF-kappaB signaling	BP	1	CARD10,LRRC19,BCL3,RBCK1,TLR3,IKBKE,TIRAP,NFKBIA,TRAF4	cyan	VSMC_M2
GO:0008643	0.27	0.83	10	112	carbohydrate transport	BP	1	APPL2,KLF15,CLIP3,IGF1,SLC5A3,SLC45A3,ERFE,RNASEL,MFSD12,SLC2A8	cyan	VSMC_M2
GO:0045682	0.27	0.86	5	50	regulation of epidermis development	BP	1	KIAA1324L,ZFP36,BMP4,RARRES3,ZFP36L1	cyan	VSMC_M2
GO:0046660	0.27	0.84	8	88	female sex differentiation	BP	1	ZFPM2,BAX,FZD4,WT1,SRC,ARRB2,SLIT2,NUPR1	cyan	VSMC_M2
GO:1903828	0.28	0.83	9	99	negative regulation of cellular protein localization	BP	1	OS9,DCLK1,PKDCC,TP53INP2,LZTS2,TMBIM1,SNX33,TMEM98,INPP5E	cyan	VSMC_M2
GO:0045069	0.28	0.85	6	62	regulation of viral genome replication	BP	1	PLSCR1,RNASEL,ADAR,ISG15,OAS2,BST2	cyan	VSMC_M2
GO:0001909	0.28	0.85	6	61	leukocyte mediated cytotoxicity	BP	1	ULBP2,LAMP1,TUSC2,B2M,ARRB2,PLEKHM2	cyan	VSMC_M2
GO:0032784	0.28	0.86	5	49	regulation of DNA-templated transcription, elongation	BP	1	NELFCD,ELL3,TCEA2,NELFB,HEXIM1	cyan	VSMC_M2
GO:0002703	0.28	0.82	12	136	regulation of leukocyte mediated immunity	BP	1	STAT6,HMOX1,LAMP1,SLC15A4,TLR3,CD81,FES,B2M,ARRB2,IL27RA,CD55,BST2	cyan	VSMC_M2
GO:0021543	0.28	0.82	11	127	pallium development	BP	1	GLI3,BAX,TMEM108,BBS2,PHACTR1,LEF1,TACC2,CCDC141,SLIT2,PPP1R9B,PTPRS	cyan	VSMC_M2
GO:0046173	0.28	0.86	5	49	polyol biosynthetic process	BP	1	IP6K1,PCBD1,QDPR,GBA,ABCA2	cyan	VSMC_M2
GO:0061053	0.28	0.85	6	63	somite development	BP	1	COBL,SFRP2,LEF1,TP53,MED12,FOXC2	cyan	VSMC_M2
GO:0006820	0.28	0.79	26	319	anion transport	BP	1	SLC17A7,SLC6A9,SLC26A11,SLC4A9,FOLR2,SLC15A4,SLC7A2,SLC38A7,GLRB,SV2A,SLC16A9,CLCN2,ADORA2A,PSAP,WNK4,GIPC1,CLCN6,SLC51B,SLC16A2,ABCC1,MFSD12,SLC10A3,SLC2A8,CLIC2,CLIC3,RAB11B	cyan	VSMC_M2
GO:0009266	0.28	0.82	12	137	response to temperature stimulus	BP	1	DAXX,HMOX1,TRPM3,APPL2,IGF1,NFKBIA,NR2F6,DNAJB6,ARRB2,PRKACA,NTRK1,HSBP1	cyan	VSMC_M2
GO:0044264	0.28	0.84	7	75	cellular polysaccharide metabolic process	BP	1	STK40,GAA,IGF1,STBD1,EXT2,PHKG1,B4GALT5	cyan	VSMC_M2
GO:0002292	0.28	0.86	5	50	T cell differentiation involved in immune response	BP	1	STAT6,BCL3,LEF1,TMEM98,ZFPM1	cyan	VSMC_M2
GO:2001235	0.28	0.83	9	98	positive regulation of apoptotic signaling pathway	BP	1	BAX,RBCK1,PRKCD,ADORA2A,TP53,NUPR1,TRAF7,INCA1,PML	cyan	VSMC_M2
GO:0046907	0.28	0.76	95	1261	intracellular transport	BP	1	RAB5B,OS9,RABL2A,TBC1D22A,GGA1,APPL2,TBC1D2,TBC1D17,GLI3,AP2A1,STOM,RHOB,BAX,DENND2A,BIN1,APOE,BCL3,CAMK1,EHD3,CMTM6,HGS,TBC1D5,RFTN1,DCLK1,LAMP1,TMEM108,CLIP3,GNPTAB,REEP5,CHMP4B,CHMP3,EDEM2,ERGIC3,NDRG4,STBD1,PRKCD,SRC,CACNB3,ARHGAP1,SYS1,LZTS2,CTSA,CD81,AGFG1,CTTN,TPCN2,SGSM1,VPS11,KIF1A,FAM53B,TMEM50A,NFKBIA,M6PR,FYCO1,RPGR,HOMER3,BMP4,MAP1S,HDAC6,B3GAT3,JUP,AKAP5,GABARAP,GIPC1,ERBB2,PRKACA,TP53,ERGIC1,NPC2,SLC51B,SNX33,ZDHHC9,UBXN6,NAGPA,CPT2,WDR81,ABCD1,SGSM2,TSC2,RHOT2,RAB11FIP3,ENTR1,HSBP1,MON1B,ABCA2,RPS15,GAS1,RAB43,GRASP,PML,VPS26B,STX3,RAB11B,EMD,UBL5	cyan	VSMC_M2
GO:0120009	0.28	0.87	4	38	intermembrane lipid transfer	BP	1	APOE,OSBPL5,STARD3,NPC2	cyan	VSMC_M2

GO:0032984	0.28	0.80	16	195	protein-containing complex disassembly	BP	1	PYM1,GSN,CHMP3,FYCO1,ADD1,CAPZB,MAP1S,TECPR1,HDAC6,UBQLN4,GBA,PPP1R9B,MCOLN1,FLII,SH3GL1,IST1	cyan	VSMC_M2
GO:0015698	0.28	0.82	10	113	inorganic anion transport	BP	1	SLC17A7,SLC26A11,SLC4A9,GLRB,CLCN2,WNK4,CLCN6,ABCC1,CLIC2,CLIC3	cyan	VSMC_M2
GO:1903522	0.28	0.80	15	179	regulation of blood circulation	BP	1	BIN1,EHD3,GAA,SCN1B,SNTA1,GNAO1,CTNNA3,KCND3,JUP,PRKACA,SLC8A3,GATA4,CALM3,CLIC2,RNLS	cyan	VSMC_M2
GO:1903531	0.28	0.83	9	99	negative regulation of secretion by cell	BP	1	HMOX1,APOE,RHBDF2,RAB11FIP1,GNAI2,HADH,RAB11FIP3,RHBDF1,CBARP	cyan	VSMC_M2
GO:0050769	0.28	0.80	15	181	positive regulation of neurogenesis	BP	1	PLXNB2,GLI3,NRP1,BIN1,MAN2A1,TGM2,STK25,ELL3,RND2,SERPINE2,SLIT2,ASPA,IL34,IST1,SERPINF1	cyan	VSMC_M2
GO:0022409	0.28	0.80	15	176	positive regulation of cell-cell adhesion	BP	1	FLOT1,AFDN,GLI3,PNP,IGF1,SRC,CD81,TJP1,LEF1,B2M,ALOX15,IL27RA,TNFRSF14,CD55,PLPP3	cyan	VSMC_M2
GO:0097193	0.28	0.79	20	242	intrinsic apoptotic signaling pathway	BP	1	GRINA,HMOX1,BAX,BCL3,SFRP2,PRKCD,SRC,MAPK8IP1,IKBKE,STK25,ELL3,TMEM161A,EPHA2,CASP9,TP53BP2,TP53,PDK2,NUPR1,ABL1,PML	cyan	VSMC_M2
GO:0042177	0.28	0.83	9	101	negative regulation of protein catabolic process	BP	1	EIF3H,NOP53,ATRAID,TIMP2,CTSA,FURIN,SERPINE2,GIPC1,PML	cyan	VSMC_M2
GO:0002275	0.28	0.85	6	62	myeloid cell activation involved in immune response	BP	1	HMOX1,FES,GRN,CPLX2,PTGDS,SBNO2	cyan	VSMC_M2
GO:0035821	0.28	0.84	7	75	modulation of process of other organism	BP	1	CTDP1,GSDMD,LRRC19,STOM,APOE,ATG7,LEF1	cyan	VSMC_M2
GO:0060349	0.29	0.84	7	76	bone morphogenesis	BP	1	GLI3,RARG,SFRP2,EXT2,LTBP3,BMP4,ACP5	cyan	VSMC_M2
GO:0042180	0.29	0.81	13	150	cellular ketone metabolic process	BP	1	APPL2,COQ8B,COQ9,SLC45A3,ERFE,CLCN2,AIFM2,STARD3,UBIAD1,PDK2,ABCD1,HAGH,H6PD	cyan	VSMC_M2
GO:0043303	0.29	0.87	4	38	mast cell degranulation	BP	1	HMOX1,FES,CPLX2,PTGDS	cyan	VSMC_M2
GO:0032964	0.29	0.87	4	38	collagen biosynthetic process	BP	1	VIM,BMP4,ARRB2,PDGFRB	cyan	VSMC_M2
GO:0034332	0.29	0.87	4	39	adherens junction organization	BP	1	SRC,TJP1,ADD1,DLG5	cyan	VSMC_M2
GO:0006836	0.29	0.81	12	139	neurotransmitter transport	BP	1	FLOT1,CADPS2,SLC17A7,SLC6A9,SV2A,ADCY1,ADORA2A,GIPC1,CPLX2,DVL1,CALM3,STX3	cyan	VSMC_M2
GO:1904951	0.29	0.79	21	257	positive regulation of establishment of protein localization	BP	1	GLI3,STOM,CAMK1,APBB1,IGF1,EDEM2,PRKCD,SRC,CACNB3,CD81,VPS11,ADORA2A,B3GAT3,JUP,AKAP5,ERBB2,PRKACA,SLC51B,PHPT1,EMD,UBL5	cyan	VSMC_M2
GO:0042752	0.29	0.83	8	89	regulation of circadian rhythm	BP	1	ATG7,ADCY1,ADORA2A,NR2F6,TP53,MTA1,PTGDS,PML	cyan	VSMC_M2
GO:0070228	0.29	0.87	4	38	regulation of lymphocyte apoptotic process	BP	1	ST3GAL1,BAX,BMP4,TP53	cyan	VSMC_M2
GO:0010611	0.29	0.85	5	51	regulation of cardiac muscle hypertrophy	BP	1	CTDP1,MLIP,IGF1,GATA5,CDK9	cyan	VSMC_M2
GO:0010675	0.29	0.81	10	114	regulation of cellular carbohydrate metabolic process	BP	1	KAT2B,IGF1,SRC,SLC45A3,ERFE,TP53,PDK2,NUPR1,FAM3A,CBFA2T3	cyan	VSMC_M2
GO:0042475	0.29	0.84	6	63	odontogenesis of dentin-containing tooth	BP	1	GLI3,BAX,LRP4,GNAO1,LEF1,BMP4	cyan	VSMC_M2
GO:1901362	0.29	0.74	222	3012	organic cyclic compound biosynthetic process	BP	1	CTDP1,TSHZ1,PMEL,STAT6,MOXD1,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,CYB5R3,TCF20,DAXX,TEF,PTPRK,IBA57,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,APOE,UROD,BCL3,SLC6A9,CAMK1,TEP1,PNP,ZFP36,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,ACSS2,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,CLCN2,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,ACAT1,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,STARD3,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,HSD3B7,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12,NUPR1,SHC1,PBXIP1,KANK2,PPCDC,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,MFSD12,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,UAP1L1,SBNO2,EDF1,AXIN1,RERE,POLRMT,H6PD,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,FPGS,PBX3,TK2,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,PDXK,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0051353	0.29	0.85	5	50	positive regulation of oxidoreductase activity	BP	1	APOE,GNAI2,CCS,ABL1,CALM3	cyan	VSMC_M2
GO:2000059	0.29	0.86	4	39	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	EIF3H,NOP53,GIPC1,PML	cyan	VSMC_M2
GO:0051298	0.29	0.84	6	64	centrosome duplication	BP	1	KAT2B,POC1B,CHMP4B,CHMP3,ARHGEF10,FBXW5	cyan	VSMC_M2
GO:0050819	0.29	0.86	4	38	negative regulation of coagulation	BP	1	APOE,SERPING1,PRKCD,SERPINE2	cyan	VSMC_M2
GO:0098732	0.29	0.82	9	102	macromolecule deacylation	BP	1	TRERF1,NDN,TPPP,TBL1Y,HDAC5,HDAC6,TP53,ELMSAN1,MTA1	cyan	VSMC_M2
GO:0014897	0.29	0.83	7	77	striated muscle hypertrophy	BP	1	CTDP1,MLIP,KLF15,IGF1,GATA5,GATA4,CDK9	cyan	VSMC_M2
GO:0051851	0.30	0.85	5	51	modulation by host of symbiont process	BP	1	CTDP1,LRRC19,STOM,APOE,LEF1	cyan	VSMC_M2
GO:0051781	0.30	0.84	6	63	positive regulation of cell division	BP	1	CDC14C,CHMP3,VEGFD,VEGFB,GIPC1,CENPV	cyan	VSMC_M2
GO:0034763	0.30	0.82	8	88	negative regulation of transmembrane transport	BP	1	APPL2,BIN1,SLC6A9,CACNB3,LINC02210-CRHR1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0030534	0.30	0.82	8	90	adult behavior	BP	1	EHMT2,SLITRK6,GLRB,BBS2,CSTB,ARRB2,PBX3,EN1	cyan	VSMC_M2
GO:0050679	0.30	0.80	13	154	positive regulation of epithelial cell proliferation	BP	1	HMOX1,NRP1,FGFR1,IGF1,PLCG1,VEGFD,ECM1,GRN,VEGFB,BMP4,STAT5A,ERBB2,AR	cyan	VSMC_M2
GO:0055092	0.30	0.84	6	63	sterol homeostasis	BP	1	APOE,PLSCR3,NPC2,ABCD1,LCAT,ABCA2	cyan	VSMC_M2
GO:0009411	0.30	0.80	11	127	response to UV	BP	1	PTPRK,BAX,BCL3,SMPD1,PRKCD,MMP2,TMEM161A,CASP9,TP53,PML,BMF	cyan	VSMC_M2
GO:0071674	0.30	0.80	11	126	mononuclear cell migration	BP	1	PLA2G7,XG,ECM1,NBL1,IL27RA,SLIT2,HSD3B7,GBA,TNFRSF14,IL34,RPS19	cyan	VSMC_M2
GO:0090288	0.30	0.83	7	78	negative regulation of cellular response to growth factor stimulus	BP	1	HGS,ADGRA2,SFRP2,NBL1,SLIT2,EPN2,ABL1	cyan	VSMC_M2
GO:0044782	0.30	0.77	23	288	cilium organization	BP	1	CDC14C,KCTD17,RSPH9,BBS9,GSN,CCDC114,MARK4,EHD3,DZIP1,POC1B,WWTR1,BBS2,VANGL2,RPGR,CC2D2A,HDAC6,CROCC,WDR90,ENTR1,DNAAF1,ATMIN,ATP6V0D1,TMEM250	cyan	VSMC_M2
GO:1903035	0.30	0.84	6	64	negative regulation of response to wounding	BP	1	APOE,SERPING1,PRKCD,RGMA,SERPINE2,PTPRS	cyan	VSMC_M2
GO:1904064	0.30	0.81	9	103	positive regulation of cation transmembrane transport	BP	1	BAX,SLC6A9,EHD3,CACNB3,PLCG1,CAPN3,WNK4,ABL1,CALM3	cyan	VSMC_M2

GO:0042490	0.30	0.85	5	52	mechanoreceptor differentiation	BP	1	SLITRK6,BMP4,NAGLU,NTRK1,SDC4	cyan	VSMC_M2
GO:0045446	0.30	0.82	8	91	endothelial cell differentiation	BP	1	AFDN,NRP1,TJP1,HEG1,ADD1,BMP4,PTPRS,EDF1	cyan	VSMC_M2
GO:0034762	0.30	0.76	31	396	regulation of transmembrane transport	BP	1	APPL2,KCNQ5,STOM,KLF15,BAX,BIN1,SLC6A9,EHD3,CLIP3,SCN1B,IGF1,SNTA1,CACNB3,PLCG1,CAPN3,CACNA2D2,TPCN2,ERFE,CLCN2,RNASEL,LINC02210-CRHR1,KCND3,CAPN1,WNK4,PRKACA,ABL1,CBARP,KCND2,CALM3,CLIC2,CLIC3	cyan	VSMC_M2
GO:0071900	0.30	0.77	24	300	regulation of protein serine/threonine kinase activity	BP	1	FZD4,CAB39L,APOE,CAMK1,HGS,KAT2B,FGFR1,SMPD1,MAP3K12,SFRP2,PRKCD,SRC,MAPK8IP1,HEG1,BMP4,ERBB2,GBA,PDGFRB,ABL1,IL34,INCA1,SLC8A3,HEXIM1,CALM3	cyan	VSMC_M2
GO:0051260	0.30	0.80	11	128	protein homooligomerization	BP	1	GSDMD,KCTD17,APPL2,SHKBP1,EHD3,RNF213,DISP1,B2M,KCND3,MCOLN1,KCND2	cyan	VSMC_M2
GO:0015800	0.30	0.86	4	39	acidic amino acid transport	BP	1	SLC17A7,SLC38A7,ADORA2A,GIPC1	cyan	VSMC_M2
GO:0050919	0.30	0.86	4	40	negative chemotaxis	BP	1	SEMA3B,SEMA4B,SEMA6C,SLIT2	cyan	VSMC_M2
GO:0031638	0.30	0.86	4	38	zymogen activation	BP	1	FURIN,CLEC3B,C1R,SERPINE2	cyan	VSMC_M2
GO:0043299	0.30	0.84	5	51	leukocyte degranulation	BP	1	HMOX1,LAMP1,FES,CPLX2,PTGDS	cyan	VSMC_M2
GO:0002250	0.30	0.78	20	244	adaptive immune response	BP	1	STAT6,IRF1,BCL3,RFTN1,SLC15A4,SERPING1,PRKCD,CD81,LEF1,B2M,C1R,C1S,ALOX15,IL17RA,IL27RA,MCOLN1,TMEM98,C6,TNFRSF14,CD55	cyan	VSMC_M2
GO:0010824	0.30	0.86	4	39	regulation of centrosome duplication	BP	1	KAT2B,CHMP4B,CHMP3,FBXW5	cyan	VSMC_M2
GO:0043244	0.30	0.81	9	107	regulation of protein-containing complex disassembly	BP	1	GSN,FYCO1,ADD1,CAPZB,MAP1S,HDAC6,UBQLN4,GBA,FLII	cyan	VSMC_M2
GO:0002279	0.30	0.86	4	39	mast cell activation involved in immune response	BP	1	HMOX1,FES,CPLX2,PTGDS	cyan	VSMC_M2
GO:0150116	0.30	0.83	6	65	regulation of cell-substrate junction organization	BP	1	NRP1,EFNA5,EPHA3,SRC,ABL1,SDC4	cyan	VSMC_M2
GO:0007173	0.30	0.82	8	90	epidermal growth factor receptor signaling pathway	BP	1	EFEMP1,RHBDF2,SHKBP1,SRC,PLCG1,SHC1,RHBDF1,ABL1	cyan	VSMC_M2
GO:0048701	0.30	0.86	4	40	embryonic cranial skeleton morphogenesis	BP	1	GLI3,BMP4,MED12,FOXC2	cyan	VSMC_M2
GO:0014743	0.30	0.84	5	52	regulation of muscle hypertrophy	BP	1	CTDP1,MLIP,IGF1,GATA5,CDK9	cyan	VSMC_M2
GO:0045661	0.30	0.86	4	39	regulation of myoblast differentiation	BP	1	CAPN3,BOC,BMP4,ZFP36L1	cyan	VSMC_M2
GO:0098927	0.31	0.86	4	40	vesicle-mediated transport between endosomal compartments	BP	1	CHMP3,SRC,VPS11,WDR81	cyan	VSMC_M2
GO:0071453	0.31	0.79	12	142	cellular response to oxygen levels	BP	1	HMOX1,NOP53,ATG7,ANGPT4,SRC,CACNB3,PTGIS,ZFP36L1,TP53,ATP6V0D1,SLC8A3,KCND2	cyan	VSMC_M2
GO:0014896	0.31	0.82	7	78	muscle hypertrophy	BP	1	CTDP1,MLIP,KLF15,IGF1,GATA5,GATA4,CDK9	cyan	VSMC_M2
GO:0060324	0.31	0.85	4	40	face development	BP	1	RRAS,RARG,MMP2,LEF1	cyan	VSMC_M2
GO:0031110	0.31	0.82	7	79	regulation of microtubule polymerization or depolymerization	BP	1	CLIP3,GAS2L1,FES,PRUNE1,MAP1S,HDAC6,ABL1	cyan	VSMC_M2
GO:0043457	0.31	0.85	4	39	regulation of cellular respiration	BP	1	NOP53,NUPR1,ABCD1,CBFA2T3	cyan	VSMC_M2
GO:0002312	0.31	0.83	6	64	B cell activation involved in immune response	BP	1	STAT6,ST3GAL1,BCL3,SLC15A4,IL27RA,ABL1	cyan	VSMC_M2
GO:0002712	0.31	0.85	4	39	regulation of B cell mediated immunity	BP	1	STAT6,SLC15A4,IL27RA,CD55	cyan	VSMC_M2
GO:0002889	0.31	0.85	4	39	regulation of immunoglobulin mediated immune response	BP	1	STAT6,SLC15A4,IL27RA,CD55	cyan	VSMC_M2
GO:0051966	0.31	0.85	4	40	regulation of synaptic transmission, glutamatergic	BP	1	TSHZ3,ADORA2A,SERPINE2,NTRK1	cyan	VSMC_M2
GO:1990830	0.31	0.82	7	77	cellular response to leukemia inhibitory factor	BP	1	FZD4,SOCS3,RPS16,RARG,TEX14,SBNO2,PML	cyan	VSMC_M2
GO:0001885	0.31	0.84	5	53	endothelial cell development	BP	1	AFDN,TJP1,HEG1,ADD1,PTPRS	cyan	VSMC_M2
GO:0014068	0.31	0.83	6	66	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	FGFR1,IGF1,SRC,NTRK1,PDGFRB,ROR1	cyan	VSMC_M2
GO:0010676	0.31	0.85	4	40	positive regulation of cellular carbohydrate metabolic process	BP	1	KAT2B,IGF1,SRC,SLC45A3	cyan	VSMC_M2
GO:0044260	0.31	0.71	430	5916	cellular macromolecule metabolic process	BP	1	CTDP1,TSHZ1,PYM1,STAT6,TCF21,OS9,MGAT4B,FLOT1,PPP6R2,MSH5,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,DEPTOR,B3GALT4,TCF20,DAXX,FBXO32,TEF,PTPRK,ST3GAL1,CDC14C,TEAD3,MTCH1,TLE1,CARD10,KCTD17,NFIB,TRERF1,GCNT1,HMOX1,ACO1,CUL9,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,P3H1,NAT14,GPNMB,EFEMP1,RRAGC,EEPD1,MEIS1,RNF144A,STK40,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,RPL18,PARP12,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,FZD4,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,BCL3,MIF4GD,AGAP3,ATRAID,SLC6A9,ATG7,SOCS3,CAMK1,EHD3,PLD3,TEP1,RNF170,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,GAA,PAK4,SGSH,RNF213,ARAP1,RPL15,HGS,KAT2B,TBC1D5,EIF3K,RHOG,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,TPP1,CLIP3,GTF3A,SLC15A4,ANGPT4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,GNPTAB,IGF1,TLR3,SNTA1,MAN2A1,WT1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,GALNT18,GGCX,POU6F1,SERPING1,CAST,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,STBD1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,MMP2,PTPN13,EXT2,STAT1,ABHD14B,MOB2,GFRA2,CD81,NDN,PHKG1,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,MRPL36,PCSK6,CSTB,ZNF496,NFKB1,GNAI2,SPOCD1,TPPP,B4GALT4,HIST1H1C,PKNOX2,RGMA,BCL9,UBA7,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,SSH3,APH1A,MN1,DCAF11,VEGFD,GCNT7,WDR6,ECM1,REC8,CTSK,GRK5,NELFCD,CASP10,ADCY1,FES,MINDY1,FURIN,VPS11,BCL9L,HEG1,RFX5,GATA5,B4GAT1,H	cyan	VSMC_M2
GO:0072384	0.31	0.82	7	78	organelle transport along microtubule	BP	1	LAMP1,KIF1A,FYCO1,MAP1S,HDAC6,RHOT2,HSBP1	cyan	VSMC_M2
GO:0001952	0.31	0.80	9	105	regulation of cell-matrix adhesion	BP	1	RRAS,NRP1,EFNA5,EPHA3,SRC,JUP,ADAM15,ABL1,SDC4	cyan	VSMC_M2
GO:0043255	0.31	0.82	7	78	regulation of carbohydrate biosynthetic process	BP	1	AP2A1,KAT2B,IGF1,NFKB1,ERFE,PDK2,FAM3A	cyan	VSMC_M2
GO:0051046	0.31	0.75	34	434	regulation of secretion	BP	1	HMOX1,P3H1,CADPS2,APOE,RHBDF2,HGS,RAB11FIP1,LAMP1,APBB1,IGF1,EFNA5,TPCN2,GNAI2,HADH,DISP1,SV2A,RHBDD3,ADCY1,FES,LINC02210-CRHR1,ADORA2A,WNK4,GIPC1,CPLX2,RASL10B,LLGL1,DVL1,PHPT1,RAB11FIP3,RHBDF1,OAS2,CBARP,CALM3,SDC4	cyan	VSMC_M2
GO:0048678	0.31	0.82	6	65	response to axon injury	BP	1	BAX,RGMA,LAMB2,GRN,NTRK1,PTPRS	cyan	VSMC_M2
GO:0006606	0.31	0.79	11	129	protein import into nucleus	BP	1	APPL2,GLI3,BCL3,PRKCD,FAM53B,NFKBIA,BMP4,JUP,TP53,TSC2,PML	cyan	VSMC_M2
GO:0032602	0.31	0.82	6	64	chemokine production	BP	1	HMOX1,TLR3,TIRAP,EPHA2,IL17RA,ZFPM1	cyan	VSMC_M2
GO:0032642	0.31	0.82	6	64	regulation of chemokine production	BP	1	HMOX1,TLR3,TIRAP,EPHA2,IL17RA,ZFPM1	cyan	VSMC_M2
GO:0050954	0.31	0.80	10	120	sensory perception of mechanical stimulus	BP	1	FZD4,SLITRK6,EPYC,HEXB,CACNB3,SERPINE2,NTRK1,ROR1,PIEZO2,SERPINB6	cyan	VSMC_M2

GO:0033365	0.31	0.74	56	737	protein localization to organelle	BP	1	OS9,PACSIN2,GGA1,CARD10,APPL2,BBS9,GLI3,NRP1,BAX,NOP53,MARK4,BCL3,DZIP1,HGS,DCLK1,LAMP1,TPP1,GNPTAB,CHMP4B,WWTR1,PRKCD,SRC,BBS2,SYS1,LZTS2,CD81,TRIM8,GAS2L1,VPS11,FAM53B,NFKBIA,M6PR,BMP4,CC2D2A,CROCC,DNAJB6,JUP,PRKACA,TP53,GLMP,PPP1R9B,TMEM98,NAGPA,GLIS2,DVL1,ISG15,TSC2,NPHP4,INPP5E,RAB11FIP3,ENTR1,MON1B,ZBTB7A,PML,CALM3,UBLS	cyan	VSMC_M2
GO:2000116	0.31	0.78	14	167	regulation of cysteine-type endopeptidase activity	BP	1	MTCH1,GSN,BAX,CAST,SFRP2,SRC,CASP10,ADORA2A,DNAJB6,ARRB2,CASP9,PML,CARD8,PSMB9	cyan	VSMC_M2
GO:0060998	0.31	0.83	5	54	regulation of dendritic spine development	BP	1	APOE,CAMK1,KIF1A,DLG5,PTPRS	cyan	VSMC_M2
GO:0018130	0.31	0.71	213	2900	heterocycle biosynthetic process	BP	1	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,IBA57,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,APOE,UROD,BCL3,SLC6A9,CAMK1,TEP1,PNP,ZFP36,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,ACSS2,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,ACAT1,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12,NUPR1,SHC1,PBXIP1,KANK2,PPCDC,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,UAP1L1,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,FPGS,PBX3,TK2,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,PDXK,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0014706	0.32	0.76	24	307	striated muscle tissue development	BP	1	CTDP1,MYL6B,TCF21,FLOT1,ZFPM2,MEIS1,EFNB2,IGF1,WT1,NDRG4,BCL9,LEF1,HEG1,GATA5,BMP4,ARRB2,NUPR1,PDGFRB,EEF2,NPRL3,FOXC2,GATA4,ZFPM1,EMD	cyan	VSMC_M2
GO:0120193	0.32	0.83	5	54	tight junction organization	BP	1	AFDN,TJP1,EPHA2,PRKACA,NPHP4	cyan	VSMC_M2
GO:1903037	0.32	0.77	17	206	regulation of leukocyte cell-cell adhesion	BP	1	IRF1,GPNMB,GLI3,PNP,IGF1,SRC,CD81,LEF1,B2M,ADORA2A,BMP4,DLG5,ERBB2,IL27RA,TNFRSF14,CD55,SDC4	cyan	VSMC_M2
GO:0006357	0.32	0.72	132	1784	regulation of transcription by RNA polymerase II	BP	1	CTDP1,TSHZ1,STAT6,TCF21,EHMT2,ZFPM2,IRF1,TCF20,TEF,TEAD3,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,MEIS3,BCL3,CAMK1,ZFP36,KAT2B,APBB1,LMO1,RARG,IGF1,TLR3,WT1,TSHZ3,POU6F1,PLSCR1,HEXB,SFRP2,WWTR1,ZHX3,FOXF2,SORBS3,STAT1,ABHD14B,CD81,NDN,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,SOX5,ECM1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,ELL3,NFKBIA,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,NR2F6,ZBTB3,JUP,WIZ,MYRF,ZBTB17,TCF12,RFX1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,PBXIP1,KANK2,MTA1,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,TCF3,SBNO2,TCF25,BRD3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,ATN1,JUNB,GATA4,GLI4,CDK9,ZNF74,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0009261	0.32	0.85	4	40	ribonucleotide catabolic process	BP	1	PNP,ACAT1,ABCD1,DPYD	cyan	VSMC_M2
GO:0035725	0.32	0.79	10	120	sodium ion transmembrane transport	BP	1	SLC17A7,STOM,SLC6A9,SLC4A9,ATP4A,SCN1B,SNTA1,TPCN2,WNK4,SLC8A3	cyan	VSMC_M2
GO:0001837	0.32	0.79	11	131	epithelial to mesenchymal transition	BP	1	FGFR1,SFRP2,WWTR1,EPHA3,FOXF2,LEF1,BCL9L,ELL3,BMP4,DLG5,ADAM15	cyan	VSMC_M2
GO:0002448	0.32	0.85	4	40	mast cell mediated immunity	BP	1	HMOX1,FES,CPLX2,PTGDS	cyan	VSMC_M2
GO:0002753	0.32	0.83	5	53	cytoplasmic pattern recognition receptor signaling pathway	BP	1	IRF3,NOP53,SLC15A4,NFKBIA,DHX58	cyan	VSMC_M2
GO:0070169	0.32	0.85	4	41	positive regulation of biomineral tissue development	BP	1	ATRAID,PKDCC,BMP4,ISG15	cyan	VSMC_M2
GO:0002028	0.32	0.82	6	66	regulation of sodium ion transport	BP	1	STOM,SCN1B,SNTA1,WNK4,SERPINE2,MLLT6	cyan	VSMC_M2
GO:0008284	0.32	0.73	52	681	positive regulation of cell population proliferation	BP	1	ZFPM2,HMOX1,MEIS1,GLI3,FLT3LG,NRP1,MEIS3,PNP,FOLR2,RHOG,FGFR1,IL5RA,EFNB2,RARG,IGF1,SFRP2,WWTR1,TGM2,PLCG1,MMP2,STAT1,CD81,CHRNA7,TJP1,TIRAP,GNAI2,LEF1,VEGFD,ECM1,GRK5,ELL3,LTBP3,CAPN1,GRN,VEGFB,BMP4,STAT5A,ERBB2,IL27RA,AR,SHC1,PBXIP1,PDGFRB,IL13RA1,CRIP2,ABL1,IL34,CD55,PML,TMEM250,STX3,BST2	cyan	VSMC_M2
GO:0014812	0.32	0.81	7	79	muscle cell migration	BP	1	NRP1,IGF1,NDRG4,SRC,ARPC5,SLIT2,PDGFRB	cyan	VSMC_M2
GO:0051101	0.32	0.80	8	91	regulation of DNA binding	BP	1	HMOX1,BCL3,IGF1,LEF1,NFKBIA,EDF1,ZBTB7A,CALM3	cyan	VSMC_M2
GO:0070227	0.32	0.83	5	52	lymphocyte apoptotic process	BP	1	ST3GAL1,GLI3,BAX,BMP4,TP53	cyan	VSMC_M2
GO:0050772	0.32	0.82	6	68	positive regulation of axonogenesis	BP	1	PLXNB2,NRP1,STK25,RND2,SLIT2,IST1	cyan	VSMC_M2
GO:1990823	0.32	0.81	7	78	response to leukemia inhibitory factor	BP	1	FZD4,SOCS3,RPS16,RARG,TEX14,SBNO2,PML	cyan	VSMC_M2
GO:0002699	0.32	0.78	12	142	positive regulation of immune effector process	BP	1	STAT6,HMOX1,APPL2,LAMP1,CD81,FES,B2M,DHX58,GPRC5B,TNFRSF14,CD55,RPS19	cyan	VSMC_M2
GO:0006111	0.32	0.84	4	40	regulation of gluconeogenesis	BP	1	KAT2B,ERFE,PDK2,FAM3A	cyan	VSMC_M2
GO:0061024	0.32	0.73	46	599	membrane organization	BP	1	FLOT1,PACSIN2,MTCH1,APPL2,ATP10D,ELMO1,GSN,BAX,BIN1,APOE,FOLR2,HGS,RFTN1,RHOG,SMPD1,CHMP4B,CHMP3,PLSCR1,GLRB,PRKCD,LRP4,OSBPL5,VPS11,USE1,ALOX15,MYRF,PLEKHM2,PLSCR3,STARD3,AR,TMEM175,TP53,CPLX2,NPC2,ATP8B2,SNX33,ABCC1,ABCD1,DVL1,AGRN,RHOT2,ABCA2,ZNF205,CALM3,STX3,EMD	cyan	VSMC_M2

GO:0045664	0.32	0.78	12	145	regulation of neuron differentiation	BP	1	MEIS1,GLI3,BIN1,TIMP2,FGFR1,SFRP2,B2M,BMP4,NBL1,TCF12,GPRC5B,TCF3	cyan	VSMC_M2
GO:0008654	0.32	0.76	18	222	phospholipid biosynthetic process	BP	1	CHKB,SLC44A1,SOCS3,GPAT4,LPCAT4,PLSCR1,HEXB,PTDSS1,PIK3C2B,IP6K1,PLD2,ALOX15,PLSCR3,SLC44A2,PIGQ,INPP5E,LCAT,ABCA2	cyan	VSMC_M2
GO:0048260	0.32	0.84	4	41	positive regulation of receptor-mediated endocytosis	BP	1	AP2A1,TBC1D5,B2M,ARRB2	cyan	VSMC_M2
GO:0009792	0.33	0.73	41	537	embryo development ending in birth or egg hatching	BP	1	PLXNB2,ZFPM2,COBL,GLI3,SOCS3,FGFR1,RARG,IGF1,MAN2A1,SFRP2,PLCG1,RGMA,LEF1,FURIN,HEG1,VANGL2,PLCD3,BMP4,CC2D2A,DNAJB6,FKBP10,EPHA2,PRKACA,ZFP36L1,PCGF2,AR,TP53,HOXB1,HOXB2,HOXB4,MED12,C6,CPT2,DVL1,TSC2,RPL13,FOXC2,ABL1,JUNB,SDC4,EN1	cyan	VSMC_M2
GO:0007189	0.33	0.81	7	80	adenylate cyclase-activating G protein-coupled receptor signaling pathway	BP	1	ADGRD1,ARRDC3,GNAI2,ADGRB2,ADCY1,LINC02210-CRHR1,ADORA2A	cyan	VSMC_M2
GO:0048863	0.33	0.77	14	171	stem cell differentiation	BP	1	NRP1,SEMA3B,SOX5,SEMA4B,SEMA6C,ELL3,LTBP3,BMP4,TP53,HOXB4,NELFB,FOXC2,ABL1,GATA4	cyan	VSMC_M2
GO:0034605	0.33	0.83	5	53	cellular response to heat	BP	1	DAXX,HMOX1,DNAJB6,PRKACA,HSBP1	cyan	VSMC_M2
GO:0003006	0.33	0.73	52	685	developmental process involved in reproduction	BP	1	TCF21,ADAMTS2,EHMT2,ZFPM2,RPS6KA2,MEA1,ITGB8,GLI3,BAX,FZD4,SOCS3,DZIP1,TPPP2,CATSPERG,RARG,IGF1,TLR3,WT1,GGT7,CTSB,HEXB,SFRP2,NDRG3,SRC,BBS2,FOXF2,AGFG1,SPOCD1,LEF1,REC8,ELL3,WNT2B,PLCD3,PSAP,BMP4,DNAJB6,ARRB2,SERPINE2,PRKACA,ZFP36L1,NTRK1,SLIT2,AR,PPP1R9B,ADAM15,NUPR1,PDGFRB,PLAC1,SERPINF1,JUNB,GATA4,PYGO2	cyan	VSMC_M2
GO:1903578	0.33	0.81	6	66	regulation of ATP metabolic process	BP	1	IGF1,TP53,NUPR1,ABCD1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0070507	0.33	0.78	11	135	regulation of microtubule cytoskeleton organization	BP	1	CLIP3,EFNA5,CHMP4B,EPHA3,TPPP,GAS2L1,FES,PRUNE1,MAP1S,HDAC6,ABL1	cyan	VSMC_M2
GO:0007159	0.33	0.76	19	234	leukocyte cell-cell adhesion	BP	1	IRF1,GCNT1,GPNMB,GLI3,PNP,IGF1,SRC,CD81,LEF1,B2M,ADORA2A,BMP4,DLG5,ERBB2,IL27RA,TNFRSF14,CERCAM,CD55,SDC4	cyan	VSMC_M2
GO:0071868	0.33	0.81	6	66	cellular response to monoamine stimulus	BP	1	TGM2,GNAO1,ARRB2,PRKACA,ABL1,RGS8	cyan	VSMC_M2
GO:0071870	0.33	0.81	6	66	cellular response to catecholamine stimulus	BP	1	TGM2,GNAO1,ARRB2,PRKACA,ABL1,RGS8	cyan	VSMC_M2
GO:0046323	0.33	0.82	5	54	glucose import	BP	1	APPL2,KLF15,IGF1,ERFE,RNASEL	cyan	VSMC_M2
GO:0045778	0.33	0.84	4	42	positive regulation of ossification	BP	1	ATRAID,PKDCC,BMP4,ISG15	cyan	VSMC_M2
GO:0016043	0.33	0.70	336	4652	cellular component organization	BP	1	CTDP1,MMP19,PYM1,PMEL,RAB5B,ADAMTS2,FLOT1,MSH5,EHMT2,PLXNB2,EIF3H,RPS6KA2,AFDN,DEPTOR,PACSIN2,TAPBP,DAXX,TGFBI,PTPRK,ARHGAP18,IBA57,CDC14C,GSDMD,MTCH1,CARD10,KCTD17,NFIB,KIFC2,ARHGAP39,CUL9,TRPM3,APPL2,ATP10D,RSPH9,HIGD2A,PLA2G7,P3H1,BBS9,ELMO1,COBL,AKT1S1,GLI3,AP2A1,GSN,SLC17A7,NRP1,RHOB,BAX,CCDC114,NOP53,LURAP1,FZD4,MARK4,VIM,BIN1,APOE,BCL3,ATG7,LTBP4,SHKBP1,SLITRK6,CAMK1,EHD3,TEP1,DZIP1,TPPP2,GAA,PAK4,RNF213,ARAP1,NPTX1,FOLR2,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,EFNB2,POC1B,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,TPP1,MMP17,CLIP3,PPFIBP2,ANGPT4,EIF3F,RARG,SCN1B,GNPTAB,IGF1,REEP5,SNTA1,MAN2A1,WT1,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,CAST,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,LRP4,BBS2,MMS19,FOXF2,GNAO1,PDLIM2,C15orf62,PYROXD2,SORBS3,NISCH,MMP2,PNPLA2,LZTS2,PHACTR1,HPS6,NDN,CHRNA7,IKBKE,OSBPL5,CAPN3,TJP1,TIRAP,CTTN,BOC,TPCN2,SEMA3B,TPPP,HIST1H1C,RGMA,DISP1,B4GALT5,SV2A,SSH3,EGFL6,LAMB2,EXOC8,NDUFAF3,REC8,SEMA4B,CTSK,NCKIPSD,GAS2L1,ADCY1,FES,PRUNE1,FURIN,VPS11,SEMA6C,TACC2,HEG1,VANGL2,KIF1A,RERG,PARD3B,STK25,OLFML2B,MUS81,CTNNA3,WIPF1,ARPC5,MOV10,LTBP3,B2M,DPF2,KCND3,ARHGEF10,BCR,ADORA2A,FYCO1,RPGR,AIFM2,ADAMTS7,CDC42BPG,GRN,HDAC5,GPC2,RND2,VAT1,ADD1,BMP4,NAGLU,MAEA,NBL1,CAPZB,MAP1S,CC2D2A,TECPR1,DLG5,USE1,HDAC6,PQBP1,ARHGEF10L,WDR45,PLD2,CROCC,DNAJB6,FKBP10,ARRB2,JUP,ALOX15,EPHA2,MYRF,GABARAP,PLEKHM	cyan	VSMC_M2
GO:0046928	0.33	0.81	6	66	regulation of neurotransmitter secretion	BP	1	ADCY1,ADORA2A,GIPC1,CPLX2,DVL1,CALM3	cyan	VSMC_M2
GO:0002763	0.33	0.84	4	40	positive regulation of myeloid leukocyte differentiation	BP	1	LEF1,FES,ZFP36L1,IL34	cyan	VSMC_M2
GO:0035303	0.33	0.79	9	106	regulation of dephosphorylation	BP	1	PPP6R2,SMPD1,PRKCD,SRC,GNAI2,GBA,PPP1R9B,PDGFRB,CALM3	cyan	VSMC_M2
GO:0010717	0.33	0.80	7	80	regulation of epithelial to mesenchymal transition	BP	1	SFRP2,WWTR1,EPHA3,LEF1,BCL9L,ELL3,BMP4	cyan	VSMC_M2
GO:0042594	0.33	0.77	13	158	response to starvation	BP	1	EHMT2,RRAGC,ATG7,ZFP36,TBC1D5,GAS2L1,WNT2B,ACAT1,WDR45,GABARAP,TP53,GBA,NPRL3	cyan	VSMC_M2
GO:1904645	0.33	0.84	4	41	response to amyloid-beta	BP	1	IGF1,MMP2,CHRNA7,ABCC1	cyan	VSMC_M2
GO:0010883	0.33	0.84	4	41	regulation of lipid storage	BP	1	PNPLA2,IKBKE,NFKB1,NFKBIA	cyan	VSMC_M2
GO:0042147	0.33	0.80	7	80	retrograde transport, endosome to Golgi	BP	1	GGA1,TBC1D17,DENND2A,EHD3,TBC1D5,SGSM2,VPS26B	cyan	VSMC_M2
GO:0001892	0.33	0.81	6	67	embryonic placenta development	BP	1	SOCS3,LEF1,PLCD3,DNAJB6,ZFP36L1,JUNB	cyan	VSMC_M2
GO:0002548	0.33	0.84	4	40	monocyte chemotaxis	BP	1	PLA2G7,NBL1,SLIT2,RPS19	cyan	VSMC_M2
GO:0051149	0.33	0.82	5	53	positive regulation of muscle cell differentiation	BP	1	CAMK1,EFNB2,IGF1,BMP4,ARRB2	cyan	VSMC_M2
GO:0007623	0.33	0.77	13	160	circadian rhythm	BP	1	KLF9,DBP,ATG7,ADCY1,ADORA2A,NAGLU,NR2F6,NTRK1,TP53,MTA1,PTGDS,KCND2,PML	cyan	VSMC_M2
GO:0070925	0.33	0.72	53	705	organelle assembly	BP	1	EHMT2,CDC14C,KCTD17,KIFC2,RSPH9,BBS9,GSN,CCDC114,NOP53,MARK4,ATG7,EHD3,DZIP1,HGS,KAT2B,POC1B,CHMP4B,CHMP3,TP53INP2,PATL1,WWTR1,SRC,BBS2,LZTS2,CAPN3,VPS11,VANGL2,ARHGEF10,RPGR,CC2D2A,HDAC6,WDR45,CROCC,GABARAP,UBQLN2,TMEM175,NUPR1,PDGFRB,FLII,PTPRS,TRAF7,WDR90,ENTR1,NPRL3,DNAAF1,ATMIN,IST1,ATP6V0D1,RPS15,RAB43,RPS19,TMEM250,SDC4	cyan	VSMC_M2
GO:0045860	0.33	0.74	24	305	positive regulation of protein kinase activity	BP	1	DAXX,CARD10,FZD4,CAB39L,CAMK1,FGFR1,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,PRKCD,SRC,TIRAP,ERBB2,GPRC5B,PDGFRB,MAP2K3,TRAF4,AXIN1,ABL1,IL34,CALM3,SDC4	cyan	VSMC_M2
GO:1901800	0.33	0.78	9	104	positive regulation of proteasomal protein catabolic process	BP	1	RNF144A,NOP53,GABARAP,UBQLN2,GBA,NUPR1,DVL1,ELOB,CBFA2T3	cyan	VSMC_M2
GO:0007422	0.34	0.81	6	69	peripheral nervous system development	BP	1	SLC5A3,ADGRB2,LAMB2,ARHGEF10,ERBB2,MED12	cyan	VSMC_M2

GO:0043242	0.34	0.81	6	70	negative regulation of protein-containing complex disassembly	BP	1	GSN,ADD1,CAPZB,HDAC6,UBQLN4,FLII	cyan	VSMC_M2
GO:0008064	0.34	0.76	13	159	regulation of actin polymerization or depolymerization	BP	1	ARHGAP18,GSN,BIN1,PRKCD,C15orf62,CTTN,SSH3,ARPC5,ADD1,CAPZB,ALOX15,SLIT2,FLII	cyan	VSMC_M2
GO:0110151	0.34	0.83	4	42	positive regulation of biomineralization	BP	1	ATRAID,PKDCC,BMP4,ISG15	cyan	VSMC_M2
GO:0071887	0.34	0.80	7	79	leukocyte apoptotic process	BP	1	ST3GAL1,GLI3,IRF3,BAX,BMP4,CASP9,TP53	cyan	VSMC_M2
GO:1901606	0.34	0.81	6	65	alpha-amino acid catabolic process	BP	1	DDAH2,AASS,SCLY,ACAT1,QDPR,ASPA	cyan	VSMC_M2
GO:0031103	0.34	0.83	4	42	axon regeneration	BP	1	RGMA,LAMB2,GRN,PTPRS	cyan	VSMC_M2
GO:0003018	0.34	0.75	16	200	vascular process in circulatory system	BP	1	AKAP12,SLC44A1,APOE,SLC6A9,SLC7A2,SNTA1,SRC,EXT2,SLC5A3,TJP1,ADORA2A,SLIT2,SLC16A2,ABCC1,FOXC2,ABCA2	cyan	VSMC_M2
GO:0050853	0.34	0.83	4	41	B cell receptor signaling pathway	BP	1	BAX,RFTN1,CD81,ABL1	cyan	VSMC_M2
GO:0043434	0.34	0.74	24	308	response to peptide hormone	BP	1	STAT6,GCNT1,APPL2,KLF15,SOCS3,KAT2B,PRKCD,SRC,STAT1,NFKB1,GNAI2,HADH,ERFE,PHEX,LINC02210-CRHR1,HDAC5,QDPR,STAT5A,ZFP36L1,PDK2,SHC1,TSC2,FOXC2,SLC2A8	cyan	VSMC_M2
GO:0051057	0.34	0.82	5	55	positive regulation of small GTPase mediated signal transduction	BP	1	IGF1,SRC,TGM2,NTRK1,PDGFRB	cyan	VSMC_M2
GO:0002237	0.34	0.75	19	236	response to molecule of bacterial origin	BP	1	AKAP12,IRF3,VIM,ZFP36,GGT7,SRC,BPI,TIRAP,NFKB1,NFKBIA,B2M,CASP9,PLSCR3,ACP5,SBNO2,ABL1,CD55,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0031334	0.34	0.75	16	199	positive regulation of protein-containing complex assembly	BP	1	GSN,BAX,BIN1,TPPP2,SRC,C15orf62,TIRAP,CTTN,TPPP,FES,ARPC5,ALOX15,TP53,WARS,ISG15,BMF	cyan	VSMC_M2
GO:0051817	0.34	0.80	6	67	modulation of process of other organism involved in symbiotic interaction	BP	1	CTDP1,LRRC19,STOM,APOE,ATG7,LEF1	cyan	VSMC_M2
GO:0051402	0.34	0.75	16	198	neuron apoptotic process	BP	1	HMOX1,AKT1S1,NRP1,BAX,APOE,ADORA2A,GRN,ARRB2,CASP9,NTRK1,TP53,GBA,NUPR1,RETREG1,ATN1,EN1	cyan	VSMC_M2
GO:1903530	0.34	0.73	31	399	regulation of secretion by cell	BP	1	HMOX1,P3H1,CADPS2,APOE,RHBDF2,HGS,RAB11FIP1,LAMP1,APBB1,IGF1,EFNA5,TPCN2,GNAI2,HADH,DISP1,RHBDD3,ADCY1,FES,LINC02210-CRHR1,ADORA2A,GIPC1,CPLX2,RASL10B,LLGL1,DVL1,PHPT1,RAB11FIP3,RHBDF1,CBARP,CALM3,SDC4	cyan	VSMC_M2
GO:0051170	0.34	0.77	11	132	import into nucleus	BP	1	APPL2,GLI3,BCL3,PRKCD,FAM53B,NFKBIA,BMP4,JUP,TP53,TSC2,PML	cyan	VSMC_M2
GO:0060147	0.34	0.83	4	41	regulation of posttranscriptional gene silencing	BP	1	ZFP36,BMP4,TP53,ADAR	cyan	VSMC_M2
GO:0035050	0.34	0.81	5	55	embryonic heart tube development	BP	1	NDRG4,VANGL2,FOXC2,DNAAF1,GATA4	cyan	VSMC_M2
GO:0044257	0.34	0.71	52	685	cellular protein catabolic process	BP	1	OS9,EIF3H,KCTD17,CUL9,RNF144A,NOP53,TRIM13,APOE,AGAP3,ATRAID,RNF213,TPP1,RBCK1,CHMP4B,TP53INP2,EDEM2,CTSB,WWTR1,FOXF2,CD81,UBA7,DCAF11,CTSK,FURIN,VPS11,MAGEF1,ADAMTS7,MAEA,HDAC6,ARRB2,GABARAP,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,MTA1,CLPP,UBXN6,WDR81,DVL1,ISG15,ELOB,FBXW5,AXIN1,RHBDF1,CBFA2T3,RNF166,ABCA2,PML,PSMB9	cyan	VSMC_M2
GO:0019216	0.34	0.74	20	251	regulation of lipid metabolic process	BP	1	APPL2,APOE,PRKCD,SRC,PNPLA2,CD81,SLC45A3,NFKB1,ERFE,CLCN2,PSAP,NPC2,PDK2,PDGFRB,ABCD1,EDF1,FAM3A,H6PD,ABCA2,EEF1A2	cyan	VSMC_M2
GO:0030326	0.34	0.78	8	96	embryonic limb morphogenesis	BP	1	GLI3,BAX,RARG,SFRP2,LRP4,LEF1,BMP4,EN1	cyan	VSMC_M2
GO:0035113	0.34	0.78	8	96	embryonic appendage morphogenesis	BP	1	GLI3,BAX,RARG,SFRP2,LRP4,LEF1,BMP4,EN1	cyan	VSMC_M2
GO:0006874	0.34	0.74	22	283	cellular calcium ion homeostasis	BP	1	GRINA,KCTD17,BAX,APOE,ACKR4,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,PRKACA,GRIA1,MCOLN1,ABL1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0002768	0.34	0.76	13	158	immune response-regulating cell surface receptor signaling pathway	BP	1	APPL2,BAX,RFTN1,RBCK1,PLSCR1,PRKCD,SRC,CACNB3,PLCG1,CD81,PLD2,PHPT1,ABL1	cyan	VSMC_M2
GO:0030832	0.34	0.76	13	160	regulation of actin filament length	BP	1	ARHGAP18,GSN,BIN1,PRKCD,C15orf62,CTTN,SSH3,ARPC5,ADD1,CAPZB,ALOX15,SLIT2,FLII	cyan	VSMC_M2
GO:0034765	0.34	0.73	25	323	regulation of ion transmembrane transport	BP	1	KCNQ5,STOM,BAX,BIN1,SLC6A9,EHD3,SCN1B,SNTA1,CACNB3,PLCG1,CAPN3,CACNA2D2,TPCN2,CLCN2,LINC02210-CRHR1,KCND3,CAPN1,WNK4,PRKACA,ABL1,CBARP,KCND2,CALM3,CLIC2,CLIC3	cyan	VSMC_M2
GO:0032370	0.34	0.81	5	55	positive regulation of lipid transport	BP	1	EEPD1,APOE,PRKCD,ERFE,NFKBIA	cyan	VSMC_M2
GO:0002562	0.34	0.81	5	54	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	STAT6,SLC15A4,LEF1,IL27RA,TCF3	cyan	VSMC_M2
GO:0016444	0.34	0.81	5	54	somatic cell DNA recombination	BP	1	STAT6,SLC15A4,LEF1,IL27RA,TCF3	cyan	VSMC_M2
GO:0046635	0.35	0.83	4	41	positive regulation of alpha-beta T cell activation	BP	1	GLI3,PNP,CD81,CD55	cyan	VSMC_M2
GO:0055085	0.35	0.70	78	1047	transmembrane transport	BP	1	TRPM3,APPL2,ATP10D,KCNQ5,SLC44A1,SLC17A7,STOM,KLF15,BAX,UQCRH,BIN1,ABCB8,SLC6A9,EHD3,SLC26A11,SLC4A9,FOLR2,CLIP3,SLC15A4,SLC7A2,ATP4A,SCN1B,IGF1,SNTA1,SLC38A7,GLRB,CACNB3,PLCG1,SLC5A3,SLC45A3,CHRNA7,CAPN3,CACNA2D2,TPCN2,SV2A,ANXA9,ERFE,SLC16A9,CLCN2,TCN2,RNASEL,LINC02210-CRHR1,KCND3,ORAI2,CAPN1,WNK4,CHRNE,PRKACA,CLCN6,TMEM175,ORAI3,SLC51B,SLC16A2,ATP8B2,SPNS1,SLC44A2,GRIA1,ATOX1,ABCC1,MCOLN1,PIEZO2,CPT2,MFSD12,ABCD1,SLC10A3,ABL1,SLC2A8,ATP6V0D1,ABCA2,CNNM3,SLC8A3,CBARP,KCND2,CALM3,CLIC2,LASP1,CLIC3,MPV17	cyan	VSMC_M2
GO:0034754	0.35	0.79	7	79	cellular hormone metabolic process	BP	1	CYP2S1,PLB1,PNPLA2,CLCN2,STARD3,DHRS13,DGAT1	cyan	VSMC_M2
GO:0051881	0.35	0.80	6	66	regulation of mitochondrial membrane potential	BP	1	BAX,SRC,TUSC2,ADORA2A,ABCD1,ABL1	cyan	VSMC_M2
GO:0002706	0.35	0.78	8	92	regulation of lymphocyte mediated immunity	BP	1	STAT6,LAMP1,SLC15A4,CD81,B2M,ARRB2,IL27RA,CD55	cyan	VSMC_M2
GO:0072089	0.35	0.81	5	54	stem cell proliferation	BP	1	SFRP2,LTBP3,WNT2B,ZFP36L1,GBA	cyan	VSMC_M2
GO:0035082	0.35	0.81	5	55	axoneme assembly	BP	1	RSPH9,CCDC114,BBS2,CC2D2A,DNAAF1	cyan	VSMC_M2
GO:0090066	0.35	0.72	32	418	regulation of anatomical structure size	BP	1	DEPTOR,ARHGAP18,AKT1S1,GSN,NRP1,BIN1,APOE,RARG,SNTA1,CHMP3,PRKCD,C15orf62,EXT2,CTTN,SEMA3B,RGMA,SSH3,SEMA4B,SEMA6C,ARPC5,ADORA2A,RND2,ADD1,CAPZB,ALOX15,CLCN6,SLIT2,FLII,PTPRS,FOXC2,ABL1,IST1	cyan	VSMC_M2
GO:0048871	0.35	0.72	29	378	multicellular organismal homeostasis	BP	1	STAT6,APPL2,BAX,POC1B,TPP1,CHMP4B,TP53INP2,ARRDC3,WWTR1,SRC,DECR1,BBS2,EXT2,NDN,TJP1,HADH,IP6K1,CTSK,LTBP3,B2M,LDB2,CROCC,PRKACA,GBA,ACP5,SIGLEC15,CPT2,NPHP4,FOXC2	cyan	VSMC_M2
GO:0072678	0.35	0.82	4	42	T cell migration	BP	1	XG,ECM1,IL27RA,TNFRSF14	cyan	VSMC_M2
GO:0006809	0.35	0.81	5	55	nitric oxide biosynthetic process	BP	1	DDAH2,CYB5R3,PTGIS,ACP5,GCHFR	cyan	VSMC_M2

GO:0008625	0.35	0.79	6	67	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	DAXX,HMOX1,BAX,SFRP2,TMBIM1,GABARAP	cyan	VSMC_M2
GO:0055007	0.35	0.78	8	96	cardiac muscle cell differentiation	BP	1	CTDP1,EFNB2,IGF1,WT1,BMP4,ARRB2,PDGFRB,GATA4	cyan	VSMC_M2
GO:0031109	0.35	0.77	9	109	microtubule polymerization or depolymerization	BP	1	TPPP2,CLIP3,TPPP,GAS2L1,FES,PRUNE1,MAP1S,HDAC6,ABL1	cyan	VSMC_M2
GO:0051259	0.35	0.74	14	174	protein complex oligomerization	BP	1	GSDMD,KCTD17,TRPM3,APPL2,SHKBP1,EHD3,RNF213,DISP1,B2M,KCND3,TP53,MCOLN1,ISG15,KCND2	cyan	VSMC_M2
GO:0010720	0.36	0.73	18	231	positive regulation of cell development	BP	1	PLXNB2,GLI3,NRP1,BIN1,MAN2A1,TGM2,STK25,ELL3,RND2,ADD1,BMP4,SERPINE2,SLIT2,ASPA,ABL1,IL34,IST1,SERPINF1	cyan	VSMC_M2
GO:0048524	0.36	0.80	5	55	positive regulation of viral process	BP	1	STOM,TRIM21,CHMP3,ADAR,TMEM250	cyan	VSMC_M2
GO:0032496	0.36	0.73	18	225	response to lipopolysaccharide	BP	1	AKAP12,IRF3,VIM,ZFP36,GGT7,SRC,BPI,TIRAP,NFKB1,NFKBIA,CASP9,PLSCR3,ACP5,SBNO2,ABL1,CD55,CARD8,NFKBIL1	cyan	VSMC_M2
GO:0099072	0.36	0.82	4	43	regulation of postsynaptic membrane neurotransmitter receptor levels	BP	1	PORCN,CLSTN1,GRASP,STX3	cyan	VSMC_M2
GO:0071214	0.36	0.73	21	267	cellular response to abiotic stimulus	BP	1	IRF1,PTPRK,RHOB,BAX,SMPD1,TLR3,SFRP2,PRKCD,MMP2,CAPN3,NFKB1,TMEM161A,CASP9,ZFP36L1,TP53,MCOLN1,PIEZO2,NMT2,SERPINB6,BMF,RAB11B	cyan	VSMC_M2
GO:0104004	0.36	0.73	21	267	cellular response to environmental stimulus	BP	1	IRF1,PTPRK,RHOB,BAX,SMPD1,TLR3,SFRP2,PRKCD,MMP2,CAPN3,NFKB1,TMEM161A,CASP9,ZFP36L1,TP53,MCOLN1,PIEZO2,NMT2,SERPINB6,BMF,RAB11B	cyan	VSMC_M2
GO:1901568	0.36	0.80	5	54	fatty acid derivative metabolic process	BP	1	GGT7,ACAT1,ALOX15,ABCD1,DGAT1	cyan	VSMC_M2
GO:0060966	0.36	0.82	4	42	regulation of gene silencing by RNA	BP	1	ZFP36,BMP4,TP53,ADAR	cyan	VSMC_M2
GO:1903351	0.36	0.80	5	55	cellular response to dopamine	BP	1	TGM2,GNAO1,ARRB2,ABL1,RGS8	cyan	VSMC_M2
GO:0035384	0.36	0.82	4	42	thioester biosynthetic process	BP	1	ACSS1,ACSS2,ACAT1,PDK2	cyan	VSMC_M2
GO:0071616	0.36	0.82	4	42	acyl-CoA biosynthetic process	BP	1	ACSS1,ACSS2,ACAT1,PDK2	cyan	VSMC_M2
GO:0060688	0.36	0.82	4	42	regulation of morphogenesis of a branching structure	BP	1	WNT2B,BMP4,AR,ABL1	cyan	VSMC_M2
GO:0002090	0.36	0.81	4	43	regulation of receptor internalization	BP	1	FLOT1,TBC1D5,ARRB2,UBQLN2	cyan	VSMC_M2
GO:0045599	0.36	0.81	4	43	negative regulation of fat cell differentiation	BP	1	ZADH2,ZFPM2,WWTR1,ZFPM1	cyan	VSMC_M2
GO:0021700	0.36	0.73	16	204	developmental maturation	BP	1	RPS6KA2,MTCH1,GPAT4,IGF1,MMP2,TUSC2,B4GALT5,REC8,MAEA,PRKACA,GBA,AGRN,RERE,CLSTN1,NFIA,ZBTB7A	cyan	VSMC_M2
GO:1900542	0.36	0.80	5	56	regulation of purine nucleotide metabolic process	BP	1	IGF1,PDK2,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0098656	0.36	0.74	13	161	anion transmembrane transport	BP	1	SLC17A7,SLC6A9,SLC26A11,SLC4A9,FOLR2,SLC15A4,SLC7A2,SLC38A7,GLRB,CLCN6,ABCC1,MFSD12,CLIC2	cyan	VSMC_M2
GO:0006464	0.36	0.67	208	2859	cellular protein modification process	BP	1	CTDP1,OS9,MGAT4B,FLOT1,PPP6R2,EHMT2,PLXNB2,RPS6KA2,DEPTOR,B3GALT4,DAXX,FBXO32,PTPRK,ST3GAL1,CDC14C,CARD10,TRERF1,GCNT1,CUL9,TRIM14,GALNT12,P3H1,GPNMB,EFEMP1,RNF144A,STK40,AKT1S1,STK17A,AASS,NRP1,KLF15,BAX,PARP12,NOP53,FKRP,TRIM13,FZD4,CAB39L,MARK4,AGBL5,APOE,ATG7,SOCS3,CAMK1,RNF170,PAK4,RNF213,HGS,KAT2B,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,CLIP3,ANGPT4,EIF3F,MAP3K12,RBCK1,IGF1,TLR3,SNTA1,MAN2A1,EFNA5,DPY19L3,GALNT18,GGCX,EDEM2,ARRDC3,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,RIOX2,FOXF2,MAPK8IP1,PTPN13,EXT2,MOB2,GFRA2,CD81,NDN,PHKG1,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,GNAI2,TPPP,B4GALT4,HIST1H1C,UBA7,LEF1,TBL1Y,B4GALT5,SSH3,DCAF11,VEGFD,GCNT7,GRK5,FES,MINDY1,VPS11,HEG1,B4GAT1,STK25,ATG4B,RNASEL,MAGEF1,PHEX,DTX2,BCR,ADORA2A,CDC42BPG,HDAC5,VEGFB,MACROD1,WNK4,BMP4,MAEA,PORCN,HDAC6,B3GAT3,WDR45,FKBP10,ARRB2,EPHA2,GABARAP,FNTB,ERBB2,BRAT1,PRKACA,NTRK1,PCGF2,MLLT6,SLIT2,TP53,KAT8,ELMSAN1,PDK2,MED12,GBA,PPP1R9B,SLC51B,NUPR1,SHC1,PBXIP1,ADAR,TEX14,WARS,ULK3,GPRC5B,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,ZDHHC9,TRAF4,PTPRS,KDM4B,NAGPA,DVL1,ISG15,ELOB,E4F1,DPH7,TRAF7,TNFRSF14,TSC2,FBXW5,PHPT1,UNKL,PIGQ,AXIN1,RNF166,ABL1,IL34,INCA1,ABCA2,RPS15,DTX3,SLC8A3,HEXIM1,TRIM26,NMT2,PML,PLPP3,HS3ST3B1,CALM3,CPPED1,CDK9,SDC4,ADPRHL2,MACROD2,AL157935.2,PYGO2,GTF2H4,UBL5	cyan	VSMC_M2
GO:0036211	0.36	0.67	208	2859	protein modification process	BP	1	CTDP1,OS9,MGAT4B,FLOT1,PPP6R2,EHMT2,PLXNB2,RPS6KA2,DEPTOR,B3GALT4,DAXX,FBXO32,PTPRK,ST3GAL1,CDC14C,CARD10,TRERF1,GCNT1,CUL9,TRIM14,GALNT12,P3H1,GPNMB,EFEMP1,RNF144A,STK40,AKT1S1,STK17A,AASS,NRP1,KLF15,BAX,PARP12,NOP53,FKRP,TRIM13,FZD4,CAB39L,MARK4,AGBL5,APOE,ATG7,SOCS3,CAMK1,RNF170,PAK4,RNF213,HGS,KAT2B,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,CLIP3,ANGPT4,EIF3F,MAP3K12,RBCK1,IGF1,TLR3,SNTA1,MAN2A1,EFNA5,DPY19L3,GALNT18,GGCX,EDEM2,ARRDC3,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,RIOX2,FOXF2,MAPK8IP1,PTPN13,EXT2,MOB2,GFRA2,CD81,NDN,PHKG1,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,GNAI2,TPPP,B4GALT4,HIST1H1C,UBA7,LEF1,TBL1Y,B4GALT5,SSH3,DCAF11,VEGFD,GCNT7,GRK5,FES,MINDY1,VPS11,HEG1,B4GAT1,STK25,ATG4B,RNASEL,MAGEF1,PHEX,DTX2,BCR,ADORA2A,CDC42BPG,HDAC5,VEGFB,MACROD1,WNK4,BMP4,MAEA,PORCN,HDAC6,B3GAT3,WDR45,FKBP10,ARRB2,EPHA2,GABARAP,FNTB,ERBB2,BRAT1,PRKACA,NTRK1,PCGF2,MLLT6,SLIT2,TP53,KAT8,ELMSAN1,PDK2,MED12,GBA,PPP1R9B,SLC51B,NUPR1,SHC1,PBXIP1,ADAR,TEX14,WARS,ULK3,GPRC5B,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,ZDHHC9,TRAF4,PTPRS,KDM4B,NAGPA,DVL1,ISG15,ELOB,E4F1,DPH7,TRAF7,TNFRSF14,TSC2,FBXW5,PHPT1,UNKL,PIGQ,AXIN1,RNF166,ABL1,IL34,INCA1,ABCA2,RPS15,DTX3,SLC8A3,HEXIM1,TRIM26,NMT2,PML,PLPP3,HS3ST3B1,CALM3,CPPED1,CDK9,SDC4,ADPRHL2,MACROD2,AL157935.2,PYGO2,GTF2H4,UBL5	cyan	VSMC_M2
GO:0014032	0.36	0.78	6	69	neural crest cell development	BP	1	NRP1,SEMA3B,SEMA4B,SEMA6C,BMP4,FOXC2	cyan	VSMC_M2

GO:0006875	0.36	0.71	29	381	cellular metal ion homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,BAX,APOE,SLC6A9,ACKR4,ATP4A,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,ERFE,CYB561,PRKACA,GRIA1,MCOLN1,ABL1,ATP6V0D1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0051261	0.37	0.77	8	99	protein depolymerization	BP	1	GSN,ADD1,CAPZB,MAP1S,HDAC6,PPP1R9B,FLII,SH3GL1	cyan	VSMC_M2
GO:0034654	0.37	0.66	207	2841	nucleobase-containing compound biosynthetic process	BP	1	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,APOE,BCL3,CAMK1,TEP1,PNP,ZFP36,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,TSHZ3,ACSS2,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,NMNAT2,TCEA3,ELL3,NFKBIA,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,ACAT1,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,PDK2,MED12,NUPR1,SHC1,PBXIP1,KANK2,PPCDC,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,UAP1L1,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,TK2,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:0032760	0.37	0.78	6	69	positive regulation of tumor necrosis factor production	BP	1	AKAP12,TLR3,TIRAP,FRMD8,TMEM106A,OAS2	cyan	VSMC_M2
GO:0006835	0.37	0.80	5	56	dicarboxylic acid transport	BP	1	SLC17A7,FOLR2,SLC38A7,ADORA2A,GIPC1	cyan	VSMC_M2
GO:0045667	0.37	0.76	9	109	regulation of osteoblast differentiation	BP	1	GLI3,ATRAID,IGF1,SFRP2,WWTR1,ZHX3,BMP4,PRKACA,SMOC1	cyan	VSMC_M2
GO:0002244	0.37	0.76	8	96	hematopoietic progenitor cell differentiation	BP	1	DPF2,BMP4,TP53,HOXB4,ADAR,EEF2,ABL1,SLC8A3	cyan	VSMC_M2
GO:0042476	0.37	0.76	8	95	odontogenesis	BP	1	GLI3,BAX,SRC,LRP4,GNAO1,LEF1,PHEX,BMP4	cyan	VSMC_M2
GO:0045444	0.37	0.73	15	188	fat cell differentiation	BP	1	ZADH2,ZFPM2,BBS9,ZFP36,CLIP3,SFRP2,WWTR1,BBS2,LMO3,RNASEL,HDAC6,ZFP36L1,RETREG1,ZBTB7A,ZFPM1	cyan	VSMC_M2
GO:0043367	0.37	0.79	5	56	CD4-positive, alpha-beta T cell differentiation	BP	1	STAT6,BCL3,LEF1,TMEM98,ZFPM1	cyan	VSMC_M2
GO:0010906	0.37	0.76	8	96	regulation of glucose metabolic process	BP	1	KAT2B,IGF1,SRC,SLC45A3,ERFE,TP53,PDK2,FAM3A	cyan	VSMC_M2
GO:0043154	0.37	0.79	5	55	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	SFRP2,SRC,ADORA2A,DNAJB6,ARRB2	cyan	VSMC_M2
GO:0071675	0.37	0.77	7	81	regulation of mononuclear cell migration	BP	1	PLA2G7,ECM1,NBL1,IL27RA,SLIT2,TNFRSF14,IL34	cyan	VSMC_M2
GO:0045604	0.37	0.81	4	44	regulation of epidermal cell differentiation	BP	1	ZFP36,BMP4,RARRES3,ZFP36L1	cyan	VSMC_M2
GO:0005977	0.37	0.79	5	57	glycogen metabolic process	BP	1	STK40,GAA,IGF1,STBD1,PHKG1	cyan	VSMC_M2
GO:0072523	0.37	0.81	4	43	purine-containing compound catabolic process	BP	1	PNP,ACAT1,ABCD1,DPYD	cyan	VSMC_M2
GO:0032527	0.37	0.81	4	43	protein exit from endoplasmic reticulum	BP	1	OS9,EDEM2,CD81,SLC51B	cyan	VSMC_M2
GO:0045913	0.37	0.79	5	57	positive regulation of carbohydrate metabolic process	BP	1	KAT2B,IGF1,SRC,SLC45A3,NFKB1	cyan	VSMC_M2
GO:0032526	0.37	0.77	7	84	response to retinoic acid	BP	1	FZD4,RARG,EPHA3,TMEM161A,PDGFRB,SLC10A3,SERPINF1	cyan	VSMC_M2
GO:0000122	0.37	0.68	52	694	negative regulation of transcription by RNA polymerase II	BP	1	STAT6,TCF21,EHMT2,ZFPM2,NFIB,MLIP,ZBTB45,AASS,GLI3,IRF3,NOP53,ZFP36,APBB1,LMO1,RARG,WT1,POU6F1,WWTR1,SORBS3,STAT1,NDN,NFKB1,HIST1H1C,LEF1,RFX5,MAGEF1,DPF2,HDAC5,MXD4,BMP4,LDB2,NR2F6,ZBTB17,PCGF2,AR,TP53,HOXB4,KANK2,MTA1,MOSPD1,GLIS2,E4F1,TCF3,TCF25,FOXC2,HSBP1,ZNF205,HEXIM1,ZBTB7A,ATN1,ZFPM1,EN1	cyan	VSMC_M2
GO:0042102	0.37	0.79	5	55	positive regulation of T cell proliferation	BP	1	PNP,IGF1,CD81,IL27RA,CD55	cyan	VSMC_M2
GO:1903533	0.37	0.78	6	69	regulation of protein targeting	BP	1	STOM,CACNB3,VPS11,ERBB2,SLC51B,UBL5	cyan	VSMC_M2
GO:0032623	0.37	0.81	4	43	interleukin-2 production	BP	1	PNP,ZFP36,HOMER3,ABL1	cyan	VSMC_M2
GO:0032663	0.37	0.81	4	43	regulation of interleukin-2 production	BP	1	PNP,ZFP36,HOMER3,ABL1	cyan	VSMC_M2
GO:0007204	0.37	0.72	15	194	positive regulation of cytosolic calcium ion concentration	BP	1	BAX,ACKR4,CACNB3,TGM2,PLCG1,CAPN3,TPCN2,PRKACA,MCOLN1,ABL1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:1901292	0.37	0.78	6	69	nucleoside phosphate catabolic process	BP	1	PNP,NEIL2,ACAT1,NUDT13,ABCD1,DPYD	cyan	VSMC_M2
GO:0008277	0.37	0.76	8	96	regulation of G protein-coupled receptor signaling pathway	BP	1	ARRDC3,GNAI2,GRK5,ARRB2,UBQLN2,PPP1R9B,NMT2,RGS10	cyan	VSMC_M2
GO:0006366	0.38	0.66	136	1862	transcription by RNA polymerase II	BP	1	CTDP1,TSHZ1,STAT6,TCF21,EHMT2,ZFPM2,IRF1,TCF20,TEF,TEAD3,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,MEIS3,BCL3,CAMK1,ZFP36,KAT2B,APBB1,LMO1,RARG,IGF1,TLR3,WT1,TSHZ3,POU6F1,PLSCR1,HEXB,SFRP2,WWTR1,ZHX3,FOXF2,SORBS3,STAT1,ABHD14B,CD81,NDN,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,SOX5,ECM1,NELFCD,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,ELL3,NFKBIA,DPF2,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,NR2F6,ZBTB3,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,RFX1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,PBXIP1,KANK2,MTA1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,SBNO2,TCF25,BRD3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,NFIA,ABCA2,ZNF205,HEXIM1,ZBTB7A,ATN1,JUNB,GATA4,GLI4,CDK9,ZNF74,ZBTB47,GTF2H4,ZFPM1,EN1	cyan	VSMC_M2
GO:1903350	0.38	0.79	5	56	response to dopamine	BP	1	TGM2,GNAO1,ARRB2,ABL1,RGS8	cyan	VSMC_M2

GO:0032768	0.38	0.80	4	43	regulation of monooxygenase activity	BP	1	DDAH2,APOE,NFKB1,CALM3	cyan	VSMC_M2
GO:0015711	0.38	0.71	18	228	organic anion transport	BP	1	SLC17A7,SLC6A9,SLC4A9,FOLR2,SLC15A4,SLC7A2,SLC38A7,SV2A,SLC16A9,ADORA2A,PSAP,GIPC1,SLC51B,SLC16A2,ABCC1,MFSD12,SLC10A3,SLC2A8	cyan	VSMC_M2
GO:0044238	0.38	0.65	552	7641	primary metabolic process	BP	1	CTDP1,TSHZ1,ZADH2,MMP19,PYM1,RBMS2,STAT6,TCF21,OS9,ADAMTS2,MGAT4B,FLOT1,CHKB,DDAH2,PPP6R2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,CFB,EIF3H,RPS6KA2,IRF1,DEPTOR,B3GALT4,CYB5R3,TCF20,DAXX,NAGA,FBXO32,TEF,PTPRK,ST3GAL1,CDC14C,TEAD3,MTCH1,TLE1,GGA1,CARD10,KCTD17,NFIB,TRERF1,GCNT1,HMOX1,ACO1,CUL9,KLF9,APPL2,PLA2G7,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,ITGB8,P3H1,NAT14,GPNMB,SLC44A1,BCKDHB,EFEMP1,RRAGC,EEPD1,MEIS1,RNF144A,IAH1,STK40,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,RPL18,PARP12,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,ACSS1,FZD4,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,BCL3,MIF4GD,AGAP3,ATRAID,SLC6A9,ACAA1,ATG7,CYP2S1,LTBP4,CAPN5,PLB1,SOCS3,CAMK1,PLD3,TEP1,OSBPL10,RNF170,PNP,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,GAA,PAK4,SGSH,ECH1,RNF213,GPAT4,RPL15,HGS,KAT2B,EIF3K,RHOG,DCXR,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PGGHG,PKDCC,TPP1,MMP17,CLIP3,GTF3A,SLC15A4,ANGPT4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,GNPTAB,IGF1,CYP4V2,TLR3,SNTA1,MAN2A1,WT1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,GGCX,POU6F1,LPCAT4,SERPING1,CAST,LACTB2,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,STBD1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,DECR1,PLBD2,PLCG1,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,NISCH,MMP2,PTPN13,PTDSS1,EXT2,SLC5A3,PNPLA2,PIK3C2B,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,SLC45A3,PHKG1,GUSB,CHRNA7,TRIM8,IKBKE,OSBPL5,CAPN3,NADSYN1,TIRAP,MRPL36,PCSK6,RNPEP,CSTB,ZNF496,NFKB1,GNAI2,SPOCD1,TPPP,B4GALT4,HIST1H1C,RXNO2,RGMA,BCL9,UBA7,LEF1,T	cyan	VSMC_M2
GO:0045598	0.38	0.75	9	109	regulation of fat cell differentiation	BP	1	ZADH2,ZFPM2,ZFP36,SFRP2,WWTR1,LMO3,HDAC6,ZFP36L1,ZFPM1	cyan	VSMC_M2
GO:0006140	0.38	0.79	5	57	regulation of nucleotide metabolic process	BP	1	IGF1,PDK2,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0035249	0.38	0.79	5	57	synaptic transmission, glutamatergic	BP	1	SLC17A7,TSHZ3,ADORA2A,SERPINE2,NTRK1	cyan	VSMC_M2
GO:0030177	0.38	0.74	10	124	positive regulation of Wnt signaling pathway	BP	1	ADGRA2,SFRP2,SRC,NFKB1,LEF1,FAM53B,JUP,PBXIP1,GPRC5B,ABL1	cyan	VSMC_M2
GO:0048736	0.38	0.73	11	140	appendage development	BP	1	GLI3,BAX,KAT2B,PKDCC,RARG,SFRP2,LRP4,LEF1,BMP4,SMOC1,EN1	cyan	VSMC_M2
GO:0060173	0.38	0.73	11	140	limb development	BP	1	GLI3,BAX,KAT2B,PKDCC,RARG,SFRP2,LRP4,LEF1,BMP4,SMOC1,EN1	cyan	VSMC_M2
GO:0009799	0.38	0.75	8	98	specification of symmetry	BP	1	NDRG4,PCSK6,VANGL2,BMP4,NBL1,CC2D2A,DNAAF1,GATA4	cyan	VSMC_M2
GO:0045834	0.38	0.75	9	109	positive regulation of lipid metabolic process	BP	1	APOE,PRKCD,SRC,PNPLA2,CD81,SLC45A3,PDGFRB,ABCD1,EEF1A2	cyan	VSMC_M2
GO:0007269	0.38	0.74	9	110	neurotransmitter secretion	BP	1	CADPS2,SV2A,ADCY1,ADORA2A,GIPC1,CPLX2,DVL1,CALM3,STX3	cyan	VSMC_M2
GO:0099643	0.38	0.74	9	110	signal release from synapse	BP	1	CADPS2,SV2A,ADCY1,ADORA2A,GIPC1,CPLX2,DVL1,CALM3,STX3	cyan	VSMC_M2
GO:0043502	0.38	0.77	6	71	regulation of muscle adaptation	BP	1	CTDP1,FBXO32,MLIP,IGF1,GATA5,CDK9	cyan	VSMC_M2
GO:0000018	0.38	0.76	7	83	regulation of DNA recombination	BP	1	STAT6,SLC15A4,MMS19,HIST1H1C,MAGEF1,IL27RA,UBQLN4	cyan	VSMC_M2
GO:0051438	0.38	0.80	4	43	regulation of ubiquitin-protein transferase activity	BP	1	ARRDC3,AXIN1,ABL1,RPS15	cyan	VSMC_M2
GO:0030101	0.38	0.80	4	43	natural killer cell activation	BP	1	ULBP2,LAMP1,TUSC2,RHBDD3	cyan	VSMC_M2
GO:0043488	0.38	0.73	11	137	regulation of mRNA stability	BP	1	VIM,ZFP36,SAMD4B,PATL1,PRKCD,IKBKE,TIRAP,RNASEL,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0071692	0.38	0.70	21	271	protein localization to extracellular region	BP	1	P3H1,APOE,RHBDF2,RAB11FIP1,APBB1,GNPTAB,IGF1,EFNA5,HADH,DISP1,RHBDD3,M6PR,ADORA2A,NBL1,PORCN,LLGL1,NAGPA,PHPT1,RAB11FIP3,RHBDF1,RAB11B	cyan	VSMC_M2
GO:0043627	0.38	0.78	5	57	response to estrogen	BP	1	HMOX1,GLI3,AR,GBA,PDGFRB	cyan	VSMC_M2
GO:0072593	0.38	0.72	14	176	reactive oxygen species metabolic process	BP	1	STK17A,DCXR,PRKCD,SLC5A3,TUSC2,GNAI2,CCS,HDAC6,TP53,ACP5,PDGFRB,ABCD1,ZNF205,MPV17	cyan	VSMC_M2
GO:0003170	0.38	0.78	5	58	heart valve development	BP	1	GATA5,BMP4,SLIT2,GATA4,ZFPM1	cyan	VSMC_M2
GO:0030834	0.39	0.80	4	46	regulation of actin filament depolymerization	BP	1	GSN,ADD1,CAPZB,FLII	cyan	VSMC_M2
GO:0006073	0.39	0.78	5	58	cellular glucan metabolic process	BP	1	STK40,GAA,IGF1,STBD1,PHKG1	cyan	VSMC_M2
GO:0044042	0.39	0.78	5	58	glucan metabolic process	BP	1	STK40,GAA,IGF1,STBD1,PHKG1	cyan	VSMC_M2
GO:0071478	0.39	0.72	12	150	cellular response to radiation	BP	1	PTPRK,RHOB,BAX,SMPD1,SFRP2,PRKCD,MMP2,TMEM161A,CASP9,TP53,NMT2,BMF	cyan	VSMC_M2
GO:0006807	0.39	0.64	526	7284	nitrogen compound metabolic process	BP	1	CTDP1,TSHZ1,MMP19,PYM1,RBMS2,STAT6,MOXD1,TCF21,OS9,ADAMTS2,MGAT4B,GNS,FLOT1,CHKB,DDAH2,PPP6R2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,CFB,EIF3H,RPS6KA2,IRF1,DEPTOR,B3GALT4,CYB5R3,TAPBP,TCF20,DAXX,NAGA,FBXO32,TEF,PTPRK,ST3GAL1,IBA57,CDC14C,TEAD3,MTCH1,TLE1,GGA1,OPLAH,CARD10,KCTD17,NFIB,TRERF1,GCNT1,HMOX1,ACO1,CUL9,KLF9,PLA2G7,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,ITGB8,P3H1,NAT14,GPNMB,SLC44A1,BCKDHB,EFEMP1,RRAGC,EEPD1,MEIS1,RNF144A,STK40,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,RPL18,PARP12,NOP53,ABTB1,BICRA,MEIS3,FKRP,TRIM13,ACSS1,FZD4,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,UROD,BCL3,ETHE1,MIF4GD,AGAP3,ATRAID,SLC6A9,ATG7,LTBP4,CAPN5,PLB1,SOCS3,CAMK1,PLD3,TEP1,OSBPL10,RNF170,PNP,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,PAK4,SGSH,RNF213,GPAT4,RPL15,HGS,KAT2B,EIF3K,RHOG,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,TPP1,MMP17,CLIP3,GTF3A,SLC15A4,ANGPT4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,GNPTAB,IGF1,TLR3,SNTA1,MAN2A1,WT1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,GALNT18,GGCX,POU6F1,LPCAT4,SERPING1,CAST,LACTB2,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,MMP2,PTPN13,PTDSS1,EXT2,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,PHKG1,GUSB,CHRNA7,TRIM8,IKBKE,OSBPL5,CAPN3,NADSYN1,TIRAP,MRPL36,PCSK6,RNPEP,CSTB,ZNF496,NFKB1,GNAI2,SPOCD1,TPPP,B4GALT4,HIST1H1C,RXNO2,RGMA,BCL9,UBA7,LEF1,T	cyan	VSMC_M2

GO:0051302	0.39	0.73	11	138	regulation of cell division	BP	1	CDC14C,CHMP3,SFRP2,VEGFD,VEGFB,GIPC1,TEX14,CENPV,RAB11FIP3,ENTR1,CALM3	cyan	VSMC_M2
GO:0060038	0.39	0.80	4	45	cardiac muscle cell proliferation	BP	1	ZFPM2,MEIS1,NDRG4,FOXC2	cyan	VSMC_M2
GO:0007611	0.39	0.72	14	183	learning or memory	BP	1	EHMT2,APOE,NDRG4,CHRNA7,ADCY1,PTCHD1,B2M,NTRK1,PPP1R9B,GRIA1,SLC8A3,SERPINF1,LRRN4,EN1	cyan	VSMC_M2
GO:1902905	0.39	0.71	14	179	positive regulation of supramolecular fiber organization	BP	1	GSN,NRP1,BIN1,APOE,C15orf62,SORBS3,CTTN,FES,ARPC5,ARHGEF10,ARHGEF10L,ALOX15,ABL1,SDC4	cyan	VSMC_M2
GO:0038066	0.39	0.79	4	44	p38MAPK cascade	BP	1	ZFP36,BMP4,ZFP36L1,MAP2K3	cyan	VSMC_M2
GO:0051224	0.39	0.74	8	96	negative regulation of protein transport	BP	1	OS9,APOE,RHBDF2,RAB11FIP1,PKDCC,HADH,RAB11FIP3,RHBDF1	cyan	VSMC_M2
GO:0007043	0.39	0.74	8	99	cell-cell junction assembly	BP	1	AFDN,TJP1,HEG1,DLG5,JUP,EPHA2,PRKACA,NPHP4	cyan	VSMC_M2
GO:0008202	0.39	0.70	17	217	steroid metabolic process	BP	1	CYB5R3,APOE,ACAA1,SMPD1,CYP4V2,OSBPL5,NFKB1,STS,CLCN2,ACAT1,STARD3,HSD3B7,NPC2,GBA,H6PD,LCAT,ABCA2	cyan	VSMC_M2
GO:0032635	0.39	0.74	8	96	interleukin-6 production	BP	1	TLR3,BPI,TIRAP,TMEM106A,ARRB2,IL17RA,IL27RA,GBA	cyan	VSMC_M2
GO:0032675	0.39	0.74	8	96	regulation of interleukin-6 production	BP	1	TLR3,BPI,TIRAP,TMEM106A,ARRB2,IL17RA,IL27RA,GBA	cyan	VSMC_M2
GO:0010718	0.39	0.79	4	45	positive regulation of epithelial to mesenchymal transition	BP	1	WWTR1,LEF1,BCL9L,BMP4	cyan	VSMC_M2
GO:0048259	0.39	0.75	7	85	regulation of receptor-mediated endocytosis	BP	1	FLOT1,AP2A1,TBC1D5,B2M,ARRB2,UBQLN2,ABCA2	cyan	VSMC_M2
GO:0055074	0.39	0.69	22	291	calcium ion homeostasis	BP	1	GRINA,KCTD17,BAX,APOE,ACKR4,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,PRKACA,GRIA1,MCOLN1,ABL1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0072331	0.39	0.72	11	139	signal transduction by p53 class mediator	BP	1	BAX,NOP53,BCL3,ELL3,TP53BP2,TP53,PDK2,NUPR1,RPS15,HEXIM1,PML	cyan	VSMC_M2
GO:0022412	0.39	0.70	19	247	cellular process involved in reproduction in multicellular organism	BP	1	EHMT2,RPS6KA2,BAX,FZD4,DZIP1,FOLR2,IGF1,WT1,HEXB,SRC,BBS2,REC8,BMP4,ARRB2,PRKACA,SLIT2,TEX14,SLC2A8,PYGO2	cyan	VSMC_M2
GO:0014902	0.39	0.75	7	86	myotube differentiation	BP	1	FLOT1,PLD3,IGF1,CD81,BCL9,HDAC5,PTGFRN	cyan	VSMC_M2
GO:0060420	0.40	0.77	5	58	regulation of heart growth	BP	1	CTDP1,ZFPM2,MEIS1,IGF1,WT1	cyan	VSMC_M2
GO:1901879	0.40	0.76	6	75	regulation of protein depolymerization	BP	1	GSN,ADD1,CAPZB,MAP1S,HDAC6,FLII	cyan	VSMC_M2
GO:0050900	0.40	0.69	19	245	leukocyte migration	BP	1	GCNT1,HMOX1,PLA2G7,RHOG,SRC,CD81,TIRAP,XG,VEGFD,ECM1,VEGFB,NBL1,IL27RA,SLIT2,HSD3B7,GBA,TNFRSF14,IL34,RPS19	cyan	VSMC_M2
GO:0032637	0.40	0.77	5	57	interleukin-8 production	BP	1	LRRC19,BCL3,TLR3,BPI,TIRAP	cyan	VSMC_M2
GO:0033866	0.40	0.77	5	57	nucleoside bisphosphate biosynthetic process	BP	1	ACSS1,ACSS2,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0034030	0.40	0.77	5	57	ribonucleoside bisphosphate biosynthetic process	BP	1	ACSS1,ACSS2,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0034033	0.40	0.77	5	57	purine nucleoside bisphosphate biosynthetic process	BP	1	ACSS1,ACSS2,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0031100	0.40	0.77	5	58	animal organ regeneration	BP	1	HMOX1,GLI3,RPS16,FPGS,RPS15	cyan	VSMC_M2
GO:0071248	0.40	0.72	11	141	cellular response to metal ion	BP	1	DAXX,HMOX1,SMPD1,CAPN3,ADCY1,B2M,ADD1,ALOX15,MCOLN1,SERPINF1,JUNB	cyan	VSMC_M2
GO:1902743	0.40	0.79	4	45	regulation of lamellipodium organization	BP	1	SRC,CAPZB,EPHA2,SLIT2	cyan	VSMC_M2
GO:0001947	0.40	0.79	4	45	heart looping	BP	1	NDRG4,VANGL2,DNAAF1,GATA4	cyan	VSMC_M2
GO:0035107	0.40	0.73	9	115	appendage morphogenesis	BP	1	GLI3,BAX,PKDCC,RARG,SFRP2,LRP4,LEF1,BMP4,EN1	cyan	VSMC_M2
GO:0035108	0.40	0.73	9	115	limb morphogenesis	BP	1	GLI3,BAX,PKDCC,RARG,SFRP2,LRP4,LEF1,BMP4,EN1	cyan	VSMC_M2
GO:0080164	0.40	0.79	4	45	regulation of nitric oxide metabolic process	BP	1	DDAH2,PTGIS,TMEM106A,ACP5	cyan	VSMC_M2
GO:0048864	0.40	0.75	6	72	stem cell development	BP	1	NRP1,SEMA3B,SEMA4B,SEMA6C,BMP4,FOXC2	cyan	VSMC_M2
GO:0007259	0.40	0.73	8	98	receptor signaling pathway via JAK-STAT	BP	1	STAT6,BCL3,SOCS3,HGS,IGF1,STAT1,STAT5A,OCIAD2	cyan	VSMC_M2
GO:0048660	0.40	0.72	10	124	regulation of smooth muscle cell proliferation	BP	1	HMOX1,APOE,IGF1,NDRG4,TGM2,MMP2,STAT1,GNAI2,BMP4,PDGFRB	cyan	VSMC_M2
GO:0001960	0.40	0.77	5	58	negative regulation of cytokine-mediated signaling pathway	BP	1	ECM1,SLIT2,ADAR,ISG15,CARD8	cyan	VSMC_M2
GO:0010469	0.40	0.73	9	112	regulation of signaling receptor activity	BP	1	NPTXR,NRP1,SLC6A9,NPTX1,PRKCD,SRC,CAPN1,HDAC6,SHC1	cyan	VSMC_M2
GO:0051347	0.40	0.67	33	441	positive regulation of transferase activity	BP	1	DAXX,CARD10,FZD4,CAB39L,CAMK1,FGFR1,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,ARRDC3,PRKCD,EPHA3,SRC,CD81,CHRNA7,TIRAP,RARRES3,EPHA2,ERBB2,NTRK1,GPRC5B,PDGFRB,MAP2K3,ROR1,TRAF4,AXIN1,ABL1,IL34,EEF1A2,CALM3,SDC4	cyan	VSMC_M2
GO:1902652	0.41	0.72	9	111	secondary alcohol metabolic process	BP	1	CYB5R3,APOE,SMPD1,OSBPL5,STARD3,NPC2,GBA,IDH3G,LCAT	cyan	VSMC_M2
GO:0006766	0.41	0.75	6	71	vitamin metabolic process	BP	1	NFKB1,RLBP1,UBIAD1,ABCC1,FPGS,PDXK	cyan	VSMC_M2
GO:1903557	0.41	0.75	6	72	positive regulation of tumor necrosis factor superfamily cytokine production	BP	1	AKAP12,TLR3,TIRAP,FRMD8,TMEM106A,OAS2	cyan	VSMC_M2
GO:0051480	0.41	0.69	16	212	regulation of cytosolic calcium ion concentration	BP	1	BAX,ACKR4,CACNB3,TGM2,PLCG1,CAPN3,TPCN2,PRKACA,GRIA1,MCOLN1,ABL1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0051153	0.41	0.75	6	72	regulation of striated muscle cell differentiation	BP	1	CTDP1,EFNB2,IGF1,HDAC5,BMP4,ARRB2	cyan	VSMC_M2
GO:0042255	0.41	0.78	4	45	ribosome assembly	BP	1	NOP53,TRAF7,RPS15,RPS19	cyan	VSMC_M2
GO:0002819	0.41	0.72	9	111	regulation of adaptive immune response	BP	1	STAT6,IRF1,SLC15A4,CD81,B2M,ALOX15,IL27RA,TNFRSF14,CD55	cyan	VSMC_M2
GO:1901880	0.41	0.76	5	62	negative regulation of protein depolymerization	BP	1	GSN,ADD1,CAPZB,HDAC6,FLII	cyan	VSMC_M2
GO:0021537	0.41	0.70	14	184	telencephalon development	BP	1	NFIB,GLI3,BAX,TMEM108,BBS2,PHACTR1,LEF1,TACC2,CCDC141,BMP4,SLIT2,PPP1R9B,PTPRS,SLC8A3	cyan	VSMC_M2
GO:0030520	0.41	0.78	4	46	intracellular estrogen receptor signaling pathway	BP	1	SRC,VPS11,AR,KANK2	cyan	VSMC_M2
GO:0060537	0.41	0.67	24	323	muscle tissue development	BP	1	CTDP1,MYL6B,TCF21,FLOT1,ZFPM2,MEIS1,EFNB2,IGF1,WT1,NDRG4,BCL9,LEF1,HEG1,GATA5,BMP4,ARRB2,NUPR1,PDGFRB,EEF2,NPRL3,FOXC2,GATA4,ZFPM1,EMD	cyan	VSMC_M2
GO:0006094	0.41	0.76	5	58	gluconeogenesis	BP	1	KAT2B,ERFE,G6PC3,PDK2,FAM3A	cyan	VSMC_M2
GO:0030216	0.41	0.75	6	74	keratinocyte differentiation	BP	1	ZFP36,BCR,RARRES3,EPHA2,KAZN,ZFP36L1	cyan	VSMC_M2

GO:0019219	0.41	0.62	206	2852	regulation of nucleobase-containing compound metabolic process	BP	1	CTDP1,TSHZ1,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,CAMK1,ZFP36,SAMD4B,KAT2B,RHOG,TRIM21,APBB1,SLC15A4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TMEM161A,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,WIZ,MYRF,ZBTB17,TCF12,ERBB2,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,PDK2,MED12,NUPR1,SHC1,PBXIP1,KANK2,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,HSBP1,ATMIN,PBX3,OAS2,NFIA,ABCA2,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,AHNAK2,ZBTB47,GTF2H4,MPV17,ZFPM1,EN1	cyan	VSMC_M2
GO:0010822	0.41	0.76	5	59	positive regulation of mitochondrion organization	BP	1	BAX,CAMKK2,TP53,ZNF205,BMF	cyan	VSMC_M2
GO:0019079	0.41	0.73	8	99	viral genome replication	BP	1	STOM,PLSCR1,RNASEL,ADAR,ISG15,OAS2,NFIA,BST2	cyan	VSMC_M2
GO:0010811	0.41	0.73	8	100	positive regulation of cell-substrate adhesion	BP	1	RRAS,NRP1,EGFL6,JUP,ALOX15,ABL1,SDC4,COL8A1	cyan	VSMC_M2
GO:0014031	0.41	0.74	6	73	mesenchymal cell development	BP	1	NRP1,SEMA3B,SEMA4B,SEMA6C,BMP4,FOXC2	cyan	VSMC_M2
GO:0043588	0.41	0.70	13	171	skin development	BP	1	ADAMTS2,ZFP36,ARRDC3,LRP4,BCR,RARRES3,LDB2,JUP,EPHA2,KAZN,ZFP36L1,GBA,KRT25	cyan	VSMC_M2
GO:0050852	0.41	0.73	7	85	T cell receptor signaling pathway	BP	1	RFTN1,RBCK1,CACNB3,PLCG1,CD81,PHPT1,ABL1	cyan	VSMC_M2
GO:0043270	0.41	0.69	14	182	positive regulation of ion transport	BP	1	BAX,SLC6A9,EHD3,SCN1B,CACNB3,PLCG1,CAPN3,ADORA2A,WNK4,ARRB2,MLLT6,PDGFRB,ABL1,CALM3	cyan	VSMC_M2
GO:0034767	0.41	0.72	9	114	positive regulation of ion transmembrane transport	BP	1	BAX,SLC6A9,EHD3,CACNB3,PLCG1,CAPN3,WNK4,ABL1,CALM3	cyan	VSMC_M2
GO:0097120	0.41	0.77	4	46	receptor localization to synapse	BP	1	CLSTN1,GRASP,LRRC7,STX3	cyan	VSMC_M2
GO:0072676	0.42	0.74	6	72	lymphocyte migration	BP	1	XG,ECM1,IL27RA,HSD3B7,GBA,TNFRSF14	cyan	VSMC_M2
GO:0009063	0.42	0.73	7	84	cellular amino acid catabolic process	BP	1	DDAH2,BCKDHB,AASS,ECHS1,ACAT1,QDPR,ASPA	cyan	VSMC_M2
GO:0061640	0.42	0.73	7	87	cytoskeleton-dependent cytokinesis	BP	1	RHOB,CHMP4B,CHMP3,LZTS2,SNX33,IST1,TMEM250	cyan	VSMC_M2
GO:1902105	0.42	0.69	15	193	regulation of leukocyte differentiation	BP	1	IRF1,GLI3,LRRC17,TMEM176B,PNP,TLR3,LEF1,FES,BMP4,ERBB2,ZFP36L1,ABL1,IL34,TMEM176A,ZFPM1	cyan	VSMC_M2
GO:0070167	0.42	0.74	6	74	regulation of biomineral tissue development	BP	1	ATRAID,PKDCC,ECM1,LTBP3,BMP4,ISG15	cyan	VSMC_M2
GO:0090596	0.42	0.69	15	198	sensory organ morphogenesis	BP	1	TSHZ1,EFEMP1,MEIS1,GLI3,BAX,SLITRK6,RARG,MAN2A1,FOXF2,WNT2B,BMP4,NAGLU,EPHA2,DVL1,COL8A1	cyan	VSMC_M2
GO:0031401	0.42	0.64	55	747	positive regulation of protein modification process	BP	1	FLOT1,DAXX,CARD10,GPNMB,NRP1,NOP53,FZD4,CAB39L,ATG7,CAMK1,FGFR1,SMPD1,CLIP3,ANGPT4,MAP3K12,IGF1,TLR3,EFNA5,ARRDC3,CAMKK2,SFRP2,PRKCD,SRC,LRP4,MOB2,CD81,NDN,CHRNA7,TIRAP,VEGFD,VEGFB,BMP4,HDAC6,ARRB2,GABARAP,ERBB2,BRAT1,NTRK1,TP53,GBA,SLC51B,NUPR1,GPRC5B,PDGFRB,MTA1,MAP2K3,TRAF4,DVL1,TNFRSF14,AXIN1,ABL1,IL34,CALM3,CDK9,SDC4	cyan	VSMC_M2
GO:0010761	0.42	0.77	4	46	fibroblast migration	BP	1	AKAP12,APPL2,PML,SDC4	cyan	VSMC_M2
GO:0050803	0.42	0.69	13	170	regulation of synapse structure or activity	BP	1	SLC17A7,APOE,SLITRK6,CAMK1,LZTS3,LRP4,KIF1A,DLG5,NTRK1,PTPRS,AGRN,CLSTN1,ABL1	cyan	VSMC_M2
GO:0050732	0.42	0.77	4	46	negative regulation of peptidyl-tyrosine phosphorylation	BP	1	SOCS3,SH3BP5,SFRP2,PRKCD	cyan	VSMC_M2
GO:0043281	0.42	0.69	12	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MTCH1,GSN,BAX,SFRP2,SRC,CASP10,ADORA2A,DNAJB6,ARRB2,CASP9,PML,CARD8	cyan	VSMC_M2
GO:0002761	0.42	0.73	7	86	regulation of myeloid leukocyte differentiation	BP	1	LRRC17,TLR3,LEF1,FES,ZFP36L1,IL34,ZFPM1	cyan	VSMC_M2
GO:0046785	0.42	0.74	6	74	microtubule polymerization	BP	1	TPPP2,CLIP3,TPPP,FES,PRUNE1,ABL1	cyan	VSMC_M2
GO:0034220	0.42	0.63	56	765	ion transmembrane transport	BP	1	TRPM3,ATP10D,KCNQ5,SLC17A7,STOM,BAX,UQCRH,BIN1,ABCB8,SLC6A9,EHD3,SLC26A11,SLC4A9,FOLR2,SLC15A4,SLC7A2,ATP4A,SCN1B,SNTA1,SLC38A7,GLRB,CACNB3,PLCG1,CHRNA7,CAPN3,CACNA2D2,TPCN2,ANXA9,CLCN2,TCN2,LINC02210-CRHR1,KCND3,ORAI2,CAPN1,WNK4,CHRNE,PRKACA,CLCN6,TMEM175,ORAI3,ATP8B2,GRIA1,ATOX1,ABCC1,MCOLN1,PIEZO2,MFSD12,ABL1,ATP6V0D1,SLC8A3,CBARP,KCND2,CALM3,CLIC2,LASP1,CLIC3	cyan	VSMC_M2
GO:0040014	0.42	0.77	4	47	regulation of multicellular organism growth	BP	1	GPAT4,IGF1,BBS2,STAT5A	cyan	VSMC_M2
GO:0043506	0.42	0.77	4	46	regulation of JUN kinase activity	BP	1	FZD4,MAP3K12,SFRP2,MAPK8IP1	cyan	VSMC_M2
GO:0007098	0.42	0.71	9	115	centrosome cycle	BP	1	MARK4,KAT2B,POC1B,CHMP4B,CHMP3,FES,ARHGEF10,CROCC,FBXW5	cyan	VSMC_M2
GO:0070482	0.42	0.67	21	280	response to oxygen levels	BP	1	HMOX1,NOP53,ATG7,ANGPT4,SRC,CACNB3,MMP2,CHRNA7,PTGIS,VEGFD,VEGFB,ZFP36L1,TP53,ADAM15,PDGFRB,CBFA2T3,SLC2A8,ATP6V0D1,SLC8A3,KCND2,PML	cyan	VSMC_M2
GO:0043551	0.42	0.77	4	47	regulation of phosphatidylinositol 3-kinase activity	BP	1	SOCS3,SRC,PDGFRB,WDR81	cyan	VSMC_M2
GO:0048857	0.42	0.77	4	46	neural nucleus development	BP	1	NFIB,HOXB1,HOXB2,CALM3	cyan	VSMC_M2
GO:0000041	0.42	0.72	7	86	transition metal ion transport	BP	1	SLC6A9,ARHGAP1,TCN2,B2M,ATOX1,MCOLN1,RAB11B	cyan	VSMC_M2
GO:0010817	0.42	0.66	25	331	regulation of hormone levels	BP	1	FZD4,CYP2S1,LTBP4,PLB1,RAB11FIP1,EFNA5,CTSB,PNPLA2,PCSK6,NFKB1,HADH,CTSK,FURIN,CLCN2,LINC02210-CRHR1,STARD3,SLC16A2,RASL10B,DHRS13,PHPT1,RAB11FIP3,H6PD,CHST8,DGAT1,RAB11B	cyan	VSMC_M2
GO:0090559	0.43	0.75	5	59	regulation of membrane permeability	BP	1	BAX,HEG1,TP53,RHOT2,ZNF205	cyan	VSMC_M2

GO:0030003	0.43	0.64	32	434	cellular cation homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,BAX,APOE,SLC6A9,SLC4A9,ACKR4,ATP4A,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,ERFE,CYB561,GRN,PRKACA,TMEM175,GRIA1,MCOLN1,ABL1,ATP6V0D1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0061371	0.43	0.76	4	47	determination of heart left/right asymmetry	BP	1	NDRG4,VANGL2,DNAAF1,GATA4	cyan	VSMC_M2
GO:0031341	0.43	0.76	4	46	regulation of cell killing	BP	1	LAMP1,B2M,ARRB2,CD55	cyan	VSMC_M2
GO:1902893	0.43	0.76	4	47	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	NFIB,WT1,BMP4,TP53	cyan	VSMC_M2
GO:1902807	0.43	0.74	5	60	negative regulation of cell cycle G1/S phase transition	BP	1	GPNMB,APBB1,TP53,KANK2,PML	cyan	VSMC_M2
GO:0110149	0.43	0.73	6	75	regulation of biomineralization	BP	1	ATRAID,PKDCC,ECM1,LTBP3,BMP4,ISG15	cyan	VSMC_M2
GO:0006081	0.43	0.76	4	46	cellular aldehyde metabolic process	BP	1	CLCN2,DHRS13,HAGH,PDXK	cyan	VSMC_M2
GO:0036294	0.43	0.69	10	129	cellular response to decreased oxygen levels	BP	1	HMOX1,NOP53,ANGPT4,SRC,CACNB3,PTGIS,ZFP36L1,TP53,SLC8A3,KCND2	cyan	VSMC_M2
GO:0098660	0.43	0.63	42	574	inorganic ion transmembrane transport	BP	1	TRPM3,KCNQ5,SLC17A7,STOM,BAX,UQCRH,BIN1,ABCB8,SLC6A9,EHD3,SLC26A11,SLC4A9,SLC15A4,ATP4A,SCN1B,SNTA1,GLRB,CACNB3,PLCG1,CHRNA7,CAPN3,CACNA2D2,TPCN2,ANXA9,TCN2,LINC02210-CRHR1,KCND3,ORAI2,WNK4,PRKACA,CLCN6,TMEM175,ORAI3,ATOX1,MCOLN1,ABL1,ATP6V0D1,SLC8A3,CBARP,KCND2,CALM3,CLIC2	cyan	VSMC_M2
GO:0007416	0.43	0.69	10	132	synapse assembly	BP	1	PLXNB2,SLITRK6,EFNB2,LRP4,DLG5,NTRK1,PTPRS,DVL1,AGRN,CLSTN1	cyan	VSMC_M2
GO:0046503	0.43	0.76	4	47	glycerolipid catabolic process	BP	1	PLA2G7,PNPLA2,DAGLA,PNPLA7	cyan	VSMC_M2
GO:0038127	0.43	0.71	8	102	ERBB signaling pathway	BP	1	EFEMP1,RHBDF2,SHKBP1,SRC,PLCG1,SHC1,RHBDF1,ABL1	cyan	VSMC_M2
GO:1904950	0.43	0.71	8	100	negative regulation of establishment of protein localization	BP	1	OS9,APOE,RHBDF2,RAB11FIP1,PKDCC,HADH,RAB11FIP3,RHBDF1	cyan	VSMC_M2
GO:0034446	0.43	0.71	7	89	substrate adhesion-dependent cell spreading	BP	1	NRP1,FZD4,EFNA5,SRC,ATRNL1,LAMB2,ABL1	cyan	VSMC_M2
GO:0010629	0.43	0.62	56	766	negative regulation of gene expression	BP	1	PYM1,HMOX1,APPL2,ITGB8,GPNMB,VIM,APOE,BCL3,ZFP36,SAMD4B,KAT2B,IGF1,PATL1,CAST,SFRP2,PRKCD,BPI,CHRNA7,IKBKE,TIRAP,TUSC2,NFKB1,SPOCD1,LEF1,FURIN,GATA5,HELZ2,RNASEL,MOV10,HOMER3,BMP4,ZNF503,DHX58,ARRB2,EPHA2,SERPINE2,ZFP36L1,IL27RA,TP53,GBA,ADAR,ACP5,CENPV,TMEM98,PTPRS,ABCD1,INPP5E,MIR197,GAS1,MEX3D,SERPINF1,PML,CARD8,NFKBIL1,BST2,ZFPM1	cyan	VSMC_M2
GO:0021536	0.44	0.76	4	47	diencephalon development	BP	1	NRP1,BAX,PTCHD1,BMP4	cyan	VSMC_M2
GO:0016125	0.44	0.70	9	114	sterol metabolic process	BP	1	CYB5R3,APOE,SMPD1,CYP4V2,OSBPL5,STARD3,NPC2,GBA,LCAT	cyan	VSMC_M2
GO:0060113	0.44	0.76	4	48	inner ear receptor cell differentiation	BP	1	SLITRK6,BMP4,NAGLU,SDC4	cyan	VSMC_M2
GO:0014015	0.44	0.75	4	48	positive regulation of gliogenesis	BP	1	BIN1,SERPINE2,ASPA,IL34	cyan	VSMC_M2
GO:0032273	0.44	0.69	9	116	positive regulation of protein polymerization	BP	1	GSN,BIN1,TPPP2,C15orf62,CTTN,TPPP,FES,ARPC5,ALOX15	cyan	VSMC_M2
GO:1904062	0.44	0.65	18	241	regulation of cation transmembrane transport	BP	1	STOM,BAX,BIN1,SLC6A9,EHD3,SCN1B,SNTA1,CACNB3,PLCG1,CAPN3,LINC02210-CRHR1,CAPN1,WNK4,PRKACA,ABL1,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0002274	0.44	0.67	12	156	myeloid leukocyte activation	BP	1	HMOX1,ITGB8,TLR3,PLSCR1,PRKCD,BPI,FES,GRN,TMEM106A,CPLX2,PTGDS,SBNO2	cyan	VSMC_M2
GO:0048659	0.44	0.68	10	128	smooth muscle cell proliferation	BP	1	HMOX1,APOE,IGF1,NDRG4,TGM2,MMP2,STAT1,GNAI2,BMP4,PDGFRB	cyan	VSMC_M2
GO:0048477	0.44	0.73	5	62	oogenesis	BP	1	RPS6KA2,IGF1,HEXB,SRC,REC8	cyan	VSMC_M2
GO:0009267	0.44	0.68	10	130	cellular response to starvation	BP	1	EHMT2,RRAGC,ATG7,GAS2L1,WNT2B,WDR45,GABARAP,TP53,GBA,NPRL3	cyan	VSMC_M2
GO:0009611	0.44	0.63	31	422	response to wounding	BP	1	HMOX1,GLI3,NRP1,BAX,APOE,ZFP36,SMPD1,IGF1,GGCX,SERPING1,PLSCR1,PRKCD,SRC,HPS6,RGMA,LAMB2,FIBP,ADORA2A,GRN,FKBP10,ALOX15,SERPINE2,ERBB2,ZFP36L1,NTRK1,PDGFRB,PTPRS,FOXC2,PLPP3,GATA4,SDC4	cyan	VSMC_M2
GO:0010952	0.44	0.68	11	142	positive regulation of peptidase activity	BP	1	MTCH1,GSN,BAX,SFRP2,APH1A,CASP10,GRN,PCOLCE,CASP9,PML,CARD8	cyan	VSMC_M2
GO:0001890	0.44	0.69	9	117	placenta development	BP	1	ITGB8,SOCS3,CTSB,LEF1,PLCD3,DNAJB6,ZFP36L1,PLAC1,JUNB	cyan	VSMC_M2
GO:0035914	0.44	0.75	4	48	skeletal muscle cell differentiation	BP	1	BCL9,NUPR1,EEF2,EMD	cyan	VSMC_M2
GO:0007568	0.44	0.65	19	252	aging	BP	1	ATG7,TIMP2,SERPING1,PRKCD,GNAO1,B2M,CASP9,NTRK1,TP53,GBA,PPP1R9B,ULK3,PDGFRB,MAP2K3,EEF2,ABL1,KRT25,SERPINF1,PML	cyan	VSMC_M2
GO:0009306	0.45	0.65	20	266	protein secretion	BP	1	P3H1,APOE,RHBDF2,RAB11FIP1,APBB1,GNPTAB,IGF1,EFNA5,HADH,DISP1,RHBDD3,M6PR,ADORA2A,PORCN,LLGL1,NAGPA,PHPT1,RAB11FIP3,RHBDF1,RAB11B	cyan	VSMC_M2
GO:0035592	0.45	0.65	20	266	establishment of protein localization to extracellular region	BP	1	P3H1,APOE,RHBDF2,RAB11FIP1,APBB1,GNPTAB,IGF1,EFNA5,HADH,DISP1,RHBDD3,M6PR,ADORA2A,PORCN,LLGL1,NAGPA,PHPT1,RAB11FIP3,RHBDF1,RAB11B	cyan	VSMC_M2
GO:0061614	0.45	0.75	4	48	pri-miRNA transcription by RNA polymerase II	BP	1	NFIB,WT1,BMP4,TP53	cyan	VSMC_M2
GO:0031113	0.45	0.75	4	49	regulation of microtubule polymerization	BP	1	CLIP3,FES,PRUNE1,ABL1	cyan	VSMC_M2
GO:1902882	0.45	0.72	6	74	regulation of response to oxidative stress	BP	1	ATG7,GGT7,AIFM2,HDAC6,ABCD1,GATA4	cyan	VSMC_M2
GO:0060761	0.45	0.73	5	61	negative regulation of response to cytokine stimulus	BP	1	ECM1,SLIT2,ADAR,ISG15,CARD8	cyan	VSMC_M2
GO:0001708	0.45	0.73	5	62	cell fate specification	BP	1	EHMT2,GLI3,NRP1,SFRP2,AR	cyan	VSMC_M2
GO:0061013	0.45	0.67	11	144	regulation of mRNA catabolic process	BP	1	VIM,ZFP36,SAMD4B,PATL1,PRKCD,IKBKE,TIRAP,RNASEL,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0044265	0.45	0.60	69	947	cellular macromolecule catabolic process	BP	1	PYM1,OS9,EIF3H,KCTD17,CUL9,RNF144A,BAX,NOP53,TRIM13,VIM,APOE,AGAP3,ATRAID,ZFP36,SAMD4B,SGSH,RNF213,TPP1,RBCK1,CHMP4B,TP53INP2,PATL1,EDEM2,CTSB,WWTR1,PRKCD,FOXF2,CD81,IKBKE,TIRAP,UBA7,DCAF11,CTSK,FURIN,VPS11,HELZ2,RNASEL,MAGEF1,MUS81,MOV10,ADAMTS7,MAEA,HDAC6,ARRB2,GABARAP,GIPC1,PRKACA,ZFP36L1,UBQLN2,UBQLN4,GBA,NUPR1,MTA1,CLPP,UBXN6,WDR81,DVL1,ISG15,ELOB,FBXW5,AXIN1,RHBDF1,CBFA2T3,RNF166,OAS2,ABCA2,MEX3D,PML,PSMB9	cyan	VSMC_M2
GO:0051058	0.45	0.75	4	49	negative regulation of small GTPase mediated signal transduction	BP	1	TIMP2,HEG1,CGNL1,SLIT2	cyan	VSMC_M2
GO:0002708	0.45	0.73	5	61	positive regulation of lymphocyte mediated immunity	BP	1	STAT6,LAMP1,CD81,B2M,CD55	cyan	VSMC_M2

GO:0097529	0.45	0.67	11	142	myeloid leukocyte migration	BP	1	PLA2G7,RHOG,CD81,TIRAP,XG,VEGFD,VEGFB,NBL1,SLIT2,IL34,RPS19	cyan	VSMC_M2
GO:0030278	0.45	0.70	7	91	regulation of ossification	BP	1	ATRAID,PKDCC,LRP4,ECM1,LTBP3,BMP4,ISG15	cyan	VSMC_M2
GO:0019319	0.45	0.72	5	61	hexose biosynthetic process	BP	1	KAT2B,ERFE,G6PC3,PDK2,FAM3A	cyan	VSMC_M2
GO:0031102	0.45	0.74	4	49	neuron projection regeneration	BP	1	RGMA,LAMB2,GRN,PTPRS	cyan	VSMC_M2
GO:0009247	0.45	0.72	5	61	glycolipid biosynthetic process	BP	1	B3GALT4,ST3GAL1,B4GALT5,PIGQ,AL157935.2	cyan	VSMC_M2
GO:0007517	0.45	0.64	19	259	muscle organ development	BP	1	MYL6B,TCF21,FLOT1,ZFPM2,IGF1,WT1,POU6F1,CAPN3,BCL9,LEF1,DISP1,HEG1,BMP4,TCF12,NUPR1,EEF2,FOXC2,ZFPM1,EMD	cyan	VSMC_M2
GO:0010810	0.46	0.66	13	175	regulation of cell-substrate adhesion	BP	1	RRAS,NRP1,FZD4,EFNA5,EPHA3,SRC,EGFL6,JUP,ALOX15,ADAM15,ABL1,SDC4,COL8A1	cyan	VSMC_M2
GO:0055008	0.46	0.74	4	50	cardiac muscle tissue morphogenesis	BP	1	ZFPM2,HEG1,FOXC2,ZFPM1	cyan	VSMC_M2
GO:0016447	0.46	0.74	4	48	somatic recombination of immunoglobulin gene segments	BP	1	STAT6,SLC15A4,IL27RA,TCF3	cyan	VSMC_M2
GO:0097305	0.46	0.66	13	174	response to alcohol	BP	1	EHMT2,KLF9,RPL15,ADCY1,JUP,SLIT2,PPP1R9B,ADAM15,EEF2,H6PD,ABCA2,CALM3,RGS19	cyan	VSMC_M2
GO:0002702	0.46	0.70	6	75	positive regulation of production of molecular mediator of immune response	BP	1	STAT6,CD81,B2M,GPRC5B,TNFRSF14,CD55	cyan	VSMC_M2
GO:0002381	0.46	0.74	4	48	immunoglobulin production involved in immunoglobulin-mediated immune response	BP	1	STAT6,SLC15A4,B2M,IL27RA	cyan	VSMC_M2
GO:0000281	0.46	0.72	5	63	mitotic cytokinesis	BP	1	RHOB,CHMP4B,CHMP3,LZTS2,SNX33	cyan	VSMC_M2
GO:0042632	0.46	0.72	5	62	cholesterol homeostasis	BP	1	APOE,PLSCR3,NPC2,LCAT,ABCA2	cyan	VSMC_M2
GO:0006090	0.46	0.70	6	76	pyruvate metabolic process	BP	1	ME3,IGF1,PDK2,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0014033	0.46	0.70	6	77	neural crest cell differentiation	BP	1	NRP1,SEMA3B,SEMA4B,SEMA6C,BMP4,FOXC2	cyan	VSMC_M2
GO:0032722	0.46	0.73	4	48	positive regulation of chemokine production	BP	1	HMOX1,TLR3,TIRAP,IL17RA	cyan	VSMC_M2
GO:0022604	0.46	0.63	19	261	regulation of cell morphogenesis	BP	1	PLXNB2,ARHGAP18,NRP1,RHOB,FZD4,ARAP1,RHOG,EFNA5,HEXB,SRC,C15orf62,FES,BCL9L,MOV10,RND2,CAPZB,ZMYM3,DVL1,ABL1	cyan	VSMC_M2
GO:0034250	0.46	0.67	10	130	positive regulation of cellular amide metabolic process	BP	1	PYM1,PLXNB2,VIM,BCL3,MIF4GD,PRKCD,CHRNA7,ERBB2,EEF2,ABCA2	cyan	VSMC_M2
GO:0008203	0.46	0.68	8	103	cholesterol metabolic process	BP	1	CYB5R3,APOE,SMPD1,OSBPL5,STARD3,NPC2,GBA,LCAT	cyan	VSMC_M2
GO:1901264	0.46	0.71	5	61	carbohydrate derivative transport	BP	1	SLC15A4,G6PC3,PSAP,NPC2,ABCD1	cyan	VSMC_M2
GO:0050708	0.46	0.64	15	200	regulation of protein secretion	BP	1	P3H1,APOE,RHBDF2,RAB11FIP1,APBB1,IGF1,EFNA5,HADH,DISP1,RHBDD3,ADORA2A,LLGL1,PHPT1,RAB11FIP3,RHBDF1	cyan	VSMC_M2
GO:0019217	0.46	0.71	5	62	regulation of fatty acid metabolic process	BP	1	APPL2,SLC45A3,ERFE,PDK2,ABCD1	cyan	VSMC_M2
GO:1902305	0.46	0.73	4	50	regulation of sodium ion transmembrane transport	BP	1	STOM,SCN1B,SNTA1,WNK4	cyan	VSMC_M2
GO:0019932	0.47	0.64	16	218	second-messenger-mediated signaling	BP	1	DDAH2,APOE,ACKR4,IGF1,CAMKK2,PLCG1,TPCN2,ADGRB2,ADCY1,HOMER3,PRKACA,PDK2,PPP1R9B,MCOLN1,CALM3,CLIC2	cyan	VSMC_M2
GO:1901361	0.47	0.61	29	395	organic cyclic compound catabolic process	BP	1	PYM1,MOXD1,HMOX1,BAX,VIM,APOE,ACAA1,PNP,ZFP36,SAMD4B,PATL1,NEIL2,PRKCD,IKBKE,TIRAP,STS,HELZ2,RNASEL,MUS81,MOV10,ACAT1,NUDT13,QDPR,ZFP36L1,ABCC1,ABCD1,DPYD,OAS2,MEX3D	cyan	VSMC_M2
GO:0098655	0.47	0.60	45	623	cation transmembrane transport	BP	1	TRPM3,KCNQ5,SLC17A7,STOM,BAX,UQCRH,BIN1,ABCB8,SLC6A9,EHD3,SLC4A9,SLC15A4,SLC7A2,ATP4A,SCN1B,SNTA1,SLC38A7,CACNB3,PLCG1,CHRNA7,CAPN3,CACNA2D2,TPCN2,ANXA9,TCN2,LINC02210-CRHR1,KCND3,ORAI2,CAPN1,WNK4,CHRNE,PRKACA,TMEM175,ORAI3,ATOX1,MCOLN1,PIEZO2,MFSD12,ABL1,ATP6V0D1,SLC8A3,CBARP,KCND2,CALM3,CLIC2	cyan	VSMC_M2
GO:0003143	0.47	0.73	4	50	embryonic heart tube morphogenesis	BP	1	NDRG4,VANGL2,DNAAF1,GATA4	cyan	VSMC_M2
GO:0036473	0.47	0.70	6	76	cell death in response to oxidative stress	BP	1	ATG7,PRKCD,STK25,HDAC6,PML,GATA4	cyan	VSMC_M2
GO:0055013	0.47	0.71	5	65	cardiac muscle cell development	BP	1	CTDP1,IGF1,BMP4,PDGFRB,GATA4	cyan	VSMC_M2
GO:0048706	0.47	0.67	8	105	embryonic skeletal system development	BP	1	GLI3,BMP4,PCGF2,HOXB1,HOXB2,HOXB4,MED12,FOXC2	cyan	VSMC_M2
GO:0051899	0.47	0.71	5	66	membrane depolarization	BP	1	SCN1B,SRC,ADORA2A,ABCD1,ABL1	cyan	VSMC_M2
GO:0090263	0.47	0.68	7	92	positive regulation of canonical Wnt signaling pathway	BP	1	ADGRA2,SFRP2,SRC,NFKB1,FAM53B,JUP,GPRC5B	cyan	VSMC_M2
GO:0045185	0.47	0.69	6	80	maintenance of protein location	BP	1	OS9,GSN,DZIP1,NFKBIA,NBL1,PML	cyan	VSMC_M2
GO:0060191	0.47	0.71	5	63	regulation of lipase activity	BP	1	FGFR1,PCSK6,FURIN,PDGFRB,ABL1	cyan	VSMC_M2
GO:1903051	0.47	0.72	4	50	negative regulation of proteolysis involved in cellular protein catabolic process	BP	1	EIF3H,NOP53,GIPC1,PML	cyan	VSMC_M2
GO:0048193	0.47	0.62	19	259	Golgi vesicle transport	BP	1	TAPBP,GGA1,AP2A1,EHD3,LAMP1,PKDCC,ERGIC3,BBS2,EXOC2,SYS1,OSBPL5,TMEM115,EXOC8,USE1,ERGIC1,LLGL1,SGSM2,GAS1,PLPP3	cyan	VSMC_M2
GO:0050870	0.47	0.66	10	130	positive regulation of T cell activation	BP	1	GLI3,PNP,IGF1,SRC,CD81,LEF1,B2M,IL27RA,TNFRSF14,CD55	cyan	VSMC_M2
GO:0098662	0.47	0.59	39	541	inorganic cation transmembrane transport	BP	1	TRPM3,KCNQ5,SLC17A7,STOM,BAX,UQCRH,BIN1,ABCB8,SLC6A9,EHD3,SLC4A9,SLC15A4,ATP4A,SCN1B,SNTA1,CACNB3,PLCG1,CHRNA7,CAPN3,CACNA2D2,TPCN2,ANXA9,TCN2,LINC02210-CRHR1,KCND3,ORAI2,WNK4,PRKACA,TMEM175,ORAI3,ATOX1,MCOLN1,ABL1,ATP6V0D1,SLC8A3,CBARP,KCND2,CALM3,CLIC2	cyan	VSMC_M2
GO:0033002	0.48	0.64	13	174	muscle cell proliferation	BP	1	ZFPM2,HMOX1,MEIS1,APOE,IGF1,NDRG4,TGM2,MMP2,STAT1,GNAI2,BMP4,PDGFRB,FOXC2	cyan	VSMC_M2
GO:0071456	0.48	0.66	9	119	cellular response to hypoxia	BP	1	HMOX1,NOP53,ANGPT4,SRC,PTGIS,ZFP36L1,TP53,SLC8A3,KCND2	cyan	VSMC_M2
GO:0016311	0.48	0.61	25	342	dephosphorylation	BP	1	CTDP1,PPP6R2,HDDC2,PTPRK,CDC14C,SMPD1,PRKCD,SRC,PTPN13,GNAI2,SSH3,TNS3,PRUNE1,G6PC3,GBA,PPP1R9B,ACP5,PDGFRB,PTPRS,PHPT1,INPP5E,PLPP2,PLPP3,CALM3,CPPED1	cyan	VSMC_M2
GO:0050878	0.48	0.62	20	273	regulation of body fluid levels	BP	1	APOE,GPAT4,GGCX,SERPING1,PLSCR1,PRKCD,SRC,EXT2,HPS6,GNAI2,HEG1,FIBP,ADORA2A,WNK4,STAT5A,SERPINE2,PRKACA,MLLT6,GBA,OAS2	cyan	VSMC_M2

GO:0022607	0.48	0.56	159	2230	cellular component assembly	BP	1	FLOT1,EHMT2,PLXNB2,EIF3H,AFDN,PACSIN2,TAPBP,DAXX,PTPRK,ARHGAP18,IBA57,CDC14C,GSDMD,CARD10,KCTD17,KIFC2,TRPM3,APPL2,RSPH9,HIGD2A,BBS9,COBL,GSN,NRP1,BAX,CCDC114,NOP53,MARK4,BIN1,APOE,ATG7,SHKBP1,SLITRK6,EHD3,DZIP1,TPPP2,RNF213,ARAP1,HGS,KAT2B,EIF3K,RFTN1,RHOG,EFNB2,POC1B,CLIP3,ANGPT4,EIF3F,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,WWTR1,PRKCD,EPHA3,SRC,LRP4,BBS2,MMS19,C15orf62,SORBS3,LZTS2,PHACTR1,IKBKE,CAPN3,TJP1,TIRAP,CTTN,TPPP,HIST1H1C,DISP1,SV2A,SSH3,LAMB2,NDUFAF3,REC8,FES,PRUNE1,VPS11,HEG1,VANGL2,STK25,WIPF1,ARPC5,LTBP3,B2M,KCND3,ARHGEF10,BCR,RPGR,ADD1,CAPZB,CC2D2A,DLG5,HDAC6,ARHGEF10L,WDR45,CROCC,DNAJB6,FKBP10,JUP,ALOX15,EPHA2,GABARAP,CGNL1,SMIM20,PRKACA,UBQLN2,NTRK1,SLIT2,TMEM175,TP53,GBA,PPP1R9B,NUPR1,ADAR,WARS,CENPV,PDGFRB,MCOLN1,FLII,LLGL1,PTPRS,DVL1,AGRN,ISG15,ELOB,TRAF7,SLC9A3R2,NDOR1,NPHP4,WDR90,ENTR1,AXIN1,NPRL3,CLSTN1,AIF1L,ABL1,DNAAF1,ATMIN,IST1,LCAT,ATP6V0D1,ABCA2,RPS15,KCND2,RAB43,DGAT1,PML,RPS19,GEMIN8,CARD8,BMF,GCHFR,TMEM250,SDC4,TSPAN4	cyan	VSMC_M2
GO:0051963	0.48	0.69	6	79	regulation of synapse assembly	BP	1	SLITRK6,DLG5,NTRK1,PTPRS,AGRN,CLSTN1	cyan	VSMC_M2
GO:0036465	0.48	0.70	5	64	synaptic vesicle recycling	BP	1	SLC17A7,PLD2,STON2,SH3GL1,CALM3	cyan	VSMC_M2
GO:0051146	0.48	0.62	16	220	striated muscle cell differentiation	BP	1	CTDP1,FLOT1,PLD3,EFNB2,IGF1,WT1,CD81,CAPN3,BCL9,HDAC5,BMP4,ARRB2,PDGFRB,FLII,PTGFRN,GATA4	cyan	VSMC_M2
GO:0097696	0.48	0.66	8	105	receptor signaling pathway via STAT	BP	1	STAT6,BCL3,SOCS3,HGS,IGF1,STAT1,STAT5A,OCIAD2	cyan	VSMC_M2
GO:0006873	0.48	0.59	32	444	cellular ion homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,BAX,APOE,SLC6A9,SLC4A9,ACKR4,ATP4A,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,ERFE,CYB561,GRN,PRKACA,TMEM175,GRIA1,MCOLN1,ABL1,ATP6V0D1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0017038	0.48	0.63	13	174	protein import	BP	1	APPL2,GLI3,APOE,BCL3,PRKCD,FAM53B,NFKBIA,BMP4,JUP,TP53,SNX33,TSC2,PML	cyan	VSMC_M2
GO:0097581	0.48	0.68	6	78	lamellipodium organization	BP	1	SRC,CTTN,ARPC5,CAPZB,EPHA2,SLIT2	cyan	VSMC_M2
GO:0045639	0.48	0.68	6	77	positive regulation of myeloid cell differentiation	BP	1	STAT1,LEF1,FES,ZFP36L1,ISG15,IL34	cyan	VSMC_M2
GO:0046620	0.48	0.68	6	78	regulation of organ growth	BP	1	CTDP1,ZFPM2,MEIS1,IGF1,WT1,FOXC2	cyan	VSMC_M2
GO:0071840	0.48	0.54	343	4827	cellular component organization or biogenesis	BP	1	CTDP1,MMP19,PYM1,PMEL,RAB5B,ADAMTS2,FLOT1,MSH5,EHMT2,PLXNB2,EIF3H,RPS6KA2,AFDN,DEPTOR,PACSIN2,TAPBP,DAXX,TGFBI,PTPRK,ARHGAP18,IBA57,CDC14C,GSDMD,MTCH1,CARD10,KCTD17,NFIB,KIFC2,ARHGAP39,CUL9,TRPM3,APPL2,ATP10D,RSPH9,HIGD2A,PLA2G7,P3H1,BBS9,ELMO1,COBL,AKT1S1,GLI3,AP2A1,GSN,SLC17A7,NRP1,RHOB,BAX,CCDC114,NOP53,LURAP1,FZD4,MARK4,VIM,BIN1,APOE,BCL3,ATG7,LTBP4,SHKBP1,SLITRK6,CAMK1,EHD3,TEP1,DZIP1,TPPP2,RPS16,GAA,PAK4,RNF213,ARAP1,NPTX1,FOLR2,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,EFNB2,POC1B,DCLK1,SMPD1,TMEM108,LZTS3,APBB1,TPP1,MMP17,CLIP3,PPFIBP2,GTF3A,ANGPT4,EIF3F,RARG,SCN1B,GNPTAB,IGF1,REEP5,SNTA1,MAN2A1,WT1,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,CAST,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,NDRG4,NDRG3,GLRB,PRKCD,EPHA3,SRC,CACNB3,LRP4,RIOX2,BBS2,MMS19,FOXF2,GNAO1,PDLIM2,C15orf62,PYROXD2,SORBS3,NISCH,MMP2,PNPLA2,LZTS2,PHACTR1,HPS6,NDN,CHRNA7,IKBKE,OSBPL5,CAPN3,TJP1,TIRAP,MRPL36,CTTN,BOC,TPCN2,SEMA3B,TPPP,HIST1H1C,RGMA,DISP1,B4GALT5,SV2A,SSH3,EGFL6,LAMB2,EXOC8,NDUFAF3,REC8,SEMA4B,CTSK,NCKIPSD,GAS2L1,ADCY1,FES,PRUNE1,FURIN,VPS11,SEMA6C,TACC2,HEG1,VANGL2,KIF1A,RERG,PARD3B,STK25,OLFML2B,RNASEL,MUS81,CTNNA3,WIPF1,ARPC5,MOV10,LTBP3,B2M,DPF2,KCND3,ARHGEF10,BCR,ADORA2A,FYCO1,RPGR,AIFM2,ADAMTS7,CDC42BPG,GRN,HDAC5,GPC2,RND2,VAT1,ADD1,BMP4,NAGLU,MAEA,LDB2,NBL1,CAPZB,MAP1S,CC2D2A,TECPR1,DLG5,USE1,HDAC6,PQBP1,ARHGEF10L,WDR45,PLD2,CROCC,DNAJB6,FKBP10,ARRB2,JUP	cyan	VSMC_M2
GO:0006112	0.48	0.69	5	65	energy reserve metabolic process	BP	1	STK40,GAA,IGF1,STBD1,PHKG1	cyan	VSMC_M2
GO:0006898	0.49	0.62	14	192	receptor-mediated endocytosis	BP	1	FLOT1,AP2A1,APOE,TBC1D5,TMEM108,CD81,CTTN,TPCN2,B2M,M6PR,ARRB2,UBQLN2,GRIA1,ABCA2	cyan	VSMC_M2
GO:0043487	0.49	0.64	11	148	regulation of RNA stability	BP	1	VIM,ZFP36,SAMD4B,PATL1,PRKCD,IKBKE,TIRAP,RNASEL,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0048278	0.49	0.71	4	50	vesicle docking	BP	1	NDRG4,VPS11,CPLX2,STX3	cyan	VSMC_M2
GO:0006414	0.49	0.71	4	50	translational elongation	BP	1	ABTB1,EEF2,DPH7,EEF1A2	cyan	VSMC_M2
GO:0050810	0.49	0.71	4	50	regulation of steroid biosynthetic process	BP	1	APOE,NFKB1,CLCN2,H6PD	cyan	VSMC_M2
GO:0043406	0.49	0.66	7	93	positive regulation of MAP kinase activity	BP	1	FZD4,FGFR1,MAP3K12,SRC,ERBB2,PDGFRB,IL34	cyan	VSMC_M2
GO:0072503	0.49	0.60	22	306	cellular divalent inorganic cation homeostasis	BP	1	GRINA,KCTD17,BAX,APOE,ACKR4,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,PRKACA,GRIA1,MCOLN1,ABL1,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0070059	0.49	0.71	4	50	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP	1	GRINA,BAX,TP53,PML	cyan	VSMC_M2
GO:0061157	0.49	0.67	6	79	mRNA destabilization	BP	1	ZFP36,SAMD4B,PATL1,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0051262	0.49	0.69	5	66	protein tetramerization	BP	1	TRPM3,APPL2,B2M,TP53,MCOLN1	cyan	VSMC_M2
GO:0051606	0.49	0.64	10	135	detection of stimulus	BP	1	TRPM3,CACNB3,NR2F6,ARRB2,JUP,SERPINE2,NTRK1,PIEZO2,NMT2,CALM3	cyan	VSMC_M2
GO:0007281	0.49	0.62	13	177	germ cell development	BP	1	EHMT2,RPS6KA2,BAX,DZIP1,IGF1,WT1,HEXB,SRC,BBS2,REC8,BMP4,PRKACA,PYGO2	cyan	VSMC_M2
GO:0002931	0.49	0.71	4	51	response to ischemia	BP	1	CASP9,TP53,EEF2,RNLS	cyan	VSMC_M2
GO:0098661	0.49	0.71	4	51	inorganic anion transmembrane transport	BP	1	SLC26A11,GLRB,CLCN6,CLIC2	cyan	VSMC_M2
GO:0071466	0.49	0.66	7	92	cellular response to xenobiotic stimulus	BP	1	EHMT2,ACAA1,CYP2S1,TLR3,QDPR,PPP1R9B,GSTM4	cyan	VSMC_M2
GO:0030193	0.49	0.71	4	50	regulation of blood coagulation	BP	1	APOE,SERPING1,PRKCD,SERPINE2	cyan	VSMC_M2

GO:0006518	0.49	0.57	50	688	peptide metabolic process	BP	1	PYM1,PLXNB2,EIF3H,TAPBP,OPLAH,ACO1,IARS,RPL18,ABTB1,VIM,BIN1,APOE,BCL3,ETHE1,MIF4GD,RPS16,ZFP36,SAMD4B,RPL15,EIF3K,TPP1,EIF3F,IGF1,PATL1,GGT7,SPON1,CPE,CHRNA7,MRPL36,PCSK6,APH1A,FURIN,MOV10,ERBB2,ZFP36L1,WARS,EEF2,DPH7,HAGH,INPP5E,GSTM4,RPL13,ABCA2,RPS15,MEX3D,RPS19,EEF1A2,CLIC2,CLIC3,RPL36A	cyan	VSMC_M2
GO:0050807	0.49	0.62	12	165	regulation of synapse organization	BP	1	APOE,SLITRK6,CAMK1,LZTS3,LRP4,KIF1A,DLG5,NTRK1,PTPRS,AGRN,CLSTN1,ABL1	cyan	VSMC_M2
GO:0002824	0.49	0.69	5	64	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	STAT6,CD81,B2M,IL27RA,CD55	cyan	VSMC_M2
GO:0046902	0.50	0.70	4	50	regulation of mitochondrial membrane permeability	BP	1	BAX,TP53,RHOT2,ZNF205	cyan	VSMC_M2
GO:0031060	0.50	0.70	4	52	regulation of histone methylation	BP	1	EHMT2,AASS,MLLT6,PYGO2	cyan	VSMC_M2
GO:0071300	0.50	0.70	4	52	cellular response to retinoic acid	BP	1	FZD4,RARG,EPHA3,SERPINF1	cyan	VSMC_M2
GO:0051603	0.50	0.56	46	639	proteolysis involved in cellular protein catabolic process	BP	1	OS9,EIF3H,KCTD17,CUL9,RNF144A,NOP53,TRIM13,APOE,AGAP3,RNF213,RBCK1,CHMP4B,TP53INP2,EDEM2,CTSB,WWTR1,FOXF2,UBA7,DCAF11,CTSK,MAGEF1,ADAMTS7,MAEA,HDAC6,ARRB2,GABARAP,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,MTA1,CLPP,UBXN6,WDR81,DVL1,ISG15,ELOB,FBXW5,AXIN1,RHBDF1,CBFA2T3,RNF166,PML,PSMB9	cyan	VSMC_M2
GO:0033692	0.50	0.70	4	52	cellular polysaccharide biosynthetic process	BP	1	IGF1,EXT2,PHKG1,B4GALT5	cyan	VSMC_M2
GO:0048488	0.50	0.70	4	52	synaptic vesicle endocytosis	BP	1	SLC17A7,STON2,SH3GL1,CALM3	cyan	VSMC_M2
GO:0140238	0.50	0.70	4	52	presynaptic endocytosis	BP	1	SLC17A7,STON2,SH3GL1,CALM3	cyan	VSMC_M2
GO:0002688	0.51	0.65	7	92	regulation of leukocyte chemotaxis	BP	1	PLA2G7,TIRAP,VEGFD,VEGFB,NBL1,SLIT2,IL34	cyan	VSMC_M2
GO:0098739	0.51	0.63	9	123	import across plasma membrane	BP	1	SLC6A9,FOLR2,SLC15A4,SLC7A2,ATP4A,SLC5A3,WNK4,SLC16A2,SLC8A3	cyan	VSMC_M2
GO:0061045	0.51	0.69	4	52	negative regulation of wound healing	BP	1	APOE,SERPING1,PRKCD,SERPINE2	cyan	VSMC_M2
GO:0072507	0.51	0.58	23	323	divalent inorganic cation homeostasis	BP	1	GRINA,KCTD17,BAX,APOE,ACKR4,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,PRKACA,GRIA1,MCOLN1,ABL1,CNNM3,SLC8A3,CD55,PML,CALM3,CLIC2	cyan	VSMC_M2
GO:0006633	0.51	0.64	8	107	fatty acid biosynthetic process	BP	1	ACSS1,ACSS2,SLC45A3,PTGIS,ALOX15,ABCD1,PTGDS,GSTM4	cyan	VSMC_M2
GO:0019439	0.51	0.57	27	375	aromatic compound catabolic process	BP	1	PYM1,MOXD1,HMOX1,BAX,VIM,ACAA1,PNP,ZFP36,SAMD4B,PATL1,NEIL2,PRKCD,IKBKE,TIRAP,HELZ2,RNASEL,MUS81,MOV10,ACAT1,NUDT13,QDPR,ZFP36L1,ABCC1,ABCD1,DPYD,OAS2,MEX3D	cyan	VSMC_M2
GO:0046364	0.51	0.67	5	65	monosaccharide biosynthetic process	BP	1	KAT2B,ERFE,G6PC3,PDK2,FAM3A	cyan	VSMC_M2
GO:1900046	0.51	0.69	4	51	regulation of hemostasis	BP	1	APOE,SERPING1,PRKCD,SERPINE2	cyan	VSMC_M2
GO:0055076	0.51	0.63	8	107	transition metal ion homeostasis	BP	1	HMOX1,ACO1,SLC6A9,ERFE,CYB561,B2M,NEO1,ATP6V0D1	cyan	VSMC_M2
GO:0046822	0.51	0.64	7	94	regulation of nucleocytoplasmic transport	BP	1	GLI3,CAMK1,PRKCD,BMP4,JUP,PRKACA,EMD	cyan	VSMC_M2
GO:0010332	0.51	0.69	4	53	response to gamma radiation	BP	1	BAX,TRIM13,TP53,PML	cyan	VSMC_M2
GO:0046425	0.51	0.69	4	52	regulation of receptor signaling pathway via JAK-STAT	BP	1	BCL3,SOCS3,HGS,OCIAD2	cyan	VSMC_M2
GO:0010970	0.51	0.62	10	139	transport along microtubule	BP	1	LAMP1,TMEM108,CLIP3,KIF1A,FYCO1,RPGR,MAP1S,HDAC6,RHOT2,HSBP1	cyan	VSMC_M2
GO:0048878	0.51	0.54	59	832	chemical homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,APPL2,KLF15,BAX,APOE,SLC6A9,SLC4A9,ACKR4,ATP4A,SCN1B,EFNA5,HEXB,SRC,CACNB3,TGM2,PLCG1,EXT2,PNPLA2,STAT1,CHRNA7,CAPN3,TPCN2,GNAI2,SV2A,ERFE,CYB561,B2M,ADORA2A,GRN,WNK4,PLSCR3,PRKACA,MLLT6,TMEM175,NPC2,PDK2,GBA,GRIA1,NEO1,MCOLN1,ABCD1,PHPT1,ABL1,LCAT,ATP6V0D1,ABCA2,CNNM3,SLC8A3,SERPINF1,CD55,DGAT1,PML,GATA4,CALM3,CLIC2,RAB11B	cyan	VSMC_M2
GO:1905515	0.51	0.69	4	53	non-motile cilium assembly	BP	1	BBS2,VANGL2,CC2D2A,ATMIN	cyan	VSMC_M2
GO:0000288	0.51	0.69	4	53	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	BP	1	ZFP36,SAMD4B,PATL1,ZFP36L1	cyan	VSMC_M2
GO:1903034	0.52	0.62	9	123	regulation of response to wounding	BP	1	APOE,SERPING1,PRKCD,RGMA,GRN,SERPINE2,PTPRS,FOXC2,PLPP3	cyan	VSMC_M2
GO:0042306	0.52	0.68	4	52	regulation of protein import into nucleus	BP	1	GLI3,PRKCD,BMP4,JUP	cyan	VSMC_M2
GO:0010812	0.52	0.68	4	53	negative regulation of cell-substrate adhesion	BP	1	FZD4,EFNA5,SRC,ADAM15	cyan	VSMC_M2
GO:0010256	0.52	0.56	30	422	endomembrane system organization	BP	1	FLOT1,PACSIN2,GSN,BIN1,EHD3,FOLR2,HGS,SMPD1,REEP5,CHMP4B,CHMP3,PLSCR1,PRKCD,EXOC8,VPS11,STK25,MYRF,PLEKHM2,SERPINE2,PLSCR3,AR,CPLX2,ATP8B2,SNX33,DYM,ABCD1,IST1,RAB43,STX3,EMD	cyan	VSMC_M2
GO:1900407	0.52	0.66	5	66	regulation of cellular response to oxidative stress	BP	1	ATG7,AIFM2,HDAC6,ABCD1,GATA4	cyan	VSMC_M2
GO:0002821	0.52	0.66	5	66	positive regulation of adaptive immune response	BP	1	STAT6,CD81,B2M,IL27RA,CD55	cyan	VSMC_M2
GO:0050890	0.52	0.58	15	214	cognition	BP	1	EHMT2,APOE,NDRG4,CHRNA7,ADCY1,PTCHD1,B2M,DGCR2,NTRK1,PPP1R9B,GRIA1,SLC8A3,SERPINF1,LRRN4,EN1	cyan	VSMC_M2
GO:0045445	0.52	0.66	5	67	myoblast differentiation	BP	1	IGF1,CAPN3,BOC,BMP4,ZFP36L1	cyan	VSMC_M2
GO:1904888	0.52	0.68	4	54	cranial skeletal system development	BP	1	GLI3,BMP4,MED12,FOXC2	cyan	VSMC_M2
GO:0009855	0.52	0.63	7	97	determination of bilateral symmetry	BP	1	NDRG4,PCSK6,VANGL2,NBL1,CC2D2A,DNAAF1,GATA4	cyan	VSMC_M2
GO:0010921	0.52	0.66	5	68	regulation of phosphatase activity	BP	1	PPP6R2,GNAI2,PPP1R9B,PDGFRB,CALM3	cyan	VSMC_M2
GO:0060997	0.52	0.68	4	54	dendritic spine morphogenesis	BP	1	LZTS3,KIF1A,HDAC6,DVL1	cyan	VSMC_M2
GO:0044380	0.53	0.68	4	55	protein localization to cytoskeleton	BP	1	MARK4,GAS2L1,PPP1R9B,DVL1	cyan	VSMC_M2
GO:0001764	0.53	0.62	8	113	neuron migration	BP	1	PLXNB2,NRP1,BAX,FGFR1,DCLK1,PHACTR1,NDN,ASTN1	cyan	VSMC_M2
GO:0048839	0.53	0.60	10	139	inner ear development	BP	1	GLI3,SLITRK6,LRP10,BMP4,NAGLU,PDGFRB,ROR1,DVL1,SDC4,MPV17	cyan	VSMC_M2
GO:0035418	0.53	0.68	4	54	protein localization to synapse	BP	1	DVL1,CLSTN1,GRASP,STX3	cyan	VSMC_M2
GO:0010565	0.53	0.63	7	95	regulation of cellular ketone metabolic process	BP	1	APPL2,SLC45A3,ERFE,CLCN2,PDK2,ABCD1,H6PD	cyan	VSMC_M2
GO:0061014	0.53	0.64	6	82	positive regulation of mRNA catabolic process	BP	1	ZFP36,SAMD4B,PATL1,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0055021	0.53	0.68	4	53	regulation of cardiac muscle tissue growth	BP	1	CTDP1,ZFPM2,MEIS1,IGF1	cyan	VSMC_M2
GO:0045786	0.53	0.56	22	306	negative regulation of cell cycle	BP	1	RPS6KA2,PTPRK,GPNMB,RHOB,NOP53,TIMP2,KAT2B,APBB1,MUS81,BMP4,ZBTB17,TP53BP2,ZFP36L1,TP53,NUPR1,KANK2,TEX14,ABL1,INCA1,GAS1,HEXIM1,PML	cyan	VSMC_M2
GO:0050779	0.53	0.64	6	82	RNA destabilization	BP	1	ZFP36,SAMD4B,PATL1,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0098781	0.53	0.67	4	53	ncRNA transcription	BP	1	NOP53,GTF3A,ELL3,TP53	cyan	VSMC_M2

GO:0046330	0.53	0.65	5	68	positive regulation of JNK cascade	BP	1	TLR3,MAPK8IP1,TIRAP,TRAF4,AXIN1	cyan	VSMC_M2
GO:0043280	0.54	0.62	7	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MTCH1,GSN,BAX,CASP10,CASP9,PML,CARD8	cyan	VSMC_M2
GO:0045600	0.54	0.67	4	53	positive regulation of fat cell differentiation	BP	1	ZFP36,SFRP2,LMO3,ZFP36L1	cyan	VSMC_M2
GO:1904705	0.54	0.67	4	53	regulation of vascular associated smooth muscle cell proliferation	BP	1	HMOX1,IGF1,MMP2,GNAI2	cyan	VSMC_M2
GO:0034612	0.54	0.58	13	181	response to tumor necrosis factor	BP	1	AKAP12,ZFP36,SMPD1,GGT7,STAT1,NFKB1,NFKBIA,ADAMTS7,ZFP36L1,TP53,GBA,TNFRSF14,CARD8	cyan	VSMC_M2
GO:0032409	0.54	0.57	14	198	regulation of transporter activity	BP	1	STOM,SLC6A9,EHD3,SCN1B,PRKCD,CACNB3,SLC5A3,LINC02210-CRHR1,CAPN1,WNK4,PRKACA,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0010498	0.54	0.54	31	434	proteasomal protein catabolic process	BP	1	OS9,EIF3H,KCTD17,RNF144A,NOP53,TRIM13,APOE,AGAP3,RBCK1,EDEM2,WWTR1,FOXF2,DCAF11,MAEA,ARRB2,GABARAP,GIPC1,PRKACA,UBQLN2,UBQLN4,GBA,NUPR1,MTA1,UBXN6,DVL1,ELOB,FBXW5,RHBDF1,CBFA2T3,PML,PSMB9	cyan	VSMC_M2
GO:0031023	0.54	0.60	9	127	microtubule organizing center organization	BP	1	MARK4,KAT2B,POC1B,CHMP4B,CHMP3,FES,ARHGEF10,CROCC,FBXW5	cyan	VSMC_M2
GO:0098869	0.54	0.64	5	67	cellular oxidant detoxification	BP	1	SELENOW,APOE,CCS,UBIAD1,CLIC2	cyan	VSMC_M2
GO:0042886	0.54	0.57	15	210	amide transport	BP	1	TAPBP,LTBP4,FOLR2,SLC15A4,EFNA5,HADH,DISP1,LINC02210-CRHR1,PSAP,RASL10B,ABCC1,ABCD1,PHPT1,ABCA2,RAB11B	cyan	VSMC_M2
GO:0050848	0.54	0.66	4	55	regulation of calcium-mediated signaling	BP	1	IGF1,HOMER3,PDK2,CALM3	cyan	VSMC_M2
GO:0032874	0.54	0.61	7	97	positive regulation of stress-activated MAPK cascade	BP	1	TLR3,MAPK8IP1,TIRAP,STK25,BMP4,TRAF4,AXIN1	cyan	VSMC_M2
GO:0030838	0.54	0.62	6	82	positive regulation of actin filament polymerization	BP	1	GSN,BIN1,C15orf62,CTTN,ARPC5,ALOX15	cyan	VSMC_M2
GO:0030865	0.54	0.66	4	55	cortical cytoskeleton organization	BP	1	RHOB,RHOG,RND2,LLGL1	cyan	VSMC_M2
GO:0009416	0.54	0.56	17	239	response to light stimulus	BP	1	PTPRK,BAX,BCL3,SMPD1,NDRG4,PRKCD,MMP2,TMEM161A,NR2F6,CASP9,TP53,MTA1,NPHP4,NMT2,LRRN4,PML,BMF	cyan	VSMC_M2
GO:0051592	0.54	0.60	8	114	response to calcium ion	BP	1	SMPD1,CAPN3,ADCY1,ADD1,ALOX15,MCOLN1,JUNB,CALM3	cyan	VSMC_M2
GO:0055006	0.55	0.64	5	71	cardiac cell development	BP	1	CTDP1,IGF1,BMP4,PDGFRB,GATA4	cyan	VSMC_M2
GO:1903321	0.55	0.62	6	82	negative regulation of protein modification by small protein conjugation or removal	BP	1	TRIM21,CAPN3,ARRB2,ISG15,ABL1,RPS15	cyan	VSMC_M2
GO:0016445	0.55	0.66	4	54	somatic diversification of immunoglobulins	BP	1	STAT6,SLC15A4,IL27RA,TCF3	cyan	VSMC_M2
GO:0060415	0.55	0.66	4	56	muscle tissue morphogenesis	BP	1	ZFPM2,HEG1,FOXC2,ZFPM1	cyan	VSMC_M2
GO:0090101	0.55	0.61	7	101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SFRP2,BCL9L,FAM89B,NBL1,TP53,ABL1,ZBTB7A	cyan	VSMC_M2
GO:0050671	0.55	0.62	6	82	positive regulation of lymphocyte proliferation	BP	1	PNP,IGF1,CD81,TIRAP,IL27RA,CD55	cyan	VSMC_M2
GO:0010638	0.55	0.53	30	428	positive regulation of organelle organization	BP	1	KCTD17,GSN,NRP1,BAX,MARK4,BIN1,DZIP1,IGF1,CAMKK2,SRC,C15orf62,SORBS3,CTTN,FES,ARPC5,ARHGEF10,FYCO1,GRN,ARHGEF10L,CROCC,ALOX15,TP53,PDGFRB,ENTR1,ABL1,ATMIN,ZNF205,PML,BMF,SDC4	cyan	VSMC_M2
GO:0006801	0.55	0.65	4	54	superoxide metabolic process	BP	1	PRKCD,GNAI2,CCS,ACP5	cyan	VSMC_M2
GO:0032006	0.55	0.62	6	84	regulation of TOR signaling	BP	1	DEPTOR,RRAGC,AKT1S1,GBA,TSC2,NPRL3	cyan	VSMC_M2
GO:0042116	0.55	0.63	5	69	macrophage activation	BP	1	TLR3,BPI,GRN,TMEM106A,SBNO2	cyan	VSMC_M2
GO:0016239	0.55	0.65	4	56	positive regulation of macroautophagy	BP	1	HMOX1,TRIM13,FYCO1,TSC2	cyan	VSMC_M2
GO:1990874	0.55	0.65	4	54	vascular associated smooth muscle cell proliferation	BP	1	HMOX1,IGF1,MMP2,GNAI2	cyan	VSMC_M2
GO:0007569	0.55	0.60	7	98	cell aging	BP	1	PRKCD,B2M,TP53,ULK3,MAP2K3,ABL1,PML	cyan	VSMC_M2
GO:0006470	0.55	0.55	16	228	protein dephosphorylation	BP	1	CTDP1,PPP6R2,PTPRK,CDC14C,SMPD1,PRKCD,PTPN13,GNAI2,SSH3,GBA,PPP1R9B,PDGFRB,PTPRS,PHPT1,CALM3,CPPED1	cyan	VSMC_M2
GO:0007163	0.55	0.56	13	189	establishment or maintenance of cell polarity	BP	1	GSN,RHOB,RHOG,SFRP5,PARD3B,STK25,ARPC5,FAM89B,RND2,DLG5,ANKFN1,LLGL1,LRRC7	cyan	VSMC_M2
GO:0021953	0.55	0.59	8	116	central nervous system neuron differentiation	BP	1	NFIB,GLI3,NRP1,DCLK1,SCN1B,B4GALT5,B2M,SLIT2	cyan	VSMC_M2
GO:0061061	0.55	0.52	35	504	muscle structure development	BP	1	CTDP1,MYL6B,TCF21,FLOT1,ZFPM2,BIN1,CAMK1,PLD3,EFNB2,IGF1,WT1,POU6F1,PDLIM2,CD81,CAPN3,BOC,BCL9,LEF1,DISP1,HEG1,HDAC5,BMP4,ARRB2,TCF12,ZFP36L1,NUPR1,PDGFRB,FLII,EEF2,FOXC2,PTGFRN,GATA4,CDK9,ZFPM1,EMD	cyan	VSMC_M2
GO:0032411	0.55	0.61	6	85	positive regulation of transporter activity	BP	1	SLC6A9,EHD3,PRKCD,CACNB3,WNK4,CALM3	cyan	VSMC_M2
GO:0002456	0.56	0.65	4	54	T cell mediated immunity	BP	1	RFTN1,CD81,B2M,CD55	cyan	VSMC_M2
GO:0050818	0.56	0.65	4	54	regulation of coagulation	BP	1	APOE,SERPING1,PRKCD,SERPINE2	cyan	VSMC_M2
GO:0036293	0.56	0.54	18	258	response to decreased oxygen levels	BP	1	HMOX1,NOP53,ANGPT4,SRC,CACNB3,MMP2,CHRNA7,PTGIS,VEGFD,VEGFB,ZFP36L1,TP53,ADAM15,CBFA2T3,SLC2A8,SLC8A3,KCND2,PML	cyan	VSMC_M2
GO:0014855	0.56	0.65	4	56	striated muscle cell proliferation	BP	1	ZFPM2,MEIS1,NDRG4,FOXC2	cyan	VSMC_M2
GO:0030199	0.56	0.65	4	56	collagen fibril organization	BP	1	ADAMTS2,SFRP2,FKBP10,FOXC2	cyan	VSMC_M2
GO:0032946	0.56	0.61	6	83	positive regulation of mononuclear cell proliferation	BP	1	PNP,IGF1,CD81,TIRAP,IL27RA,CD55	cyan	VSMC_M2
GO:1904589	0.56	0.64	4	55	regulation of protein import	BP	1	GLI3,PRKCD,BMP4,JUP	cyan	VSMC_M2
GO:0031623	0.56	0.60	6	85	receptor internalization	BP	1	FLOT1,TBC1D5,CD81,ARRB2,UBQLN2,GRIA1	cyan	VSMC_M2
GO:0001666	0.56	0.54	17	244	response to hypoxia	BP	1	HMOX1,NOP53,ANGPT4,SRC,MMP2,CHRNA7,PTGIS,VEGFD,VEGFB,ZFP36L1,TP53,ADAM15,CBFA2T3,SLC2A8,SLC8A3,KCND2,PML	cyan	VSMC_M2
GO:0006885	0.56	0.62	5	70	regulation of pH	BP	1	SLC4A9,GRN,TMEM175,PDK2,ATP6V0D1	cyan	VSMC_M2
GO:0070304	0.56	0.59	7	99	positive regulation of stress-activated protein kinase signaling cascade	BP	1	TLR3,MAPK8IP1,TIRAP,STK25,BMP4,TRAF4,AXIN1	cyan	VSMC_M2
GO:2001243	0.57	0.60	6	83	negative regulation of intrinsic apoptotic signaling pathway	BP	1	GRINA,SFRP2,SRC,MAPK8IP1,ELL3,TMEM161A	cyan	VSMC_M2
GO:0009566	0.57	0.58	8	113	fertilization	BP	1	EHMT2,BAX,PLB1,FOLR2,HEXB,GLRB,REC8,AR	cyan	VSMC_M2
GO:0009408	0.57	0.60	6	84	response to heat	BP	1	DAXX,HMOX1,IGF1,DNAJB6,PRKACA,HSBP1	cyan	VSMC_M2
GO:0045580	0.57	0.59	7	98	regulation of T cell differentiation	BP	1	IRF1,GLI3,PNP,LEF1,BMP4,ERBB2,ABL1	cyan	VSMC_M2
GO:0010950	0.57	0.57	9	127	positive regulation of endopeptidase activity	BP	1	MTCH1,GSN,BAX,SFRP2,APH1A,CASP10,CASP9,PML,CARD8	cyan	VSMC_M2
GO:0002444	0.57	0.61	5	70	myeloid leukocyte mediated immunity	BP	1	HMOX1,TUSC2,FES,CPLX2,PTGDS	cyan	VSMC_M2
GO:0046890	0.57	0.57	9	127	regulation of lipid biosynthetic process	BP	1	APOE,PRKCD,SLC45A3,NFKB1,CLCN2,ABCD1,FAM3A,H6PD,ABCA2	cyan	VSMC_M2
GO:0006487	0.57	0.63	4	55	protein N-linked glycosylation	BP	1	MGAT4B,ST3GAL1,EXT2,NUDT14	cyan	VSMC_M2

GO:2000134	0.57	0.63	4	56	negative regulation of G1/S transition of mitotic cell cycle	BP	1	GPNMB,TP53,KANK2,PML	cyan	VSMC_M2
GO:0062012	0.57	0.53	17	243	regulation of small molecule metabolic process	BP	1	APPL2,APOE,KAT2B,IGF1,SRC,SLC45A3,NFKB1,ERFE,CLCN2,TP53,PDK2,NUPR1,ABCD1,FAM3A,H6PD,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0045216	0.57	0.56	10	146	cell-cell junction organization	BP	1	AFDN,SRC,TJP1,HEG1,ADD1,DLG5,JUP,EPHA2,PRKACA,NPHP4	cyan	VSMC_M2
GO:0043543	0.58	0.54	14	202	protein acylation	BP	1	KLF15,CAMK1,KAT2B,APBB1,CLIP3,LEF1,PORCN,PCGF2,KAT8,NUPR1,PBXIP1,ZDHHC9,NMT2,PYGO2	cyan	VSMC_M2
GO:1902806	0.58	0.57	8	115	regulation of cell cycle G1/S phase transition	BP	1	APPL2,GPNMB,APBB1,MN1,TP53,KANK2,PLPP2,PML	cyan	VSMC_M2
GO:0051147	0.58	0.56	8	115	regulation of muscle cell differentiation	BP	1	CTDP1,CAMK1,EFNB2,IGF1,HDAC5,BMP4,ARRB2,CDK9	cyan	VSMC_M2
GO:0098930	0.58	0.62	4	58	axonal transport	BP	1	TMEM108,KIF1A,HDAC6,HSBP1	cyan	VSMC_M2
GO:0043624	0.58	0.56	8	119	cellular protein complex disassembly	BP	1	GSN,ADD1,CAPZB,MAP1S,HDAC6,PPP1R9B,FLII,SH3GL1	cyan	VSMC_M2
GO:1905330	0.58	0.62	4	56	regulation of morphogenesis of an epithelium	BP	1	WNT2B,BMP4,AR,ABL1	cyan	VSMC_M2
GO:0055082	0.58	0.48	39	564	cellular chemical homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,KLF15,BAX,APOE,SLC6A9,SLC4A9,ACKR4,ATP4A,EFNA5,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,ERFE,CYB561,GRN,PRKACA,TMEM175,GRIA1,MCOLN1,PHPT1,ABL1,ATP6V0D1,ABCA2,SLC8A3,SERPINF1,CD55,PML,GATA4,CALM3,CLIC2,RAB11B	cyan	VSMC_M2
GO:1901616	0.58	0.62	4	56	organic hydroxy compound catabolic process	BP	1	MOXD1,APOE,INPP5E,LDHD	cyan	VSMC_M2
GO:0032677	0.59	0.62	4	56	regulation of interleukin-8 production	BP	1	BCL3,TLR3,BPI,TIRAP	cyan	VSMC_M2
GO:0008652	0.59	0.62	4	56	cellular amino acid biosynthetic process	BP	1	AASS,PCBD1,MRI1,DPYD	cyan	VSMC_M2
GO:0043409	0.59	0.55	9	131	negative regulation of MAPK cascade	BP	1	APOE,SMPD1,SFRP2,PRKCD,MAPK8IP1,LMO3,BMP4,GBA,ABL1	cyan	VSMC_M2
GO:0055088	0.59	0.56	8	116	lipid homeostasis	BP	1	APOE,PNPLA2,PLSCR3,NPC2,ABCD1,LCAT,ABCA2,DGAT1	cyan	VSMC_M2
GO:0044270	0.59	0.49	25	361	cellular nitrogen compound catabolic process	BP	1	PYM1,HMOX1,BAX,VIM,PNP,ZFP36,SAMD4B,PATL1,NEIL2,PRKCD,IKBKE,TIRAP,NIT1,HELZ2,RNASEL,MUS81,MOV10,ACAT1,NUDT13,ZFP36L1,ABCC1,ABCD1,DPYD,OAS2,MEX3D	cyan	VSMC_M2
GO:1903039	0.59	0.54	10	143	positive regulation of leukocyte cell-cell adhesion	BP	1	GLI3,PNP,IGF1,SRC,CD81,LEF1,B2M,IL27RA,TNFRSF14,CD55	cyan	VSMC_M2
GO:0051251	0.59	0.52	13	186	positive regulation of lymphocyte activation	BP	1	STAT6,GLI3,PNP,LAMP1,IGF1,SRC,CD81,TIRAP,LEF1,B2M,IL27RA,TNFRSF14,CD55	cyan	VSMC_M2
GO:0046916	0.59	0.57	6	86	cellular transition metal ion homeostasis	BP	1	HMOX1,ACO1,SLC6A9,ERFE,CYB561,ATP6V0D1	cyan	VSMC_M2
GO:2001021	0.59	0.59	5	72	negative regulation of response to DNA damage stimulus	BP	1	SFRP2,MAGEF1,ELL3,TMEM161A,UBQLN4	cyan	VSMC_M2
GO:0031589	0.59	0.50	20	294	cell-substrate adhesion	BP	1	PTPRK,RRAS,NRP1,FZD4,ITGBL1,EFNA5,EPHA3,SRC,SORBS3,CTTN,ATRNL1,EGFL6,LAMB2,BCR,JUP,ALOX15,ADAM15,ABL1,SDC4,COL8A1	cyan	VSMC_M2
GO:0035051	0.59	0.55	8	119	cardiocyte differentiation	BP	1	CTDP1,EFNB2,IGF1,WT1,BMP4,ARRB2,PDGFRB,GATA4	cyan	VSMC_M2
GO:0014013	0.59	0.59	5	73	regulation of gliogenesis	BP	1	BIN1,SERPINE2,TMEM98,ASPA,IL34	cyan	VSMC_M2
GO:0060538	0.59	0.54	9	132	skeletal muscle organ development	BP	1	MYL6B,TCF21,FLOT1,WT1,BCL9,DISP1,NUPR1,EEF2,EMD	cyan	VSMC_M2
GO:0007160	0.59	0.52	13	192	cell-matrix adhesion	BP	1	PTPRK,RRAS,NRP1,ITGBL1,EFNA5,EPHA3,SRC,CTTN,BCR,JUP,ADAM15,ABL1,SDC4	cyan	VSMC_M2
GO:0002690	0.59	0.59	5	71	positive regulation of leukocyte chemotaxis	BP	1	PLA2G7,TIRAP,VEGFD,VEGFB,IL34	cyan	VSMC_M2
GO:0006753	0.60	0.48	27	387	nucleoside phosphate metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,NEIL2,ABHD14B,NADSYN1,PTGIS,ADCY1,UCKL1,NMNAT2,ACAT1,NUDT13,EPHA2,PDK2,NUPR1,PPCDC,NUDT14,ABCD1,CBFA2T3,DPYD,TK2,ACOT6,ZBTB7A,DGAT1	cyan	VSMC_M2
GO:0051453	0.60	0.60	4	58	regulation of intracellular pH	BP	1	SLC4A9,GRN,TMEM175,ATP6V0D1	cyan	VSMC_M2
GO:0043583	0.60	0.52	11	162	ear development	BP	1	TSHZ1,GLI3,SLITRK6,LRP10,BMP4,NAGLU,PDGFRB,ROR1,DVL1,SDC4,MPV17	cyan	VSMC_M2
GO:0009798	0.60	0.60	4	59	axis specification	BP	1	COBL,WT1,PCSK6,BMP4	cyan	VSMC_M2
GO:0002687	0.60	0.55	7	101	positive regulation of leukocyte migration	BP	1	PLA2G7,TIRAP,XG,VEGFD,VEGFB,TNFRSF14,IL34	cyan	VSMC_M2
GO:0008360	0.60	0.53	9	134	regulation of cell shape	BP	1	PLXNB2,ARHGAP18,RHOB,ARAP1,RHOG,HEXB,C15orf62,FES,RND2	cyan	VSMC_M2
GO:0051403	0.61	0.51	13	190	stress-activated MAPK cascade	BP	1	ZFP36,MAP3K12,TLR3,SFRP2,MAPK8IP1,TIRAP,NFKB1,STK25,BMP4,ZFP36L1,MAP2K3,TRAF4,AXIN1	cyan	VSMC_M2
GO:0007368	0.61	0.56	6	90	determination of left/right symmetry	BP	1	NDRG4,PCSK6,VANGL2,CC2D2A,DNAAF1,GATA4	cyan	VSMC_M2
GO:0010038	0.61	0.49	19	279	response to metal ion	BP	1	DAXX,CUTA,HMOX1,ACO1,SMPD1,APBB1,PLSCR1,FIBIN,CAPN3,ADCY1,B2M,ADD1,QDPR,ALOX15,CASP9,MCOLN1,SERPINF1,JUNB,CALM3	cyan	VSMC_M2
GO:0032412	0.61	0.51	12	178	regulation of ion transmembrane transporter activity	BP	1	STOM,SLC6A9,EHD3,SCN1B,CACNB3,LINC02210-CRHR1,CAPN1,WNK4,PRKACA,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0019218	0.61	0.57	5	73	regulation of steroid metabolic process	BP	1	APOE,NFKB1,CLCN2,H6PD,ABCA2	cyan	VSMC_M2
GO:0043467	0.61	0.54	7	104	regulation of generation of precursor metabolites and energy	BP	1	NOP53,IGF1,TP53,NUPR1,ABCD1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0050851	0.61	0.53	8	117	antigen receptor-mediated signaling pathway	BP	1	BAX,RFTN1,RBCK1,CACNB3,PLCG1,CD81,PHPT1,ABL1	cyan	VSMC_M2
GO:0050764	0.61	0.59	4	59	regulation of phagocytosis	BP	1	APPL2,PLSCR1,TGM2,ALOX15	cyan	VSMC_M2
GO:0099111	0.61	0.51	11	165	microtubule-based transport	BP	1	LAMP1,TMEM108,CLIP3,KIF1A,FYCO1,RPGR,MAP1S,HDAC6,RHOT2,DNAAF1,HSBP1	cyan	VSMC_M2
GO:2000106	0.61	0.59	4	59	regulation of leukocyte apoptotic process	BP	1	ST3GAL1,BAX,BMP4,TP53	cyan	VSMC_M2
GO:0009913	0.61	0.53	8	120	epidermal cell differentiation	BP	1	SLITRK6,ZFP36,BCR,BMP4,RARRES3,EPHA2,KAZN,ZFP36L1	cyan	VSMC_M2
GO:0045619	0.62	0.53	8	117	regulation of lymphocyte differentiation	BP	1	IRF1,GLI3,PNP,LEF1,BMP4,ERBB2,ZFP36L1,ABL1	cyan	VSMC_M2
GO:1904892	0.62	0.59	4	59	regulation of receptor signaling pathway via STAT	BP	1	BCL3,SOCS3,HGS,OCIAD2	cyan	VSMC_M2
GO:0071241	0.62	0.51	11	165	cellular response to inorganic substance	BP	1	DAXX,HMOX1,SMPD1,CAPN3,ADCY1,B2M,ADD1,ALOX15,MCOLN1,SERPINF1,JUNB	cyan	VSMC_M2
GO:0060968	0.62	0.58	4	59	regulation of gene silencing	BP	1	ZFP36,BMP4,TP53,ADAR	cyan	VSMC_M2

GO:0065003	0.62	0.43	84	1210	protein-containing complex assembly	BP	1	EIF3H,AFDN,TAPBP,DAXX,ARHGAP18,GSDMD,CARD10,KCTD17,TRPM3,APPL2,RSPH9,HIGD2A,COBL,GSN,BAX,CCDC114,NOP53,BIN1,APOE,SHKBP1,EHD3,TPPP2,RNF213,EIF3K,CLIP3,ANGPT4,EIF3F,EFNA5,CHMP4B,CHMP3,PRKCD,SRC,C15orf62,IKBKE,CAPN3,TIRAP,CTTN,TPPP,HIST1H1C,DISP1,SV2A,SSH3,NDUFAF3,FES,PRUNE1,WIPF1,ARPC5,B2M,KCND3,ADD1,CAPZB,DLG5,HDAC6,ALOX15,SMIM20,PRKACA,SLIT2,TP53,GBA,NUPR1,ADAR,WARS,CENPV,MCOLN1,FLII,LLGL1,ISG15,ELOB,TRAF7,SLC9A3R2,AXIN1,ABL1,DNAAF1,LCAT,RPS15,KCND2,DGAT1,PML,RPS19,GEMIN8,CARD8,BMF,GCHFR,TSPAN4	cyan	VSMC_M2
GO:0051495	0.62	0.49	13	194	positive regulation of cytoskeleton organization	BP	1	GSN,NRP1,BIN1,C15orf62,SORBS3,CTTN,FES,ARPC5,ARHGEF10,ARHGEF10L,ALOX15,ABL1,SDC4	cyan	VSMC_M2
GO:0033138	0.62	0.56	5	74	positive regulation of peptidyl-serine phosphorylation	BP	1	CAMK1,SFRP2,HDAC6,ARRB2,AXIN1	cyan	VSMC_M2
GO:0061097	0.62	0.56	5	74	regulation of protein tyrosine kinase activity	BP	1	SH3BP5,SRC,SHC1,GPRC5B,IL34	cyan	VSMC_M2
GO:0048644	0.62	0.58	4	61	muscle organ morphogenesis	BP	1	ZFPM2,HEG1,FOXC2,ZFPM1	cyan	VSMC_M2
GO:0034248	0.62	0.46	27	395	regulation of cellular amide metabolic process	BP	1	PYM1,PLXNB2,EIF3H,ACO1,VIM,BIN1,APOE,BCL3,MIF4GD,ZFP36,SAMD4B,EIF3K,IGF1,PATL1,SPON1,PRKCD,CHRNA7,MOV10,ERBB2,ZFP36L1,TP53,PDK2,EEF2,DPH7,INPP5E,ABCA2,MEX3D	cyan	VSMC_M2
GO:0006096	0.62	0.58	4	60	glycolytic process	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0006757	0.62	0.58	4	60	ATP generation from ADP	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0071356	0.62	0.50	11	163	cellular response to tumor necrosis factor	BP	1	AKAP12,ZFP36,STAT1,NFKB1,NFKBIA,ADAMTS7,ZFP36L1,TP53,GBA,TNFRSF14,CARD8	cyan	VSMC_M2
GO:0051726	0.62	0.43	57	827	regulation of cell cycle	BP	1	RPS6KA2,IRF1,PTPRK,CDC14C,CUL9,APPL2,GPNMB,RHOB,BAX,HBP1,NOP53,MARK4,BIN1,TIMP2,KAT2B,TRIM21,APBB1,IGF1,CHMP4B,CHMP3,PLSCR1,SRC,MN1,WDR6,GRK5,GAS2L1,MUS81,BMP4,MAEA,WIZ,ZBTB17,GIPC1,TP53BP2,PRKACA,ZFP36L1,TP53,PRCC,PPP1R9B,NUPR1,KANK2,TEX14,CENPV,PDGFRB,E4F1,TSC2,FBXW5,RAB11FIP3,ENTR1,PLPP2,ABL1,INCA1,GAS1,HEXIM1,PML,JUNB,CALM3,CDK9	cyan	VSMC_M2
GO:1901222	0.63	0.55	5	75	regulation of NIK/NF-kappaB signaling	BP	1	LRRC19,BCL3,RBCK1,TLR3,NFKBIA	cyan	VSMC_M2
GO:0006091	0.63	0.45	27	392	generation of precursor metabolites and energy	BP	1	ACO1,STK40,NOP53,UQCRH,ACSS1,ME3,GAA,IGF1,ACSS2,STBD1,COQ9,PHKG1,WDR93,CYB561,AIFM2,ACAT1,QDPR,PGLS,TP53,GBA,NUPR1,ABCD1,IDH3G,NDOR1,H6PD,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0043412	0.63	0.40	212	3029	macromolecule modification	BP	1	CTDP1,OS9,MGAT4B,FLOT1,PPP6R2,EHMT2,PLXNB2,RPS6KA2,DEPTOR,B3GALT4,DAXX,FBXO32,PTPRK,ST3GAL1,CDC14C,CARD10,TRERF1,GCNT1,CUL9,TRIM14,GALNT12,P3H1,GPNMB,EFEMP1,RNF144A,STK40,AKT1S1,STK17A,AASS,NRP1,KLF15,BAX,PARP12,NOP53,FKRP,TRIM13,FZD4,CAB39L,MARK4,AGBL5,APOE,ATG7,SOCS3,CAMK1,RNF170,PAK4,RNF213,HGS,KAT2B,FGFR1,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,CLIP3,ANGPT4,EIF3F,MAP3K12,RBCK1,IGF1,TLR3,SNTA1,MAN2A1,WT1,EFNA5,DPY19L3,GALNT18,GGCX,EDEM2,NEIL2,ARRDC3,CAMKK2,SFRP2,WWTR1,PRKCD,EPHA3,SRC,CPE,TGM2,LRP4,RIOX2,FOXF2,MAPK8IP1,PTPN13,EXT2,MOB2,GFRA2,CD81,NDN,PHKG1,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,GNAI2,SPOCD1,TPPP,B4GALT4,HIST1H1C,UBA7,LEF1,TBL1Y,B4GALT5,SSH3,DCAF11,VEGFD,GCNT7,WDR6,GRK5,FES,MINDY1,VPS11,HEG1,B4GAT1,STK25,ATG4B,RNASEL,MAGEF1,PHEX,DTX2,BCR,ADORA2A,CDC42BPG,HDAC5,VEGFB,MACROD1,WNK4,BMP4,MAEA,PORCN,HDAC6,B3GAT3,WDR45,FKBP10,ARRB2,EPHA2,GABARAP,FNTB,ERBB2,BRAT1,PRKACA,NTRK1,PCGF2,MLLT6,SLIT2,TP53,KAT8,ELMSAN1,PDK2,MED12,GBA,PPP1R9B,SLC51B,NUPR1,SHC1,PBXIP1,ADAR,TEX14,WARS,ULK3,GPRC5B,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,ZDHHC9,TRAF4,PTPRS,KDM4B,NAGPA,DVL1,ISG15,ELOB,E4F1,DPH7,TRAF7,TNFRSF14,TSC2,FBXW5,PHPT1,UNKL,PIGQ,AXIN1,RNF166,ABL1,IL34,INCA1,ABCA2,RPS15,DTX3,SLC8A3,HEXIM1,TRIM26,NMT2,PML,PLPP3,HS3ST3B1,CALM3,CPPED1,CDK9,SDC4,ADPRHL2,MACROD2,AL157935.2,PYGO2,GTF2H4,UBL5	cyan	VSMC_M2
GO:2001056	0.63	0.52	7	105	positive regulation of cysteine-type endopeptidase activity	BP	1	MTCH1,GSN,BAX,CASP10,CASP9,PML,CARD8	cyan	VSMC_M2
GO:0033209	0.63	0.55	5	75	tumor necrosis factor-mediated signaling pathway	BP	1	STAT1,NFKBIA,TP53,TNFRSF14,CARD8	cyan	VSMC_M2
GO:0030856	0.63	0.52	7	106	regulation of epithelial cell differentiation	BP	1	ZFP36,WWTR1,STAT1,ADD1,BMP4,RARRES3,ZFP36L1	cyan	VSMC_M2
GO:0051052	0.63	0.46	20	297	regulation of DNA metabolic process	BP	1	STAT6,EHMT2,BAX,APBB1,SLC15A4,WT1,PRKCD,SRC,MMS19,HIST1H1C,MAGEF1,TMEM161A,ARRB2,IL27RA,TP53,UBQLN4,PDGFRB,PML,CDK9,MPV17	cyan	VSMC_M2
GO:0060395	0.63	0.57	4	62	SMAD protein signal transduction	BP	1	VIM,WWTR1,FAM89B,BMP4	cyan	VSMC_M2
GO:0007005	0.63	0.44	30	436	mitochondrion organization	BP	1	HIGD2A,BAX,ATG7,IGF1,MAN2A1,CAMKK2,PYROXD2,CTTN,NDUFAF3,CTSK,VPS11,AIFM2,VAT1,HDAC6,WDR45,ARRB2,GABARAP,PLSCR3,SMIM20,TP53,GBA,RETREG1,WDR81,TSC2,RHOT2,ZNF205,CALM3,BMF,MPV17,UBL5	cyan	VSMC_M2
GO:0035335	0.64	0.54	5	77	peptidyl-tyrosine dephosphorylation	BP	1	PTPRK,CDC14C,PTPN13,SSH3,PTPRS	cyan	VSMC_M2
GO:0071322	0.64	0.50	8	121	cellular response to carbohydrate stimulus	BP	1	RPS6KA2,EFNA5,PRKACA,ZFP36L1,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0090407	0.64	0.43	31	452	organophosphate biosynthetic process	BP	1	CHKB,SLC44A1,ACSS1,SOCS3,PNP,GPAT4,ACSS2,LPCAT4,PLSCR1,HEXB,PTDSS1,PIK3C2B,NADSYN1,IP6K1,PTGIS,ADCY1,UCKL1,NMNAT2,ACAT1,PLD2,ALOX15,PLSCR3,PDK2,SLC44A2,PPCDC,PIGQ,INPP5E,LCAT,TK2,ABCA2,PDXK	cyan	VSMC_M2
GO:0042060	0.64	0.45	22	329	wound healing	BP	1	HMOX1,GLI3,APOE,SMPD1,IGF1,GGCX,SERPING1,PLSCR1,PRKCD,SRC,HPS6,FIBP,ADORA2A,FKBP10,ALOX15,SERPINE2,ERBB2,PDGFRB,FOXC2,PLPP3,GATA4,SDC4	cyan	VSMC_M2
GO:0009117	0.64	0.44	26	381	nucleotide metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,NEIL2,ABHD14B,NADSYN1,PTGIS,ADCY1,UCKL1,NMNAT2,ACAT1,NUDT13,EPHA2,PDK2,NUPR1,PPCDC,ABCD1,CBFA2T3,DPYD,TK2,ACOT6,ZBTB7A,DGAT1	cyan	VSMC_M2
GO:0015908	0.64	0.56	4	60	fatty acid transport	BP	1	APOE,ERFE,CPT2,ABCD1	cyan	VSMC_M2

GO:0043161	0.64	0.44	25	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	OS9,EIF3H,KCTD17,RNF144A,NOP53,TRIM13,AGAP3,RBCK1,EDEM2,WWTR1,FOXF2,DCAF11,MAEA,ARRB2,GABARAP,GIPC1,UBQLN2,UBQLN4,GBA,MTA1,DVL1,ELOB,FBXW5,CBFA2T3,PML	cyan	VSMC_M2
GO:0106106	0.65	0.50	8	123	cold-induced thermogenesis	BP	1	STAT6,APPL2,ARRDC3,DECR1,HADH,IP6K1,CPT2,FOXC2	cyan	VSMC_M2
GO:0120161	0.65	0.50	8	123	regulation of cold-induced thermogenesis	BP	1	STAT6,APPL2,ARRDC3,DECR1,HADH,IP6K1,CPT2,FOXC2	cyan	VSMC_M2
GO:0002705	0.65	0.53	5	76	positive regulation of leukocyte mediated immunity	BP	1	STAT6,LAMP1,CD81,B2M,CD55	cyan	VSMC_M2
GO:0046700	0.65	0.43	24	357	heterocycle catabolic process	BP	1	PYM1,HMOX1,BAX,VIM,PNP,ZFP36,SAMD4B,PATL1,NEIL2,PRKCD,IKBKE,TIRAP,HELZ2,RNASEL,MUS81,MOV10,ACAT1,NUDT13,ZFP36L1,ABCC1,ABCD1,DPYD,OAS2,MEX3D	cyan	VSMC_M2
GO:0010212	0.65	0.48	9	137	response to ionizing radiation	BP	1	RHOB,BAX,TRIM13,SMPD1,SFRP2,BRAT1,TP53,MTA1,PML	cyan	VSMC_M2
GO:0055086	0.65	0.42	30	439	nucleobase-containing small molecule metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,NEIL2,ABHD14B,NADSYN1,PTGIS,ADCY1,UCKL1,NMNAT2,ACAT1,NUDT13,MACROD1,EPHA2,PDK2,NUPR1,PPCDC,NUDT14,ABCD1,UAP1L1,CBFA2T3,DPYD,TK2,ACOT6,ZBTB7A,DGAT1,MACROD2	cyan	VSMC_M2
GO:0034249	0.65	0.47	12	183	negative regulation of cellular amide metabolic process	BP	1	BIN1,APOE,ZFP36,SAMD4B,IGF1,PATL1,SPON1,CHRNA7,MOV10,ZFP36L1,INPP5E,MEX3D	cyan	VSMC_M2
GO:0030512	0.65	0.55	4	64	negative regulation of transforming growth factor beta receptor signaling pathway	BP	1	BCL9L,FAM89B,TP53,ZBTB7A	cyan	VSMC_M2
GO:0051865	0.65	0.55	4	62	protein autoubiquitination	BP	1	TRIM13,RNF213,TRIM21,MTA1	cyan	VSMC_M2
GO:2001242	0.65	0.48	9	135	regulation of intrinsic apoptotic signaling pathway	BP	1	GRINA,BAX,SFRP2,SRC,MAPK8IP1,ELL3,TMEM161A,TP53,NUPR1	cyan	VSMC_M2
GO:0120162	0.65	0.52	5	78	positive regulation of cold-induced thermogenesis	BP	1	STAT6,APPL2,DECR1,HADH,CPT2	cyan	VSMC_M2
GO:0019693	0.65	0.43	21	312	ribose phosphate metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,ABHD14B,ADCY1,UCKL1,ACAT1,EPHA2,PDK2,NUPR1,PPCDC,NUDT14,ABCD1,CBFA2T3,DPYD,ACOT6,ZBTB7A,DGAT1	cyan	VSMC_M2
GO:0008217	0.65	0.49	8	122	regulation of blood pressure	BP	1	RPS6KA2,HMOX1,NISCH,EXT2,AR,RASL10B,RENBP,RNLS	cyan	VSMC_M2
GO:0046889	0.65	0.54	4	61	positive regulation of lipid biosynthetic process	BP	1	APOE,PRKCD,SLC45A3,ABCD1	cyan	VSMC_M2
GO:0031098	0.66	0.45	13	197	stress-activated protein kinase signaling cascade	BP	1	ZFP36,MAP3K12,TLR3,SFRP2,MAPK8IP1,TIRAP,NFKB1,STK25,BMP4,ZFP36L1,MAP2K3,TRAF4,AXIN1	cyan	VSMC_M2
GO:0006913	0.66	0.44	17	257	nucleocytoplasmic transport	BP	1	APPL2,GLI3,BCL3,CAMK1,PRKCD,LZTS2,AGFG1,FAM53B,NFKBIA,BMP4,JUP,PRKACA,TP53,TSC2,RPS15,PML,EMD	cyan	VSMC_M2
GO:0051169	0.66	0.44	17	257	nuclear transport	BP	1	APPL2,GLI3,BCL3,CAMK1,PRKCD,LZTS2,AGFG1,FAM53B,NFKBIA,BMP4,JUP,PRKACA,TP53,TSC2,RPS15,PML,EMD	cyan	VSMC_M2
GO:0050864	0.66	0.50	6	93	regulation of B cell activation	BP	1	STAT6,SLC15A4,CD81,TIRAP,ZFP36L1,IL27RA	cyan	VSMC_M2
GO:0034637	0.66	0.53	4	63	cellular carbohydrate biosynthetic process	BP	1	IGF1,EXT2,PHKG1,B4GALT5	cyan	VSMC_M2
GO:0018193	0.66	0.38	68	997	peptidyl-amino acid modification	BP	1	EHMT2,RPS6KA2,P3H1,EFEMP1,NRP1,KLF15,BAX,AGBL5,SOCS3,CAMK1,KAT2B,FGFR1,SH3BP5,DCLK1,APBB1,PKDCC,CLIP3,ANGPT4,MAP3K12,IGF1,SNTA1,EFNA5,DPY19L3,GGCX,CAMKK2,SFRP2,PRKCD,EPHA3,SRC,TGM2,LRP4,CD81,IKBKE,CAPN3,HIST1H1C,LEF1,FES,BCR,CDC42BPG,HDAC6,FKBP10,ARRB2,EPHA2,ERBB2,PRKACA,NTRK1,PCGF2,MLLT6,TP53,KAT8,SHC1,PBXIP1,ULK3,GPRC5B,PDGFRB,NUDT14,MAP2K3,ROR1,ZDHHC9,DPH7,TNFRSF14,AXIN1,ABL1,IL34,NMT2,PML,CALM3,PYGO2	cyan	VSMC_M2
GO:0045921	0.66	0.53	4	63	positive regulation of exocytosis	BP	1	CADPS2,HGS,LAMP1,SDC4	cyan	VSMC_M2
GO:1903320	0.66	0.44	14	211	regulation of protein modification by small protein conjugation or removal	BP	1	DAXX,NOP53,TRIM21,ARRDC3,FOXF2,CAPN3,ARRB2,GABARAP,MTA1,ISG15,AXIN1,ABL1,RPS15,CDK9	cyan	VSMC_M2
GO:0008544	0.67	0.44	13	201	epidermis development	BP	1	KIAA1324L,SLITRK6,ZFP36,LRP4,STS,BCR,BMP4,RARRES3,LDB2,EPHA2,KAZN,ZFP36L1,KRT25	cyan	VSMC_M2
GO:0032755	0.67	0.53	4	62	positive regulation of interleukin-6 production	BP	1	TLR3,TIRAP,TMEM106A,IL17RA	cyan	VSMC_M2
GO:0043604	0.67	0.39	46	672	amide biosynthetic process	BP	1	PYM1,PLXNB2,EIF3H,B3GALT4,ST3GAL1,ACO1,IARS,RPL18,ABTB1,ACSS1,VIM,BCL3,MIF4GD,RPS16,ZFP36,SAMD4B,RPL15,EIF3K,SMPD1,EIF3F,PATL1,GGT7,ACSS2,PRKCD,MRPL36,B4GALT5,FURIN,MOV10,ACAT1,ERBB2,ZFP36L1,PDK2,GBA,WARS,CERS4,EEF2,DPH7,HAGH,INPP5E,RPL13,RPS15,MEX3D,RPS19,EEF1A2,RPL36A,AL157935.2	cyan	VSMC_M2
GO:0032414	0.67	0.51	5	80	positive regulation of ion transmembrane transporter activity	BP	1	SLC6A9,EHD3,CACNB3,WNK4,CALM3	cyan	VSMC_M2
GO:0098657	0.67	0.45	10	155	import into cell	BP	1	FLOT1,SLC6A9,FOLR2,SLC15A4,SLC7A2,ATP4A,SLC5A3,WNK4,SLC16A2,SLC8A3	cyan	VSMC_M2
GO:0006520	0.67	0.43	15	224	cellular amino acid metabolic process	BP	1	DDAH2,IARS,BCKDHB,AASS,SCLY,ECHS1,PCBD1,ACAT1,QDPR,MRI1,SLC16A2,WARS,ASPA,DPYD,FPGS	cyan	VSMC_M2
GO:0022898	0.67	0.44	12	186	regulation of transmembrane transporter activity	BP	1	STOM,SLC6A9,EHD3,SCN1B,CACNB3,LINC02210-CRHR1,CAPN1,WNK4,PRKACA,CBARP,CALM3,CLIC2	cyan	VSMC_M2
GO:0006402	0.67	0.44	13	201	mRNA catabolic process	BP	1	PYM1,VIM,ZFP36,SAMD4B,PATL1,PRKCD,IKBKE,TIRAP,HELZ2,RNASEL,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0050867	0.67	0.43	15	226	positive regulation of cell activation	BP	1	STAT6,GLI3,PNP,LAMP1,IGF1,SRC,CD81,CAPN3,TIRAP,LEF1,B2M,IL27RA,PDGFRB,TNFRSF14,CD55	cyan	VSMC_M2
GO:0072527	0.67	0.52	4	63	pyrimidine-containing compound metabolic process	BP	1	NEIL2,UCKL1,DPYD,TK2	cyan	VSMC_M2
GO:0030641	0.68	0.52	4	64	regulation of cellular pH	BP	1	SLC4A9,GRN,TMEM175,ATP6V0D1	cyan	VSMC_M2
GO:0045727	0.68	0.47	7	109	positive regulation of translation	BP	1	PYM1,PLXNB2,VIM,BCL3,MIF4GD,ERBB2,EEF2	cyan	VSMC_M2
GO:2001020	0.68	0.43	13	200	regulation of response to DNA damage stimulus	BP	1	APBB1,SFRP2,PRKCD,MMS19,MAGEF1,ELL3,TMEM161A,CASP9,TP53,UBQLN4,ABL1,PML,CDK9	cyan	VSMC_M2
GO:0009259	0.68	0.41	20	302	ribonucleotide metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,ABHD14B,ADCY1,UCKL1,ACAT1,EPHA2,PDK2,NUPR1,PPCDC,ABCD1,CBFA2T3,DPYD,ACOT6,ZBTB7A,DGAT1	cyan	VSMC_M2
GO:0018107	0.68	0.48	6	98	peptidyl-threonine phosphorylation	BP	1	MAP3K12,PRKCD,CDC42BPG,PRKACA,AXIN1,CALM3	cyan	VSMC_M2
GO:0030168	0.68	0.47	6	96	platelet activation	BP	1	APOE,PLSCR1,PRKCD,SRC,FIBP,SERPINE2	cyan	VSMC_M2
GO:0007088	0.68	0.47	6	96	regulation of mitotic nuclear division	BP	1	CUL9,IGF1,BMP4,TEX14,PDGFRB,FBXW5	cyan	VSMC_M2
GO:0046394	0.69	0.42	14	213	carboxylic acid biosynthetic process	BP	1	AASS,ACSS1,GGT7,ACSS2,SLC45A3,PTGIS,PCBD1,ALOX15,MRI1,HSD3B7,ABCD1,PTGDS,GSTM4,DPYD	cyan	VSMC_M2

GO:0034655	0.69	0.39	22	335	nucleobase-containing compound catabolic process	BP	1	PYM1,BAX,VIM,PNP,ZFP36,SAMD4B,PATL1,NEIL2,PRKCD,IKBKE,TIRAP,HELZ2,RNASEL,MUS81,MOV10,ACAT1,NUDT13,ZFP36L1,ABCD1,DPYD,OAS2,MEX3D	cyan	VSMC_M2
GO:1990748	0.69	0.48	5	79	cellular detoxification	BP	1	SELENOW,APOE,CCS,UBIAD1,CLIC2	cyan	VSMC_M2
GO:0030004	0.69	0.48	5	81	cellular monovalent inorganic cation homeostasis	BP	1	SLC4A9,ATP4A,GRN,TMEM175,ATP6V0D1	cyan	VSMC_M2
GO:0061041	0.69	0.47	6	96	regulation of wound healing	BP	1	APOE,SERPING1,PRKCD,SERPINE2,FOXC2,PLPP3	cyan	VSMC_M2
GO:0043170	0.69	0.34	496	7034	macromolecule metabolic process	BP	1	CTDP1,TSHZ1,MMP19,PYM1,RBMS2,STAT6,TCF21,OS9,ADAMTS2,MGAT4B,GNS,AKAP12,FLOT1,PPP6R2,MSH5,EHMT2,PLXNB2,ZFPM2,CFB,EIF3H,RPS6KA2,IRF1,AFDN,DEPTOR,B3GALT4,TAPBP,TCF20,DAXX,FBXO32,TEF,PTPRK,ST3GAL1,CDC14C,GSDMD,TEAD3,MTCH1,TLE1,GGA1,CARD10,KCTD17,NFIB,TRERF1,GCNT1,HMOX1,LRRC19,ACO1,CUL9,KLF9,APPL2,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,GALNT12,ITGB8,P3H1,NAT14,GPNMB,EFEMP1,TRIL,RRAGC,EEPD1,MEIS1,RNF144A,STK40,AKT1S1,STK17A,PTOV1,AASS,GLI3,SIM1,AP2A1,IRF3,GSN,NRP1,KLF15,BAX,DBP,HBP1,RPL18,PARP12,NOP53,ABTB1,BICRA,MEIS3,FKRP,LURAP1,TRIM13,FZD4,CAB39L,MARK4,VIM,AGBL5,BIN1,APOE,BCL3,MIF4GD,AGAP3,ATRAID,SLC6A9,ATG7,LTBP4,CAPN5,SOCS3,CAMK1,EHD3,PLD3,TEP1,RNF170,PNP,RPS16,TIMP2,ZFP36,CANT1,SAMD4B,GAA,PAK4,SGSH,RNF213,ARAP1,RPL15,HGS,KAT2B,TBC1D5,EIF3K,RFTN1,RHOG,FGFR1,IL5RA,SH3BP5,TRIM21,DCLK1,SMPD1,APBB1,PKDCC,TPP1,MMP17,CLIP3,GTF3A,SLC15A4,ANGPT4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,GNPTAB,IGF1,TLR3,SNTA1,MAN2A1,WT1,EFNA5,CHMP4B,DPY19L3,TP53INP2,PATL1,TSHZ3,GGT7,GALNT18,GGCX,POU6F1,SERPING1,CAST,LACTB2,EDEM2,CTSB,NEIL2,ARRDC3,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,STBD1,PRKCD,EPHA3,SRC,CPE,TGM2,BPI,LRP4,ZHX3,RIOX2,MMS19,CHST14,FOXF2,SFRP5,MAPK8IP1,SORBS3,MMP2,PTPN13,EXT2,STAT1,CTSA,ABHD14B,MOB2,GFRA2,CD81,NDN,PHKG1,GUSB,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,MRPL36,AGFG1,PCSK6,RNPEP,CSTB,TUSC2,ZNF496,NFKB1,GNAI2,SPOCD1,TPPP,B4GALT4,HIST1H1C,PKNOX2,RGMA,BCL9,UBA7,LEF1,TRIM47,STEAP3,NTRK2,ACSL1,F2RL2,SYNJ2,ANXA1	cyan	VSMC_M2
GO:0045930	0.69	0.42	12	186	negative regulation of mitotic cell cycle	BP	1	GPNMB,NOP53,TIMP2,MUS81,BMP4,ZFP36L1,TP53,KANK2,TEX14,ABL1,GAS1,PML	cyan	VSMC_M2
GO:0015980	0.69	0.40	17	259	energy derivation by oxidation of organic compounds	BP	1	ACO1,STK40,NOP53,UQCRH,ME3,GAA,IGF1,STBD1,COQ9,PHKG1,AIFM2,TP53,GBA,NUPR1,ABCD1,IDH3G,CBFA2T3	cyan	VSMC_M2
GO:0072521	0.69	0.39	21	319	purine-containing compound metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,ABHD14B,ADCY1,ACAT1,MACROD1,EPHA2,PDK2,NUPR1,PPCDC,ABCD1,CBFA2T3,DPYD,ACOT6,ZBTB7A,DGAT1,MACROD2	cyan	VSMC_M2
GO:0008037	0.69	0.46	6	97	cell recognition	BP	1	NRP1,FOLR2,EPHA3,CD81,NDN,AL157935.2	cyan	VSMC_M2
GO:0006576	0.69	0.50	4	64	cellular biogenic amine metabolic process	BP	1	MOXD1,SLC44A1,SAT2,SAT1	cyan	VSMC_M2
GO:0007018	0.70	0.39	18	283	microtubule-based movement	BP	1	KIFC2,RSPH9,CCDC114,TPPP2,LAMP1,TMEM108,CLIP3,BBS2,KIF7,KIF1A,FYCO1,RPGR,MAP1S,HDAC6,NPHP4,RHOT2,DNAAF1,HSBP1	cyan	VSMC_M2
GO:0006605	0.70	0.39	17	262	protein targeting	BP	1	OS9,STOM,HGS,GNPTAB,CHMP4B,CACNB3,VPS11,M6PR,HOMER3,GABARAP,GIPC1,ERBB2,SLC51B,ZDHHC9,NAGPA,MON1B,UBL5	cyan	VSMC_M2
GO:0016053	0.70	0.40	14	215	organic acid biosynthetic process	BP	1	AASS,ACSS1,GGT7,ACSS2,SLC45A3,PTGIS,PCBD1,ALOX15,MRI1,HSD3B7,ABCD1,PTGDS,GSTM4,DPYD	cyan	VSMC_M2
GO:0046031	0.70	0.49	4	66	ADP metabolic process	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0043933	0.70	0.34	93	1370	protein-containing complex subunit organization	BP	1	PYM1,EIF3H,AFDN,TAPBP,DAXX,ARHGAP18,GSDMD,CARD10,KCTD17,TRPM3,APPL2,RSPH9,HIGD2A,PLA2G7,COBL,GSN,BAX,CCDC114,NOP53,BIN1,APOE,SHKBP1,EHD3,TPPP2,RNF213,EIF3K,CLIP3,ANGPT4,EIF3F,EFNA5,CHMP4B,CHMP3,PRKCD,SRC,C15orf62,IKBKE,CAPN3,TIRAP,CTTN,TPPP,HIST1H1C,DISP1,SV2A,SSH3,NDUFAF3,FES,PRUNE1,WIPF1,ARPC5,B2M,KCND3,FYCO1,ADD1,CAPZB,MAP1S,TECPR1,DLG5,HDAC6,ALOX15,SMIM20,PRKACA,SLIT2,TP53,UBQLN4,GBA,PPP1R9B,NUPR1,ADAR,WARS,CENPV,MCOLN1,FLII,LLGL1,SH3GL1,ISG15,ELOB,TRAF7,SLC9A3R2,AXIN1,ABL1,DNAAF1,IST1,LCAT,RPS15,KCND2,DGAT1,PML,RPS19,GEMIN8,CARD8,BMF,GCHFR,TSPAN4	cyan	VSMC_M2
GO:0002377	0.70	0.46	5	81	immunoglobulin production	BP	1	STAT6,SLC15A4,B2M,IL27RA,TCF3	cyan	VSMC_M2
GO:0009123	0.71	0.48	4	65	nucleoside monophosphate metabolic process	BP	1	PNP,UCKL1,DPYD,TK2	cyan	VSMC_M2
GO:0140029	0.71	0.48	4	66	exocytic process	BP	1	SV2A,VPS11,CPLX2,STX3	cyan	VSMC_M2
GO:0008088	0.71	0.48	4	68	axo-dendritic transport	BP	1	TMEM108,KIF1A,HDAC6,HSBP1	cyan	VSMC_M2
GO:0070555	0.71	0.45	6	98	response to interleukin-1	BP	1	AKAP12,SMPD1,SRC,NFKB1,PTGIS,ADAMTS7	cyan	VSMC_M2
GO:0044706	0.71	0.41	10	159	multi-multicellular organism process	BP	1	TEAD3,EPYC,CTSB,HEXB,MMP2,STS,LINC02210-CRHR1,SERPINE2,AR,JUNB	cyan	VSMC_M2
GO:0090100	0.71	0.46	5	85	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	KIAA1324L,BMP4,GIPC1,NEO1,GATA4	cyan	VSMC_M2
GO:0006612	0.71	0.44	6	97	protein targeting to membrane	BP	1	STOM,CHMP4B,CACNB3,ERBB2,SLC51B,ZDHHC9	cyan	VSMC_M2
GO:1901796	0.71	0.46	5	83	regulation of signal transduction by p53 class mediator	BP	1	NOP53,ELL3,TP53,RPS15,HEXIM1	cyan	VSMC_M2
GO:0017015	0.71	0.44	6	102	regulation of transforming growth factor beta receptor signaling pathway	BP	1	LTBP4,BCL9L,FAM89B,GIPC1,TP53,ZBTB7A	cyan	VSMC_M2
GO:0060294	0.71	0.48	4	68	cilium movement involved in cell motility	BP	1	RSPH9,TPPP2,BBS2,NPHP4	cyan	VSMC_M2
GO:0007605	0.71	0.44	6	102	sensory perception of sound	BP	1	FZD4,SLITRK6,EPYC,HEXB,ROR1,SERPINB6	cyan	VSMC_M2
GO:0009636	0.71	0.40	11	174	response to toxic substance	BP	1	EHMT2,BAX,SELENOW,APOE,SCN1B,CCS,UBIAD1,NUPR1,PDGFRB,SNN,CLIC2	cyan	VSMC_M2
GO:0051783	0.71	0.43	7	114	regulation of nuclear division	BP	1	RPS6KA2,CUL9,IGF1,BMP4,TEX14,PDGFRB,FBXW5	cyan	VSMC_M2
GO:0000226	0.71	0.35	34	522	microtubule cytoskeleton organization	BP	1	CDC14C,KIFC2,CUL9,RSPH9,CCDC114,MARK4,TPPP2,KAT2B,POC1B,CLIP3,EFNA5,CHMP4B,CHMP3,EPHA3,BBS2,LZTS2,TPPP,GAS2L1,FES,PRUNE1,TACC2,PARD3B,ARHGEF10,MAP1S,CC2D2A,HDAC6,CROCC,GABARAP,ANKFN1,LLGL1,DVL1,FBXW5,ABL1,DNAAF1	cyan	VSMC_M2
GO:0015718	0.71	0.47	4	66	monocarboxylic acid transport	BP	1	SLC16A9,SLC51B,SLC16A2,SLC10A3	cyan	VSMC_M2
GO:0010927	0.71	0.45	5	87	cellular component assembly involved in morphogenesis	BP	1	CAPN3,TPPP,PDGFRB,FLII,ABCA2	cyan	VSMC_M2

GO:0140056	0.71	0.47	4	67	organelle localization by membrane tethering	BP	1	NDRG4,VPS11,CPLX2,STX3	cyan	VSMC_M2
GO:0023061	0.72	0.36	21	325	signal release	BP	1	CADPS2,FZD4,LTBP4,RAB11FIP1,EFNA5,NISCH,HADH,SV2A,ADCY1,LINC02210-CRHR1,ADORA2A,PORCN,GIPC1,CPLX2,RASL10B,DVL1,PHPT1,RAB11FIP3,CALM3,STX3,RAB11B	cyan	VSMC_M2
GO:0019725	0.72	0.34	42	638	cellular homeostasis	BP	1	GRINA,KCTD17,HMOX1,ACO1,KLF15,BAX,APOE,SLC6A9,GAA,SLC4A9,ACKR4,ATP4A,EFNA5,HEXB,CACNB3,TGM2,PLCG1,CHRNA7,CAPN3,TPCN2,SV2A,ERFE,CYB561,GRN,PRKACA,CLCN6,TMEM175,GRIA1,MCOLN1,PHPT1,RHOT2,ABL1,ATP6V0D1,ABCA2,SLC8A3,SERPINF1,CD55,PML,GATA4,CALM3,CLIC2,RAB11B	cyan	VSMC_M2
GO:1990845	0.72	0.41	8	132	adaptive thermogenesis	BP	1	STAT6,APPL2,ARRDC3,DECR1,HADH,IP6K1,CPT2,FOXC2	cyan	VSMC_M2
GO:0051591	0.72	0.47	4	68	response to cAMP	BP	1	WT1,STAT1,ZFP36L1,SLC8A3	cyan	VSMC_M2
GO:0001701	0.72	0.36	20	314	in utero embryonic development	BP	1	ZFPM2,GLI3,SOCS3,IGF1,MAN2A1,PLCG1,LEF1,FURIN,HEG1,PLCD3,DNAJB6,FKBP10,ZFP36L1,PCGF2,AR,TP53,C6,CPT2,RPL13,JUNB	cyan	VSMC_M2
GO:0071805	0.72	0.41	8	131	potassium ion transmembrane transport	BP	1	KCNQ5,BIN1,ABCB8,ATP4A,KCND3,WNK4,TMEM175,KCND2	cyan	VSMC_M2
GO:0021510	0.72	0.47	4	70	spinal cord development	BP	1	GLI3,MED12,PTPRS,PBX3	cyan	VSMC_M2
GO:0072330	0.72	0.40	9	144	monocarboxylic acid biosynthetic process	BP	1	ACSS1,ACSS2,SLC45A3,PTGIS,ALOX15,HSD3B7,ABCD1,PTGDS,GSTM4	cyan	VSMC_M2
GO:0051054	0.72	0.39	11	176	positive regulation of DNA metabolic process	BP	1	STAT6,BAX,APBB1,WT1,PRKCD,SRC,MMS19,TMEM161A,ARRB2,PDGFRB,PML	cyan	VSMC_M2
GO:0048639	0.72	0.41	8	134	positive regulation of developmental growth	BP	1	ZFPM2,NRP1,IGF1,WT1,CAPN3,RND2,AGRN,IST1	cyan	VSMC_M2
GO:0000956	0.73	0.42	6	102	nuclear-transcribed mRNA catabolic process	BP	1	PYM1,ZFP36,SAMD4B,PATL1,HELZ2,ZFP36L1	cyan	VSMC_M2
GO:0007589	0.73	0.46	4	68	body fluid secretion	BP	1	GPAT4,WNK4,STAT5A,OAS2	cyan	VSMC_M2
GO:1903844	0.73	0.42	6	104	regulation of cellular response to transforming growth factor beta stimulus	BP	1	LTBP4,BCL9L,FAM89B,GIPC1,TP53,ZBTB7A	cyan	VSMC_M2
GO:0042692	0.73	0.35	19	303	muscle cell differentiation	BP	1	CTDP1,FLOT1,BIN1,CAMK1,PLD3,EFNB2,IGF1,WT1,CD81,CAPN3,BCL9,HDAC5,BMP4,ARRB2,PDGFRB,FLII,PTGFRN,GATA4,CDK9	cyan	VSMC_M2
GO:0097306	0.73	0.45	4	71	cellular response to alcohol	BP	1	KLF9,ADCY1,JUP,ADAM15	cyan	VSMC_M2
GO:0071260	0.74	0.44	4	69	cellular response to mechanical stimulus	BP	1	IRF1,TLR3,NFKB1,PIEZO2	cyan	VSMC_M2
GO:0030901	0.74	0.44	4	69	midbrain development	BP	1	SFRP2,DLG5,CALM3,EN1	cyan	VSMC_M2
GO:0018210	0.74	0.41	6	104	peptidyl-threonine modification	BP	1	MAP3K12,PRKCD,CDC42BPG,PRKACA,AXIN1,CALM3	cyan	VSMC_M2
GO:0007596	0.74	0.37	10	164	blood coagulation	BP	1	APOE,GGCX,SERPING1,PLSCR1,PRKCD,SRC,HPS6,FIBP,ADORA2A,SERPINE2	cyan	VSMC_M2
GO:0003341	0.74	0.40	6	103	cilium movement	BP	1	RSPH9,CCDC114,TPPP2,BBS2,NPHP4,DNAAF1	cyan	VSMC_M2
GO:0051656	0.74	0.33	21	334	establishment of organelle localization	BP	1	HMOX1,LAMP1,CHMP4B,BBS2,FES,KIF1A,PARD3B,STK25,FYCO1,MAP1S,HDAC6,CROCC,STARD3,CPLX2,ANKFN1,LLGL1,PTGDS,RHOT2,HSBP1,RPS15,RAB11B	cyan	VSMC_M2
GO:1901605	0.74	0.37	9	146	alpha-amino acid metabolic process	BP	1	DDAH2,AASS,SCLY,PCBD1,ACAT1,QDPR,MRI1,ASPA,FPGS	cyan	VSMC_M2
GO:0007338	0.75	0.41	5	86	single fertilization	BP	1	PLB1,FOLR2,HEXB,GLRB,AR	cyan	VSMC_M2
GO:0001776	0.75	0.43	4	70	leukocyte homeostasis	BP	1	BAX,SLC15A4,LMO1,ABL1	cyan	VSMC_M2
GO:0044344	0.75	0.41	5	86	cellular response to fibroblast growth factor stimulus	BP	1	ZFP36,FGFR1,EXT2,FIBP,ZFP36L1	cyan	VSMC_M2
GO:0007254	0.75	0.38	8	134	JNK cascade	BP	1	MAP3K12,TLR3,SFRP2,MAPK8IP1,TIRAP,NFKB1,TRAF4,AXIN1	cyan	VSMC_M2
GO:0006641	0.75	0.43	4	70	triglyceride metabolic process	BP	1	APOE,GPAT4,PNPLA2,DGAT1	cyan	VSMC_M2
GO:0006282	0.75	0.39	7	118	regulation of DNA repair	BP	1	APBB1,MMS19,MAGEF1,TMEM161A,UBQLN4,PML,CDK9	cyan	VSMC_M2
GO:0097237	0.75	0.41	5	85	cellular response to toxic substance	BP	1	SELENOW,APOE,CCS,UBIAD1,CLIC2	cyan	VSMC_M2
GO:0009150	0.75	0.33	18	286	purine ribonucleotide metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,ABHD14B,ADCY1,ACAT1,EPHA2,PDK2,NUPR1,PPCDC,ABCD1,CBFA2T3,ACOT6,ZBTB7A,DGAT1	cyan	VSMC_M2
GO:0098659	0.75	0.43	4	71	inorganic cation import across plasma membrane	BP	1	SLC6A9,ATP4A,WNK4,SLC8A3	cyan	VSMC_M2
GO:0099587	0.75	0.43	4	71	inorganic ion import across plasma membrane	BP	1	SLC6A9,ATP4A,WNK4,SLC8A3	cyan	VSMC_M2
GO:0045927	0.75	0.35	12	199	positive regulation of growth	BP	1	ZFPM2,NRP1,RFTN1,IGF1,WT1,SFRP2,CAPN3,RND2,ERBB2,BRAT1,AGRN,IST1	cyan	VSMC_M2
GO:1905897	0.75	0.43	4	70	regulation of response to endoplasmic reticulum stress	BP	1	GRINA,BAX,UBQLN2,NUPR1	cyan	VSMC_M2
GO:0002822	0.75	0.39	6	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	STAT6,SLC15A4,CD81,B2M,IL27RA,CD55	cyan	VSMC_M2
GO:0007599	0.75	0.36	10	166	hemostasis	BP	1	APOE,GGCX,SERPING1,PLSCR1,PRKCD,SRC,HPS6,FIBP,ADORA2A,SERPINE2	cyan	VSMC_M2
GO:0050817	0.75	0.36	10	166	coagulation	BP	1	APOE,GGCX,SERPING1,PLSCR1,PRKCD,SRC,HPS6,FIBP,ADORA2A,SERPINE2	cyan	VSMC_M2
GO:0030595	0.75	0.36	9	150	leukocyte chemotaxis	BP	1	PLA2G7,TIRAP,VEGFD,VEGFB,NBL1,SLIT2,HSD3B7,IL34,RPS19	cyan	VSMC_M2
GO:0046328	0.75	0.39	6	104	regulation of JNK cascade	BP	1	TLR3,SFRP2,MAPK8IP1,TIRAP,TRAF4,AXIN1	cyan	VSMC_M2
GO:0006473	0.76	0.35	10	168	protein acetylation	BP	1	KLF15,CAMK1,KAT2B,APBB1,LEF1,PCGF2,KAT8,NUPR1,PBXIP1,PYGO2	cyan	VSMC_M2
GO:0031396	0.76	0.35	11	180	regulation of protein ubiquitination	BP	1	DAXX,ARRDC3,FOXF2,ARRB2,GABARAP,MTA1,ISG15,AXIN1,ABL1,RPS15,CDK9	cyan	VSMC_M2
GO:0031929	0.76	0.39	6	105	TOR signaling	BP	1	DEPTOR,RRAGC,AKT1S1,GBA,TSC2,NPRL3	cyan	VSMC_M2
GO:0033135	0.76	0.38	6	104	regulation of peptidyl-serine phosphorylation	BP	1	BAX,CAMK1,SFRP2,HDAC6,ARRB2,AXIN1	cyan	VSMC_M2
GO:0001959	0.76	0.37	7	119	regulation of cytokine-mediated signaling pathway	BP	1	IRF3,IKBKE,ECM1,SLIT2,ADAR,ISG15,CARD8	cyan	VSMC_M2
GO:0044773	0.76	0.42	4	71	mitotic DNA damage checkpoint signaling	BP	1	NOP53,MUS81,TP53,PML	cyan	VSMC_M2
GO:0090305	0.76	0.33	13	213	nucleic acid phosphodiester bond hydrolysis	BP	1	BAX,PLD3,ZFP36,LACTB2,PLSCR1,TATDN3,HELZ2,RNASEL,MUS81,MOV10,RNASEK,EXD3,REXO1	cyan	VSMC_M2
GO:0099175	0.76	0.41	4	73	regulation of postsynapse organization	BP	1	APOE,LZTS3,KIF1A,PTPRS	cyan	VSMC_M2
GO:0007519	0.76	0.37	7	122	skeletal muscle tissue development	BP	1	MYL6B,TCF21,FLOT1,BCL9,NUPR1,EEF2,EMD	cyan	VSMC_M2
GO:0006165	0.76	0.41	4	72	nucleoside diphosphate phosphorylation	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0030705	0.77	0.34	10	173	cytoskeleton-dependent intracellular transport	BP	1	LAMP1,TMEM108,CLIP3,KIF1A,FYCO1,RPGR,MAP1S,HDAC6,RHOT2,HSBP1	cyan	VSMC_M2
GO:1903313	0.77	0.37	6	105	positive regulation of mRNA metabolic process	BP	1	ZFP36,SAMD4B,PATL1,MOV10,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0048284	0.77	0.36	7	120	organelle fusion	BP	1	BAX,CHMP3,VPS11,VAT1,TMEM175,CPLX2,STX3	cyan	VSMC_M2
GO:0045833	0.77	0.40	4	72	negative regulation of lipid metabolic process	BP	1	APPL2,APOE,NFKB1,ABCA2	cyan	VSMC_M2
GO:0031397	0.77	0.40	4	72	negative regulation of protein ubiquitination	BP	1	ARRB2,ISG15,ABL1,RPS15	cyan	VSMC_M2

GO:0044085	0.77	0.26	166	2454	cellular component biogenesis	BP	1	FLOT1,EHMT2,PLXNB2,EIF3H,AFDN,PACSIN2,TAPBP,DAXX,PTPRK,ARHGAP18,IBA57,CDC14C,GSDMD,CARD10,KCTD17,KIFC2,TRPM3,APPL2,RSPH9,HIGD2A,BBS9,COBL,GSN,NRP1,BAX,CCDC114,NOP53,MARK4,BIN1,APOE,ATG7,SHKBP1,SLITRK6,EHD3,DZIP1,TPPP2,RPS16,RNF213,ARAP1,HGS,KAT2B,EIF3K,RFTN1,RHOG,EFNB2,POC1B,CLIP3,GTF3A,ANGPT4,EIF3F,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,WWTR1,PRKCD,EPHA3,SRC,LRP4,RIOX2,BBS2,MMS19,C15orf62,SORBS3,LZTS2,PHACTR1,IKBKE,CAPN3,TJP1,TIRAP,MRPL36,CTTN,TPPP,HIST1H1C,DISP1,SV2A,SSH3,LAMB2,NDUFAF3,REC8,FES,PRUNE1,VPS11,HEG1,VANGL2,STK25,RNASEL,WIPF1,ARPC5,LTBP3,B2M,KCND3,ARHGEF10,BCR,RPGR,ADD1,LDB2,CAPZB,CC2D2A,DLG5,HDAC6,ARHGEF10L,WDR45,CROCC,DNAJB6,FKBP10,JUP,ALOX15,EPHA2,GABARAP,CGNL1,SMIM20,PRKACA,UBQLN2,NTRK1,SLIT2,TMEM175,TP53,GBA,PPP1R9B,NUPR1,ADAR,WARS,CENPV,IMP3,PDGFRB,MCOLN1,FLI,LLGL1,PTPRS,DVL1,AGRN,ISG15,ELOB,TRAF7,SLC9A3R2,NDOR1,NPHP4,WDR90,ENTR1,AXIN1,NPRL3,CLSTN1,AIF1L,ABL1,DNAAF1,ATMIN,IST1,LCAT,ATP6V0D1,ABCA2,RPS15,KCND2,RAB43,DGAT1,PML,RPS19,GEMIN8,CARD8,BMF,GCHFR,TMEM250,SDC4,TSPAN4	cyan	VSMC_M2
GO:0071902	0.77	0.33	10	170	positive regulation of protein serine/threonine kinase activity	BP	1	FZD4,CAB39L,CAMK1,FGFR1,MAP3K12,SRC,ERBB2,PDGFRB,IL34,CALM3	cyan	VSMC_M2
GO:0048515	0.78	0.36	6	106	spermatid differentiation	BP	1	EHMT2,BAX,BBS2,REC8,PRKACA,PYGO2	cyan	VSMC_M2
GO:0009165	0.78	0.32	12	198	nucleotide biosynthetic process	BP	1	ACSS1,PNP,ACSS2,NADSYN1,PTGIS,ADCY1,UCKL1,NMNAT2,ACAT1,PDK2,PPCDC,TK2	cyan	VSMC_M2
GO:0051640	0.78	0.28	28	447	organelle localization	BP	1	HMOX1,BIN1,LAMP1,CHMP4B,NDRG4,BBS2,HPS6,FES,VPS11,KIF1A,PARD3B,STK25,FYCO1,MAP1S,HDAC6,CROCC,PLEKHM2,BRAT1,STARD3,CPLX2,ANKFN1,LLGL1,PTGDS,RHOT2,HSBP1,RPS15,STX3,RAB11B	cyan	VSMC_M2
GO:0046939	0.78	0.38	4	74	nucleotide phosphorylation	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0007565	0.78	0.33	8	139	female pregnancy	BP	1	TEAD3,EPYC,CTSB,MMP2,STS,LINC02210-CRHR1,AR,JUNB	cyan	VSMC_M2
GO:0072594	0.78	0.28	22	355	establishment of protein localization to organelle	BP	1	APPL2,GLI3,BAX,BCL3,HGS,LAMP1,GNPTAB,CHMP4B,PRKCD,VPS11,FAM53B,NFKBIA,M6PR,BMP4,JUP,TP53,NAGPA,TSC2,MON1B,PML,CALM3,UBL5	cyan	VSMC_M2
GO:0015833	0.78	0.31	11	186	peptide transport	BP	1	TAPBP,LTBP4,SLC15A4,EFNA5,HADH,DISP1,LINC02210-CRHR1,RASL10B,ABCC1,PHPT1,RAB11B	cyan	VSMC_M2
GO:0006906	0.79	0.36	5	90	vesicle fusion	BP	1	CHMP3,VPS11,TMEM175,CPLX2,STX3	cyan	VSMC_M2
GO:0006813	0.79	0.33	8	140	potassium ion transport	BP	1	KCNQ5,BIN1,ABCB8,ATP4A,KCND3,WNK4,TMEM175,KCND2	cyan	VSMC_M2
GO:0035195	0.79	0.35	6	107	gene silencing by miRNA	BP	1	ZFP36,MOV10,BMP4,TP53,ADAR,MIR197	cyan	VSMC_M2
GO:1901293	0.79	0.31	12	199	nucleoside phosphate biosynthetic process	BP	1	ACSS1,PNP,ACSS2,NADSYN1,PTGIS,ADCY1,UCKL1,NMNAT2,ACAT1,PDK2,PPCDC,TK2	cyan	VSMC_M2
GO:0001678	0.79	0.34	7	124	cellular glucose homeostasis	BP	1	KLF15,EFNA5,PRKACA,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0001659	0.79	0.33	8	141	temperature homeostasis	BP	1	STAT6,APPL2,ARRDC3,DECR1,HADH,IP6K1,CPT2,FOXC2	cyan	VSMC_M2
GO:0044774	0.79	0.38	4	74	mitotic DNA integrity checkpoint signaling	BP	1	NOP53,MUS81,TP53,PML	cyan	VSMC_M2
GO:0019941	0.79	0.27	35	550	modification-dependent protein catabolic process	BP	1	OS9,EIF3H,KCTD17,CUL9,RNF144A,NOP53,TRIM13,AGAP3,RNF213,RBCK1,TP53INP2,EDEM2,WWTR1,FOXF2,UBA7,DCAF11,MAGEF1,MAEA,HDAC6,ARRB2,GABARAP,GIPC1,UBQLN2,UBQLN4,GBA,MTA1,WDR81,DVL1,ISG15,ELOB,FBXW5,AXIN1,CBFA2T3,RNF166,PML	cyan	VSMC_M2
GO:0071774	0.79	0.36	5	91	response to fibroblast growth factor	BP	1	ZFP36,FGFR1,EXT2,FIBP,ZFP36L1	cyan	VSMC_M2
GO:1903312	0.79	0.38	4	74	negative regulation of mRNA metabolic process	BP	1	ZFP36,IKBKE,TIRAP,CDK9	cyan	VSMC_M2
GO:0071347	0.79	0.38	4	75	cellular response to interleukin-1	BP	1	AKAP12,NFKB1,PTGIS,ADAMTS7	cyan	VSMC_M2
GO:0098754	0.79	0.36	5	90	detoxification	BP	1	SELENOW,APOE,CCS,UBIAD1,CLIC2	cyan	VSMC_M2
GO:0044106	0.79	0.37	4	74	cellular amine metabolic process	BP	1	MOXD1,SLC44A1,SAT2,SAT1	cyan	VSMC_M2
GO:0006639	0.79	0.35	5	92	acylglycerol metabolic process	BP	1	APOE,GPAT4,PNPLA2,DAGLA,DGAT1	cyan	VSMC_M2
GO:1990266	0.79	0.37	4	74	neutrophil migration	BP	1	RHOG,TIRAP,XG,SLIT2	cyan	VSMC_M2
GO:0016567	0.79	0.26	42	656	protein ubiquitination	BP	1	OS9,DAXX,FBXO32,CUL9,TRIM14,RNF144A,TRIM13,SOCS3,RNF170,RNF213,TRIM21,RBCK1,ARRDC3,WWTR1,FOXF2,TRIM8,UBA7,DCAF11,VPS11,MAGEF1,DTX2,MAEA,HDAC6,ARRB2,GABARAP,PCGF2,MED12,MTA1,ISG15,ELOB,E4F1,TRAF7,FBXW5,UNKL,AXIN1,RNF166,ABL1,RPS15,DTX3,TRIM26,PML,CDK9	cyan	VSMC_M2
GO:0097530	0.80	0.35	5	91	granulocyte migration	BP	1	RHOG,TIRAP,XG,SLIT2,IL34	cyan	VSMC_M2
GO:0018394	0.80	0.31	8	143	peptidyl-lysine acetylation	BP	1	KLF15,KAT2B,APBB1,LEF1,PCGF2,KAT8,PBXIP1,PYGO2	cyan	VSMC_M2
GO:2000779	0.80	0.36	4	76	regulation of double-strand break repair	BP	1	MMS19,MAGEF1,UBQLN4,PML	cyan	VSMC_M2
GO:0006401	0.80	0.29	14	237	RNA catabolic process	BP	1	PYM1,VIM,ZFP36,SAMD4B,PATL1,PRKCD,IKBKE,TIRAP,HELZ2,RNASEL,MOV10,ZFP36L1,OAS2,MEX3D	cyan	VSMC_M2
GO:0051053	0.80	0.35	5	94	negative regulation of DNA metabolic process	BP	1	SRC,HIST1H1C,MAGEF1,TP53,UBQLN4	cyan	VSMC_M2
GO:0006638	0.80	0.34	5	93	neutral lipid metabolic process	BP	1	APOE,GPAT4,PNPLA2,DAGLA,DGAT1	cyan	VSMC_M2
GO:0061025	0.80	0.32	7	125	membrane fusion	BP	1	FOLR2,CHMP3,VPS11,USE1,TMEM175,CPLX2,STX3	cyan	VSMC_M2
GO:0006997	0.80	0.33	6	112	nucleus organization	BP	1	BIN1,CHMP4B,PML,RPS19,PYGO2,EMD	cyan	VSMC_M2
GO:0022414	0.80	0.24	67	1029	reproductive process	BP	1	TCF21,ADAMTS2,MSH5,EHMT2,ZFPM2,RPS6KA2,TEAD3,MEA1,ITGB8,GLI3,BAX,FZD4,PLB1,SOCS3,DZIP1,TPPP2,FOLR2,CATSPERG,EPYC,RARG,IGF1,TLR3,WT1,GGT7,CTSB,HEXB,SFRP2,NDRG3,GLRB,SRC,BBS2,FOXF2,MMP2,AGFG1,SPOCD1,LEF1,STS,REC8,MUS81,ELL3,LINC02210-CRHR1,WNT2B,PLCD3,PSAP,BMP4,DNAJB6,ARRB2,SERPINE2,PRKACA,ZFP36L1,SPIN4,NTRK1,SLIT2,AR,PPP1R9B,ADAM15,NUPR1,TEX14,PDGFRB,PLAC1,NPHP4,SLC2A8,SERPINF1,SELENOP,JUNB,GATA4,PYGO2	cyan	VSMC_M2
GO:0022406	0.80	0.36	4	76	membrane docking	BP	1	NDRG4,VPS11,CPLX2,STX3	cyan	VSMC_M2
GO:0071333	0.80	0.33	6	110	cellular response to glucose stimulus	BP	1	EFNA5,PRKACA,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0001539	0.80	0.36	4	79	cilium or flagellum-dependent cell motility	BP	1	RSPH9,TPPP2,BBS2,NPHP4	cyan	VSMC_M2
GO:0060285	0.80	0.36	4	79	cilium-dependent cell motility	BP	1	RSPH9,TPPP2,BBS2,NPHP4	cyan	VSMC_M2

GO:0009314	0.80	0.26	22	359	response to radiation	BP	1	PTPRK,RHOB,BAX,TRIM13,BCL3,SMPD1,SFRP2,NDRG4,PRKCD,MMP2,TMEM161A,NR2F6,CASP9,BRAT1,NTRK1,TP53,MTA1,NPHP4,NMT2,LRRN4,PML,BMF	cyan	VSMC_M2
GO:0002696	0.80	0.28	13	218	positive regulation of leukocyte activation	BP	1	STAT6,GLI3,PNP,LAMP1,IGF1,SRC,CD81,TIRAP,LEF1,B2M,IL27RA,TNFRSF14,CD55	cyan	VSMC_M2
GO:0000003	0.81	0.23	67	1031	reproduction	BP	1	TCF21,ADAMTS2,MSH5,EHMT2,ZFPM2,RPS6KA2,TEAD3,MEA1,ITGB8,GLI3,BAX,FZD4,PLB1,SOCS3,DZIP1,TPPP2,FOLR2,CATSPERG,EPYC,RARG,IGF1,TLR3,WT1,GGT7,CTSB,HEXB,SFRP2,NDRG3,GLRB,SRC,BBS2,FOXF2,MMP2,AGFG1,SPOCD1,LEF1,STS,REC8,MUS81,ELL3,LINC02210-CRHR1,WNT2B,PLCD3,PSAP,BMP4,DNAJB6,ARRB2,SERPINE2,PRKACA,ZFP36L1,SPIN4,NTRK1,SLIT2,AR,PPP1R9B,ADAM15,NUPR1,TEX14,PDGFRB,PLAC1,NPHP4,SLC2A8,SERPINF1,SELENOP,JUNB,GATA4,PYGO2	cyan	VSMC_M2
GO:0007127	0.81	0.33	5	94	meiosis I	BP	1	MSH5,EHMT2,REC8,MUS81,SLC2A8	cyan	VSMC_M2
GO:0006694	0.81	0.30	7	126	steroid biosynthetic process	BP	1	CYB5R3,APOE,NFKB1,CLCN2,STARD3,HSD3B7,H6PD	cyan	VSMC_M2
GO:0010564	0.81	0.24	32	515	regulation of cell cycle process	BP	1	RPS6KA2,CDC14C,CUL9,APPL2,GPNMB,NOP53,MARK4,KAT2B,APBB1,IGF1,CHMP4B,CHMP3,PLSCR1,MN1,MUS81,BMP4,WIZ,GIPC1,ZFP36L1,TP53,PPP1R9B,KANK2,TEX14,CENPV,PDGFRB,E4F1,FBXW5,RAB11FIP3,ENTR1,PLPP2,PML,CALM3	cyan	VSMC_M2
GO:0090174	0.81	0.32	5	94	organelle membrane fusion	BP	1	CHMP3,VPS11,TMEM175,CPLX2,STX3	cyan	VSMC_M2
GO:0009135	0.81	0.34	4	78	purine nucleoside diphosphate metabolic process	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0009179	0.81	0.34	4	78	purine ribonucleoside diphosphate metabolic process	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0034976	0.82	0.27	13	222	response to endoplasmic reticulum stress	BP	1	OS9,FLOT1,GRINA,BAX,TRIM13,EDEM2,ALOX15,UBQLN2,TP53,NUPR1,UBXN6,EEF2,PML	cyan	VSMC_M2
GO:0009308	0.82	0.34	4	77	amine metabolic process	BP	1	MOXD1,SLC44A1,SAT2,SAT1	cyan	VSMC_M2
GO:0071331	0.82	0.31	6	112	cellular response to hexose stimulus	BP	1	EFNA5,PRKACA,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0035194	0.82	0.31	6	112	post-transcriptional gene silencing by RNA	BP	1	ZFP36,MOV10,BMP4,TP53,ADAR,MIR197	cyan	VSMC_M2
GO:1902107	0.82	0.31	6	110	positive regulation of leukocyte differentiation	BP	1	GLI3,PNP,LEF1,FES,ZFP36L1,IL34	cyan	VSMC_M2
GO:1903708	0.82	0.31	6	110	positive regulation of hemopoiesis	BP	1	GLI3,PNP,LEF1,FES,ZFP36L1,IL34	cyan	VSMC_M2
GO:0060759	0.82	0.29	7	128	regulation of response to cytokine stimulus	BP	1	IRF3,IKBKE,ECM1,SLIT2,ADAR,ISG15,CARD8	cyan	VSMC_M2
GO:0031047	0.82	0.29	7	129	gene silencing by RNA	BP	1	ZFP36,SPOCD1,MOV10,BMP4,TP53,ADAR,MIR197	cyan	VSMC_M2
GO:0043632	0.82	0.23	35	561	modification-dependent macromolecule catabolic process	BP	1	OS9,EIF3H,KCTD17,CUL9,RNF144A,NOP53,TRIM13,AGAP3,RNF213,RBCK1,TP53INP2,EDEM2,WWTR1,FOXF2,UBA7,DCAF11,MAGEF1,MAEA,HDAC6,ARRB2,GABARAP,GIPC1,UBQLN2,UBQLN4,GBA,MTA1,WDR81,DVL1,ISG15,ELOB,FBXW5,AXIN1,CBFA2T3,RNF166,PML	cyan	VSMC_M2
GO:0030433	0.82	0.33	4	78	ubiquitin-dependent ERAD pathway	BP	1	OS9,TRIM13,EDEM2,UBQLN2	cyan	VSMC_M2
GO:0071326	0.82	0.30	6	113	cellular response to monosaccharide stimulus	BP	1	EFNA5,PRKACA,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0062013	0.82	0.31	5	96	positive regulation of small molecule metabolic process	BP	1	KAT2B,IGF1,SRC,SLC45A3,ABCD1	cyan	VSMC_M2
GO:0006163	0.83	0.24	18	302	purine nucleotide metabolic process	BP	1	AASS,ACSS1,PNP,GPAT4,IGF1,ACSS2,ABHD14B,ADCY1,ACAT1,EPHA2,PDK2,NUPR1,PPCDC,ABCD1,CBFA2T3,ACOT6,ZBTB7A,DGAT1	cyan	VSMC_M2
GO:0016573	0.83	0.29	7	131	histone acetylation	BP	1	KAT2B,APBB1,LEF1,PCGF2,KAT8,PBXIP1,PYGO2	cyan	VSMC_M2
GO:2000045	0.83	0.31	5	97	regulation of G1/S transition of mitotic cell cycle	BP	1	APPL2,GPNMB,TP53,KANK2,PML	cyan	VSMC_M2
GO:0055001	0.83	0.27	8	150	muscle cell development	BP	1	CTDP1,BIN1,IGF1,CAPN3,BMP4,PDGFRB,FLII,GATA4	cyan	VSMC_M2
GO:0045333	0.83	0.26	11	191	cellular respiration	BP	1	ACO1,NOP53,UQCRH,ME3,COQ9,AIFM2,GBA,NUPR1,ABCD1,IDH3G,CBFA2T3	cyan	VSMC_M2
GO:0022618	0.83	0.26	9	163	ribonucleoprotein complex assembly	BP	1	EIF3H,NOP53,EIF3K,EIF3F,ADAR,TRAF7,RPS15,RPS19,GEMIN8	cyan	VSMC_M2
GO:0032872	0.83	0.27	8	148	regulation of stress-activated MAPK cascade	BP	1	TLR3,SFRP2,MAPK8IP1,TIRAP,STK25,BMP4,TRAF4,AXIN1	cyan	VSMC_M2
GO:0016441	0.84	0.28	6	115	posttranscriptional gene silencing	BP	1	ZFP36,MOV10,BMP4,TP53,ADAR,MIR197	cyan	VSMC_M2
GO:0009185	0.84	0.31	4	81	ribonucleoside diphosphate metabolic process	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0000079	0.84	0.31	4	80	regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	KAT2B,SRC,INCA1,HEXIM1	cyan	VSMC_M2
GO:0030307	0.84	0.26	7	134	positive regulation of cell growth	BP	1	NRP1,IGF1,SFRP2,RND2,ERBB2,BRAT1,IST1	cyan	VSMC_M2
GO:0009060	0.84	0.25	9	161	aerobic respiration	BP	1	ACO1,NOP53,UQCRH,ME3,COQ9,NUPR1,ABCD1,IDH3G,CBFA2T3	cyan	VSMC_M2
GO:0018393	0.84	0.26	7	134	internal peptidyl-lysine acetylation	BP	1	KAT2B,APBB1,LEF1,PCGF2,KAT8,PBXIP1,PYGO2	cyan	VSMC_M2
GO:0080135	0.84	0.20	34	553	regulation of cellular response to stress	BP	1	GRINA,BAX,ATG7,APBB1,TLR3,SFRP2,PRKCD,MMS19,MAPK8IP1,TIRAP,RGMA,STK25,MAGEF1,ELL3,B2M,AIFM2,GRN,TMEM161A,BMP4,HDAC6,DNAJB6,CASP9,UBQLN2,TP53,UBQLN4,NUPR1,TRAF4,PTPRS,ABCD1,AXIN1,ABL1,PML,GATA4,CDK9	cyan	VSMC_M2
GO:0018105	0.84	0.23	14	249	peptidyl-serine phosphorylation	BP	1	RPS6KA2,BAX,CAMK1,DCLK1,MAP3K12,SFRP2,PRKCD,SRC,IKBKE,HDAC6,ARRB2,PRKACA,ULK3,AXIN1	cyan	VSMC_M2
GO:0032446	0.84	0.20	44	703	protein modification by small protein conjugation	BP	1	OS9,DAXX,FBXO32,CUL9,TRIM14,RNF144A,TRIM13,ATG7,SOCS3,RNF170,RNF213,TRIM21,RBCK1,ARRDC3,WWTR1,FOXF2,TRIM8,CAPN3,UBA7,DCAF11,VPS11,MAGEF1,DTX2,MAEA,HDAC6,ARRB2,GABARAP,PCGF2,MED12,MTA1,ISG15,ELOB,E4F1,TRAF7,FBXW5,UNKL,AXIN1,RNF166,ABL1,RPS15,DTX3,TRIM26,PML,CDK9	cyan	VSMC_M2
GO:0061982	0.84	0.28	5	99	meiosis I cell cycle process	BP	1	MSH5,EHMT2,REC8,MUS81,SLC2A8	cyan	VSMC_M2
GO:0007292	0.85	0.28	5	101	female gamete generation	BP	1	RPS6KA2,IGF1,HEXB,SRC,REC8	cyan	VSMC_M2
GO:0032504	0.85	0.20	35	571	multicellular organism reproduction	BP	1	ADAMTS2,EHMT2,RPS6KA2,MEA1,BAX,FZD4,DZIP1,TPPP2,FOLR2,CATSPERG,IGF1,WT1,GGT7,CTSB,HEXB,NDRG3,SRC,BBS2,AGFG1,SPOCD1,REC8,ELL3,BMP4,ARRB2,SERPINE2,PRKACA,SPIN4,SLIT2,AR,PPP1R9B,TEX14,SLC2A8,SERPINF1,JUNB,PYGO2	cyan	VSMC_M2
GO:0042593	0.85	0.24	10	183	glucose homeostasis	BP	1	APPL2,KLF15,EFNA5,PLSCR3,PRKACA,PDK2,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0007017	0.85	0.19	44	715	microtubule-based process	BP	1	CDC14C,KIFC2,CUL9,RSPH9,CCDC114,MARK4,TPPP2,KAT2B,POC1B,LAMP1,TMEM108,CLIP3,EFNA5,CHMP4B,CHMP3,EPHA3,BBS2,LZTS2,TPPP,KIF7,GAS2L1,FES,PRUNE1,TACC2,KIF1A,PARD3B,ARHGEF10,FYCO1,RPGR,MAP1S,CC2D2A,HDAC6,CROCC,GABARAP,ERBB2,ANKFN1,LLGL1,DVL1,NPHP4,FBXW5,RHOT2,ABL1,DNAAF1,HSBP1	cyan	VSMC_M2

GO:0036503	0.85	0.27	5	99	ERAD pathway	BP	1	OS9,TRIM13,EDEM2,UBQLN2,UBXN6	cyan	VSMC_M2
GO:0033500	0.85	0.23	10	184	carbohydrate homeostasis	BP	1	APPL2,KLF15,EFNA5,PLSCR3,PRKACA,PDK2,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0070302	0.85	0.24	8	151	regulation of stress-activated protein kinase signaling cascade	BP	1	TLR3,SFRP2,MAPK8IP1,TIRAP,STK25,BMP4,TRAF4,AXIN1	cyan	VSMC_M2
GO:0007286	0.85	0.27	5	100	spermatid development	BP	1	EHMT2,BBS2,REC8,PRKACA,PYGO2	cyan	VSMC_M2
GO:0035150	0.85	0.27	5	100	regulation of tube size	BP	1	APOE,SNTA1,EXT2,ADORA2A,FOXC2	cyan	VSMC_M2
GO:0035296	0.85	0.27	5	100	regulation of tube diameter	BP	1	APOE,SNTA1,EXT2,ADORA2A,FOXC2	cyan	VSMC_M2
GO:0097746	0.85	0.27	5	100	blood vessel diameter maintenance	BP	1	APOE,SNTA1,EXT2,ADORA2A,FOXC2	cyan	VSMC_M2
GO:0006475	0.85	0.25	7	136	internal protein amino acid acetylation	BP	1	KAT2B,APBB1,LEF1,PCGF2,KAT8,PBXIP1,PYGO2	cyan	VSMC_M2
GO:0006304	0.85	0.28	4	84	DNA modification	BP	1	EHMT2,WT1,NEIL2,SPOCD1	cyan	VSMC_M2
GO:0007612	0.85	0.27	5	104	learning	BP	1	NDRG4,PPP1R9B,SLC8A3,LRRN4,EN1	cyan	VSMC_M2
GO:0006511	0.85	0.19	33	542	ubiquitin-dependent protein catabolic process	BP	1	OS9,EIF3H,KCTD17,CUL9,RNF144A,NOP53,TRIM13,AGAP3,RNF213,RBCK1,TP53INP2,EDEM2,WWTR1,FOXF2,DCAF11,MAGEF1,MAEA,HDAC6,ARRB2,GABARAP,GIPC1,UBQLN2,UBQLN4,GBA,MTA1,WDR81,DVL1,ELOB,FBXW5,AXIN1,CBFA2T3,RNF166,PML	cyan	VSMC_M2
GO:0007006	0.86	0.26	5	99	mitochondrial membrane organization	BP	1	BAX,TP53,RHOT2,ZNF205,CALM3	cyan	VSMC_M2
GO:1904029	0.86	0.28	4	83	regulation of cyclin-dependent protein kinase activity	BP	1	KAT2B,SRC,INCA1,HEXIM1	cyan	VSMC_M2
GO:0007346	0.86	0.20	21	360	regulation of mitotic cell cycle	BP	1	CDC14C,CUL9,APPL2,GPNMB,NOP53,TIMP2,IGF1,MUS81,BMP4,MAEA,ZFP36L1,TP53,PPP1R9B,KANK2,TEX14,PDGFRB,E4F1,FBXW5,ABL1,GAS1,PML	cyan	VSMC_M2
GO:0022900	0.86	0.23	8	149	electron transport chain	BP	1	UQCRH,COQ9,WDR93,CYB561,AIFM2,QDPR,GBA,NDOR1	cyan	VSMC_M2
GO:0007030	0.86	0.25	6	122	Golgi organization	BP	1	EHD3,STK25,PLEKHM2,ATP8B2,DYM,RAB43	cyan	VSMC_M2
GO:0031497	0.86	0.27	4	84	chromatin assembly	BP	1	DAXX,HIST1H1C,TP53,CENPV	cyan	VSMC_M2
GO:0046488	0.86	0.23	7	138	phosphatidylinositol metabolic process	BP	1	SOCS3,PLCG1,PIK3C2B,IP6K1,PDGFRB,PIGQ,INPP5E	cyan	VSMC_M2
GO:0048609	0.87	0.18	34	563	multicellular organismal reproductive process	BP	1	ADAMTS2,EHMT2,RPS6KA2,MEA1,BAX,FZD4,DZIP1,TPPP2,CATSPERG,IGF1,WT1,GGT7,CTSB,HEXB,NDRG3,SRC,BBS2,AGFG1,SPOCD1,REC8,ELL3,BMP4,ARRB2,SERPINE2,PRKACA,SPIN4,SLIT2,AR,PPP1R9B,TEX14,SLC2A8,SERPINF1,JUNB,PYGO2	cyan	VSMC_M2
GO:0031398	0.87	0.25	5	102	positive regulation of protein ubiquitination	BP	1	ARRDC3,GABARAP,MTA1,AXIN1,CDK9	cyan	VSMC_M2
GO:0040029	0.87	0.26	4	86	regulation of gene expression, epigenetic	BP	1	KAT2B,HDAC5,HDAC6,MTA1	cyan	VSMC_M2
GO:0016570	0.87	0.18	23	399	histone modification	BP	1	EHMT2,TRERF1,AASS,KAT2B,APBB1,MAP3K12,PRKCD,RIOX2,HIST1H1C,LEF1,TBL1Y,HDAC5,HDAC6,PCGF2,MLLT6,TP53,KAT8,ELMSAN1,PBXIP1,MTA1,KDM4B,CDK9,PYGO2	cyan	VSMC_M2
GO:0071826	0.87	0.22	9	170	ribonucleoprotein complex subunit organization	BP	1	EIF3H,NOP53,EIF3K,EIF3F,ADAR,TRAF7,RPS15,RPS19,GEMIN8	cyan	VSMC_M2
GO:0001824	0.87	0.25	4	86	blastocyst development	BP	1	IGF1,FURIN,RPL13,JUNB	cyan	VSMC_M2
GO:0045471	0.88	0.25	4	87	response to ethanol	BP	1	EHMT2,RPL15,EEF2,RGS19	cyan	VSMC_M2
GO:0051897	0.88	0.25	4	88	positive regulation of protein kinase B signaling	BP	1	MEIS3,FGFR1,SRC,ARRB2	cyan	VSMC_M2
GO:0006338	0.88	0.20	9	175	chromatin remodeling	BP	1	DAXX,KAT2B,HIST1H1C,HDAC5,CENPV,KDM4B,MPND,RERE,ZBTB7A	cyan	VSMC_M2
GO:0140013	0.88	0.21	7	139	meiotic nuclear division	BP	1	MSH5,EHMT2,RPS6KA2,REC8,MUS81,TEX14,SLC2A8	cyan	VSMC_M2
GO:0032355	0.88	0.23	5	105	response to estradiol	BP	1	GGT7,CASP9,PPP1R9B,PDGFRB,EEF2	cyan	VSMC_M2
GO:1903322	0.88	0.22	6	121	positive regulation of protein modification by small protein conjugation or removal	BP	1	NOP53,ARRDC3,GABARAP,MTA1,AXIN1,CDK9	cyan	VSMC_M2
GO:0098727	0.88	0.23	5	108	maintenance of cell number	BP	1	IGF1,TRIM8,BCL9,LDB2,MED12	cyan	VSMC_M2
GO:0031056	0.88	0.22	6	124	regulation of histone modification	BP	1	EHMT2,AASS,MLLT6,TP53,CDK9,PYGO2	cyan	VSMC_M2
GO:0006333	0.88	0.23	5	106	chromatin assembly or disassembly	BP	1	DAXX,HIST1H1C,MAP1S,TP53,CENPV	cyan	VSMC_M2
GO:0001101	0.88	0.22	5	107	response to acid chemical	BP	1	RRAGC,GLRB,MMP2,NTRK1,PPP1R9B	cyan	VSMC_M2
GO:0042471	0.88	0.23	4	89	ear morphogenesis	BP	1	TSHZ1,SLITRK6,NAGLU,DVL1	cyan	VSMC_M2
GO:0014074	0.89	0.22	5	109	response to purine-containing compound	BP	1	WT1,STAT1,ADORA2A,ZFP36L1,SLC8A3	cyan	VSMC_M2
GO:0043043	0.89	0.15	34	566	peptide biosynthetic process	BP	1	PYM1,PLXNB2,EIF3H,ACO1,IARS,RPL18,ABTB1,VIM,BCL3,MIF4GD,RPS16,ZFP36,SAMD4B,RPL15,EIF3K,EIF3F,PATL1,GGT7,MRPL36,FURIN,MOV10,ERBB2,ZFP36L1,WARS,EEF2,DPH7,HAGH,INPP5E,RPL13,RPS15,MEX3D,RPS19,EEF1A2,RPL36A	cyan	VSMC_M2
GO:0006996	0.89	0.13	194	2943	organelle organization	BP	1	CTDP1,PMEL,MSH5,EHMT2,RPS6KA2,PACSIN2,DAXX,ARHGAP18,CDC14C,KCTD17,KIFC2,CUL9,RSPH9,HIGD2A,BBS9,ELMO1,COBL,GSN,NRP1,RHOB,BAX,CCDC114,NOP53,LURAP1,MARK4,VIM,BIN1,APOE,ATG7,EHD3,TEP1,DZIP1,TPPP2,GAA,PAK4,ARAP1,HGS,KAT2B,RHOG,POC1B,TMEM108,TPP1,CLIP3,GNPTAB,IGF1,REEP5,MAN2A1,EFNA5,RHPN2,CHMP4B,CHMP3,TP53INP2,PATL1,HEXB,CAMKK2,WWTR1,PRKCD,EPHA3,SRC,BBS2,PDLIM2,C15orf62,PYROXD2,SORBS3,NISCH,PNPLA2,LZTS2,PHACTR1,HPS6,CAPN3,TJP1,CTTN,TPCN2,TPPP,HIST1H1C,SSH3,EXOC8,NDUFAF3,REC8,CTSK,NCKIPSD,GAS2L1,FES,PRUNE1,VPS11,TACC2,VANGL2,PARD3B,STK25,MUS81,CTNNA3,WIPF1,ARPC5,DPF2,ARHGEF10,FYCO1,RPGR,AIFM2,CDC42BPG,GRN,HDAC5,RND2,VAT1,ADD1,BMP4,NAGLU,MAEA,CAPZB,MAP1S,CC2D2A,HDAC6,ARHGEF10L,WDR45,PLD2,CROCC,DNAJB6,ARRB2,ALOX15,GABARAP,PLEKHM2,SERPINE2,CGNL1,PLSCR3,SMIM20,UBQLN2,SLIT2,TMEM175,TP53,CPLX2,UBQLN4,GBA,PPP1R9B,ZMYM3,NUPR1,SHC1,ATP8B2,ANKFN1,ARHGAP17,TEX14,SIGLEC15,ULK3,CENPV,SNX33,PDGFRB,MCOLN1,FLII,LLGL1,PTPRS,KDM4B,DYM,MPND,RETREG1,NAGPA,WDR81,ABCD1,DVL1,AGRN,TRAF7,TSC2,NPHP4,FBXW5,PHPT1,RHOT2,WDR90,ENTR1,RERE,NPRL3,BRD3,AIF1L,ABL1,DNAAF1,ATMIN,CNN3,SLC2A8,IST1,ATP6V0D1,RPS15,KRT25,PTGFRN,ZNF205,ZBTB7A,RAB43,PML,RPS19,CALM3,BMF,TMEM250,SDC4,STX3,BST2,PYGO2,MPV17,EMD,UBL5	cyan	VSMC_M2
GO:1901991	0.89	0.19	7	142	negative regulation of mitotic cell cycle phase transition	BP	1	GPNMB,NOP53,ZFP36L1,TP53,KANK2,TEX14,PML	cyan	VSMC_M2
GO:0140014	0.89	0.17	13	244	mitotic nuclear division	BP	1	CTDP1,CDC14C,KIFC2,CUL9,IGF1,CHMP4B,REC8,ARHGEF10,BMP4,PPP1R9B,TEX14,PDGFRB,FBXW5	cyan	VSMC_M2
GO:0070585	0.90	0.20	5	107	protein localization to mitochondrion	BP	1	BAX,VPS11,ISG15,CALM3,UBL5	cyan	VSMC_M2

GO:0006310	0.90	0.16	13	245	DNA recombination	BP	1	STAT6,MSH5,TEP1,SLC15A4,MMS19,HIST1H1C,LEF1,REC8,MAGEF1,MUS81,IL27RA,UBQLN4,TCF3	cyan	VSMC_M2
GO:0009914	0.90	0.16	11	212	hormone transport	BP	1	FZD4,LTBP4,RAB11FIP1,EFNA5,HADH,LINC02210-CRHR1,SLC16A2,RASL10B,PHPT1,RAB11FIP3,RAB11B	cyan	VSMC_M2
GO:0006275	0.90	0.21	4	92	regulation of DNA replication	BP	1	EHMT2,ATG7,WIZ,TP53	cyan	VSMC_M2
GO:1903311	0.91	0.15	13	247	regulation of mRNA metabolic process	BP	1	VIM,ZFP36,SAMD4B,PATL1,PRKCD,IKBKE,TIRAP,RNASEL,MOV10,ZFP36L1,MEX3D,ZBTB7A,CDK9	cyan	VSMC_M2
GO:0043200	0.91	0.20	4	93	response to amino acid	BP	1	RRAGC,GLRB,MMP2,PPP1R9B	cyan	VSMC_M2
GO:0018209	0.91	0.15	14	267	peptidyl-serine modification	BP	1	RPS6KA2,BAX,CAMK1,DCLK1,MAP3K12,SFRP2,PRKCD,SRC,IKBKE,HDAC6,ARRB2,PRKACA,ULK3,AXIN1	cyan	VSMC_M2
GO:0046683	0.91	0.20	4	94	response to organophosphorus	BP	1	WT1,STAT1,ZFP36L1,SLC8A3	cyan	VSMC_M2
GO:0009132	0.91	0.19	4	94	nucleoside diphosphate metabolic process	BP	1	IGF1,NUPR1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0051168	0.91	0.17	6	131	nuclear export	BP	1	CAMK1,LZTS2,AGFG1,PRKACA,RPS15,EMD	cyan	VSMC_M2
GO:0010467	0.91	0.10	300	4455	gene expression	BP	1	CTDP1,TSHZ1,PYM1,RBMS2,STAT6,TCF21,ADAMTS2,AKAP12,FLOT1,EHMT2,PLXNB2,ZFPM2,EIF3H,RPS6KA2,IRF1,AFDN,TAPBP,TCF20,DAXX,TEF,PTPRK,GSDMD,TEAD3,TLE1,NFIB,TRERF1,HMOX1,LRRC19,ACO1,KLF9,APPL2,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,ITGB8,NAT14,GPNMB,EFEMP1,TRIL,RRAGC,MEIS1,STK40,PTOV1,AASS,GLI3,SIM1,IRF3,GSN,KLF15,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,FKRP,LURAP1,TRIM13,FZD4,VIM,APOE,BCL3,MIF4GD,ATRAID,CAMK1,PLD3,PNP,RPS16,ZFP36,SAMD4B,RPL15,HGS,KAT2B,EIF3K,RFTN1,RHOG,IL5RA,TRIM21,APBB1,GTF3A,SLC15A4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,GGT7,POU6F1,CAST,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,CPE,BPI,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,EXT2,STAT1,ABHD14B,CD81,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,TIRAP,MRPL36,AGFG1,PCSK6,TUSC2,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,APH1A,MN1,WDR6,ECM1,NELFCD,ADCY1,FURIN,CCS,BCL9L,HEG1,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,PHEX,ELL3,NFKBIA,MOV10,LTBP3,FRMD8,B2M,DPF2,ADORA2A,CLEC3B,PCBD1,C1R,HDAC5,TSC22D4,HOMER3,TMEM106A,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DHX58,DNAJB6,ARRB2,JUP,WIZ,EPHA2,MYRF,IL17RA,ZBTB17,TCF12,SERPINE2,ERBB2,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,ACP5,KANK2,WARS,CENPV,GPRC5B,IMP3,TMEM98,MTA1,MAP	cyan	VSMC_M2
GO:2000278	0.91	0.19	4	95	regulation of DNA biosynthetic process	BP	1	SRC,ARRB2,TP53,PDGFRB	cyan	VSMC_M2
GO:0033554	0.91	0.10	99	1561	cellular response to stress	BP	1	STAT6,OS9,FLOT1,MSH5,EHMT2,DAXX,PTPRK,GRINA,HMOX1,RRAGC,EEPD1,IRF3,RHOB,BAX,NOP53,TRIM13,BCL3,AGAP3,ATG7,ZFP36,APBB1,ANGPT4,MAP3K12,TLR3,EDEM2,NEIL2,CAMKK2,SFRP2,PRKCD,SRC,MMS19,MAPK8IP1,MMP2,IKBKE,CAPN3,TIRAP,NFKB1,RGMA,UBA7,PTGIS,LAMB2,REC8,GAS2L1,CCS,STK25,MAGEF1,MUS81,ELL3,NFKBIA,B2M,WNT2B,AIFM2,GRN,TMEM161A,MACROD1,BMP4,HDAC6,ARHGEF10L,WDR45,DNAJB6,ALOX15,EPHA2,GABARAP,CASP9,BRAT1,PRKACA,ZFP36L1,UBQLN2,PCGF2,TP53,UBQLN4,PDK2,GBA,NUPR1,ULK3,ABCC1,MTA1,MAP2K3,TRAF4,PTPRS,UBXN6,EEF2,ABCD1,AXIN1,NPRL3,ABL1,HSBP1,ATMIN,SLC8A3,KCND2,ZBTB7A,PML,SERPINB6,GATA4,CDK9,ADPRHL2,MACROD2,GTF2H4,MPV17	cyan	VSMC_M2
GO:0006412	0.91	0.12	32	548	translation	BP	1	PYM1,PLXNB2,EIF3H,ACO1,IARS,RPL18,ABTB1,VIM,BCL3,MIF4GD,RPS16,ZFP36,SAMD4B,RPL15,EIF3K,EIF3F,PATL1,GGT7,MRPL36,MOV10,ERBB2,ZFP36L1,WARS,EEF2,DPH7,INPP5E,RPL13,RPS15,MEX3D,RPS19,EEF1A2,RPL36A	cyan	VSMC_M2
GO:0034968	0.92	0.18	4	98	histone lysine methylation	BP	1	EHMT2,HIST1H1C,MLLT6,PYGO2	cyan	VSMC_M2
GO:2001022	0.92	0.18	4	95	positive regulation of response to DNA damage stimulus	BP	1	APBB1,PRKCD,MMS19,TMEM161A	cyan	VSMC_M2
GO:0140694	0.92	0.13	16	305	non-membrane-bounded organelle assembly	BP	1	KIFC2,GSN,NOP53,KAT2B,POC1B,CHMP4B,PATL1,SRC,LZTS2,CAPN3,ARHGEF10,PDGFRB,FLII,TRAF7,RPS15,RPS19	cyan	VSMC_M2
GO:0051704	0.92	0.11	42	709	multi-organism process	BP	1	ADAMTS2,EHMT2,RPS6KA2,TEAD3,MEA1,BAX,PLB1,DZIP1,TPPP2,FOLR2,CATSPERG,EPYC,IGF1,WT1,GGT7,CTSB,HEXB,NDRG3,GLRB,SRC,BBS2,MMP2,AGFG1,TPCN2,SPOCD1,STS,REC8,ELL3,LINC02210-CRHR1,BMP4,SERPINE2,PRKACA,SPIN4,AR,PPP1R9B,TEX14,SLC2A8,NMT2,SELENOP,JUNB,BST2,PYGO2	cyan	VSMC_M2
GO:0006661	0.92	0.17	5	115	phosphatidylinositol biosynthetic process	BP	1	SOCS3,PIK3C2B,IP6K1,PIGQ,INPP5E	cyan	VSMC_M2
GO:0016571	0.92	0.16	5	118	histone methylation	BP	1	EHMT2,AASS,HIST1H1C,MLLT6,PYGO2	cyan	VSMC_M2
GO:0009743	0.92	0.14	9	186	response to carbohydrate	BP	1	RPS6KA2,ATG7,EFNA5,PRKACA,ZFP36L1,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0009260	0.92	0.15	7	149	ribonucleotide biosynthetic process	BP	1	ACSS1,ACSS2,ADCY1,UCKL1,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0016050	0.92	0.12	13	255	vesicle organization	BP	1	PMEL,HGS,CHMP4B,CHMP3,EXOC8,VPS11,SERPINE2,TMEM175,CPLX2,SNX33,IST1,SDC4,STX3	cyan	VSMC_M2
GO:0010948	0.93	0.12	12	237	negative regulation of cell cycle process	BP	1	RPS6KA2,GPNMB,NOP53,KAT2B,APBB1,MUS81,BMP4,ZFP36L1,TP53,KANK2,TEX14,PML	cyan	VSMC_M2
GO:0009749	0.93	0.14	7	153	response to glucose	BP	1	ATG7,EFNA5,PRKACA,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:1903046	0.93	0.14	7	153	meiotic cell cycle process	BP	1	MSH5,EHMT2,RPS6KA2,REC8,MUS81,TEX14,SLC2A8	cyan	VSMC_M2
GO:0007093	0.93	0.15	5	117	mitotic cell cycle checkpoint signaling	BP	1	NOP53,MUS81,TP53,TEX14,PML	cyan	VSMC_M2
GO:0007276	0.93	0.10	26	469	gamete generation	BP	1	ADAMTS2,EHMT2,RPS6KA2,MEA1,BAX,DZIP1,TPPP2,CATSPERG,IGF1,WT1,GGT7,HEXB,NDRG3,SRC,BBS2,AGFG1,SPOCD1,REC8,ELL3,BMP4,PRKACA,SPIN4,AR,TEX14,SLC2A8,PYGO2	cyan	VSMC_M2
GO:0046879	0.93	0.12	10	206	hormone secretion	BP	1	FZD4,LTBP4,RAB11FIP1,EFNA5,HADH,LINC02210-CRHR1,RASL10B,PHPT1,RAB11FIP3,RAB11B	cyan	VSMC_M2
GO:0042770	0.93	0.13	7	155	signal transduction in response to DNA damage	BP	1	NOP53,BCL3,MUS81,CASP9,TP53,ABL1,PML	cyan	VSMC_M2

GO:0019953	0.93	0.09	32	565	sexual reproduction	BP	1	ADAMTS2,EHMT2,RPS6KA2,MEA1,BAX,PLB1,DZIP1,TPPP2,FOLR2,CATSPERG,IGF1,WT1,GGT7,HEXB,NDRG3,GLRB,SRC,BBS2,AGFG1,SPOCD1,REC8,ELL3,BMP4,SERPINE2,PRKACA,SPIN4,AR,PPP1R9B,TEX14,SLC2A8,SELENOP,PYGO2	cyan	VSMC_M2
GO:0045787	0.93	0.11	12	243	positive regulation of cell cycle	BP	1	CDC14C,TRIM21,IGF1,CHMP3,PLSCR1,SRC,WIZ,GIPC1,NUPR1,CENPV,PDGFRB,ABL1	cyan	VSMC_M2
GO:0030010	0.93	0.14	5	123	establishment of cell polarity	BP	1	GSN,PARD3B,FAM89B,ANKFN1,LLGL1	cyan	VSMC_M2
GO:0006413	0.93	0.15	4	99	translational initiation	BP	1	EIF3H,MIF4GD,EIF3K,EIF3F	cyan	VSMC_M2
GO:0006417	0.93	0.10	18	341	regulation of translation	BP	1	PYM1,PLXNB2,EIF3H,ACO1,VIM,BCL3,MIF4GD,ZFP36,SAMD4B,EIF3K,PATL1,MOV10,ERBB2,ZFP36L1,EEF2,DPH7,INPP5E,MEX3D	cyan	VSMC_M2
GO:0050714	0.93	0.15	4	100	positive regulation of protein secretion	BP	1	APBB1,IGF1,ADORA2A,PHPT1	cyan	VSMC_M2
GO:0051225	0.93	0.15	4	101	spindle assembly	BP	1	KIFC2,CHMP4B,LZTS2,ARHGEF10	cyan	VSMC_M2
GO:0022904	0.94	0.14	4	99	respiratory electron transport chain	BP	1	UQCRH,COQ9,AIFM2,GBA	cyan	VSMC_M2
GO:0017148	0.94	0.12	7	158	negative regulation of translation	BP	1	ZFP36,SAMD4B,PATL1,MOV10,ZFP36L1,INPP5E,MEX3D	cyan	VSMC_M2
GO:0009152	0.94	0.13	6	137	purine ribonucleotide biosynthetic process	BP	1	ACSS1,ACSS2,ADCY1,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0018205	0.94	0.10	16	313	peptidyl-lysine modification	BP	1	EHMT2,KLF15,KAT2B,APBB1,TGM2,CAPN3,HIST1H1C,LEF1,HDAC6,FKBP10,PCGF2,MLLT6,KAT8,PBXIP1,PML,PYGO2	cyan	VSMC_M2
GO:0051301	0.94	0.09	29	525	cell division	BP	1	CTDP1,CDC14C,TEAD3,RHOB,MARK4,CHMP4B,CHMP3,SFRP2,WWTR1,LZTS2,GNAI2,TPPP,LEF1,SOX5,VEGFD,PARD3B,VEGFB,MAEA,GIPC1,HOXB4,TEX14,CENPV,SNX33,E4F1,RAB11FIP3,ENTR1,IST1,CALM3,TMEM250	cyan	VSMC_M2
GO:0046390	0.94	0.11	7	156	ribose phosphate biosynthetic process	BP	1	ACSS1,ACSS2,ADCY1,UCKL1,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0051047	0.94	0.10	10	211	positive regulation of secretion	BP	1	CADPS2,HGS,LAMP1,APBB1,IGF1,GNAI2,ADORA2A,RASL10B,PHPT1,SDC4	cyan	VSMC_M2
GO:0009746	0.94	0.11	7	159	response to hexose	BP	1	ATG7,EFNA5,PRKACA,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0070647	0.94	0.08	47	806	protein modification by small protein conjugation or removal	BP	1	OS9,DAXX,FBXO32,CUL9,TRIM14,RNF144A,NOP53,TRIM13,ATG7,SOCS3,RNF170,RNF213,TRIM21,EIF3F,RBCK1,ARRDC3,WWTR1,FOXF2,TRIM8,CAPN3,UBA7,DCAF11,MINDY1,VPS11,MAGEF1,DTX2,MAEA,HDAC6,ARRB2,GABARAP,PCGF2,MED12,MTA1,ISG15,ELOB,E4F1,TRAF7,FBXW5,UNKL,AXIN1,RNF166,ABL1,RPS15,DTX3,TRIM26,PML,CDK9	cyan	VSMC_M2
GO:0072522	0.94	0.11	7	157	purine-containing compound biosynthetic process	BP	1	ACSS1,PNP,ACSS2,ADCY1,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0019827	0.94	0.13	4	106	stem cell population maintenance	BP	1	TRIM8,BCL9,LDB2,MED12	cyan	VSMC_M2
GO:0000724	0.94	0.12	5	124	double-strand break repair via homologous recombination	BP	1	MMS19,REC8,MAGEF1,MUS81,UBQLN4	cyan	VSMC_M2
GO:0090501	0.95	0.12	5	124	RNA phosphodiester bond hydrolysis	BP	1	LACTB2,HELZ2,RNASEL,MOV10,RNASEK	cyan	VSMC_M2
GO:0035967	0.95	0.13	4	103	cellular response to topologically incorrect protein	BP	1	OS9,DAXX,BAX,HDAC6	cyan	VSMC_M2
GO:1903532	0.95	0.10	9	196	positive regulation of secretion by cell	BP	1	CADPS2,HGS,LAMP1,APBB1,IGF1,ADORA2A,RASL10B,PHPT1,SDC4	cyan	VSMC_M2
GO:0072655	0.95	0.12	4	103	establishment of protein localization to mitochondrion	BP	1	BAX,VPS11,CALM3,UBL5	cyan	VSMC_M2
GO:0006352	0.95	0.12	4	105	DNA-templated transcription, initiation	BP	1	NAT14,TP53,MED12,CDK9	cyan	VSMC_M2
GO:0044843	0.95	0.10	8	180	cell cycle G1/S phase transition	BP	1	APPL2,GPNMB,APBB1,MN1,TP53,KANK2,PLPP2,PML	cyan	VSMC_M2
GO:0090068	0.95	0.10	8	180	positive regulation of cell cycle process	BP	1	CDC14C,IGF1,CHMP3,PLSCR1,WIZ,GIPC1,CENPV,PDGFRB	cyan	VSMC_M2
GO:0018022	0.95	0.12	4	108	peptidyl-lysine methylation	BP	1	EHMT2,HIST1H1C,MLLT6,PYGO2	cyan	VSMC_M2
GO:0010608	0.95	0.08	26	480	posttranscriptional regulation of gene expression	BP	1	PYM1,PLXNB2,EIF3H,ACO1,VIM,BCL3,MIF4GD,ZFP36,SAMD4B,EIF3K,PATL1,PRKCD,IKBKE,TIRAP,RNASEL,MOV10,BMP4,ERBB2,ZFP36L1,TP53,ADAR,EEF2,DPH7,INPP5E,MIR197,MEX3D	cyan	VSMC_M2
GO:0016579	0.95	0.12	4	108	protein deubiquitination	BP	1	NOP53,TRIM21,EIF3F,MINDY1	cyan	VSMC_M2
GO:0000077	0.95	0.12	4	105	DNA damage checkpoint signaling	BP	1	NOP53,MUS81,TP53,PML	cyan	VSMC_M2
GO:0000725	0.95	0.11	5	126	recombinational repair	BP	1	MMS19,REC8,MAGEF1,MUS81,UBQLN4	cyan	VSMC_M2
GO:0044703	0.95	0.07	39	688	multi-organism reproductive process	BP	1	ADAMTS2,EHMT2,RPS6KA2,TEAD3,MEA1,BAX,PLB1,DZIP1,TPPP2,FOLR2,CATSPERG,EPYC,IGF1,WT1,GGT7,CTSB,HEXB,NDRG3,GLRB,SRC,BBS2,MMP2,AGFG1,SPOCD1,STS,REC8,ELL3,LINC02210-CRHR1,BMP4,SERPINE2,PRKACA,SPIN4,AR,PPP1R9B,TEX14,SLC2A8,SELENOP,JUNB,PYGO2	cyan	VSMC_M2
GO:0034622	0.95	0.06	48	830	cellular protein-containing complex assembly	BP	1	EIF3H,TAPBP,DAXX,ARHGAP18,HIGD2A,COBL,GSN,CCDC114,NOP53,BIN1,TPPP2,EIF3K,CLIP3,ANGPT4,EIF3F,EFNA5,CHMP4B,CHMP3,PRKCD,SRC,C15orf62,CTTN,TPPP,HIST1H1C,SV2A,SSH3,NDUFAF3,FES,PRUNE1,ARPC5,B2M,ADD1,CAPZB,ALOX15,SMIM20,SLIT2,TP53,ADAR,CENPV,FLII,TRAF7,AXIN1,ABL1,DNAAF1,RPS15,RPS19,GEMIN8,CARD8	cyan	VSMC_M2
GO:0034284	0.95	0.09	7	164	response to monosaccharide	BP	1	ATG7,EFNA5,PRKACA,PHPT1,SERPINF1,GATA4,RAB11B	cyan	VSMC_M2
GO:0007052	0.95	0.11	4	109	mitotic spindle organization	BP	1	KIFC2,CHMP4B,TACC2,ARHGEF10	cyan	VSMC_M2
GO:0000280	0.95	0.07	18	355	nuclear division	BP	1	CTDP1,MSH5,EHMT2,RPS6KA2,CDC14C,KIFC2,CUL9,IGF1,CHMP4B,REC8,MUS81,ARHGEF10,BMP4,PPP1R9B,TEX14,PDGFRB,FBXW5,SLC2A8	cyan	VSMC_M2
GO:0048232	0.95	0.07	19	371	male gamete generation	BP	1	ADAMTS2,EHMT2,MEA1,BAX,DZIP1,TPPP2,CATSPERG,GGT7,NDRG3,BBS2,AGFG1,SPOCD1,REC8,ELL3,PRKACA,AR,TEX14,SLC2A8,PYGO2	cyan	VSMC_M2
GO:1901988	0.96	0.08	9	201	negative regulation of cell cycle phase transition	BP	1	GPNMB,NOP53,APBB1,MUS81,ZFP36L1,TP53,KANK2,TEX14,PML	cyan	VSMC_M2

GO:0034641	0.96	0.05	325	4878	cellular nitrogen compound metabolic process	BP	1	CTDP1,TSHZ1,PYM1,RBMS2,STAT6,MOXD1,TCF21,FLOT1,DDAH2,MSH5,NEU1,EHMT2,PLXNB2,ZFPM2,EIF3H,IRF1,B3GALT4,CYB5R3,TAPBP,TCF20,DAXX,NAGA,TEF,PTPRK,ST3GAL1,IBA57,TEAD3,TLE1,OPLAH,NFIB,TRERF1,HMOX1,ACO1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,ITGB8,NAT14,SLC44A1,EFEMP1,RRAGC,EEPD1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,BAX,DBP,HBP1,RPL18,NOP53,ABTB1,BICRA,MEIS3,TRIM13,ACSS1,FZD4,VIM,BIN1,APOE,UROD,BCL3,ETHE1,MIF4GD,SLC6A9,CAMK1,PLD3,TEP1,PNP,RPS16,ZFP36,SAMD4B,GPAT4,RPL15,KAT2B,EIF3K,RHOG,TRIM21,SMPD1,APBB1,TPP1,GTF3A,SLC15A4,EIF3F,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,GGT7,ACSS2,POU6F1,LACTB2,NEIL2,PLSCR1,HEXB,CAMKK2,SPON1,SFRP2,WWTR1,SCAND1,PRKCD,SRC,CPE,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,CHRNA7,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,MRPL36,PCSK6,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,B4GALT5,SOX5,APH1A,MN1,WDR6,ECM1,REC8,NELFCD,ADCY1,FURIN,TATDN3,BCL9L,RFX5,GATA5,NIT1,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,MUS81,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TMEM161A,TSC22D4,ACAT1,NUDT13,MACROD1,MXD4,BMP4,RARRES3,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,RNASEK,WIZ,EPHA2,MYRF,ZBTB17,TCF12,ERBB2,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,SAT2,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,PDK2,MED12,GBA,PPP1R9B,NUPR1,SHC	cyan	VSMC_M2
GO:0071897	0.96	0.09	6	150	DNA biosynthetic process	BP	1	TEP1,SRC,ARRB2,TP53,PDGFRB,TK2	cyan	VSMC_M2
GO:0016458	0.96	0.08	7	169	gene silencing	BP	1	ZFP36,SPOCD1,MOV10,BMP4,TP53,ADAR,MIR197	cyan	VSMC_M2
GO:0030072	0.96	0.08	7	168	peptide hormone secretion	BP	1	LTBP4,EFNA5,HADH,LINC02210-CRHR1,RASL10B,PHPT1,RAB11B	cyan	VSMC_M2
GO:1902850	0.96	0.09	5	133	microtubule cytoskeleton organization involved in mitosis	BP	1	KIFC2,CHMP4B,TACC2,ARHGEF10,ANKFN1	cyan	VSMC_M2
GO:0031570	0.96	0.09	4	111	DNA integrity checkpoint signaling	BP	1	NOP53,MUS81,TP53,PML	cyan	VSMC_M2
GO:0006164	0.96	0.08	6	149	purine nucleotide biosynthetic process	BP	1	ACSS1,ACSS2,ADCY1,ACAT1,PDK2,PPCDC	cyan	VSMC_M2
GO:0006302	0.96	0.07	10	225	double-strand break repair	BP	1	APBB1,MMS19,REC8,MAGEF1,MUS81,TP53,UBQLN4,MTA1,ZBTB7A,PML	cyan	VSMC_M2
GO:0007049	0.97	0.04	84	1405	cell cycle	BP	1	CTDP1,MSH5,EHMT2,RPS6KA2,IRF1,PTPRK,CDC14C,KIFC2,CUL9,APPL2,GPNMB,RHOB,BAX,HBP1,NOP53,MARK4,BIN1,CAMK1,TIMP2,PAK4,ARAP1,KAT2B,TRIM21,POC1B,APBB1,IGF1,CHMP4B,CHMP3,PLSCR1,PRKCD,SRC,LZTS2,CAPN3,TUSC2,GNAI2,TPPP,MN1,WDR6,REC8,GRK5,GAS2L1,FES,TACC2,PARD3B,MUS81,ARHGEF10,BMP4,MAEA,ZNF503,CROCC,WIZ,ZBTB17,GIPC1,TP53BP2,PRKACA,ZFP36L1,TP53,PRCC,PPP1R9B,NUPR1,KANK2,ANKFN1,TEX14,CENPV,SNX33,PDGFRB,LLGL1,E4F1,TSC2,FBXW5,RAB11FIP3,ENTR1,PLPP2,ABL1,SLC2A8,IST1,INCA1,GAS1,HEXIM1,PML,JUNB,CALM3,TMEM250,CDK9	cyan	VSMC_M2
GO:0002790	0.97	0.07	7	172	peptide secretion	BP	1	LTBP4,EFNA5,HADH,LINC02210-CRHR1,RASL10B,PHPT1,RAB11B	cyan	VSMC_M2
GO:0050657	0.97	0.07	5	135	nucleic acid transport	BP	1	FLOT1,ZFP36,RFTN1,AGFG1,ZFP36L1	cyan	VSMC_M2
GO:0050658	0.97	0.07	5	135	RNA transport	BP	1	FLOT1,ZFP36,RFTN1,AGFG1,ZFP36L1	cyan	VSMC_M2
GO:0046883	0.97	0.06	7	174	regulation of hormone secretion	BP	1	RAB11FIP1,EFNA5,HADH,LINC02210-CRHR1,RASL10B,PHPT1,RAB11FIP3	cyan	VSMC_M2
GO:0022402	0.97	0.04	54	951	cell cycle process	BP	1	CTDP1,MSH5,EHMT2,RPS6KA2,CDC14C,KIFC2,CUL9,APPL2,GPNMB,RHOB,NOP53,MARK4,ARAP1,KAT2B,POC1B,APBB1,IGF1,CHMP4B,CHMP3,PLSCR1,LZTS2,CAPN3,TPPP,MN1,REC8,FES,TACC2,MUS81,ARHGEF10,BMP4,ZNF503,CROCC,WIZ,GIPC1,ZFP36L1,TP53,PPP1R9B,KANK2,ANKFN1,TEX14,CENPV,SNX33,PDGFRB,LLGL1,E4F1,FBXW5,RAB11FIP3,ENTR1,PLPP2,SLC2A8,IST1,PML,CALM3,TMEM250	cyan	VSMC_M2
GO:1902600	0.97	0.07	4	115	proton transmembrane transport	BP	1	UQCRH,SLC15A4,ATP4A,ATP6V0D1	cyan	VSMC_M2
GO:0051236	0.97	0.07	5	138	establishment of RNA localization	BP	1	FLOT1,ZFP36,RFTN1,AGFG1,ZFP36L1	cyan	VSMC_M2
GO:0006323	0.97	0.07	4	119	DNA packaging	BP	1	DAXX,HIST1H1C,TP53,CENPV	cyan	VSMC_M2
GO:0007283	0.98	0.04	17	357	spermatogenesis	BP	1	ADAMTS2,EHMT2,MEA1,BAX,DZIP1,TPPP2,CATSPERG,GGT7,NDRG3,BBS2,AGFG1,SPOCD1,REC8,ELL3,PRKACA,AR,PYGO2	cyan	VSMC_M2
GO:0051650	0.98	0.06	5	143	establishment of vesicle localization	BP	1	BBS2,KIF1A,FYCO1,STARD3,RAB11B	cyan	VSMC_M2
GO:1901990	0.98	0.04	10	237	regulation of mitotic cell cycle phase transition	BP	1	CDC14C,APPL2,GPNMB,NOP53,ZFP36L1,TP53,PPP1R9B,KANK2,TEX14,PML	cyan	VSMC_M2
GO:0006119	0.98	0.06	4	119	oxidative phosphorylation	BP	1	UQCRH,COQ9,NUPR1,ABCD1	cyan	VSMC_M2
GO:0070646	0.98	0.06	4	125	protein modification by small protein removal	BP	1	NOP53,TRIM21,EIF3F,MINDY1	cyan	VSMC_M2
GO:0000209	0.98	0.04	8	203	protein polyubiquitination	BP	1	TRIM14,RNF144A,TRIM21,RBCK1,FOXF2,HDAC6,GABARAP,RNF166	cyan	VSMC_M2
GO:0007051	0.98	0.05	6	165	spindle organization	BP	1	KIFC2,CHMP4B,LZTS2,TPPP,TACC2,ARHGEF10	cyan	VSMC_M2
GO:0042254	0.98	0.04	11	256	ribosome biogenesis	BP	1	NOP53,RPS16,KAT2B,GTF3A,RIOX2,MRPL36,RNASEL,IMP3,TRAF7,RPS15,RPS19	cyan	VSMC_M2
GO:1901987	0.98	0.04	14	311	regulation of cell cycle phase transition	BP	1	CDC14C,APPL2,GPNMB,NOP53,APBB1,MN1,MUS81,ZFP36L1,TP53,PPP1R9B,KANK2,TEX14,PLPP2,PML	cyan	VSMC_M2
GO:0031503	0.98	0.04	7	186	protein-containing complex localization	BP	1	AGFG1,RPGR,CLSTN1,RPS15,GRASP,LRRC7,STX3	cyan	VSMC_M2
GO:0035966	0.98	0.05	5	143	response to topologically incorrect protein	BP	1	OS9,DAXX,BAX,EDEM2,HDAC6	cyan	VSMC_M2
GO:0006479	0.98	0.05	5	148	protein methylation	BP	1	EHMT2,AASS,HIST1H1C,MLLT6,PYGO2	cyan	VSMC_M2
GO:0008213	0.98	0.05	5	148	protein alkylation	BP	1	EHMT2,AASS,HIST1H1C,MLLT6,PYGO2	cyan	VSMC_M2

GO:0016070	0.98	0.02	222	3480	RNA metabolic process	BP	1	CTDP1,TSHZ1,PYM1,RBMS2,STAT6,TCF21,FLOT1,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,CAMK1,RPS16,ZFP36,SAMD4B,KAT2B,RHOG,TRIM21,APBB1,GTF3A,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,LACTB2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,WDR6,ECM1,NELFCD,ADCY1,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,RNASEK,WIZ,MYRF,ZBTB17,TCF12,ERBB2,PRKACA,ZFP36L1,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,MED12,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,KANK2,WARS,IMP3,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,NELFB,TCF3,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,RNPC3,HSBP1,ATMIN,PBX3,SNORD15B,OAS2,NFIA,ABCA2,RPS15,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,SNORD36C,RPS19,GEMIN8,PLPP3,JUNB,GATA4,GLI4,CARD8,CDK9,ZNF74,NFKBIL1,AHNAK2,ZBTB47,GTF2H4,ZFPM1,EN1,UBL5	cyan	VSMC_M2
GO:0006986	0.98	0.05	4	124	response to unfolded protein	BP	1	OS9,DAXX,BAX,EDEM2	cyan	VSMC_M2
GO:0006325	0.98	0.03	13	301	chromatin organization	BP	1	DAXX,KAT2B,HIST1H1C,DPF2,HDAC5,MAP1S,TP53,CENPV,KDM4B,MPND,RERE,BRD3,ZBTB7A	cyan	VSMC_M2
GO:0006457	0.98	0.04	6	166	protein folding	BP	1	P3H1,LTBP4,HSPB6,B2M,GRN,DNAJB6	cyan	VSMC_M2
GO:0006403	0.99	0.03	6	171	RNA localization	BP	1	FLOT1,ZFP36,RFTN1,AGFG1,ZFP36L1,MEX3D	cyan	VSMC_M2
GO:0051648	0.99	0.04	5	154	vesicle localization	BP	1	BBS2,KIF1A,FYCO1,STARD3,RAB11B	cyan	VSMC_M2
GO:0051321	0.99	0.03	7	192	meiotic cell cycle	BP	1	MSH5,EHMT2,RPS6KA2,REC8,MUS81,TEX14,SLC2A8	cyan	VSMC_M2
GO:0065004	0.99	0.04	4	132	protein-DNA complex assembly	BP	1	DAXX,HIST1H1C,TP53,CENPV	cyan	VSMC_M2
GO:0006839	0.99	0.03	8	210	mitochondrial transport	BP	1	BAX,VPS11,STARD3,TP53,CPT2,RHOT2,ZNF205,UBL5	cyan	VSMC_M2
GO:0000075	0.99	0.03	5	155	cell cycle checkpoint signaling	BP	1	NOP53,MUS81,TP53,TEX14,PML	cyan	VSMC_M2
GO:0048285	0.99	0.02	18	401	organelle fission	BP	1	CTDP1,MSH5,EHMT2,RPS6KA2,CDC14C,KIFC2,CUL9,IGF1,CHMP4B,REC8,MUS81,ARHGEF10,BMP4,PPP1R9B,TEX14,PDGFRB,FBXW5,SLC2A8	cyan	VSMC_M2
GO:0006364	0.99	0.02	7	198	rRNA processing	BP	1	NOP53,RPS16,KAT2B,RNASEL,IMP3,RPS15,RPS19	cyan	VSMC_M2
GO:0000082	0.99	0.03	5	160	G1/S transition of mitotic cell cycle	BP	1	APPL2,GPNMB,TP53,KANK2,PML	cyan	VSMC_M2
GO:0015931	0.99	0.02	6	181	nucleobase-containing compound transport	BP	1	FLOT1,ZFP36,RFTN1,AGFG1,ZFP36L1,ABCD1	cyan	VSMC_M2
GO:0046034	0.99	0.02	8	219	ATP metabolic process	BP	1	UQCRH,IGF1,COQ9,TP53,NUPR1,ABCD1,CBFA2T3,ZBTB7A	cyan	VSMC_M2
GO:0006974	0.99	0.01	35	699	cellular response to DNA damage stimulus	BP	1	MSH5,HMOX1,EEPD1,IRF3,BAX,NOP53,BCL3,APBB1,NEIL2,SFRP2,PRKCD,MMS19,IKBKE,UBA7,REC8,MAGEF1,MUS81,ELL3,TMEM161A,MACROD1,EPHA2,CASP9,BRAT1,TP53,UBQLN4,NUPR1,MTA1,ABL1,ATMIN,ZBTB7A,PML,CDK9,ADPRHL2,MACROD2,GTF2H4	cyan	VSMC_M2
GO:0090276	0.99	0.02	4	140	regulation of peptide hormone secretion	BP	1	EFNA5,HADH,RASL10B,PHPT1	cyan	VSMC_M2
GO:0002791	0.99	0.02	4	142	regulation of peptide secretion	BP	1	EFNA5,HADH,RASL10B,PHPT1	cyan	VSMC_M2
GO:0016072	0.99	0.02	7	206	rRNA metabolic process	BP	1	NOP53,RPS16,KAT2B,RNASEL,IMP3,RPS15,RPS19	cyan	VSMC_M2
GO:0098742	0.99	0.02	4	152	cell-cell adhesion via plasma-membrane adhesion molecules	BP	1	PLXNB2,GATA5,PTPRS,CLSTN1	cyan	VSMC_M2
GO:0090087	0.99	0.02	4	144	regulation of peptide transport	BP	1	EFNA5,HADH,RASL10B,PHPT1	cyan	VSMC_M2
GO:0022613	0.99	0.01	16	376	ribonucleoprotein complex biogenesis	BP	1	EIF3H,NOP53,RPS16,KAT2B,EIF3K,GTF3A,EIF3F,RIOX2,MRPL36,RNASEL,ADAR,IMP3,TRAF7,RPS15,RPS19,GEMIN8	cyan	VSMC_M2
GO:0006259	0.99	0.01	37	741	DNA metabolic process	BP	1	STAT6,MSH5,EHMT2,EEPD1,BAX,NOP53,PLD3,TEP1,APBB1,SLC15A4,WT1,NEIL2,PRKCD,SRC,MMS19,SPOCD1,HIST1H1C,LEF1,REC8,MAGEF1,MUS81,TMEM161A,ARRB2,IL27RA,TP53,UBQLN4,PDGFRB,MTA1,TCF3,ABL1,TK2,ZBTB7A,PML,CDK9,ADPRHL2,GTF2H4,MPV17	cyan	VSMC_M2
GO:0006260	0.99	0.01	8	230	DNA replication	BP	1	EHMT2,NFIB,ATG7,WIZ,TP53,E4F1,NFIA,CDK9	cyan	VSMC_M2
GO:0030073	1.00	0.02	4	149	insulin secretion	BP	1	EFNA5,HADH,PHPT1,RAB11B	cyan	VSMC_M2
GO:1903047	1.00	0.01	28	608	mitotic cell cycle process	BP	1	CTDP1,CDC14C,KIFC2,CUL9,APPL2,GPNMB,RHOB,NOP53,IGF1,CHMP4B,CHMP3,LZTS2,REC8,TACC2,MUS81,ARHGEF10,BMP4,ZFP36L1,TP53,PPP1R9B,KANK2,ANKFN1,TEX14,SNX33,PDGFRB,FBXW5,PML,CALM3	cyan	VSMC_M2
GO:0006281	1.00	0.01	19	455	DNA repair	BP	1	MSH5,EEPD1,NOP53,APBB1,NEIL2,MMS19,REC8,MAGEF1,MUS81,TMEM161A,TP53,UBQLN4,MTA1,ABL1,ZBTB7A,PML,CDK9,ADPRHL2,GTF2H4	cyan	VSMC_M2

GO:1901360	1.00	0.00	289	4575	organic cyclic compound metabolic process	BP	1	CTDP1,TSHZ1,PYM1,PMEL,RBMS2,STAT6,MOXD1,TCF21,FLOT1,MSH5,EHMT2,ZFPM2,IRF1,CYB5R3,TCF20,DAXX,TEF,PTPRK,IBA57,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,EEPD1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,VIM,APOE,UROD,BCL3,SLC6A9,ACAA1,CAMK1,PLD3,TEP1,PNP,RPS16,ZFP36,SAMD4B,GPAT4,KAT2B,RHOG,TRIM21,SMPD1,APBB1,GTF3A,SLC15A4,LMO1,MAP3K12,RBCK1,RARG,IGF1,CYP4V2,TLR3,WT1,TP53INP2,PATL1,TSHZ3,ACSS2,POU6F1,LACTB2,CTSB,NEIL2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,OSBPL5,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,STS,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,WDR6,ECM1,REC8,CTSK,NELFCD,ADCY1,TATDN3,BCL9L,RFX5,GATA5,CLCN2,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,MUS81,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TMEM161A,TSC22D4,ACAT1,NUDT13,MACROD1,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,RNASEK,WIZ,EPHA2,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,STARD3,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,HSD3B7,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,NPC2,PDK2,MED12,GBA,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,SLC16A2,KANK2,WARS,PPCDC,IMP3,ABCC1,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,MFSD12,GLIS2,ABCD1,DVL1,AG	cyan	VSMC_M2
GO:0006725	1.00	0.00	277	4410	cellular aromatic compound metabolic process	BP	1	CTDP1,TSHZ1,PYM1,PMEL,RBMS2,STAT6,MOXD1,TCF21,FLOT1,MSH5,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,IBA57,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,EEPD1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,VIM,APOE,UROD,BCL3,SLC6A9,ACAA1,CAMK1,PLD3,TEP1,PNP,RPS16,ZFP36,SAMD4B,GPAT4,KAT2B,RHOG,TRIM21,APBB1,GTF3A,SLC15A4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,ACSS2,POU6F1,LACTB2,CTSB,NEIL2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,WDR6,ECM1,REC8,CTSK,NELFCD,ADCY1,TATDN3,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,MUS81,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TMEM161A,TSC22D4,ACAT1,NUDT13,MACROD1,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,RNASEK,WIZ,EPHA2,MYRF,ZBTB17,TCF12,GIPC1,ERBB2,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,PDK2,MED12,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,SLC16A2,KANK2,WARS,PPCDC,IMP3,ABCC1,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,MFSD12,GLIS2,ABCD1,DVL1,AGRN,ELOB,E4F1,EXD3,NELFB,REXO1,TCF3,UAP1L1,SBNO2,EDF1,AXIN1,R	cyan	VSMC_M2
GO:0071824	1.00	0.01	4	163	protein-DNA complex subunit organization	BP	1	DAXX,HIST1H1C,TP53,CENPV	cyan	VSMC_M2
GO:0044772	1.00	0.00	13	350	mitotic cell cycle phase transition	BP	1	CTDP1,CDC14C,APPL2,GPNMB,NOP53,CHMP4B,ZFP36L1,TP53,PPP1R9B,KANK2,TEX14,PML,CALM3	cyan	VSMC_M2
GO:0044770	1.00	0.00	17	426	cell cycle phase transition	BP	1	CTDP1,CDC14C,APPL2,GPNMB,NOP53,APBB1,CHMP4B,MN1,MUS81,ZFP36L1,TP53,PPP1R9B,KANK2,TEX14,PLPP2,PML,CALM3	cyan	VSMC_M2
GO:0043414	1.00	0.01	8	254	macromolecule methylation	BP	1	EHMT2,AASS,WT1,SPOCD1,HIST1H1C,WDR6,MLLT6,PYGO2	cyan	VSMC_M2
GO:0033044	1.00	0.01	4	168	regulation of chromosome organization	BP	1	SRC,TEX14,CENPV,PML	cyan	VSMC_M2
GO:0090304	1.00	0.00	241	3916	nucleic acid metabolic process	BP	1	CTDP1,TSHZ1,PYM1,RBMS2,STAT6,TCF21,FLOT1,MSH5,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,EEPD1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,FZD4,VIM,APOE,BCL3,CAMK1,PLD3,TEP1,RPS16,ZFP36,SAMD4B,KAT2B,RHOG,TRIM21,APBB1,GTF3A,SLC15A4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,POU6F1,LACTB2,NEIL2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,WDR6,ECM1,REC8,NELFCD,ADCY1,TATDN3,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,RNASEL,MAGEF1,MUS81,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TMEM161A,TSC22D4,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,RNASEK,WIZ,MYRF,ZBTB17,TCF12,ERBB2,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,MED12,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,KANK2,WARS,IMP3,PDGFRB,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,DVL1,AGRN,ELOB,E4F1,EXD3,NELFB,REXO1,TCF3,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,RNPC3,HSBP1,ATMIN,PBX3,TK2,SNORD15B,OAS2,NFIA,ABCA2,RPS15,MEX3D,ZNF205,HEXIM1,ZBTB7A,TRIM26,ATN1,PML,SNORD36C,RPS19,GEMIN8,PLPP3,JUNB,GATA4,GLI4,	cyan	VSMC_M2
GO:0000278	1.00	0.00	33	729	mitotic cell cycle	BP	1	CTDP1,CDC14C,KIFC2,CUL9,APPL2,GPNMB,RHOB,NOP53,TIMP2,IGF1,CHMP4B,CHMP3,LZTS2,REC8,TACC2,MUS81,ARHGEF10,BMP4,MAEA,ZFP36L1,TP53,PPP1R9B,KANK2,ANKFN1,TEX14,SNX33,PDGFRB,E4F1,FBXW5,ABL1,GAS1,PML,CALM3	cyan	VSMC_M2
GO:0071103	1.00	0.00	5	200	DNA conformation change	BP	1	DAXX,HIST1H1C,TP53,CENPV,ABL1	cyan	VSMC_M2

GO:0006139	1.00	0.00	262	4274	nucleobase-containing compound metabolic process	BP	1	CTDP1,TSHZ1,PYM1,RBMS2,STAT6,TCF21,FLOT1,MSH5,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,EEPD1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,VIM,APOE,BCL3,CAMK1,PLD3,TEP1,PNP,RPS16,ZFP36,SAMD4B,GPAT4,KAT2B,RHOG,TRIM21,APBB1,GTF3A,SLC15A4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,ACSS2,POU6F1,LACTB2,NEIL2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,WDR6,ECM1,REC8,NELFCD,ADCY1,TATDN3,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,MUS81,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TMEM161A,TSC22D4,ACAT1,NUDT13,MACROD1,MXD4,BMP4,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,RNASEK,WIZ,EPHA2,MYRF,ZBTB17,TCF12,ERBB2,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,PDK2,MED12,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,KANK2,WARS,PPCDC,IMP3,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,ABCD1,DVL1,AGRN,ELOB,E4F1,EXD3,NELFB,REXO1,TCF3,UAP1L1,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,RNPC3,HSBP1,ATMIN,DPYD,FPGS,PBX3,TK2,SNO	cyan	VSMC_M2
GO:0046483	1.00	0.00	268	4376	heterocycle metabolic process	BP	1	CTDP1,TSHZ1,PYM1,RBMS2,STAT6,TCF21,FLOT1,MSH5,EHMT2,ZFPM2,IRF1,TCF20,DAXX,TEF,PTPRK,IBA57,TEAD3,TLE1,NFIB,TRERF1,HMOX1,KLF9,MLIP,IARS,ZBTB45,ZSCAN18,TRIM14,NAT14,EFEMP1,RRAGC,EEPD1,MEIS1,PTOV1,AASS,GLI3,SIM1,IRF3,KLF15,BAX,DBP,HBP1,NOP53,BICRA,MEIS3,TRIM13,ACSS1,FZD4,VIM,APOE,UROD,BCL3,SLC6A9,CAMK1,PLD3,TEP1,PNP,RPS16,ZFP36,SAMD4B,GPAT4,KAT2B,RHOG,TRIM21,APBB1,GTF3A,SLC15A4,LMO1,MAP3K12,RBCK1,RARG,IGF1,TLR3,WT1,TP53INP2,PATL1,TSHZ3,ACSS2,POU6F1,LACTB2,NEIL2,PLSCR1,HEXB,CAMKK2,SFRP2,WWTR1,SCAND1,PRKCD,SRC,ZHX3,RIOX2,MMS19,FOXF2,SFRP5,MAPK8IP1,SORBS3,STAT1,ABHD14B,CD81,NDN,TRIM8,IKBKE,CAPN3,NADSYN1,TIRAP,ZNF496,NFKB1,SPOCD1,HIST1H1C,PKNOX2,RGMA,BCL9,LEF1,TBL1Y,GTF2IRD2,PTGIS,SOX5,MN1,WDR6,ECM1,REC8,NELFCD,ADCY1,TATDN3,BCL9L,RFX5,GATA5,HELZ2,SLC2A4RG,UCKL1,RNASEL,MAGEF1,MUS81,NMNAT2,TCEA3,ELL3,NFKBIA,MOV10,DPF2,ADORA2A,PCBD1,HDAC5,TMEM161A,TSC22D4,ACAT1,NUDT13,MACROD1,MXD4,BMP4,QDPR,LDB2,TCEA2,STAT5A,ZNF503,NR2F6,HDAC6,ZBTB3,PQBP1,DNAJB6,ARRB2,JUP,RNASEK,WIZ,EPHA2,MYRF,ZBTB17,TCF12,ERBB2,PRKACA,ZFP36L1,IL27RA,RFX1,SPIN4,NTRK1,PCGF2,ZNF771,MLLT6,AR,TP53,GLMP,KAT8,HOXB1,HOXB2,HOXB4,ELMSAN1,UBQLN4,PDK2,MED12,PPP1R9B,NUPR1,SHC1,PBXIP1,ADAR,KANK2,WARS,PPCDC,IMP3,ABCC1,PDGFRB,NUDT14,MTA1,MAP2K3,ROR1,MLLT1,MOSPD1,MPND,GLIS2,ABCD1,DVL1,AGRN,ELOB,E4F1,EXD3,NELFB,REXO1,TCF3,UAP1L1,SBNO2,EDF1,AXIN1,RERE,POLRMT,TCF25,BRD3,CBFA2T3,FOXC2,ABL1,RNPC3,H	cyan	VSMC_M2
GO:0032259	1.00	0.00	8	290	methylation	BP	1	EHMT2,AASS,WT1,SPOCD1,HIST1H1C,WDR6,MLLT6,PYGO2	cyan	VSMC_M2
GO:0098813	1.00	0.00	5	230	nuclear chromosome segregation	BP	1	EHMT2,CHMP4B,REC8,MUS81,TEX14	cyan	VSMC_M2
GO:0016071	1.00	0.00	22	586	mRNA metabolic process	BP	1	PYM1,VIM,ZFP36,SAMD4B,PATL1,PRKCD,IKBKE,TIRAP,HELZ2,RNASEL,MOV10,PQBP1,PRKACA,ZFP36L1,TP53,ADAR,RNPC3,MEX3D,ZBTB7A,GEMIN8,CDK9,UBL5	cyan	VSMC_M2
GO:0007059	1.00	0.00	7	288	chromosome segregation	BP	1	EHMT2,CHMP4B,PLSCR1,MMS19,REC8,MUS81,TEX14	cyan	VSMC_M2
GO:0034470	1.00	0.00	9	345	ncRNA processing	BP	1	NOP53,RPS16,KAT2B,WDR6,RNASEL,ADAR,IMP3,RPS15,RPS19	cyan	VSMC_M2
GO:0034660	1.00	0.00	12	412	ncRNA metabolic process	BP	1	IARS,NOP53,RPS16,KAT2B,NFKB1,WDR6,RNASEL,ADAR,WARS,IMP3,RPS15,RPS19	cyan	VSMC_M2
GO:0000377	1.00	0.00	5	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1	PQBP1,RNPC3,ZBTB7A,GEMIN8,UBL5	cyan	VSMC_M2
GO:0000398	1.00	0.00	5	255	mRNA splicing, via spliceosome	BP	1	PQBP1,RNPC3,ZBTB7A,GEMIN8,UBL5	cyan	VSMC_M2
GO:0000375	1.00	0.00	5	259	RNA splicing, via transesterification reactions	BP	1	PQBP1,RNPC3,ZBTB7A,GEMIN8,UBL5	cyan	VSMC_M2
GO:0008380	1.00	0.00	9	356	RNA splicing	BP	1	RRAGC,WT1,PQBP1,PPP1R9B,RNPC3,ZBTB7A,GEMIN8,AHNAK2,UBL5	cyan	VSMC_M2
GO:0006397	1.00	0.00	10	407	mRNA processing	BP	1	RNASEL,PQBP1,PRKACA,ZFP36L1,ADAR,RNPC3,ZBTB7A,GEMIN8,CDK9,UBL5	cyan	VSMC_M2
GO:0051276	1.00	0.00	21	682	chromosome organization	BP	1	EHMT2,DAXX,TEP1,KAT2B,CHMP4B,SRC,HIST1H1C,REC8,DPF2,HDAC5,MAP1S,TP53,TEX14,CENPV,KDM4B,MPND,RERE,BRD3,ABL1,ZBTB7A,PML	cyan	VSMC_M2
GO:0006396	1.00	0.00	26	950	RNA processing	BP	1	RBMS2,RRAGC,NOP53,RPS16,KAT2B,WT1,WDR6,RNASEL,BMP4,PQBP1,PRKACA,ZFP36L1,TP53,PPP1R9B,ADAR,IMP3,RNPC3,SNORD15B,RPS15,ZBTB7A,SNORD36C,RPS19,GEMIN8,CDK9,AHNAK2,UBL5	cyan	VSMC_M2

GO:0023052	0.00	1.00	381	4258	signaling	BP	3E-05	MBP,DOK6,GDF11,BCL2,RNF41,IFNGR1,CITED2,STX11,SASH1,IRAK3,GRIP1,MDM2,DDR1,RGS22,RNF19A,SOD2,ABRA,ANGPT1,FAM19A5,SMOC2,SCUBE1,GJA1,TRDN,TPD52L1,LAMA2,EP300,BRD8,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,RASL11B,VLDLR,UNC13B,PPP1R9A,CD274,PDK4,IL18R1,RNF149,CREB3,REST,ICA1,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,PREPL,EDN2,SYT5,ABCA1,PTPN3,SVEP1,TBX18,CHN2,MAP3K7,DOCK4,KIDINS220,MDFIC,GPR63,FZD8,EPHB6,SESN1,JADE1,MAP3K8,HIPK2,GATA2,APBB1IP,LIMS2,SNRK,TPT1,ITGA8,TENM4,ITGA9,INHBB,GPR39,HRH1,LMO7,NXPH2,BABAM2,RALGAPA2,LBH,NDRG2,KCNE3,POLB,LMCD1,ARHGEF17,THRB,PLCB4,ACTN4,ADAM9,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,COL4A1,COL4A2,PCDHB4,CDC42EP3,CYP1B1,PCLO,SEMA3C,TF,APLP1,FLT3,AMOTL2,ZDHHC2,RIC3,MAP3K1,NCOR2,FFAR3,PTPRG,CHD7,LATS2,HIPK3,ANKRD1,KIAA0355,CPEB3,NCK1,SORBS2,ADM,CD180,SCN8A,SH3RF1,MRVI1,ATOH8,CLCN3,GRK7,TCF7L1,WWC2,TEAD1,MCTP1,ARHGEF3,PTH,KIF13B,RNF34,CDKL2,G3BP2,CLU,BLNK,GPR87,APP,PDGFC,RXFP1,ABCC8,PTPN11,ADCY6,LBP,HERPUD1,TMEM64,JMY,DCBLD2,PTPN22,PKP4,HNF4A,CHAC1,GDF6,FMOD,SERINC3,ADA,RCAN1,NGF,EDN1,JAM3,CD47,NFASC,SEMA5A,LPL,MX1,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,PPP1R12B,DAPP1,RGS2,EYA2,NCOA3,ACTN2,ZNF106,PFKL,LRP5,KCTD10,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,TM7SF3,GALNT3,PRKCA,GNB4,AFAP1L2,TXNIP,MID1,PLXNA2,SESN2,SHTN1,CAMK2D,ABCC9,ADCY5,CTSS,LRP2,CFLAR,GABBR1,INPP5F,FGFR2,CASTOR1,	darkgreen	VSMC_M4
GO:0007154	0.00	1.00	383	4300	cell communication	BP	3E-05	MBP,DOK6,GDF11,BCL2,RNF41,IFNGR1,CITED2,STX11,SASH1,IRAK3,GRIP1,MDM2,DDR1,RGS22,RNF19A,SOD2,ABRA,ANGPT1,FAM19A5,SMOC2,SCUBE1,GJA1,TRDN,TPD52L1,LAMA2,EP300,BRD8,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,RASL11B,VLDLR,UNC13B,PPP1R9A,CD274,PDK4,IL18R1,RNF149,CREB3,REST,ICA1,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,SLC2A1,TGFBR1,PREPL,EDN2,SYT5,ABCA1,PTPN3,SVEP1,TBX18,CHN2,MAP3K7,DOCK4,KIDINS220,MDFIC,GPR63,FZD8,EPHB6,SESN1,JADE1,MAP3K8,HIPK2,GATA2,APBB1IP,LIMS2,SNRK,TPT1,ITGA8,TENM4,ITGA9,INHBB,GPR39,HRH1,NXPH2,BABAM2,RALGAPA2,LBH,NDRG2,POLB,LMCD1,ARHGEF17,THRB,PLCB4,ACTN4,ADAM9,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,COL4A1,COL4A2,PCDHB4,CDC42EP3,CYP1B1,PCLO,SEMA3C,TF,APLP1,FLT3,AMOTL2,ZDHHC2,RIC3,MAP3K1,NCOR2,FFAR3,PTPRG,CHD7,LATS2,HIPK3,ANKRD1,KIAA0355,CPEB3,NCK1,SORBS2,ADM,MAP1LC3A,CD180,SCN8A,SH3RF1,MRVI1,ATOH8,CLCN3,GRK7,TCF7L1,WWC2,TEAD1,MCTP1,ARHGEF3,PTH,KIF13B,RNF34,CDKL2,G3BP2,CLU,BLNK,GPR87,APP,PDGFC,RXFP1,ABCC8,PTPN11,ADCY6,LBP,HERPUD1,TMEM64,JMY,DCBLD2,PTPN22,PKP4,HNF4A,CHAC1,GDF6,FMOD,SERINC3,ADA,RCAN1,NGF,EDN1,JAM3,CD47,NFASC,SEMA5A,LPL,MX1,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,PPP1R12B,DAPP1,RGS2,EYA2,NCOA3,ACTN2,ZNF106,PFKL,LRP5,KCTD10,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,TM7SF3,GALNT3,PRKCA,GNB4,AFAP1L2,TXNIP,MID1,PLXNA2,SESN2,SHTN1,CAMK2D,ADCY5,CTSS,LRP2,CFLAR,GABBR1,INPP5F,FGFR2,CAS	darkgreen	VSMC_M4
GO:0007165	0.00	1.00	348	3919	signal transduction	BP	0.00019	MBP,DOK6,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,GRIP1,MDM2,DDR1,RGS22,SOD2,ABRA,ANGPT1,FAM19A5,SMOC2,SCUBE1,GJA1,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,RASL11B,VLDLR,UNC13B,PPP1R9A,CD274,PDK4,IL18R1,RNF149,CREB3,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,EDN2,ABCA1,PTPN3,SVEP1,TBX18,CHN2,MAP3K7,DOCK4,KIDINS220,MDFIC,GPR63,FZD8,EPHB6,SESN1,JADE1,MAP3K8,HIPK2,GATA2,APBB1IP,LIMS2,SNRK,TPT1,ITGA8,TENM4,ITGA9,INHBB,GPR39,HRH1,NXPH2,BABAM2,RALGAPA2,LBH,NDRG2,POLB,LMCD1,ARHGEF17,THRB,PLCB4,ACTN4,ADAM9,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,COL4A1,COL4A2,CDC42EP3,CYP1B1,PCLO,SEMA3C,TF,APLP1,FLT3,AMOTL2,MAP3K1,NCOR2,FFAR3,PTPRG,LATS2,HIPK3,ANKRD1,KIAA0355,NCK1,SORBS2,ADM,CD180,SH3RF1,MRVI1,ATOH8,GRK7,TCF7L1,WWC2,TEAD1,MCTP1,ARHGEF3,PTH,KIF13B,RNF34,CDKL2,G3BP2,CLU,BLNK,GPR87,APP,PDGFC,RXFP1,PTPN11,ADCY6,LBP,HERPUD1,TMEM64,JMY,DCBLD2,PTPN22,HNF4A,CHAC1,GDF6,FMOD,SERINC3,ADA,RCAN1,NGF,EDN1,CD47,SEMA5A,LPL,MX1,RAB29,ADIPOR1,FNDC5,RIPOR2,PPP1R12B,DAPP1,RGS2,EYA2,NCOA3,ACTN2,ZNF106,LRP5,KCTD10,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,GALNT3,PRKCA,GNB4,AFAP1L2,TXNIP,MID1,PLXNA2,SESN2,SHTN1,CAMK2D,ADCY5,CTSS,LRP2,CFLAR,GABBR1,INPP5F,FGFR2,CASTOR1,TP53BP1,PRKD1,NCSTN,PI4KB,F11R,TRIM63,PLXNB1,ZRANB1,STRN3,RAPH1,ARID5B,ITGA6,ATF6,RAPGEF4,INSYN2,AKAP6,DDR2,GPRC5A,MAP3K13,LRP6,HIP1,PRDX4,HSPB1,SER	darkgreen	VSMC_M4
GO:0051270	0.00	1.00	98	830	regulation of cellular component movement	BP	0.00133	BCL2,RNF41,CITED2,SASH1,MDM2,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,ADGRB1,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,TGFBR1,EDN2,DOCK4,TCAF1,GATA2,LRCH1,ACTN4,ADAM9,CYP1B1,SEMA3C,TF,AMOTL2,PTPRG,NCK1,ATOH8,MCTP1,CHST2,APP,PDGFC,ABCC8,ANXA3,LBP,ADA,EDN1,JAM3,CD47,SEMA5A,ADIPOR1,RIPOR2,TNNT2,FEZ1,PREX1,LGMN,PRKCA,PARD6B,PLXNA2,SHTN1,CAMK2D,MYLK,INPP5F,PRKD1,PLXNB1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,CACNA1C,PPARGC1A,ACTN1,NUMB,BBS4,MAPRE2,PAK3,MMP28,GAS2L2,RHOT1,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,CSF1,CDH13,PLCG2,F3,LMO4,CYR61,NEXN,SLC8A1,CD151,PLN,FGF9,CCR6,ICAM1,PIK3C2A,PRKG1,FAM83H	darkgreen	VSMC_M4

GO:0010646	0.00	1.00	235	2513	regulation of cell communication	BP	0.00298	DOK6,GDF11,BCL2,RNF41,CITED2,SASH1,IRAK3,MDM2,RGS22,RNF19A,SOD2,ABRA,ANGPT1,SMOC2,SCUBE1,GJA1,TRDN,TPD52L1,LAMA2,EP300,ADGRB1,DAPK1,TLE4,GNAQ,MLLT3,LEP,CDKN2B,WFS1,PIP5K1B,DOCK8,SH3RF3,KANK1,RASL11B,UNC13B,PPP1R9A,IL18R1,RNF149,CREB3,REST,ICA1,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,PREPL,ABCA1,PTPN3,TBX18,CHN2,MAP3K7,MDFIC,SESN1,JADE1,HIPK2,GATA2,LIMS2,TPT1,INHBB,HRH1,RALGAPA2,LBH,NDRG2,LMCD1,ARHGEF17,PLCB4,ACTN4,ADAM9,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,CYP1B1,APLP1,FLT3,ZDHHC2,NCOR2,FFAR3,CHD7,LATS2,HIPK3,ANKRD1,CPEB3,NCK1,ADM,CD180,SH3RF1,GRK7,TCF7L1,WWC2,MCTP1,ARHGEF3,PTH,RNF34,CLU,APP,PDGFC,ABCC8,PTPN11,LBP,HERPUD1,TMEM64,PTPN22,HNF4A,CHAC1,GDF6,SERINC3,ADA,RCAN1,NGF,EDN1,CD47,SEMA5A,RAB29,ABCG1,ADIPOR1,KDM5B,RIPOR2,RGS2,EYA2,NCOA3,PFKL,LRP5,KCTD10,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,TM7SF3,PRKCA,AFAP1L2,MID1,SESN2,CAMK2D,ADCY5,LRP2,CFLAR,INPP5F,FGFR2,CASTOR1,PRKD1,NCSTN,F11R,PLXNB1,ZRANB1,STRN3,ITGA6,ATF6,AKAP6,GPRC5A,MAP3K13,HIP1,HSPB1,SERPINE1,ACHE,ATP6AP2,ARHGAP20,RDX,UNC5B,MAOA,IGFBP2,NBR1,SYNPO2L,CYP19A1,TNFSF10,DACT1,NLGN1,HIF1A,IQSEC3,GNAI1,FBXL20,PPARGC1A,RORA,SIPA1L1,SLIT3,TGFB3,ADRA1B,SMAD6,NPTN,NRK,MAPRE2,CDH2,PAK3,NOMO1,GAS2L2,SH3TC2,FST,RHOT1,CRLF3,ARHGAP28,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,TLE2,FLNA,PLEKHG5,VAMP7,CSF1,CDH13,PLCG2,TERF2IP,F3,GLG1,ARHGAP29,BCAR3,CYR61,SYDE2,WLS,MIR99A,ITPR1,VNN1,SLC8A1,ADAMTSL2,TLR1,FRZB,LOX,	darkgreen	VSMC_M4
GO:2000145	0.00	1.00	91	772	regulation of cell motility	BP	0.00323	BCL2,RNF41,CITED2,SASH1,MDM2,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,ADGRB1,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,TGFBR1,EDN2,DOCK4,TCAF1,GATA2,LRCH1,ACTN4,ADAM9,CYP1B1,SEMA3C,TF,AMOTL2,PTPRG,NCK1,ATOH8,MCTP1,CHST2,APP,PDGFC,ABCC8,ANXA3,LBP,ADA,EDN1,JAM3,CD47,SEMA5A,ADIPOR1,RIPOR2,PREX1,LGMN,PRKCA,PARD6B,PLXNA2,SHTN1,MYLK,INPP5F,PRKD1,PLXNB1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,PPARGC1A,NUMB,BBS4,MAPRE2,PAK3,MMP28,GAS2L2,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,CSF1,CDH13,PLCG2,F3,LMO4,CYR61,NEXN,SLC8A1,CD151,FGF9,CCR6,ICAM1,PIK3C2A,PRKG1,FAM83H	darkgreen	VSMC_M4
GO:0032879	0.00	1.00	199	2074	regulation of localization	BP	0.00334	BCL2,RNF41,SLC35D3,CITED2,SASH1,MDM2,SOD2,ANGPT1,C4A,FAM19A5,SMOC2,GJA1,TRDN,LAMA2,ADGRB1,DAPK1,SH3GL2,LEP,WFS1,LIMCH1,DDX58,DOCK8,KANK1,UNC13B,PPP1R9A,CD274,RIC1,CREB3,REST,ICA1,RECK,TGFBR1,PREPL,EDN2,SYT5,ABCA1,PTPN3,SNAP91,DOCK4,MDFIC,TCAF1,GATA2,LRCH1,INHBB,KCNE3,RAB2B,ACTN4,ADAM9,FGF14,ATP2C1,CYP1B1,PCLO,SEMA3C,TF,AMOTL2,ZDHHC2,RIC3,FFAR3,FXYD1,PTPRG,CHD7,LATS2,ANKRD1,NCK1,PAM,SCN8A,ATOH8,OCLN,MCTP1,CHST2,JPH1,PTH,CLU,APP,ATXN2,PDGFC,ABCC8,ANXA3,PTPN11,PTX3,LBP,ATG13,HNF4A,ADA,EDN1,JAM3,CD47,SEMA5A,LPL,RAB29,ABCG1,ADIPOR1,KDM5B,RIPOR2,RGS2,TNNT2,ACTN2,PFKL,LRP5,FEZ1,PREX1,HTR2B,LGMN,TM7SF3,PRKCA,SEC24B,MFGE8,PARD6B,ATP9A,PLXNA2,SESN2,ARV1,SHTN1,CAMK2D,ADCY5,CTSS,MYLK,INPP5F,PTPN14,PRKD1,PLXNB1,ITGA6,RAPGEF4,AKAP6,DDR2,HIP1,HSPB1,SERPINE1,ACHE,CRYAB,RDX,EXPH5,MAOB,CYP19A1,NLGN1,WDR1,HIF1A,OPN3,CACNA1C,ADGRE2,GNAI1,FBXL20,PPARGC1A,ACTN1,NPPB,DISP3,NUMB,TGFB3,KCNK10,BBS4,NPTN,MAPRE2,CDH2,PAK3,MMP28,GAS2L2,ABLIM3,SH3TC2,RHOT1,DNAJC6,DAB2,LGALS9,PRKAA2,TMEM59,ATCAY,DAPK3,SLC43A2,PLXNB3,FLNA,VAMP7,HCN2,AHCYL1,CSF1,MBTPS1,CDH13,PLCG2,F3,LRSAM1,LMO4,CYR61,NEXN,WLS,KCNE4,ITPR1,SLC8A1,CD151,PLN,FGF9,TMEM38A,CCR6,SARAF,ICAM1,PIK3C2A,ORMDL3,YAP1,PRKG1,BMP6,FAM83H,SCP2	darkgreen	VSMC_M4
GO:0003012	0.00	1.00	48	332	muscle system process	BP	0.00343	GJA1,TRDN,LEP,TPM2,EDN2,CALD1,DOCK4,PPP1R13L,KCNE3,LMCD1,FOXO1,FXYD1,SORBS2,MYL9,ABCC8,ADA,EDN1,PPP1R12B,RGS2,TNNT2,ACTN2,NPNT,HTR2B,PRKCA,CAMK2D,MYLK,CFLAR,INPP5F,TRIM63,AKAP6,CRYAB,APBB2,CACNA1C,PPARGC1A,SGCA,ADRA1B,CNN1,DAPK3,FLNA,CCDC78,KCNE4,SLC8A1,TBX20,PLN,TMEM38A,PIK3C2A,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:0030334	0.00	1.00	87	735	regulation of cell migration	BP	0.0042	BCL2,RNF41,CITED2,SASH1,MDM2,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,ADGRB1,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,TGFBR1,EDN2,DOCK4,TCAF1,GATA2,LRCH1,ACTN4,ADAM9,CYP1B1,SEMA3C,AMOTL2,PTPRG,NCK1,ATOH8,MCTP1,CHST2,APP,PDGFC,ABCC8,ANXA3,LBP,ADA,EDN1,JAM3,CD47,SEMA5A,ADIPOR1,RIPOR2,PREX1,LGMN,PRKCA,PARD6B,PLXNA2,SHTN1,MYLK,PRKD1,PLXNB1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,PPARGC1A,NUMB,MAPRE2,PAK3,MMP28,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,CSF1,CDH13,PLCG2,F3,LMO4,CYR61,NEXN,SLC8A1,CD151,FGF9,CCR6,ICAM1,PIK3C2A,PRKG1,FAM83H	darkgreen	VSMC_M4

GO:0050896	0.00	1.00	475	5876	response to stimulus	BP	0.0042	MBP,ZNF516,DOK6,GDF11,BCL2,RNF41,IFNGR1,CITED2,SHPRH,SASH1,IRAK3,GRIP1,MDM2,DDR1,RGS22,IPCEF1,SOD2,OXR1,ABRA,ANGPT1,C4A,FAM19A5,PKDREJ,RNASET2,SMOC2,SCUBE1,GJA1,TRDN,TPD52L1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,RASL11B,VLDLR,UNC13B,C2orf40,PPP1R9A,CD274,PON2,PDK4,IL18R1,RNF149,CREB3,REST,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,SLC2A1,TGFBR1,EDN2,SYT5,SLC17A5,ABCA1,PTPN3,SVEP1,TBX18,CHN2,MAP3K7,NT5C3A,DOCK4,KIDINS220,MDFIC,GPR63,PAPPA,FZD8,EPHB6,SESN1,JADE1,MAP3K8,HIPK2,GATA2,APBB1IP,LIMS2,ABHD12,TMEM135,LRCH1,SNRK,MRC1,TPT1,ITGA8,TENM4,ITGA9,INHBB,GPR39,HRH1,NXPH2,BABAM2,RALGAPA2,LBH,STT3B,NDRG2,POLB,LMCD1,ARHGEF17,THRB,PLCB4,ACTN4,ADAM9,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,COL4A1,COL4A2,CDC42EP3,CYP1B1,CPNE4,PCLO,SEMA3C,TF,APLP1,FLT3,AMOTL2,MAP3K1,NCOR2,FFAR3,HPN,PTPRG,CHD7,LATS2,HIPK3,ANKRD1,KIAA0355,CPEB3,TRIM23,NCK1,SORBS2,ADM,MAP1LC3A,PAM,CD180,SH3RF1,MRVI1,ATOH8,GRK7,OCLN,TCF7L1,WWC2,TEAD1,MCTP1,CHST2,ARHGEF3,PTH,KIF13B,RNF34,CDKL2,G3BP2,CLU,ENTPD1,BLNK,GPM6A,MEIS2,GPR87,MYL9,APP,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,PTPN11,PTX3,ADCY6,LBP,NEK4,HERPUD1,PROS1,TMEM64,JMY,DCBLD2,CHD6,PTPN22,TANC1,HNF4A,CHAC1,GDF6,FMOD,SERINC3,ADA,RCAN1,IFIT1,NGF,PDZD7,EDN1,JAM3,CD47,NFASC,PLA2G4F,N4BP1,SMARCAD1,MARCH6,SEMA5A,LPL,MX1,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,PPP1R12B,CCD	darkgreen	VSMC_M4
GO:0023051	0.00	1.00	234	2524	regulation of signaling	BP	0.00438	DOK6,GDF11,BCL2,RNF41,CITED2,SASH1,IRAK3,MDM2,RGS22,RNF19A,SOD2,ABRA,ANGPT1,SMOC2,SCUBE1,GJA1,TPD52L1,LAMA2,EP300,ADGRB1,DAPK1,TLE4,GNAQ,MLLT3,LEP,CDKN2B,WFS1,PIP5K1B,DOCK8,SH3RF3,KANK1,RASL11B,UNC13B,PPP1R9A,IL18R1,RNF149,CREB3,REST,ICA1,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,PREPL,ABCA1,PTPN3,TBX18,CHN2,MAP3K7,MDFIC,SESN1,JADE1,HIPK2,GATA2,LIMS2,TPT1,INHBB,HRH1,LMO7,RALGAPA2,LBH,NDRG2,LMCD1,ARHGEF17,PLCB4,ACTN4,ADAM9,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,CYP1B1,APLP1,FLT3,ZDHHC2,NCOR2,FFAR3,CHD7,LATS2,HIPK3,ANKRD1,CPEB3,NCK1,ADM,CD180,SH3RF1,GRK7,TCF7L1,WWC2,MCTP1,ARHGEF3,PTH,RNF34,CLU,APP,PDGFC,ABCC8,PTPN11,LBP,HERPUD1,TMEM64,PTPN22,HNF4A,CHAC1,GDF6,SERINC3,ADA,RCAN1,NGF,EDN1,CD47,SEMA5A,RAB29,ABCG1,ADIPOR1,KDM5B,RIPOR2,RGS2,EYA2,NCOA3,PFKL,LRP5,KCTD10,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,TM7SF3,PRKCA,AFAP1L2,MID1,SESN2,ADCY5,LRP2,CFLAR,INPP5F,FGFR2,CASTOR1,PRKD1,NCSTN,F11R,PLXNB1,ZRANB1,STRN3,ITGA6,ATF6,AKAP6,GPRC5A,MAP3K13,HIP1,HSPB1,SERPINE1,ACHE,ATP6AP2,ARHGAP20,RDX,UNC5B,MAOA,IGFBP2,NBR1,SYNPO2L,CYP19A1,TNFSF10,DACT1,NLGN1,HIF1A,IQSEC3,GNAI1,FBXL20,PPARGC1A,RORA,SIPA1L1,SLIT3,TGFB3,ADRA1B,SMAD6,NPTN,NRK,MAPRE2,CDH2,PAK3,NOMO1,GAS2L2,SH3TC2,FST,RHOT1,CRLF3,ARHGAP28,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,TLE2,FLNA,PLEKHG5,VAMP7,CSF1,CDH13,PLCG2,TERF2IP,F3,GLG1,ARHGAP29,BCAR3,CYR61,SYDE2,WLS,MIR99A,ITPR1,VNN1,SLC8A1,ADAMTSL2,TLR1,FRZB,LOX,TBX20,IT	darkgreen	VSMC_M4
GO:0009605	0.00	1.00	169	1770	response to external stimulus	BP	0.00559	BCL2,IFNGR1,CITED2,SASH1,IRAK3,MDM2,SOD2,ANGPT1,C4A,FAM19A5,PKDREJ,RNASET2,SMOC2,GJA1,TRDN,LAMA2,EP300,ADGRB1,DAPK1,GNAQ,LEP,CDKN2B,DDX58,CD274,PDK4,CREB3,ZAP70,SLC2A1,EDN2,SLC17A5,ABCA1,MAP3K7,NT5C3A,DOCK4,EPHB6,SESN1,ABHD12,TMEM135,MRC1,TPT1,INHBB,HRH1,ADAM9,FOXO1,SEMA3C,TF,MAP3K1,FFAR3,HPN,CHD7,ANKRD1,TRIM23,NCK1,ADM,MAP1LC3A,CD180,GRK7,PTH,G3BP2,CLU,GPM6A,MEIS2,APP,SHROOM3,ABCC8,ANXA3,PTPN11,PTX3,LBP,PROS1,PTPN22,SERINC3,ADA,IFIT1,PDZD7,EDN1,JAM3,CD47,NFASC,N4BP1,SEMA5A,LPL,MX1,RAB29,RIPOR2,CCDC80,FEZ1,NPNT,PREX1,MST1R,LGMN,ROBO3,SUN1,PRKCA,TXNIP,CFI,PLXNA2,SESN2,ABCC9,INPP5F,FGFR2,RBM4B,USP53,PRKD1,F11R,PLXNB1,GABARAPL1,HSPB1,SERPINE1,C1RL,UNC5B,MAOB,IGFBP2,ATG14,PCSK1N,HIF1A,OPN3,ADGRE2,PPARGC1A,RORA,CALCOCO2,SLIT3,SMAD6,BBS4,NPTN,GP2,CDH2,ULK2,PAK3,MMP28,LGALS9,SKP2,PRKAA2,DAPK3,PLXNB3,FLNA,PLEKHG5,VAMP7,CSF1,MAP1LC3B2,CDH13,PLCG2,VCAM1,F3,ABCA4,LRSAM1,CYR61,IFI44,NEXN,VNN1,SLC8A1,TLR1,BNIP3,ADAMTS5,LOX,REG4,ZNF175,CDKN1A,MFAP4,CCR6,HOPX,GABARAPL2,ICAM1,C15orf48,STC2,PRKG1,BMP6,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:0040012	0.00	1.00	91	796	regulation of locomotion	BP	0.00755	BCL2,RNF41,CITED2,SASH1,MDM2,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,ADGRB1,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,TGFBR1,EDN2,DOCK4,TCAF1,GATA2,LRCH1,ACTN4,ADAM9,CYP1B1,SEMA3C,TF,AMOTL2,PTPRG,NCK1,ATOH8,MCTP1,CHST2,APP,PDGFC,ABCC8,ANXA3,LBP,ADA,EDN1,JAM3,CD47,SEMA5A,ADIPOR1,RIPOR2,PREX1,LGMN,PRKCA,PARD6B,PLXNA2,SHTN1,MYLK,INPP5F,PRKD1,PLXNB1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,PPARGC1A,NUMB,BBS4,MAPRE2,PAK3,MMP28,GAS2L2,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,CSF1,CDH13,PLCG2,F3,LMO4,CYR61,NEXN,SLC8A1,CD151,FGF9,CCR6,ICAM1,PIK3C2A,PRKG1,FAM83H	darkgreen	VSMC_M4

GO:0035556	0.00	1.00	195	2063	intracellular signal transduction	BP	0.00843	MBP,DOK6,BCL2,RNF41,SASH1,IRAK3,GRIP1,MDM2,SOD2,ABRA,ANGPT1,GJA1,TPD52L1,EP300,DAPK1,LEP,WFS1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,UNC13B,PPP1R9A,IL18R1,RNF149,CREB3,ZAP70,TGFBR1,EDN2,ABCA1,PTPN3,CHN2,MAP3K7,DOCK4,MDFIC,SESN1,MAP3K8,HIPK2,SNRK,TPT1,HRH1,BABAM2,RALGAPA2,LBH,NDRG2,POLB,LMCD1,ARHGEF17,PLCB4,ACTN4,ADAM9,FOXO1,RASSF2,ATP2C1,CDC42EP3,CYP1B1,PCLO,TF,FLT3,AMOTL2,MAP3K1,LATS2,HIPK3,ANKRD1,KIAA0355,NCK1,ADM,SH3RF1,MRVI1,WWC2,TEAD1,MCTP1,ARHGEF3,PTH,RNF34,G3BP2,CLU,BLNK,APP,PDGFC,PTPN11,ADCY6,HERPUD1,JMY,PTPN22,CHAC1,GDF6,SERINC3,ADA,RCAN1,NGF,EDN1,SEMA5A,ADIPOR1,RIPOR2,RGS2,KCTD10,NPNT,PREX1,PLCL1,HTR2B,MST1R,PRKCA,MID1,SESN2,SHTN1,CAMK2D,ADCY5,LRP2,CFLAR,INPP5F,FGFR2,CASTOR1,TP53BP1,PRKD1,PI4KB,F11R,PLXNB1,RAPGEF4,AKAP6,MAP3K13,HIP1,PRDX4,HSPB1,CRYAB,ATP6AP2,ARHGAP20,RDX,UNC5B,NBR1,SYNPO2L,TNFSF10,DACT1,NLGN1,MAEL,HIF1A,IQSEC3,APBB2,CACNA1C,MYZAP,GNAI1,ADGRL1,NPPB,RORA,SIPA1L1,ADRA1B,NPTN,NRK,MAPRE2,CDH2,PAK3,RHOT1,ARHGAP28,LGALS9,PATJ,NPR3,PRKAA2,DAPK3,ADCY9,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,VCAM1,TERF2IP,F3,ARHGAP29,BCAR3,CYR61,SYDE2,WLS,ITPR1,VNN1,SLC8A1,BNIP3,LOX,C10orf71,PLN,SRPK3,CDKN1A,FGF9,EDA,NCALD,NACC2,TMEM38A,CCR6,ICAM1,PIK3C2A,YAP1,PRKG1,MAFA,DDIT4	darkgreen	VSMC_M4
GO:0003008	0.00	1.00	129	1240	system process	BP	0.00843	MBP,BCL2,MDM2,SOD2,ANGPT1,GJA1,TRDN,EP300,SH3GL2,LEP,WFS1,VLDLR,UNC13B,TPM2,PPP1R9A,SLC2A1,EDN2,SVEP1,TBX18,CALD1,DOCK4,HIPK2,PPP1R13L,TENM4,INHBB,HRH1,KCNE3,LMCD1,THRB,FOXO1,TUSC3,WASF3,FFAR3,FXYD1,HPN,CHD7,CPEB3,SORBS2,ADM,SCN8A,GRK7,OCLN,MEIS2,MYL9,APP,SCARB2,ABCC8,PTPN11,ADCY6,SLC26A7,TANC1,ADA,RCAN1,NGF,PDZD7,EDN1,JAM3,NFASC,RIPOR2,PPP1R12B,RGS2,TNNT2,ACTN2,LRP5,NPNT,HTR2B,LGMN,PRKCA,ABLIM1,CAMK2D,ABCC9,ADCY5,MYLK,LRP2,CFLAR,CTSZ,INPP5F,USP53,FABP2,NCSTN,F11R,TRIM63,SLC25A12,PPEF1,ATF6,INSYN2,AKAP6,CRYGS,CRYAB,ATP6AP2,NLGN1,WDR1,HIF1A,APBB2,CACNA1C,PPARGC1A,NPPB,SGCA,MAGT1,ADRA1B,CNN1,KCNK10,KIAA0556,BBS4,NPTN,NPR3,RBFOX1,DAPK3,SCNN1D,FLNA,CCDC78,SLC2A5,ABCA4,KCNE4,ITPR1,SLC8A1,TBX20,TMPRSS11E,PLN,NCALD,TMEM38A,HOPX,ICAM1,PIK3C2A,ORMDL3,YAP1,PRKG1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0030335	0.00	1.00	57	443	positive regulation of cell migration	BP	0.00843	BCL2,SASH1,MDM2,SOD2,ANGPT1,SMOC2,DOCK8,CD274,CREB3,TGFBR1,EDN2,DOCK4,GATA2,ACTN4,ADAM9,SEMA3C,ATOH8,APP,PDGFC,ANXA3,LBP,EDN1,JAM3,CD47,SEMA5A,RIPOR2,PREX1,LGMN,PRKCA,SHTN1,MYLK,PRKD1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,NUMB,MAPRE2,PAK3,DAB2,LGALS9,DAPK3,FLNA,CSF1,CDH13,PLCG2,F3,CYR61,SLC8A1,CD151,FGF9,CCR6,ICAM1,PIK3C2A,FAM83H	darkgreen	VSMC_M4
GO:0051272	0.00	1.00	59	466	positive regulation of cellular component movement	BP	0.00843	BCL2,SASH1,MDM2,SOD2,ANGPT1,SMOC2,DOCK8,CD274,CREB3,TGFBR1,EDN2,DOCK4,GATA2,ACTN4,ADAM9,SEMA3C,TF,ATOH8,APP,PDGFC,ANXA3,LBP,EDN1,JAM3,CD47,SEMA5A,RIPOR2,FEZ1,PREX1,LGMN,PRKCA,SHTN1,MYLK,PRKD1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,NUMB,MAPRE2,PAK3,DAB2,LGALS9,DAPK3,FLNA,CSF1,CDH13,PLCG2,F3,CYR61,SLC8A1,CD151,FGF9,CCR6,ICAM1,PIK3C2A,FAM83H	darkgreen	VSMC_M4
GO:2000147	0.00	1.00	58	455	positive regulation of cell motility	BP	0.00843	BCL2,SASH1,MDM2,SOD2,ANGPT1,SMOC2,DOCK8,CD274,CREB3,TGFBR1,EDN2,DOCK4,GATA2,ACTN4,ADAM9,SEMA3C,TF,ATOH8,APP,PDGFC,ANXA3,LBP,EDN1,JAM3,CD47,SEMA5A,RIPOR2,PREX1,LGMN,PRKCA,SHTN1,MYLK,PRKD1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,NUMB,MAPRE2,PAK3,DAB2,LGALS9,DAPK3,FLNA,CSF1,CDH13,PLCG2,F3,CYR61,SLC8A1,CD151,FGF9,CCR6,ICAM1,PIK3C2A,FAM83H	darkgreen	VSMC_M4
GO:0006936	0.00	1.00	38	256	muscle contraction	BP	0.01099	GJA1,TRDN,TPM2,EDN2,CALD1,DOCK4,PPP1R13L,KCNE3,FXYD1,MYL9,ADA,EDN1,PPP1R12B,RGS2,TNNT2,ACTN2,NPNT,HTR2B,CAMK2D,MYLK,TRIM63,CRYAB,APBB2,CACNA1C,SGCA,ADRA1B,CNN1,DAPK3,FLNA,CCDC78,KCNE4,SLC8A1,TBX20,PLN,TMEM38A,PIK3C2A,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:0044057	0.00	1.00	52	398	regulation of system process	BP	0.01099	MDM2,GJA1,TRDN,LEP,UNC13B,EDN2,TBX18,DOCK4,TENM4,INHBB,HRH1,KCNE3,LMCD1,THRB,FOXO1,WASF3,FXYD1,ADM,MYL9,APP,ABCC8,PTPN11,ADA,EDN1,PPP1R12B,RGS2,TNNT2,NPNT,PRKCA,CAMK2D,ABCC9,TRIM63,SLC25A12,AKAP6,NLGN1,CACNA1C,PPARGC1A,NPPB,SGCA,ADRA1B,CNN1,DAPK3,FLNA,KCNE4,SLC8A1,PLN,TMEM38A,HOPX,ICAM1,ORMDL3,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0040017	0.00	1.00	58	462	positive regulation of locomotion	BP	0.01269	BCL2,SASH1,MDM2,SOD2,ANGPT1,SMOC2,DOCK8,CD274,CREB3,TGFBR1,EDN2,DOCK4,GATA2,ACTN4,ADAM9,SEMA3C,TF,ATOH8,APP,PDGFC,ANXA3,LBP,EDN1,JAM3,CD47,SEMA5A,RIPOR2,PREX1,LGMN,PRKCA,SHTN1,MYLK,PRKD1,ITGA6,DDR2,HSPB1,SERPINE1,RDX,HIF1A,NUMB,MAPRE2,PAK3,DAB2,LGALS9,DAPK3,FLNA,CSF1,CDH13,PLCG2,F3,CYR61,SLC8A1,CD151,FGF9,CCR6,ICAM1,PIK3C2A,FAM83H	darkgreen	VSMC_M4

GO:0008015	0.00	1.00	49	369	blood circulation	BP	0.01307	MDM2,SOD2,ANGPT1,GJA1,TRDN,SH3GL2,LEP,EDN2,TBX18,DOCK4,PPP1R13L,HRH1,KCNE3,THRB,FFAR3,FXYD1,CHD7,ADM,OCLN,ABCC8,ADCY6,ADA,EDN1,RGS2,TNNT2,LRP5,HTR2B,CAMK2D,ABCC9,CTSZ,F11R,ATP6AP2,CACNA1C,NPPB,ADRA1B,NPR3,FLNA,SLC2A5,KCNE4,SLC8A1,TBX20,PLN,NCALD,TMEM38A,HOPX,ICAM1,PIK3C2A,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0016477	0.00	1.00	118	1120	cell migration	BP	0.01307	BCL2,RNF41,CITED2,SASH1,MDM2,DDR1,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,MRTFA,ADGRB1,LEP,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,ZAP70,TGFBR1,EDN2,PEX13,DOCK4,TCAF1,GATA2,LRCH1,HRH1,ACTN4,FMNL2,ADAM9,CYP1B1,SEMA3C,AMOTL2,PTPRG,NCK1,SH3RF1,ATOH8,WWC2,MCTP1,CHST2,GPM6A,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,ADA,EDN1,JAM3,CD47,SEMA5A,ADIPOR1,RIPOR2,LRP5,PREX1,HTR2B,MST1R,LGMN,SDC3,SUN1,PRKCA,PARD6B,PLXNA2,SHTN1,MYLK,PRKD1,F11R,PLXNB1,ZRANB1,ARID5B,ITGA6,DDR2,HSPB1,SERPINE1,RDX,WDR1,HIF1A,ADGRE2,PPARGC1A,NUMB,FAT2,MAPRE2,GP2,CDH2,PAK3,MMP28,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,VCAM1,F3,LMO4,CYR61,SYDE2,NEXN,SLC8A1,CD151,LOX,TBX20,FGF9,CCR6,ICAM1,PIK3C2A,SDC2,PRKG1,FAM83H,DDIT4	darkgreen	VSMC_M4
GO:0051384	0.00	1.00	20	104	response to glucocorticoid	BP	0.01307	BCL2,REST,IGFBP7,PAPPA,ADAM9,FOXO1,FLT3,ADM,PAM,ANXA3,EDN1,CFLAR,TRIM63,MAOB,IGFBP2,SLIT3,CDKN1A,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0030198	0.00	1.00	37	250	extracellular matrix organization	BP	0.01774	COL23A1,DDR1,SMOC2,RIC1,RECK,ECM2,TGFBR1,ANTXR1,COL4A1,COL4A2,CYP1B1,APLP1,HPN,APP,RXFP1,PTX3,FMOD,COL4A4,CCDC80,NPNT,NID1,CTSS,CFLAR,QSOX1,DDR2,PRDX4,COLGALT2,P4HA1,MMP1,ANGPTL7,MMP28,CYR61,ADAMTSL2,ADAMTS5,LOX,CST3,MFAP4	darkgreen	VSMC_M4
GO:0045229	0.00	1.00	37	251	external encapsulating structure organization	BP	0.01774	COL23A1,DDR1,SMOC2,RIC1,RECK,ECM2,TGFBR1,ANTXR1,COL4A1,COL4A2,CYP1B1,APLP1,HPN,APP,RXFP1,PTX3,FMOD,COL4A4,CCDC80,NPNT,NID1,CTSS,CFLAR,QSOX1,DDR2,PRDX4,COLGALT2,P4HA1,MMP1,ANGPTL7,MMP28,CYR61,ADAMTSL2,ADAMTS5,LOX,CST3,MFAP4	darkgreen	VSMC_M4
GO:0009725	0.00	1.00	74	652	response to hormone	BP	0.01774	BCL2,CITED2,MDM2,GJA1,EP300,BRD8,LEP,KANK1,PDK4,REST,IGFBP7,SLC2A1,PAPPA,INHBB,LBH,THRB,ADAM9,FOXO1,FLT3,NCOR2,FFAR3,HPN,LATS2,NCK1,ADM,PAM,PTH,RXFP1,ABCC8,ANXA3,PTPN11,ADCY6,EDN1,LPL,ADIPOR1,NCOA3,ACTN2,ZNF106,LRP5,TXNIP,SESN2,CTSS,LRP2,CFLAR,WDTC1,TRIM63,STRN3,LRP6,RDX,MAOB,IGFBP2,TNFSF10,GNAI1,PPARGC1A,SLIT3,TGFB3,SMAD6,BBS4,DAB2,SKP2,PRKAA2,LCN8,AHCYL1,SORT1,BCAR3,LOX,PLN,CDKN1A,ICAM1,PIK3C2A,STC2,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0043062	0.00	1.00	37	251	extracellular structure organization	BP	0.01774	COL23A1,DDR1,SMOC2,RIC1,RECK,ECM2,TGFBR1,ANTXR1,COL4A1,COL4A2,CYP1B1,APLP1,HPN,APP,RXFP1,PTX3,FMOD,COL4A4,CCDC80,NPNT,NID1,CTSS,CFLAR,QSOX1,DDR2,PRDX4,COLGALT2,P4HA1,MMP1,ANGPTL7,MMP28,CYR61,ADAMTSL2,ADAMTS5,LOX,CST3,MFAP4	darkgreen	VSMC_M4
GO:0007166	0.00	1.00	181	1935	cell surface receptor signaling pathway	BP	0.01775	DOK6,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,DDR1,ANGPT1,SMOC2,SCUBE1,EP300,BRD8,ADGRB1,TLE4,GNAQ,MLLT3,LEP,CDKN2B,KANK1,RASL11B,VLDLR,UNC13B,PPP1R9A,CD274,PDK4,IL18R1,RECK,ZAP70,TGFBR1,EDN2,ABCA1,PTPN3,SVEP1,TBX18,MAP3K7,KIDINS220,MDFIC,FZD8,EPHB6,JADE1,HIPK2,GATA2,LIMS2,ITGA8,ITGA9,INHBB,NDRG2,ACTN4,ADAM9,CRIM1,FOXO1,RASSF2,COL4A1,COL4A2,CYP1B1,SEMA3C,TF,FLT3,AMOTL2,MAP3K1,FFAR3,PTPRG,LATS2,NCK1,SORBS2,CD180,SH3RF1,ATOH8,TCF7L1,RNF34,BLNK,GPR87,APP,PDGFC,PTPN11,LBP,TMEM64,PTPN22,HNF4A,CHAC1,GDF6,FMOD,ADA,NGF,EDN1,CD47,SEMA5A,MX1,RAB29,ADIPOR1,EYA2,ZNF106,LRP5,NPNT,MST1R,LGMN,GALNT3,PRKCA,AFAP1L2,TXNIP,PLXNA2,SHTN1,ADCY5,LRP2,CFLAR,INPP5F,FGFR2,PRKD1,NCSTN,PLXNB1,ZRANB1,ARID5B,ITGA6,INSYN2,DDR2,GPRC5A,LRP6,HIP1,HSPB1,SERPINE1,ATP6AP2,UNC5B,IGFBP2,TNFSF10,DACT1,LMTK2,NLGN1,HIF1A,ADGRE2,ADGRL1,NPPB,DISP3,FGFRL1,RORA,SIPA1L1,SLIT3,TGFB3,SMAD6,BBS4,NPTN,CDH2,PAK3,NOMO1,SH3TC2,FST,CRLF3,DAB2,PRKAA2,DAPK3,PLXNB3,TLE2,FLNA,CSF1,SORT1,CDH13,PLCG2,F3,GLG1,BCAR3,CYR61,WLS,MIR99A,ADAMTSL2,FRZB,LOX,CD59,TBX20,ITM2C,LYPD6,PLN,TMEM170B,FGF9,EDA,CCR6,ICAM1,PIK3C2A,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0048870	0.00	1.00	126	1234	cell motility	BP	0.01828	BCL2,RNF41,CITED2,SASH1,MDM2,DDR1,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,MRTFA,ADGRB1,LEP,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,ZAP70,TGFBR1,EDN2,PEX13,DOCK4,TCAF1,GATA2,ENKUR,LRCH1,HRH1,ACTN4,FMNL2,ADAM9,CYP1B1,SEMA3C,TF,AMOTL2,PTPRG,NCK1,SH3RF1,ATOH8,WWC2,MCTP1,CHST2,GPM6A,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,JMY,ADA,EDN1,JAM3,CD47,SEMA5A,ADIPOR1,DNAH7,RIPOR2,LRP5,PREX1,HTR2B,MST1R,LGMN,SDC3,SUN1,PRKCA,PARD6B,PLXNA2,SHTN1,MYLK,INPP5F,PRKD1,F11R,PLXNB1,ZRANB1,ARID5B,ITGA6,DDR2,HSPB1,SERPINE1,RDX,WDR1,HIF1A,ADGRE2,PPARGC1A,NUMB,BBS4,FAT2,MAPRE2,GP2,CDH2,PAK3,MMP28,GAS2L2,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,VCAM1,F3,LMO4,CYR61,SYDE2,NEXN,SLC8A1,CD151,LOX,TBX20,FGF9,DSTN,CCR6,ICAM1,PIK3C2A,SDC2,PRKG1,FAM83H,DDIT4	darkgreen	VSMC_M4

GO:0051674	0.00	1.00	126	1234	localization of cell	BP	0.01828	BCL2,RNF41,CITED2,SASH1,MDM2,DDR1,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,MRTFA,ADGRB1,LEP,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,ZAP70,TGFBR1,EDN2,PEX13,DOCK4,TCAF1,GATA2,ENKUR,LRCH1,HRH1,ACTN4,FMNL2,ADAM9,CYP1B1,SEMA3C,TF,AMOTL2,PTPRG,NCK1,SH3RF1,ATOH8,WWC2,MCTP1,CHST2,GPM6A,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,JMY,ADA,EDN1,JAM3,CD47,SEMA5A,ADIPOR1,DNAH7,RIPOR2,LRP5,PREX1,HTR2B,MST1R,LGMN,SDC3,SUN1,PRKCA,PARD6B,PLXNA2,SHTN1,MYLK,INPP5F,PRKD1,F11R,PLXNB1,ZRANB1,ARID5B,ITGA6,DDR2,HSPB1,SERPINE1,RDX,WDR1,HIF1A,ADGRE2,PPARGC1A,NUMB,BBS4,FAT2,MAPRE2,GP2,CDH2,PAK3,MMP28,GAS2L2,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,VCAM1,F3,LMO4,CYR61,SYDE2,NEXN,SLC8A1,CD151,LOX,TBX20,FGF9,DSTN,CCR6,ICAM1,PIK3C2A,SDC2,PRKG1,FAM83H,DDIT4	darkgreen	VSMC_M4
GO:0019932	0.00	1.00	33	218	second-messenger-mediated signaling	BP	0.02145	PPP1R9A,ZAP70,EDN2,HRH1,LMCD1,PCLO,ADM,MRVI1,MCTP1,ADA,RCAN1,EDN1,RGS2,HTR2B,CAMK2D,RAPGEF4,AKAP6,CACNA1C,GNAI1,ADGRL1,NPPB,CDH13,PLCG2,VCAM1,ITPR1,SLC8A1,C10orf71,PLN,NCALD,TMEM38A,CCR6,PRKG1,MAFA	darkgreen	VSMC_M4
GO:0040011	0.00	1.00	135	1349	locomotion	BP	0.02387	BCL2,RNF41,CITED2,SASH1,MDM2,DDR1,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,EP300,MRTFA,ADGRB1,LEP,LIMCH1,DDX58,DOCK8,KANK1,CD274,CREB3,RECK,ZAP70,TGFBR1,EDN2,PEX13,DOCK4,TCAF1,EPHB6,GATA2,ENKUR,LRCH1,HRH1,ACTN4,FMNL2,ADAM9,CYP1B1,SEMA3C,TF,AMOTL2,PTPRG,NCK1,SH3RF1,ATOH8,WWC2,MCTP1,CHST2,GPM6A,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,JMY,ADA,RCAN1,EDN1,JAM3,CD47,NFASC,SEMA5A,ADIPOR1,DNAH7,RIPOR2,LRP5,FEZ1,PREX1,HTR2B,MST1R,LGMN,ROBO3,SDC3,SUN1,PRKCA,PARD6B,PLXNA2,SHTN1,MYLK,INPP5F,PRKD1,F11R,PLXNB1,ZRANB1,ARID5B,ITGA6,DDR2,HSPB1,SERPINE1,RDX,UNC5B,WDR1,HIF1A,ADGRE2,PPARGC1A,NUMB,SLIT3,BBS4,NPTN,FAT2,MAPRE2,GP2,CDH2,PAK3,MMP28,GAS2L2,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,VCAM1,F3,LMO4,CYR61,SYDE2,NEXN,SLC8A1,CD151,LOX,TBX20,FGF9,DSTN,CCR6,ICAM1,PIK3C2A,SDC2,PRKG1,FAM83H,DDIT4	darkgreen	VSMC_M4
GO:0051049	0.00	1.00	125	1276	regulation of transport	BP	0.02462	BCL2,SLC35D3,MDM2,ANGPT1,C4A,GJA1,TRDN,DAPK1,SH3GL2,LEP,WFS1,UNC13B,PPP1R9A,RIC1,REST,ICA1,PREPL,SYT5,ABCA1,PTPN3,SNAP91,MDFIC,TCAF1,GATA2,INHBB,KCNE3,RAB2B,ACTN4,ADAM9,FGF14,ATP2C1,PCLO,TF,ZDHHC2,FFAR3,FXYD1,CHD7,ANKRD1,PAM,SCN8A,OCLN,MCTP1,JPH1,PTH,CLU,APP,ATXN2,ABCC8,PTPN11,PTX3,ATG13,HNF4A,ADA,EDN1,CD47,RAB29,ABCG1,KDM5B,RGS2,TNNT2,ACTN2,PFKL,LRP5,FEZ1,TM7SF3,SEC24B,MFGE8,ATP9A,ARV1,CAMK2D,ADCY5,CTSS,MYLK,INPP5F,PTPN14,PRKD1,RAPGEF4,AKAP6,HIP1,SERPINE1,ACHE,CRYAB,RDX,EXPH5,MAOB,CYP19A1,NLGN1,WDR1,HIF1A,OPN3,CACNA1C,ADGRE2,FBXL20,PPARGC1A,NPPB,DISP3,NUMB,TGFB3,KCNK10,CDH2,ABLIM3,SH3TC2,RHOT1,DNAJC6,DAB2,LGALS9,SLC43A2,FLNA,VAMP7,HCN2,AHCYL1,MBTPS1,CDH13,PLCG2,LRSAM1,WLS,KCNE4,SLC8A1,CD151,PLN,TMEM38A,SARAF,ICAM1,BMP6,SCP2	darkgreen	VSMC_M4
GO:0009966	0.00	1.00	203	2237	regulation of signal transduction	BP	0.02462	DOK6,GDF11,BCL2,RNF41,CITED2,SASH1,IRAK3,MDM2,RGS22,SOD2,ABRA,ANGPT1,SMOC2,SCUBE1,GJA1,TPD52L1,EP300,DAPK1,TLE4,GNAQ,MLLT3,LEP,CDKN2B,WFS1,PIP5K1B,DOCK8,SH3RF3,KANK1,RASL11B,UNC13B,IL18R1,RNF149,CREB3,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,ABCA1,PTPN3,TBX18,CHN2,MAP3K7,MDFIC,SESN1,JADE1,HIPK2,GATA2,LIMS2,TPT1,INHBB,RALGAPA2,LBH,NDRG2,LMCD1,ARHGEF17,ACTN4,ADAM9,CRIM1,FOXO1,RASSF2,ATP2C1,CYP1B1,APLP1,FLT3,NCOR2,FFAR3,LATS2,HIPK3,ANKRD1,NCK1,ADM,CD180,SH3RF1,GRK7,TCF7L1,WWC2,ARHGEF3,PTH,RNF34,CLU,APP,PDGFC,PTPN11,LBP,HERPUD1,TMEM64,PTPN22,CHAC1,GDF6,SERINC3,ADA,RCAN1,NGF,EDN1,CD47,SEMA5A,RAB29,ADIPOR1,RIPOR2,RGS2,EYA2,NCOA3,KCTD10,NPNT,PREX1,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,MID1,SESN2,LRP2,CFLAR,INPP5F,FGFR2,CASTOR1,PRKD1,F11R,PLXNB1,ZRANB1,STRN3,ITGA6,ATF6,AKAP6,GPRC5A,MAP3K13,HIP1,HSPB1,SERPINE1,ATP6AP2,ARHGAP20,RDX,UNC5B,MAOA,IGFBP2,NBR1,SYNPO2L,TNFSF10,DACT1,NLGN1,HIF1A,IQSEC3,GNAI1,PPARGC1A,RORA,SIPA1L1,SLIT3,TGFB3,ADRA1B,SMAD6,NPTN,NRK,MAPRE2,CDH2,PAK3,NOMO1,GAS2L2,SH3TC2,FST,CRLF3,ARHGAP28,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,TLE2,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,TERF2IP,F3,GLG1,ARHGAP29,BCAR3,CYR61,SYDE2,WLS,MIR99A,ITPR1,VNN1,ADAMTSL2,TLR1,FRZB,LOX,TBX20,ITM2C,C10orf71,LYPD6,TMEM170B,FGF9,EDA,NACC2,ICAM1,YAP1,IGFBPL1,BMP6,DDIT4	darkgreen	VSMC_M4

GO:0048731	0.00	1.00	308	3556	system development	BP	0.02681	MBP,ZNF516,GDF11,BCL2,IFNGR1,CITED2,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,CDSN,GRHL2,SOD2,ANGPT1,FAM19A5,TRPS1,SMOC2,SCUBE1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,MLLT3,LEP,CDKN2B,WFS1,KANK1,SGCB,VLDLR,C2orf40,PPP1R9A,CD274,IL18R1,REST,RECK,ZAP70,SLC2A1,TGFBR1,EDN2,PTPN3,SVEP1,TBX18,PEX13,CALD1,ANTXR1,KIDINS220,FZD8,EPHB6,GYS1,ITSN2,HIPK2,JRKL,GATA2,HS6ST1,LIMS2,ITM2B,PPP1R13L,SNRK,ITGA8,TENM4,INHBB,SMARCD3,PCDH9,PFKFB3,FOSL2,LBH,NDRG2,POLB,SALL2,THRB,ADAM9,TACC1,CRIM1,FGF14,FOXO1,TRPC4,RASSF2,COL4A1,COL4A2,ANKLE2,PCDHB4,CYP1B1,PCLO,SEMA3C,TMEM178A,TF,APLP1,FLT3,AMOTL2,WASF3,NCOR2,HPN,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,NCK1,SORBS2,ADM,PAM,SCN8A,SH3RF1,ATOH8,TEAD1,FAM172A,JPH1,PTH,KIF13B,CLU,BLNK,GPM6A,MEIS2,APP,SCARB2,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,PTPN11,PTX3,ADCY6,TMEM64,PTPN22,HNF4A,CHAC1,GDF6,NAB1,ADA,RCAN1,NGF,PDZD7,EDN1,JAM3,GPRIN3,NFASC,ETS2,SEMA5A,BACE2,RAB29,ADIPOR1,COL4A4,KDM5B,RIPOR2,MARCKSL1,RGS2,RBM20,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,MST1R,ROBO3,NID1,SUN1,PRKCA,GNB4,TXNIP,SEC24B,ABLIM1,MFGE8,PARD6B,PLXNA2,SHTN1,P4HTM,NGRN,MYLK,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,TP53BP1,PTPN14,PRKD1,NCSTN,PLXNB1,SLC25A12,RAPH1,ARID5B,ITGA6,ZNF365,ATF6,TAGLN,AKAP6,DDR2,MAP3K13,ID3,LRP6,PRDX4,LNPK,CRYGS,HSPB1,CUX1,MFAP5,SERPINE1,ACHE,CRYAB,ATP6AP2,PAPPA2,UNC5B,EXPH5,MAOB,NBR1,EZH1,SYNPO2L,CYP19A1,TNFSF10,DACT1,LMTK2,NLGN1,SPEG,WDR1,HIF1A,OPN3,ZBTB1	darkgreen	VSMC_M4
GO:0009607	0.00	1.00	87	856	response to biotic stimulus	BP	0.02741	BCL2,IFNGR1,SASH1,IRAK3,SOD2,C4A,RNASET2,GJA1,TRDN,EP300,ADGRB1,DAPK1,LEP,WFS1,DDX58,CD274,ZAP70,SLC17A5,ABCA1,MAP3K7,NT5C3A,MRC1,TPT1,ADAM9,TF,CHD7,ANKRD1,TRIM23,NCK1,ADM,CD180,G3BP2,CLU,GPM6A,ABCC8,ANXA3,PTPN11,PTX3,LBP,PTPN22,SERINC3,IFIT1,EDN1,CD47,N4BP1,MX1,RAB29,CCDC80,MST1R,PRKCA,TXNIP,CFI,ABCC9,FGFR2,PRKD1,HSPB1,SERPINE1,C1RL,MAOB,HIF1A,PPARGC1A,CALCOCO2,SMAD6,GP2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,VCAM1,LRSAM1,IFI44,VNN1,TLR1,BNIP3,ADAMTS5,REG4,ZNF175,MFAP4,ICAM1,C15orf48,YAP1,IGFBPL1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0009719	0.00	1.00	121	1202	response to endogenous stimulus	BP	0.02741	BCL2,CITED2,MDM2,SMOC2,GJA1,EP300,BRD8,SH3GL2,LEP,CDKN2B,KANK1,RASL11B,PDK4,REST,IGFBP7,SLC2A1,TGFBR1,ABCA1,MAP3K7,KIDINS220,PAPPA,SESN1,HIPK2,INHBB,HRH1,LBH,THRB,ADAM9,CRIM1,FOXO1,COL4A1,COL4A2,APLP1,FLT3,NCOR2,FFAR3,HPN,LATS2,ANKRD1,CPEB3,NCK1,ADM,PAM,PTH,APP,PDGFC,RXFP1,ABCC8,ANXA3,PTPN11,ADCY6,PTPN22,GDF6,FMOD,NGF,EDN1,LPL,ADIPOR1,KDM5B,NCOA3,ACTN2,ZNF106,LRP5,NPNT,HTR2B,LGMN,GALNT3,TXNIP,SESN2,ADCY5,CTSS,LRP2,CFLAR,WDTC1,FGFR2,CASTOR1,NCSTN,TRIM63,STRN3,AKAP6,LRP6,RDX,MAOB,IGFBP2,TNFSF10,GNAI1,PPARGC1A,FGFRL1,SLIT3,TGFB3,SMAD6,BBS4,NPTN,FST,DAB2,SKP2,PRKAA2,FLNA,LCN8,HCN2,AHCYL1,SORT1,CDH13,VCAM1,GLG1,BCAR3,CYR61,SLC8A1,ADAMTSL2,LOX,TBX20,PLN,CDKN1A,FGF9,TMEM38A,ICAM1,PIK3C2A,STC2,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:1903019	0.00	1.00	6	13	negative regulation of glycoprotein metabolic process	BP	0.02988	ITM2B,PTX3,BACE2,TMEM59,ITM2C,CST3	darkgreen	VSMC_M4
GO:0009653	0.00	1.00	194	2050	anatomical structure morphogenesis	BP	0.03118	MBP,BCL2,CITED2,SASH1,UST,GRIP1,MDM2,DDR1,CDSN,GRHL2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,EP300,MRTFA,ADGRB1,SH3GL2,MLLT3,LEP,KANK1,VLDLR,PPP1R9A,RECK,TGFBR1,LMBRD1,SVEP1,TBX18,CALD1,ANTXR1,KIDINS220,EPHB6,ITSN2,HIPK2,GATA2,LIMS2,TMEM135,PPP1R13L,ITGA8,TENM4,SMARCD3,POLB,THRB,ACTN4,FMNL2,ADAM9,FOXO1,COL4A1,COL4A2,CDC42EP3,CYP1B1,SEMA3C,APLP1,AMOTL2,WASF3,HPN,CHD7,ANKRD1,MARCH5,ADM,PAM,ATOH8,KIF13B,CLU,GPM6A,MEIS2,APP,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,PTPN11,TANC1,HNF4A,NAB1,ADA,NGF,PDZD7,EDN1,JAM3,NFASC,ETS2,SEMA5A,KDM5B,RIPOR2,EYA2,TNNT2,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,ROBO3,PRKCA,SEC24B,ABLIM1,MFGE8,PARD6B,PLXNA2,SHTN1,MYLK,LRP2,CFLAR,CTSZ,FGFR2,PTPN14,PRKD1,F11R,PLXNB1,ZRANB1,RAPH1,ARID5B,ITGA6,ZNF365,MAP3K13,ID3,LRP6,LNPK,CRYGS,HSPB1,CUX1,MFAP5,SERPINE1,CRYAB,ATP6AP2,PAPPA2,RDX,UNC5B,EZH1,SYNPO2L,DACT1,LMTK2,NLGN1,WDR1,MAEL,HIF1A,CACNA1C,PPARGC1A,ACTN1,NPPB,FGFRL1,RORA,SIPA1L1,NUMB,SLIT3,TGFB3,SMAD6,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,FST,ANGPTL4,DAB2,CDH18,MYO10,DAPK3,PLXNB3,TLE2,FLNA,CSF1,CDH13,F3,GLG1,BCAR3,LMO4,CYR61,NEXN,WLS,AFF3,CCDC136,CD151,SPINK2,BNIP3,ADAMTS5,FRZB,LOX,TBX20,CST3,CSRP1,FGF9,EDA,HOPX,ICAM1,PIK3C2A,SDC2,YAP1,MYL12B,BMP6	darkgreen	VSMC_M4
GO:0007167	0.00	1.00	84	752	enzyme linked receptor protein signaling pathway	BP	0.03168	DOK6,GDF11,CITED2,DDR1,ANGPT1,SMOC2,EP300,LEP,CDKN2B,KANK1,RASL11B,PDK4,ZAP70,TGFBR1,PTPN3,SVEP1,MAP3K7,EPHB6,HIPK2,INHBB,ADAM9,CRIM1,FOXO1,RASSF2,COL4A1,COL4A2,TF,FLT3,FFAR3,PTPRG,LATS2,NCK1,ATOH8,BLNK,PDGFC,PTPN11,HNF4A,GDF6,FMOD,NGF,ADIPOR1,ZNF106,NPNT,MST1R,LGMN,GALNT3,AFAP1L2,TXNIP,LRP2,FGFR2,PRKD1,ARID5B,DDR2,GPRC5A,HIP1,HSPB1,IGFBP2,LMTK2,HIF1A,NPPB,FGFRL1,SIPA1L1,TGFB3,SMAD6,NPTN,PAK3,NOMO1,SH3TC2,FST,DAB2,CSF1,SORT1,CDH13,F3,GLG1,BCAR3,CYR61,ADAMTSL2,LOX,TBX20,FGF9,PIK3C2A,BMP6,DDIT4	darkgreen	VSMC_M4

GO:0010033	0.00	1.00	201	2273	response to organic substance	BP	0.03617	BCL2,IFNGR1,CITED2,SASH1,IRAK3,MDM2,SOD2,ANGPT1,SMOC2,GJA1,EP300,BRD8,DAPK1,TLE4,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,DDX58,DOCK8,KANK1,RASL11B,UNC13B,CD274,PDK4,IL18R1,CREB3,REST,IGFBP7,SLC2A1,TGFBR1,EDN2,ABCA1,MAP3K7,KIDINS220,PAPPA,SESN1,HIPK2,GATA2,LRCH1,MRC1,INHBB,HRH1,LBH,STT3B,POLB,THRB,ACTN4,ADAM9,CRIM1,FOXO1,COL4A1,COL4A2,CYP1B1,APLP1,FLT3,NCOR2,FFAR3,HPN,LATS2,ANKRD1,CPEB3,NCK1,ADM,MAP1LC3A,PAM,CD180,OCLN,PTH,CLU,MEIS2,APP,PDGFC,RXFP1,ABCC8,ANXA3,PTPN11,ADCY6,LBP,HERPUD1,PTPN22,HNF4A,CHAC1,GDF6,FMOD,ADA,IFIT1,NGF,EDN1,CD47,PLA2G4F,MARCH6,LPL,MX1,ABCG1,ADIPOR1,KDM5B,RIPOR2,RGS2,NCOA3,ACTN2,ZNF106,PFKL,LRP5,FEZ1,NPNT,HTR2B,MST1R,LGMN,TM7SF3,GALNT3,PRKCA,TXNIP,SESN2,ABCC9,ADCY5,CTSS,LRP2,CFLAR,WDTC1,FGFR2,CASTOR1,PRKD1,NCSTN,TRIM63,STRN3,ARID5B,ITGA6,ATF6,AKAP6,ID3,LRP6,HSPB1,EIF4A2,SERPINE1,ACHE,CRYAB,RDX,MAOB,IGFBP2,CYP19A1,TNFSF10,JKAMP,HIF1A,GNAI1,PPARGC1A,FAF2,FGFRL1,RORA,CALCOCO2,SLIT3,TGFB3,SMAD6,EPG5,BBS4,NPTN,PAK3,HSPB3,FST,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,FLNA,LCN8,SLC2A5,HCN2,AHCYL1,CSF1,SORT1,MBTPS1,CDH13,PLCG2,VCAM1,F3,GLG1,BCAR3,CYR61,MIR99A,AFF3,SLC8A1,ADAMTSL2,TLR1,FBXO27,CD83,LOX,TBX20,PLN,CDKN1A,FGF9,TMEM38A,CCR6,ICAM1,PIK3C2A,STC2,YAP1,BMP6,MAFA,DDIT4	darkgreen	VSMC_M4
GO:0043207	0.00	1.00	83	820	response to external biotic stimulus	BP	0.03617	BCL2,IFNGR1,SASH1,IRAK3,SOD2,C4A,RNASET2,GJA1,TRDN,EP300,ADGRB1,DAPK1,LEP,DDX58,CD274,ZAP70,SLC17A5,ABCA1,MAP3K7,NT5C3A,MRC1,TPT1,ADAM9,TF,CHD7,ANKRD1,TRIM23,NCK1,ADM,CD180,G3BP2,CLU,GPM6A,ABCC8,ANXA3,PTPN11,PTX3,LBP,PTPN22,SERINC3,IFIT1,EDN1,CD47,N4BP1,MX1,RAB29,CCDC80,MST1R,PRKCA,CFI,ABCC9,FGFR2,PRKD1,HSPB1,SERPINE1,C1RL,MAOB,HIF1A,PPARGC1A,CALCOCO2,SMAD6,GP2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,VCAM1,LRSAM1,IFI44,VNN1,TLR1,BNIP3,ADAMTS5,REG4,ZNF175,MFAP4,ICAM1,C15orf48,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0051707	0.00	1.00	83	820	response to other organism	BP	0.03617	BCL2,IFNGR1,SASH1,IRAK3,SOD2,C4A,RNASET2,GJA1,TRDN,EP300,ADGRB1,DAPK1,LEP,DDX58,CD274,ZAP70,SLC17A5,ABCA1,MAP3K7,NT5C3A,MRC1,TPT1,ADAM9,TF,CHD7,ANKRD1,TRIM23,NCK1,ADM,CD180,G3BP2,CLU,GPM6A,ABCC8,ANXA3,PTPN11,PTX3,LBP,PTPN22,SERINC3,IFIT1,EDN1,CD47,N4BP1,MX1,RAB29,CCDC80,MST1R,PRKCA,CFI,ABCC9,FGFR2,PRKD1,HSPB1,SERPINE1,C1RL,MAOB,HIF1A,PPARGC1A,CALCOCO2,SMAD6,GP2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,VCAM1,LRSAM1,IFI44,VNN1,TLR1,BNIP3,ADAMTS5,REG4,ZNF175,MFAP4,ICAM1,C15orf48,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0007188	0.00	1.00	22	129	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	BP	0.03662	ADGRB1,GNAQ,ABCA1,APLP1,FFAR3,ADM,PTH,RXFP1,ADCY6,EDN1,RGS2,PRKCA,ADCY5,GABBR1,ADGRE2,GNAI1,ADGRL1,ADRA1B,NPR3,ADCY9,FLNA,PLN	darkgreen	VSMC_M4
GO:0022610	0.00	1.00	110	1050	biological adhesion	BP	0.03848	MBP,BCL2,CITED2,DDR1,CDSN,GRHL2,ANGPT1,LAMA2,ADGRB1,LEP,LIMCH1,DOCK8,KANK1,CD274,TMEM8B,ECM2,IGFBP7,ZAP70,SVEP1,ANTXR1,MAP3K8,APBB1IP,LIMS2,TESK2,ITGA8,TENM4,ITGA9,INHBB,PCDH9,LMO7,CD93,ACTN4,ADAM9,ATP2C1,PCDHB4,CYP1B1,VEZT,APLP1,ZDHHC2,FBLN7,NCK1,CHST2,ENTPD1,MYL9,APP,PTPN11,PTPN22,PKP4,ADA,JAM3,CD47,NFASC,SEMA5A,RIPOR2,CCDC80,ACTN2,FEZ1,NPNT,PREX1,ROBO3,NID1,PRKCA,MFGE8,PLXNA2,F11R,PLXNB1,SNED1,ITGA6,DDR2,LRP6,HSPB1,COL26A1,SERPINE1,ACHE,RDX,IGFBP2,AOC3,NLGN1,ADGRE2,ADGRL1,ACTN1,FGFRL1,SMAD6,NPTN,FAT2,CDH2,LGALS9,CDH18,MYO10,DAPK3,PLXNB3,FLNA,CSF1,CDH13,VCAM1,CYR61,NEXN,VNN1,PCDHGA1,CD151,FAT3,PCDHB2,CD83,CSRP1,EDA,MFAP4,ICAM1,PRKG1,BMP6,PLEKHA2	darkgreen	VSMC_M4
GO:1902531	0.00	1.00	127	1309	regulation of intracellular signal transduction	BP	0.03848	DOK6,BCL2,RNF41,SASH1,IRAK3,MDM2,SOD2,ABRA,ANGPT1,GJA1,TPD52L1,EP300,LEP,WFS1,PIP5K1B,DOCK8,SH3RF3,KANK1,IL18R1,RNF149,CREB3,ZAP70,TGFBR1,ABCA1,CHN2,MAP3K7,MDFIC,SESN1,HIPK2,TPT1,RALGAPA2,LBH,NDRG2,LMCD1,ARHGEF17,ACTN4,ADAM9,FOXO1,RASSF2,ATP2C1,FLT3,HIPK3,ANKRD1,NCK1,SH3RF1,WWC2,ARHGEF3,RNF34,CLU,APP,PDGFC,PTPN11,HERPUD1,PTPN22,GDF6,SERINC3,ADA,RCAN1,NGF,EDN1,SEMA5A,ADIPOR1,RIPOR2,RGS2,KCTD10,NPNT,PREX1,HTR2B,MST1R,PRKCA,MID1,SESN2,LRP2,CFLAR,INPP5F,FGFR2,CASTOR1,PRKD1,F11R,PLXNB1,AKAP6,MAP3K13,HIP1,HSPB1,ATP6AP2,ARHGAP20,RDX,UNC5B,NBR1,SYNPO2L,TNFSF10,DACT1,NLGN1,HIF1A,IQSEC3,GNAI1,RORA,SIPA1L1,ADRA1B,NPTN,NRK,MAPRE2,CDH2,PAK3,ARHGAP28,LGALS9,PRKAA2,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,TERF2IP,F3,ARHGAP29,BCAR3,CYR61,SYDE2,WLS,ITPR1,VNN1,C10orf71,FGF9,EDA,NACC2,ICAM1,DDIT4	darkgreen	VSMC_M4
GO:0031960	0.00	1.00	20	117	response to corticosteroid	BP	0.03848	BCL2,REST,IGFBP7,PAPPA,ADAM9,FOXO1,FLT3,ADM,PAM,ANXA3,EDN1,CFLAR,TRIM63,MAOB,IGFBP2,SLIT3,CDKN1A,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4

GO:0006874	0.00	1.00	38	283	cellular calcium ion homeostasis	BP	0.03848	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,RIC3,CHD7,MICU2,ADM,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,AKAP6,LRP6,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2	darkgreen	VSMC_M4
GO:0051239	0.00	1.00	177	1937	regulation of multicellular organismal process	BP	0.04019	MBP,ZNF516,BCL2,IFNGR1,CITED2,SASH1,IRAK3,MDM2,LAPTM4B,GRHL2,ANGPT1,FAM19A5,TRPS1,SMOC2,GJA1,TRDN,LAMA2,ADGRB1,LEP,DDX58,UNC13B,CD274,PDK4,IL18R1,REST,RECK,ZAP70,TGFBR1,EDN2,ABCA1,TBX18,MAP3K7,DOCK4,HIPK2,GATA2,TENM4,INHBB,SMARCD3,HRH1,LBH,NDRG2,KCNE3,LMCD1,THRB,ADAM9,FOXO1,RASSF2,COL4A2,CYP1B1,SEMA3C,TMEM178A,TF,WASF3,FFAR3,FXYD1,HPN,PTPRG,CHD7,LATS2,ADM,SH3RF1,ATOH8,WWC2,PTH,CLU,MEIS2,MYL9,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,PROS1,TMEM64,PTPN22,HNF4A,GDF6,ADA,NGF,EDN1,CD47,N4BP1,SEMA5A,LPL,ADIPOR1,KDM5B,PPP1R12B,RGS2,TNNT2,NCOA3,NPNT,PLCL1,HTR2B,LGMN,PRKCA,AFAP1L2,PLXNA2,SHTN1,P4HTM,CAMK2D,ABCC9,LRP2,FGFR2,TP53BP1,PRKD1,F11R,TRIM63,PLXNB1,SLC25A12,ZNF365,AKAP6,DDR2,MAP3K13,PRDX4,LNPK,HSPB1,CUX1,SERPINE1,ACHE,ATP6AP2,NBR1,NLGN1,MAEL,HIF1A,CACNA1C,PPARGC1A,NPPB,ANGPTL7,RORA,NUMB,SGCA,TGFB3,ADRA1B,CNN1,SMAD6,FAXDC2,NPTN,MAPRE2,ULK2,PAK3,FST,ANGPTL4,DAB2,LGALS9,NPR3,DAPK3,PLXNB3,FLNA,VAMP7,CSF1,PLCG2,F3,GLG1,CYR61,KCNE4,VNN1,SLC8A1,TLR1,ADAMTS5,FRZB,CD83,LOX,TBX20,LRRC24,CST3,PLN,MAFF,TMEM38A,CCR6,HOPX,ICAM1,PIK3C2A,ORMDL3,YAP1,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0090257	0.00	1.00	27	179	regulation of muscle system process	BP	0.04019	EDN2,DOCK4,LMCD1,FOXO1,MYL9,ABCC8,ADA,EDN1,PPP1R12B,RGS2,TNNT2,NPNT,PRKCA,CAMK2D,TRIM63,AKAP6,CACNA1C,PPARGC1A,SGCA,ADRA1B,CNN1,DAPK3,SLC8A1,PLN,TMEM38A,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:0035150	0.00	1.00	18	100	regulation of tube size	BP	0.04019	SOD2,GJA1,LEP,EDN2,DOCK4,HRH1,ADM,ADCY6,EDN1,RGS2,HTR2B,NPPB,ADRA1B,NPR3,SLC8A1,ICAM1,PIK3C2A,PRKG1	darkgreen	VSMC_M4
GO:0035296	0.00	1.00	18	100	regulation of tube diameter	BP	0.04019	SOD2,GJA1,LEP,EDN2,DOCK4,HRH1,ADM,ADCY6,EDN1,RGS2,HTR2B,NPPB,ADRA1B,NPR3,SLC8A1,ICAM1,PIK3C2A,PRKG1	darkgreen	VSMC_M4
GO:0097746	0.00	1.00	18	100	blood vessel diameter maintenance	BP	0.04019	SOD2,GJA1,LEP,EDN2,DOCK4,HRH1,ADM,ADCY6,EDN1,RGS2,HTR2B,NPPB,ADRA1B,NPR3,SLC8A1,ICAM1,PIK3C2A,PRKG1	darkgreen	VSMC_M4
GO:0007155	0.00	1.00	109	1044	cell adhesion	BP	0.04019	MBP,BCL2,CITED2,DDR1,CDSN,GRHL2,ANGPT1,LAMA2,ADGRB1,LEP,LIMCH1,DOCK8,KANK1,CD274,TMEM8B,ECM2,IGFBP7,ZAP70,SVEP1,ANTXR1,MAP3K8,APBB1IP,LIMS2,TESK2,ITGA8,TENM4,ITGA9,PCDH9,LMO7,CD93,ACTN4,ADAM9,ATP2C1,PCDHB4,CYP1B1,VEZT,APLP1,ZDHHC2,FBLN7,NCK1,CHST2,ENTPD1,MYL9,APP,PTPN11,PTPN22,PKP4,ADA,JAM3,CD47,NFASC,SEMA5A,RIPOR2,CCDC80,ACTN2,FEZ1,NPNT,PREX1,ROBO3,NID1,PRKCA,MFGE8,PLXNA2,F11R,PLXNB1,SNED1,ITGA6,DDR2,LRP6,HSPB1,COL26A1,SERPINE1,ACHE,RDX,IGFBP2,AOC3,NLGN1,ADGRE2,ADGRL1,ACTN1,FGFRL1,SMAD6,NPTN,FAT2,CDH2,LGALS9,CDH18,MYO10,DAPK3,PLXNB3,FLNA,CSF1,CDH13,VCAM1,CYR61,NEXN,VNN1,PCDHGA1,CD151,FAT3,PCDHB2,CD83,CSRP1,EDA,MFAP4,ICAM1,PRKG1,BMP6,PLEKHA2	darkgreen	VSMC_M4
GO:0048583	0.00	1.00	244	2834	regulation of response to stimulus	BP	0.04019	DOK6,GDF11,BCL2,RNF41,CITED2,SASH1,IRAK3,MDM2,RGS22,SOD2,OXR1,ABRA,ANGPT1,C4A,FAM19A5,SMOC2,SCUBE1,GJA1,TPD52L1,EP300,DAPK1,TLE4,GNAQ,MLLT3,LEP,CDKN2B,WFS1,DDX58,PIP5K1B,DOCK8,SH3RF3,KANK1,RASL11B,UNC13B,CD274,IL18R1,RNF149,CREB3,REST,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,EDN2,ABCA1,PTPN3,TBX18,CHN2,MAP3K7,MDFIC,SESN1,JADE1,HIPK2,GATA2,LIMS2,ABHD12,TPT1,INHBB,BABAM2,RALGAPA2,LBH,NDRG2,LMCD1,ARHGEF17,ACTN4,ADAM9,CRIM1,FOXO1,RASSF2,ATP2C1,CYP1B1,SEMA3C,APLP1,FLT3,MAP3K1,NCOR2,FFAR3,LATS2,HIPK3,ANKRD1,NCK1,ADM,CD180,SH3RF1,GRK7,OCLN,TCF7L1,WWC2,MCTP1,ARHGEF3,PTH,RNF34,CLU,BLNK,APP,PDGFC,ABCC8,PTPN11,LBP,NEK4,HERPUD1,PROS1,TMEM64,PTPN22,CHAC1,GDF6,SERINC3,ADA,RCAN1,IFIT1,NGF,EDN1,JAM3,CD47,N4BP1,SEMA5A,LPL,RAB29,ADIPOR1,RIPOR2,RGS2,EYA2,NCOA3,KCTD10,NPNT,PREX1,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,CFI,MID1,SESN2,CAMK2D,CTSS,MYLK,LRP2,CFLAR,INPP5F,FGFR2,CASTOR1,TP53BP1,PRKD1,F11R,TRIM63,PLXNB1,ZRANB1,STRN3,ITGA6,ZNF365,ATF6,AKAP6,GPRC5A,MAP3K13,HIP1,HSPB1,SERPINE1,C1RL,ATP6AP2,ARHGAP20,RDX,UNC5B,MAOA,IGFBP2,NBR1,SYNPO2L,TNFSF10,DACT1,NLGN1,HIF1A,IQSEC3,ADGRE2,GNAI1,PPARGC1A,RORA,SIPA1L1,SGCA,SLIT3,TGFB3,ADRA1B,SMAD6,EPG5,BBS4,NPTN,NRK,MAPRE2,CDH2,PAK3,NOMO1,MMP28,GAS2L2,SH3TC2,FST,CRLF3,ARHGAP28,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,TLE2,FLNA,PLEKHG5,VAMP7,CSF1,CDH13,PLCG2,TERF2IP,F3,GLG1,ARHGAP29,BCAR3,LRSAM1,CYR61,SYDE2,WLS,MIR99A,ITPR1,VNN1,ADAMTSL2,TLR1,FRZB,LOX,CD58,TBX20,ITM2C,S1C,ST1,LYPD6,T	darkgreen	VSMC_M4
GO:0003013	0.00	1.00	53	437	circulatory system process	BP	0.04019	MDM2,SOD2,ANGPT1,GJA1,TRDN,SH3GL2,LEP,SLC2A1,EDN2,SVEP1,TBX18,DOCK4,PPP1R13L,HRH1,KCNE3,THRB,FFAR3,FXYD1,CHD7,ADM,OCLN,ABCC8,ADCY6,ADA,EDN1,RGS2,TNNT2,LRP5,HTR2B,CAMK2D,ABCC9,LRP2,CTSZ,F11R,ATP6AP2,CACNA1C,NPPB,ADRA1B,NPR3,FLNA,SLC2A5,KCNE4,SLC8A1,TBX20,PLN,NCALD,TMEM38A,HOPX,ICAM1,PIK3C2A,YAP1,PRKG1,BMP6	darkgreen	VSMC_M4

GO:0033993	0.00	1.00	71	657	response to lipid	BP	0.04019	BCL2,SASH1,IRAK3,MDM2,SOD2,GJA1,EP300,LEP,CD274,PDK4,REST,IGFBP7,TGFBR1,ABCA1,PAPPA,GATA2,MRC1,LBH,ADAM9,FOXO1,FLT3,NCOR2,FFAR3,ANKRD1,ADM,PAM,CD180,PTH,CLU,ABCC8,ANXA3,ADCY6,LBP,PTPN22,EDN1,LPL,ABCG1,NCOA3,PRKCA,TXNIP,ADCY5,CFLAR,FGFR2,TRIM63,STRN3,ID3,LRP6,SERPINE1,CRYAB,MAOB,IGFBP2,CYP19A1,GNAI1,PPARGC1A,RORA,SLIT3,TGFB3,SMAD6,DAB2,LGALS9,SKP2,PLCG2,VCAM1,LOX,PLN,CDKN1A,ICAM1,STC2,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0065009	0.00	1.00	203	2307	regulation of molecular function	BP	0.04521	MBP,BCL2,SASH1,IRAK3,MDM2,DDR1,GRHL2,ABRA,ANGPT1,C4A,GJA1,TRDN,TPD52L1,EP300,DAPK1,GNAQ,LEP,CDKN2B,WFS1,DDX58,FAM122A,DOCK8,DCUN1D4,VLDLR,TPM2,PPP1R9A,RIC1,IL18R1,REST,RECK,SNX13,TGFBR1,EDN2,PTPN3,CHN2,MAP3K7,ANTXR1,DOCK4,KIDINS220,TCAF1,EPHB6,ITSN2,HIPK2,RCBTB2,LRCH1,SMARCD3,USP6NL,ITIH5,RALGAPA2,KCNE3,ARHGEF17,ACTN4,ADAM9,CRIM1,FGF14,RASSF2,ANKLE2,CYP1B1,FLT3,FXYD1,DENND5A,LATS2,HIPK3,TRIM23,NCK1,SH3RF1,ARHGEF3,JPH1,PTH,RNF34,G3BP2,CLU,GPR87,APP,SCARB2,PDGFC,RXFP1,ABCC8,ANXA3,PTX3,CCNT1,HERPUD1,PROS1,TMEM64,JMY,PTPN22,PKP4,AKTIP,RCAN1,IFIT1,RBL2,NGF,EDN1,RIPOR2,PPP1R12B,RGS2,TNNT2,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,SERINC2,AFAP1L2,TXNIP,PLXNA2,SESN2,CAMK2D,CTSS,CFLAR,CTSZ,WDTC1,FGFR2,TP53BP1,PRKD1,NCSTN,F11R,PLXNB1,ARID5B,ITGA6,RAPGEF4,AKAP6,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,HSPB1,EIF4A2,SERPINE1,CRYAB,ARHGAP20,RDX,AOC3,ATG14,TNFSF10,DACT1,LMTK2,NLGN1,RABEP1,PCSK1N,HIF1A,IQSEC3,CCPG1,PPP1R36,CACNA1C,PPARGC1A,FAF2,SIPA1L1,MAT2B,CCNG1,TOM1L1,MAPRE2,EVI5L,ANGPTL4,ARHGAP28,DAB2,LGALS9,OCRL,NPR3,FAM122C,PLXNB3,FLNA,PLEKHG5,AHCYL1,CSF1,SORT1,PPP1R26,PLCG2,TBC1D13,TERF2IP,F3,ARHGAP29,BCAR3,LMO4,CYR61,SYDE2,ZFP90,KCNE4,SLC8A1,DNAJA2,SPINK2,LOX,CST3,XIRP1,LYPD6,PLN,CDKN1A,EDA,PPM1E,RFK,CNTD2,HOPX,GABARAPL2,ICAM1,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:0032501	0.00	1.00	407	5003	multicellular organismal process	BP	0.0457	MBP,ZNF516,GDF11,BCL2,SLC35D3,IFNGR1,CITED2,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,CDSN,GRHL2,SOD2,OXR1,ANGPT1,FAM19A5,TRPS1,SMOC2,SCUBE1,AFF4,GJA1,TRDN,LAMA2,EP300,ADGRB1,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,DDX58,KANK1,SGCB,VLDLR,UNC13B,SPATA6L,TPM2,C2orf40,PPP1R9A,CD274,PDK4,IL18R1,REST,RECK,IGFBP7,ZAP70,SLC2A1,TGFBR1,LMBRD1,EDN2,ABCA1,PTPN3,SVEP1,TBX18,PEX13,MAP3K7,CALD1,ANTXR1,DOCK4,KIDINS220,PAPPA,FZD8,EPHB6,GYS1,ITSN2,HIPK2,JRKL,GATA2,HS6ST1,ENKUR,LIMS2,ABHD12,ITM2B,PPP1R13L,SNRK,TPT1,TESK2,ITGA8,TENM4,INHBB,SMARCD3,PCDH9,HRH1,PFKFB3,FOSL2,LBH,NDRG2,KCNE3,POLB,LMCD1,SALL2,THRB,ADAM9,TACC1,CRIM1,FGF14,FOXO1,TRPC4,RASSF2,COL4A1,COL4A2,ANKLE2,PCDHB4,CYP1B1,PCLO,SEMA3C,GTSF1,TMEM178A,TF,APLP1,FLT3,AMOTL2,TUSC3,WASF3,NCOR2,FFAR3,FXYD1,HPN,PTPRG,DENND5A,CHD7,LATS2,ANKRD1,CPEB3,NCK1,SORBS2,ADM,PAM,SCN8A,SH3RF1,ATOH8,CLCN3,GRK7,OCLN,WWC2,TEAD1,CHST2,FAM172A,JPH1,PTH,KIF13B,CLU,ENTPD1,BLNK,GPM6A,MEIS2,MYL9,APP,SCARB2,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,PTPN11,PTX3,ADCY6,LBP,PROS1,TMEM64,SLC26A7,PTPN22,TANC1,HNF4A,CHAC1,GDF6,NAB1,ADA,RCAN1,NGF,PDZD7,EDN1,JAM3,GPRIN3,CD47,NFASC,ETS2,N4BP1,SEMA5A,BACE2,LPL,RAB29,ABCG1,ADIPOR1,COL4A4,KDM5B,RIPOR2,PPP1R12B,MARCKSL1,RGS2,EYA2,RBM20,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,ROBO3,NID1,SUN1,PRKCA,GNB4,AFAP1L2,TXNIP,SEC24B,ABLIM1,MFGE8,PARD6B,MID1,PLXNA2,SHTN1,P4HTM,CAMK2D,AB	darkgreen	VSMC_M4
GO:0061061	0.00	1.00	58	504	muscle structure development	BP	0.04813	BCL2,CITED2,MDM2,SOD2,LAMA2,EP300,MRTFA,ADGRB1,SGCB,REST,TGFBR1,TBX18,SMARCD3,ACTN4,CHD7,ANKRD1,SORBS2,ADM,JPH1,TANC1,RCAN1,EDN1,RIPOR2,RGS2,TNNT2,ACTN2,NPNT,MYLK,LRP2,CFLAR,FGFR2,ARID5B,TAGLN,AKAP6,ID3,CRYAB,SYNPO2L,SPEG,WDR1,ZBTB18,ACTN1,FGFRL1,RORA,SGCA,CDH2,RBFOX1,SORT1,SLC8A1,ADAMTS5,LOX,TBX20,PDLIM3,CSRP1,SRPK3,MAFF,FGF9,HLF,HOPX	darkgreen	VSMC_M4
GO:0055074	0.00	1.00	38	291	calcium ion homeostasis	BP	0.05091	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,RIC3,CHD7,MICU2,ADM,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,AKAP6,LRP6,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2	darkgreen	VSMC_M4
GO:0006915	0.00	1.00	131	1436	apoptotic process	BP	0.05091	BCL2,RNF41,CITED2,MDM2,SOD2,OXR1,ANGPT1,GJA1,TPD52L1,EP300,DAPK1,LEP,WFS1,DOCK8,SH3RF3,UNC13B,CD274,PDK4,CREB3,REST,TGFBR1,MAP3K7,JADE1,HIPK2,GATA2,LIMS2,PPP1R13L,TPT1,NAA16,INHBB,EXOG,BABAM2,POLB,THRB,ACTN4,FOXO1,RASSF2,ANKLE2,CYP1B1,APLP1,FLT3,HPN,LATS2,HIPK3,ANKRD1,NCK1,ADM,SLC25A4,SH3RF1,PTH,RNF34,CLU,APP,HERPUD1,JMY,CHAC1,GDF6,SERINC3,ADA,AKTIP,NGF,EDN1,SEMA5A,MX1,EYA2,ACTN2,LRP5,HTR2B,LGMN,ZMAT3,PRKCA,TXNIP,CAMK2D,LRP2,CFLAR,CTSZ,FGFR2,USP53,PRKD1,NCSTN,ITGA6,ATF6,ID3,LRP6,HIP1,HSPB1,SERPINE1,CRYAB,PDE1A,UNC5B,GULP1,TNFSF10,RABEP1,MAEL,HIF1A,OPN3,DDX41,PPARGC1A,ACTN1,TEX11,SLIT3,TGFB3,SMAD6,PAK3,RHOT1,ANGPTL4,DAB2,LGALS9,SKP2,TM2D1,PRKAA2,ATCAY,DAPK3,FLNA,AHCYL1,SORT1,CYR61,ITPR1,VNN1,BNIP3,FRZB,LOX,ITM2C,CDKN1A,RASSF3,RFK,NACC2,ICAM1,ORMDL3,YAP1,DDIT4	darkgreen	VSMC_M4

GO:0012501	0.00	1.00	134	1474	programmed cell death	BP	0.05091	BCL2,RNF41,CITED2,MDM2,CDSN,SOD2,OXR1,ANGPT1,GJA1,TPD52L1,EP300,DAPK1,LEP,WFS1,DOCK8,SH3RF3,UNC13B,CD274,PDK4,CREB3,REST,TGFBR1,MAP3K7,JADE1,HIPK2,GATA2,LIMS2,PPP1R13L,TPT1,NAA16,INHBB,EXOG,BABAM2,POLB,THRB,ACTN4,FOXO1,RASSF2,ANKLE2,CYP1B1,APLP1,FLT3,HPN,LATS2,HIPK3,ANKRD1,NCK1,ADM,SLC25A4,SH3RF1,PTH,RNF34,CLU,APP,HERPUD1,JMY,CHAC1,GDF6,SERINC3,ADA,AKTIP,NGF,EDN1,SEMA5A,MX1,EYA2,ACTN2,LRP5,HTR2B,LGMN,ZMAT3,TM7SF3,PRKCA,TXNIP,CAMK2D,LRP2,CFLAR,CTSZ,FGFR2,USP53,PRKD1,NCSTN,ITGA6,ATF6,ID3,LRP6,HIP1,HSPB1,SERPINE1,CRYAB,PDE1A,UNC5B,GULP1,TNFSF10,RABEP1,MAEL,HIF1A,OPN3,DDX41,PPARGC1A,ACTN1,TEX11,SLIT3,TGFB3,SMAD6,PAK3,RHOT1,ANGPTL4,DAB2,LGALS9,SKP2,TM2D1,PRKAA2,ATCAY,DAPK3,FLNA,AHCYL1,SORT1,PLCG2,CYR61,ITPR1,VNN1,BNIP3,FRZB,LOX,ITM2C,CDKN1A,RASSF3,RFK,NACC2,ICAM1,ORMDL3,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0050850	0.00	1.00	7	20	positive regulation of calcium-mediated signaling	BP	0.05091	ZAP70,LMCD1,ADA,AKAP6,CDH13,PLCG2,C10orf71	darkgreen	VSMC_M4
GO:1903522	0.00	1.00	27	179	regulation of blood circulation	BP	0.05091	MDM2,GJA1,TRDN,LEP,EDN2,TBX18,DOCK4,HRH1,KCNE3,THRB,FXYD1,ADM,ADA,EDN1,RGS2,TNNT2,CAMK2D,ABCC9,CACNA1C,ADRA1B,FLNA,KCNE4,SLC8A1,PLN,TMEM38A,HOPX,ICAM1	darkgreen	VSMC_M4
GO:0006928	0.00	1.00	150	1565	movement of cell or subcellular component	BP	0.05091	BCL2,RNF41,CITED2,SASH1,MDM2,DDR1,SOD2,ANGPT1,FAM19A5,SMOC2,GJA1,LAMA2,MRTFA,ADGRB1,LEP,LIMCH1,DDX58,DOCK8,KANK1,CD274,DYNC1I1,CREB3,RECK,ZAP70,TGFBR1,EDN2,PEX13,DOCK4,TCAF1,EPHB6,GATA2,ENKUR,LRCH1,HRH1,KCNE3,ACTN4,FMNL2,ADAM9,CYP1B1,SEMA3C,DNHD1,TF,AMOTL2,PTPRG,NCK1,SH3RF1,ATOH8,WWC2,MCTP1,CHST2,KIF13B,GPM6A,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,JMY,ADA,EDN1,JAM3,CD47,NFASC,MYO1B,SEMA5A,ADIPOR1,DNAH7,RIPOR2,TNNT2,LRP5,FEZ1,PREX1,HTR2B,MST1R,LGMN,ROBO3,SDC3,SUN1,PRKCA,PARD6B,PLXNA2,SHTN1,CAMK2D,MYLK,INPP5F,PRKD1,F11R,PLXNB1,DYNC1I2,ZRANB1,ARID5B,ITGA6,AP3B2,DDR2,HSPB1,SERPINE1,RDX,UNC5B,WDR1,HIF1A,CACNA1C,ADGRE2,PPARGC1A,ACTN1,NUMB,SLIT3,IFT43,KIAA0556,BBS4,NPTN,FAT2,MAPRE2,GP2,CDH2,PAK3,MMP28,GAS2L2,RHOT1,DAB2,LGALS9,DAPK3,PLXNB3,FLNA,PLEKHG5,VAMP7,CSF1,CDH13,PLCG2,VCAM1,F3,LMO4,CYR61,SYDE2,NEXN,KCNE4,SLC8A1,CD151,LOX,TBX20,PLN,FGF9,DSTN,CCR6,ICAM1,PIK3C2A,SDC2,PRKG1,FAM83H,DDIT4	darkgreen	VSMC_M4
GO:0048584	0.00	1.00	137	1488	positive regulation of response to stimulus	BP	0.05091	DOK6,GDF11,BCL2,CITED2,SASH1,ABRA,ANGPT1,C4A,SMOC2,SCUBE1,GJA1,TPD52L1,EP300,MLLT3,LEP,CDKN2B,DDX58,SH3RF3,KANK1,CD274,IL18R1,CREB3,RECK,ZAP70,TGFBR1,EDN2,MAP3K7,HIPK2,GATA2,LIMS2,INHBB,BABAM2,LMCD1,ACTN4,ADAM9,RASSF2,ATP2C1,CYP1B1,FLT3,FFAR3,ANKRD1,NCK1,CD180,SH3RF1,OCLN,ARHGEF3,PTH,CLU,BLNK,APP,PDGFC,PTPN11,LBP,HERPUD1,PTPN22,GDF6,SERINC3,ADA,NGF,EDN1,CD47,SEMA5A,LPL,RAB29,ADIPOR1,RIPOR2,EYA2,NPNT,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,CFI,MID1,MYLK,LRP2,CFLAR,FGFR2,TP53BP1,PRKD1,F11R,PLXNB1,ZRANB1,ATF6,AKAP6,MAP3K13,HIP1,HSPB1,SERPINE1,C1RL,ATP6AP2,UNC5B,MAOA,SYNPO2L,TNFSF10,DACT1,NLGN1,HIF1A,TGFB3,ADRA1B,NPTN,MAPRE2,CDH2,PAK3,GAS2L2,CRLF3,DAB2,LGALS9,SKP2,DAPK3,FLNA,PLEKHG5,VAMP7,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,LRSAM1,CYR61,WLS,TLR1,CD59,TBX20,ITM2C,C10orf71,LYPD6,FGF9,EDA,MFAP4,NACC2,CCR6,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:0010880	0.00	1.00	8	24	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	0.05195	TRDN,CHD7,CAMK2D,AKAP6,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0031666	0.00	1.00	4	6	positive regulation of lipopolysaccharide-mediated signaling pathway	BP	0.05195	SASH1,CD180,PRKCA,BMP6	darkgreen	VSMC_M4
GO:0048856	0.00	1.00	349	4193	anatomical structure development	BP	0.05505	MBP,ZNF516,GDF11,BCL2,IFNGR1,CITED2,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,CDSN,GRHL2,SOD2,ANGPT1,FAM19A5,TRPS1,SMOC2,SCUBE1,AFF4,GJA1,LAMA2,EP300,MRTFA,ADGRB1,SH3GL2,MLLT3,LEP,CDKN2B,WFS1,KANK1,SGCB,VLDLR,C2orf40,PPP1R9A,CD274,RIC1,IL18R1,REST,RECK,IGFBP7,ZAP70,SLC2A1,TGFBR1,LMBRD1,EDN2,PTPN3,SVEP1,TBX18,PEX13,CALD1,ANTXR1,KIDINS220,FZD8,EPHB6,GYS1,ITSN2,HIPK2,JRKL,GATA2,HS6ST1,ENKUR,LIMS2,TMEM135,ITM2B,PPP1R13L,SNRK,TPT1,ITGA8,TENM4,INHBB,SMARCD3,PCDH9,PFKFB3,FOSL2,LBH,NDRG2,POLB,SALL2,THRB,ACTN4,FMNL2,ADAM9,TACC1,CRIM1,FGF14,FOXO1,TRPC4,RASSF2,ATP2C1,COL4A1,COL4A2,ANKLE2,PCDHB4,CDC42EP3,CYP1B1,PCLO,SEMA3C,TMEM178A,TF,APLP1,FLT3,AMOTL2,WASF3,NCOR2,HPN,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,MARCH5,NCK1,SORBS2,ADM,PAM,SCN8A,SH3RF1,ATOH8,TEAD1,CHST2,FAM172A,JPH1,PTH,KIF13B,CLU,BLNK,GPM6A,MEIS2,APP,SCARB2,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,PTPN11,PTX3,ADCY6,TMEM64,PTPN22,TANC1,HNF4A,CHAC1,GDF6,CPQ,NAB1,ADA,RCAN1,NGF,PDZD7,EDN1,JAM3,GPRIN3,NFASC,ETS2,SEMA5A,BACE2,RAB29,ADIPOR1,COL4A4,KDM5B,RIPOR2,MARCKSL1,RGS2,EYA2,RBM20,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,MST1R,ROBO3,NID1,SUN1,PRKCA,GNB4,TXNIP,SEC24B,ABLIM1,MFGE8,PARD6B,MID1,PLXNA2,SHTN1,P4HTM,NGRN,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,TP53BP1,PTPN14,PRKD1,NCSTN,F11R,PLXNB1,ZRANB1,SLC25A12,RAPH1,ARID5B,ITGA6,ZNF365,ATF6,TAGLN,AKAP6,DDR2,MAP3K13,ID3,LRP6,PRDX4,LNPK,CRYGS,HSPB1,CUX1,MFAP5,	darkgreen	VSMC_M4

GO:0007275	0.00	1.00	322	3815	multicellular organism development	BP	0.05505	MBP,ZNF516,GDF11,BCL2,IFNGR1,CITED2,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,CDSN,GRHL2,SOD2,ANGPT1,FAM19A5,TRPS1,SMOC2,SCUBE1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,MLLT3,LEP,CDKN2B,WFS1,KANK1,SGCB,VLDLR,C2orf40,PPP1R9A,CD274,IL18R1,REST,RECK,IGFBP7,ZAP70,SLC2A1,TGFBR1,LMBRD1,EDN2,PTPN3,SVEP1,TBX18,PEX13,CALD1,ANTXR1,KIDINS220,FZD8,EPHB6,GYS1,ITSN2,HIPK2,JRKL,GATA2,HS6ST1,ENKUR,LIMS2,ITM2B,PPP1R13L,SNRK,ITGA8,TENM4,INHBB,SMARCD3,PCDH9,PFKFB3,FOSL2,LBH,NDRG2,POLB,SALL2,THRB,ADAM9,TACC1,CRIM1,FGF14,FOXO1,TRPC4,RASSF2,COL4A1,COL4A2,ANKLE2,PCDHB4,CYP1B1,PCLO,SEMA3C,TMEM178A,TF,APLP1,FLT3,AMOTL2,WASF3,NCOR2,HPN,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,NCK1,SORBS2,ADM,PAM,SCN8A,SH3RF1,ATOH8,TEAD1,CHST2,FAM172A,JPH1,PTH,KIF13B,CLU,BLNK,GPM6A,MEIS2,APP,SCARB2,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,PTPN11,PTX3,ADCY6,TMEM64,PTPN22,HNF4A,CHAC1,GDF6,NAB1,ADA,RCAN1,NGF,PDZD7,EDN1,JAM3,GPRIN3,NFASC,ETS2,SEMA5A,BACE2,RAB29,ADIPOR1,COL4A4,KDM5B,RIPOR2,MARCKSL1,RGS2,EYA2,RBM20,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,MST1R,ROBO3,NID1,SUN1,PRKCA,GNB4,TXNIP,SEC24B,ABLIM1,MFGE8,PARD6B,MID1,PLXNA2,SHTN1,P4HTM,NGRN,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,TP53BP1,PTPN14,PRKD1,NCSTN,F11R,PLXNB1,SLC25A12,RAPH1,ARID5B,ITGA6,ZNF365,ATF6,TAGLN,AKAP6,DDR2,MAP3K13,ID3,LRP6,PRDX4,LNPK,CRYGS,HSPB1,CUX1,MFAP5,SERPINE1,ACHE,CRYAB,ATP6AP2,PAPPA2,UNC5B,EXPH5,MAOB,NBR1,EZH1,SYNPO2L,CYP19A1,TNFSF1	darkgreen	VSMC_M4
GO:0008016	0.00	1.00	23	144	regulation of heart contraction	BP	0.06395	MDM2,GJA1,TRDN,EDN2,TBX18,KCNE3,THRB,FXYD1,ADM,ADA,EDN1,RGS2,TNNT2,CAMK2D,ABCC9,CACNA1C,ADRA1B,FLNA,KCNE4,SLC8A1,PLN,TMEM38A,HOPX	darkgreen	VSMC_M4
GO:0019722	0.00	1.00	23	147	calcium-mediated signaling	BP	0.06395	PPP1R9A,ZAP70,EDN2,LMCD1,MCTP1,ADA,RCAN1,EDN1,HTR2B,CAMK2D,AKAP6,CACNA1C,ADGRL1,CDH13,PLCG2,VCAM1,ITPR1,SLC8A1,C10orf71,PLN,NCALD,TMEM38A,CCR6	darkgreen	VSMC_M4
GO:0051716	0.00	1.00	403	5042	cellular response to stimulus	BP	0.06395	MBP,DOK6,GDF11,BCL2,RNF41,IFNGR1,CITED2,SHPRH,SASH1,IRAK3,GRIP1,MDM2,DDR1,RGS22,IPCEF1,SOD2,OXR1,ABRA,ANGPT1,FAM19A5,SMOC2,SCUBE1,GJA1,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,RASL11B,VLDLR,UNC13B,C2orf40,PPP1R9A,CD274,PDK4,IL18R1,RNF149,CREB3,REST,RECK,IGFBP7,ZAP70,FRMPD1,SNX13,SLC2A1,TGFBR1,EDN2,SYT5,ABCA1,PTPN3,SVEP1,TBX18,CHN2,MAP3K7,DOCK4,KIDINS220,MDFIC,GPR63,FZD8,EPHB6,SESN1,JADE1,MAP3K8,HIPK2,GATA2,APBB1IP,LIMS2,LRCH1,SNRK,MRC1,TPT1,ITGA8,TENM4,ITGA9,INHBB,GPR39,HRH1,NXPH2,BABAM2,RALGAPA2,LBH,STT3B,NDRG2,POLB,LMCD1,ARHGEF17,THRB,PLCB4,ACTN4,ADAM9,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,COL4A1,COL4A2,CDC42EP3,CYP1B1,CPNE4,PCLO,SEMA3C,TF,APLP1,FLT3,AMOTL2,MAP3K1,NCOR2,FFAR3,PTPRG,LATS2,HIPK3,ANKRD1,KIAA0355,CPEB3,NCK1,SORBS2,ADM,MAP1LC3A,CD180,SH3RF1,MRVI1,ATOH8,GRK7,OCLN,TCF7L1,WWC2,TEAD1,MCTP1,ARHGEF3,PTH,KIF13B,RNF34,CDKL2,G3BP2,CLU,BLNK,GPR87,APP,PDGFC,SHROOM3,RXFP1,ABCC8,PTPN11,ADCY6,LBP,NEK4,HERPUD1,TMEM64,JMY,DCBLD2,CHD6,PTPN22,HNF4A,CHAC1,GDF6,FMOD,SERINC3,ADA,RCAN1,IFIT1,NGF,EDN1,JAM3,CD47,PLA2G4F,N4BP1,SMARCAD1,MARCH6,SEMA5A,LPL,MX1,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,PPP1R12B,DAPP1,RGS2,EYA2,NCOA3,ACTN2,ZNF106,LRP5,KCTD10,FEZ1,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,ZMAT3,TM7SF3,GALNT3,PRKCA,GNB4,AFAP1L2,TXNIP,MID1,PLXNA2,SESN2,SHTN1,CAMK2D,ADCY5,CTSS,	darkgreen	VSMC_M4
GO:0043067	0.00	1.00	105	1119	regulation of programmed cell death	BP	0.06442	BCL2,CITED2,MDM2,CDSN,SOD2,OXR1,ANGPT1,GJA1,TPD52L1,DAPK1,LEP,WFS1,DOCK8,UNC13B,CD274,PDK4,CREB3,REST,TGFBR1,HIPK2,GATA2,LIMS2,TPT1,NAA16,INHBB,BABAM2,ACTN4,FOXO1,RASSF2,ANKLE2,CYP1B1,FLT3,HPN,LATS2,HIPK3,ANKRD1,NCK1,ADM,SLC25A4,SH3RF1,PTH,RNF34,CLU,HERPUD1,JMY,SERINC3,ADA,NGF,EDN1,SEMA5A,EYA2,ACTN2,LRP5,HTR2B,LGMN,ZMAT3,TM7SF3,PRKCA,TXNIP,CAMK2D,LRP2,CFLAR,CTSZ,FGFR2,ITGA6,ATF6,ID3,LRP6,HIP1,HSPB1,SERPINE1,CRYAB,PDE1A,UNC5B,TNFSF10,MAEL,HIF1A,OPN3,PPARGC1A,ACTN1,TEX11,TGFB3,SMAD6,PAK3,ANGPTL4,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,FLNA,SORT1,PLCG2,CYR61,VNN1,BNIP3,FRZB,LOX,ITM2C,CDKN1A,RASSF3,NACC2,ICAM1,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0033002	0.00	1.00	25	174	muscle cell proliferation	BP	0.067	CITED2,MDM2,SOD2,ANGPT1,FAM19A5,GJA1,TGFBR1,TENM4,NDRG2,PTPN11,EDN1,CFLAR,FGFR2,PDE1A,PPARGC1A,TGFB3,CNN1,SKP2,NPR3,CDH13,TBX20,CDKN1A,FGF9,YAP1,PRKG1	darkgreen	VSMC_M4
GO:1904036	0.00	1.00	9	34	negative regulation of epithelial cell apoptotic process	BP	0.067	ANGPT1,WFS1,GATA2,SEMA5A,CFLAR,SERPINE1,ANGPTL4,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0009617	0.00	1.00	42	362	response to bacterium	BP	0.06736	SASH1,IRAK3,SOD2,GJA1,TRDN,ADGRB1,CD274,SLC17A5,ABCA1,MRC1,ADAM9,TF,CHD7,ANKRD1,ADM,CD180,GPM6A,ABCC8,ANXA3,LBP,PTPN22,EDN1,RAB29,CCDC80,PRKCA,FGFR2,PRKD1,SERPINE1,MAOB,PPARGC1A,SMAD6,LGALS9,PLCG2,VCAM1,IFI44,TLR1,BNIP3,ADAMTS5,REG4,ICAM1,C15orf48,BMP6	darkgreen	VSMC_M4
GO:0035633	0.00	1.00	9	32	maintenance of blood-brain barrier	BP	0.07069	MBP,ANGPT1,GJA1,LAMA2,SH3GL2,OCLN,ABCC8,JAM3,F11R	darkgreen	VSMC_M4

GO:0051240	0.00	1.00	103	1050	positive regulation of multicellular organismal process	BP	0.07457	MBP,ZNF516,BCL2,IFNGR1,CITED2,SASH1,IRAK3,SMOC2,GJA1,ADGRB1,LEP,DDX58,UNC13B,CD274,IL18R1,REST,ZAP70,TGFBR1,EDN2,ABCA1,MAP3K7,HIPK2,GATA2,TENM4,INHBB,SMARCD3,HRH1,LBH,CYP1B1,WASF3,FFAR3,CHD7,ADM,PTH,CLU,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,TMEM64,PTPN22,GDF6,ADA,NGF,EDN1,SEMA5A,LPL,ADIPOR1,KDM5B,RGS2,NCOA3,NPNT,HTR2B,PRKCA,AFAP1L2,PLXNA2,SHTN1,CAMK2D,LRP2,FGFR2,TP53BP1,PRKD1,PLXNB1,SLC25A12,ZNF365,AKAP6,MAP3K13,HSPB1,CUX1,SERPINE1,ACHE,ATP6AP2,NLGN1,HIF1A,PPARGC1A,NPPB,RORA,NUMB,TGFB3,ADRA1B,NPTN,PAK3,FST,ANGPTL4,DAB2,LGALS9,PLXNB3,VAMP7,CSF1,PLCG2,F3,CYR61,VNN1,SLC8A1,TLR1,CD83,TBX20,LRRC24,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:0046885	0.00	1.00	7	20	regulation of hormone biosynthetic process	BP	0.07606	REST,FFAR3,ADM,HIF1A,PPARGC1A,STC2,BMP6	darkgreen	VSMC_M4
GO:0071310	0.00	1.00	161	1784	cellular response to organic substance	BP	0.0848	BCL2,IFNGR1,CITED2,SASH1,IRAK3,MDM2,SOD2,ANGPT1,SMOC2,GJA1,EP300,BRD8,DAPK1,TLE4,SH3GL2,LEP,CDKN2B,WFS1,DDX58,DOCK8,KANK1,RASL11B,UNC13B,CD274,PDK4,IL18R1,CREB3,REST,IGFBP7,TGFBR1,EDN2,ABCA1,MAP3K7,KIDINS220,SESN1,HIPK2,LRCH1,MRC1,INHBB,HRH1,LBH,THRB,ACTN4,ADAM9,CRIM1,FOXO1,COL4A1,COL4A2,CYP1B1,APLP1,FLT3,NCOR2,FFAR3,LATS2,ANKRD1,CPEB3,NCK1,CD180,OCLN,PTH,CLU,APP,PDGFC,RXFP1,ABCC8,PTPN11,ADCY6,LBP,HERPUD1,PTPN22,GDF6,FMOD,IFIT1,NGF,EDN1,CD47,PLA2G4F,LPL,MX1,ABCG1,ADIPOR1,KDM5B,RIPOR2,NCOA3,ACTN2,ZNF106,LRP5,FEZ1,NPNT,HTR2B,MST1R,LGMN,TM7SF3,GALNT3,PRKCA,SESN2,ADCY5,CTSS,LRP2,CFLAR,WDTC1,FGFR2,CASTOR1,PRKD1,NCSTN,STRN3,ARID5B,ITGA6,ATF6,AKAP6,ID3,LRP6,HSPB1,EIF4A2,SERPINE1,RDX,IGFBP2,HIF1A,GNAI1,PPARGC1A,FGFRL1,RORA,SLIT3,TGFB3,SMAD6,EPG5,BBS4,NPTN,PAK3,FST,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,FLNA,SLC2A5,HCN2,AHCYL1,CSF1,SORT1,MBTPS1,PLCG2,VCAM1,F3,GLG1,BCAR3,CYR61,MIR99A,SLC8A1,ADAMTSL2,LOX,TBX20,FGF9,TMEM38A,CCR6,ICAM1,PIK3C2A,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0006995	0.00	1.00	4	8	cellular response to nitrogen starvation	BP	0.08503	MAP1LC3A,GABARAPL1,MAP1LC3B2,GABARAPL2	darkgreen	VSMC_M4
GO:0043562	0.00	1.00	4	8	cellular response to nitrogen levels	BP	0.08503	MAP1LC3A,GABARAPL1,MAP1LC3B2,GABARAPL2	darkgreen	VSMC_M4
GO:0014070	0.00	1.00	73	703	response to organic cyclic compound	BP	0.08517	BCL2,IRAK3,MDM2,SOD2,GJA1,EP300,LEP,DDX58,REST,IGFBP7,TGFBR1,ABCA1,PAPPA,HRH1,LBH,ADAM9,FOXO1,CYP1B1,APLP1,FLT3,NCOR2,ANKRD1,ADM,MAP1LC3A,PAM,PTH,CLU,APP,ANXA3,ADCY6,ADA,IFIT1,EDN1,PLA2G4F,NCOA3,HTR2B,TXNIP,ABCC9,ADCY5,CFLAR,NCSTN,TRIM63,STRN3,ITGA6,AKAP6,ID3,LRP6,CRYAB,MAOB,IGFBP2,CYP19A1,GNAI1,PPARGC1A,RORA,SLIT3,TGFB3,EPG5,PAK3,DAB2,SKP2,FLNA,HCN2,SLC8A1,CD83,LOX,PLN,CDKN1A,TMEM38A,ICAM1,STC2,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0014808	0.00	1.00	8	26	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	0.08578	TRDN,CHD7,CAMK2D,AKAP6,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:1903514	0.00	1.00	8	26	release of sequestered calcium ion into cytosol by endoplasmic reticulum	BP	0.08578	TRDN,CHD7,CAMK2D,AKAP6,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0030155	0.00	1.00	60	541	regulation of cell adhesion	BP	0.09667	MBP,BCL2,CITED2,DDR1,CDSN,ANGPT1,LAMA2,LEP,LIMCH1,DOCK8,KANK1,CD274,ECM2,ZAP70,MAP3K8,APBB1IP,LIMS2,LMO7,ACTN4,ADAM9,CYP1B1,ZDHHC2,NCK1,CHST2,PTPN11,PTPN22,PKP4,ADA,JAM3,CD47,SEMA5A,RIPOR2,CCDC80,NPNT,PREX1,NID1,PRKCA,PLXNA2,F11R,PLXNB1,ITGA6,COL26A1,SERPINE1,RDX,IGFBP2,LGALS9,MYO10,DAPK3,PLXNB3,FLNA,CSF1,CDH13,VCAM1,CYR61,VNN1,CD83,ICAM1,PRKG1,BMP6,PLEKHA2	darkgreen	VSMC_M4
GO:0044419	0.00	1.00	90	948	biological process involved in interspecies interaction between organisms	BP	0.1003	BCL2,IFNGR1,SASH1,IRAK3,SOD2,C4A,RNASET2,GJA1,TRDN,EP300,ADGRB1,DAPK1,LEP,DDX58,CD274,REST,ZAP70,SLC17A5,ABCA1,MAP3K7,NT5C3A,MRC1,TPT1,INHBB,ADAM9,TF,HPN,CHD7,ANKRD1,TRIM23,NCK1,ADM,CD180,G3BP2,CLU,GPM6A,SCARB2,ABCC8,ANXA3,PTPN11,PTX3,LBP,CCNT1,PTPN22,SERINC3,IFIT1,EDN1,CD47,N4BP1,MX1,RAB29,CCDC80,MST1R,PRKCA,CFI,ABCC9,FGFR2,PRKD1,F11R,HSPB1,SERPINE1,C1RL,MAOB,HIF1A,PPARGC1A,CALCOCO2,SMAD6,GP2,ULK2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,VCAM1,LRSAM1,IFI44,VNN1,TLR1,BNIP3,ADAMTS5,REG4,ZNF175,MFAP4,ICAM1,C15orf48,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0044321	0.00	1.00	6	16	response to leptin	BP	0.1003	LEP,INHBB,EDN1,ADIPOR1,LRP2,BBS4	darkgreen	VSMC_M4
GO:0072503	0.00	1.00	38	306	cellular divalent inorganic cation homeostasis	BP	0.1003	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,RIC3,CHD7,MICU2,ADM,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,AKAP6,LRP6,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2	darkgreen	VSMC_M4

GO:0009967	0.00	1.00	107	1127	positive regulation of signal transduction	BP	0.10411	DOK6,GDF11,CITED2,SASH1,ABRA,ANGPT1,SMOC2,SCUBE1,GJA1,TPD52L1,EP300,MLLT3,LEP,CDKN2B,SH3RF3,KANK1,IL18R1,RECK,ZAP70,TGFBR1,MAP3K7,HIPK2,LIMS2,INHBB,LMCD1,ACTN4,ADAM9,RASSF2,ATP2C1,CYP1B1,FLT3,ANKRD1,NCK1,CD180,SH3RF1,ARHGEF3,PTH,APP,PDGFC,PTPN11,LBP,PTPN22,GDF6,SERINC3,ADA,NGF,EDN1,SEMA5A,RAB29,ADIPOR1,NPNT,HTR2B,MST1R,PRKCA,AFAP1L2,MID1,LRP2,CFLAR,FGFR2,PRKD1,F11R,PLXNB1,ZRANB1,ATF6,AKAP6,MAP3K13,HIP1,ATP6AP2,UNC5B,MAOA,SYNPO2L,TNFSF10,DACT1,NLGN1,HIF1A,TGFB3,ADRA1B,NPTN,MAPRE2,CDH2,GAS2L2,CRLF3,DAB2,LGALS9,SKP2,DAPK3,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,CYR61,WLS,TLR1,TBX20,ITM2C,C10orf71,LYPD6,FGF9,EDA,NACC2,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:0042981	0.00	1.00	101	1092	regulation of apoptotic process	BP	0.10411	BCL2,CITED2,MDM2,SOD2,OXR1,ANGPT1,GJA1,TPD52L1,DAPK1,LEP,WFS1,DOCK8,UNC13B,CD274,PDK4,CREB3,REST,TGFBR1,HIPK2,GATA2,LIMS2,TPT1,NAA16,INHBB,BABAM2,ACTN4,FOXO1,RASSF2,ANKLE2,CYP1B1,FLT3,HPN,LATS2,HIPK3,ANKRD1,NCK1,ADM,SH3RF1,PTH,RNF34,CLU,HERPUD1,JMY,SERINC3,ADA,NGF,EDN1,SEMA5A,EYA2,ACTN2,LRP5,HTR2B,LGMN,ZMAT3,PRKCA,TXNIP,CAMK2D,LRP2,CFLAR,CTSZ,FGFR2,ITGA6,ATF6,ID3,LRP6,HIP1,HSPB1,SERPINE1,CRYAB,PDE1A,UNC5B,TNFSF10,MAEL,HIF1A,OPN3,PPARGC1A,ACTN1,TEX11,TGFB3,SMAD6,PAK3,ANGPTL4,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,FLNA,SORT1,CYR61,VNN1,BNIP3,FRZB,LOX,ITM2C,CDKN1A,RASSF3,NACC2,ICAM1,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0007189	0.00	1.00	15	80	adenylate cyclase-activating G protein-coupled receptor signaling pathway	BP	0.10696	ADGRB1,GNAQ,ABCA1,APLP1,ADM,PTH,RXFP1,ADCY6,PRKCA,ADCY5,ADGRE2,ADGRL1,ADRA1B,ADCY9,PLN	darkgreen	VSMC_M4
GO:0010647	0.00	1.00	117	1251	positive regulation of cell communication	BP	0.10696	DOK6,GDF11,CITED2,SASH1,ABRA,ANGPT1,SMOC2,SCUBE1,GJA1,TRDN,TPD52L1,LAMA2,EP300,MLLT3,LEP,CDKN2B,SH3RF3,KANK1,PPP1R9A,IL18R1,RECK,ZAP70,TGFBR1,MAP3K7,HIPK2,LIMS2,INHBB,LMCD1,ACTN4,ADAM9,RASSF2,ATP2C1,CYP1B1,FLT3,ZDHHC2,ANKRD1,NCK1,CD180,SH3RF1,ARHGEF3,PTH,APP,PDGFC,PTPN11,LBP,PTPN22,GDF6,SERINC3,ADA,NGF,EDN1,SEMA5A,RAB29,ABCG1,ADIPOR1,NPNT,HTR2B,MST1R,LGMN,TM7SF3,PRKCA,AFAP1L2,MID1,LRP2,CFLAR,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,ZRANB1,ATF6,AKAP6,MAP3K13,HIP1,ATP6AP2,UNC5B,MAOA,SYNPO2L,CYP19A1,TNFSF10,DACT1,NLGN1,HIF1A,TGFB3,ADRA1B,NPTN,MAPRE2,CDH2,GAS2L2,CRLF3,DAB2,LGALS9,SKP2,DAPK3,FLNA,PLEKHG5,VAMP7,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,CYR61,WLS,TLR1,TBX20,ITM2C,C10orf71,LYPD6,FGF9,EDA,NACC2,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:0003231	0.00	1.00	18	101	cardiac ventricle development	BP	0.10932	CITED2,MDM2,GRHL2,TGFBR1,PPP1R13L,SMARCD3,SEMA3C,CHD7,TNNT2,LRP2,FGFR2,HIF1A,FGFRL1,SLIT3,SMAD6,LMO4,CYR61,TBX20	darkgreen	VSMC_M4
GO:0006937	0.00	1.00	19	121	regulation of muscle contraction	BP	0.10932	EDN2,DOCK4,MYL9,ADA,EDN1,PPP1R12B,RGS2,TNNT2,NPNT,CAMK2D,CACNA1C,ADRA1B,CNN1,DAPK3,SLC8A1,PLN,TMEM38A,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:0051480	0.00	1.00	29	212	regulation of cytosolic calcium ion concentration	BP	0.10932	BCL2,GJA1,TRDN,EDN2,GATA2,TRPC4,TMEM178A,RIC3,CHD7,ADM,SLC35G1,JPH1,TMEM64,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,AKAP6,LRP6,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A,CCR6	darkgreen	VSMC_M4
GO:0042060	0.00	1.00	40	329	wound healing	BP	0.10932	DDR1,FAM19A5,SMOC2,SCUBE1,GJA1,MRTFA,GNAQ,KANK1,TGFBR1,GATA2,ITGA9,OCLN,ENTPD1,MYL9,ABCC8,PROS1,DCBLD2,HNF4A,EDN1,PRKCA,MYLK,CFLAR,FGFR2,F11R,LNPK,HSPB1,SERPINE1,HIF1A,TGFB3,FLNA,PLCG2,F3,CYR61,CD151,LOX,CD59,CSRP1,CDKN1A,YAP1,PRKG1	darkgreen	VSMC_M4
GO:0042221	0.00	1.00	243	2921	response to chemical	BP	0.11034	MBP,BCL2,IFNGR1,CITED2,SASH1,IRAK3,MDM2,IPCEF1,SOD2,OXR1,ANGPT1,SMOC2,GJA1,LAMA2,EP300,BRD8,DAPK1,TLE4,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,DDX58,DOCK8,KANK1,RASL11B,UNC13B,PPP1R9A,CD274,PON2,PDK4,IL18R1,RNF149,CREB3,REST,IGFBP7,SLC2A1,TGFBR1,EDN2,SYT5,ABCA1,MAP3K7,DOCK4,KIDINS220,PAPPA,EPHB6,SESN1,HIPK2,GATA2,TMEM135,LRCH1,MRC1,INHBB,HRH1,LBH,STT3B,POLB,THRB,ACTN4,ADAM9,CRIM1,FOXO1,COL4A1,COL4A2,CYP1B1,CPNE4,SEMA3C,TF,APLP1,FLT3,NCOR2,FFAR3,HPN,CHD7,LATS2,ANKRD1,CPEB3,NCK1,ADM,MAP1LC3A,PAM,CD180,OCLN,PTH,CLU,MEIS2,APP,PDGFC,RXFP1,ABCC8,ANXA3,PTPN11,ADCY6,LBP,HERPUD1,CHD6,PTPN22,HNF4A,CHAC1,GDF6,FMOD,ADA,IFIT1,NGF,EDN1,JAM3,CD47,NFASC,PLA2G4F,MARCH6,SEMA5A,LPL,MX1,ABCG1,ADIPOR1,KDM5B,RIPOR2,RGS2,TNNT2,NCOA3,ACTN2,ZNF106,PFKL,LRP5,FEZ1,NPNT,PREX1,HTR2B,MST1R,LGMN,ROBO3,TM7SF3,GALNT3,PRKCA,TXNIP,PLXNA2,SESN2,CAMK2D,ABCC9,ADCY5,CTSS,MYLK,LRP2,CFLAR,WDTC1,FGFR2,CASTOR1,PRKD1,NCSTN,CYBRD1,TRIM63,PLXNB1,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,AKAP6,ID3,LRP6,PRDX4,HSPB1,EIF4A2,SERPINE1,ACHE,CRYAB,RDX,UNC5B,MAOB,IGFBP2,AOC3,FMO4,CYP19A1,TNFSF10,NLGN1,JKAMP,HIF1A,ADGRE2,GNAI1,PPARGC1A,FAF2,FGFRL1,RORA,CALCOCO2,SLIT3,TGFB3,SMAD6,EPG5,BBS4,NPTN,PAK3,MMP28,HSPB3,FST,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,PLXNB3,FLNA,LCN8,PLEKHG5,SLC2A5,HCN2,AHCYL1,CSF1,SORT1,MBTPS1,CDH13,PLCG2,VCAM1,F3,GLG1,BCAR3,LRRC8C,CYR61,NEXN,MIR99A,AFF3,VNN1,SLC8A1,ADAMTSL2,TLR1,FBXO27,BNIP3,CD83,LOX,TBX20,PLN,CDKN1A,FGF9,PPM1F,TMEM38A,CCR	darkgreen	VSMC_M4

GO:0030029	0.00	1.00	72	662	actin filament-based process	BP	0.11485	BCL2,GJA1,MRTFA,LIMCH1,KANK1,TPM2,PPP1R9A,TGFBR1,CALD1,ANTXR1,TESK2,KCNE3,ARHGEF17,ACTN4,FMNL2,ATP2C1,CDC42EP3,TF,AMOTL2,WASF3,ANKRD1,EPB41L4A,NCK1,SORBS2,PAM,SHROOM3,JMY,EDN1,JAM3,CD47,MYO1B,SEMA5A,MARCKSL1,TNNT2,ACTN2,PREX1,SHTN1,CAMK2D,CFLAR,SYNPO2,F11R,HIP1,RDX,SYNPO2L,WDR1,IQSEC3,CACNA1C,MICAL3,ACTN1,SIPA1L1,TGFB3,CNN1,NRK,SPECC1,SYNPO,PAK3,GAS2L2,PLS3,ABLIM3,ARHGAP28,DAPK3,FLNA,SPTAN1,KCNE4,XIRP1,PDLIM3,CSRP1,PLN,PPM1E,DSTN,ICAM1,PRKG1	darkgreen	VSMC_M4
GO:0030036	0.00	1.00	66	600	actin cytoskeleton organization	BP	0.11487	BCL2,MRTFA,LIMCH1,KANK1,TPM2,PPP1R9A,TGFBR1,CALD1,ANTXR1,TESK2,ARHGEF17,ACTN4,FMNL2,ATP2C1,CDC42EP3,TF,AMOTL2,WASF3,ANKRD1,EPB41L4A,NCK1,SORBS2,PAM,SHROOM3,JMY,EDN1,JAM3,CD47,MYO1B,SEMA5A,MARCKSL1,TNNT2,ACTN2,PREX1,SHTN1,CFLAR,SYNPO2,F11R,HIP1,RDX,SYNPO2L,WDR1,IQSEC3,MICAL3,ACTN1,SIPA1L1,TGFB3,CNN1,NRK,SPECC1,SYNPO,PAK3,GAS2L2,PLS3,ABLIM3,ARHGAP28,DAPK3,FLNA,SPTAN1,XIRP1,PDLIM3,CSRP1,PPM1E,DSTN,ICAM1,PRKG1	darkgreen	VSMC_M4
GO:0070887	0.00	1.00	192	2230	cellular response to chemical stimulus	BP	0.11507	BCL2,IFNGR1,CITED2,SASH1,IRAK3,MDM2,IPCEF1,SOD2,OXR1,ANGPT1,SMOC2,GJA1,EP300,BRD8,DAPK1,TLE4,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,DDX58,DOCK8,KANK1,RASL11B,UNC13B,PPP1R9A,CD274,PDK4,IL18R1,RNF149,CREB3,REST,IGFBP7,SLC2A1,TGFBR1,EDN2,SYT5,ABCA1,MAP3K7,DOCK4,KIDINS220,SESN1,HIPK2,LRCH1,MRC1,INHBB,HRH1,LBH,THRB,ACTN4,ADAM9,CRIM1,FOXO1,COL4A1,COL4A2,CYP1B1,CPNE4,TF,APLP1,FLT3,NCOR2,FFAR3,LATS2,ANKRD1,CPEB3,NCK1,MAP1LC3A,CD180,OCLN,PTH,CLU,APP,PDGFC,RXFP1,ABCC8,PTPN11,ADCY6,LBP,HERPUD1,CHD6,PTPN22,HNF4A,GDF6,FMOD,IFIT1,NGF,EDN1,JAM3,CD47,PLA2G4F,SEMA5A,LPL,MX1,ABCG1,ADIPOR1,KDM5B,RIPOR2,NCOA3,ACTN2,ZNF106,LRP5,FEZ1,NPNT,PREX1,HTR2B,MST1R,LGMN,TM7SF3,GALNT3,PRKCA,SESN2,CAMK2D,ADCY5,CTSS,MYLK,LRP2,CFLAR,WDTC1,FGFR2,CASTOR1,PRKD1,NCSTN,STRN3,ARID5B,ITGA6,ATF6,AKAP6,ID3,LRP6,PRDX4,HSPB1,EIF4A2,SERPINE1,ACHE,RDX,IGFBP2,FMO4,NLGN1,HIF1A,ADGRE2,GNAI1,PPARGC1A,FGFRL1,RORA,SLIT3,TGFB3,SMAD6,EPG5,BBS4,NPTN,PAK3,MMP28,FST,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,PLXNB3,FLNA,PLEKHG5,SLC2A5,HCN2,AHCYL1,CSF1,SORT1,MBTPS1,PLCG2,VCAM1,F3,GLG1,BCAR3,LRRC8C,CYR61,MIR99A,VNN1,SLC8A1,ADAMTSL2,BNIP3,LOX,TBX20,FGF9,PPM1E,TMEM38A,CCR6,ICAM1,PIK3C2A,STC2,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0072359	0.00	1.00	92	902	circulatory system development	BP	0.11507	CITED2,SASH1,MDM2,GRHL2,SOD2,ANGPT1,FAM19A5,SMOC2,SCUBE1,GJA1,EP300,ADGRB1,LEP,SGCB,REST,RECK,TGFBR1,SVEP1,TBX18,CALD1,ANTXR1,GYS1,HIPK2,GATA2,PPP1R13L,TENM4,SMARCD3,COL4A1,COL4A2,CYP1B1,SEMA3C,AMOTL2,CHD7,ANKRD1,SORBS2,ADM,PAM,ABCC8,ANXA3,PTPN11,EDN1,JAM3,SEMA5A,RGS2,RBM20,TNNT2,ACTN2,LRP5,HTR2B,PRKCA,SEC24B,MFGE8,MYLK,LRP2,CFLAR,FGFR2,PTPN14,PRKD1,AKAP6,ID3,HSPB1,SERPINE1,UNC5B,SYNPO2L,HIF1A,CACNA1C,NPPB,ANGPTL7,FGFRL1,RORA,SLIT3,SMAD6,BBS4,CDH2,ANGPTL4,FLNA,CDH13,VCAM1,F3,LMO4,CYR61,SLC8A1,LOX,TBX20,PDLIM3,PLN,CDKN1A,FGF9,HOPX,PIK3C2A,YAP1,CRELD1	darkgreen	VSMC_M4
GO:0006939	0.00	1.00	15	84	smooth muscle contraction	BP	0.11507	EDN2,DOCK4,ADA,EDN1,RGS2,NPNT,HTR2B,MYLK,APBB2,CNN1,DAPK3,SLC8A1,PIK3C2A,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:0016339	0.00	1.00	7	22	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	BP	0.11507	ATP2C1,PCDHB4,NLGN1,CDH2,CDH18,CDH13,PCDHB2	darkgreen	VSMC_M4
GO:0023056	0.00	1.00	117	1258	positive regulation of signaling	BP	0.11507	DOK6,GDF11,CITED2,SASH1,ABRA,ANGPT1,SMOC2,SCUBE1,GJA1,TPD52L1,LAMA2,EP300,MLLT3,LEP,CDKN2B,SH3RF3,KANK1,PPP1R9A,IL18R1,RECK,ZAP70,TGFBR1,MAP3K7,HIPK2,LIMS2,INHBB,LMCD1,ACTN4,ADAM9,RASSF2,ATP2C1,CYP1B1,FLT3,ZDHHC2,ANKRD1,NCK1,CD180,SH3RF1,ARHGEF3,PTH,APP,PDGFC,PTPN11,LBP,PTPN22,GDF6,SERINC3,ADA,NGF,EDN1,SEMA5A,RAB29,ABCG1,ADIPOR1,NPNT,HTR2B,MST1R,LGMN,TM7SF3,PRKCA,AFAP1L2,MID1,LRP2,CFLAR,INPP5F,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,ZRANB1,ATF6,AKAP6,MAP3K13,HIP1,ATP6AP2,UNC5B,MAOA,SYNPO2L,CYP19A1,TNFSF10,DACT1,NLGN1,HIF1A,TGFB3,ADRA1B,NPTN,MAPRE2,CDH2,GAS2L2,CRLF3,DAB2,LGALS9,SKP2,DAPK3,FLNA,PLEKHG5,VAMP7,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,CYR61,WLS,TLR1,TBX20,ITM2C,C10orf71,LYPD6,FGF9,EDA,NACC2,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:1903530	0.00	1.00	45	399	regulation of secretion by cell	BP	0.11507	GJA1,LEP,UNC13B,PPP1R9A,RIC1,REST,ICA1,PREPL,SYT5,GATA2,INHBB,RAB2B,ADAM9,PCLO,FFAR3,CHD7,ANKRD1,PAM,MCTP1,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ATP9A,ADCY5,RAPGEF4,ACHE,EXPH5,MAOB,CYP19A1,NLGN1,HIF1A,ADGRE2,FBXL20,TGFB3,RHOT1,LGALS9,VAMP7,WLS,BMP6	darkgreen	VSMC_M4

GO:0050793	0.00	1.00	167	1852	regulation of developmental process	BP	0.11507	BCL2,CITED2,SASH1,UST,GRIP1,MDM2,GRHL2,SOD2,FAM19A5,TRPS1,SMOC2,GJA1,LAMA2,ADGRB1,MLLT3,LEP,KANK1,VLDLR,PPP1R9A,REST,RECK,ZAP70,TGFBR1,ABCA1,TBX18,ITSN2,HIPK2,GATA2,PLEKHB2,LIMS2,TMEM135,PPP1R13L,TPT1,TENM4,SMARCD3,LBH,ACTN4,FMNL2,ADAM9,CRIM1,FOXO1,RASSF2,COL4A2,CDC42EP3,CYP1B1,SEMA3C,TMEM178A,WASF3,HPN,CHD7,LATS2,CPEB3,MARCH5,ADM,SH3RF1,ATOH8,WWC2,PTH,KIF13B,MEIS2,APP,SHROOM3,ABCC8,ANXA3,PTPN11,NEK4,TMEM64,HNF4A,GDF6,NAB1,ADA,NGF,EDN1,SEMA5A,LPL,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,RGS2,NCOA3,LRP5,FEZ1,NPNT,PREX1,LGMN,PRKCA,SEC24B,PLXNA2,SHTN1,P4HTM,LRP2,CFLAR,INPP5F,FGFR2,TP53BP1,PRKD1,F11R,PLXNB1,ZRANB1,SLC25A12,ZNF365,AKAP6,DDR2,MAP3K13,ID3,LNPK,HSPB1,CUX1,SERPINE1,RDX,NBR1,DACT1,NLGN1,WDR1,MAEL,HIF1A,ADGRL1,PPARGC1A,NPPB,ZC4H2,DISP3,ANGPTL7,RORA,SIPA1L1,NUMB,TGFB3,SMAD6,FAXDC2,NPTN,CDH2,ULK2,PAK3,FST,ANGPTL4,DAB2,LGALS9,MYO10,RBFOX1,DAPK3,PLXNB3,FLNA,CSF1,SORT1,F3,GLG1,LMO4,CYR61,VNN1,SLC8A1,BNIP3,FRZB,CD83,LOX,TBX20,LRRC24,CST3,MAFF,CDKN1A,FGF9,HOPX,ICAM1,SDC2,YAP1,MYL12B,BMP6	darkgreen	VSMC_M4
GO:1904706	0.00	1.00	6	20	negative regulation of vascular associated smooth muscle cell proliferation	BP	0.11507	SOD2,FAM19A5,TGFB3,CNN1,CDKN1A,PRKG1	darkgreen	VSMC_M4
GO:0009888	0.00	1.00	131	1389	tissue development	BP	0.11507	ZNF516,GDF11,BCL2,CITED2,MDM2,DDR1,CDSN,GRHL2,TRPS1,SCUBE1,GJA1,LAMA2,EP300,MRTFA,MLLT3,LEP,SGCB,TGFBR1,SVEP1,TBX18,PPP1R13L,TPT1,ITGA8,TENM4,FOSL2,LBH,THRB,ADAM9,FOXO1,ATP2C1,COL4A1,COL4A2,CYP1B1,SEMA3C,HPN,CHD7,ANKRD1,SORBS2,ADM,ATOH8,FAM172A,PTH,SHROOM3,RXFP1,PTPN11,HNF4A,GDF6,NAB1,ADA,RCAN1,PDZD7,EDN1,ETS2,SEMA5A,ADIPOR1,KDM5B,RIPOR2,RGS2,EYA2,TNNT2,NCOA3,ACTN2,LRP5,NPNT,HTR2B,TXNIP,SEC24B,PLXNA2,MYLK,LRP2,CFLAR,CTSZ,FGFR2,F11R,ARID5B,ITGA6,TAGLN,AKAP6,DDR2,ID3,LRP6,LNPK,CRYGS,SERPINE1,ATP6AP2,RDX,EXPH5,NBR1,DACT1,WDR1,HIF1A,OPN3,ZBTB18,PPARGC1A,PLOD1,NPPB,TGFB3,SMAD6,BBS4,CDH2,FST,DAB2,RBFOX1,BGN,FLNA,CCDC78,CSF1,GLG1,LMO4,CYR61,WLS,SLC8A1,ADAMTSL2,CD151,FRZB,LOX,TBX20,CSRP1,PLN,SRPK3,MAFF,CDKN1A,EDA,HLF,HOPX,ICAM1,STC2,YAP1,BMP6,FAM83H,CRELD1	darkgreen	VSMC_M4
GO:0045785	0.00	1.00	37	306	positive regulation of cell adhesion	BP	0.11507	CITED2,ANGPT1,LEP,DOCK8,CD274,ECM2,ZAP70,MAP3K8,APBB1IP,LIMS2,ADAM9,NCK1,CHST2,PTPN11,PTPN22,ADA,CD47,CCDC80,NPNT,PREX1,NID1,PRKCA,F11R,ITGA6,COL26A1,IGFBP2,LGALS9,MYO10,FLNA,CSF1,CDH13,VCAM1,CYR61,VNN1,CD83,ICAM1,PLEKHA2	darkgreen	VSMC_M4
GO:0032502	0.00	1.00	371	4589	developmental process	BP	0.11507	MBP,ZNF516,GDF11,BCL2,IFNGR1,CITED2,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,CDSN,GRHL2,SOD2,ANGPT1,FAM19A5,TRPS1,SMOC2,SCUBE1,AFF4,GJA1,ZHX1,LAMA2,EP300,MRTFA,ADGRB1,SH3GL2,MLLT3,LEP,CDKN2B,WFS1,KANK1,SGCB,VLDLR,UNC13B,SPATA6L,C2orf40,PPP1R9A,CD274,RIC1,IL18R1,REST,RECK,IGFBP7,ZAP70,SLC2A1,TGFBR1,LMBRD1,EDN2,ABCA1,PTPN3,SVEP1,TBX18,PEX13,CALD1,ANTXR1,KIDINS220,FZD8,EPHB6,GYS1,ITSN2,HIPK2,JRKL,GATA2,PLEKHB2,HS6ST1,ENKUR,LIMS2,TMEM135,ITM2B,PPP1R13L,SNRK,TPT1,TESK2,ITGA8,TENM4,ELF1,INHBB,SMARCD3,PCDH9,PFKFB3,FOSL2,LBH,NDRG2,POLB,SALL2,THRB,ACTN4,FMNL2,ADAM9,TACC1,CRIM1,FGF14,FOXO1,TRPC4,RASSF2,ATP2C1,COL4A1,COL4A2,ANKLE2,PCDHB4,CDC42EP3,CYP1B1,PCLO,SEMA3C,GTSF1,TMEM178A,TF,APLP1,FLT3,AMOTL2,WASF3,ZDHHC2,NCOR2,HPN,PTPRG,DENND5A,CHD7,LATS2,ANKRD1,CPEB3,MARCH5,NCK1,SORBS2,ADM,PAM,SCN8A,SH3RF1,ATOH8,CLCN3,WWC2,TEAD1,CHST2,FAM172A,JPH1,PTH,KIF13B,CDKL2,CLU,BLNK,GPM6A,MEIS2,APP,SCARB2,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,PTPN11,PTX3,ADCY6,NEK4,TMEM64,PTPN22,TANC1,HNF4A,CHAC1,GDF6,CPQ,NAB1,ADA,RCAN1,RBL2,NGF,PDZD7,EDN1,JAM3,GPRIN3,NFASC,ETS2,SEMA5A,BACE2,LPL,RAB29,ABCG1,ADIPOR1,COL4A4,FNDC5,KDM5B,RIPOR2,MARCKSL1,RGS2,EYA2,RBM20,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,MST1R,LGMN,ROBO3,NID1,SUN1,PRKCA,GNB4,TXNIP,SEC24B,ABLIM1,MFGE8,PARD6B,MID1,PLXNA2,SHTN1,P4HTM,NGRN,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,TP53BP1,PTPN14,PRKD1,NCSTN,F11R,PLXNB1,ZR	darkgreen	VSMC_M4
GO:0006940	0.00	1.00	10	46	regulation of smooth muscle contraction	BP	0.11507	EDN2,DOCK4,ADA,EDN1,RGS2,NPNT,CNN1,DAPK3,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:0072507	0.00	1.00	39	323	divalent inorganic cation homeostasis	BP	0.12323	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,RIC3,CHD7,MICU2,ADM,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,CNNM2,HTR2B,CAMK2D,ADCY5,PRKD1,AKAP6,LRP6,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2	darkgreen	VSMC_M4
GO:1902459	0.00	1.00	4	7	positive regulation of stem cell population maintenance	BP	0.12328	REST,LBH,NCOA3,YAP1	darkgreen	VSMC_M4
GO:0032350	0.00	1.00	8	30	regulation of hormone metabolic process	BP	0.12669	REST,FFAR3,HPN,ADM,HIF1A,PPARGC1A,STC2,BMP6	darkgreen	VSMC_M4
GO:0071706	0.00	1.00	18	115	tumor necrosis factor superfamily cytokine production	BP	0.13247	IFNGR1,IRAK3,ANGPT1,LEP,DDX58,CD274,CLU,APP,ABCC8,PTPN11,LBP,PTPN22,CD47,LPL,HSPB1,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4
GO:1903555	0.00	1.00	18	115	regulation of tumor necrosis factor superfamily cytokine production	BP	0.13247	IFNGR1,IRAK3,ANGPT1,LEP,DDX58,CD274,CLU,APP,ABCC8,PTPN11,LBP,PTPN22,CD47,LPL,HSPB1,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4

GO:0071495	0.00	1.00	100	1018	cellular response to endogenous stimulus	BP	0.13693	CITED2,MDM2,SMOC2,GJA1,EP300,BRD8,SH3GL2,LEP,CDKN2B,KANK1,RASL11B,PDK4,REST,IGFBP7,TGFBR1,MAP3K7,KIDINS220,SESN1,HIPK2,INHBB,HRH1,LBH,THRB,ADAM9,CRIM1,FOXO1,COL4A1,COL4A2,APLP1,FLT3,NCOR2,FFAR3,LATS2,ANKRD1,CPEB3,NCK1,PTH,APP,PDGFC,RXFP1,PTPN11,ADCY6,PTPN22,GDF6,FMOD,NGF,EDN1,LPL,ADIPOR1,KDM5B,NCOA3,ACTN2,ZNF106,NPNT,HTR2B,LGMN,GALNT3,SESN2,ADCY5,CTSS,LRP2,CFLAR,WDTC1,FGFR2,CASTOR1,NCSTN,STRN3,AKAP6,RDX,IGFBP2,PPARGC1A,FGFRL1,SLIT3,TGFB3,SMAD6,BBS4,NPTN,FST,DAB2,SKP2,PRKAA2,FLNA,HCN2,AHCYL1,SORT1,VCAM1,GLG1,BCAR3,CYR61,SLC8A1,ADAMTSL2,LOX,TBX20,FGF9,TMEM38A,ICAM1,PIK3C2A,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0044093	0.00	1.00	108	1151	positive regulation of molecular function	BP	0.14115	MBP,BCL2,SASH1,IRAK3,DDR1,GRHL2,ABRA,ANGPT1,TRDN,TPD52L1,EP300,DAPK1,GNAQ,LEP,DDX58,DOCK8,DCUN1D4,VLDLR,PPP1R9A,RIC1,IL18R1,REST,SNX13,EDN2,CHN2,MAP3K7,ANTXR1,TCAF1,EPHB6,HIPK2,USP6NL,RALGAPA2,KCNE3,ACTN4,ADAM9,FGF14,RASSF2,FLT3,PTH,CLU,APP,PDGFC,ABCC8,ANXA3,CCNT1,JMY,PKP4,AKTIP,NGF,EDN1,RIPOR2,TNNT2,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,PREX1,PLCL1,HTR2B,MST1R,LGMN,SERINC2,AFAP1L2,CTSS,CFLAR,FGFR2,TP53BP1,PRKD1,NCSTN,F11R,PLXNB1,ARID5B,ITGA6,AKAP6,DDR2,GPRC5A,MAP3K13,LRP6,HIP1,ATG14,TNFSF10,DACT1,LMTK2,HIF1A,CACNA1C,PPARGC1A,SIPA1L1,TOM1L1,MAPRE2,EVI5L,LGALS9,NPR3,CSF1,PLCG2,TBC1D13,TERF2IP,F3,ARHGAP29,BCAR3,LMO4,CYR61,SYDE2,CDKN1A,EDA,RFK,GABARAPL2,ICAM1	darkgreen	VSMC_M4
GO:0097190	0.00	1.00	49	471	apoptotic signaling pathway	BP	0.14115	BCL2,RNF41,MDM2,SOD2,TPD52L1,EP300,DAPK1,WFS1,CREB3,TGFBR1,HIPK2,TPT1,INHBB,POLB,CYP1B1,NCK1,SH3RF1,PTH,RNF34,CLU,HERPUD1,JMY,CHAC1,SERINC3,NGF,EYA2,PRKCA,CFLAR,ITGA6,HIP1,HSPB1,SERPINE1,UNC5B,TNFSF10,MAEL,HIF1A,RHOT1,TM2D1,DAPK3,SORT1,ITPR1,VNN1,BNIP3,ITM2C,CDKN1A,NACC2,ICAM1,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0070296	0.00	1.00	8	29	sarcoplasmic reticulum calcium ion transport	BP	0.14342	TRDN,CHD7,CAMK2D,AKAP6,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:1903018	0.00	1.00	8	35	regulation of glycoprotein metabolic process	BP	0.14344	BCL2,ITM2B,PTX3,BACE2,NCSTN,TMEM59,ITM2C,CST3	darkgreen	VSMC_M4
GO:0032760	0.00	1.00	13	69	positive regulation of tumor necrosis factor production	BP	0.14344	IFNGR1,LEP,DDX58,CLU,APP,ABCC8,PTPN11,LBP,LPL,HSPB1,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0051336	0.00	1.00	75	754	regulation of hydrolase activity	BP	0.14344	MBP,MDM2,C4A,DAPK1,GNAQ,DOCK8,TPM2,RIC1,REST,RECK,SNX13,CHN2,ANTXR1,IRCH1,USP6NL,ITIH5,RALGAPA2,CRIM1,SH3RF1,PTH,RNF34,APP,SCARB2,PTX3,HERPUD1,PROS1,TMEM64,PKP4,RCAN1,NGF,RIPOR2,RGS2,TNNT2,NPNT,PREX1,HTR2B,LGMN,PLXNA2,CAMK2D,CFLAR,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,ITGA6,HIP1,SERPINE1,CRYAB,RDX,TNFSF10,PCSK1N,CCPG1,PPP1R36,SIPA1L1,MAPRE2,EVI5L,ANGPTL4,LGALS9,OCRL,PLXNB3,SORT1,PPP1R26,TBC1D13,F3,ARHGAP29,BCAR3,CYR61,SYDE2,SPINK2,CST3,PLN,GABARAPL2,ICAM1,PRKG1	darkgreen	VSMC_M4
GO:0008219	0.00	1.00	138	1587	cell death	BP	0.1446	BCL2,RNF41,CITED2,MDM2,CDSN,SOD2,OXR1,ANGPT1,GJA1,TPD52L1,EP300,DAPK1,LEP,WFS1,DOCK8,SH3RF3,UNC13B,CD274,PDK4,CREB3,REST,TGFBR1,MAP3K7,JADE1,HIPK2,GATA2,LIMS2,PPP1R13L,TPT1,NAA16,INHBB,EXOG,BABAM2,FOSL2,POLB,THRB,ACTN4,FOXO1,RASSF2,ANKLE2,CYP1B1,APLP1,FLT3,HPN,LATS2,HIPK3,ANKRD1,NCK1,ADM,SLC25A4,SH3RF1,PTH,RNF34,CLU,APP,HERPUD1,JMY,CHAC1,GDF6,SERINC3,ADA,AKTIP,NGF,EDN1,SEMA5A,MX1,RAB29,EYA2,ACTN2,LRP5,HTR2B,LGMN,ZMAT3,TM7SF3,PRKCA,TXNIP,CAMK2D,LRP2,CFLAR,CTSZ,FGFR2,USP53,PRKD1,NCSTN,ITGA6,ATF6,ID3,LRP6,HIP1,HSPB1,SERPINE1,CRYAB,PDE1A,UNC5B,GULP1,TNFSF10,RABEP1,MAEL,HIF1A,OPN3,DDX41,PPARGC1A,ACTN1,TEX11,SLIT3,TGFB3,SMAD6,PAK3,RHOT1,ANGPTL4,DAB2,LGALS9,SKP2,TM2D1,PRKAA2,ATCAY,DAPK3,FLNA,AHCYL1,CSF1,SORT1,PLCG2,CYR61,ITPR1,VNN1,BNIP3,FRZB,LOX,ITM2C,CDKN1A,RASSF3,RFK,NACC2,TMEM123,ICAM1,ORMDL3,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0042310	0.00	1.00	12	62	vasoconstriction	BP	0.1464	GJA1,LEP,EDN2,DOCK4,HRH1,ADM,EDN1,HTR2B,ADRA1B,SLC8A1,ICAM1,PIK3C2A	darkgreen	VSMC_M4
GO:0007186	0.00	1.00	50	458	G protein-coupled receptor signaling pathway	BP	0.1464	FAM19A5,ADGRB1,GNAQ,FRMPD1,ABCA1,GPR63,FZD8,GPR39,HRH1,NXPH2,PLCB4,APLP1,FFAR3,ADM,GRK7,PTH,GPR87,RXFP1,ADCY6,ADA,EDN1,RGS2,ACTN2,PREX1,HTR2B,PRKCA,GNB4,ADCY5,GABBR1,RAPGEF4,GPRC5A,GPR160,PCSK1N,OPN3,ADGRE2,GNAI1,ADGRL1,NPPB,ADRA1B,GAS2L2,LMBRD2,TM2D1,NPR3,ADCY9,FLNA,AHCYL1,SORT1,BCAR3,PLN,CCR6	darkgreen	VSMC_M4
GO:0046886	0.00	1.00	4	8	positive regulation of hormone biosynthetic process	BP	0.1464	ADM,HIF1A,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0010039	0.00	1.00	7	26	response to iron ion	BP	0.14839	BCL2,MDM2,TF,MAP1LC3A,CYBRD1,HIF1A,BMP6	darkgreen	VSMC_M4
GO:0044557	0.00	1.00	4	8	relaxation of smooth muscle	BP	0.15173	ABCC8,RGS2,SLC8A1,PRKG1	darkgreen	VSMC_M4

GO:0048522	0.00	1.00	337	4212	positive regulation of cellular process	BP	0.15173	MBP,ZNF516,DOK6,GDF11,BCL2,RNF41,SLC35D3,IFNGR1,CITED2,SASH1,GRIP1,MDM2,DDR1,RNF19A,GRHL2,SOD2,ABRA,ANGPT1,C4A,SMOC2,SCUBE1,GJA1,TRDN,TPD52L1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DOCK8,SH3RF3,KANK1,DCUN1D4,VLDLR,UNC13B,PPP1R9A,CD274,IL18R1,CREB3,REST,RECK,ECM2,ZAP70,TGFBR1,EDN2,ABCA1,MAP3K7,ANTXR1,DOCK4,KIDINS220,MDFIC,TCAF1,EPHB6,SESN1,JADE1,MAP3K8,ITSN2,HIPK2,GATA2,APBB1IP,LIMS2,ZNF398,PPP1R13L,TENM4,NAA16,ELF1,INHBB,SMARCD3,HRH1,LMO7,BABAM2,FOSL2,LBH,LIPT2,KCNE3,LMCD1,RAB2B,SALL2,THRB,ACTN4,ADAM9,TACC1,FGF14,FOXO1,RASSF2,ATP2C1,ANKLE2,CDC42EP3,CYP1B1,SEMA3C,TF,FLT3,WASF3,ZDHHC2,RIC3,FXYD1,HPN,CHD7,LATS2,ANKRD1,PCGF5,CPEB3,MARCH5,NCK1,ADM,CD180,SLC25A4,SH3RF1,ATOH8,CLCN3,OCLN,TEAD1,CHST2,ARHGEF3,PTH,EXTL3,G3BP2,CLU,MED12L,GPM6A,MEIS2,APP,SCARB2,PDGFC,ABCC8,ANXA3,PTPN11,PTX3,LBP,NEK4,CCNT1,HERPUD1,TMEM64,JMY,ATG13,CHD6,PTPN22,PKP4,HNF4A,GDF6,SERINC3,ADA,AKTIP,NGF,EDN1,JAM3,CD47,ETS2,SEMA5A,LPL,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,CDC80,MARCKSL1,RGS2,EYA2,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,FEZ1,NPNT,PREX1,HTR2B,MST1R,LGMN,ZMAT3,TM7SF3,NID1,PRKCA,AFAP1L2,TXNIP,MFGE8,MID1,PLXNA2,SESN2,SHTN1,CAMK2D,CTSS,NGRN,MYLK,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,SYNPO2,TP53BP1,PRKD1,NCSTN,F11R,PLXNB1,ZRANB1,SLC25A12,ARID5B,ITGA6,ZNF365,ATF6,AKAP6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,LNPK,FAM129A,HSPB1,CLIC4,SCN3A4,SERPINE1,CRYAB,PDE1A,UNC5B	darkgreen	VSMC_M4
GO:0003206	0.00	1.00	17	101	cardiac chamber morphogenesis	BP	0.15173	CITED2,MDM2,GRHL2,TGFBR1,PPP1R13L,SMARCD3,SEMA3C,CHD7,TNNT2,LRP2,FGFR2,HIF1A,FGFRL1,SLIT3,SMAD6,CYR61,TBX20	darkgreen	VSMC_M4
GO:0003015	0.00	1.00	25	180	heart process	BP	0.15369	MDM2,GJA1,TRDN,EDN2,TBX18,PPP1R13L,KCNE3,THRB,FXYD1,ADM,ADA,EDN1,RGS2,TNNT2,CAMK2D,ABCC9,CACNA1C,ADRA1B,FLNA,KCNE4,SLC8A1,PLN,TMEM38A,HOPX,YAP1	darkgreen	VSMC_M4
GO:0009611	0.00	1.00	47	422	response to wounding	BP	0.15369	BCL2,DDR1,FAM19A5,SMOC2,SCUBE1,GJA1,MRTFA,GNAQ,KANK1,TGFBR1,GATA2,ITGA9,INHBB,ADM,OCLN,ENTPD1,MYL9,ABCC8,PROS1,DCBLD2,HNF4A,EDN1,JAM3,PRKCA,MYLK,CFLAR,INPP5F,FGFR2,F11R,ID3,LNPK,HSPB1,SERPINE1,HIF1A,TGFB3,FLNA,PLCG2,F3,CYR61,CD151,BNIP3,LOX,CD59,CSRP1,CDKN1A,YAP1,PRKG1	darkgreen	VSMC_M4
GO:0048871	0.00	1.00	43	378	multicellular organismal homeostasis	BP	0.15369	MBP,ZNF516,BCL2,SLC35D3,ANGPT1,GJA1,LAMA2,SH3GL2,LEP,WFS1,PDK4,IL18R1,SLC2A1,EDN2,GATA2,PPP1R13L,FOXO1,TF,CLCN3,OCLN,PTH,PDGFC,ABCC8,PTPN11,ADCY6,TMEM64,JAM3,ADIPOR1,PLCL1,PRKCA,F11R,HSPB1,ACHE,APBB2,PPARGC1A,BBS4,NPR3,PRKAA2,CSF1,ABCA4,ADAMTS5,YAP1,BMP6	darkgreen	VSMC_M4
GO:0042445	0.00	1.00	19	133	hormone metabolic process	BP	0.15369	HSD17B6,LEP,REST,CYP1B1,FFAR3,HPN,ADM,PTPN11,CPQ,BACE2,CTSZ,ATP6AP2,CYP19A1,PCSK1N,HIF1A,PPARGC1A,PCSK4,STC2,BMP6	darkgreen	VSMC_M4
GO:0048662	0.00	1.00	9	44	negative regulation of smooth muscle cell proliferation	BP	0.15369	SOD2,FAM19A5,NDRG2,PPARGC1A,TGFB3,CNN1,NPR3,CDKN1A,PRKG1	darkgreen	VSMC_M4
GO:0060537	0.00	1.00	39	323	muscle tissue development	BP	0.15369	BCL2,CITED2,GJA1,EP300,SGCB,TGFBR1,TBX18,PPP1R13L,TENM4,SEMA3C,CHD7,ANKRD1,SORBS2,RCAN1,EDN1,RIPOR2,RGS2,EYA2,TNNT2,ACTN2,MYLK,LRP2,CFLAR,FGFR2,AKAP6,ZBTB18,PPARGC1A,NPPB,RBFOX1,SLC8A1,LOX,TBX20,CSRP1,PLN,SRPK3,MAFF,HLF,HOPX,YAP1	darkgreen	VSMC_M4
GO:0072593	0.00	1.00	23	176	reactive oxygen species metabolic process	BP	0.15369	BCL2,RNF41,SOD2,ADGRB1,LEP,PDK4,SESN1,CYP1B1,CLCN3,EDN1,PREX1,SESN2,CFLAR,PRDX4,CRYAB,MAOB,HIF1A,PLCG2,CYR61,BNIP3,CDKN1A,RFK,DDIT4	darkgreen	VSMC_M4
GO:0043086	0.00	1.00	56	555	negative regulation of catalytic activity	BP	0.15369	IRAK3,MDM2,C4A,GNAQ,CDKN2B,FAM122A,RECK,LRCH1,ITIH5,CRIM1,LATS2,HIPK3,NCK1,SH3RF1,RNF34,GPR87,APP,ANXA3,PTX3,HERPUD1,PROS1,PTPN22,IFIT1,NGF,PPP1R12B,RGS2,TNNT2,LRP5,TXNIP,WDTC1,F11R,GPRC5A,LRP6,HSPB1,EIF4A2,SERPINE1,CRYAB,RDX,AOC3,LMTK2,PCSK1N,PPP1R36,FAF2,ANGPTL4,NPR3,FAM122C,PLXNB3,SORT1,PPP1R26,SLC8A1,SPINK2,CST3,PLN,CDKN1A,PPM1E,ORMDL3	darkgreen	VSMC_M4
GO:0032352	0.00	1.00	5	13	positive regulation of hormone metabolic process	BP	0.15369	HPN,ADM,HIF1A,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0006897	0.00	1.00	50	444	endocytosis	BP	0.15473	ANGPT1,ADGRB1,SH3GL2,VLDLR,LMBRD1,SYT5,ABCA1,SNAP91,ITSN2,GATA2,MRC1,TF,APLP1,ADM,CLCN3,MCTP1,CLU,APP,ATXN2,SCARB2,PTX3,LBP,LRP5,HTR2B,CFI,MFGE8,ATP9A,LRP2,INPP5F,PRKD1,PI4KB,LRP6,HIP1,SERPINE1,ACHE,GULP1,NLGN1,RABEP1,NUMB,MARCH2,DNAJC6,DAB2,VAMP7,SORT1,FNBP1,CDH13,PLCG2,LRSAM1,CD151,PIK3C2A	darkgreen	VSMC_M4
GO:0060047	0.00	1.00	24	172	heart contraction	BP	0.15669	MDM2,GJA1,TRDN,EDN2,TBX18,PPP1R13L,KCNE3,THRB,FXYD1,ADM,ADA,EDN1,RGS2,TNNT2,CAMK2D,ABCC9,CACNA1C,ADRA1B,FLNA,KCNE4,SLC8A1,PLN,TMEM38A,HOPX	darkgreen	VSMC_M4
GO:0010941	0.00	1.00	109	1223	regulation of cell death	BP	0.15897	BCL2,CITED2,MDM2,CDSN,SOD2,OXR1,ANGPT1,GJA1,TPD52L1,DAPK1,LEP,WFS1,DOCK8,UNC13B,CD274,PDK4,CREB3,REST,TGFBR1,HIPK2,GATA2,LIMS2,TPT1,NAA16,INHBB,BABAM2,ACTN4,FOXO1,RASSF2,ANKLE2,CYP1B1,FLT3,HPN,LATS2,HIPK3,ANKRD1,NCK1,ADM,SLC25A4,SH3RF1,PTH,RNF34,CLU,HERPUD1,JMY,SERINC3,ADA,NGF,EDN1,SEMA5A,RAB29,EYA2,ACTN2,LRP5,HTR2B,LGMN,ZMAT3,TM7SF3,PRKCA,TXNIP,CAMK2D,LRP2,CFLAR,CTSZ,FGFR2,PRKD1,ITGA6,ATF6,ID3,LRP6,HIP1,HSPB1,SERPINE1,CRYAB,PDE1A,UNC5B,TNFSF10,MAEL,HIF1A,OPN3,PPARGC1A,ACTN1,TEX11,TGFB3,SMAD6,PAK3,ANGPTL4,DAB2,LGALS9,SKP2,PRKAA2,DAPK3,FLNA,CSF1,SORT1,PLCG2,CYR61,VNN1,BNIP3,FRZB,LOX,ITM2C,CDKN1A,RASSF3,NACC2,ICAM1,ORMDL3,YAP1,DDIT4	darkgreen	VSMC_M4

GO:0051046	0.00	1.00	47	434	regulation of secretion	BP	0.15918	GJA1,LEP,UNC13B,PPP1R9A,RIC1,REST,ICA1,PREPL,SYT5,GATA2,INHBB,RAB2B,ADAM9,PCLO,FFAR3,CHD7,ANKRD1,PAM,MCTP1,ABCC8,PTPN11,HNF4A,ADA,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ATP9A,ADCY5,RAPGEF4,ACHE,EXPH5,MAOB,CYP19A1,NLGN1,HIF1A,ADGRE2,FBXL20,NPPB,TGFB3,RHOT1,LGALS9,VAMP7,WLS,BMP6	darkgreen	VSMC_M4
GO:0007169	0.00	1.00	55	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	0.17026	DOK6,DDR1,ANGPT1,SMOC2,LEP,KANK1,PDK4,ZAP70,PTPN3,SVEP1,EPHB6,CRIM1,FOXO1,RASSF2,COL4A1,COL4A2,FLT3,FFAR3,PTPRG,NCK1,BLNK,PDGFC,PTPN11,NGF,ADIPOR1,ZNF106,MST1R,LGMN,GALNT3,AFAP1L2,TXNIP,FGFR2,PRKD1,ARID5B,DDR2,GPRC5A,HIP1,HSPB1,IGFBP2,LMTK2,HIF1A,FGFRL1,SIPA1L1,NPTN,PAK3,SH3TC2,CSF1,SORT1,CDH13,F3,BCAR3,LOX,FGF9,PIK3C2A,DDIT4	darkgreen	VSMC_M4
GO:0060411	0.00	1.00	12	59	cardiac septum morphogenesis	BP	0.17068	CITED2,MDM2,TGFBR1,SEMA3C,CHD7,LRP2,FGFR2,FGFRL1,SLIT3,SMAD6,CYR61,TBX20	darkgreen	VSMC_M4
GO:0060395	0.00	1.00	12	62	SMAD protein signal transduction	BP	0.17286	GDF11,TGFBR1,HIPK2,INHBB,TF,ATOH8,HNF4A,GDF6,TGFB3,SMAD6,DAB2,BMP6	darkgreen	VSMC_M4
GO:0001894	0.00	1.00	25	189	tissue homeostasis	BP	0.17286	MBP,BCL2,ANGPT1,GJA1,LAMA2,SH3GL2,PDK4,SLC2A1,GATA2,TF,CLCN3,OCLN,PTH,ABCC8,PTPN11,TMEM64,JAM3,PRKCA,F11R,HSPB1,APBB2,BBS4,CSF1,ABCA4,YAP1	darkgreen	VSMC_M4
GO:0048659	0.00	1.00	18	128	smooth muscle cell proliferation	BP	0.17286	MDM2,SOD2,FAM19A5,GJA1,NDRG2,PTPN11,EDN1,FGFR2,PDE1A,PPARGC1A,TGFB3,CNN1,SKP2,NPR3,CDH13,CDKN1A,FGF9,PRKG1	darkgreen	VSMC_M4
GO:1903557	0.00	1.00	13	72	positive regulation of tumor necrosis factor superfamily cytokine production	BP	0.17526	IFNGR1,LEP,DDX58,CLU,APP,ABCC8,PTPN11,LBP,LPL,HSPB1,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0050794	0.00	1.00	572	7581	regulation of cellular process	BP	0.17526	MBP,ZNF516,DOK6,GDF11,BCL2,RNF41,SLC35D3,IFNGR1,CITED2,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,CDSN,RGS22,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,FAM19A5,TRPS1,SMOC2,SCUBE1,GJA1,ZHX1,TRDN,TPD52L1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,DCUN1D4,RASL11B,VLDLR,UNC13B,C2orf40,PPP1R9A,CD274,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,TMEM8B,REST,ICA1,RECK,ECM2,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,PREPL,EDN2,SYT5,ABCA1,ZNF331,PTPN3,SVEP1,SNAP91,TBX18,CHN2,MAP3K7,ANTXR1,DOCK4,KIDINS220,MDFIC,GPR63,TCAF1,FZD8,EPHB6,SESN1,JADE1,MAP3K8,ITSN2,HIPK2,GATA2,PLEKHB2,APBB1IP,LIMS2,TMEM135,ZNF398,ITM2B,PPP1R13L,LRCH1,SNRK,TPT1,ITGA8,TENM4,GGA3,NAA16,ELF1,ITGA9,INHBB,SMARCD3,USP6NL,GPR39,HRH1,LMO7,ITIH5,NXPH2,BABAM2,FOSL2,RALGAPA2,LBH,NDRG2,LIPT2,KCNE3,POLB,LMCD1,ARHGEF17,RAB2B,SALL2,THRB,PLCB4,ACTN4,SATB1,ADAM9,TACC1,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,COL4A1,COL4A2,ANKLE2,CDC42EP3,CYP1B1,PCLO,SEMA3C,TMEM178A,LMNTD2,TF,EBF4,APLP1,FLT3,AMOTL2,WASF3,ZDHHC2,RIC3,MAP3K1,MIER3,NCOR2,FFAR3,FXYD1,HPN,PTPRG,DENND5A,ZC3H6,CHD7,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,KIAA0355,CPEB3,MARCH5,NCK1,SORBS2,ADM,RNF141,PAM,CD180,SLC25A4,SCN8A,SH3RF1,MRVI1,ATOH8,CLCN3,GRK7,OCLN,TCF7L1,WWC2,TEAD1,MCTP1,CHST2,ARHGEF3,FAM172A,JPH1,PTH,KIF13B,EXTL3,RNF34,CDKL2,G3BP2,CLU,BLNK,MED12L,GPM6A,MEIS2,GPR87,APP,ATX	darkgreen	VSMC_M4
GO:0098609	0.00	1.00	63	592	cell-cell adhesion	BP	0.17526	MBP,BCL2,CITED2,CDSN,LEP,DOCK8,CD274,ZAP70,MAP3K8,LIMS2,ITGA8,TENM4,PCDH9,CD93,ADAM9,ATP2C1,PCDHB4,CYP1B1,VEZT,ZDHHC2,NCK1,CHST2,MYL9,PTPN11,PTPN22,PKP4,ADA,JAM3,CD47,RIPOR2,NPNT,ROBO3,PRKCA,F11R,ITGA6,LRP6,HSPB1,RDX,IGFBP2,NLGN1,ADGRL1,FGFRL1,NPTN,FAT2,CDH2,LGALS9,CDH18,MYO10,PLXNB3,FLNA,CDH13,VCAM1,CYR61,NEXN,VNN1,PCDHGA1,FAT3,PCDHB2,CD83,CSRP1,ICAM1,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0010955	0.00	1.00	6	23	negative regulation of protein processing	BP	0.17526	MDM2,CHAC1,CTSZ,SERPINE1,TMEM59,GLG1	darkgreen	VSMC_M4
GO:1903318	0.00	1.00	6	23	negative regulation of protein maturation	BP	0.17526	MDM2,CHAC1,CTSZ,SERPINE1,TMEM59,GLG1	darkgreen	VSMC_M4
GO:0042692	0.00	1.00	36	303	muscle cell differentiation	BP	0.17526	BCL2,MDM2,SOD2,MRTFA,ADGRB1,SGCB,TBX18,SMARCD3,ACTN4,ANKRD1,SORBS2,ADM,TANC1,RCAN1,EDN1,RIPOR2,RGS2,TNNT2,ACTN2,NPNT,CFLAR,FGFR2,AKAP6,SYNPO2L,SPEG,WDR1,ACTN1,RORA,CDH2,SORT1,SLC8A1,ADAMTS5,LOX,CSRP1,FGF9,HOPX	darkgreen	VSMC_M4
GO:0032640	0.00	1.00	17	111	tumor necrosis factor production	BP	0.17526	IFNGR1,IRAK3,ANGPT1,LEP,DDX58,CLU,APP,ABCC8,PTPN11,LBP,PTPN22,CD47,LPL,HSPB1,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0032680	0.00	1.00	17	111	regulation of tumor necrosis factor production	BP	0.17526	IFNGR1,IRAK3,ANGPT1,LEP,DDX58,CLU,APP,ABCC8,PTPN11,LBP,PTPN22,CD47,LPL,HSPB1,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0010038	0.00	1.00	33	279	response to metal ion	BP	0.17526	BCL2,MDM2,SOD2,SYT5,ADAM9,CPNE4,TF,MAP1LC3A,PAM,PTH,APP,ABCC8,EDN1,TNNT2,LGMN,TXNIP,CAMK2D,NCSTN,CYBRD1,SLC25A12,MAOB,IGFBP2,NLGN1,HIF1A,PPARGC1A,PRKAA2,AHCYL1,PLCG2,VCAM1,BNIP3,PLN,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0035809	0.00	1.00	5	15	regulation of urine volume	BP	0.17526	ADM,ADCY6,EDN1,NPPB,NPR3	darkgreen	VSMC_M4
GO:1905603	0.00	1.00	4	8	regulation of blood-brain barrier permeability	BP	0.17856	ANGPT1,SH3GL2,OCLN,ABCC8	darkgreen	VSMC_M4
GO:0043069	0.00	1.00	66	681	negative regulation of programmed cell death	BP	0.17895	BCL2,CITED2,MDM2,CDSN,SOD2,OXR1,ANGPT1,LEP,WFS1,DOCK8,PDK4,CREB3,TGFBR1,HIPK2,GATA2,LIMS2,TPT1,NAA16,BABAM2,FOXO1,ANKLE2,HPN,HIPK3,SLC25A4,SH3RF1,PTH,RNF34,CLU,HERPUD1,ADA,NGF,EDN1,SEMA5A,EYA2,HTR2B,LGMN,TM7SF3,PRKCA,LRP2,CFLAR,FGFR2,ITGA6,LRP6,HSPB1,SERPINE1,CRYAB,UNC5B,MAEL,HIF1A,OPN3,PPARGC1A,TEX11,TGFB3,SMAD6,ANGPTL4,DAB2,PRKAA2,FLNA,PLCG2,CYR61,VNN1,BNIP3,CDKN1A,ICAM1,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0002687	0.00	1.00	15	101	positive regulation of leukocyte migration	BP	0.18225	DOCK8,CREB3,EDN2,APP,LBP,EDN1,JAM3,CD47,RIPOR2,LGMN,SERPINE1,LGALS9,CSF1,CCR6,ICAM1	darkgreen	VSMC_M4
GO:1904705	0.00	1.00	10	53	regulation of vascular associated smooth muscle cell proliferation	BP	0.18334	MDM2,SOD2,FAM19A5,GJA1,EDN1,TGFB3,CNN1,CDKN1A,FGF9,PRKG1	darkgreen	VSMC_M4

GO:1902533	0.00	1.00	71	731	positive regulation of intracellular signal transduction	BP	0.19273	DOK6,SASH1,ABRA,ANGPT1,GJA1,TPD52L1,EP300,LEP,SH3RF3,IL18R1,ZAP70,TGFBR1,MAP3K7,HIPK2,LMCD1,ACTN4,ADAM9,RASSF2,ATP2C1,FLT3,ANKRD1,NCK1,SH3RF1,ARHGEF3,APP,PDGFC,PTPN11,PTPN22,GDF6,SERINC3,ADA,NGF,EDN1,SEMA5A,NPNT,HTR2B,MST1R,PRKCA,MID1,LRP2,CFLAR,FGFR2,PRKD1,F11R,PLXNB1,AKAP6,MAP3K13,HIP1,UNC5B,SYNPO2L,TNFSF10,NLGN1,ADRA1B,NPTN,MAPRE2,CDH2,LGALS9,FLNA,PLEKHG5,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,WLS,C10orf71,FGF9,EDA,NACC2,ICAM1	darkgreen	VSMC_M4
GO:0050921	0.00	1.00	16	109	positive regulation of chemotaxis	BP	0.19359	SMOC2,CREB3,EDN2,LBP,EDN1,SEMA5A,RIPOR2,LGMN,PRKD1,HSPB1,SERPINE1,LGALS9,CSF1,CDH13,F3,CCR6	darkgreen	VSMC_M4
GO:0003073	0.00	1.00	11	60	regulation of systemic arterial blood pressure	BP	0.19359	SOD2,GJA1,EDN2,ADM,EDN1,CTSZ,ATP6AP2,NPPB,ADRA1B,SLC2A5,NCALD	darkgreen	VSMC_M4
GO:0007507	0.00	1.00	53	474	heart development	BP	0.19359	CITED2,MDM2,GRHL2,SCUBE1,GJA1,EP300,SGCB,REST,TGFBR1,TBX18,GYS1,PPP1R13L,TENM4,SMARCD3,SEMA3C,CHD7,ANKRD1,SORBS2,ADM,PAM,PTPN11,EDN1,RGS2,RBM20,TNNT2,ACTN2,HTR2B,SEC24B,LRP2,FGFR2,AKAP6,ID3,SYNPO2L,HIF1A,CACNA1C,NPPB,FGFRL1,SLIT3,SMAD6,BBS4,FLNA,VCAM1,LMO4,CYR61,SLC8A1,LOX,TBX20,PDLIM3,PLN,CDKN1A,HOPX,YAP1,CRELD1	darkgreen	VSMC_M4
GO:0048545	0.00	1.00	31	258	response to steroid hormone	BP	0.196	BCL2,MDM2,EP300,REST,IGFBP7,PAPPA,LBH,ADAM9,FOXO1,FLT3,NCOR2,ADM,PAM,ANXA3,EDN1,TXNIP,CFLAR,TRIM63,STRN3,MAOB,IGFBP2,SLIT3,TGFB3,DAB2,SKP2,LOX,CDKN1A,ICAM1,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:1990874	0.00	1.00	10	54	vascular associated smooth muscle cell proliferation	BP	0.19975	MDM2,SOD2,FAM19A5,GJA1,EDN1,TGFB3,CNN1,CDKN1A,FGF9,PRKG1	darkgreen	VSMC_M4
GO:0050789	0.00	1.00	592	7907	regulation of biological process	BP	0.20232	MBP,ZNF516,DOK6,GDF11,BCL2,RNF41,SLC35D3,IFNGR1,CITED2,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,CDSN,RGS22,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,FAM19A5,TRPS1,SMOC2,SCUBE1,AFF4,GJA1,ZHX1,TRDN,TPD52L1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,DCUN1D4,RASL11B,VLDLR,UNC13B,C2orf40,PPP1R9A,CD274,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,TMEM8B,REST,ICA1,RECK,ECM2,IGFBP7,ZAP70,FRMPD1,SNX13,TGFBR1,PREPL,EDN2,SYT5,ABCA1,ZNF331,PTPN3,SVEP1,SNAP91,TBX18,CHN2,MAP3K7,ANTXR1,DOCK4,KIDINS220,MDFIC,GPR63,TCAF1,FZD8,EPHB6,SESN1,JADE1,MAP3K8,ITSN2,HIPK2,GATA2,PLEKHB2,APBB1IP,LIMS2,ABHD12,TMEM135,ZNF398,ITM2B,PPP1R13L,LRCH1,SNRK,TPT1,ITGA8,TENM4,GGA3,NAA16,ELF1,ITGA9,INHBB,SMARCD3,USP6NL,GPR39,HRH1,LMO7,ITIH5,NXPH2,BABAM2,FOSL2,RALGAPA2,LBH,NDRG2,LIPT2,KCNE3,POLB,LMCD1,ARHGEF17,RAB2B,SALL2,THRB,PLCB4,ACTN4,FMNL2,SATB1,ADAM9,TACC1,CRIM1,FGF14,FOXO1,RASSF2,ATP2C1,COL4A1,COL4A2,ANKLE2,CDC42EP3,CYP1B1,PCLO,SEMA3C,TMEM178A,LMNTD2,TF,EBF4,APLP1,FLT3,AMOTL2,WASF3,ZDHHC2,RIC3,MAP3K1,MIER3,NCOR2,FFAR3,FXYD1,HPN,FBLN7,PTPRG,DENND5A,ZC3H6,CHD7,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,KIAA0355,CPEB3,MARCH5,NCK1,SORBS2,ADM,RNF141,PAM,CD180,SLC25A4,SCN8A,SH3RF1,MRVI1,ATOH8,CLCN3,GRK7,OCLN,TCF7L1,WWC2,TEAD1,MCTP1,CHST2,ARHGEF3,FAM172A,JPH1,PTH,KIF13B,EXTL3,RNF34,CDKL2,G3BP2,CLU,BLNK,MED12L,	darkgreen	VSMC_M4
GO:0051091	0.00	1.00	26	204	positive regulation of DNA-binding transcription factor activity	BP	0.20232	IRAK3,ABRA,EP300,DDX58,IL18R1,MAP3K7,HIPK2,CLU,APP,ANXA3,JMY,EDN1,LRP5,CFLAR,TP53BP1,PRKD1,ARID5B,DDR2,MAP3K13,LRP6,PPARGC1A,LGALS9,PLCG2,TERF2IP,EDA,ICAM1	darkgreen	VSMC_M4
GO:0023061	0.00	1.00	37	325	signal release	BP	0.20232	STX11,GJA1,LEP,UNC13B,PPP1R9A,REST,ICA1,PREPL,SYT5,ABCA1,INHBB,PCLO,FFAR3,CHD7,ADM,MCTP1,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,MAOB,CYP19A1,NLGN1,HIF1A,FBXL20,RHOT1,VAMP7,WLS,BMP6,MAFA	darkgreen	VSMC_M4
GO:0003044	0.00	1.00	7	30	regulation of systemic arterial blood pressure mediated by a chemical signal	BP	0.20232	SOD2,EDN2,EDN1,CTSZ,ATP6AP2,ADRA1B,SLC2A5	darkgreen	VSMC_M4
GO:0050790	0.00	1.00	157	1823	regulation of catalytic activity	BP	0.20574	MBP,BCL2,SASH1,IRAK3,MDM2,DDR1,GRHL2,ANGPT1,C4A,TPD52L1,DAPK1,GNAQ,LEP,CDKN2B,FAM122A,DOCK8,DCUN1D4,VLDLR,TPM2,PPP1R9A,RIC1,REST,RECK,SNX13,EDN2,CHN2,MAP3K7,ANTXR1,DOCK4,KIDINS220,EPHB6,ITSN2,RCBTB2,LRCH1,USP6NL,ITIH5,RALGAPA2,ARHGEF17,ADAM9,CRIM1,RASSF2,ANKLE2,FLT3,DENND5A,LATS2,HIPK3,TRIM23,NCK1,SH3RF1,ARHGEF3,PTH,RNF34,CLU,GPR87,APP,SCARB2,PDGFC,RXFP1,ANXA3,PTX3,CCNT1,HERPUD1,PROS1,TMEM64,PTPN22,PKP4,RCAN1,IFIT1,RBL2,NGF,EDN1,RIPOR2,PPP1R12B,RGS2,TNNT2,LRP5,ARRDC4,NPNT,PREX1,HTR2B,MST1R,LGMN,SERINC2,AFAP1L2,TXNIP,PLXNA2,SESN2,CAMK2D,CFLAR,WDTC1,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,ITGA6,RAPGEF4,DDR2,GPRC5A,MAP3K13,LRP6,HIP1,HSPB1,EIF4A2,SERPINE1,CRYAB,ARHGAP20,RDX,AOC3,ATG14,TNFSF10,LMTK2,RABEP1,PCSK1N,HIF1A,IQSEC3,CCPG1,PPP1R36,CACNA1C,FAF2,SIPA1L1,MAT2B,CCNG1,TOM1L1,MAPRE2,EVI5L,ANGPTL4,ARHGAP28,LGALS9,OCRL,NPR3,FAM122C,PLXNB3,PLEKHG5,CSF1,SORT1,PPP1R26,TBC1D13,F3,ARHGAP29,BCAR3,LMO4,CYR61,SYDE2,SLC8A1,DNAJA2,SPINK2,CST3,PLN,CDKN1A,PPM1E,RFK,CNTD2,GABARAPL2,ICAM1,ORMDL3,PRKG1	darkgreen	VSMC_M4
GO:2001028	0.00	1.00	5	15	positive regulation of endothelial cell chemotaxis	BP	0.20791	SMOC2,SEMA5A,LGMN,PRKD1,HSPB1	darkgreen	VSMC_M4
GO:0051346	0.00	1.00	28	242	negative regulation of hydrolase activity	BP	0.22399	MDM2,C4A,RECK,LRCH1,ITIH5,CRIM1,SH3RF1,RNF34,APP,PTX3,HERPUD1,PROS1,NGF,RGS2,TNNT2,F11R,SERPINE1,CRYAB,RDX,PCSK1N,PPP1R36,ANGPTL4,PLXNB3,SORT1,PPP1R26,SPINK2,CST3,PLN	darkgreen	VSMC_M4

GO:0022603	0.00	1.00	77	761	regulation of anatomical structure morphogenesis	BP	0.22427	CITED2,SASH1,UST,GRIP1,FAM19A5,SMOC2,GJA1,ADGRB1,MLLT3,LEP,KANK1,PPP1R9A,RECK,TBX18,ITSN2,HIPK2,GATA2,LIMS2,TMEM135,TENM4,ACTN4,FMNL2,COL4A2,CDC42EP3,CYP1B1,SEMA3C,WASF3,HPN,MARCH5,ADM,KIF13B,SHROOM3,ABCC8,ANXA3,HNF4A,ADA,NGF,EDN1,SEMA5A,PREX1,PRKCA,SEC24B,PLXNA2,SHTN1,FGFR2,PRKD1,F11R,PLXNB1,ZRANB1,MAP3K13,HSPB1,CUX1,SERPINE1,RDX,DACT1,NLGN1,WDR1,HIF1A,PPARGC1A,NPPB,SIPA1L1,CDH2,ULK2,PAK3,ANGPTL4,DAB2,MYO10,DAPK3,PLXNB3,FLNA,CSF1,F3,BNIP3,CST3,ICAM1,SDC2,MYL12B	darkgreen	VSMC_M4
GO:0097067	0.00	1.00	5	14	cellular response to thyroid hormone stimulus	BP	0.22747	BRD8,THRB,CTSS,RDX,PPARGC1A	darkgreen	VSMC_M4
GO:0006875	0.00	1.00	42	381	cellular metal ion homeostasis	BP	0.22932	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,CYBRD1,AKAP6,LRP6,HIF1A,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2,BMP6	darkgreen	VSMC_M4
GO:0010508	0.00	1.00	16	105	positive regulation of autophagy	BP	0.23481	DAPK1,MAP3K7,SESN1,FOXO1,SLC25A4,SESN2,PRKD1,ATF6,HIF1A,CALCOCO2,PRKAA2,TMEM59,LRSAM1,BNIP3,PIK3C2A,ORMDL3	darkgreen	VSMC_M4
GO:0007193	0.00	1.00	9	45	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	BP	0.23534	FFAR3,ADCY6,EDN1,RGS2,ADCY5,GABBR1,GNAI1,NPR3,FLNA	darkgreen	VSMC_M4
GO:0097066	0.00	1.00	6	21	response to thyroid hormone	BP	0.2354	BRD8,THRB,HPN,CTSS,RDX,PPARGC1A	darkgreen	VSMC_M4
GO:0044092	0.00	1.00	75	806	negative regulation of molecular function	BP	0.23713	IRAK3,MDM2,C4A,TRDN,GNAQ,CDKN2B,WFS1,FAM122A,RECK,LRCH1,ITIH5,KCNE3,CRIM1,CYP1B1,LATS2,HIPK3,NCK1,SH3RF1,RNF34,G3BP2,GPR87,APP,ANXA3,PTX3,HERPUD1,PROS1,PTPN22,IFIT1,NGF,RIPOR2,PPP1R12B,RGS2,TNNT2,ACTN2,LRP5,TXNIP,CAMK2D,CTSZ,WDTC1,F11R,GPRC5A,ID3,LRP6,HSPB1,EIF4A2,SERPINE1,CRYAB,RDX,AOC3,DACT1,LMTK2,PCSK1N,PPP1R36,PPARGC1A,FAF2,ANGPTL4,ARHGAP28,DAB2,NPR3,FAM122C,PLXNB3,FLNA,SORT1,PPP1R26,ZFP90,KCNE4,SLC8A1,SPINK2,CST3,XIRP1,LYPD6,PLN,CDKN1A,PPM1E,ORMDL3	darkgreen	VSMC_M4
GO:0003018	0.00	1.00	26	200	vascular process in circulatory system	BP	0.24035	SOD2,ANGPT1,GJA1,SH3GL2,LEP,SLC2A1,EDN2,DOCK4,HRH1,ADM,OCLN,ABCC8,ADCY6,EDN1,RGS2,HTR2B,ABCC9,LRP2,NPPB,ADRA1B,NPR3,SLC8A1,ICAM1,PIK3C2A,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0051128	0.00	1.00	164	1877	regulation of cellular component organization	BP	0.24527	BCL2,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,ANGPT1,GJA1,EP300,ADGRB1,SH3GL2,MLLT3,LIMCH1,FAM122A,KANK1,VLDLR,UNC13B,PPP1R9A,RIC1,IGFBP7,TGFBR1,ABCA1,SNAP91,ANTXR1,KIDINS220,JADE1,ITSN2,GATA2,TMEM135,USP6NL,ADAM9,CDC42EP3,SEMA3C,LMNTD2,TF,WASF3,ZDHHC2,HPN,PTPRG,DENND5A,CHPT1,ANKRD1,MARCH5,NCK1,PAM,SLC25A4,OCLN,MCTP1,KIF13B,EXTL3,G3BP2,CLU,GPM6A,APP,ATXN2,SCARB2,ABCC8,PTPN11,ADCY6,JMY,DCBLD2,HNF4A,NGF,EDN1,JAM3,CD47,SEMA5A,RAB29,ABCG1,ADIPOR1,RIPOR2,RGS2,PDE4DIP,ACTN2,LRP5,FEZ1,PREX1,MID1,PLXNA2,SESN2,SHTN1,CAMK2D,CFLAR,CTSZ,INPP5F,SYNPO2,PRKD1,F11R,PLXNB1,ITGA6,ZNF365,AKAP6,DDR2,MAP3K13,HIP1,LNPK,CUX1,SERPINE1,CRYAB,PAPPA2,RDX,SYNPO2L,MMP1,TNFSF10,DACT1,NLGN1,WDR1,HIF1A,GNAI1,ADGRL1,PPARGC1A,NPPB,ANGPTL7,SIPA1L1,NUMB,CALCOCO2,SLIT3,TGFB3,SMAD6,TOM1L1,BBS4,NPTN,MAPRE2,SYNPO,CDH2,ULK2,PAK3,GAS2L2,EVI5L,RHOT1,CRLF3,ARHGAP28,DNAJC6,DAB2,PATJ,PRKAA2,MYO10,DAPK3,PLXNB3,FLNA,CDH13,PLCG2,SPTAN1,TERF2IP,LRSAM1,LMO4,NEXN,CD151,BNIP3,FRZB,TBX20,LRRC24,ITM2C,CST3,OSGIN2,CDKN1A,PPM1E,DSTN,ICAM1,SDC2,YAP1,IGFBPL1,BMP6	darkgreen	VSMC_M4
GO:0048660	0.00	1.00	17	124	regulation of smooth muscle cell proliferation	BP	0.24527	MDM2,SOD2,FAM19A5,GJA1,NDRG2,EDN1,FGFR2,PDE1A,PPARGC1A,TGFB3,CNN1,SKP2,NPR3,CDH13,CDKN1A,FGF9,PRKG1	darkgreen	VSMC_M4
GO:0055001	0.00	1.00	21	150	muscle cell development	BP	0.24527	BCL2,SGCB,TBX18,ACTN4,ANKRD1,SORBS2,ADM,RCAN1,EDN1,RIPOR2,RGS2,TNNT2,ACTN2,CFLAR,AKAP6,SYNPO2L,WDR1,ACTN1,SLC8A1,LOX,CSRP1	darkgreen	VSMC_M4
GO:0045216	0.00	1.00	21	146	cell-cell junction organization	BP	0.24527	GRHL2,GJA1,TGFBR1,SVEP1,LIMS2,OCLN,ABCC8,PKP4,JAM3,PRKCA,PARD6B,F11R,RDX,WDR1,NUMB,TGFB3,CDH2,PATJ,CDH18,FLNA,BMP6	darkgreen	VSMC_M4
GO:0007517	0.00	1.00	31	259	muscle organ development	BP	0.24825	BCL2,CITED2,LAMA2,EP300,ADGRB1,SGCB,TGFBR1,CHD7,ANKRD1,JPH1,RCAN1,RIPOR2,TNNT2,MYLK,LRP2,CFLAR,FGFR2,ARID5B,TAGLN,ID3,CRYAB,SPEG,ZBTB18,FGFRL1,SGCA,RBFOX1,LOX,TBX20,SRPK3,MAFF,HLF	darkgreen	VSMC_M4
GO:0009409	0.00	1.00	8	39	response to cold	BP	0.24825	ZNF516,SOD2,TMEM135,FOXO1,ADM,LPL,PCSK1N,PPARGC1A	darkgreen	VSMC_M4
GO:0061035	0.00	1.00	11	61	regulation of cartilage development	BP	0.25293	TRPS1,LEP,TGFBR1,PTH,PTPN11,GDF6,LNPK,GLG1,CYR61,FRZB,BMP6	darkgreen	VSMC_M4
GO:0014706	0.00	1.00	36	307	striated muscle tissue development	BP	0.25293	BCL2,CITED2,GJA1,EP300,SGCB,TGFBR1,TBX18,PPP1R13L,TENM4,SEMA3C,CHD7,ANKRD1,SORBS2,RCAN1,EDN1,RIPOR2,RGS2,EYA2,TNNT2,ACTN2,LRP2,CFLAR,FGFR2,AKAP6,ZBTB18,NPPB,RBFOX1,SLC8A1,LOX,TBX20,PLN,SRPK3,MAFF,HLF,HOPX,YAP1	darkgreen	VSMC_M4
GO:1901222	0.00	1.00	12	75	regulation of NIK/NF-kappaB signaling	BP	0.25839	SASH1,EP300,IL18R1,ACTN4,RASSF2,APP,PTPN22,EDN1,ADIPOR1,LGALS9,TERF2IP,EDA	darkgreen	VSMC_M4
GO:0007015	0.00	1.00	42	373	actin filament organization	BP	0.25839	BCL2,LIMCH1,KANK1,TPM2,PPP1R9A,TGFBR1,CALD1,CDC42EP3,TF,WASF3,NCK1,SORBS2,SHROOM3,JMY,CD47,MYO1B,SEMA5A,MARCKSL1,TNNT2,ACTN2,PREX1,SHTN1,SYNPO2,F11R,HIP1,RDX,SYNPO2L,WDR1,MICAL3,ACTN1,TGFB3,SYNPO,PAK3,GAS2L2,PLS3,ARHGAP28,FLNA,SPTAN1,XIRP1,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4

GO:0060249	0.00	1.00	27	218	anatomical structure homeostasis	BP	0.2584	MBP,BCL2,ANGPT1,GJA1,LAMA2,SH3GL2,PDK4,SLC2A1,GATA2,TF,CLCN3,OCLN,PTH,ABCC8,PTPN11,TMEM64,JAM3,PRKCA,F11R,HSPB1,HIF1A,APBB2,BBS4,CSF1,ABCA4,LOX,YAP1	darkgreen	VSMC_M4
GO:0007204	0.00	1.00	25	194	positive regulation of cytosolic calcium ion concentration	BP	0.26104	BCL2,GJA1,TRDN,EDN2,GATA2,RIC3,CHD7,ADM,JPH1,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,AKAP6,LRP6,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A,CCR6	darkgreen	VSMC_M4
GO:0010648	0.00	1.00	96	1047	negative regulation of cell communication	BP	0.26184	BCL2,IRAK3,MDM2,RGS22,SOD2,GJA1,TLE4,MLLT3,LEP,WFS1,KANK1,RASL11B,PPP1R9A,RNF149,CREB3,REST,SNX13,TGFBR1,PTPN3,TBX18,SESN1,JADE1,HIPK2,GATA2,TPT1,INHBB,LBH,NDRG2,CRIM1,FOXO1,RASSF2,APLP1,NCOR2,LATS2,HIPK3,NCK1,ADM,SH3RF1,WWC2,RNF34,CLU,ABCC8,PTPN11,HERPUD1,TMEM64,PTPN22,CHAC1,ADA,RCAN1,EDN1,CD47,ADIPOR1,RIPOR2,RGS2,EYA2,PFKL,KCTD10,HTR2B,LGMN,SESN2,LRP2,CFLAR,INPP5F,CASTOR1,STRN3,ITGA6,GPRC5A,HSPB1,SERPINE1,ACHE,UNC5B,IGFBP2,DACT1,HIF1A,GNAI1,RORA,SLIT3,TGFB3,SMAD6,CDH2,NOMO1,FST,DAB2,PRKAA2,TLE2,GLG1,MIR99A,ITPR1,VNN1,ADAMTSL2,FRZB,TBX20,TMEM170B,ICAM1,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0071677	0.00	1.00	8	41	positive regulation of mononuclear cell migration	BP	0.26631	DOCK8,CREB3,APP,CD47,LGMN,SERPINE1,LGALS9,CCR6	darkgreen	VSMC_M4
GO:0023057	0.00	1.00	96	1048	negative regulation of signaling	BP	0.26663	BCL2,IRAK3,MDM2,RGS22,SOD2,GJA1,TLE4,MLLT3,LEP,WFS1,KANK1,RASL11B,PPP1R9A,RNF149,CREB3,REST,SNX13,TGFBR1,PTPN3,TBX18,SESN1,JADE1,HIPK2,GATA2,TPT1,INHBB,LBH,NDRG2,CRIM1,FOXO1,RASSF2,APLP1,NCOR2,LATS2,HIPK3,NCK1,ADM,SH3RF1,WWC2,RNF34,CLU,ABCC8,PTPN11,HERPUD1,TMEM64,PTPN22,CHAC1,ADA,RCAN1,EDN1,CD47,ADIPOR1,RIPOR2,RGS2,EYA2,PFKL,KCTD10,HTR2B,LGMN,SESN2,LRP2,CFLAR,INPP5F,CASTOR1,STRN3,ITGA6,GPRC5A,HSPB1,SERPINE1,ACHE,UNC5B,IGFBP2,DACT1,HIF1A,GNAI1,RORA,SLIT3,TGFB3,SMAD6,CDH2,NOMO1,FST,DAB2,PRKAA2,TLE2,GLG1,MIR99A,ITPR1,VNN1,ADAMTSL2,FRZB,TBX20,TMEM170B,ICAM1,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0003208	0.00	1.00	11	57	cardiac ventricle morphogenesis	BP	0.26668	GRHL2,TGFBR1,PPP1R13L,SMARCD3,SEMA3C,CHD7,TNNT2,LRP2,FGFR2,HIF1A,TBX20	darkgreen	VSMC_M4
GO:0042983	0.00	1.00	4	11	amyloid precursor protein biosynthetic process	BP	0.26863	ITM2B,BACE2,NCSTN,ITM2C	darkgreen	VSMC_M4
GO:0042984	0.00	1.00	4	11	regulation of amyloid precursor protein biosynthetic process	BP	0.26863	ITM2B,BACE2,NCSTN,ITM2C	darkgreen	VSMC_M4
GO:0048513	0.00	1.00	213	2529	animal organ development	BP	0.2708	MBP,ZNF516,BCL2,CITED2,MDM2,DDR1,CDSN,GRHL2,ANGPT1,TRPS1,SCUBE1,GJA1,LAMA2,EP300,ADGRB1,MLLT3,LEP,CDKN2B,WFS1,SGCB,VLDLR,IL18R1,REST,ZAP70,SLC2A1,TGFBR1,EDN2,PTPN3,TBX18,PEX13,GYS1,HIPK2,GATA2,LIMS2,PPP1R13L,SNRK,ITGA8,TENM4,INHBB,SMARCD3,PCDH9,PFKFB3,FOSL2,LBH,NDRG2,POLB,SALL2,THRB,ADAM9,TACC1,FOXO1,RASSF2,COL4A1,CYP1B1,SEMA3C,TMEM178A,TF,APLP1,FLT3,NCOR2,HPN,PTPRG,CHD7,ANKRD1,SORBS2,ADM,PAM,SH3RF1,TEAD1,FAM172A,JPH1,PTH,BLNK,GPM6A,MEIS2,APP,PDGFC,RXFP1,ANXA3,PTPN11,PTX3,TMEM64,PTPN22,HNF4A,GDF6,NAB1,ADA,RCAN1,PDZD7,EDN1,JAM3,SEMA5A,ADIPOR1,COL4A4,KDM5B,RIPOR2,RGS2,RBM20,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,NID1,SUN1,PRKCA,GNB4,TXNIP,SEC24B,ABLIM1,PLXNA2,P4HTM,MYLK,LRP2,CFLAR,CTSZ,FGFR2,NCSTN,PLXNB1,ARID5B,ITGA6,ZNF365,ATF6,TAGLN,AKAP6,DDR2,ID3,LRP6,PRDX4,LNPK,CRYGS,MFAP5,SERPINE1,ACHE,CRYAB,PAPPA2,EXPH5,MAOB,NBR1,EZH1,SYNPO2L,CYP19A1,TNFSF10,DACT1,SPEG,WDR1,HIF1A,OPN3,ZBTB18,CACNA1C,PPARGC1A,ACTN1,NPPB,ZC4H2,ANGPTL7,FGFRL1,RORA,NUMB,TEX11,SGCA,SLIT3,TGFB3,SMAD6,FAXDC2,BBS4,CDH2,PLS3,FST,DAB2,LGALS9,SMARCA1,RBFOX1,BGN,TLE2,FLNA,CSF1,PLCG2,VCAM1,GLG1,BCAR3,LMO4,CYR61,WLS,VNN1,SLC8A1,ADAMTSL2,BNIP3,ADAMTS5,FRZB,CD83,LOX,TBX20,PDLIM3,PLN,SRPK3,MAFF,CDKN1A,FGF9,EDA,HLF,CCR6,HOPX,ICAM1,STC2,YAP1,PRKG1,BMP6,FAM83H,DDIT4,CRELD1	darkgreen	VSMC_M4
GO:0001666	0.00	1.00	29	244	response to hypoxia	BP	0.2732	BCL2,CITED2,MDM2,SOD2,EP300,LEP,REST,SLC2A1,HIPK2,ANKRD1,ADM,PAM,ADA,EDN1,CFLAR,CRYAB,HIF1A,PPARGC1A,PLOD1,RORA,TGFB3,ANGPTL4,VCAM1,ITPR1,SLC8A1,BNIP3,ICAM1,STC2,DDIT4	darkgreen	VSMC_M4
GO:1901700	0.00	1.00	110	1234	response to oxygen-containing compound	BP	0.27554	BCL2,SASH1,IRAK3,MDM2,SOD2,OXR1,GJA1,DAPK1,GNAQ,LEP,KANK1,UNC13B,CD274,PDK4,IGFBP7,SLC2A1,TGFBR1,ABCA1,SESN1,MRC1,INHBB,HRH1,POLB,ADAM9,FOXO1,COL4A1,CYP1B1,APLP1,NCOR2,FFAR3,ANKRD1,CPEB3,NCK1,ADM,MAP1LC3A,PAM,CD180,PTH,CLU,APP,PDGFC,ABCC8,PTPN11,ADCY6,LBP,PTPN22,HNF4A,ADA,EDN1,LPL,ABCG1,ADIPOR1,RGS2,NCOA3,ACTN2,ZNF106,PFKL,LRP5,HTR2B,LGMN,PRKCA,TXNIP,SESN2,ABCC9,ADCY5,CFLAR,WDTC1,FGFR2,CASTOR1,PRKD1,NCSTN,STRN3,AKAP6,ID3,LRP6,SERPINE1,ACHE,CRYAB,MAOB,IGFBP2,CYP19A1,TNFSF10,HIF1A,GNAI1,PPARGC1A,RORA,SLIT3,TGFB3,SMAD6,LGALS9,PRKAA2,FLNA,SLC2A5,HCN2,AHCYL1,SORT1,PLCG2,VCAM1,BCAR3,SLC8A1,BNIP3,PLN,CDKN1A,ICAM1,PIK3C2A,STC2,YAP1,BMP6,MAFA,DDIT4	darkgreen	VSMC_M4
GO:0048771	0.00	1.00	18	129	tissue remodeling	BP	0.27668	MDM2,GJA1,LEP,PDK4,RASSF2,SEMA3C,TF,CHD7,PTH,TMEM64,LRP5,PRKCA,DDR2,HIF1A,TGFB3,BGN,FLNA,CST3	darkgreen	VSMC_M4

GO:0051094	0.00	1.00	92	982	positive regulation of developmental process	BP	0.28007	BCL2,CITED2,SASH1,GRIP1,MDM2,SOD2,SMOC2,GJA1,ADGRB1,LEP,VLDLR,PPP1R9A,REST,ZAP70,TGFBR1,ITSN2,HIPK2,GATA2,LIMS2,PPP1R13L,TENM4,SMARCD3,LBH,ADAM9,CYP1B1,CHD7,CPEB3,MARCH5,ADM,ATOH8,PTH,ANXA3,TMEM64,GDF6,ADA,NGF,EDN1,SEMA5A,LPL,FNDC5,KDM5B,RIPOR2,NCOA3,LRP5,FEZ1,NPNT,PREX1,PRKCA,PLXNA2,SHTN1,LRP2,FGFR2,TP53BP1,PRKD1,F11R,PLXNB1,ZNF365,AKAP6,DDR2,MAP3K13,HSPB1,CUX1,SERPINE1,NLGN1,HIF1A,ADGRL1,PPARGC1A,ZC4H2,NUMB,TGFB3,FAXDC2,NPTN,PAK3,FST,ANGPTL4,DAB2,LGALS9,PLXNB3,FLNA,CSF1,F3,CYR61,VNN1,SLC8A1,BNIP3,FRZB,CD83,TBX20,LRRC24,HOPX,YAP1,BMP6	darkgreen	VSMC_M4
GO:0042446	0.00	1.00	9	47	hormone biosynthetic process	BP	0.28114	HSD17B6,REST,FFAR3,ADM,CYP19A1,HIF1A,PPARGC1A,STC2,BMP6	darkgreen	VSMC_M4
GO:0033629	0.00	1.00	4	10	negative regulation of cell adhesion mediated by integrin	BP	0.2816	CYP1B1,PTPN11,JAM3,SERPINE1	darkgreen	VSMC_M4
GO:0040008	0.00	1.00	53	518	regulation of growth	BP	0.28208	BCL2,CITED2,DDR1,GJA1,BRD8,LEP,WFS1,FAM122A,TMEM8B,IGFBP7,TGFBR1,JADE1,ITSN2,SEMA3C,HPN,CHD7,LATS2,CHPT1,WWC2,EXTL3,APP,DCBLD2,HNF4A,NGF,EDN1,SEMA5A,ADIPOR1,RGS2,LGMN,ZMAT3,SESN2,SHTN1,CAMK2D,FGFR2,AKAP6,MAP3K13,CRYAB,PAPPA2,IGFBP2,MAEL,HIF1A,NPPB,SLIT3,ULK2,CRLF3,CSF1,FRZB,TBX20,OSGIN2,CDKN1A,HOPX,YAP1,IGFBPL1	darkgreen	VSMC_M4
GO:0010561	0.00	1.00	4	11	negative regulation of glycoprotein biosynthetic process	BP	0.28579	ITM2B,BACE2,TMEM59,ITM2C	darkgreen	VSMC_M4
GO:0033688	0.00	1.00	6	22	regulation of osteoblast proliferation	BP	0.28579	BCL2,LRP5,FGFR2,PLXNB1,NPR3,CYR61	darkgreen	VSMC_M4
GO:0046879	0.00	1.00	25	206	hormone secretion	BP	0.28579	GJA1,LEP,REST,ICA1,INHBB,PCLO,FFAR3,CHD7,ADM,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,CYP19A1,HIF1A,VAMP7,BMP6,MAFA	darkgreen	VSMC_M4
GO:1904035	0.00	1.00	11	65	regulation of epithelial cell apoptotic process	BP	0.28579	ANGPT1,WFS1,GATA2,SEMA5A,CFLAR,SERPINE1,PPARGC1A,ANGPTL4,SORT1,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0048523	0.00	1.00	291	3647	negative regulation of cellular process	BP	0.2872	MBP,BCL2,RNF41,CITED2,IRAK3,MDM2,DDR1,LAPTM4B,CDSN,RGS22,GRHL2,SOD2,OXR1,ANGPT1,C4A,FAM19A5,TRPS1,GJA1,ZHX1,TRDN,EP300,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,FAM122A,DOCK8,KANK1,RASL11B,PPP1R9A,CD274,RIC1,PDK4,RNF149,CREB3,ZNF169,REST,RECK,IGFBP7,SNX13,TGFBR1,ABCA1,PTPN3,TBX18,ANTXR1,MDFIC,TCAF1,SESN1,JADE1,HIPK2,GATA2,LIMS2,ZNF398,ITM2B,PPP1R13L,LRCH1,TPT1,GGA3,NAA16,INHBB,ITIH5,BABAM2,LBH,NDRG2,KCNE3,LMCD1,THRB,ACTN4,SATB1,CRIM1,FOXO1,RASSF2,ANKLE2,CYP1B1,SEMA3C,TMEM178A,APLP1,MIER3,NCOR2,FXYD1,HPN,PTPRG,DENND5A,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,CPEB3,MARCH5,NCK1,ADM,SLC25A4,SH3RF1,ATOH8,OCLN,WWC2,MCTP1,JPH1,PTH,RNF34,CLU,MEIS2,APP,ATXN2,ABCC8,PTPN11,PTX3,ADCY6,CCNT1,HERPUD1,PROS1,TMEM64,DCBLD2,PTPN22,HNF4A,CHAC1,NAB1,ADA,RCAN1,RBL2,NGF,EDN1,JAM3,CD47,ETS2,N4BP1,SEMA5A,BACE2,LPL,RAB29,ABCG1,ADIPOR1,KDM5B,RIPOR2,RGS2,EYA2,MXI1,ACTN2,PFKL,LRP5,KCTD10,FEZ1,HTR2B,LGMN,TM7SF3,PRKCA,TXNIP,MID1,ATP9A,PLXNA2,SESN2,YEATS2,CAMK2D,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,CASTOR1,TP53BP1,PTPN14,PRKD1,F11R,PLXNB1,QSOX1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,AKAP6,GPRC5A,ID3,LRP6,PRDX4,FAM129A,HSPB1,EIF4A2,CUX1,SERPINE1,ACHE,CRYAB,RDX,UNC5B,MAOB,IGFBP2,NBR1,EZH1,ATG14,DACT1,NLGN1,SPEG,MAEL,SIN3B,PCSK1N,HIF1A,OPN3,ZBTB18,APBB2,PPP1R36,CACNA1C,ZBTB4,GNAI1,PPARGC1A,ACTN1,NPPB,DISP3,FGFRL1,RORA,NUMB,CHD3,TEX11,SLIT3,TGFB3,CNN1,SMAD6,TOM1L1,CD	darkgreen	VSMC_M4
GO:0010817	0.00	1.00	36	331	regulation of hormone levels	BP	0.2872	HSD17B6,GJA1,LEP,REST,ICA1,INHBB,CYP1B1,PCLO,FFAR3,HPN,CHD7,ADM,ABCC8,PTPN11,HNF4A,CPQ,EDN1,BACE2,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ADCY5,CTSZ,RAPGEF4,ATP6AP2,CYP19A1,PCSK1N,HIF1A,PPARGC1A,PCSK4,VAMP7,STC2,BMP6,MAFA	darkgreen	VSMC_M4
GO:0060548	0.00	1.00	70	754	negative regulation of cell death	BP	0.2872	BCL2,CITED2,MDM2,CDSN,SOD2,OXR1,ANGPT1,LEP,WFS1,DOCK8,PDK4,CREB3,REST,TGFBR1,HIPK2,GATA2,LIMS2,TPT1,NAA16,BABAM2,FOXO1,ANKLE2,HPN,HIPK3,NCK1,SLC25A4,SH3RF1,PTH,RNF34,CLU,HERPUD1,ADA,NGF,EDN1,SEMA5A,EYA2,HTR2B,LGMN,TM7SF3,PRKCA,LRP2,CFLAR,FGFR2,PRKD1,ITGA6,LRP6,HSPB1,SERPINE1,CRYAB,UNC5B,MAEL,HIF1A,OPN3,PPARGC1A,TEX11,TGFB3,SMAD6,ANGPTL4,DAB2,PRKAA2,FLNA,CSF1,PLCG2,CYR61,VNN1,BNIP3,CDKN1A,ICAM1,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0090100	0.00	1.00	14	85	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.2872	GDF11,CITED2,EP300,CDKN2B,TGFBR1,HIPK2,INHBB,GDF6,NPNT,TGFB3,DAB2,CYR61,TBX20,BMP6	darkgreen	VSMC_M4
GO:0070482	0.00	1.00	32	280	response to oxygen levels	BP	0.29051	BCL2,CITED2,MDM2,SOD2,EP300,LEP,REST,SLC2A1,HIPK2,POLB,FOXO1,ANKRD1,ADM,PAM,ADA,EDN1,CFLAR,CRYAB,HIF1A,PPARGC1A,PLOD1,RORA,TGFB3,ANGPTL4,VCAM1,ITPR1,SLC8A1,BNIP3,CDKN1A,ICAM1,STC2,DDIT4	darkgreen	VSMC_M4

GO:0065008	0.00	1.00	228	2770	regulation of biological quality	BP	0.29206	MBP,ZNF516,BCL2,HSD17B6,SLC35D3,CITED2,STX11,GRIP1,MDM2,DDR1,LAPTM4B,SOD2,ANGPT1,SCUBE1,GJA1,TRDN,LAMA2,EP300,ADGRB1,SH3GL2,GNAQ,LEP,WFS1,KANK1,UNC13B,PPP1R9A,PDK4,IL18R1,RNF149,REST,ICA1,SLC2A1,PREPL,EDN2,SYT5,ABCA1,PTPN3,TBX18,DOCK4,HIPK2,GATA2,PPP1R13L,TPT1,GGA3,NAA16,INHBB,HRH1,KCNE3,POLB,THRB,FMNL2,FGF14,FOXO1,TRPC4,RASSF2,ATP2C1,CDC42EP3,CYP1B1,PCLO,SEMA3C,TMEM178A,TF,FLT3,WASF3,ZDHHC2,RIC3,NCOR2,FFAR3,FXYD1,HPN,CHD7,MICU2,CPEB3,NCK1,ADM,PAM,SLC25A4,SCN8A,CLCN3,OCLN,SLC35G1,MCTP1,JPH1,PTH,CLU,ENTPD1,GPM6A,MYL9,APP,PDGFC,SHROOM3,ABCC8,HECTD4,PTPN11,ADCY6,HERPUD1,PROS1,TMEM64,JMY,HNF4A,CPQ,ADA,IFIT1,NGF,EDN1,JAM3,SEMA5A,BACE2,LPL,ABCG1,CNNM2,ADIPOR1,KDM5B,RGS2,EYA2,TNNT2,ACTN2,PFKL,LRP5,PREX1,PLCL1,HTR2B,LGMN,TM7SF3,PRKCA,ATP9A,PLXNA2,SESN2,ARV1,SHTN1,P4HTM,CAMK2D,ADCY5,GABBR1,CTSZ,WDTC1,USP53,PRKD1,NCSTN,F11R,CYBRD1,PLXNB1,RAPGEF4,INSYN2,AKAP6,MAP3K13,LRP6,HIP1,PRDX4,LNPK,HSPB1,SERPINE1,ACHE,CRYAB,ATP6AP2,RDX,MAOA,MAOB,ATG14,FBXL5,CYP19A1,DACT1,NLGN1,WDR1,PCSK1N,HIF1A,APBB2,CACNA1C,ADGRL1,FBXL20,PPARGC1A,NPPB,DISP3,RORA,SIPA1L1,NUMB,ADRA1B,KCNK10,BBS4,NPTN,CDH2,ULK2,PAK3,GAS2L2,RHOT1,ANGPTL4,ARHGAP28,LGALS9,NPR3,PRKAA2,MYO10,DAPK3,PLXNB3,PCSK4,FLNA,VAMP7,SLC2A5,HCN2,CSF1,PLCG2,SPTAN1,F3,ABCA4,KCNE4,ITPR1,SLC8A1,BNIP3,ADAMTS5,LOX,CD59,LRRC24,CSRP1,PLN,NCALD,DSTN,TMEM38A,TMEM123,CCR6,JCAM1,PIK3C2A,ORMDL3,STC2,YAP1,ATP6V	darkgreen	VSMC_M4
GO:0050900	0.00	1.00	28	245	leukocyte migration	BP	0.29206	LEP,DOCK8,CREB3,ZAP70,EDN2,LRCH1,HRH1,CHST2,APP,LBP,ADA,EDN1,JAM3,CD47,RIPOR2,PREX1,LGMN,F11R,SERPINE1,WDR1,ADGRE2,GP2,MMP28,LGALS9,CSF1,VCAM1,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0002237	0.00	1.00	27	236	response to molecule of bacterial origin	BP	0.29332	SASH1,IRAK3,SOD2,GJA1,CD274,ABCA1,MRC1,ADAM9,ANKRD1,ADM,CD180,ABCC8,LBP,PTPN22,EDN1,PRKCA,FGFR2,SERPINE1,MAOB,PPARGC1A,SMAD6,LGALS9,PLCG2,VCAM1,TLR1,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0032496	0.00	1.00	26	225	response to lipopolysaccharide	BP	0.29916	SASH1,IRAK3,SOD2,GJA1,CD274,ABCA1,MRC1,ADAM9,ANKRD1,ADM,CD180,ABCC8,LBP,PTPN22,EDN1,PRKCA,FGFR2,SERPINE1,MAOB,PPARGC1A,SMAD6,LGALS9,PLCG2,VCAM1,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0002685	0.00	1.00	19	152	regulation of leukocyte migration	BP	0.29921	DOCK8,CREB3,EDN2,LRCH1,CHST2,APP,LBP,ADA,EDN1,JAM3,CD47,RIPOR2,LGMN,SERPINE1,MMP28,LGALS9,CSF1,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0048518	0.00	1.00	354	4533	positive regulation of biological process	BP	0.30391	MBP,ZNF516,DOK6,GDF11,BCL2,RNF41,SLC35D3,IFNGR1,CITED2,SASH1,IRAK3,GRIP1,MDM2,DDR1,RNF19A,GRHL2,SOD2,ABRA,ANGPT1,C4A,SMOC2,SCUBE1,GJA1,TRDN,TPD52L1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DOCK8,SH3RF3,KANK1,DCUN1D4,VLDLR,UNC13B,PPP1R9A,CD274,IL18R1,CREB3,REST,RECK,ECM2,ZAP70,TGFBR1,EDN2,ABCA1,MAP3K7,ANTXR1,DOCK4,KIDINS220,MDFIC,TCAF1,EPHB6,SESN1,JADE1,MAP3K8,ITSN2,HIPK2,GATA2,APBB1IP,LIMS2,ZNF398,PPP1R13L,TENM4,GGA3,NAA16,ELF1,INHBB,SMARCD3,HRH1,LMO7,BABAM2,FOSL2,LBH,LIPT2,KCNE3,LMCD1,RAB2B,SALL2,THRB,ACTN4,ADAM9,TACC1,FGF14,FOXO1,RASSF2,ATP2C1,ANKLE2,CDC42EP3,CYP1B1,SEMA3C,TF,FLT3,WASF3,ZDHHC2,RIC3,NCOR2,FFAR3,FXYD1,HPN,FBLN7,CHD7,LATS2,ANKRD1,PCGF5,CPEB3,MARCH5,NCK1,ADM,CD180,SLC25A4,SH3RF1,ATOH8,CLCN3,OCLN,TEAD1,CHST2,ARHGEF3,PTH,EXTL3,G3BP2,CLU,BLNK,MED12L,GPM6A,MEIS2,APP,SCARB2,PDGFC,ABCC8,ANXA3,PTPN11,PTX3,LBP,NEK4,CCNT1,HERPUD1,TMEM64,JMY,ATG13,CHD6,PTPN22,PKP4,HNF4A,GDF6,SERINC3,ADA,AKTIP,IFIT1,NGF,EDN1,JAM3,CD47,ETS2,SEMA5A,LPL,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,CCDC80,MARCKSL1,RGS2,EYA2,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,FEZ1,NPNT,PREX1,HTR2B,MST1R,LGMN,ZMAT3,TM7SF3,NID1,PRKCA,AFAP1L2,TXNIP,CFI,MFGE8,MID1,PLXNA2,SESN2,SHTN1,CAMK2D,CTSS,NGRN,MYLK,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,RBM4B,SYNPO2,TP53BP1,PRKD1,NCSTN,F11R,PLXNB1,ZRANB1,SLC25A12,ARID5B,ITGA6,ZNF365,ATF6,AKAP6,NPAS3,DDR2	darkgreen	VSMC_M4
GO:0019229	0.00	1.00	9	47	regulation of vasoconstriction	BP	0.30586	GJA1,LEP,EDN2,DOCK4,HRH1,ADM,EDN1,ADRA1B,ICAM1	darkgreen	VSMC_M4
GO:2000352	0.00	1.00	6	24	negative regulation of endothelial cell apoptotic process	BP	0.30586	ANGPT1,GATA2,SEMA5A,SERPINE1,ANGPTL4,ICAM1	darkgreen	VSMC_M4
GO:0031589	0.00	1.00	35	294	cell-substrate adhesion	BP	0.30903	BCL2,DDR1,ANGPT1,LIMCH1,KANK1,TMEM8B,ECM2,ANTXR1,LIMS2,TESK2,ITGA8,ACTN4,ADAM9,PTPN11,JAM3,CCDC80,ACTN2,NPNT,PREX1,NID1,SNED1,ITGA6,COL26A1,SERPINE1,ACTN1,SMAD6,FAT2,DAPK3,FLNA,CSF1,CDH13,VCAM1,CYR61,EDA,PLEKHA2	darkgreen	VSMC_M4
GO:0032757	0.01	1.00	8	41	positive regulation of interleukin-8 production	BP	0.31129	LEP,DDX58,LBP,AFAP1L2,SERPINE1,LGALS9,F3,TLR1	darkgreen	VSMC_M4
GO:0035767	0.01	1.00	6	24	endothelial cell chemotaxis	BP	0.31202	SMOC2,SEMA5A,LGMN,PRKD1,HSPB1,PLEKHG5	darkgreen	VSMC_M4
GO:0006956	0.01	1.00	6	27	complement activation	BP	0.31202	C4A,CLU,CFI,C1RL,CD59,MFAP4	darkgreen	VSMC_M4
GO:0032635	0.01	1.00	14	96	interleukin-6 production	BP	0.3197	MBP,IRAK3,LEP,DDX58,APP,PTPN11,LBP,PTPN22,CD47,LPL,AFAP1L2,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0032675	0.01	1.00	14	96	regulation of interleukin-6 production	BP	0.3197	MBP,IRAK3,LEP,DDX58,APP,PTPN11,LBP,PTPN22,CD47,LPL,AFAP1L2,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4

GO:0065007	0.01	1.00	619	8375	biological regulation	BP	0.32432	MBP,ZNF516,DOK6,GDF11,BCL2,RNF41,HSD17B6,SLC35D3,IFNGR1,CITED2,STX11,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,CDSN,RGS22,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,FAM19A5,TRPS1,SMOC2,SCUBE1,AFF4,GJA1,ZHX1,TRDN,TPD52L1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,DCUN1D4,RASL11B,VLDLR,UNC13B,TPM2,C2orf40,PPP1R9A,CD274,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,TMEM8B,REST,ICA1,RECK,ECM2,IGFBP7,ZAP70,FRMPD1,SNX13,SLC2A1,TGFBR1,PREPL,EDN2,SYT5,ABCA1,ZNF331,PTPN3,SVEP1,SNAP91,TBX18,CHN2,MAP3K7,ANTXR1,DOCK4,KIDINS220,MDFIC,GPR63,TCAF1,FZD8,EPHB6,SESN1,JADE1,MAP3K8,ITSN2,HIPK2,GATA2,PLEKHB2,APBB1IP,LIMS2,ABHD12,TMEM135,ZNF398,RCBTB2,ITM2B,PPP1R13L,LRCH1,SNRK,TPT1,ITGA8,TENM4,GGA3,NAA16,ELF1,ITGA9,INHBB,SMARCD3,USP6NL,GPR39,HRH1,LMO7,ITIH5,NXPH2,BABAM2,FOSL2,RALGAPA2,LBH,NDRG2,LIPT2,KCNE3,POLB,LMCD1,ARHGEF17,RAB2B,SALL2,THRB,PLCB4,ACTN4,FMNL2,SATB1,ADAM9,TACC1,CRIM1,FGF14,FOXO1,TRPC4,RASSF2,ATP2C1,COL4A1,COL4A2,ANKLE2,CDC42EP3,CYP1B1,PCLO,SEMA3C,TMEM178A,LMNTD2,TF,EBF4,APLP1,FLT3,AMOTL2,WASF3,ZDHHC2,RIC3,MAP3K1,MIER3,NCOR2,FFAR3,FXYD1,HPN,FBLN7,PTPRG,DENND5A,ZC3H6,CHD7,MICU2,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,KIAA0355,CPEB3,MARCH5,TRIM23,NCK1,SORBS2,ADM,RNF141,PAM,CD180,SLC25A4,SCN8A,SH3RF1,MRVI1,ATOH8,CLCN3,GRK7,OCLN,TCF7L1,WWC2,SLC35G1,TEAD1,MCTP1,CHST2,ARHGEF3,FAM1	darkgreen	VSMC_M4
GO:0044706	0.01	1.00	20	159	multi-multicellular organism process	BP	0.33298	BCL2,CITED2,DDR1,GJA1,LEP,RECK,IGFBP7,SLC2A1,PAPPA,ADM,PAM,RXFP1,ABCC8,EDN1,RGS2,IGFBP2,TGFB3,LGALS9,MAFF,STC2	darkgreen	VSMC_M4
GO:0097435	0.01	1.00	63	622	supramolecular fiber organization	BP	0.33499	BCL2,MDM2,TRDN,LIMCH1,KANK1,TPM2,PPP1R9A,TGFBR1,CALD1,CDC42EP3,CYP1B1,TF,WASF3,ANKRD1,NCK1,SORBS2,OCLN,CLU,APP,SHROOM3,JMY,FMOD,EDN1,CD47,MYO1B,SEMA5A,MARCKSL1,TNNT2,ACTN2,PREX1,MID1,SHTN1,CFLAR,SYNPO2,F11R,DDR2,HIP1,COLGALT2,MFAP5,CRYAB,RDX,P4HA1,SYNPO2L,WDR1,MICAL3,ACTN1,TGFB3,SYNPO,PAK3,GAS2L2,PLS3,ARHGAP28,DAPK3,FLNA,SPTAN1,LOX,CST3,XIRP1,CSRP1,PPM1E,MFAP4,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0032103	0.01	1.00	31	286	positive regulation of response to external stimulus	BP	0.33545	SASH1,SMOC2,EP300,CREB3,EDN2,MAP3K7,FFAR3,CD180,APP,LBP,EDN1,CD47,SEMA5A,LPL,RIPOR2,LGMN,PRKCA,PRKD1,HSPB1,SERPINE1,PAK3,LGALS9,FLNA,VAMP7,CSF1,CDH13,PLCG2,F3,LRSAM1,CCR6,BMP6	darkgreen	VSMC_M4
GO:0043066	0.01	1.00	62	662	negative regulation of apoptotic process	BP	0.33545	BCL2,CITED2,MDM2,SOD2,OXR1,ANGPT1,LEP,WFS1,DOCK8,PDK4,CREB3,TGFBR1,HIPK2,GATA2,LIMS2,TPT1,NAA16,BABAM2,FOXO1,ANKLE2,HPN,HIPK3,SH3RF1,PTH,RNF34,CLU,HERPUD1,ADA,NGF,EDN1,SEMA5A,EYA2,HTR2B,LGMN,PRKCA,LRP2,CFLAR,FGFR2,ITGA6,LRP6,HSPB1,SERPINE1,CRYAB,UNC5B,MAEL,HIF1A,OPN3,PPARGC1A,TEX11,TGFB3,SMAD6,ANGPTL4,DAB2,PRKAA2,FLNA,CYR61,VNN1,BNIP3,CDKN1A,ICAM1,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0010975	0.01	1.00	42	376	regulation of neuron projection development	BP	0.34503	UST,MDM2,EP300,KANK1,VLDLR,PPP1R9A,KIDINS220,SEMA3C,PTPRG,DENND5A,ANKRD1,NCK1,KIF13B,SCARB2,ADCY6,NGF,SEMA5A,RAB29,RGS2,FEZ1,PREX1,PLXNA2,SHTN1,CFLAR,CTSZ,INPP5F,PRKD1,PLXNB1,ITGA6,ZNF365,MAP3K13,CUX1,NLGN1,SIPA1L1,NPTN,CDH2,ULK2,PAK3,PLXNB3,FLNA,ITM2C,SDC2	darkgreen	VSMC_M4
GO:0038063	0.01	1.00	4	9	collagen-activated tyrosine kinase receptor signaling pathway	BP	0.34621	DDR1,COL4A1,COL4A2,DDR2	darkgreen	VSMC_M4
GO:0010460	0.01	1.00	5	17	positive regulation of heart rate	BP	0.34621	EDN2,ADM,ADA,EDN1,ADRA1B	darkgreen	VSMC_M4
GO:0140352	0.01	1.00	60	618	export from cell	BP	0.34621	STX11,GJA1,LEP,UNC13B,PPP1R9A,RIC1,REST,ICA1,PREPL,SYT5,ABCA1,GATA2,INHBB,SYNGR2,KCNE3,RAB2B,ADAM9,PCLO,FFAR3,FXYD1,CHD7,ANKRD1,EXOC6,ADM,PAM,SLC35G1,MCTP1,ABCC8,ANXA3,PTPN11,HNF4A,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ATP9A,ADCY5,RAPGEF4,ACHE,EXPH5,MAOB,CYP19A1,NLGN1,HIF1A,SYT16,MICAL3,ADGRE2,FBXL20,TGFB3,RHOT1,LGALS9,VAMP7,WLS,KCNE4,SLC8A1,PIK3C2A,BMP6,MAFA	darkgreen	VSMC_M4
GO:1901224	0.01	1.00	9	51	positive regulation of NIK/NF-kappaB signaling	BP	0.35149	SASH1,EP300,IL18R1,ACTN4,APP,EDN1,LGALS9,TERF2IP,EDA	darkgreen	VSMC_M4

GO:0048519	0.01	0.99	312	3961	negative regulation of biological process	BP	0.35495	MBP,BCL2,RNF41,IFNGR1,CITED2,IRAK3,MDM2,DDR1,LAPTM4B,CDSN,RGS22,GRHL2,SOD2,OXR1,ANGPT1,C4A,FAM19A5,TRPS1,GJA1,ZHX1,TRDN,EP300,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,FAM122A,DOCK8,KANK1,RASL11B,PPP1R9A,CD274,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,IGFBP7,SNX13,TGFBR1,ABCA1,PTPN3,TBX18,ANTXR1,DOCK4,MDFIC,TCAF1,SESN1,JADE1,HIPK2,GATA2,LIMS2,ZNF398,ITM2B,PPP1R13L,LRCH1,TPT1,GGA3,NAA16,INHBB,ITIH5,BABAM2,LBH,NDRG2,KCNE3,LMCD1,THRB,ACTN4,SATB1,CRIM1,FOXO1,RASSF2,COL4A2,ANKLE2,CYP1B1,SEMA3C,TMEM178A,APLP1,MIER3,NCOR2,FXYD1,HPN,PTPRG,DENND5A,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,CPEB3,MARCH5,NCK1,ADM,SLC25A4,SH3RF1,ATOH8,OCLN,WWC2,MCTP1,FAM172A,JPH1,PTH,RNF34,CLU,MEIS2,APP,ATXN2,ABCC8,PTPN11,PTX3,ADCY6,LBP,CCNT1,HERPUD1,PROS1,TMEM64,DCBLD2,PTPN22,HNF4A,CHAC1,NAB1,ADA,RCAN1,IFIT1,RBL2,NGF,EDN1,JAM3,CD47,ETS2,N4BP1,SEMA5A,BACE2,LPL,MX1,RAB29,ABCG1,ADIPOR1,KDM5B,RIPOR2,RGS2,EYA2,MXI1,ACTN2,PFKL,LRP5,KCTD10,FEZ1,PLCL1,HTR2B,LGMN,TM7SF3,PRKCA,TXNIP,HELZ,MID1,ATP9A,PLXNA2,SESN2,YEATS2,CAMK2D,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,CASTOR1,TP53BP1,PTPN14,PRKD1,F11R,TRIM63,PLXNB1,QSOX1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,AKAP6,GPRC5A,ID3,LRP6,PRDX4,FAM129A,HSPB1,EIF4A2,CUX1,SERPINE1,ACHE,CRYAB,RDX,UNC5B,MAOB,IGFBP2,NBR1,EZH1,ATG14,DACT1,NLGN1,SPEG,MAEL,SIN3B,PCSK1N,HIF1A,OPN3,ZBTB18,APBB2,PPP1R36,CACNA1C,ZBTB4,GNAI1,PPARGC1A,ACTN1,NPPB,DIS	darkgreen	VSMC_M4
GO:0030154	0.01	1.00	245	2966	cell differentiation	BP	0.35495	ZNF516,BCL2,IFNGR1,CITED2,UST,GRIP1,MDM2,DDR1,CDSN,GRHL2,SOD2,ANGPT1,TRPS1,SCUBE1,AFF4,GJA1,ZHX1,LAMA2,EP300,MRTFA,ADGRB1,SH3GL2,MLLT3,LEP,CDKN2B,KANK1,SGCB,VLDLR,PPP1R9A,IL18R1,REST,RECK,ZAP70,TGFBR1,ABCA1,TBX18,PEX13,ANTXR1,KIDINS220,FZD8,EPHB6,ITSN2,HIPK2,GATA2,PLEKHB2,HS6ST1,LIMS2,PPP1R13L,SNRK,ITGA8,TENM4,ELF1,INHBB,SMARCD3,FOSL2,LBH,NDRG2,THRB,ACTN4,ADAM9,CRIM1,FOXO1,TRPC4,RASSF2,COL4A1,COL4A2,SEMA3C,GTSF1,TMEM178A,TF,FLT3,WASF3,HPN,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,NCK1,SORBS2,ADM,SH3RF1,ATOH8,FAM172A,PTH,KIF13B,CLU,BLNK,GPM6A,MEIS2,APP,SCARB2,SHROOM3,RXFP1,ABCC8,PTPN11,PTX3,ADCY6,TMEM64,PTPN22,TANC1,HNF4A,CHAC1,GDF6,NAB1,ADA,RCAN1,RBL2,NGF,PDZD7,EDN1,JAM3,GPRIN3,NFASC,ETS2,SEMA5A,BACE2,LPL,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,RGS2,EYA2,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,ROBO3,SUN1,PRKCA,TXNIP,SEC24B,PARD6B,PLXNA2,SHTN1,P4HTM,NGRN,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,RAPH1,ARID5B,ITGA6,ZNF365,TAGLN,AKAP6,DDR2,MAP3K13,ID3,LRP6,HIP1,LNPK,CUX1,SERPINE1,ACHE,RDX,UNC5B,EXPH5,NBR1,SYNPO2L,LMTK2,NLGN1,SPEG,WDR1,MAEL,HIF1A,OPN3,DDX41,PPARGC1A,ACTN1,ZC4H2,DISP3,RORA,SIPA1L1,NUMB,SLIT3,TGFB3,SMAD6,FAXDC2,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,SH3TC2,FST,DAB2,LGALS9,SMARCA1,MARF1,RBFOX1,ATCAY,DAPK3,PLXNB3,PCSK4,FLNA,CCDC78,CSF1,SORT1,PLCG2,VCAM1,GLG1,LMO4,CYR61,NEXN,VNN1,SLC8A1,CCDC136,SPINK2,BNIP3,ADAMTS5,FRZB,CD83,LOX,TBX	darkgreen	VSMC_M4
GO:0006911	0.01	1.00	8	39	phagocytosis, engulfment	BP	0.35495	ADGRB1,ABCA1,GATA2,CLCN3,MFGE8,GULP1,VAMP7,PLCG2	darkgreen	VSMC_M4
GO:0050886	0.01	1.00	9	49	endocrine process	BP	0.35598	GJA1,LEP,EDN2,INHBB,PTPN11,EDN1,CTSZ,ATP6AP2,BMP6	darkgreen	VSMC_M4
GO:0009914	0.01	1.00	25	212	hormone transport	BP	0.35818	GJA1,LEP,REST,ICA1,INHBB,PCLO,FFAR3,CHD7,ADM,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,CYP19A1,HIF1A,VAMP7,BMP6,MAFA	darkgreen	VSMC_M4
GO:0022898	0.01	1.00	23	186	regulation of transmembrane transporter activity	BP	0.35818	BCL2,GJA1,TRDN,DAPK1,PTPN3,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,JPH1,APP,ABCC8,ACTN2,CAMK2D,CTSS,AKAP6,NLGN1,PPARGC1A,AHCYL1,PLCG2,KCNE4,PLN	darkgreen	VSMC_M4
GO:0045861	0.01	1.00	24	213	negative regulation of proteolysis	BP	0.35818	MDM2,C4A,RECK,PTPN3,HIPK2,ITIH5,CRIM1,SH3RF1,RNF34,APP,HERPUD1,PROS1,CHAC1,NGF,N4BP1,CTSZ,SERPINE1,CRYAB,PCSK1N,TMEM59,GLG1,SPINK2,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:0006898	0.01	1.00	24	192	receptor-mediated endocytosis	BP	0.35818	ANGPT1,SH3GL2,VLDLR,LMBRD1,SNAP91,ITSN2,MRC1,TF,ADM,CLU,ATXN2,SCARB2,HTR2B,LRP2,INPP5F,PI4KB,LRP6,HIP1,SERPINE1,ACHE,NUMB,DNAJC6,DAB2,PLCG2	darkgreen	VSMC_M4
GO:0006873	0.01	1.00	46	444	cellular ion homeostasis	BP	0.35818	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,KCNE3,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,CYBRD1,AKAP6,LRP6,ATP6AP2,HIF1A,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0051050	0.01	1.00	64	660	positive regulation of transport	BP	0.36008	SLC35D3,MDM2,ANGPT1,C4A,GJA1,TRDN,LEP,WFS1,UNC13B,ABCA1,TCAF1,GATA2,INHBB,KCNE3,RAB2B,ACTN4,ADAM9,FGF14,ATP2C1,TF,ZDHHC2,FXYD1,ANKRD1,OCLN,PTH,CLU,ABCC8,PTPN11,PTX3,ATG13,EDN1,CD47,RAB29,ABCG1,ACTN2,FEZ1,TM7SF3,MFGE8,CTSS,MYLK,PRKD1,AKAP6,HIP1,SERPINE1,ACHE,RDX,EXPH5,CYP19A1,NLGN1,HIF1A,OPN3,NPPB,TGFB3,CDH2,ABLIM3,DAB2,FLNA,VAMP7,AHCYL1,PLCG2,WLS,CD151,BMP6,SCP2	darkgreen	VSMC_M4
GO:0002027	0.01	1.00	12	73	regulation of heart rate	BP	0.36174	MDM2,EDN2,KCNE3,ADM,ADA,EDN1,CAMK2D,CACNA1C,ADRA1B,KCNE4,SLC8A1,PLN	darkgreen	VSMC_M4
GO:0072678	0.01	1.00	8	42	T cell migration	BP	0.36277	DOCK8,ZAP70,LRCH1,APP,RIPOR2,F11R,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0003300	0.01	1.00	12	75	cardiac muscle hypertrophy	BP	0.36529	LEP,LMCD1,FOXO1,SORBS2,EDN1,RGS2,HTR2B,PRKCA,CAMK2D,INPP5F,TRIM63,AKAP6	darkgreen	VSMC_M4
GO:0032946	0.01	1.00	12	83	positive regulation of mononuclear cell proliferation	BP	0.36533	BCL2,LEP,CD274,ZAP70,NCK1,PTPN22,ADA,IGFBP2,LGALS9,CSF1,VCAM1,CDKN1A	darkgreen	VSMC_M4

GO:2001026	0.01	1.00	5	18	regulation of endothelial cell chemotaxis	BP	0.36533	SMOC2,SEMA5A,LGMN,PRKD1,HSPB1	darkgreen	VSMC_M4
GO:0034330	0.01	1.00	58	541	cell junction organization	BP	0.36533	BCL2,GRHL2,GJA1,ADGRB1,LIMCH1,UNC13B,PPP1R9A,REST,TGFBR1,SVEP1,LIMS2,TESK2,COL4A1,PCDHB4,PCLO,WASF3,ZDHHC2,OCLN,GPM6A,APP,ABCC8,PTPN11,PKP4,TANC1,JAM3,NFASC,RAB29,ACTN2,LGMN,PRKCA,PARD6B,F11R,PLXNB1,ITGA6,ZNF365,ACHE,RDX,NLGN1,WDR1,APBB2,ADGRL1,ACTN1,ZC4H2,SIPA1L1,NUMB,TGFB3,NPTN,MAPRE2,SYNPO,CDH2,PAK3,PATJ,CDH18,DAPK3,FLNA,PCDHB2,LRRC24,BMP6	darkgreen	VSMC_M4
GO:0034616	0.01	1.00	4	12	response to laminar fluid shear stress	BP	0.36541	ABCA1,ADAM9,TGFB3,SMAD6	darkgreen	VSMC_M4
GO:0030003	0.01	1.00	45	434	cellular cation homeostasis	BP	0.36541	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,HTR2B,CAMK2D,ADCY5,PRKD1,CYBRD1,AKAP6,LRP6,ATP6AP2,HIF1A,CACNA1C,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0032469	0.01	1.00	6	24	endoplasmic reticulum calcium ion homeostasis	BP	0.36541	BCL2,WFS1,APP,HERPUD1,CAMK2D,ITPR1	darkgreen	VSMC_M4
GO:0055065	0.01	1.00	45	438	metal ion homeostasis	BP	0.36541	BCL2,GJA1,TRDN,WFS1,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,CNNM2,HTR2B,CAMK2D,ADCY5,PRKD1,CYBRD1,AKAP6,LRP6,FBXL5,HIF1A,CACNA1C,NPPB,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2,BMP6	darkgreen	VSMC_M4
GO:0016486	0.01	1.00	5	18	peptide hormone processing	BP	0.36541	BACE2,CTSZ,ATP6AP2,PCSK1N,PCSK4	darkgreen	VSMC_M4
GO:0140448	0.01	1.00	5	18	signaling receptor ligand precursor processing	BP	0.36541	BACE2,CTSZ,ATP6AP2,PCSK1N,PCSK4	darkgreen	VSMC_M4
GO:0010862	0.01	1.00	7	32	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	0.36541	GDF11,TGFBR1,INHBB,GDF6,TGFB3,DAB2,BMP6	darkgreen	VSMC_M4
GO:0070665	0.01	1.00	13	93	positive regulation of leukocyte proliferation	BP	0.36541	BCL2,LEP,CD274,ZAP70,NCK1,PTH,PTPN22,ADA,IGFBP2,LGALS9,CSF1,VCAM1,CDKN1A	darkgreen	VSMC_M4
GO:0060326	0.01	1.00	24	206	cell chemotaxis	BP	0.36593	SMOC2,CREB3,EDN2,DOCK4,HRH1,LBP,EDN1,JAM3,SEMA5A,RIPOR2,PREX1,LGMN,PRKD1,HSPB1,SERPINE1,ADGRE2,MMP28,LGALS9,PLXNB3,PLEKHG5,CSF1,VCAM1,LOX,CCR6	darkgreen	VSMC_M4
GO:0060627	0.01	1.00	42	403	regulation of vesicle-mediated transport	BP	0.36629	ANGPT1,C4A,SH3GL2,REST,PREPL,SYT5,SNAP91,GATA2,RAB2B,ATP2C1,PCLO,TF,ZDHHC2,MCTP1,CLU,ATXN2,PTX3,CD47,RAB29,ACTN2,MFGE8,ATP9A,INPP5F,PRKD1,RAPGEF4,HIP1,SERPINE1,RDX,EXPH5,NLGN1,ADGRE2,FBXL20,NUMB,DNAJC6,DAB2,LGALS9,VAMP7,MBTPS1,CDH13,PLCG2,LRSAM1,CD151	darkgreen	VSMC_M4
GO:0035265	0.01	1.00	18	134	organ growth	BP	0.368	BCL2,CITED2,GJA1,LEP,TGFBR1,TENM4,LATS2,SORBS2,WWC2,PTPN11,EDN1,RGS2,FGFR2,AKAP6,DDR2,MAEL,TBX20,YAP1	darkgreen	VSMC_M4
GO:0022008	0.01	0.99	118	1272	neurogenesis	BP	0.368	BCL2,IFNGR1,UST,GRIP1,MDM2,DDR1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,LEP,KANK1,VLDLR,PPP1R9A,REST,TGFBR1,PEX13,KIDINS220,FZD8,EPHB6,ITSN2,HIPK2,GATA2,HS6ST1,TENM4,SMARCD3,THRB,TRPC4,SEMA3C,WASF3,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,NCK1,ADM,SH3RF1,ATOH8,KIF13B,CLU,GPM6A,APP,SCARB2,ABCC8,PTPN11,ADCY6,CHAC1,NAB1,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,BACE2,RAB29,RGS2,FEZ1,PREX1,ROBO3,SUN1,SEC24B,PARD6B,PLXNA2,SHTN1,NGRN,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,NCSTN,PLXNB1,RAPH1,ITGA6,ZNF365,MAP3K13,ID3,LRP6,CUX1,UNC5B,LMTK2,NLGN1,WDR1,HIF1A,ZC4H2,DISP3,RORA,SIPA1L1,NUMB,SLIT3,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,SH3TC2,SMARCA1,ATCAY,DAPK3,PLXNB3,FLNA,CSF1,VCAM1,LMO4,NEXN,BNIP3,TBX20,ITM2C,SDC2,YAP1,PRKG1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0044320	0.01	1.00	4	12	cellular response to leptin stimulus	BP	0.368	LEP,INHBB,ADIPOR1,BBS4	darkgreen	VSMC_M4
GO:0043408	0.01	1.00	50	502	regulation of MAPK cascade	BP	0.37141	DOK6,RNF41,SASH1,IRAK3,ANGPT1,TPD52L1,LEP,SH3RF3,RNF149,TGFBR1,MAP3K7,MDFIC,HIPK2,LBH,NDRG2,ADAM9,FOXO1,RASSF2,FLT3,HIPK3,SH3RF1,APP,PDGFC,PTPN11,PTPN22,GDF6,EDN1,RGS2,NPNT,HTR2B,MST1R,PRKCA,MID1,CFLAR,FGFR2,MAP3K13,ATP6AP2,NBR1,DACT1,ADRA1B,NPTN,NRK,CDH2,PAK3,LGALS9,PLCG2,BCAR3,CYR61,FGF9,ICAM1	darkgreen	VSMC_M4
GO:0003205	0.01	1.00	19	135	cardiac chamber development	BP	0.37141	CITED2,MDM2,GRHL2,TGFBR1,PPP1R13L,SMARCD3,SEMA3C,CHD7,TNNT2,LRP2,FGFR2,HIF1A,FGFRL1,SLIT3,SMAD6,LMO4,CYR61,TBX20,CRELD1	darkgreen	VSMC_M4
GO:0045823	0.01	1.00	6	25	positive regulation of heart contraction	BP	0.37325	EDN2,ADM,ADA,EDN1,RGS2,ADRA1B	darkgreen	VSMC_M4
GO:2001257	0.01	1.00	16	116	regulation of cation channel activity	BP	0.37594	TRDN,DAPK1,KCNE3,FGF14,JPH1,APP,ABCC8,ACTN2,CAMK2D,CTSS,AKAP6,NLGN1,PPARGC1A,PLCG2,KCNE4,PLN	darkgreen	VSMC_M4
GO:0045595	0.01	0.99	104	1153	regulation of cell differentiation	BP	0.3777	BCL2,MDM2,GRHL2,SOD2,TRPS1,GJA1,LEP,KANK1,REST,RECK,ZAP70,TGFBR1,ABCA1,GATA2,PLEKHB2,LIMS2,PPP1R13L,TENM4,SMARCD3,LBH,ACTN4,CRIM1,FOXO1,RASSF2,SEMA3C,TMEM178A,HPN,CHD7,ADM,SH3RF1,ATOH8,PTH,MEIS2,APP,ABCC8,PTPN11,TMEM64,GDF6,ADA,NGF,EDN1,SEMA5A,LPL,ABCG1,ADIPOR1,FNDC5,RIPOR2,RGS2,NCOA3,LRP5,FEZ1,NPNT,PREX1,PRKCA,PLXNA2,SHTN1,P4HTM,LRP2,FGFR2,PRKD1,F11R,PLXNB1,ZNF365,AKAP6,DDR2,MAP3K13,ID3,LNPK,CUX1,SERPINE1,NBR1,NLGN1,WDR1,HIF1A,ZC4H2,DISP3,RORA,NUMB,TGFB3,SMAD6,FAXDC2,NPTN,ULK2,PAK3,FST,DAB2,LGALS9,RBFOX1,PLXNB3,FLNA,CSF1,SORT1,GLG1,CYR61,VNN1,FRZB,CD83,LOX,TBX20,MAFF,FGF9,HOPX,YAP1,BMP6	darkgreen	VSMC_M4
GO:0055082	0.01	1.00	56	564	cellular chemical homeostasis	BP	0.37855	BCL2,GJA1,TRDN,WFS1,UNC13B,EDN2,GATA2,TPT1,KCNE3,FOXO1,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,ABCC8,HERPUD1,TMEM64,EDN1,ABCG1,LRP5,HTR2B,CAMK2D,ADCY5,WDTC1,PRKD1,CYBRD1,AKAP6,LRP6,ATP6AP2,HIF1A,CACNA1C,PPARGC1A,ADRA1B,NPTN,PRKAA2,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,ICAM1,ORMDL3,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4

GO:0046620	0.01	1.00	12	78	regulation of organ growth	BP	0.38201	CITED2,GJA1,TGFBR1,LATS2,WWC2,EDN1,RGS2,FGFR2,AKAP6,MAEL,TBX20,YAP1	darkgreen	VSMC_M4
GO:0090075	0.01	1.00	6	25	relaxation of muscle	BP	0.38387	ABCC8,RGS2,CAMK2D,SLC8A1,PLN,PRKG1	darkgreen	VSMC_M4
GO:0010881	0.01	1.00	5	18	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	BP	0.38454	CAMK2D,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0120035	0.01	0.99	54	524	regulation of plasma membrane bounded cell projection organization	BP	0.39126	UST,MDM2,EP300,KANK1,VLDLR,PPP1R9A,TGFBR1,KIDINS220,CDC42EP3,SEMA3C,PTPRG,DENND5A,ANKRD1,NCK1,OCLN,KIF13B,GPM6A,SCARB2,ADCY6,NGF,SEMA5A,RAB29,RIPOR2,RGS2,FEZ1,PREX1,PLXNA2,SHTN1,CFLAR,CTSZ,INPP5F,PRKD1,PLXNB1,ITGA6,ZNF365,MAP3K13,CUX1,RDX,NLGN1,SIPA1L1,TGFB3,BBS4,NPTN,CDH2,ULK2,PAK3,EVI5L,MYO10,PLXNB3,FLNA,ITM2C,ICAM1,SDC2,YAP1	darkgreen	VSMC_M4
GO:0002790	0.01	1.00	21	172	peptide secretion	BP	0.39126	GJA1,LEP,REST,ICA1,ABCA1,INHBB,PCLO,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,HIF1A,MAFA	darkgreen	VSMC_M4
GO:0098542	0.01	0.99	54	574	defense response to other organism	BP	0.3929	BCL2,IFNGR1,IRAK3,C4A,RNASET2,EP300,ADGRB1,DAPK1,LEP,DDX58,ZAP70,MAP3K7,NT5C3A,MRC1,TF,TRIM23,CD180,G3BP2,CLU,ANXA3,PTPN11,PTX3,LBP,PTPN22,SERINC3,IFIT1,EDN1,CD47,N4BP1,MX1,MST1R,CFI,ABCC9,PRKD1,SERPINE1,C1RL,CALCOCO2,GP2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,LRSAM1,VNN1,TLR1,BNIP3,ADAMTS5,ZNF175,MFAP4,ICAM1,DDIT4	darkgreen	VSMC_M4
GO:0007399	0.01	0.99	164	1867	nervous system development	BP	0.39291	MBP,GDF11,BCL2,IFNGR1,CITED2,UST,GRIP1,MDM2,DDR1,GRHL2,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,LEP,KANK1,VLDLR,C2orf40,PPP1R9A,REST,RECK,SLC2A1,TGFBR1,PEX13,KIDINS220,FZD8,EPHB6,ITSN2,HIPK2,JRKL,GATA2,HS6ST1,ITM2B,ITGA8,TENM4,SMARCD3,PCDH9,PFKFB3,NDRG2,THRB,TACC1,CRIM1,FGF14,TRPC4,COL4A1,ANKLE2,PCDHB4,PCLO,SEMA3C,APLP1,WASF3,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,NCK1,ADM,PAM,SCN8A,SH3RF1,ATOH8,KIF13B,CLU,GPM6A,MEIS2,APP,SCARB2,PDGFC,SHROOM3,ABCC8,ANXA3,PTPN11,ADCY6,CHAC1,NAB1,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,BACE2,RAB29,MARCKSL1,RGS2,FEZ1,PREX1,MST1R,ROBO3,SUN1,GNB4,SEC24B,PARD6B,PLXNA2,SHTN1,NGRN,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,NCSTN,PLXNB1,SLC25A12,RAPH1,ITGA6,ZNF365,MAP3K13,ID3,LRP6,CUX1,ACHE,ATP6AP2,UNC5B,MAOB,EZH1,DACT1,LMTK2,NLGN1,WDR1,HIF1A,ADGRL1,PPARGC1A,ZC4H2,DISP3,RORA,SIPA1L1,NUMB,SLIT3,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,SH3TC2,SMARCA1,RBFOX1,ATCAY,DAPK3,PLXNB3,FLNA,CSF1,VCAM1,LMO4,NEXN,WLS,SLC8A1,PCDHB2,BNIP3,TBX20,LRRC24,ITM2C,FGF9,ORMDL3,SDC2,YAP1,PRKG1,BMP6,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:0002684	0.01	0.99	51	542	positive regulation of immune system process	BP	0.39787	BCL2,IRAK3,C4A,EP300,LEP,DDX58,DOCK8,CD274,IL18R1,CREB3,ZAP70,EDN2,MAP3K7,MAP3K8,GATA2,FFAR3,NCK1,CLU,BLNK,APP,PTPN11,LBP,TMEM64,PTPN22,ADA,EDN1,JAM3,CD47,RAB29,RIPOR2,LGMN,PRKCA,CFI,TP53BP1,SERPINE1,C1RL,IGFBP2,ADGRE2,PAK3,LGALS9,VAMP7,CSF1,PLCG2,VCAM1,VNN1,CD83,CD59,CDKN1A,MFAP4,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0014897	0.01	1.00	12	77	striated muscle hypertrophy	BP	0.39856	LEP,LMCD1,FOXO1,SORBS2,EDN1,RGS2,HTR2B,PRKCA,CAMK2D,INPP5F,TRIM63,AKAP6	darkgreen	VSMC_M4
GO:0008217	0.01	1.00	16	122	regulation of blood pressure	BP	0.40536	SOD2,GJA1,LEP,EDN2,FFAR3,ADM,EDN1,LRP5,CTSZ,F11R,ATP6AP2,NPPB,ADRA1B,NPR3,SLC2A5,NCALD	darkgreen	VSMC_M4
GO:0003215	0.01	1.00	5	18	cardiac right ventricle morphogenesis	BP	0.40536	PPP1R13L,SMARCD3,SEMA3C,CHD7,TBX20	darkgreen	VSMC_M4
GO:0008542	0.01	1.00	7	31	visual learning	BP	0.40536	HRH1,MEIS2,APP,ABCC8,TANC1,HIF1A,NPTN	darkgreen	VSMC_M4
GO:0046883	0.01	1.00	21	174	regulation of hormone secretion	BP	0.40536	GJA1,LEP,REST,ICA1,INHBB,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ADCY5,CYP19A1,HIF1A,VAMP7,BMP6	darkgreen	VSMC_M4
GO:0071216	0.01	1.00	19	157	cellular response to biotic stimulus	BP	0.40536	SASH1,WFS1,CD274,ABCA1,MRC1,ADAM9,ANKRD1,CD180,LBP,PTPN22,PRKCA,TXNIP,SERPINE1,PPARGC1A,PLCG2,TLR1,ICAM1,IGFBPL1,BMP6	darkgreen	VSMC_M4
GO:0042592	0.01	0.99	113	1295	homeostatic process	BP	0.40536	MBP,ZNF516,BCL2,SLC35D3,CITED2,SOD2,ANGPT1,GJA1,TRDN,LAMA2,SH3GL2,LEP,WFS1,UNC13B,PDK4,IL18R1,SLC2A1,EDN2,ABCA1,PTPN3,HIPK2,GATA2,PPP1R13L,TPT1,KCNE3,POLB,FOXO1,TRPC4,RASSF2,ATP2C1,TMEM178A,TF,FLT3,RIC3,CHD7,MICU2,ADM,CLCN3,OCLN,SLC35G1,JPH1,PTH,APP,PDGFC,ABCC8,HECTD4,PTPN11,ADCY6,HERPUD1,TMEM64,HNF4A,ADA,IFIT1,EDN1,JAM3,BACE2,LPL,ABCG1,CNNM2,ADIPOR1,LRP5,PLCL1,HTR2B,PRKCA,SESN2,P4HTM,CAMK2D,ADCY5,WDTC1,PRKD1,NCSTN,F11R,CYBRD1,AKAP6,LRP6,PRDX4,HSPB1,ACHE,ATP6AP2,FBXL5,HIF1A,APBB2,CACNA1C,PPARGC1A,NPPB,DISP3,RORA,ADRA1B,BBS4,NPTN,CDH2,RHOT1,ANGPTL4,LGALS9,NPR3,PRKAA2,CSF1,PLCG2,ABCA4,ITPR1,SLC8A1,BNIP3,ADAMTS5,LOX,PLN,TMEM38A,CCR6,ICAM1,ORMDL3,STC2,YAP1,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0036293	0.01	1.00	29	258	response to decreased oxygen levels	BP	0.40536	BCL2,CITED2,MDM2,SOD2,EP300,LEP,REST,SLC2A1,HIPK2,ANKRD1,ADM,PAM,ADA,EDN1,CFLAR,CRYAB,HIF1A,PPARGC1A,PLOD1,RORA,TGFB3,ANGPTL4,VCAM1,ITPR1,SLC8A1,BNIP3,ICAM1,STC2,DDIT4	darkgreen	VSMC_M4
GO:0002693	0.01	1.00	4	13	positive regulation of cellular extravasation	BP	0.40536	JAM3,CD47,RIPOR2,ICAM1	darkgreen	VSMC_M4
GO:1903524	0.01	1.00	6	26	positive regulation of blood circulation	BP	0.40673	EDN2,ADM,ADA,EDN1,RGS2,ADRA1B	darkgreen	VSMC_M4
GO:0030836	0.01	1.00	4	11	positive regulation of actin filament depolymerization	BP	0.40673	SEMA5A,ACTN2,WDR1,DSTN	darkgreen	VSMC_M4
GO:0014896	0.01	1.00	12	78	muscle hypertrophy	BP	0.40673	LEP,LMCD1,FOXO1,SORBS2,EDN1,RGS2,HTR2B,PRKCA,CAMK2D,INPP5F,TRIM63,AKAP6	darkgreen	VSMC_M4
GO:0051279	0.01	1.00	10	58	regulation of release of sequestered calcium ion into cytosol	BP	0.40673	TRDN,CHD7,JPH1,CAMK2D,PRKD1,AKAP6,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4

GO:0098771	0.01	0.99	50	502	inorganic ion homeostasis	BP	0.40699	BCL2,GJA1,TRDN,WFS1,PDK4,EDN2,GATA2,TPT1,KCNE3,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,CNNM2,HTR2B,CAMK2D,ADCY5,PRKD1,CYBRD1,AKAP6,LRP6,ATP6AP2,FBXL5,HIF1A,CACNA1C,NPPB,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0031344	0.01	0.99	55	538	regulation of cell projection organization	BP	0.40726	UST,GRIP1,MDM2,EP300,KANK1,VLDLR,PPP1R9A,TGFBR1,KIDINS220,CDC42EP3,SEMA3C,PTPRG,DENND5A,ANKRD1,NCK1,OCLN,KIF13B,GPM6A,SCARB2,ADCY6,NGF,SEMA5A,RAB29,RIPOR2,RGS2,FEZ1,PREX1,PLXNA2,SHTN1,CFLAR,CTSZ,INPP5F,PRKD1,PLXNB1,ITGA6,ZNF365,MAP3K13,CUX1,RDX,NLGN1,SIPA1L1,TGFB3,BBS4,NPTN,CDH2,ULK2,PAK3,EVI5L,MYO10,PLXNB3,FLNA,ITM2C,ICAM1,SDC2,YAP1	darkgreen	VSMC_M4
GO:0000165	0.01	0.99	56	579	MAPK cascade	BP	0.40793	MBP,DOK6,RNF41,SASH1,IRAK3,ANGPT1,TPD52L1,LEP,SH3RF3,RNF149,TGFBR1,PTPN3,MAP3K7,MDFIC,MAP3K8,HIPK2,LBH,NDRG2,ADAM9,FOXO1,RASSF2,TF,FLT3,MAP3K1,HIPK3,SH3RF1,APP,PDGFC,PTPN11,PTPN22,GDF6,EDN1,RGS2,NPNT,HTR2B,MST1R,PRKCA,MID1,CFLAR,FGFR2,MAP3K13,CRYAB,ATP6AP2,NBR1,DACT1,ADRA1B,NPTN,NRK,CDH2,PAK3,LGALS9,PLCG2,BCAR3,CYR61,FGF9,ICAM1	darkgreen	VSMC_M4
GO:0032755	0.01	1.00	10	62	positive regulation of interleukin-6 production	BP	0.40793	MBP,LEP,DDX58,APP,PTPN11,LBP,LPL,LGALS9,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0003279	0.01	1.00	14	88	cardiac septum development	BP	0.40793	CITED2,MDM2,TGFBR1,SEMA3C,CHD7,LRP2,FGFR2,FGFRL1,SLIT3,SMAD6,LMO4,CYR61,TBX20,CRELD1	darkgreen	VSMC_M4
GO:0044060	0.01	1.00	5	20	regulation of endocrine process	BP	0.40793	GJA1,LEP,INHBB,PTPN11,BMP6	darkgreen	VSMC_M4
GO:0009100	0.01	0.99	32	299	glycoprotein metabolic process	BP	0.40846	DSEL,BCL2,UST,LEP,HS6ST1,ITM2B,STT3B,TUSC3,ST3GAL5,EXTL3,PTX3,DPY19L4,MARCH6,BACE2,B3GNT7,GALNT3,B3GALNT2,MAN2A2,NDST3,NCSTN,CHST15,FUT11,HIF1A,MAGT1,GALNT10,TMEM59,BGN,EXTL2,ST6GALNAC3,FBXO27,ITM2C,CST3	darkgreen	VSMC_M4
GO:0043269	0.01	0.99	45	444	regulation of ion transport	BP	0.40902	BCL2,GJA1,TRDN,DAPK1,LEP,WFS1,SYT5,PTPN3,TCAF1,KCNE3,ACTN4,FGF14,TF,FXYD1,CHD7,SCN8A,JPH1,APP,ABCC8,EDN1,RGS2,ACTN2,CAMK2D,CTSS,MYLK,PRKD1,AKAP6,MAOB,NLGN1,WDR1,CACNA1C,PPARGC1A,KCNK10,SLC43A2,FLNA,VAMP7,HCN2,AHCYL1,PLCG2,KCNE4,SLC8A1,PLN,TMEM38A,SARAF,ICAM1	darkgreen	VSMC_M4
GO:0048016	0.01	1.00	9	48	inositol phosphate-mediated signaling	BP	0.40982	EDN2,HRH1,LMCD1,RCAN1,EDN1,AKAP6,PLCG2,ITPR1,C10orf71	darkgreen	VSMC_M4
GO:0002026	0.01	1.00	5	18	regulation of the force of heart contraction	BP	0.40982	EDN2,ADM,CAMK2D,SLC8A1,PLN	darkgreen	VSMC_M4
GO:0048869	0.01	0.99	248	3033	cellular developmental process	BP	0.41288	ZNF516,BCL2,IFNGR1,CITED2,UST,GRIP1,MDM2,DDR1,CDSN,GRHL2,SOD2,ANGPT1,TRPS1,SCUBE1,AFF4,GJA1,ZHX1,LAMA2,EP300,MRTFA,ADGRB1,SH3GL2,MLLT3,LEP,CDKN2B,KANK1,SGCB,VLDLR,C2orf40,PPP1R9A,IL18R1,REST,RECK,ZAP70,TGFBR1,ABCA1,TBX18,PEX13,ANTXR1,KIDINS220,FZD8,EPHB6,ITSN2,HIPK2,GATA2,PLEKHB2,HS6ST1,LIMS2,PPP1R13L,SNRK,ITGA8,TENM4,ELF1,INHBB,SMARCD3,FOSL2,LBH,NDRG2,THRB,ACTN4,ADAM9,CRIM1,FOXO1,TRPC4,RASSF2,COL4A1,COL4A2,SEMA3C,GTSF1,TMEM178A,TF,FLT3,WASF3,HPN,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,MARCH5,NCK1,SORBS2,ADM,SH3RF1,ATOH8,FAM172A,PTH,KIF13B,CLU,BLNK,GPM6A,MEIS2,APP,SCARB2,SHROOM3,RXFP1,ABCC8,PTPN11,PTX3,ADCY6,NEK4,TMEM64,PTPN22,TANC1,HNF4A,CHAC1,GDF6,NAB1,ADA,RCAN1,RBL2,NGF,PDZD7,EDN1,JAM3,GPRIN3,NFASC,ETS2,SEMA5A,BACE2,LPL,RAB29,ABCG1,ADIPOR1,FNDC5,KDM5B,RIPOR2,RGS2,EYA2,TNNT2,NCOA3,ACTN2,LRP5,FEZ1,NPNT,PREX1,HTR2B,ROBO3,SUN1,PRKCA,TXNIP,SEC24B,PARD6B,PLXNA2,SHTN1,P4HTM,NGRN,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,RAPH1,ARID5B,ITGA6,ZNF365,TAGLN,AKAP6,DDR2,MAP3K13,ID3,LRP6,HIP1,LNPK,CUX1,SERPINE1,ACHE,RDX,UNC5B,EXPH5,NBR1,SYNPO2L,LMTK2,NLGN1,SPEG,WDR1,MAEL,HIF1A,OPN3,DDX41,PPARGC1A,ACTN1,ZC4H2,DISP3,RORA,SIPA1L1,NUMB,SLIT3,TGFB3,SMAD6,FAXDC2,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,SH3TC2,FST,DAB2,LGALS9,SMARCA1,MARF1,RBFOX1,ATCAY,DAPK3,PLXNB3,PCSK4,FLNA,CCDC78,CSF1,SORT1,PLCG2,VCAM1,GLG1,LMO4,CYR61,NEXN,VNN1,SLC8A1,CCDC136,SPINK2,BNIP3,ADAMT	darkgreen	VSMC_M4
GO:0051209	0.01	1.00	13	82	release of sequestered calcium ion into cytosol	BP	0.41667	TRDN,CHD7,JPH1,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0010893	0.01	1.00	4	13	positive regulation of steroid biosynthetic process	BP	0.41878	ADM,ABCG1,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0045214	0.01	1.00	7	33	sarcomere organization	BP	0.42099	ANKRD1,EDN1,TNNT2,ACTN2,SYNPO2L,WDR1,CSRP1	darkgreen	VSMC_M4
GO:0045667	0.01	1.00	15	109	regulation of osteoblast differentiation	BP	0.42505	REST,CRIM1,RASSF2,TMEM64,LRP5,NPNT,FGFR2,PRKD1,DDR2,ID3,NBR1,SMAD6,CYR61,YAP1,BMP6	darkgreen	VSMC_M4
GO:0019935	0.01	1.00	10	57	cyclic-nucleotide-mediated signaling	BP	0.42538	PCLO,ADM,MRVI1,RGS2,HTR2B,RAPGEF4,AKAP6,GNAI1,NPPB,PRKG1	darkgreen	VSMC_M4
GO:0032677	0.01	1.00	9	56	regulation of interleukin-8 production	BP	0.42538	LEP,DDX58,LBP,PTPN22,AFAP1L2,SERPINE1,LGALS9,F3,TLR1	darkgreen	VSMC_M4
GO:0090092	0.01	0.99	24	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.42538	GDF11,CITED2,EP300,CDKN2B,RASL11B,TGFBR1,HIPK2,INHBB,CRIM1,LATS2,GDF6,NPNT,LRP2,TGFB3,SMAD6,NOMO1,FST,DAB2,GLG1,CYR61,ADAMTSL2,LOX,TBX20,BMP6	darkgreen	VSMC_M4
GO:0043114	0.01	1.00	8	40	regulation of vascular permeability	BP	0.42538	ANGPT1,SH3GL2,HRH1,ADM,OCLN,ABCC8,NPPB,BMP6	darkgreen	VSMC_M4
GO:0060314	0.01	1.00	5	20	regulation of ryanodine-sensitive calcium-release channel activity	BP	0.42538	TRDN,JPH1,CAMK2D,AKAP6,PLN	darkgreen	VSMC_M4

GO:0046903	0.01	0.99	63	673	secretion	BP	0.42538	STX11,DDR1,GJA1,LEP,UNC13B,PPP1R9A,RIC1,REST,ICA1,PREPL,SYT5,ABCA1,GATA2,INHBB,SYNGR2,RAB2B,ADAM9,TRPC4,PCLO,NCOR2,FFAR3,CHD7,ANKRD1,EXOC6,ADM,PAM,MCTP1,ABCC8,ANXA3,PTPN11,SLC26A7,HNF4A,ADA,EDN1,PLA2G4F,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ATP9A,ADCY5,RAPGEF4,ACHE,EXPH5,MAOB,CYP19A1,NLGN1,HIF1A,SYT16,MICAL3,ADGRE2,FBXL20,NPPB,TGFB3,RHOT1,LGALS9,NPR3,VAMP7,WLS,PIK3C2A,BMP6,MAFA	darkgreen	VSMC_M4
GO:0055080	0.01	0.99	49	494	cation homeostasis	BP	0.42546	BCL2,GJA1,TRDN,WFS1,PDK4,EDN2,GATA2,TPT1,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,CNNM2,HTR2B,CAMK2D,ADCY5,PRKD1,CYBRD1,AKAP6,LRP6,ATP6AP2,FBXL5,HIF1A,CACNA1C,NPPB,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0043470	0.01	1.00	8	41	regulation of carbohydrate catabolic process	BP	0.42548	EP300,APP,SCARB2,SLC25A12,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0032940	0.01	0.99	55	574	secretion by cell	BP	0.42548	STX11,GJA1,LEP,UNC13B,PPP1R9A,RIC1,REST,ICA1,PREPL,SYT5,ABCA1,GATA2,INHBB,SYNGR2,RAB2B,ADAM9,PCLO,FFAR3,CHD7,ANKRD1,EXOC6,ADM,PAM,MCTP1,ABCC8,ANXA3,PTPN11,HNF4A,EDN1,ABCG1,KDM5B,PFKL,LRP5,TM7SF3,ATP9A,ADCY5,RAPGEF4,ACHE,EXPH5,MAOB,CYP19A1,NLGN1,HIF1A,SYT16,MICAL3,ADGRE2,FBXL20,TGFB3,RHOT1,LGALS9,VAMP7,WLS,PIK3C2A,BMP6,MAFA	darkgreen	VSMC_M4
GO:0001829	0.01	1.00	4	13	trophectodermal cell differentiation	BP	0.42548	CITED2,ADA,HOPX,YAP1	darkgreen	VSMC_M4
GO:0008202	0.01	0.99	24	217	steroid metabolic process	BP	0.42548	HSD17B6,LEP,VLDLR,REST,IGFBP7,ABCA1,CYP1B1,ADM,APP,ABCG1,LRP5,LGMN,ARV1,LRP2,CYP19A1,PPARGC1A,DISP3,RORA,FAXDC2,PRKAA2,MBTPS1,SLC27A5,BMP6,SCP2	darkgreen	VSMC_M4
GO:0120178	0.01	1.00	6	29	steroid hormone biosynthetic process	BP	0.42667	HSD17B6,REST,ADM,CYP19A1,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0001667	0.01	0.99	38	360	ameboidal-type cell migration	BP	0.43059	SASH1,ANGPT1,SMOC2,GJA1,ADGRB1,KANK1,TGFBR1,GATA2,ADAM9,CYP1B1,SEMA3C,AMOTL2,PTPRG,ATOH8,ANXA3,PTPN11,EDN1,SEMA5A,ADIPOR1,LRP5,HTR2B,LGMN,PRKCA,PRKD1,ARID5B,DDR2,HSPB1,HIF1A,FAT2,MAPRE2,CDH2,PAK3,PLEKHG5,CDH13,PLCG2,SLC8A1,CCR6,PIK3C2A	darkgreen	VSMC_M4
GO:0051283	0.01	1.00	13	83	negative regulation of sequestering of calcium ion	BP	0.43059	TRDN,CHD7,JPH1,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0040007	0.01	0.99	70	742	growth	BP	0.43059	BCL2,CITED2,DDR1,GRHL2,GJA1,EP300,BRD8,SH3GL2,LEP,WFS1,FAM122A,TMEM8B,IGFBP7,TGFBR1,JADE1,ITSN2,PPP1R13L,TENM4,SEMA3C,HPN,CHD7,LATS2,CHPT1,SORBS2,ADM,WWC2,EXTL3,APP,PTPN11,PTX3,DCBLD2,HNF4A,CPQ,NGF,EDN1,SEMA5A,ADIPOR1,KDM5B,RGS2,LGMN,ZMAT3,SESN2,SHTN1,CAMK2D,CFLAR,WDTC1,FGFR2,RAPH1,ARID5B,AKAP6,DDR2,MAP3K13,CRYAB,PAPPA2,IGFBP2,MAEL,HIF1A,NPPB,SGCA,SLIT3,ULK2,CRLF3,CSF1,FRZB,TBX20,OSGIN2,CDKN1A,HOPX,YAP1,IGFBPL1	darkgreen	VSMC_M4
GO:1904062	0.01	0.99	27	241	regulation of cation transmembrane transport	BP	0.43059	TRDN,DAPK1,PTPN3,KCNE3,ACTN4,FGF14,FXYD1,CHD7,JPH1,APP,ABCC8,RGS2,ACTN2,CAMK2D,CTSS,PRKD1,AKAP6,NLGN1,CACNA1C,PPARGC1A,SLC43A2,FLNA,PLCG2,KCNE4,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:1902905	0.01	0.99	22	179	positive regulation of supramolecular fiber organization	BP	0.43059	LIMCH1,TGFBR1,CDC42EP3,WASF3,NCK1,OCLN,CLU,APP,JMY,EDN1,CD47,SEMA5A,ACTN2,SYNPO2,SYNPO2L,WDR1,TGFB3,SYNPO,FLNA,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0055090	0.01	1.00	5	21	acylglycerol homeostasis	BP	0.43059	HNF4A,LPL,SESN2,RORA,ANGPTL4	darkgreen	VSMC_M4
GO:0070328	0.01	1.00	5	21	triglyceride homeostasis	BP	0.43059	HNF4A,LPL,SESN2,RORA,ANGPTL4	darkgreen	VSMC_M4
GO:0140353	0.01	1.00	6	28	lipid export from cell	BP	0.43059	LEP,PTPN11,EDN1,KDM5B,CYP19A1,BMP6	darkgreen	VSMC_M4
GO:0032870	0.01	0.99	46	450	cellular response to hormone stimulus	BP	0.4312	MDM2,GJA1,EP300,BRD8,LEP,KANK1,PDK4,REST,IGFBP7,INHBB,LBH,THRB,FOXO1,FLT3,NCOR2,FFAR3,LATS2,NCK1,PTH,RXFP1,PTPN11,ADCY6,EDN1,LPL,ADIPOR1,NCOA3,ACTN2,ZNF106,CTSS,CFLAR,WDTC1,STRN3,RDX,IGFBP2,PPARGC1A,SLIT3,BBS4,DAB2,SKP2,PRKAA2,AHCYL1,BCAR3,ICAM1,PIK3C2A,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0098742	0.01	0.99	21	152	cell-cell adhesion via plasma-membrane adhesion molecules	BP	0.43325	MBP,TENM4,PCDH9,ATP2C1,PCDHB4,ROBO3,NLGN1,ADGRL1,FGFRL1,NPTN,FAT2,CDH2,CDH18,PLXNB3,CDH13,VCAM1,NEXN,PCDHGA1,FAT3,PCDHB2,ICAM1	darkgreen	VSMC_M4
GO:0045597	0.01	0.99	61	639	positive regulation of cell differentiation	BP	0.43325	BCL2,MDM2,SOD2,GJA1,REST,ZAP70,TGFBR1,GATA2,LIMS2,PPP1R13L,TENM4,SMARCD3,ADM,ATOH8,TMEM64,GDF6,ADA,NGF,EDN1,SEMA5A,LPL,FNDC5,RIPOR2,NCOA3,LRP5,FEZ1,NPNT,PREX1,PRKCA,PLXNA2,SHTN1,LRP2,PRKD1,F11R,PLXNB1,ZNF365,AKAP6,DDR2,MAP3K13,CUX1,SERPINE1,HIF1A,ZC4H2,NUMB,TGFB3,FAXDC2,NPTN,PAK3,DAB2,LGALS9,PLXNB3,FLNA,CSF1,CYR61,VNN1,FRZB,CD83,TBX20,HOPX,YAP1,BMP6	darkgreen	VSMC_M4
GO:0034762	0.01	0.99	41	396	regulation of transmembrane transport	BP	0.43325	BCL2,GJA1,TRDN,DAPK1,LEP,PTPN3,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,CHD7,SCN8A,OCLN,JPH1,PTH,APP,ABCC8,PTPN11,EDN1,RGS2,ACTN2,CAMK2D,CTSS,PRKD1,AKAP6,NLGN1,WDR1,OPN3,CACNA1C,PPARGC1A,KCNK10,SLC43A2,FLNA,HCN2,AHCYL1,PLCG2,KCNE4,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:2001234	0.01	0.99	21	187	negative regulation of apoptotic signaling pathway	BP	0.43544	BCL2,MDM2,SOD2,WFS1,CREB3,TGFBR1,TPT1,SH3RF1,RNF34,CLU,HERPUD1,EYA2,CFLAR,ITGA6,HSPB1,SERPINE1,UNC5B,HIF1A,VNN1,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0055021	0.01	1.00	9	53	regulation of cardiac muscle tissue growth	BP	0.44094	CITED2,GJA1,TGFBR1,EDN1,RGS2,FGFR2,AKAP6,TBX20,YAP1	darkgreen	VSMC_M4
GO:0033687	0.01	1.00	6	27	osteoblast proliferation	BP	0.44094	BCL2,LRP5,FGFR2,PLXNB1,NPR3,CYR61	darkgreen	VSMC_M4
GO:0051282	0.01	1.00	13	84	regulation of sequestering of calcium ion	BP	0.44169	TRDN,CHD7,JPH1,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0010634	0.01	0.99	18	143	positive regulation of epithelial cell migration	BP	0.4466	SASH1,ANGPT1,SMOC2,GATA2,ADAM9,ATOH8,ANXA3,EDN1,SEMA5A,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,MAPRE2,PLCG2,CCR6,PIK3C2A	darkgreen	VSMC_M4

GO:0032637	0.01	1.00	9	57	interleukin-8 production	BP	0.4466	LEP,DDX58,LBP,PTPN22,AFAP1L2,SERPINE1,LGALS9,F3,TLR1	darkgreen	VSMC_M4
GO:0007267	0.01	0.99	102	1146	cell-cell signaling	BP	0.44683	MBP,STX11,RNF19A,GJA1,LAMA2,ADGRB1,TLE4,GNAQ,MLLT3,LEP,KANK1,UNC13B,PPP1R9A,REST,ICA1,RECK,PREPL,SYT5,ABCA1,TBX18,MDFIC,FZD8,JADE1,INHBB,HRH1,NDRG2,PLCB4,FGF14,PCDHB4,PCLO,AMOTL2,ZDHHC2,RIC3,FFAR3,CHD7,LATS2,CPEB3,ADM,CLCN3,TCF7L1,MCTP1,PTH,APP,ABCC8,PTPN11,TMEM64,PKP4,HNF4A,NGF,EDN1,SEMA5A,ABCG1,KDM5B,PFKL,LRP5,PLCL1,HTR2B,LGMN,TM7SF3,ADCY5,GABBR1,FGFR2,NCSTN,ZRANB1,RAPGEF4,INSYN2,LRP6,ACHE,ATP6AP2,MAOB,IGFBP2,CYP19A1,TNFSF10,DACT1,NLGN1,HIF1A,CACNA1C,GNAI1,FBXL20,SIPA1L1,ADRA1B,NPTN,CDH2,RHOT1,DAB2,PRKAA2,DAPK3,TLE2,FLNA,VAMP7,HCN2,PLCG2,WLS,PCDHB2,FRZB,LYPD6,TMEM170B,FGF9,EDA,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0043434	0.01	0.99	33	308	response to peptide hormone	BP	0.44683	MDM2,GJA1,LEP,KANK1,PDK4,SLC2A1,INHBB,FOXO1,FFAR3,NCK1,ADM,ABCC8,PTPN11,ADCY6,EDN1,LPL,ADIPOR1,ACTN2,ZNF106,LRP5,SESN2,CFLAR,WDTC1,LRP6,TNFSF10,GNAI1,AHCYL1,SORT1,BCAR3,PLN,ICAM1,PIK3C2A,STC2	darkgreen	VSMC_M4
GO:0060393	0.01	1.00	8	44	regulation of pathway-restricted SMAD protein phosphorylation	BP	0.44805	GDF11,TGFBR1,INHBB,GDF6,TGFB3,SMAD6,DAB2,BMP6	darkgreen	VSMC_M4
GO:0010595	0.01	1.00	14	105	positive regulation of endothelial cell migration	BP	0.45778	SASH1,ANGPT1,SMOC2,GATA2,ATOH8,ANXA3,EDN1,SEMA5A,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,PIK3C2A	darkgreen	VSMC_M4
GO:0010522	0.01	1.00	11	71	regulation of calcium ion transport into cytosol	BP	0.46149	BCL2,TRDN,CHD7,JPH1,CAMK2D,PRKD1,AKAP6,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0042311	0.01	1.00	6	31	vasodilation	BP	0.46194	SOD2,GJA1,RGS2,NPPB,NPR3,PRKG1	darkgreen	VSMC_M4
GO:0000422	0.01	1.00	11	71	autophagy of mitochondrion	BP	0.46194	MAP1LC3A,SLC25A4,ATG13,GABARAPL1,ATG14,HIF1A,PPARGC1A,ULK2,MAP1LC3B2,BNIP3,GABARAPL2	darkgreen	VSMC_M4
GO:0061726	0.01	1.00	11	71	mitochondrion disassembly	BP	0.46194	MAP1LC3A,SLC25A4,ATG13,GABARAPL1,ATG14,HIF1A,PPARGC1A,ULK2,MAP1LC3B2,BNIP3,GABARAPL2	darkgreen	VSMC_M4
GO:0009612	0.01	0.99	21	176	response to mechanical stimulus	BP	0.46194	CITED2,PKDREJ,GJA1,SLC2A1,ABHD12,MAP3K1,HPN,ANKRD1,MEIS2,PTPN11,PDZD7,EDN1,SUN1,TXNIP,USP53,F11R,IGFBP2,CDH2,SLC8A1,BNIP3,BMP6	darkgreen	VSMC_M4
GO:0006959	0.01	1.00	11	84	humoral immune response	BP	0.46194	BCL2,C4A,TF,CLU,BLNK,CFI,C1RL,CD83,CD59,MFAP4,CCR6	darkgreen	VSMC_M4
GO:0090132	0.01	0.99	29	262	epithelium migration	BP	0.46194	SASH1,GRHL2,ANGPT1,SMOC2,ADGRB1,KANK1,TGFBR1,GATA2,ADAM9,CYP1B1,PTPRG,ATOH8,ANXA3,PTPN11,EDN1,SEMA5A,ADIPOR1,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,FAT2,MAPRE2,PLEKHG5,CDH13,PLCG2,CCR6,PIK3C2A	darkgreen	VSMC_M4
GO:0071875	0.01	1.00	5	19	adrenergic receptor signaling pathway	BP	0.46194	RGS2,ADRA1B,LMBRD2,ADCY9,PLN	darkgreen	VSMC_M4
GO:0006952	0.01	0.99	82	949	defense response	BP	0.46255	BCL2,IFNGR1,IRAK3,C4A,RNASET2,SCUBE1,GJA1,EP300,ADGRB1,DAPK1,LEP,DDX58,IL18R1,ZAP70,MAP3K7,NT5C3A,ABHD12,MRC1,INHBB,HRH1,POLB,TF,FFAR3,TRIM23,ADM,CD180,CHST2,G3BP2,CLU,BLNK,APP,ANXA3,PTPN11,PTX3,LBP,PTPN22,SERINC3,ADA,IFIT1,EDN1,JAM3,CD47,N4BP1,LPL,MX1,MST1R,AFAP1L2,CFI,ABCC9,PRKD1,F11R,SERPINE1,C1RL,AOC3,HIF1A,ADGRE2,FBXL20,RORA,CALCOCO2,GP2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,VCAM1,F3,LRSAM1,VNN1,TLR1,BNIP3,ADAMTS5,CD83,CST3,ZNF175,MFAP4,CCR6,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0060070	0.01	0.99	28	250	canonical Wnt signaling pathway	BP	0.46368	TLE4,GNAQ,MLLT3,KANK1,RECK,TBX18,FZD8,JADE1,LATS2,TCF7L1,TMEM64,SEMA5A,LRP5,FGFR2,LRP6,ATP6AP2,IGFBP2,DACT1,CDH2,DAB2,DAPK3,TLE2,WLS,FRZB,LYPD6,TMEM170B,EDA,YAP1	darkgreen	VSMC_M4
GO:0010649	0.01	1.00	4	14	regulation of cell communication by electrical coupling	BP	0.46404	GJA1,TRDN,CAMK2D,SLC8A1	darkgreen	VSMC_M4
GO:0038061	0.01	0.99	13	99	NIK/NF-kappaB signaling	BP	0.46775	SASH1,EP300,IL18R1,MAP3K7,ACTN4,RASSF2,APP,PTPN22,EDN1,ADIPOR1,LGALS9,TERF2IP,EDA	darkgreen	VSMC_M4
GO:0010811	0.01	0.99	14	100	positive regulation of cell-substrate adhesion	BP	0.46775	ECM2,LIMS2,PTPN11,CCDC80,NPNT,PREX1,NID1,ITGA6,COL26A1,FLNA,CSF1,CDH13,CYR61,PLEKHA2	darkgreen	VSMC_M4
GO:0048878	0.01	0.99	76	832	chemical homeostasis	BP	0.46775	BCL2,SOD2,GJA1,TRDN,LEP,WFS1,UNC13B,PDK4,EDN2,ABCA1,PTPN3,GATA2,TPT1,KCNE3,FOXO1,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,ABCC8,HECTD4,PTPN11,ADCY6,HERPUD1,TMEM64,HNF4A,IFIT1,EDN1,BACE2,LPL,ABCG1,CNNM2,ADIPOR1,LRP5,HTR2B,SESN2,CAMK2D,ADCY5,WDTC1,PRKD1,CYBRD1,AKAP6,LRP6,ATP6AP2,FBXL5,HIF1A,CACNA1C,PPARGC1A,NPPB,DISP3,RORA,ADRA1B,NPTN,ANGPTL4,PRKAA2,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,ICAM1,ORMDL3,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0032409	0.01	0.99	23	198	regulation of transporter activity	BP	0.47128	BCL2,GJA1,TRDN,DAPK1,PTPN3,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,JPH1,APP,ABCC8,ACTN2,CAMK2D,CTSS,AKAP6,NLGN1,PPARGC1A,AHCYL1,PLCG2,KCNE4,PLN	darkgreen	VSMC_M4
GO:0030072	0.01	0.99	20	168	peptide hormone secretion	BP	0.47172	GJA1,LEP,REST,ICA1,INHBB,PCLO,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,HIF1A,MAFA	darkgreen	VSMC_M4
GO:0071398	0.01	1.00	6	29	cellular response to fatty acid	BP	0.47273	PDK4,FFAR3,EDN1,LPL,ID3,PPARGC1A	darkgreen	VSMC_M4
GO:0010559	0.01	1.00	6	31	regulation of glycoprotein biosynthetic process	BP	0.47273	BCL2,ITM2B,BACE2,NCSTN,TMEM59,ITM2C	darkgreen	VSMC_M4
GO:0055017	0.01	1.00	11	72	cardiac muscle tissue growth	BP	0.47729	CITED2,GJA1,TGFBR1,TENM4,SORBS2,EDN1,RGS2,FGFR2,AKAP6,TBX20,YAP1	darkgreen	VSMC_M4
GO:0050708	0.01	0.99	23	200	regulation of protein secretion	BP	0.47736	GJA1,LEP,UNC13B,REST,ICA1,INHBB,ADAM9,ANKRD1,PAM,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,ACHE,EXPH5,HIF1A,TGFB3,WLS,BMP6	darkgreen	VSMC_M4
GO:1901998	0.01	1.00	6	31	toxin transport	BP	0.4781	CD274,ANTXR1,RAB29,ABCG1,LRP6,BNIP3	darkgreen	VSMC_M4
GO:0048738	0.01	0.99	23	186	cardiac muscle tissue development	BP	0.4781	CITED2,GJA1,SGCB,TGFBR1,TBX18,PPP1R13L,TENM4,CHD7,ANKRD1,SORBS2,EDN1,RGS2,TNNT2,ACTN2,LRP2,FGFR2,AKAP6,NPPB,SLC8A1,TBX20,PLN,HOPX,YAP1	darkgreen	VSMC_M4

GO:0071496	0.01	0.99	29	267	cellular response to external stimulus	BP	0.4781	BCL2,MDM2,GJA1,LEP,CDKN2B,PDK4,SLC2A1,SESN1,INHBB,FOXO1,MAP3K1,ANKRD1,MAP1LC3A,PTPN11,LPL,SESN2,PRKD1,F11R,GABARAPL1,ATG14,SKP2,PRKAA2,MAP1LC3B2,VCAM1,BNIP3,CDKN1A,GABARAPL2,ICAM1,BMP6	darkgreen	VSMC_M4
GO:1990868	0.01	1.00	8	48	response to chemokine	BP	0.4781	DOCK8,LRCH1,EDN1,RIPOR2,HIF1A,SLIT3,LOX,CCR6	darkgreen	VSMC_M4
GO:1990869	0.01	1.00	8	48	cellular response to chemokine	BP	0.4781	DOCK8,LRCH1,EDN1,RIPOR2,HIF1A,SLIT3,LOX,CCR6	darkgreen	VSMC_M4
GO:0007565	0.01	0.99	17	139	female pregnancy	BP	0.4781	BCL2,CITED2,DDR1,GJA1,LEP,RECK,IGFBP7,SLC2A1,PAPPA,ADM,PAM,ABCC8,RGS2,IGFBP2,TGFB3,LGALS9,STC2	darkgreen	VSMC_M4
GO:0048873	0.01	1.00	5	22	homeostasis of number of cells within a tissue	BP	0.4781	BCL2,GATA2,PTH,PTPN11,CSF1	darkgreen	VSMC_M4
GO:0006700	0.01	1.00	4	14	C21-steroid hormone biosynthetic process	BP	0.47907	REST,ADM,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0071219	0.01	0.99	16	133	cellular response to molecule of bacterial origin	BP	0.48209	SASH1,CD274,ABCA1,MRC1,ADAM9,ANKRD1,CD180,LBP,PTPN22,PRKCA,SERPINE1,PPARGC1A,PLCG2,TLR1,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0002690	0.01	1.00	10	71	positive regulation of leukocyte chemotaxis	BP	0.48486	CREB3,EDN2,LBP,EDN1,RIPOR2,LGMN,SERPINE1,LGALS9,CSF1,CCR6	darkgreen	VSMC_M4
GO:2001233	0.01	0.99	29	292	regulation of apoptotic signaling pathway	BP	0.48786	BCL2,MDM2,SOD2,TPD52L1,WFS1,CREB3,TGFBR1,TPT1,INHBB,NCK1,SH3RF1,RNF34,CLU,HERPUD1,SERINC3,EYA2,CFLAR,ITGA6,HSPB1,SERPINE1,UNC5B,TNFSF10,HIF1A,DAPK3,VNN1,ITM2C,NACC2,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0003007	0.01	0.99	24	197	heart morphogenesis	BP	0.48887	CITED2,MDM2,GRHL2,TGFBR1,PPP1R13L,SMARCD3,SEMA3C,CHD7,ANKRD1,TNNT2,HTR2B,SEC24B,LRP2,FGFR2,SYNPO2L,HIF1A,FGFRL1,SLIT3,SMAD6,BBS4,FLNA,CYR61,TBX20,YAP1	darkgreen	VSMC_M4
GO:1903039	0.01	0.99	17	143	positive regulation of leukocyte cell-cell adhesion	BP	0.48941	LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,CHST2,PTPN11,PTPN22,ADA,CD47,IGFBP2,LGALS9,VCAM1,VNN1,CD83,ICAM1	darkgreen	VSMC_M4
GO:0046640	0.01	1.00	5	22	regulation of alpha-beta T cell proliferation	BP	0.49687	CD274,ZAP70,SH3RF1,PTPN22,LGALS9	darkgreen	VSMC_M4
GO:0090130	0.01	0.99	29	266	tissue migration	BP	0.50178	SASH1,GRHL2,ANGPT1,SMOC2,ADGRB1,KANK1,TGFBR1,GATA2,ADAM9,CYP1B1,PTPRG,ATOH8,ANXA3,PTPN11,EDN1,SEMA5A,ADIPOR1,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,FAT2,MAPRE2,PLEKHG5,CDH13,PLCG2,CCR6,PIK3C2A	darkgreen	VSMC_M4
GO:0030182	0.01	0.99	99	1067	neuron differentiation	BP	0.50178	BCL2,UST,GRIP1,MDM2,DDR1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,LEP,KANK1,VLDLR,PPP1R9A,REST,TGFBR1,KIDINS220,FZD8,EPHB6,ITSN2,HIPK2,GATA2,HS6ST1,TENM4,THRB,SEMA3C,PTPRG,DENND5A,ANKRD1,CPEB3,NCK1,ADM,ATOH8,KIF13B,GPM6A,APP,SCARB2,PTPN11,ADCY6,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,RAB29,RGS2,FEZ1,PREX1,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,NGRN,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,PLXNB1,RAPH1,ITGA6,ZNF365,MAP3K13,ID3,LRP6,CUX1,UNC5B,LMTK2,NLGN1,HIF1A,ZC4H2,DISP3,RORA,SIPA1L1,NUMB,SLIT3,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,SMARCA1,ATCAY,DAPK3,PLXNB3,FLNA,VCAM1,LMO4,NEXN,TBX20,ITM2C,SDC2,PRKG1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0002688	0.01	0.99	12	92	regulation of leukocyte chemotaxis	BP	0.50178	CREB3,EDN2,LBP,EDN1,JAM3,RIPOR2,LGMN,SERPINE1,MMP28,LGALS9,CSF1,CCR6	darkgreen	VSMC_M4
GO:1902176	0.01	1.00	4	16	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	BP	0.50236	SOD2,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0032330	0.01	1.00	8	46	regulation of chondrocyte differentiation	BP	0.50268	TRPS1,TGFBR1,PTH,PTPN11,GDF6,LNPK,GLG1,BMP6	darkgreen	VSMC_M4
GO:0050848	0.01	1.00	9	55	regulation of calcium-mediated signaling	BP	0.50268	ZAP70,LMCD1,ADA,RCAN1,AKAP6,CDH13,PLCG2,ITPR1,C10orf71	darkgreen	VSMC_M4
GO:0051208	0.01	0.99	13	87	sequestering of calcium ion	BP	0.50899	TRDN,CHD7,JPH1,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0007632	0.02	1.00	7	35	visual behavior	BP	0.5152	HRH1,MEIS2,APP,ABCC8,TANC1,HIF1A,NPTN	darkgreen	VSMC_M4
GO:0006958	0.02	1.00	4	16	complement activation, classical pathway	BP	0.52	C4A,CLU,CFI,C1RL	darkgreen	VSMC_M4
GO:0009187	0.02	1.00	7	33	cyclic nucleotide metabolic process	BP	0.52	PTH,ADCY6,ADCY5,PDE1A,NPPB,RORA,ADCY9	darkgreen	VSMC_M4
GO:0050878	0.02	0.99	29	273	regulation of body fluid levels	BP	0.52603	DDR1,SCUBE1,GJA1,GNAQ,WFS1,NCOR2,ADM,PAM,ENTPD1,MYL9,ADCY6,PROS1,HNF4A,ADA,EDN1,PRKCA,F11R,LNPK,HSPB1,SERPINE1,HIF1A,NPPB,NPR3,FLNA,PLCG2,F3,CD59,CSRP1,PRKG1	darkgreen	VSMC_M4
GO:0032412	0.02	0.99	21	178	regulation of ion transmembrane transporter activity	BP	0.52603	TRDN,DAPK1,PTPN3,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,JPH1,APP,ABCC8,ACTN2,CAMK2D,CTSS,AKAP6,NLGN1,PPARGC1A,AHCYL1,PLCG2,KCNE4,PLN	darkgreen	VSMC_M4
GO:0010562	0.02	0.99	63	669	positive regulation of phosphorus metabolic process	BP	0.52873	GDF11,BCL2,SASH1,DDR1,ANGPT1,TPD52L1,LEP,LIMCH1,VLDLR,PPP1R9A,TGFBR1,MAP3K7,EPHB6,HIPK2,INHBB,HRH1,ADAM9,RASSF2,ANKLE2,TF,FLT3,PTH,CLU,APP,PDGFC,PTPN11,CCNT1,GDF6,AKTIP,NGF,EDN1,NPNT,HTR2B,MST1R,AFAP1L2,FGFR2,PRKD1,SLC25A12,ITGA6,DDR2,GPRC5A,MAP3K13,FAM129A,ATG14,LMTK2,HIF1A,PPARGC1A,TGFB3,TOM1L1,FAXDC2,NPTN,DAB2,PRKAA2,CSF1,PLCG2,TERF2IP,BCAR3,LMO4,CYR61,CDKN1A,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0045937	0.02	0.99	63	669	positive regulation of phosphate metabolic process	BP	0.52873	GDF11,BCL2,SASH1,DDR1,ANGPT1,TPD52L1,LEP,LIMCH1,VLDLR,PPP1R9A,TGFBR1,MAP3K7,EPHB6,HIPK2,INHBB,HRH1,ADAM9,RASSF2,ANKLE2,TF,FLT3,PTH,CLU,APP,PDGFC,PTPN11,CCNT1,GDF6,AKTIP,NGF,EDN1,NPNT,HTR2B,MST1R,AFAP1L2,FGFR2,PRKD1,SLC25A12,ITGA6,DDR2,GPRC5A,MAP3K13,FAM129A,ATG14,LMTK2,HIF1A,PPARGC1A,TGFB3,TOM1L1,FAXDC2,NPTN,DAB2,PRKAA2,CSF1,PLCG2,TERF2IP,BCAR3,LMO4,CYR61,CDKN1A,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4

GO:0048468	0.02	0.99	139	1587	cell development	BP	0.52873	BCL2,IFNGR1,CITED2,UST,GRIP1,MDM2,DDR1,CDSN,GRHL2,AFF4,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,LEP,KANK1,SGCB,VLDLR,PPP1R9A,REST,RECK,TBX18,ANTXR1,KIDINS220,EPHB6,ITSN2,GATA2,HS6ST1,LIMS2,ITGA8,TENM4,INHBB,SMARCD3,FOSL2,THRB,ACTN4,SEMA3C,WASF3,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,NCK1,SORBS2,ADM,FAM172A,KIF13B,CLU,GPM6A,APP,SCARB2,SHROOM3,ABCC8,PTPN11,PTX3,ADCY6,HNF4A,RCAN1,NGF,PDZD7,EDN1,JAM3,GPRIN3,NFASC,SEMA5A,BACE2,RAB29,RIPOR2,RGS2,TNNT2,ACTN2,LRP5,FEZ1,PREX1,HTR2B,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,RAPH1,ARID5B,ITGA6,ZNF365,AKAP6,MAP3K13,CUX1,ACHE,RDX,UNC5B,EXPH5,SYNPO2L,LMTK2,NLGN1,WDR1,HIF1A,ACTN1,SIPA1L1,NUMB,SLIT3,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,SH3TC2,MARF1,ATCAY,PLXNB3,PCSK4,FLNA,NEXN,SLC8A1,CCDC136,SPINK2,FRZB,LOX,TBX20,ITM2C,CSRP1,CDKN1A,CCR6,ICAM1,SDC2,YAP1,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0010951	0.02	0.99	16	137	negative regulation of endopeptidase activity	BP	0.52873	MDM2,C4A,RECK,ITIH5,CRIM1,SH3RF1,RNF34,APP,HERPUD1,PROS1,NGF,SERPINE1,CRYAB,PCSK1N,SPINK2,CST3	darkgreen	VSMC_M4
GO:0030511	0.02	1.00	6	28	positive regulation of transforming growth factor beta receptor signaling pathway	BP	0.52873	CITED2,EP300,CDKN2B,HIPK2,NPNT,DAB2	darkgreen	VSMC_M4
GO:1903846	0.02	1.00	6	28	positive regulation of cellular response to transforming growth factor beta stimulus	BP	0.52873	CITED2,EP300,CDKN2B,HIPK2,NPNT,DAB2	darkgreen	VSMC_M4
GO:0050671	0.02	0.99	11	82	positive regulation of lymphocyte proliferation	BP	0.53222	BCL2,LEP,CD274,ZAP70,NCK1,PTPN22,ADA,IGFBP2,LGALS9,VCAM1,CDKN1A	darkgreen	VSMC_M4
GO:0070059	0.02	0.99	8	50	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP	0.53222	BCL2,WFS1,CREB3,NCK1,HERPUD1,CHAC1,SERINC3,ITPR1	darkgreen	VSMC_M4
GO:2000026	0.02	0.99	91	1014	regulation of multicellular organismal development	BP	0.53222	CITED2,SASH1,GRHL2,FAM19A5,TRPS1,SMOC2,GJA1,LAMA2,ADGRB1,LEP,REST,RECK,ZAP70,TGFBR1,TBX18,HIPK2,GATA2,TENM4,SMARCD3,RASSF2,COL4A2,CYP1B1,SEMA3C,TMEM178A,WASF3,CHD7,ADM,SH3RF1,ATOH8,PTH,MEIS2,ABCC8,ANXA3,PTPN11,TMEM64,HNF4A,GDF6,ADA,NGF,EDN1,SEMA5A,RGS2,NCOA3,PRKCA,PLXNA2,SHTN1,P4HTM,LRP2,FGFR2,PRKD1,F11R,PLXNB1,SLC25A12,ZNF365,AKAP6,DDR2,MAP3K13,LNPK,HSPB1,CUX1,SERPINE1,NBR1,NLGN1,HIF1A,NPPB,ANGPTL7,NUMB,TGFB3,FAXDC2,NPTN,ULK2,PAK3,FST,ANGPTL4,LGALS9,PLXNB3,CSF1,F3,GLG1,CYR61,VNN1,SLC8A1,FRZB,CD83,LOX,TBX20,LRRC24,MAFF,HOPX,YAP1,BMP6	darkgreen	VSMC_M4
GO:0051130	0.02	0.99	80	870	positive regulation of cellular component organization	BP	0.5324	GRIP1,ANGPT1,EP300,ADGRB1,SH3GL2,LIMCH1,VLDLR,UNC13B,PPP1R9A,TGFBR1,ABCA1,KIDINS220,GATA2,ADAM9,CDC42EP3,TF,WASF3,ZDHHC2,ANKRD1,MARCH5,NCK1,SLC25A4,OCLN,G3BP2,CLU,GPM6A,APP,SCARB2,ABCC8,PTPN11,JMY,NGF,EDN1,CD47,SEMA5A,ABCG1,RIPOR2,RGS2,ACTN2,LRP5,FEZ1,PLXNA2,SHTN1,CFLAR,SYNPO2,PRKD1,PLXNB1,ITGA6,DDR2,MAP3K13,HIP1,LNPK,CUX1,SERPINE1,SYNPO2L,MMP1,TNFSF10,NLGN1,WDR1,HIF1A,ADGRL1,PPARGC1A,CALCOCO2,TGFB3,BBS4,NPTN,MAPRE2,SYNPO,PAK3,DAB2,PLXNB3,FLNA,PLCG2,LRSAM1,CD151,BNIP3,LRRC24,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0060828	0.02	0.99	24	210	regulation of canonical Wnt signaling pathway	BP	0.54056	TLE4,GNAQ,MLLT3,KANK1,RECK,TBX18,JADE1,LATS2,TMEM64,SEMA5A,FGFR2,ATP6AP2,IGFBP2,DACT1,CDH2,DAB2,DAPK3,TLE2,WLS,FRZB,LYPD6,TMEM170B,EDA,YAP1	darkgreen	VSMC_M4
GO:0061572	0.02	0.99	18	141	actin filament bundle organization	BP	0.54154	LIMCH1,PPP1R9A,TGFBR1,CALD1,CD47,MYO1B,SHTN1,SYNPO2,F11R,RDX,SYNPO2L,ACTN1,TGFB3,SYNPO,PLS3,ARHGAP28,FLNA,PPM1E	darkgreen	VSMC_M4
GO:0046888	0.02	0.99	8	48	negative regulation of hormone secretion	BP	0.54582	GJA1,LEP,REST,INHBB,ABCC8,PTPN11,EDN1,PFKL	darkgreen	VSMC_M4
GO:0051145	0.02	0.99	9	57	smooth muscle cell differentiation	BP	0.54968	SOD2,MRTFA,SGCB,TBX18,SMARCD3,ADM,NPNT,FGFR2,FGF9	darkgreen	VSMC_M4
GO:0052548	0.02	0.99	27	270	regulation of endopeptidase activity	BP	0.55202	MBP,MDM2,C4A,DAPK1,REST,RECK,ITIH5,CRIM1,SH3RF1,RNF34,APP,HERPUD1,PROS1,NGF,LGMN,CFLAR,NCSTN,HIP1,SERPINE1,CRYAB,TNFSF10,PCSK1N,LGALS9,F3,CYR61,SPINK2,CST3	darkgreen	VSMC_M4
GO:0010959	0.02	0.99	28	263	regulation of metal ion transport	BP	0.55345	BCL2,GJA1,TRDN,WFS1,PTPN3,KCNE3,ACTN4,FGF14,TF,FXYD1,CHD7,JPH1,ABCC8,ACTN2,CAMK2D,MYLK,PRKD1,AKAP6,CACNA1C,FLNA,AHCYL1,PLCG2,KCNE4,SLC8A1,PLN,TMEM38A,SARAF,ICAM1	darkgreen	VSMC_M4
GO:0070232	0.02	1.00	5	24	regulation of T cell apoptotic process	BP	0.55613	DOCK8,CD274,ADA,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:1901522	0.02	1.00	5	21	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	BP	0.55613	EP300,CREB3,CHD6,SESN2,HIF1A	darkgreen	VSMC_M4
GO:0071675	0.02	0.99	11	81	regulation of mononuclear cell migration	BP	0.55613	DOCK8,CREB3,LRCH1,APP,CD47,RIPOR2,LGMN,SERPINE1,LGALS9,CSF1,CCR6	darkgreen	VSMC_M4
GO:0031664	0.02	1.00	4	17	regulation of lipopolysaccharide-mediated signaling pathway	BP	0.5568	SASH1,CD180,PRKCA,BMP6	darkgreen	VSMC_M4
GO:0002223	0.02	1.00	4	13	stimulatory C-type lectin receptor signaling pathway	BP	0.5568	EP300,MAP3K7,PAK3,PLCG2	darkgreen	VSMC_M4
GO:1990840	0.02	1.00	4	13	response to lectin	BP	0.5568	EP300,MAP3K7,PAK3,PLCG2	darkgreen	VSMC_M4
GO:1990858	0.02	1.00	4	13	cellular response to lectin	BP	0.5568	EP300,MAP3K7,PAK3,PLCG2	darkgreen	VSMC_M4
GO:0006910	0.02	1.00	4	15	phagocytosis, recognition	BP	0.5568	ADGRB1,PTX3,LBP,MFGE8	darkgreen	VSMC_M4
GO:0022409	0.02	0.99	20	176	positive regulation of cell-cell adhesion	BP	0.56015	CITED2,LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,CHST2,PTPN11,PTPN22,ADA,CD47,F11R,IGFBP2,LGALS9,MYO10,VCAM1,VNN1,CD83,ICAM1	darkgreen	VSMC_M4
GO:2001243	0.02	0.99	11	83	negative regulation of intrinsic apoptotic signaling pathway	BP	0.56015	BCL2,MDM2,SOD2,WFS1,CREB3,TPT1,CLU,HERPUD1,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0045087	0.02	0.99	43	459	innate immune response	BP	0.5666	IFNGR1,IRAK3,C4A,RNASET2,EP300,ADGRB1,DAPK1,LEP,DDX58,ZAP70,MAP3K7,MRC1,TRIM23,CD180,G3BP2,CLU,PTPN11,PTX3,LBP,PTPN22,SERINC3,IFIT1,EDN1,CD47,N4BP1,MX1,MST1R,CFI,PRKD1,C1RL,CALCOCO2,GP2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,VNN1,TLR1,MFAP4,ICAM1	darkgreen	VSMC_M4

GO:0120193	0.02	0.99	9	54	tight junction organization	BP	0.56664	GRHL2,GJA1,TGFBR1,SVEP1,OCLN,ABCC8,F11R,TGFB3,PATJ	darkgreen	VSMC_M4
GO:0015833	0.02	0.99	21	186	peptide transport	BP	0.57042	GJA1,LEP,REST,ICA1,ABCA1,INHBB,PCLO,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,HIF1A,MAFA	darkgreen	VSMC_M4
GO:0071222	0.02	0.99	15	126	cellular response to lipopolysaccharide	BP	0.57058	SASH1,CD274,ABCA1,MRC1,ADAM9,ANKRD1,CD180,LBP,PTPN22,PRKCA,SERPINE1,PPARGC1A,PLCG2,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0010566	0.02	1.00	4	15	regulation of ketone biosynthetic process	BP	0.57058	REST,ADM,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0099024	0.02	0.99	8	47	plasma membrane invagination	BP	0.57058	ADGRB1,ABCA1,GATA2,CLCN3,MFGE8,GULP1,VAMP7,PLCG2	darkgreen	VSMC_M4
GO:0060389	0.02	0.99	8	47	pathway-restricted SMAD protein phosphorylation	BP	0.57111	GDF11,TGFBR1,INHBB,GDF6,TGFB3,SMAD6,DAB2,BMP6	darkgreen	VSMC_M4
GO:0043500	0.02	0.99	12	88	muscle adaptation	BP	0.57111	LMCD1,FOXO1,EDN1,RGS2,PRKCA,CAMK2D,CFLAR,INPP5F,TRIM63,AKAP6,PPARGC1A,SGCA	darkgreen	VSMC_M4
GO:0006694	0.02	0.99	15	126	steroid biosynthetic process	BP	0.57344	HSD17B6,LEP,REST,IGFBP7,ADM,ABCG1,ARV1,CYP19A1,PPARGC1A,FAXDC2,PRKAA2,MBTPS1,SLC27A5,BMP6,SCP2	darkgreen	VSMC_M4
GO:0045123	0.02	0.99	8	50	cellular extravasation	BP	0.57758	LEP,CHST2,JAM3,CD47,RIPOR2,F11R,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:0014823	0.02	0.99	9	57	response to activity	BP	0.57789	SOD2,LEP,COL4A2,EDN1,FNDC5,HIF1A,PPARGC1A,PRKAA2,BMP6	darkgreen	VSMC_M4
GO:0031175	0.02	0.99	75	784	neuron projection development	BP	0.58167	BCL2,UST,GRIP1,MDM2,DDR1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,KIDINS220,EPHB6,ITSN2,SEMA3C,PTPRG,DENND5A,ANKRD1,CPEB3,NCK1,ADM,KIF13B,GPM6A,APP,SCARB2,PTPN11,ADCY6,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,RAB29,RGS2,FEZ1,PREX1,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,PLXNB1,RAPH1,ITGA6,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,ATCAY,PLXNB3,FLNA,NEXN,ITM2C,SDC2,PRKG1	darkgreen	VSMC_M4
GO:0042886	0.02	0.99	23	210	amide transport	BP	0.58341	GJA1,LEP,REST,ICA1,ABCA1,INHBB,PCLO,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,EDN1,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,LRP2,RAPGEF4,HIF1A,SLC14A1,MAFA	darkgreen	VSMC_M4
GO:0061042	0.02	1.00	4	16	vascular wound healing	BP	0.58341	FAM19A5,SMOC2,GATA2,SERPINE1	darkgreen	VSMC_M4
GO:0009968	0.02	0.99	85	973	negative regulation of signal transduction	BP	0.58455	BCL2,IRAK3,MDM2,RGS22,SOD2,TLE4,MLLT3,WFS1,KANK1,RASL11B,RNF149,CREB3,SNX13,TGFBR1,PTPN3,TBX18,SESN1,JADE1,HIPK2,GATA2,TPT1,LBH,NDRG2,CRIM1,FOXO1,RASSF2,APLP1,NCOR2,LATS2,HIPK3,NCK1,ADM,SH3RF1,WWC2,RNF34,CLU,HERPUD1,TMEM64,PTPN22,CHAC1,ADA,RCAN1,CD47,ADIPOR1,RIPOR2,RGS2,EYA2,KCTD10,HTR2B,LGMN,SESN2,LRP2,CFLAR,INPP5F,CASTOR1,STRN3,ITGA6,GPRC5A,HSPB1,SERPINE1,UNC5B,IGFBP2,DACT1,HIF1A,RORA,SLIT3,TGFB3,SMAD6,CDH2,NOMO1,FST,DAB2,PRKAA2,TLE2,GLG1,MIR99A,ITPR1,VNN1,ADAMTSL2,FRZB,TBX20,TMEM170B,ICAM1,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0002376	0.02	0.98	134	1656	immune system process	BP	0.58455	MBP,BCL2,IFNGR1,CITED2,IRAK3,ANGPT1,C4A,RNASET2,EP300,ADGRB1,DAPK1,MLLT3,LEP,CDKN2B,DDX58,DOCK8,CD274,IL18R1,CREB3,REST,ZAP70,TGFBR1,EDN2,MAP3K7,NT5C3A,MAP3K8,HIPK2,GATA2,APBB1IP,LRCH1,SNRK,MRC1,HRH1,CD93,POLB,ADAM9,RASSF2,SEMA3C,TMEM178A,TF,FLT3,MAP3K1,FFAR3,CHD7,TRIM23,NCK1,CD180,SH3RF1,CHST2,KIF13B,G3BP2,CLU,BLNK,MEIS2,APP,ANXA3,PTPN11,PTX3,LBP,TMEM64,PTPN22,SERINC3,ADA,IFIT1,EDN1,JAM3,CD47,N4BP1,MX1,RAB29,RIPOR2,LRP5,PREX1,MST1R,LGMN,SIAE,PRKCA,CFI,P4HTM,ABCC9,CTSS,FGFR2,CTSF,TP53BP1,PRKD1,NCSTN,F11R,RAPGEF4,MFAP5,SERPINE1,C1RL,IGFBP2,TNFSF10,WDR1,HIF1A,CACNA1C,ADGRE2,ACTN1,RORA,CALCOCO2,TGFB3,SMAD6,FAXDC2,EPG5,GP2,PAK3,MMP28,FST,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,VCAM1,LRSAM1,LMO4,IFI44,VNN1,CD151,TLR1,BNIP3,ADAMTS5,CD83,LOX,CD59,ZNF175,CDKN1A,EDA,MFAP4,CCR6,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:1901698	0.02	0.99	75	845	response to nitrogen compound	BP	0.58455	IRAK3,MDM2,GJA1,GNAQ,LEP,WFS1,DDX58,KANK1,PDK4,SLC2A1,ABCA1,SESN1,INHBB,HRH1,STT3B,FOXO1,COL4A1,APLP1,FLT3,NCOR2,FFAR3,CPEB3,NCK1,ADM,MAP1LC3A,APP,PDGFC,ABCC8,PTPN11,ADCY6,HERPUD1,PTPN22,ADA,IFIT1,EDN1,MARCH6,LPL,ADIPOR1,RGS2,ACTN2,ZNF106,LRP5,HTR2B,LGMN,SESN2,ABCC9,ADCY5,CFLAR,WDTC1,CASTOR1,NCSTN,AKAP6,LRP6,ACHE,TNFSF10,JKAMP,GNAI1,PPARGC1A,FAF2,EPG5,FLNA,HCN2,AHCYL1,SORT1,CDH13,VCAM1,BCAR3,SLC8A1,FBXO27,PLN,CDKN1A,TMEM38A,ICAM1,PIK3C2A,STC2	darkgreen	VSMC_M4
GO:0010631	0.02	0.99	28	261	epithelial cell migration	BP	0.58455	SASH1,ANGPT1,SMOC2,ADGRB1,KANK1,TGFBR1,GATA2,ADAM9,CYP1B1,PTPRG,ATOH8,ANXA3,PTPN11,EDN1,SEMA5A,ADIPOR1,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,FAT2,MAPRE2,PLEKHG5,CDH13,PLCG2,CCR6,PIK3C2A	darkgreen	VSMC_M4
GO:0050810	0.02	0.99	8	50	regulation of steroid biosynthetic process	BP	0.58455	LEP,REST,IGFBP7,ADM,ABCG1,PPARGC1A,MBTPS1,BMP6	darkgreen	VSMC_M4
GO:0022612	0.02	0.99	13	95	gland morphogenesis	BP	0.58455	BCL2,DDR1,LIMS2,POLB,SEMA3C,HPN,KDM5B,LRP5,CFLAR,FGFR2,TGFB3,CSF1,EDA	darkgreen	VSMC_M4
GO:2001237	0.02	0.99	11	79	negative regulation of extrinsic apoptotic signaling pathway	BP	0.58455	BCL2,TGFBR1,SH3RF1,RNF34,EYA2,CFLAR,ITGA6,SERPINE1,UNC5B,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0034284	0.02	0.99	19	164	response to monosaccharide	BP	0.58601	SOD2,GJA1,LEP,UNC13B,HNF4A,LPL,ABCG1,PFKL,LRP5,TXNIP,SESN2,ADCY5,HIF1A,PPARGC1A,PRKAA2,SLC2A5,SLC8A1,ICAM1,MAFA	darkgreen	VSMC_M4
GO:0003281	0.02	0.99	10	60	ventricular septum development	BP	0.58601	CITED2,MDM2,TGFBR1,LRP2,FGFR2,FGFRL1,SLIT3,SMAD6,LMO4,CYR61	darkgreen	VSMC_M4

GO:0009887	0.02	0.99	73	784	animal organ morphogenesis	BP	0.58601	BCL2,CITED2,MDM2,DDR1,CDSN,GRHL2,LAMA2,EP300,MLLT3,TGFBR1,TBX18,HIPK2,GATA2,LIMS2,PPP1R13L,SMARCD3,POLB,THRB,FOXO1,SEMA3C,APLP1,HPN,CHD7,ANKRD1,ADM,PAM,MEIS2,PDGFC,NAB1,PDZD7,EDN1,KDM5B,TNNT2,LRP5,NPNT,HTR2B,SEC24B,ABLIM1,MYLK,LRP2,CFLAR,CTSZ,FGFR2,ARID5B,ITGA6,ID3,MFAP5,SERPINE1,PAPPA2,SYNPO2L,DACT1,HIF1A,FGFRL1,SLIT3,TGFB3,SMAD6,BBS4,CDH2,FST,DAB2,TLE2,FLNA,CSF1,GLG1,BCAR3,CYR61,ADAMTS5,FRZB,TBX20,FGF9,EDA,YAP1,BMP6	darkgreen	VSMC_M4
GO:0060420	0.02	0.99	9	58	regulation of heart growth	BP	0.58601	CITED2,GJA1,TGFBR1,EDN1,RGS2,FGFR2,AKAP6,TBX20,YAP1	darkgreen	VSMC_M4
GO:0097193	0.02	0.99	25	242	intrinsic apoptotic signaling pathway	BP	0.58601	BCL2,MDM2,SOD2,EP300,WFS1,CREB3,HIPK2,TPT1,POLB,CYP1B1,NCK1,CLU,HERPUD1,JMY,CHAC1,SERINC3,HSPB1,MAEL,HIF1A,ITPR1,VNN1,BNIP3,CDKN1A,NACC2,DDIT4	darkgreen	VSMC_M4
GO:0010882	0.02	1.00	5	23	regulation of cardiac muscle contraction by calcium ion signaling	BP	0.58601	CAMK2D,CACNA1C,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0042102	0.02	0.99	8	55	positive regulation of T cell proliferation	BP	0.58601	LEP,CD274,ZAP70,NCK1,PTPN22,IGFBP2,LGALS9,VCAM1	darkgreen	VSMC_M4
GO:0006979	0.02	0.99	34	357	response to oxidative stress	BP	0.58601	BCL2,MDM2,IPCEF1,SOD2,OXR1,DAPK1,PON2,REST,SESN1,ADAM9,FOXO1,CYP1B1,MAP1LC3A,MCTP1,APP,PTPN11,CHD6,ADA,RCAN1,EDN1,TXNIP,SESN2,PRKD1,PRDX4,HSPB1,CRYAB,HIF1A,PPARGC1A,ANGPTL7,PRKAA2,VNN1,SLC8A1,BNIP3,MSRB3	darkgreen	VSMC_M4
GO:0038065	0.02	1.00	4	12	collagen-activated signaling pathway	BP	0.58602	DDR1,COL4A1,COL4A2,DDR2	darkgreen	VSMC_M4
GO:0045926	0.02	0.99	22	195	negative regulation of growth	BP	0.59034	BCL2,CITED2,GJA1,JADE1,SEMA3C,WWC2,DCBLD2,HNF4A,SEMA5A,ADIPOR1,RGS2,LGMN,SESN2,CRYAB,HIF1A,NPPB,SLIT3,ULK2,CRLF3,FRZB,OSGIN2,CDKN1A	darkgreen	VSMC_M4
GO:0048259	0.02	0.99	12	85	regulation of receptor-mediated endocytosis	BP	0.59177	ANGPT1,SH3GL2,SNAP91,TF,CLU,ATXN2,HIP1,SERPINE1,NUMB,DNAJC6,DAB2,PLCG2	darkgreen	VSMC_M4
GO:0016239	0.02	0.99	9	56	positive regulation of macroautophagy	BP	0.59232	MAP3K7,SESN1,SLC25A4,SESN2,HIF1A,CALCOCO2,PRKAA2,LRSAM1,BNIP3	darkgreen	VSMC_M4
GO:0007178	0.02	0.99	30	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.59755	GDF11,CITED2,EP300,CDKN2B,RASL11B,TGFBR1,MAP3K7,HIPK2,INHBB,ADAM9,CRIM1,TF,LATS2,ATOH8,HNF4A,GDF6,FMOD,NPNT,LRP2,TGFB3,SMAD6,NOMO1,FST,DAB2,GLG1,CYR61,ADAMTSL2,LOX,TBX20,BMP6	darkgreen	VSMC_M4
GO:0046849	0.02	0.99	10	69	bone remodeling	BP	0.59945	GJA1,LEP,PDK4,RASSF2,TF,PTH,TMEM64,LRP5,PRKCA,TGFB3	darkgreen	VSMC_M4
GO:1902235	0.02	1.00	5	26	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	BP	0.60089	WFS1,CREB3,NCK1,HERPUD1,SERINC3	darkgreen	VSMC_M4
GO:0002220	0.02	1.00	4	14	innate immune response activating cell surface receptor signaling pathway	BP	0.60089	EP300,MAP3K7,PAK3,PLCG2	darkgreen	VSMC_M4
GO:0060142	0.02	1.00	4	17	regulation of syncytium formation by plasma membrane fusion	BP	0.60089	ADGRB1,ADAM9,RIPOR2,CFLAR	darkgreen	VSMC_M4
GO:0060419	0.02	0.99	11	77	heart growth	BP	0.60089	CITED2,GJA1,TGFBR1,TENM4,SORBS2,EDN1,RGS2,FGFR2,AKAP6,TBX20,YAP1	darkgreen	VSMC_M4
GO:0150146	0.02	1.00	4	14	cell junction disassembly	BP	0.60089	TGFBR1,ABCC8,TGFB3,MAPRE2	darkgreen	VSMC_M4
GO:0072583	0.02	0.99	8	46	clathrin-dependent endocytosis	BP	0.60089	SH3GL2,LMBRD1,SNAP91,ITSN2,INPP5F,HIP1,DNAJC6,DAB2	darkgreen	VSMC_M4
GO:0032366	0.02	1.00	5	23	intracellular sterol transport	BP	0.60089	ABCA1,ABCG1,ARV1,LRP6,SCP2	darkgreen	VSMC_M4
GO:0032367	0.02	1.00	5	23	intracellular cholesterol transport	BP	0.60089	ABCA1,ABCG1,ARV1,LRP6,SCP2	darkgreen	VSMC_M4
GO:0010810	0.02	0.99	21	175	regulation of cell-substrate adhesion	BP	0.60268	BCL2,DDR1,LIMCH1,KANK1,ECM2,LIMS2,ACTN4,PTPN11,CCDC80,NPNT,PREX1,NID1,ITGA6,COL26A1,SERPINE1,DAPK3,FLNA,CSF1,CDH13,CYR61,PLEKHA2	darkgreen	VSMC_M4
GO:1902932	0.02	1.00	4	17	positive regulation of alcohol biosynthetic process	BP	0.6051	HRH1,PTH,ABCG1,BMP6	darkgreen	VSMC_M4
GO:0050920	0.02	0.99	19	167	regulation of chemotaxis	BP	0.6051	SMOC2,CREB3,EDN2,SEMA3C,LBP,EDN1,JAM3,SEMA5A,RIPOR2,LGMN,PRKD1,HSPB1,SERPINE1,MMP28,LGALS9,CSF1,CDH13,F3,CCR6	darkgreen	VSMC_M4
GO:0019725	0.02	0.98	59	638	cellular homeostasis	BP	0.6051	BCL2,GJA1,TRDN,WFS1,UNC13B,EDN2,GATA2,TPT1,KCNE3,FOXO1,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,ABCC8,HERPUD1,TMEM64,EDN1,ABCG1,LRP5,HTR2B,CAMK2D,ADCY5,WDTC1,PRKD1,CYBRD1,AKAP6,LRP6,PRDX4,ATP6AP2,HIF1A,CACNA1C,PPARGC1A,ADRA1B,NPTN,RHOT1,PRKAA2,PLCG2,ITPR1,SLC8A1,BNIP3,LOX,PLN,TMEM38A,CCR6,ICAM1,ORMDL3,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0032233	0.02	0.99	9	56	positive regulation of actin filament bundle assembly	BP	0.6051	LIMCH1,TGFBR1,CD47,SYNPO2,SYNPO2L,TGFB3,SYNPO,FLNA,PPM1E	darkgreen	VSMC_M4
GO:0032231	0.02	0.99	13	92	regulation of actin filament bundle assembly	BP	0.6051	LIMCH1,PPP1R9A,TGFBR1,CD47,SYNPO2,F11R,RDX,SYNPO2L,TGFB3,SYNPO,ARHGAP28,FLNA,PPM1E	darkgreen	VSMC_M4
GO:1900271	0.02	0.99	6	33	regulation of long-term synaptic potentiation	BP	0.60538	PPP1R9A,ZDHHC2,APP,LGMN,NCSTN,NPTN	darkgreen	VSMC_M4
GO:0050870	0.02	0.99	15	130	positive regulation of T cell activation	BP	0.60639	LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,PTPN11,PTPN22,ADA,CD47,IGFBP2,LGALS9,VCAM1,VNN1,CD83	darkgreen	VSMC_M4
GO:0055119	0.02	1.00	4	15	relaxation of cardiac muscle	BP	0.60639	RGS2,CAMK2D,SLC8A1,PLN	darkgreen	VSMC_M4
GO:0051051	0.02	0.99	31	314	negative regulation of transport	BP	0.61279	BCL2,ANGPT1,GJA1,TRDN,LEP,PPP1R9A,REST,MDFIC,INHBB,KCNE3,MCTP1,ATXN2,ABCC8,PTPN11,ADA,EDN1,CD47,RGS2,ACTN2,PFKL,ATP9A,CAMK2D,PRKD1,CRYAB,MAOB,LGALS9,SLC43A2,LRSAM1,KCNE4,PLN,ICAM1	darkgreen	VSMC_M4
GO:0001944	0.02	0.98	58	607	vasculature development	BP	0.61663	CITED2,SASH1,MDM2,SOD2,ANGPT1,FAM19A5,SMOC2,ADGRB1,LEP,SGCB,RECK,TGFBR1,SVEP1,CALD1,ANTXR1,HIPK2,GATA2,COL4A1,COL4A2,CYP1B1,SEMA3C,AMOTL2,CHD7,ADM,ABCC8,ANXA3,EDN1,JAM3,SEMA5A,LRP5,PRKCA,SEC24B,MFGE8,MYLK,LRP2,CFLAR,FGFR2,PTPN14,PRKD1,HSPB1,SERPINE1,UNC5B,HIF1A,NPPB,ANGPTL7,RORA,SMAD6,CDH2,ANGPTL4,FLNA,CDH13,F3,CYR61,LOX,TBX20,FGF9,PIK3C2A,YAP1	darkgreen	VSMC_M4

GO:0070848	0.02	0.98	55	570	response to growth factor	BP	0.61663	CITED2,MDM2,SMOC2,EP300,SH3GL2,CDKN2B,RASL11B,TGFBR1,MAP3K7,KIDINS220,HIPK2,ADAM9,CRIM1,COL4A2,FLT3,LATS2,ANKRD1,PTH,MEIS2,APP,ANXA3,PTPN11,GDF6,FMOD,NGF,EDN1,KDM5B,FEZ1,NPNT,LGMN,GALNT3,LRP2,CFLAR,FGFR2,PRKD1,HSPB1,RDX,HIF1A,PPARGC1A,FGFRL1,TGFB3,SMAD6,NPTN,FST,DAB2,SORT1,VCAM1,GLG1,CYR61,ADAMTSL2,LOX,TBX20,FGF9,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0071407	0.02	0.98	44	448	cellular response to organic cyclic compound	BP	0.61748	MDM2,EP300,LEP,DDX58,REST,ABCA1,HRH1,LBH,FOXO1,CYP1B1,APLP1,FLT3,NCOR2,ANKRD1,CLU,APP,ADCY6,IFIT1,EDN1,PLA2G4F,NCOA3,HTR2B,ADCY5,CFLAR,NCSTN,STRN3,ITGA6,AKAP6,ID3,LRP6,GNAI1,PPARGC1A,RORA,EPG5,PAK3,DAB2,SKP2,FLNA,HCN2,SLC8A1,TMEM38A,ICAM1,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0048008	0.02	0.99	8	48	platelet-derived growth factor receptor signaling pathway	BP	0.61748	PDGFC,PTPN11,TXNIP,ARID5B,HIP1,F3,LOX,PIK3C2A	darkgreen	VSMC_M4
GO:0016192	0.02	0.98	103	1192	vesicle-mediated transport	BP	0.61871	STX11,GRIP1,LAPTM4B,ANGPT1,C4A,ADGRB1,SH3GL2,LEP,VLDLR,UNC13B,RIC1,REST,LMAN2L,PREPL,LMBRD1,SYT5,ABCA1,DOP1A,SNAP91,ITSN2,GATA2,MRC1,TMCC1,GGA3,USP6NL,CD93,SYNGR2,RAB2B,FGF14,ATP2C1,PCLO,TF,APLP1,ZDHHC2,DENND5A,TRIM23,EXOC6,ADM,CLCN3,MCTP1,CLU,APP,ATXN2,SCARB2,ANXA3,PTX3,LBP,AKTIP,CD47,MYO1B,RAB29,ACTN2,LRP5,HTR2B,MST1R,TINAGL1,SEC24B,CFI,MFGE8,ATP9A,LRP2,INPP5F,PRKD1,PI4KB,RAPGEF4,AP3B2,LRP6,HIP1,CUX1,SERPINE1,ACHE,RDX,EXPH5,GULP1,ATG14,LMTK2,NLGN1,RABEP1,SYT16,AP1S3,MICAL3,ADGRE2,FBXL20,NUMB,EPG5,GP2,CDH2,MARCH2,DNAJC6,DAB2,LGALS9,FLNA,VAMP7,SORT1,FNBP1,MBTPS1,CDH13,PLCG2,LRSAM1,CD151,NCALD,GABARAPL2,PIK3C2A	darkgreen	VSMC_M4
GO:0019218	0.02	0.99	10	73	regulation of steroid metabolic process	BP	0.61871	LEP,REST,IGFBP7,ADM,ABCG1,ARV1,PPARGC1A,RORA,MBTPS1,BMP6	darkgreen	VSMC_M4
GO:0031663	0.02	0.99	7	44	lipopolysaccharide-mediated signaling pathway	BP	0.61871	SASH1,CD180,LBP,PTPN22,PRKCA,PLCG2,BMP6	darkgreen	VSMC_M4
GO:0032868	0.02	0.99	23	206	response to insulin	BP	0.62041	LEP,KANK1,PDK4,SLC2A1,INHBB,FOXO1,FFAR3,NCK1,ADM,ABCC8,PTPN11,LPL,ADIPOR1,ZNF106,SESN2,CFLAR,WDTC1,TNFSF10,SORT1,BCAR3,PLN,ICAM1,PIK3C2A	darkgreen	VSMC_M4
GO:0045444	0.02	0.99	21	188	fat cell differentiation	BP	0.62217	ZNF516,EP300,LEP,GATA2,INHBB,FOXO1,TMEM64,GDF6,LPL,FNDC5,RGS2,LRP5,ARID5B,PPARGC1A,RORA,SMAD6,BBS4,SORT1,BNIP3,FRZB,YAP1	darkgreen	VSMC_M4
GO:0050801	0.02	0.98	51	542	ion homeostasis	BP	0.62298	BCL2,GJA1,TRDN,WFS1,PDK4,EDN2,PTPN3,GATA2,TPT1,KCNE3,TRPC4,ATP2C1,TMEM178A,TF,RIC3,CHD7,MICU2,ADM,CLCN3,SLC35G1,JPH1,PTH,APP,HERPUD1,TMEM64,EDN1,CNNM2,HTR2B,CAMK2D,ADCY5,PRKD1,CYBRD1,AKAP6,LRP6,ATP6AP2,FBXL5,HIF1A,CACNA1C,NPPB,ADRA1B,NPTN,PLCG2,ITPR1,SLC8A1,BNIP3,PLN,TMEM38A,CCR6,STC2,ATP6V0E1,BMP6	darkgreen	VSMC_M4
GO:0030308	0.02	0.99	18	153	negative regulation of cell growth	BP	0.62298	BCL2,GJA1,JADE1,SEMA3C,DCBLD2,HNF4A,SEMA5A,ADIPOR1,RGS2,SESN2,CRYAB,NPPB,SLIT3,ULK2,CRLF3,FRZB,OSGIN2,CDKN1A	darkgreen	VSMC_M4
GO:0022411	0.02	0.98	38	375	cellular component disassembly	BP	0.62303	IRAK3,DDR1,TGFBR1,SMARCD3,EXOG,HPN,MAP1LC3A,SLC25A4,ABCC8,ATG13,SEMA5A,ACTN2,PRKCA,MID1,CTSS,DDR2,GABARAPL1,RDX,ATG14,MMP1,WDR1,HIF1A,MICAL3,PPARGC1A,CALCOCO2,TGFB3,EPG5,MAPRE2,ULK2,DNAJC6,MAP1LC3B2,SPTAN1,BNIP3,ADAMTS5,CST3,DSTN,GABARAPL2,DDIT4	darkgreen	VSMC_M4
GO:0010977	0.02	0.99	15	116	negative regulation of neuron projection development	BP	0.62414	MDM2,KANK1,SEMA3C,PTPRG,DENND5A,ADCY6,SEMA5A,RAB29,CTSZ,INPP5F,ZNF365,NLGN1,ULK2,FLNA,ITM2C	darkgreen	VSMC_M4
GO:0006165	0.02	0.99	10	72	nucleoside diphosphate phosphorylation	BP	0.62414	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,AK7,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0009628	0.02	0.98	77	891	response to abiotic stimulus	BP	0.62414	ZNF516,BCL2,CITED2,MDM2,SOD2,PKDREJ,GJA1,EP300,GNAQ,LEP,REST,IGFBP7,SLC2A1,HIPK2,ABHD12,TMEM135,HRH1,BABAM2,POLB,FOXO1,MAP3K1,HPN,ANKRD1,ADM,PAM,GRK7,MEIS2,APP,ABCC8,PTPN11,TANC1,ADA,PDZD7,EDN1,N4BP1,LPL,LRP5,HTR2B,LGMN,SUN1,TXNIP,CTSS,MYLK,CFLAR,RBM4B,USP53,TP53BP1,F11R,TRIM63,CRYAB,PAPPA2,IGFBP2,MMP1,PCSK1N,HIF1A,OPN3,PPARGC1A,PLOD1,RORA,TGFB3,NPTN,CDH2,ANGPTL4,VCAM1,ABCA4,LRRC8C,ITPR1,SLC8A1,DNAJA2,BNIP3,CDKN1A,MFAP4,ICAM1,STC2,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0097305	0.02	0.99	20	174	response to alcohol	BP	0.62414	MDM2,SOD2,LEP,IGFBP7,TGFBR1,ABCA1,POLB,PTH,ADCY6,RGS2,ADCY5,FGFR2,LRP6,MAOB,GNAI1,SLIT3,PRKAA2,VCAM1,CDKN1A,ICAM1	darkgreen	VSMC_M4
GO:1901652	0.02	0.98	37	375	response to peptide	BP	0.62478	MDM2,GJA1,LEP,KANK1,PDK4,SLC2A1,INHBB,FOXO1,FFAR3,NCK1,ADM,APP,ABCC8,PTPN11,ADCY6,PTPN22,EDN1,LPL,ADIPOR1,ACTN2,ZNF106,LRP5,LGMN,SESN2,CFLAR,WDTC1,LRP6,TNFSF10,GNAI1,AHCYL1,SORT1,VCAM1,BCAR3,PLN,ICAM1,PIK3C2A,STC2	darkgreen	VSMC_M4
GO:0001508	0.02	0.99	14	99	action potential	BP	0.62478	GJA1,GNAQ,PTPN3,TBX18,KCNE3,SCN8A,CAMK2D,USP53,AKAP6,CACNA1C,FLNA,HCN2,KCNE4,SLC8A1	darkgreen	VSMC_M4
GO:0097529	0.02	0.99	16	142	myeloid leukocyte migration	BP	0.62797	CREB3,EDN2,HRH1,LBP,EDN1,JAM3,CD47,RIPOR2,PREX1,LGMN,SERPINE1,WDR1,ADGRE2,GP2,MMP28,CSF1	darkgreen	VSMC_M4
GO:0009132	0.02	0.99	12	94	nucleoside diphosphate metabolic process	BP	0.62855	EP300,ENTPD3,ENTPD1,APP,PFKL,ENO2,HIF1A,PPARGC1A,AK7,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0034765	0.02	0.98	33	323	regulation of ion transmembrane transport	BP	0.63217	TRDN,DAPK1,PTPN3,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,CHD7,SCN8A,JPH1,APP,ABCC8,RGS2,ACTN2,CAMK2D,CTSS,PRKD1,AKAP6,NLGN1,WDR1,CACNA1C,PPARGC1A,KCNK10,SLC43A2,FLNA,HCN2,AHCYL1,PLCG2,KCNE4,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0001938	0.02	0.99	11	78	positive regulation of endothelial cell proliferation	BP	0.63274	TGFBR1,GATA2,SEMA5A,HTR2B,PRKCA,PRKD1,HIF1A,PLXNB3,CDH13,F3,BMP6	darkgreen	VSMC_M4

GO:0071396	0.02	0.98	41	422	cellular response to lipid	BP	0.63291	SASH1,EP300,LEP,CD274,PDK4,REST,ABCA1,MRC1,LBH,ADAM9,FOXO1,FLT3,NCOR2,FFAR3,ANKRD1,CD180,CLU,ADCY6,LBP,PTPN22,EDN1,LPL,NCOA3,PRKCA,ADCY5,CFLAR,FGFR2,STRN3,ID3,LRP6,SERPINE1,GNAI1,PPARGC1A,RORA,DAB2,SKP2,PLCG2,ICAM1,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:1903053	0.02	0.99	7	43	regulation of extracellular matrix organization	BP	0.63481	DDR1,RIC1,ANTXR1,CFLAR,DDR2,ANGPTL7,CST3	darkgreen	VSMC_M4
GO:0043243	0.02	0.99	6	29	positive regulation of protein-containing complex disassembly	BP	0.63481	SEMA5A,ACTN2,WDR1,CALCOCO2,BNIP3,DSTN	darkgreen	VSMC_M4
GO:1903844	0.02	0.99	14	104	regulation of cellular response to transforming growth factor beta stimulus	BP	0.63481	CITED2,EP300,CDKN2B,RASL11B,HIPK2,LATS2,NPNT,CFLAR,TGFB3,SMAD6,DAB2,GLG1,ADAMTSL2,LOX	darkgreen	VSMC_M4
GO:0042327	0.02	0.98	57	612	positive regulation of phosphorylation	BP	0.63481	GDF11,BCL2,SASH1,DDR1,ANGPT1,TPD52L1,LEP,LIMCH1,VLDLR,PPP1R9A,TGFBR1,MAP3K7,EPHB6,HIPK2,INHBB,ADAM9,RASSF2,TF,FLT3,CLU,APP,PDGFC,PTPN11,CCNT1,GDF6,AKTIP,NGF,EDN1,HTR2B,MST1R,AFAP1L2,FGFR2,PRKD1,ITGA6,DDR2,GPRC5A,MAP3K13,FAM129A,ATG14,LMTK2,HIF1A,TGFB3,TOM1L1,FAXDC2,NPTN,DAB2,PRKAA2,CSF1,PLCG2,TERF2IP,BCAR3,LMO4,CYR61,CDKN1A,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0010466	0.02	0.99	16	145	negative regulation of peptidase activity	BP	0.63481	MDM2,C4A,RECK,ITIH5,CRIM1,SH3RF1,RNF34,APP,HERPUD1,PROS1,NGF,SERPINE1,CRYAB,PCSK1N,SPINK2,CST3	darkgreen	VSMC_M4
GO:0046633	0.02	0.99	5	25	alpha-beta T cell proliferation	BP	0.63481	CD274,ZAP70,SH3RF1,PTPN22,LGALS9	darkgreen	VSMC_M4
GO:0043410	0.03	0.98	35	356	positive regulation of MAPK cascade	BP	0.63481	DOK6,SASH1,ANGPT1,TPD52L1,LEP,SH3RF3,TGFBR1,MAP3K7,HIPK2,ADAM9,RASSF2,FLT3,SH3RF1,APP,PDGFC,PTPN11,PTPN22,GDF6,EDN1,NPNT,HTR2B,MST1R,PRKCA,MID1,CFLAR,FGFR2,MAP3K13,ADRA1B,NPTN,CDH2,LGALS9,PLCG2,BCAR3,FGF9,ICAM1	darkgreen	VSMC_M4
GO:0006950	0.03	0.98	210	2715	response to stress	BP	0.63481	ZNF516,BCL2,IFNGR1,CITED2,SHPRH,SASH1,IRAK3,MDM2,DDR1,IPCEF1,SOD2,OXR1,C4A,FAM19A5,RNASET2,SMOC2,SCUBE1,GJA1,TPD52L1,EP300,MRTFA,ADGRB1,DAPK1,GNAQ,LEP,CDKN2B,WFS1,DDX58,SH3RF3,KANK1,C2orf40,PON2,PDK4,IL18R1,CREB3,REST,IGFBP7,ZAP70,SLC2A1,TGFBR1,ABCA1,MAP3K7,NT5C3A,MDFIC,SESN1,HIPK2,GATA2,ABHD12,TMEM135,MRC1,TPT1,ITGA9,INHBB,HRH1,BABAM2,STT3B,POLB,ADAM9,FOXO1,RASSF2,CYP1B1,TF,FFAR3,HIPK3,ANKRD1,TRIM23,NCK1,ADM,MAP1LC3A,PAM,CD180,SH3RF1,OCLN,MCTP1,CHST2,G3BP2,CLU,ENTPD1,BLNK,MYL9,APP,ABCC8,ANXA3,PTPN11,PTX3,LBP,NEK4,HERPUD1,PROS1,JMY,DCBLD2,CHD6,PTPN22,HNF4A,CHAC1,GDF6,SERINC3,ADA,RCAN1,IFIT1,EDN1,JAM3,CD47,N4BP1,SMARCAD1,MARCH6,LPL,MX1,EYA2,MST1R,ZMAT3,TM7SF3,PRKCA,AFAP1L2,TXNIP,CFI,MID1,SESN2,ABCC9,MYLK,CFLAR,INPP5F,FGFR2,TP53BP1,PRKD1,F11R,ZNF365,ATF6,MAP3K13,ID3,PRDX4,LNPK,GABARAPL1,FAM129A,HSPB1,SERPINE1,CRYAB,C1RL,PAPPA2,NBR1,AOC3,ATG14,DACT1,JKAMP,MAEL,PCSK1N,HIF1A,ADGRE2,ZBTB4,FBXL20,ZFYVE26,PPARGC1A,PLOD1,FAF2,ANGPTL7,RORA,CALCOCO2,TGFB3,SMAD6,GP2,ULK2,PAK3,HSPB3,ANGPTL4,LGALS9,SKP2,MARF1,PRKAA2,DAPK3,FLNA,VAMP7,CSF1,MAP1LC3B2,MBTPS1,PLCG2,VCAM1,TERF2IP,F3,LRSAM1,CDC7,LRRC8C,CYR61,ITPR1,VNN1,SLC8A1,DNAJA2,CD151,TLR1,FBXO27,BNIP3,ADAMTS5,EXOS,CD83,LOX,CD59,CST3,CSRP1,MSRB3,ZNF175,CDKN1A,MFAP4,NACC2,CCR6,GABARAPL2,ICAM1,STC2,YAP1,PRKG1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0110053	0.03	0.99	26	237	regulation of actin filament organization	BP	0.63481	LIMCH1,KANK1,PPP1R9A,TGFBR1,CDC42EP3,WASF3,NCK1,JMY,CD47,SEMA5A,ACTN2,PREX1,SYNPO2,F11R,RDX,SYNPO2L,WDR1,TGFB3,SYNPO,PAK3,ARHGAP28,FLNA,SPTAN1,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0002758	0.03	1.00	4	15	innate immune response-activating signal transduction	BP	0.63481	EP300,MAP3K7,PAK3,PLCG2	darkgreen	VSMC_M4
GO:0043085	0.03	0.98	77	875	positive regulation of catalytic activity	BP	0.63481	MBP,BCL2,SASH1,DDR1,GRHL2,ANGPT1,TPD52L1,DAPK1,GNAQ,LEP,DOCK8,DCUN1D4,VLDLR,PPP1R9A,RIC1,REST,SNX13,EDN2,CHN2,MAP3K7,ANTXR1,EPHB6,USP6NL,RALGAPA2,ADAM9,RASSF2,FLT3,PTH,CLU,APP,PDGFC,CCNT1,PKP4,EDN1,TNNT2,ARRDC4,NPNT,PREX1,HTR2B,MST1R,LGMN,SERINC2,AFAP1L2,CFLAR,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,ITGA6,DDR2,GPRC5A,MAP3K13,HIP1,ATG14,TNFSF10,LMTK2,HIF1A,CACNA1C,SIPA1L1,TOM1L1,MAPRE2,EVI5L,LGALS9,NPR3,CSF1,TBC1D13,F3,ARHGAP29,BCAR3,LMO4,CYR61,SYDE2,CDKN1A,RFK,GABARAPL2,ICAM1	darkgreen	VSMC_M4
GO:0086064	0.03	0.99	5	23	cell communication by electrical coupling involved in cardiac conduction	BP	0.63481	GJA1,TRDN,CAMK2D,CACNA1C,SLC8A1	darkgreen	VSMC_M4
GO:0045940	0.03	1.00	4	18	positive regulation of steroid metabolic process	BP	0.63481	ADM,ABCG1,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0010611	0.03	0.99	8	51	regulation of cardiac muscle hypertrophy	BP	0.63481	LMCD1,FOXO1,EDN1,RGS2,PRKCA,CAMK2D,TRIM63,AKAP6	darkgreen	VSMC_M4
GO:0042330	0.03	0.98	42	427	taxis	BP	0.63481	ANGPT1,SMOC2,LAMA2,EP300,CREB3,EDN2,DOCK4,EPHB6,HRH1,SEMA3C,APP,LBP,EDN1,JAM3,NFASC,SEMA5A,RIPOR2,FEZ1,PREX1,LGMN,ROBO3,PLXNA2,PRKD1,PLXNB1,HSPB1,SERPINE1,UNC5B,ADGRE2,SLIT3,NPTN,MMP28,LGALS9,PLXNB3,PLEKHG5,CSF1,CDH13,VCAM1,F3,CYR61,NEXN,LOX,CCR6	darkgreen	VSMC_M4
GO:0030220	0.03	1.00	4	16	platelet formation	BP	0.63481	EP300,PTPN11,WDR1,ACTN1	darkgreen	VSMC_M4
GO:0036344	0.03	1.00	4	16	platelet morphogenesis	BP	0.63481	EP300,PTPN11,WDR1,ACTN1	darkgreen	VSMC_M4
GO:1901881	0.03	1.00	4	15	positive regulation of protein depolymerization	BP	0.63481	SEMA5A,ACTN2,WDR1,DSTN	darkgreen	VSMC_M4
GO:0031345	0.03	0.99	18	150	negative regulation of cell projection organization	BP	0.63481	MDM2,KANK1,SEMA3C,PTPRG,DENND5A,ADCY6,SEMA5A,RAB29,CTSZ,INPP5F,ZNF365,NLGN1,ULK2,EVI5L,PLXNB3,FLNA,ITM2C,YAP1	darkgreen	VSMC_M4

GO:1901701	0.03	0.98	78	887	cellular response to oxygen-containing compound	BP	0.63481	SASH1,MDM2,SOD2,OXR1,GJA1,DAPK1,GNAQ,LEP,KANK1,UNC13B,CD274,PDK4,ABCA1,SESN1,MRC1,INHBB,HRH1,ADAM9,FOXO1,COL4A1,CYP1B1,APLP1,FFAR3,ANKRD1,CPEB3,NCK1,MAP1LC3A,CD180,CLU,APP,PDGFC,PTPN11,ADCY6,LBP,PTPN22,EDN1,LPL,ABCG1,ADIPOR1,NCOA3,ACTN2,ZNF106,LRP5,HTR2B,LGMN,PRKCA,SESN2,ADCY5,CFLAR,WDTC1,FGFR2,CASTOR1,PRKD1,NCSTN,AKAP6,ID3,LRP6,SERPINE1,ACHE,HIF1A,GNAI1,PPARGC1A,RORA,PRKAA2,FLNA,SLC2A5,HCN2,AHCYL1,PLCG2,VCAM1,BCAR3,SLC8A1,BNIP3,ICAM1,PIK3C2A,YAP1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0014829	0.03	0.99	5	24	vascular associated smooth muscle contraction	BP	0.63481	EDN2,DOCK4,EDN1,SLC8A1,PIK3C2A	darkgreen	VSMC_M4
GO:0060401	0.03	0.99	16	126	cytosolic calcium ion transport	BP	0.63481	BCL2,TRDN,CHD7,MICU2,SLC35G1,JPH1,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0001558	0.03	0.98	34	339	regulation of cell growth	BP	0.63481	BCL2,DDR1,GJA1,FAM122A,IGFBP7,TGFBR1,JADE1,ITSN2,SEMA3C,HPN,CHPT1,EXTL3,DCBLD2,HNF4A,NGF,EDN1,SEMA5A,ADIPOR1,RGS2,SESN2,SHTN1,CAMK2D,AKAP6,MAP3K13,CRYAB,PAPPA2,NPPB,SLIT3,ULK2,CRLF3,FRZB,OSGIN2,CDKN1A,IGFBPL1	darkgreen	VSMC_M4
GO:0052547	0.03	0.98	28	294	regulation of peptidase activity	BP	0.63481	MBP,MDM2,C4A,DAPK1,REST,RECK,ANTXR1,ITIH5,CRIM1,SH3RF1,RNF34,APP,HERPUD1,PROS1,NGF,LGMN,CFLAR,NCSTN,HIP1,SERPINE1,CRYAB,TNFSF10,PCSK1N,LGALS9,F3,CYR61,SPINK2,CST3	darkgreen	VSMC_M4
GO:0014855	0.03	0.99	9	56	striated muscle cell proliferation	BP	0.63799	CITED2,ANGPT1,GJA1,TGFBR1,TENM4,CFLAR,FGFR2,TBX20,YAP1	darkgreen	VSMC_M4
GO:0006986	0.03	0.99	14	124	response to unfolded protein	BP	0.6402	EP300,WFS1,CREB3,STT3B,NCK1,HERPUD1,CHAC1,TM7SF3,ATF6,HSPB1,JKAMP,FAF2,HSPB3,MBTPS1	darkgreen	VSMC_M4
GO:0070661	0.03	0.99	21	201	leukocyte proliferation	BP	0.6402	BCL2,LEP,DOCK8,CD274,ZAP70,FLT3,NCK1,CD180,SH3RF1,PTH,CLU,PTPN22,ADA,NCSTN,IGFBP2,LGALS9,NPR3,CSF1,VCAM1,CD151,CDKN1A	darkgreen	VSMC_M4
GO:0003171	0.03	0.99	5	23	atrioventricular valve development	BP	0.6402	MDM2,SLIT3,SMAD6,CYR61,TBX20	darkgreen	VSMC_M4
GO:1903428	0.03	1.00	4	17	positive regulation of reactive oxygen species biosynthetic process	BP	0.6402	SOD2,ADGRB1,CLCN3,PLCG2	darkgreen	VSMC_M4
GO:0002691	0.03	0.99	5	26	regulation of cellular extravasation	BP	0.6402	CHST2,JAM3,CD47,RIPOR2,ICAM1	darkgreen	VSMC_M4
GO:0001936	0.03	0.99	14	111	regulation of endothelial cell proliferation	BP	0.64126	GJA1,LEP,TGFBR1,GATA2,ATOH8,SEMA5A,HTR2B,PRKCA,PRKD1,HIF1A,PLXNB3,CDH13,F3,BMP6	darkgreen	VSMC_M4
GO:0034405	0.03	0.99	6	31	response to fluid shear stress	BP	0.64301	CITED2,GJA1,ABCA1,ADAM9,TGFB3,SMAD6	darkgreen	VSMC_M4
GO:0090066	0.03	0.98	41	418	regulation of anatomical structure size	BP	0.64757	SOD2,GJA1,LEP,KANK1,PPP1R9A,EDN2,DOCK4,HRH1,CDC42EP3,SEMA3C,WASF3,NCK1,ADM,CLCN3,ADCY6,JMY,NGF,EDN1,SEMA5A,RGS2,ACTN2,PREX1,HTR2B,SHTN1,WDTC1,MAP3K13,RDX,WDR1,NPPB,ADRA1B,ULK2,PAK3,ARHGAP28,NPR3,SPTAN1,SLC8A1,DSTN,TMEM123,ICAM1,PIK3C2A,PRKG1	darkgreen	VSMC_M4
GO:0046939	0.03	0.99	10	74	nucleotide phosphorylation	BP	0.64775	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,AK7,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0043068	0.03	0.98	39	422	positive regulation of programmed cell death	BP	0.64775	SOD2,TPD52L1,DAPK1,LEP,UNC13B,CD274,REST,TGFBR1,INHBB,FOXO1,RASSF2,CYP1B1,LATS2,ANKRD1,NCK1,ADM,CLU,JMY,SERINC3,ZMAT3,TXNIP,CAMK2D,CTSZ,ITGA6,ATF6,ID3,TNFSF10,PPARGC1A,TGFB3,PAK3,LGALS9,DAPK3,SORT1,CYR61,BNIP3,FRZB,ITM2C,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0010742	0.03	0.99	5	25	macrophage derived foam cell differentiation	BP	0.65352	EP300,ABCA1,LPL,ABCG1,CSF1	darkgreen	VSMC_M4
GO:0090077	0.03	0.99	5	25	foam cell differentiation	BP	0.65352	EP300,ABCA1,LPL,ABCG1,CSF1	darkgreen	VSMC_M4
GO:0043065	0.03	0.98	38	410	positive regulation of apoptotic process	BP	0.65412	SOD2,TPD52L1,DAPK1,LEP,UNC13B,CD274,REST,TGFBR1,INHBB,FOXO1,RASSF2,CYP1B1,LATS2,ANKRD1,NCK1,ADM,CLU,JMY,SERINC3,ZMAT3,TXNIP,CAMK2D,CTSZ,ITGA6,ATF6,ID3,TNFSF10,PPARGC1A,TGFB3,PAK3,LGALS9,DAPK3,SORT1,CYR61,BNIP3,FRZB,ITM2C,NACC2	darkgreen	VSMC_M4
GO:0032924	0.03	0.99	6	31	activin receptor signaling pathway	BP	0.66142	CITED2,TGFBR1,INHBB,GDF6,NOMO1,FST	darkgreen	VSMC_M4
GO:0051017	0.03	0.99	17	139	actin filament bundle assembly	BP	0.66142	LIMCH1,PPP1R9A,TGFBR1,CALD1,CD47,MYO1B,SYNPO2,F11R,RDX,SYNPO2L,ACTN1,TGFB3,SYNPO,PLS3,ARHGAP28,FLNA,PPM1E	darkgreen	VSMC_M4
GO:0010243	0.03	0.98	70	793	response to organonitrogen compound	BP	0.66142	IRAK3,MDM2,GJA1,LEP,WFS1,KANK1,PDK4,SLC2A1,ABCA1,SESN1,INHBB,HRH1,STT3B,FOXO1,COL4A1,APLP1,FLT3,NCOR2,FFAR3,CPEB3,NCK1,ADM,MAP1LC3A,APP,PDGFC,ABCC8,PTPN11,ADCY6,HERPUD1,PTPN22,ADA,EDN1,MARCH6,LPL,ADIPOR1,RGS2,ACTN2,ZNF106,LRP5,HTR2B,LGMN,SESN2,ABCC9,ADCY5,CFLAR,WDTC1,CASTOR1,NCSTN,AKAP6,LRP6,TNFSF10,JKAMP,GNAI1,PPARGC1A,FAF2,FLNA,HCN2,AHCYL1,SORT1,CDH13,VCAM1,BCAR3,SLC8A1,FBXO27,PLN,CDKN1A,TMEM38A,ICAM1,PIK3C2A,STC2	darkgreen	VSMC_M4
GO:0042391	0.03	0.98	31	302	regulation of membrane potential	BP	0.66142	BCL2,SOD2,GJA1,TRDN,GNAQ,UNC13B,PPP1R9A,PTPN3,TBX18,KCNE3,FGF14,FXYD1,SCN8A,APP,EDN1,ACTN2,CAMK2D,GABBR1,USP53,INSYN2,AKAP6,NLGN1,WDR1,CACNA1C,KCNK10,FLNA,HCN2,KCNE4,SLC8A1,BNIP3,PLN	darkgreen	VSMC_M4
GO:0031667	0.03	0.98	35	362	response to nutrient levels	BP	0.66301	BCL2,MDM2,SOD2,LEP,CDKN2B,PDK4,SLC2A1,ABCA1,SESN1,TMEM135,INHBB,FOXO1,ADM,MAP1LC3A,PTH,ADA,LPL,SESN2,PRKD1,GABARAPL1,IGFBP2,ATG14,PCSK1N,PPARGC1A,BBS4,ULK2,PRKAA2,MAP1LC3B2,VCAM1,SLC8A1,BNIP3,CDKN1A,GABARAPL2,ICAM1,STC2	darkgreen	VSMC_M4
GO:0009306	0.03	0.98	27	266	protein secretion	BP	0.66301	GJA1,LEP,UNC13B,REST,ICA1,ABCA1,INHBB,ADAM9,PCLO,ANKRD1,PAM,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,ACHE,EXPH5,HIF1A,TGFB3,WLS,BMP6,MAFA	darkgreen	VSMC_M4
GO:0035592	0.03	0.98	27	266	establishment of protein localization to extracellular region	BP	0.66301	GJA1,LEP,UNC13B,REST,ICA1,ABCA1,INHBB,ADAM9,PCLO,ANKRD1,PAM,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,ACHE,EXPH5,HIF1A,TGFB3,WLS,BMP6,MAFA	darkgreen	VSMC_M4
GO:0042594	0.03	0.99	18	158	response to starvation	BP	0.66301	BCL2,PDK4,SLC2A1,SESN1,INHBB,FOXO1,ADM,MAP1LC3A,SESN2,PRKD1,GABARAPL1,ATG14,PPARGC1A,ULK2,PRKAA2,MAP1LC3B2,CDKN1A,GABARAPL2	darkgreen	VSMC_M4
GO:0042982	0.03	0.99	9	65	amyloid precursor protein metabolic process	BP	0.66301	IFNGR1,ITM2B,GGA3,CLU,BACE2,ABCG1,NCSTN,ACHE,ITM2C	darkgreen	VSMC_M4

GO:0000902	0.03	0.98	76	799	cell morphogenesis	BP	0.66301	BCL2,UST,GRIP1,DDR1,GRHL2,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,ANTXR1,KIDINS220,EPHB6,ITSN2,LIMS2,ITGA8,ACTN4,FMNL2,CDC42EP3,SEMA3C,WASF3,HPN,KIF13B,CLU,GPM6A,APP,SHROOM3,PTPN11,NGF,PDZD7,NFASC,SEMA5A,FEZ1,PREX1,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,LRP2,FGFR2,F11R,PLXNB1,ZRANB1,RAPH1,ZNF365,MAP3K13,CUX1,RDX,UNC5B,LMTK2,NLGN1,WDR1,MAEL,ACTN1,SIPA1L1,NUMB,SLIT3,NPTN,NRK,CDH2,ULK2,PAK3,CDH18,MYO10,DAPK3,PLXNB3,FLNA,NEXN,ICAM1,SDC2,YAP1,MYL12B	darkgreen	VSMC_M4
GO:0007157	0.03	0.99	6	29	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	BP	0.66301	TENM4,NLGN1,ADGRL1,CDH2,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:0043502	0.03	0.99	10	71	regulation of muscle adaptation	BP	0.66458	LMCD1,FOXO1,EDN1,RGS2,PRKCA,CAMK2D,TRIM63,AKAP6,PPARGC1A,SGCA	darkgreen	VSMC_M4
GO:0014743	0.03	0.99	8	52	regulation of muscle hypertrophy	BP	0.66516	LMCD1,FOXO1,EDN1,RGS2,PRKCA,CAMK2D,TRIM63,AKAP6	darkgreen	VSMC_M4
GO:0060428	0.03	0.99	5	26	lung epithelium development	BP	0.66516	GRHL2,THRB,FGFR2,ADAMTSL2,YAP1	darkgreen	VSMC_M4
GO:0071560	0.03	0.98	23	199	cellular response to transforming growth factor beta stimulus	BP	0.66781	CITED2,EP300,CDKN2B,RASL11B,TGFBR1,MAP3K7,HIPK2,ADAM9,COL4A2,LATS2,ANKRD1,FMOD,EDN1,NPNT,CFLAR,FGFR2,PPARGC1A,TGFB3,SMAD6,DAB2,GLG1,ADAMTSL2,LOX	darkgreen	VSMC_M4
GO:0061041	0.03	0.99	12	96	regulation of wound healing	BP	0.66952	FAM19A5,SMOC2,GJA1,KANK1,OCLN,ABCC8,PROS1,EDN1,MYLK,SERPINE1,F3,PRKG1	darkgreen	VSMC_M4
GO:0051924	0.03	0.98	19	172	regulation of calcium ion transport	BP	0.67138	BCL2,GJA1,TRDN,WFS1,KCNE3,FGF14,CHD7,JPH1,CAMK2D,MYLK,PRKD1,AKAP6,CACNA1C,PLCG2,SLC8A1,PLN,TMEM38A,SARAF,ICAM1	darkgreen	VSMC_M4
GO:0032007	0.03	0.99	6	33	negative regulation of TOR signaling	BP	0.67138	SESN1,SESN2,CASTOR1,HIF1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0060612	0.03	0.99	6	32	adipose tissue development	BP	0.67138	ZNF516,LEP,LRP5,ARID5B,PPARGC1A,CSF1	darkgreen	VSMC_M4
GO:0008284	0.03	0.98	60	681	positive regulation of cell population proliferation	BP	0.67138	BCL2,MDM2,GJA1,LEP,CD274,ZAP70,TGFBR1,EDN2,HIPK2,GATA2,SMARCD3,FOSL2,LBH,FLT3,HPN,NCK1,ADM,PTH,MEIS2,PDGFC,PTPN22,ADA,EDN1,CD47,SEMA5A,KDM5B,MARCKSL1,LRP5,HTR2B,MST1R,LGMN,PRKCA,LRP2,CFLAR,CTSZ,FGFR2,PRKD1,DDR2,IGFBP2,HIF1A,CCPG1,PPARGC1A,DISP3,TGFB3,LGALS9,SKP2,PLXNB3,FLNA,CSF1,CDH13,VCAM1,F3,CDC7,CYR61,DNAJA2,TBX20,CDKN1A,FGF9,YAP1,BMP6	darkgreen	VSMC_M4
GO:0042325	0.03	0.98	84	967	regulation of phosphorylation	BP	0.67138	GDF11,BCL2,SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,EP300,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,VLDLR,PPP1R9A,TGFBR1,MAP3K7,EPHB6,HIPK2,INHBB,ADAM9,RASSF2,ANKLE2,TF,FLT3,LATS2,HIPK3,NCK1,OCLN,CLU,APP,PDGFC,PTPN11,CCNT1,PTPN22,GDF6,AKTIP,RBL2,NGF,EDN1,RGS2,LRP5,PLCL1,HTR2B,MST1R,AFAP1L2,SESN2,INPP5F,FGFR2,PRKD1,ITGA6,DDR2,GPRC5A,MAP3K13,LRP6,FAM129A,HSPB1,ATG14,LMTK2,HIF1A,PPARGC1A,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,DAB2,PRKAA2,CSF1,PLCG2,TERF2IP,BCAR3,LMO4,CYR61,SLC8A1,LOX,CDKN1A,FGF9,PPM1E,CNTD2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0035272	0.03	0.99	6	34	exocrine system development	BP	0.67586	POLB,SEMA3C,FGFR2,TGFB3,WLS,EDA	darkgreen	VSMC_M4
GO:0097553	0.03	0.99	13	95	calcium ion transmembrane import into cytosol	BP	0.6767	TRDN,CHD7,JPH1,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0043271	0.03	0.99	12	93	negative regulation of ion transport	BP	0.68223	BCL2,TRDN,LEP,KCNE3,RGS2,ACTN2,CAMK2D,MAOB,SLC43A2,KCNE4,PLN,ICAM1	darkgreen	VSMC_M4
GO:0046887	0.03	0.99	11	86	positive regulation of hormone secretion	BP	0.68304	GJA1,LEP,INHBB,PTPN11,EDN1,ABCG1,TM7SF3,CYP19A1,HIF1A,VAMP7,BMP6	darkgreen	VSMC_M4
GO:0007520	0.03	0.99	5	25	myoblast fusion	BP	0.68304	ADGRB1,TANC1,RIPOR2,CFLAR,ADAMTS5	darkgreen	VSMC_M4
GO:0019220	0.03	0.98	92	1074	regulation of phosphate metabolic process	BP	0.68304	GDF11,BCL2,SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,EP300,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,VLDLR,PPP1R9A,PDK4,TGFBR1,MAP3K7,EPHB6,HIPK2,INHBB,HRH1,ADAM9,RASSF2,ANKLE2,TF,FLT3,LATS2,HIPK3,NCK1,OCLN,PTH,CLU,APP,PDGFC,PTPN11,CCNT1,PTPN22,GDF6,AKTIP,RCAN1,RBL2,NGF,EDN1,RGS2,LRP5,NPNT,PLCL1,HTR2B,MST1R,AFAP1L2,SESN2,INPP5F,FGFR2,PRKD1,SLC25A12,ITGA6,DDR2,GPRC5A,MAP3K13,LRP6,FAM129A,HSPB1,ATG14,LMTK2,HIF1A,PPP1R36,PPARGC1A,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,DAB2,PRKAA2,CSF1,PPP1R26,PLCG2,TERF2IP,BCAR3,LMO4,CYR61,SLC8A1,LOX,CDKN1A,FGF9,PPM1E,CNTD2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0051174	0.03	0.98	92	1074	regulation of phosphorus metabolic process	BP	0.68304	GDF11,BCL2,SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,EP300,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,VLDLR,PPP1R9A,PDK4,TGFBR1,MAP3K7,EPHB6,HIPK2,INHBB,HRH1,ADAM9,RASSF2,ANKLE2,TF,FLT3,LATS2,HIPK3,NCK1,OCLN,PTH,CLU,APP,PDGFC,PTPN11,CCNT1,PTPN22,GDF6,AKTIP,RCAN1,RBL2,NGF,EDN1,RGS2,LRP5,NPNT,PLCL1,HTR2B,MST1R,AFAP1L2,SESN2,INPP5F,FGFR2,PRKD1,SLC25A12,ITGA6,DDR2,GPRC5A,MAP3K13,LRP6,FAM129A,HSPB1,ATG14,LMTK2,HIF1A,PPP1R36,PPARGC1A,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,DAB2,PRKAA2,CSF1,PPP1R26,PLCG2,TERF2IP,BCAR3,LMO4,CYR61,SLC8A1,LOX,CDKN1A,FGF9,PPM1E,CNTD2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0071385	0.03	0.99	7	43	cellular response to glucocorticoid stimulus	BP	0.68304	REST,FOXO1,FLT3,EDN1,CFLAR,ICAM1,DDIT4	darkgreen	VSMC_M4
GO:0030073	0.03	0.98	17	149	insulin secretion	BP	0.68376	GJA1,LEP,REST,ICA1,INHBB,PCLO,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,HIF1A,MAFA	darkgreen	VSMC_M4
GO:0048260	0.03	0.99	7	41	positive regulation of receptor-mediated endocytosis	BP	0.687	ANGPT1,TF,CLU,HIP1,SERPINE1,DAB2,PLCG2	darkgreen	VSMC_M4
GO:0090278	0.03	0.99	6	34	negative regulation of peptide hormone secretion	BP	0.68979	LEP,REST,INHBB,ABCC8,PTPN11,PFKL	darkgreen	VSMC_M4
GO:0042476	0.03	0.99	12	95	odontogenesis	BP	0.69065	FOXO1,ADM,PAM,EDN1,FGFR2,ID3,SERPINE1,TGFB3,FST,CSF1,ADAMTS5,EDA	darkgreen	VSMC_M4
GO:0009101	0.03	0.98	25	245	glycoprotein biosynthetic process	BP	0.69065	DSEL,BCL2,UST,HS6ST1,ITM2B,STT3B,TUSC3,ST3GAL5,EXTL3,DPY19L4,BACE2,B3GNT7,GALNT3,B3GALNT2,MAN2A2,NDST3,NCSTN,CHST15,FUT11,MAGT1,GALNT10,TMEM59,EXTL2,ST6GALNAC3,ITM2C	darkgreen	VSMC_M4
GO:1903531	0.03	0.99	12	99	negative regulation of secretion by cell	BP	0.69333	GJA1,LEP,PPP1R9A,REST,INHBB,ABCC8,PTPN11,EDN1,PFKL,ATP9A,MAOB,LGALS9	darkgreen	VSMC_M4

GO:0003148	0.03	0.99	5	23	outflow tract septum morphogenesis	BP	0.69333	SEMA3C,LRP2,FGFR2,SMAD6,TBX20	darkgreen	VSMC_M4
GO:0060713	0.03	0.99	4	18	labyrinthine layer morphogenesis	BP	0.69333	GRHL2,ADM,FGFR2,CYR61	darkgreen	VSMC_M4
GO:0036037	0.03	0.99	4	17	CD8-positive, alpha-beta T cell activation	BP	0.69333	BCL2,CD274,SH3RF1,PTPN22	darkgreen	VSMC_M4
GO:0031346	0.03	0.98	32	302	positive regulation of cell projection organization	BP	0.69333	GRIP1,EP300,VLDLR,PPP1R9A,TGFBR1,KIDINS220,CDC42EP3,ANKRD1,NCK1,OCLN,GPM6A,SCARB2,NGF,SEMA5A,RIPOR2,RGS2,FEZ1,PLXNA2,SHTN1,CFLAR,PRKD1,PLXNB1,ITGA6,MAP3K13,CUX1,NLGN1,TGFB3,BBS4,NPTN,PAK3,PLXNB3,FLNA	darkgreen	VSMC_M4
GO:0060402	0.03	0.98	14	107	calcium ion transport into cytosol	BP	0.69513	BCL2,TRDN,CHD7,JPH1,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0120255	0.03	0.99	4	17	olefinic compound biosynthetic process	BP	0.69643	REST,ADM,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0071363	0.03	0.98	52	545	cellular response to growth factor stimulus	BP	0.69643	CITED2,MDM2,SMOC2,EP300,SH3GL2,CDKN2B,RASL11B,TGFBR1,MAP3K7,KIDINS220,HIPK2,ADAM9,CRIM1,COL4A2,FLT3,LATS2,ANKRD1,APP,PTPN11,GDF6,FMOD,NGF,EDN1,KDM5B,FEZ1,NPNT,LGMN,GALNT3,LRP2,CFLAR,FGFR2,PRKD1,HSPB1,RDX,HIF1A,PPARGC1A,FGFRL1,TGFB3,SMAD6,NPTN,FST,DAB2,SORT1,VCAM1,GLG1,CYR61,ADAMTSL2,LOX,TBX20,FGF9,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0048857	0.03	0.99	7	46	neural nucleus development	BP	0.69643	MBP,BCL2,NDRG2,GNB4,SEC24B,MAOB,FGF9	darkgreen	VSMC_M4
GO:0090559	0.03	0.99	8	59	regulation of membrane permeability	BP	0.69701	BCL2,LAPTM4B,SLC25A4,JAM3,EYA2,F11R,RHOT1,BNIP3	darkgreen	VSMC_M4
GO:0043116	0.03	0.99	4	16	negative regulation of vascular permeability	BP	0.69701	ANGPT1,SH3GL2,ADM,ABCC8	darkgreen	VSMC_M4
GO:0051048	0.03	0.98	13	110	negative regulation of secretion	BP	0.70225	GJA1,LEP,PPP1R9A,REST,INHBB,ABCC8,PTPN11,ADA,EDN1,PFKL,ATP9A,MAOB,LGALS9	darkgreen	VSMC_M4
GO:0001974	0.03	0.99	6	34	blood vessel remodeling	BP	0.70605	MDM2,SEMA3C,CHD7,BGN,FLNA,CST3	darkgreen	VSMC_M4
GO:2000404	0.03	0.99	5	28	regulation of T cell migration	BP	0.70787	DOCK8,LRCH1,APP,RIPOR2,CCR6	darkgreen	VSMC_M4
GO:1901699	0.03	0.98	48	508	cellular response to nitrogen compound	BP	0.70787	MDM2,GJA1,GNAQ,LEP,DDX58,KANK1,PDK4,SESN1,INHBB,HRH1,FOXO1,COL4A1,APLP1,FFAR3,CPEB3,NCK1,APP,PDGFC,PTPN11,ADCY6,PTPN22,IFIT1,EDN1,LPL,ADIPOR1,ACTN2,ZNF106,HTR2B,LGMN,SESN2,ADCY5,CFLAR,WDTC1,CASTOR1,NCSTN,AKAP6,ACHE,PPARGC1A,EPG5,FLNA,HCN2,AHCYL1,VCAM1,BCAR3,SLC8A1,TMEM38A,ICAM1,PIK3C2A	darkgreen	VSMC_M4
GO:0007156	0.03	0.98	13	88	homophilic cell adhesion via plasma membrane adhesion molecules	BP	0.71547	PCDH9,PCDHB4,ROBO3,NPTN,FAT2,CDH2,CDH18,PLXNB3,CDH13,NEXN,PCDHGA1,FAT3,PCDHB2	darkgreen	VSMC_M4
GO:0048699	0.03	0.97	105	1177	generation of neurons	BP	0.71586	BCL2,UST,GRIP1,MDM2,DDR1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,LEP,KANK1,VLDLR,PPP1R9A,REST,TGFBR1,PEX13,KIDINS220,FZD8,EPHB6,ITSN2,HIPK2,GATA2,HS6ST1,TENM4,SMARCD3,THRB,SEMA3C,PTPRG,DENND5A,CHD7,ANKRD1,CPEB3,NCK1,ADM,SH3RF1,ATOH8,KIF13B,GPM6A,APP,SCARB2,ABCC8,PTPN11,ADCY6,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,RAB29,RGS2,FEZ1,PREX1,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,NGRN,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,PLXNB1,RAPH1,ITGA6,ZNF365,MAP3K13,ID3,LRP6,CUX1,UNC5B,LMTK2,NLGN1,HIF1A,ZC4H2,DISP3,RORA,SIPA1L1,NUMB,SLIT3,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,SMARCA1,ATCAY,DAPK3,PLXNB3,FLNA,VCAM1,LMO4,NEXN,TBX20,ITM2C,SDC2,YAP1,PRKG1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0035295	0.03	0.97	76	849	tube development	BP	0.71586	BCL2,CITED2,SASH1,DDR1,GRHL2,ANGPT1,FAM19A5,SMOC2,GJA1,EP300,ADGRB1,LEP,RECK,TGFBR1,EDN2,CALD1,HIPK2,GATA2,THRB,COL4A1,COL4A2,CYP1B1,SEMA3C,AMOTL2,CHD7,ADM,ATOH8,PDGFC,SHROOM3,RXFP1,ABCC8,ANXA3,ADA,EDN1,JAM3,SEMA5A,KDM5B,LRP5,NPNT,PRKCA,SEC24B,MFGE8,PLXNA2,MYLK,LRP2,CTSZ,FGFR2,PRKD1,HSPB1,SERPINE1,ATP6AP2,UNC5B,DACT1,HIF1A,NPPB,RORA,TGFB3,SMAD6,BBS4,CDH2,ANGPTL4,FLNA,CSF1,CDH13,F3,LMO4,CYR61,ADAMTSL2,LOX,TBX20,CDKN1A,FGF9,EDA,HOPX,PIK3C2A,YAP1	darkgreen	VSMC_M4
GO:2001259	0.03	0.99	8	52	positive regulation of cation channel activity	BP	0.71586	TRDN,KCNE3,FGF14,ABCC8,ACTN2,CTSS,AKAP6,PLCG2	darkgreen	VSMC_M4
GO:0060306	0.03	0.99	5	23	regulation of membrane repolarization	BP	0.71586	KCNE3,AKAP6,WDR1,FLNA,KCNE4	darkgreen	VSMC_M4
GO:0048646	0.03	0.97	79	877	anatomical structure formation involved in morphogenesis	BP	0.71586	CITED2,SASH1,GRHL2,ANGPT1,FAM19A5,SMOC2,GJA1,EP300,ADGRB1,LEP,RECK,TGFBR1,TBX18,CALD1,HIPK2,GATA2,ITGA8,TENM4,SMARCD3,ADAM9,FOXO1,COL4A1,COL4A2,CYP1B1,SEMA3C,AMOTL2,ANKRD1,ADM,ATOH8,SHROOM3,ABCC8,ANXA3,PTPN11,TANC1,ADA,EDN1,JAM3,ETS2,SEMA5A,RIPOR2,EYA2,TNNT2,ACTN2,PRKCA,SEC24B,MFGE8,PLXNA2,LRP2,CFLAR,FGFR2,PTPN14,PRKD1,LRP6,HSPB1,SERPINE1,UNC5B,SYNPO2L,WDR1,HIF1A,ACTN1,NPPB,RORA,BBS4,ANGPTL4,FLNA,CDH13,F3,LMO4,CYR61,WLS,CCDC136,SPINK2,ADAMTS5,TBX20,CSRP1,EDA,HOPX,PIK3C2A,YAP1	darkgreen	VSMC_M4
GO:1901264	0.03	0.99	8	61	carbohydrate derivative transport	BP	0.71764	SLC35D3,GJA1,VLDLR,SLC25A4,LBP,CD47,ABCG1,LRRC8C	darkgreen	VSMC_M4
GO:0090276	0.03	0.98	16	140	regulation of peptide hormone secretion	BP	0.72175	GJA1,LEP,REST,ICA1,INHBB,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,HIF1A	darkgreen	VSMC_M4
GO:0002792	0.03	0.99	6	35	negative regulation of peptide secretion	BP	0.72175	LEP,REST,INHBB,ABCC8,PTPN11,PFKL	darkgreen	VSMC_M4
GO:1903532	0.03	0.98	21	196	positive regulation of secretion by cell	BP	0.72175	GJA1,LEP,UNC13B,GATA2,INHBB,RAB2B,ADAM9,ANKRD1,PTPN11,EDN1,ABCG1,TM7SF3,ACHE,EXPH5,CYP19A1,NLGN1,HIF1A,TGFB3,VAMP7,WLS,BMP6	darkgreen	VSMC_M4
GO:0070555	0.03	0.98	12	98	response to interleukin-1	BP	0.72175	IRAK3,MAP3K7,ANKRD1,APP,EDN1,CD47,PRKCA,TRIM63,HIF1A,RORA,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0042044	0.03	0.99	4	19	fluid transport	BP	0.72235	EDN1,SLC14A1,AHCYL1,ITPR1	darkgreen	VSMC_M4
GO:0002274	0.03	0.98	17	156	myeloid leukocyte activation	BP	0.72256	IFNGR1,EDN2,GATA2,CD93,ADAM9,CLU,APP,ANXA3,LBP,PREX1,ADGRE2,RORA,LGALS9,VAMP7,CSF1,PLCG2,TLR1	darkgreen	VSMC_M4
GO:1903202	0.03	0.99	6	38	negative regulation of oxidative stress-induced cell death	BP	0.72256	SOD2,OXR1,REST,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:2001236	0.03	0.98	14	121	regulation of extrinsic apoptotic signaling pathway	BP	0.72421	BCL2,TGFBR1,SH3RF1,RNF34,EYA2,CFLAR,ITGA6,SERPINE1,UNC5B,TNFSF10,DAPK3,ITM2C,ICAM1,YAP1	darkgreen	VSMC_M4

GO:0007596	0.04	0.98	18	164	blood coagulation	BP	0.72596	SCUBE1,GNAQ,ENTPD1,MYL9,PROS1,HNF4A,EDN1,PRKCA,F11R,LNPK,HSPB1,SERPINE1,FLNA,PLCG2,F3,CD59,CSRP1,PRKG1	darkgreen	VSMC_M4
GO:0001775	0.04	0.97	60	692	cell activation	BP	0.72596	BCL2,IFNGR1,EP300,LEP,DOCK8,CD274,IL18R1,ZAP70,TGFBR1,EDN2,MAP3K8,GATA2,APBB1IP,CD93,ADAM9,FLT3,CHD7,NCK1,CD180,SH3RF1,KIF13B,CLU,BLNK,MYL9,APP,ANXA3,PTPN11,LBP,PTPN22,ADA,EDN1,CD47,BACE2,RAB29,RIPOR2,PREX1,PRKCA,TP53BP1,NCSTN,F11R,HSPB1,IGFBP2,ADGRE2,RORA,LGALS9,FLNA,VAMP7,CSF1,PLCG2,VCAM1,LMO4,VNN1,CD151,TLR1,CD83,CSRP1,CDKN1A,CCR6,ICAM1,PRKG1	darkgreen	VSMC_M4
GO:1904752	0.04	0.99	5	26	regulation of vascular associated smooth muscle cell migration	BP	0.72663	MDM2,FAM19A5,DOCK4,FGF9,PRKG1	darkgreen	VSMC_M4
GO:0007160	0.04	0.98	22	192	cell-matrix adhesion	BP	0.72663	BCL2,DDR1,LIMCH1,TMEM8B,ECM2,TESK2,ITGA8,ADAM9,PTPN11,JAM3,ACTN2,NPNT,NID1,SNED1,SERPINE1,ACTN1,DAPK3,CSF1,CDH13,VCAM1,EDA,PLEKHA2	darkgreen	VSMC_M4
GO:0055093	0.04	0.99	4	19	response to hyperoxia	BP	0.72663	POLB,FOXO1,BNIP3,CDKN1A	darkgreen	VSMC_M4
GO:0051092	0.04	0.98	14	119	positive regulation of NF-kappaB transcription factor activity	BP	0.72978	IRAK3,EP300,IL18R1,MAP3K7,CLU,APP,CFLAR,PRKD1,MAP3K13,LGALS9,PLCG2,TERF2IP,EDA,ICAM1	darkgreen	VSMC_M4
GO:0006862	0.04	0.99	5	28	nucleotide transport	BP	0.73258	GJA1,SLC25A4,CD47,EPG5,LRRC8C	darkgreen	VSMC_M4
GO:0048644	0.04	0.99	9	61	muscle organ morphogenesis	BP	0.73258	TGFBR1,CHD7,ANKRD1,TNNT2,MYLK,LRP2,FGFR2,ARID5B,TBX20	darkgreen	VSMC_M4
GO:0060048	0.04	0.98	13	103	cardiac muscle contraction	BP	0.73258	GJA1,PPP1R13L,KCNE3,RGS2,TNNT2,CAMK2D,CACNA1C,ADRA1B,FLNA,KCNE4,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0031669	0.04	0.98	20	182	cellular response to nutrient levels	BP	0.73258	BCL2,MDM2,LEP,CDKN2B,PDK4,SLC2A1,SESN1,INHBB,FOXO1,MAP1LC3A,LPL,SESN2,PRKD1,GABARAPL1,ATG14,PRKAA2,MAP1LC3B2,CDKN1A,GABARAPL2,ICAM1	darkgreen	VSMC_M4
GO:0006935	0.04	0.98	41	426	chemotaxis	BP	0.73258	ANGPT1,SMOC2,LAMA2,CREB3,EDN2,DOCK4,EPHB6,HRH1,SEMA3C,APP,LBP,EDN1,JAM3,NFASC,SEMA5A,RIPOR2,FEZ1,PREX1,LGMN,ROBO3,PLXNA2,PRKD1,PLXNB1,HSPB1,SERPINE1,UNC5B,ADGRE2,SLIT3,NPTN,MMP28,LGALS9,PLXNB3,PLEKHG5,CSF1,CDH13,VCAM1,F3,CYR61,NEXN,LOX,CCR6	darkgreen	VSMC_M4
GO:0051592	0.04	0.98	14	114	response to calcium ion	BP	0.73258	SYT5,ADAM9,CPNE4,EDN1,TNNT2,LGMN,TXNIP,CAMK2D,NCSTN,SLC25A12,NLGN1,PRKAA2,AHCYL1,PLCG2	darkgreen	VSMC_M4
GO:0061448	0.04	0.98	22	203	connective tissue development	BP	0.73258	ZNF516,TRPS1,LEP,TGFBR1,PTH,RXFP1,PTPN11,GDF6,EDN1,LRP5,CFLAR,ARID5B,LNPK,HIF1A,PPARGC1A,BGN,CSF1,GLG1,CYR61,FRZB,LOX,BMP6	darkgreen	VSMC_M4
GO:0007417	0.04	0.97	72	795	central nervous system development	BP	0.73258	MBP,BCL2,IFNGR1,CITED2,GRHL2,SH3GL2,LEP,VLDLR,C2orf40,RECK,SLC2A1,PEX13,EPHB6,JRKL,GATA2,ITGA8,TENM4,PCDH9,PFKFB3,NDRG2,TACC1,TRPC4,COL4A1,ANKLE2,APLP1,WASF3,PTPRG,CHD7,PAM,CLU,MEIS2,APP,PDGFC,ANXA3,PTPN11,SEMA5A,BACE2,MARCKSL1,RGS2,FEZ1,SUN1,GNB4,SEC24B,PLXNA2,LRP2,FGFR2,NCSTN,ZNF365,ID3,LRP6,ATP6AP2,MAOB,EZH1,WDR1,HIF1A,PPARGC1A,ZC4H2,RORA,NUMB,BBS4,CDH2,SMARCA1,FLNA,LMO4,WLS,SLC8A1,BNIP3,TBX20,FGF9,PRKG1,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:0031668	0.04	0.98	22	205	cellular response to extracellular stimulus	BP	0.73258	BCL2,MDM2,LEP,CDKN2B,PDK4,SLC2A1,SESN1,INHBB,FOXO1,MAP1LC3A,LPL,SESN2,PRKD1,GABARAPL1,ATG14,SKP2,PRKAA2,MAP1LC3B2,VCAM1,CDKN1A,GABARAPL2,ICAM1	darkgreen	VSMC_M4
GO:0007435	0.04	0.99	5	26	salivary gland morphogenesis	BP	0.73258	POLB,SEMA3C,FGFR2,TGFB3,EDA	darkgreen	VSMC_M4
GO:0048585	0.04	0.97	102	1229	negative regulation of response to stimulus	BP	0.73258	BCL2,IRAK3,MDM2,RGS22,SOD2,OXR1,FAM19A5,GJA1,TLE4,MLLT3,LEP,WFS1,KANK1,RASL11B,RNF149,CREB3,SNX13,TGFBR1,PTPN3,TBX18,SESN1,JADE1,HIPK2,GATA2,TPT1,LBH,NDRG2,CRIM1,FOXO1,RASSF2,SEMA3C,APLP1,NCOR2,LATS2,HIPK3,NCK1,ADM,SH3RF1,WWC2,MCTP1,RNF34,CLU,ABCC8,HERPUD1,PROS1,TMEM64,PTPN22,CHAC1,ADA,RCAN1,EDN1,CD47,SEMA5A,LPL,ADIPOR1,RIPOR2,RGS2,EYA2,KCTD10,HTR2B,LGMN,SESN2,LRP2,CFLAR,INPP5F,CASTOR1,TP53BP1,STRN3,ITGA6,GPRC5A,HSPB1,SERPINE1,UNC5B,IGFBP2,DACT1,HIF1A,RORA,SLIT3,TGFB3,SMAD6,BBS4,CDH2,NOMO1,MMP28,FST,DAB2,LGALS9,PRKAA2,TLE2,GLG1,MIR99A,ITPR1,VNN1,ADAMTSL2,FRZB,CD59,TBX20,TMEM170B,ICAM1,YAP1,PRKG1,DDIT4	darkgreen	VSMC_M4
GO:0035966	0.04	0.98	15	143	response to topologically incorrect protein	BP	0.73258	EP300,WFS1,CREB3,STT3B,NCK1,CLU,HERPUD1,CHAC1,TM7SF3,ATF6,HSPB1,JKAMP,FAF2,HSPB3,MBTPS1	darkgreen	VSMC_M4
GO:0097530	0.04	0.98	11	91	granulocyte migration	BP	0.73258	EDN2,HRH1,LBP,EDN1,JAM3,RIPOR2,PREX1,WDR1,ADGRE2,GP2,CSF1	darkgreen	VSMC_M4
GO:0071456	0.04	0.98	14	119	cellular response to hypoxia	BP	0.73258	BCL2,CITED2,MDM2,HIPK2,ANKRD1,EDN1,CFLAR,HIF1A,PPARGC1A,RORA,SLC8A1,BNIP3,ICAM1,STC2	darkgreen	VSMC_M4
GO:0071692	0.04	0.98	27	271	protein localization to extracellular region	BP	0.73258	GJA1,LEP,UNC13B,REST,ICA1,ABCA1,INHBB,ADAM9,PCLO,ANKRD1,PAM,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,RAPGEF4,ACHE,EXPH5,HIF1A,TGFB3,WLS,BMP6,MAFA	darkgreen	VSMC_M4
GO:0046031	0.04	0.99	9	66	ADP metabolic process	BP	0.73258	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0002791	0.04	0.98	16	142	regulation of peptide secretion	BP	0.73258	GJA1,LEP,REST,ICA1,INHBB,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,HIF1A	darkgreen	VSMC_M4
GO:0030278	0.04	0.98	12	91	regulation of ossification	BP	0.73258	BCL2,PTH,PTPN11,DDR2,NBR1,HIF1A,TGFB3,SMAD6,CSF1,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:1901654	0.04	0.98	17	151	response to ketone	BP	0.73258	IGFBP7,FOXO1,ADCY6,EDN1,TXNIP,ADCY5,CFLAR,MAOB,GNAI1,SLIT3,TGFB3,PRKAA2,PLN,CDKN1A,ICAM1,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0009410	0.04	0.98	30	314	response to xenobiotic stimulus	BP	0.73258	BCL2,MDM2,SOD2,RNF149,REST,ABCA1,CYP1B1,SEMA3C,ANKRD1,PAM,PTH,ABCC8,HNF4A,ADA,EDN1,LPL,HTR2B,TXNIP,MAOB,IGFBP2,FMO4,PPARGC1A,RORA,PRKAA2,BCAR3,SLC8A1,LOX,CDKN1A,PPM1E,ICAM1	darkgreen	VSMC_M4
GO:2000177	0.04	0.99	9	62	regulation of neural precursor cell proliferation	BP	0.73272	GATA2,LIMS2,SMARCD3,LRP2,CTSZ,HIF1A,DISP3,CDH2,FLNA	darkgreen	VSMC_M4

GO:0070228	0.04	0.99	6	38	regulation of lymphocyte apoptotic process	BP	0.73298	DOCK8,CD274,ADA,HIF1A,LGALS9,ORMDL3	darkgreen	VSMC_M4
GO:0000768	0.04	0.99	6	34	syncytium formation by plasma membrane fusion	BP	0.73783	ADGRB1,ADAM9,TANC1,RIPOR2,CFLAR,ADAMTS5	darkgreen	VSMC_M4
GO:0140253	0.04	0.99	6	34	cell-cell fusion	BP	0.73783	ADGRB1,ADAM9,TANC1,RIPOR2,CFLAR,ADAMTS5	darkgreen	VSMC_M4
GO:0060341	0.04	0.97	60	675	regulation of cellular localization	BP	0.74411	BCL2,SLC35D3,MDM2,ANGPT1,TRDN,LEP,MDFIC,TCAF1,GATA2,ATP2C1,ZDHHC2,RIC3,CHD7,LATS2,JPH1,PTPN11,ATG13,RAB29,ABCG1,RIPOR2,TNNT2,ACTN2,LRP5,FEZ1,SEC24B,PARD6B,ATP9A,SESN2,ARV1,CAMK2D,ADCY5,INPP5F,PTPN14,PRKD1,AKAP6,CRYAB,RDX,NLGN1,HIF1A,CACNA1C,ADGRE2,GNAI1,NUMB,NPTN,CDH2,ABLIM3,SH3TC2,RHOT1,DAB2,LGALS9,PRKAA2,TMEM59,FLNA,VAMP7,SLC8A1,PLN,TMEM38A,ORMDL3,YAP1,SCP2	darkgreen	VSMC_M4
GO:0010035	0.04	0.97	40	435	response to inorganic substance	BP	0.74411	BCL2,MDM2,SOD2,SYT5,ADAM9,FOXO1,CYP1B1,CPNE4,TF,MAP1LC3A,PAM,PTH,APP,ABCC8,PTPN11,ADA,EDN1,TNNT2,LGMN,TXNIP,CAMK2D,CFLAR,NCSTN,CYBRD1,SLC25A12,CRYAB,MAOB,IGFBP2,NLGN1,HIF1A,PPARGC1A,PRKAA2,AHCYL1,PLCG2,VCAM1,SLC8A1,BNIP3,PLN,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0051047	0.04	0.98	22	211	positive regulation of secretion	BP	0.74411	GJA1,LEP,UNC13B,GATA2,INHBB,RAB2B,ADAM9,ANKRD1,PTPN11,EDN1,ABCG1,TM7SF3,ACHE,EXPH5,CYP19A1,NLGN1,HIF1A,NPPB,TGFB3,VAMP7,WLS,BMP6	darkgreen	VSMC_M4
GO:0051248	0.04	0.97	69	813	negative regulation of protein metabolic process	BP	0.74593	IRAK3,MDM2,LAPTM4B,OXR1,ANGPT1,C4A,ADGRB1,DAPK1,SH3GL2,GNAQ,CDKN2B,RIC1,RECK,PTPN3,HIPK2,ITM2B,GGA3,INHBB,ITIH5,CRIM1,RASSF2,FXYD1,LATS2,HIPK3,CPEB3,NCK1,SH3RF1,OCLN,RNF34,CLU,APP,PTX3,HERPUD1,PROS1,PTPN22,CHAC1,NGF,EDN1,N4BP1,BACE2,RGS2,LRP5,SESN2,CTSZ,INPP5F,GPRC5A,LRP6,FAM129A,HSPB1,SERPINE1,CRYAB,ATG14,PCSK1N,PPARGC1A,SMAD6,PRKAA2,TMEM59,DAPK3,FLNA,TERF2IP,GLG1,SLC8A1,SPINK2,ITM2C,CST3,CDKN1A,PPM1E,GABARAPL2,DDIT4	darkgreen	VSMC_M4
GO:0006955	0.04	0.97	83	1012	immune response	BP	0.74836	MBP,BCL2,IFNGR1,IRAK3,ANGPT1,C4A,RNASET2,EP300,ADGRB1,DAPK1,LEP,DDX58,CD274,IL18R1,ZAP70,MAP3K7,NT5C3A,GATA2,APBB1IP,MRC1,SEMA3C,TF,MAP3K1,FFAR3,TRIM23,CD180,G3BP2,CLU,BLNK,APP,ANXA3,PTPN11,PTX3,LBP,PTPN22,SERINC3,ADA,IFIT1,EDN1,JAM3,CD47,N4BP1,MX1,RAB29,MST1R,CFI,ABCC9,CTSS,TP53BP1,PRKD1,RAPGEF4,SERPINE1,C1RL,TNFSF10,ADGRE2,RORA,CALCOCO2,TGFB3,SMAD6,EPG5,GP2,PAK3,LGALS9,SKP2,DAPK3,VAMP7,CSF1,PLCG2,LRSAM1,IFI44,VNN1,TLR1,BNIP3,ADAMTS5,CD83,CD59,ZNF175,EDA,MFAP4,CCR6,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0061337	0.04	0.98	11	76	cardiac conduction	BP	0.74836	GJA1,TRDN,TBX18,KCNE3,CAMK2D,ABCC9,CACNA1C,FLNA,KCNE4,SLC8A1,PLN	darkgreen	VSMC_M4
GO:0000302	0.04	0.98	18	177	response to reactive oxygen species	BP	0.74836	BCL2,MDM2,SOD2,SESN1,ADAM9,FOXO1,CYP1B1,MAP1LC3A,PTPN11,ADA,EDN1,TXNIP,SESN2,CRYAB,HIF1A,PPARGC1A,SLC8A1,BNIP3	darkgreen	VSMC_M4
GO:0008631	0.04	0.99	6	39	intrinsic apoptotic signaling pathway in response to oxidative stress	BP	0.74836	BCL2,SOD2,CYP1B1,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0050817	0.04	0.98	18	166	coagulation	BP	0.74836	SCUBE1,GNAQ,ENTPD1,MYL9,PROS1,HNF4A,EDN1,PRKCA,F11R,LNPK,HSPB1,SERPINE1,FLNA,PLCG2,F3,CD59,CSRP1,PRKG1	darkgreen	VSMC_M4
GO:0034390	0.04	0.99	4	20	smooth muscle cell apoptotic process	BP	0.74836	SOD2,EDN1,LRP6,PDE1A	darkgreen	VSMC_M4
GO:0034391	0.04	0.99	4	20	regulation of smooth muscle cell apoptotic process	BP	0.74836	SOD2,EDN1,LRP6,PDE1A	darkgreen	VSMC_M4
GO:0007599	0.04	0.98	18	166	hemostasis	BP	0.74968	SCUBE1,GNAQ,ENTPD1,MYL9,PROS1,HNF4A,EDN1,PRKCA,F11R,LNPK,HSPB1,SERPINE1,FLNA,PLCG2,F3,CD59,CSRP1,PRKG1	darkgreen	VSMC_M4
GO:0030111	0.04	0.98	28	277	regulation of Wnt signaling pathway	BP	0.74968	TLE4,GNAQ,MLLT3,KANK1,RECK,TBX18,MDFIC,JADE1,LATS2,TCF7L1,APP,TMEM64,SEMA5A,FGFR2,ZRANB1,ATP6AP2,IGFBP2,DACT1,CDH2,DAB2,DAPK3,TLE2,WLS,FRZB,LYPD6,TMEM170B,EDA,YAP1	darkgreen	VSMC_M4
GO:0032970	0.04	0.97	34	337	regulation of actin filament-based process	BP	0.75273	LIMCH1,KANK1,PPP1R9A,TGFBR1,CDC42EP3,WASF3,NCK1,PAM,JMY,EDN1,JAM3,CD47,SEMA5A,TNNT2,ACTN2,PREX1,CAMK2D,SYNPO2,F11R,RDX,SYNPO2L,WDR1,CACNA1C,TGFB3,SYNPO,PAK3,ARHGAP28,DAPK3,FLNA,SPTAN1,PLN,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0007548	0.04	0.98	22	206	sex differentiation	BP	0.75288	BCL2,CITED2,LEP,TGFBR1,INHBB,CHD7,CDKL2,PTPN11,PTX3,HNF4A,LRP2,ARID5B,PRDX4,CYP19A1,TNFSF10,TEX11,SLIT3,FST,FLNA,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0048638	0.04	0.98	27	257	regulation of developmental growth	BP	0.75408	BCL2,CITED2,GJA1,LEP,TGFBR1,ITSN2,SEMA3C,CHD7,LATS2,WWC2,APP,NGF,EDN1,SEMA5A,RGS2,LGMN,SHTN1,FGFR2,AKAP6,MAP3K13,MAEL,ULK2,CSF1,TBX20,CDKN1A,HOPX,YAP1	darkgreen	VSMC_M4
GO:1902903	0.04	0.97	33	327	regulation of supramolecular fiber organization	BP	0.7558	LIMCH1,KANK1,PPP1R9A,TGFBR1,CDC42EP3,WASF3,NCK1,OCLN,CLU,APP,JMY,EDN1,CD47,SEMA5A,ACTN2,PREX1,MID1,SYNPO2,F11R,CRYAB,RDX,SYNPO2L,WDR1,TGFB3,SYNPO,PAK3,ARHGAP28,DAPK3,FLNA,SPTAN1,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0022617	0.04	0.99	7	47	extracellular matrix disassembly	BP	0.75838	DDR1,HPN,CTSS,DDR2,MMP1,ADAMTS5,CST3	darkgreen	VSMC_M4
GO:0071674	0.04	0.98	14	126	mononuclear cell migration	BP	0.75909	DOCK8,CREB3,ZAP70,LRCH1,APP,CD47,RIPOR2,LGMN,F11R,SERPINE1,LGALS9,CSF1,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0009991	0.04	0.97	36	385	response to extracellular stimulus	BP	0.75909	BCL2,MDM2,SOD2,LEP,CDKN2B,PDK4,SLC2A1,ABCA1,SESN1,TMEM135,INHBB,FOXO1,ADM,MAP1LC3A,PTH,ADA,LPL,SESN2,PRKD1,GABARAPL1,IGFBP2,ATG14,PCSK1N,PPARGC1A,BBS4,ULK2,SKP2,PRKAA2,MAP1LC3B2,VCAM1,SLC8A1,BNIP3,CDKN1A,GABARAPL2,ICAM1,STC2	darkgreen	VSMC_M4
GO:2000134	0.04	0.98	8	56	negative regulation of G1/S transition of mitotic cell cycle	BP	0.76103	BCL2,MDM2,CDKN2B,JADE1,RBL2,DACT1,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0060391	0.04	0.99	4	17	positive regulation of SMAD protein signal transduction	BP	0.76103	TGFBR1,TGFB3,DAB2,BMP6	darkgreen	VSMC_M4
GO:0071384	0.04	0.99	7	46	cellular response to corticosteroid stimulus	BP	0.76103	REST,FOXO1,FLT3,EDN1,CFLAR,ICAM1,DDIT4	darkgreen	VSMC_M4
GO:2001135	0.04	0.99	4	18	regulation of endocytic recycling	BP	0.76103	ZDHHC2,ACTN2,ATP9A,INPP5F	darkgreen	VSMC_M4

GO:0090087	0.04	0.98	16	144	regulation of peptide transport	BP	0.76103	GJA1,LEP,REST,ICA1,INHBB,FFAR3,CHD7,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,HIF1A	darkgreen	VSMC_M4
GO:0002066	0.04	0.99	6	35	columnar/cuboidal epithelial cell development	BP	0.76103	HNF4A,HIF1A,CDH2,CDKN1A,YAP1,BMP6	darkgreen	VSMC_M4
GO:0070613	0.04	0.99	7	52	regulation of protein processing	BP	0.76322	MDM2,HPN,CHAC1,CTSZ,SERPINE1,TMEM59,GLG1	darkgreen	VSMC_M4
GO:1900542	0.04	0.98	8	56	regulation of purine nucleotide metabolic process	BP	0.76422	EP300,PDK4,APP,SLC25A12,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0006949	0.04	0.99	6	35	syncytium formation	BP	0.76422	ADGRB1,ADAM9,TANC1,RIPOR2,CFLAR,ADAMTS5	darkgreen	VSMC_M4
GO:1903034	0.04	0.98	14	123	regulation of response to wounding	BP	0.76422	FAM19A5,SMOC2,GJA1,KANK1,OCLN,ABCC8,PROS1,EDN1,MYLK,INPP5F,SERPINE1,FLNA,F3,PRKG1	darkgreen	VSMC_M4
GO:0008209	0.04	0.99	4	22	androgen metabolic process	BP	0.76468	HSD17B6,ADM,CYP19A1,PPARGC1A	darkgreen	VSMC_M4
GO:0010324	0.04	0.98	8	54	membrane invagination	BP	0.76659	ADGRB1,ABCA1,GATA2,CLCN3,MFGE8,GULP1,VAMP7,PLCG2	darkgreen	VSMC_M4
GO:0019934	0.04	0.99	4	19	cGMP-mediated signaling	BP	0.76659	MRVI1,HTR2B,NPPB,PRKG1	darkgreen	VSMC_M4
GO:0030100	0.04	0.98	19	174	regulation of endocytosis	BP	0.76659	ANGPT1,SH3GL2,SNAP91,GATA2,TF,MCTP1,CLU,ATXN2,PRKD1,HIP1,SERPINE1,NLGN1,NUMB,DNAJC6,DAB2,CDH13,PLCG2,LRSAM1,CD151	darkgreen	VSMC_M4
GO:0086001	0.04	0.98	9	58	cardiac muscle cell action potential	BP	0.76659	GJA1,TBX18,KCNE3,CAMK2D,CACNA1C,FLNA,HCN2,KCNE4,SLC8A1	darkgreen	VSMC_M4
GO:0006110	0.04	0.99	6	34	regulation of glycolytic process	BP	0.76659	EP300,APP,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0048666	0.04	0.97	80	877	neuron development	BP	0.76659	BCL2,UST,GRIP1,MDM2,DDR1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,LEP,KANK1,VLDLR,PPP1R9A,KIDINS220,EPHB6,ITSN2,TENM4,THRB,SEMA3C,PTPRG,DENND5A,ANKRD1,CPEB3,NCK1,ADM,KIF13B,GPM6A,APP,SCARB2,PTPN11,ADCY6,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,RAB29,RGS2,FEZ1,PREX1,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,PLXNB1,RAPH1,ITGA6,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,ATCAY,PLXNB3,FLNA,NEXN,ITM2C,SDC2,PRKG1	darkgreen	VSMC_M4
GO:0032989	0.04	0.97	59	609	cellular component morphogenesis	BP	0.76854	BCL2,UST,GRIP1,DDR1,GJA1,LAMA2,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,KIDINS220,EPHB6,ITSN2,TENM4,SEMA3C,ANKRD1,KIF13B,GPM6A,APP,PTPN11,NGF,EDN1,NFASC,SEMA5A,TNNT2,ACTN2,FEZ1,ROBO3,PARD6B,PLXNA2,SHTN1,LRP2,CFLAR,FGFR2,PLXNB1,RAPH1,ZNF365,MAP3K13,CUX1,UNC5B,SYNPO2L,LMTK2,NLGN1,WDR1,SIPA1L1,NUMB,SLIT3,NPTN,NRK,CDH2,ULK2,PAK3,PLXNB3,NEXN,CCDC136,SPINK2,CSRP1,SDC2	darkgreen	VSMC_M4
GO:0099623	0.04	0.99	4	17	regulation of cardiac muscle cell membrane repolarization	BP	0.76891	KCNE3,WDR1,FLNA,KCNE4	darkgreen	VSMC_M4
GO:0030239	0.04	0.98	8	51	myofibril assembly	BP	0.76891	ANKRD1,EDN1,TNNT2,ACTN2,CFLAR,SYNPO2L,WDR1,CSRP1	darkgreen	VSMC_M4
GO:0061037	0.04	0.99	5	29	negative regulation of cartilage development	BP	0.76891	LEP,TGFBR1,PTH,PTPN11,FRZB	darkgreen	VSMC_M4
GO:0042542	0.04	0.98	13	118	response to hydrogen peroxide	BP	0.76929	BCL2,MDM2,SOD2,ADAM9,FOXO1,CYP1B1,MAP1LC3A,PTPN11,ADA,TXNIP,CRYAB,SLC8A1,BNIP3	darkgreen	VSMC_M4
GO:2000310	0.04	0.99	4	18	regulation of NMDA receptor activity	BP	0.76978	DAPK1,APP,NLGN1,PPARGC1A	darkgreen	VSMC_M4
GO:0007431	0.04	0.99	5	27	salivary gland development	BP	0.76978	POLB,SEMA3C,FGFR2,TGFB3,EDA	darkgreen	VSMC_M4
GO:0071559	0.04	0.98	23	205	response to transforming growth factor beta	BP	0.76978	CITED2,EP300,CDKN2B,RASL11B,TGFBR1,MAP3K7,HIPK2,ADAM9,COL4A2,LATS2,ANKRD1,FMOD,EDN1,NPNT,CFLAR,FGFR2,PPARGC1A,TGFB3,SMAD6,DAB2,GLG1,ADAMTSL2,LOX	darkgreen	VSMC_M4
GO:1904738	0.04	0.99	5	27	vascular associated smooth muscle cell migration	BP	0.76978	MDM2,FAM19A5,DOCK4,FGF9,PRKG1	darkgreen	VSMC_M4
GO:1903169	0.04	0.98	13	110	regulation of calcium ion transmembrane transport	BP	0.77039	TRDN,KCNE3,FGF14,CHD7,JPH1,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0045987	0.04	0.99	4	20	positive regulation of smooth muscle contraction	BP	0.77039	EDN2,ADA,EDN1,NPNT	darkgreen	VSMC_M4
GO:0009267	0.04	0.98	15	130	cellular response to starvation	BP	0.77522	BCL2,PDK4,SLC2A1,SESN1,INHBB,FOXO1,MAP1LC3A,SESN2,PRKD1,GABARAPL1,ATG14,PRKAA2,MAP1LC3B2,CDKN1A,GABARAPL2	darkgreen	VSMC_M4
GO:0014031	0.04	0.98	10	73	mesenchymal cell development	BP	0.77924	BCL2,CITED2,SEMA3C,FAM172A,EDN1,SEMA5A,HTR2B,HIF1A,CDH2,TBX20	darkgreen	VSMC_M4
GO:0001819	0.04	0.97	29	304	positive regulation of cytokine production	BP	0.7808	MBP,IFNGR1,IRAK3,LEP,DDX58,CD274,IL18R1,MAP3K7,CYP1B1,FFAR3,CLU,APP,ABCC8,PTPN11,LBP,PTPN22,LPL,HTR2B,AFAP1L2,HSPB1,SERPINE1,ATP6AP2,HIF1A,RORA,LGALS9,PLCG2,F3,TLR1,CD83	darkgreen	VSMC_M4
GO:1902930	0.04	0.99	6	37	regulation of alcohol biosynthetic process	BP	0.78467	REST,HRH1,PTH,ABCG1,MBTPS1,BMP6	darkgreen	VSMC_M4
GO:0032722	0.04	0.98	7	48	positive regulation of chemokine production	BP	0.78583	MBP,FFAR3,APP,LBP,LPL,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0006140	0.04	0.98	8	57	regulation of nucleotide metabolic process	BP	0.78583	EP300,PDK4,APP,SLC25A12,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0051489	0.04	0.98	7	44	regulation of filopodium assembly	BP	0.78646	PPP1R9A,TGFBR1,GPM6A,RIPOR2,NLGN1,TGFB3,MYO10	darkgreen	VSMC_M4
GO:0009190	0.04	0.99	4	17	cyclic nucleotide biosynthetic process	BP	0.78646	ADCY6,ADCY5,NPPB,ADCY9	darkgreen	VSMC_M4
GO:0052652	0.04	0.99	4	17	cyclic purine nucleotide metabolic process	BP	0.78646	ADCY6,ADCY5,NPPB,ADCY9	darkgreen	VSMC_M4
GO:1904019	0.04	0.98	11	86	epithelial cell apoptotic process	BP	0.78646	ANGPT1,WFS1,GATA2,SEMA5A,CFLAR,SERPINE1,PPARGC1A,ANGPTL4,SORT1,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0071466	0.04	0.98	11	92	cellular response to xenobiotic stimulus	BP	0.78646	RNF149,REST,ABCA1,CYP1B1,ANKRD1,HNF4A,EDN1,FMO4,RORA,PRKAA2,PPM1E	darkgreen	VSMC_M4
GO:0016125	0.04	0.98	13	114	sterol metabolic process	BP	0.78646	LEP,VLDLR,ABCA1,CYP1B1,APP,ABCG1,LRP5,ARV1,CYP19A1,DISP3,FAXDC2,PRKAA2,MBTPS1	darkgreen	VSMC_M4
GO:0007266	0.04	0.98	14	116	Rho protein signal transduction	BP	0.78648	ABRA,KANK1,ABCA1,CDC42EP3,ARHGEF3,PTH,RIPOR2,KCTD10,SHTN1,F11R,SYNPO2L,PLEKHG5,CDH13,ARHGAP29	darkgreen	VSMC_M4
GO:0070542	0.04	0.98	7	49	response to fatty acid	BP	0.78648	PDK4,FOXO1,FFAR3,EDN1,LPL,ID3,PPARGC1A	darkgreen	VSMC_M4
GO:0060986	0.04	0.99	5	27	endocrine hormone secretion	BP	0.78648	GJA1,LEP,INHBB,PTPN11,BMP6	darkgreen	VSMC_M4
GO:0055002	0.04	0.98	8	52	striated muscle cell development	BP	0.78692	ANKRD1,EDN1,TNNT2,ACTN2,CFLAR,SYNPO2L,WDR1,CSRP1	darkgreen	VSMC_M4
GO:0017015	0.05	0.98	13	102	regulation of transforming growth factor beta receptor signaling pathway	BP	0.79107	CITED2,EP300,CDKN2B,RASL11B,HIPK2,LATS2,NPNT,TGFB3,SMAD6,DAB2,GLG1,ADAMTSL2,LOX	darkgreen	VSMC_M4
GO:0016049	0.05	0.97	38	399	cell growth	BP	0.79107	BCL2,DDR1,GJA1,SH3GL2,FAM122A,IGFBP7,TGFBR1,JADE1,ITSN2,SEMA3C,HPN,CHPT1,SORBS2,EXTL3,APP,DCBLD2,HNF4A,NGF,EDN1,SEMA5A,ADIPOR1,RGS2,SESN2,SHTN1,CAMK2D,RAPH1,AKAP6,MAP3K13,CRYAB,PAPPA2,NPPB,SLIT3,ULK2,CRLF3,FRZB,OSGIN2,CDKN1A,IGFBPL1	darkgreen	VSMC_M4
GO:0045933	0.05	0.99	5	30	positive regulation of muscle contraction	BP	0.79107	EDN2,ADA,EDN1,RGS2,NPNT	darkgreen	VSMC_M4
GO:2000351	0.05	0.99	6	39	regulation of endothelial cell apoptotic process	BP	0.79282	ANGPT1,GATA2,SEMA5A,SERPINE1,ANGPTL4,ICAM1	darkgreen	VSMC_M4

GO:0010506	0.05	0.97	27	268	regulation of autophagy	BP	0.79282	BCL2,EP300,DAPK1,LEP,MAP3K7,SESN1,FOXO1,SLC25A4,PTPN22,FEZ1,HTR2B,SESN2,PRKD1,QSOX1,ATF6,HSPB1,HIF1A,CALCOCO2,PRKAA2,TMEM59,DAPK3,LRSAM1,ITPR1,BNIP3,PIK3C2A,ORMDL3,ATP6V0E1	darkgreen	VSMC_M4
GO:0060444	0.05	0.99	4	18	branching involved in mammary gland duct morphogenesis	BP	0.79795	DDR1,KDM5B,LRP5,CSF1	darkgreen	VSMC_M4
GO:0008306	0.05	0.98	8	53	associative learning	BP	0.80032	HRH1,MEIS2,APP,ABCC8,TANC1,LGMN,HIF1A,NPTN	darkgreen	VSMC_M4
GO:2001242	0.05	0.98	14	135	regulation of intrinsic apoptotic signaling pathway	BP	0.80208	BCL2,MDM2,SOD2,WFS1,CREB3,TPT1,NCK1,CLU,HERPUD1,SERINC3,HSPB1,HIF1A,VNN1,NACC2	darkgreen	VSMC_M4
GO:0051403	0.05	0.97	20	190	stress-activated MAPK cascade	BP	0.80208	SASH1,TPD52L1,LEP,SH3RF3,MAP3K7,MDFIC,HIPK2,FOXO1,RASSF2,HIPK3,SH3RF1,APP,PTPN22,GDF6,MID1,MAP3K13,CRYAB,NBR1,DACT1,LGALS9	darkgreen	VSMC_M4
GO:0050679	0.05	0.97	17	154	positive regulation of epithelial cell proliferation	BP	0.80208	TGFBR1,GATA2,HPN,SEMA5A,KDM5B,HTR2B,PRKCA,CFLAR,FGFR2,PRKD1,HIF1A,PLXNB3,CDH13,F3,FGF9,YAP1,BMP6	darkgreen	VSMC_M4
GO:0006869	0.05	0.97	27	273	lipid transport	BP	0.80208	LEP,VLDLR,SLC2A1,ABCA1,ESYT3,CLU,SCARB2,PTPN11,LBP,EDN1,PLA2G4F,ABCG1,KDM5B,ATP9A,ARV1,FABP2,LRP6,GULP1,CYP19A1,DISP3,STOML1,VAMP7,ABCA4,SLC27A5,PRELID2,BMP6,SCP2	darkgreen	VSMC_M4
GO:1900273	0.05	0.99	4	19	positive regulation of long-term synaptic potentiation	BP	0.80208	ZDHHC2,APP,LGMN,NPTN	darkgreen	VSMC_M4
GO:0060603	0.05	0.99	5	26	mammary gland duct morphogenesis	BP	0.80208	DDR1,KDM5B,LRP5,FGFR2,CSF1	darkgreen	VSMC_M4
GO:2000369	0.05	0.99	4	19	regulation of clathrin-dependent endocytosis	BP	0.80208	SH3GL2,SNAP91,DNAJC6,DAB2	darkgreen	VSMC_M4
GO:0046323	0.05	0.98	8	54	glucose import	BP	0.80293	LEP,SLC2A1,OCLN,PTH,PTPN11,SESN2,OPN3,SORT1	darkgreen	VSMC_M4
GO:0010743	0.05	0.99	4	20	regulation of macrophage derived foam cell differentiation	BP	0.80444	ABCA1,LPL,ABCG1,CSF1	darkgreen	VSMC_M4
GO:0035994	0.05	0.99	4	20	response to muscle stretch	BP	0.80461	ANKRD1,EDN1,CDH2,SLC8A1	darkgreen	VSMC_M4
GO:0070252	0.05	0.98	10	70	actin-mediated cell contraction	BP	0.80767	GJA1,LIMCH1,KCNE3,TNNT2,SHTN1,CAMK2D,CACNA1C,FLNA,KCNE4,PLN	darkgreen	VSMC_M4
GO:0051146	0.05	0.97	23	220	striated muscle cell differentiation	BP	0.80767	BCL2,ADGRB1,SGCB,TBX18,ANKRD1,SORBS2,TANC1,RCAN1,EDN1,RIPOR2,RGS2,TNNT2,ACTN2,CFLAR,AKAP6,SYNPO2L,WDR1,CDH2,SORT1,SLC8A1,ADAMTS5,CSRP1,HOPX	darkgreen	VSMC_M4
GO:0060323	0.05	0.99	5	28	head morphogenesis	BP	0.80767	EP300,PTPN11,ARID5B,ATP6AP2,TGFB3	darkgreen	VSMC_M4
GO:0010043	0.05	0.99	5	32	response to zinc ion	BP	0.80767	SOD2,PAM,ABCC8,VCAM1,PLN	darkgreen	VSMC_M4
GO:0051179	0.05	0.96	345	4586	localization	BP	0.80767	BCL2,RNF41,SLC35D3,CITED2,STX11,SASH1,GRIP1,MDM2,DDR1,LAPTM4B,IPCEF1,SOD2,ABRA,ANGPT1,C4A,FAM19A5,PKDREJ,SMOC2,CALHM5,GJA1,TRDN,LAMA2,MRTFA,ADGRB1,DAPK1,SH3GL2,LEP,WFS1,LIMCH1,DDX58,DOCK8,KANK1,VLDLR,UNC13B,PPP1R9A,CD274,RIC1,DYNC1I1,CREB3,REST,ICA1,RECK,ZAP70,FRMPD1,LMAN2L,SNX13,SLC2A1,TGFBR1,PREPL,LMBRD1,EDN2,SYT5,SLC17A5,ABCA1,PTPN3,DOP1A,SNAP91,PEX13,ANTXR1,DOCK4,MDFIC,TCAF1,SLC37A3,ITSN2,GATA2,ENKUR,LRCH1,MRC1,TPT1,TMCC1,GGA3,INHBB,USP6NL,HRH1,CD93,SYNGR2,KCNE3,RAB2B,ACTN4,TM9SF2,FMNL2,ADAM9,FGF14,TRPC4,SLC16A3,ATP2C1,CYP1B1,PCLO,SEMA3C,EML4,TF,APLP1,AMOTL2,TUSC3,ZDHHC2,RIC3,NCOR2,FFAR3,FXYD1,HPN,PTPRG,DENND5A,CHD7,MICU2,LATS2,ANKRD1,MARCH5,TRIM23,NCK1,EXOC6,ADM,ESYT3,PAM,SLC25A4,SCN8A,SH3RF1,ATOH8,CLCN3,OCLN,WWC2,SLC35G1,MCTP1,CHST2,JPH1,PTH,KIF13B,G3BP2,CLU,GPM6A,APP,ATXN2,SCARB2,PDGFC,SHROOM3,ABCC8,ANXA3,PTPN11,PTX3,LBP,HERPUD1,SLC26A7,JMY,ATG13,HNF4A,SERINC3,ADA,AKTIP,IFIT1,PDZD7,EDN1,JAM3,CD47,NFASC,PLA2G4F,ANO5,MYO1B,SEMA5A,LPL,RAB29,ABCG1,CNNM2,ADIPOR1,DNAH7,KDM5B,RIPOR2,RGS2,EYA2,TNNT2,ACTN2,PFKL,LRP5,ARRDC4,FEZ1,NPNT,PREX1,HTR2B,MST1R,LGMN,TINAGL1,ZMAT3,TM7SF3,SDC3,SUN1,PRKCA,TXNIP,SEC24B,CFI,MFGE8,PARD6B,MID1,ATP9A,PLXNA2,SESN2,ARV1,SHTN1,CAMK2D,ABCC9,ADCY5,CTSS,MYLK,LRP2,INPP5F,FABP2,PTPN14,PRKD1,PI4KB,NBEAL1,F11R,CYBRD1,PLXNB1,DYNC1I2,ZRANB1,SLC25A12,ARID5B,ITGA6,RAPGEF4,AP3B2,AKAP6,DDR2,LRP6,HIP1,HSPB1,CUX1,SERPINE1,ACHE,CRYAB,RDX,EXPH5,MAOB,GLUL1,ATG14,F	darkgreen	VSMC_M4
GO:0010644	0.05	0.99	5	27	cell communication by electrical coupling	BP	0.80767	GJA1,TRDN,CAMK2D,CACNA1C,SLC8A1	darkgreen	VSMC_M4
GO:0061298	0.05	0.99	4	16	retina vasculature development in camera-type eye	BP	0.80767	COL4A1,CYP1B1,LRP5,HIF1A	darkgreen	VSMC_M4
GO:0001932	0.05	0.96	72	845	regulation of protein phosphorylation	BP	0.80767	GDF11,BCL2,SASH1,IRAK3,ANGPT1,TPD52L1,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,VLDLR,PPP1R9A,TGFBR1,MAP3K7,HIPK2,INHBB,ADAM9,RASSF2,FLT3,LATS2,HIPK3,NCK1,OCLN,CLU,APP,PDGFC,PTPN11,CCNT1,PTPN22,GDF6,AKTIP,NGF,EDN1,RGS2,LRP5,PLCL1,HTR2B,MST1R,AFAP1L2,SESN2,INPP5F,PRKD1,DDR2,GPRC5A,MAP3K13,LRP6,FAM129A,HSPB1,ATG14,PPARGC1A,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,DAB2,CSF1,PLCG2,TERF2IP,BCAR3,CYR61,SLC8A1,LOX,CDKN1A,FGF9,PPM1E,CNTD2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0002209	0.05	0.99	4	19	behavioral defense response	BP	0.80767	BCL2,GJA1,EP300,FBXL20	darkgreen	VSMC_M4
GO:0042116	0.05	0.98	9	69	macrophage activation	BP	0.80767	IFNGR1,EDN2,CD93,CLU,APP,LBP,RORA,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0009746	0.05	0.97	17	159	response to hexose	BP	0.80767	GJA1,UNC13B,HNF4A,LPL,ABCG1,PFKL,LRP5,TXNIP,SESN2,ADCY5,HIF1A,PPARGC1A,PRKAA2,SLC2A5,SLC8A1,ICAM1,MAFA	darkgreen	VSMC_M4
GO:0050766	0.05	0.98	6	38	positive regulation of phagocytosis	BP	0.80767	C4A,GATA2,PTX3,CD47,MFGE8,PLCG2	darkgreen	VSMC_M4
GO:0050873	0.05	0.98	6	40	brown fat cell differentiation	BP	0.80767	ZNF516,LEP,FNDC5,RGS2,PPARGC1A,BNIP3	darkgreen	VSMC_M4
GO:1903317	0.05	0.98	7	54	regulation of protein maturation	BP	0.80767	MDM2,HPN,CHAC1,CTSZ,SERPINE1,TMEM59,GLG1	darkgreen	VSMC_M4
GO:0032943	0.05	0.97	18	179	mononuclear cell proliferation	BP	0.80767	BCL2,LEP,DOCK8,CD274,ZAP70,FLT3,NCK1,CD180,SH3RF1,PTPN22,ADA,NCSTN,IGFBP2,LGALS9,CSF1,VCAM1,CD151,CDKN1A	darkgreen	VSMC_M4
GO:0060038	0.05	0.98	7	45	cardiac muscle cell proliferation	BP	0.80767	CITED2,GJA1,TGFBR1,TENM4,FGFR2,TBX20,YAP1	darkgreen	VSMC_M4
GO:0032386	0.05	0.97	28	290	regulation of intracellular transport	BP	0.80767	SLC35D3,MDM2,ANGPT1,LEP,MDFIC,TCAF1,ZDHHC2,PTPN11,ATG13,RAB29,TNNT2,ACTN2,FEZ1,SEC24B,ATP9A,ARV1,INPP5F,PTPN14,PRKD1,CRYAB,RDX,ABLIM3,SH3TC2,RHOT1,DAB2,FLNA,PLN,SCP2	darkgreen	VSMC_M4
GO:0060043	0.05	0.98	6	37	regulation of cardiac muscle cell proliferation	BP	0.80767	CITED2,GJA1,TGFBR1,FGFR2,TBX20,YAP1	darkgreen	VSMC_M4

GO:0071277	0.05	0.98	9	63	cellular response to calcium ion	BP	0.80767	SYT5,CPNE4,EDN1,LGMN,CAMK2D,NCSTN,NLGN1,PRKAA2,PLCG2	darkgreen	VSMC_M4
GO:0008207	0.05	0.99	4	22	C21-steroid hormone metabolic process	BP	0.80767	REST,ADM,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0045766	0.05	0.97	15	133	positive regulation of angiogenesis	BP	0.80767	SASH1,SMOC2,HIPK2,GATA2,CYP1B1,ADM,ANXA3,SEMA5A,PRKCA,PRKD1,HSPB1,SERPINE1,HIF1A,ANGPTL4,F3	darkgreen	VSMC_M4
GO:1904018	0.05	0.97	15	133	positive regulation of vasculature development	BP	0.80767	SASH1,SMOC2,HIPK2,GATA2,CYP1B1,ADM,ANXA3,SEMA5A,PRKCA,PRKD1,HSPB1,SERPINE1,HIF1A,ANGPTL4,F3	darkgreen	VSMC_M4
GO:0051491	0.05	0.99	5	27	positive regulation of filopodium assembly	BP	0.80767	TGFBR1,GPM6A,RIPOR2,NLGN1,TGFB3	darkgreen	VSMC_M4
GO:0002347	0.05	0.99	4	22	response to tumor cell	BP	0.80767	DAPK1,CD274,TXNIP,IGFBPL1	darkgreen	VSMC_M4
GO:0046660	0.05	0.98	11	88	female sex differentiation	BP	0.80767	BCL2,LEP,INHBB,CHD7,PTX3,LRP2,ARID5B,CYP19A1,SLIT3,FST,ICAM1	darkgreen	VSMC_M4
GO:0007602	0.05	0.99	4	22	phototransduction	BP	0.80767	GNAQ,GRK7,OPN3,ABCA4	darkgreen	VSMC_M4
GO:0034219	0.05	0.98	11	86	carbohydrate transmembrane transport	BP	0.80767	LEP,SLC2A1,SLC17A5,OCLN,PTH,PTPN11,EDN1,SESN2,OPN3,SLC2A5,SORT1	darkgreen	VSMC_M4
GO:0030336	0.05	0.97	23	223	negative regulation of cell migration	BP	0.80767	BCL2,RNF41,CITED2,FAM19A5,GJA1,ADGRB1,LIMCH1,KANK1,RECK,TCAF1,LRCH1,CYP1B1,PTPRG,MCTP1,ABCC8,ADA,ADIPOR1,RIPOR2,SERPINE1,PPARGC1A,MMP28,PLXNB3,PRKG1	darkgreen	VSMC_M4
GO:0015865	0.05	0.99	4	22	purine nucleotide transport	BP	0.80767	GJA1,SLC25A4,CD47,LRRC8C	darkgreen	VSMC_M4
GO:0015868	0.05	0.99	4	22	purine ribonucleotide transport	BP	0.80767	GJA1,SLC25A4,CD47,LRRC8C	darkgreen	VSMC_M4
GO:0051503	0.05	0.99	4	22	adenine nucleotide transport	BP	0.80767	GJA1,SLC25A4,CD47,LRRC8C	darkgreen	VSMC_M4
GO:1902882	0.05	0.98	9	74	regulation of response to oxidative stress	BP	0.80767	SOD2,OXR1,REST,SESN1,MCTP1,SESN2,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0042110	0.05	0.97	29	310	T cell activation	BP	0.80767	BCL2,LEP,DOCK8,CD274,IL18R1,ZAP70,MAP3K8,APBB1IP,CHD7,NCK1,SH3RF1,KIF13B,PTPN11,PTPN22,ADA,CD47,RAB29,RIPOR2,PREX1,NCSTN,IGFBP2,RORA,LGALS9,VCAM1,VNN1,CD151,CD83,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0002696	0.05	0.97	21	218	positive regulation of leukocyte activation	BP	0.80767	BCL2,LEP,DOCK8,CD274,ZAP70,MAP3K8,GATA2,NCK1,PTPN11,LBP,PTPN22,ADA,CD47,TP53BP1,IGFBP2,LGALS9,VAMP7,VCAM1,VNN1,CD83,CDKN1A	darkgreen	VSMC_M4
GO:0006914	0.05	0.96	41	450	autophagy	BP	0.80767	BCL2,RNF41,EP300,DAPK1,LEP,MAP3K7,SESN1,FOXO1,MAP1LC3A,SLC25A4,CLU,ATG13,PTPN22,FEZ1,HTR2B,SESN2,SYNPO2,PRKD1,QSOX1,ATF6,GABARAPL1,HSPB1,NBR1,ATG14,HIF1A,PPARGC1A,CALCOCO2,EPG5,ATG4A,ULK2,PRKAA2,TMEM59,DAPK3,MAP1LC3B2,LRSAM1,ITPR1,BNIP3,GABARAPL2,PIK3C2A,ORMDL3,ATP6V0E1	darkgreen	VSMC_M4
GO:0061919	0.05	0.96	41	450	process utilizing autophagic mechanism	BP	0.80767	BCL2,RNF41,EP300,DAPK1,LEP,MAP3K7,SESN1,FOXO1,MAP1LC3A,SLC25A4,CLU,ATG13,PTPN22,FEZ1,HTR2B,SESN2,SYNPO2,PRKD1,QSOX1,ATF6,GABARAPL1,HSPB1,NBR1,ATG14,HIF1A,PPARGC1A,CALCOCO2,EPG5,ATG4A,ULK2,PRKAA2,TMEM59,DAPK3,MAP1LC3B2,LRSAM1,ITPR1,BNIP3,GABARAPL2,PIK3C2A,ORMDL3,ATP6V0E1	darkgreen	VSMC_M4
GO:0031324	0.05	0.96	149	1896	negative regulation of cellular metabolic process	BP	0.80767	BCL2,CITED2,IRAK3,MDM2,LAPTM4B,OXR1,ANGPT1,C4A,TRPS1,GJA1,ZHX1,EP300,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,RIC1,ZNF169,REST,RECK,PTPN3,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,ITIH5,LBH,LMCD1,THRB,SATB1,CRIM1,FOXO1,RASSF2,ANKLE2,MIER3,NCOR2,FXYD1,ZC3H6,LATS2,HIPK3,ANKRD1,CPEB3,NCK1,SH3RF1,ATOH8,OCLN,WWC2,RNF34,CLU,MEIS2,APP,ATXN2,PTX3,CCNT1,HERPUD1,PROS1,PTPN22,HNF4A,CHAC1,NAB1,NGF,EDN1,ETS2,N4BP1,BACE2,KDM5B,RGS2,MXI1,LRP5,FEZ1,HTR2B,TXNIP,SESN2,YEATS2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,TP53BP1,QSOX1,SLC25A12,STRN3,ARID5B,GPRC5A,ID3,LRP6,FAM129A,HSPB1,EIF4A2,CUX1,SERPINE1,CRYAB,EZH1,ATG14,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,OPN3,ZBTB18,APBB2,PPP1R36,ZBTB4,PPARGC1A,CHD3,SMAD6,FST,DAB2,PRKAA2,TMEM59,ATCAY,DAPK3,TLE2,FLNA,PPP1R26,TERF2IP,GLG1,ZFP90,SLC8A1,SPINK2,BNIP3,TBX20,ITM2C,CST3,ZNF425,ZNF175,CDKN1A,ZNF572,PPM1E,NACC2,ZNF79,HOPX,GABARAPL2,ORMDL3,YAP1,HKR1,BMP6,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:0008643	0.05	0.97	13	112	carbohydrate transport	BP	0.80767	SLC35D3,LEP,SLC2A1,SLC17A5,SLC37A3,OCLN,PTH,PTPN11,EDN1,SESN2,OPN3,SLC2A5,SORT1	darkgreen	VSMC_M4
GO:0022407	0.05	0.97	28	293	regulation of cell-cell adhesion	BP	0.80767	MBP,CITED2,CDSN,LEP,DOCK8,CD274,ZAP70,MAP3K8,ZDHHC2,NCK1,CHST2,PTPN11,PTPN22,ADA,CD47,RIPOR2,PRKCA,F11R,RDX,IGFBP2,LGALS9,MYO10,VCAM1,VNN1,CD83,ICAM1,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0045907	0.05	0.99	4	22	positive regulation of vasoconstriction	BP	0.80767	GJA1,HRH1,ADRA1B,ICAM1	darkgreen	VSMC_M4
GO:0001935	0.05	0.97	14	123	endothelial cell proliferation	BP	0.80767	GJA1,LEP,TGFBR1,GATA2,ATOH8,SEMA5A,HTR2B,PRKCA,PRKD1,HIF1A,PLXNB3,CDH13,F3,BMP6	darkgreen	VSMC_M4
GO:0051090	0.05	0.96	31	328	regulation of DNA-binding transcription factor activity	BP	0.80767	IRAK3,ABRA,EP300,WFS1,DDX58,IL18R1,MAP3K7,HIPK2,CYP1B1,G3BP2,CLU,APP,ANXA3,JMY,EDN1,LRP5,CFLAR,TP53BP1,PRKD1,ARID5B,DDR2,MAP3K13,ID3,LRP6,PPARGC1A,LGALS9,FLNA,PLCG2,TERF2IP,EDA,ICAM1	darkgreen	VSMC_M4
GO:0140058	0.05	0.98	5	28	neuron projection arborization	BP	0.80767	GRIP1,LRP2,ZNF365,MAP3K13,NLGN1	darkgreen	VSMC_M4
GO:0060669	0.05	0.99	4	21	embryonic placenta morphogenesis	BP	0.80767	GRHL2,ADM,FGFR2,CYR61	darkgreen	VSMC_M4
GO:0014909	0.05	0.98	9	67	smooth muscle cell migration	BP	0.80767	BCL2,MDM2,DDR1,FAM19A5,DOCK4,SERPINE1,PPARGC1A,FGF9,PRKG1	darkgreen	VSMC_M4
GO:0009268	0.05	0.98	5	31	response to pH	BP	0.80767	GJA1,PAM,ABCC8,LGMN,CTSS	darkgreen	VSMC_M4
GO:0071867	0.05	0.98	9	69	response to monoamine	BP	0.80767	HRH1,APLP1,APP,ADCY6,HTR2B,ADCY5,NCSTN,PPARGC1A,FLNA	darkgreen	VSMC_M4
GO:0071869	0.05	0.98	9	69	response to catecholamine	BP	0.80767	HRH1,APLP1,APP,ADCY6,HTR2B,ADCY5,NCSTN,PPARGC1A,FLNA	darkgreen	VSMC_M4
GO:0060632	0.05	0.98	5	32	regulation of microtubule-based movement	BP	0.80767	FEZ1,BBS4,GAS2L2,RHOT1,CCR6	darkgreen	VSMC_M4
GO:0050714	0.05	0.97	12	100	positive regulation of protein secretion	BP	0.80767	GJA1,UNC13B,ADAM9,ANKRD1,ABCG1,TM7SF3,ACHE,EXPH5,HIF1A,TGFB3,WLS,BMP6	darkgreen	VSMC_M4
GO:0060541	0.05	0.97	18	163	respiratory system development	BP	0.80767	GRHL2,EP300,EDN2,THRB,CHD7,RXFP1,ADA,SEC24B,CTSZ,FGFR2,FGFRL1,TGFB3,ADAMTSL2,LOX,FGF9,EDA,HOPX,YAP1	darkgreen	VSMC_M4
GO:2000377	0.06	0.97	13	120	regulation of reactive oxygen species metabolic process	BP	0.80767	BCL2,RNF41,SOD2,ADGRB1,LEP,CYP1B1,CLCN3,CFLAR,CRYAB,HIF1A,PLCG2,BNIP3,CDKN1A	darkgreen	VSMC_M4
GO:1903580	0.06	0.98	5	29	positive regulation of ATP metabolic process	BP	0.80767	APP,SLC25A12,HIF1A,PPARGC1A,PRKAA2	darkgreen	VSMC_M4

GO:1902175	0.06	0.99	4	23	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	BP	0.80767	SOD2,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0045321	0.06	0.96	50	586	leukocyte activation	BP	0.80767	BCL2,IFNGR1,EP300,LEP,DOCK8,CD274,IL18R1,ZAP70,EDN2,MAP3K8,GATA2,APBB1IP,CD93,ADAM9,FLT3,CHD7,NCK1,CD180,SH3RF1,KIF13B,CLU,BLNK,APP,ANXA3,PTPN11,LBP,PTPN22,ADA,EDN1,CD47,RAB29,RIPOR2,PREX1,TP53BP1,NCSTN,IGFBP2,ADGRE2,RORA,LGALS9,VAMP7,CSF1,PLCG2,VCAM1,VNN1,CD151,TLR1,CD83,CDKN1A,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0010976	0.06	0.97	16	140	positive regulation of neuron projection development	BP	0.80767	EP300,VLDLR,PPP1R9A,KIDINS220,ANKRD1,NCK1,SCARB2,RGS2,FEZ1,CFLAR,PRKD1,ITGA6,NPTN,PAK3,PLXNB3,FLNA	darkgreen	VSMC_M4
GO:0001990	0.06	0.99	4	23	regulation of systemic arterial blood pressure by hormone	BP	0.80767	EDN2,EDN1,CTSZ,ATP6AP2	darkgreen	VSMC_M4
GO:0090090	0.06	0.97	13	113	negative regulation of canonical Wnt signaling pathway	BP	0.80767	TLE4,MLLT3,TBX18,JADE1,LATS2,TMEM64,IGFBP2,DACT1,CDH2,DAB2,TLE2,FRZB,TMEM170B	darkgreen	VSMC_M4
GO:0033628	0.06	0.98	6	40	regulation of cell adhesion mediated by integrin	BP	0.80767	ADAM9,CYP1B1,PTPN11,ADA,JAM3,SERPINE1	darkgreen	VSMC_M4
GO:1902807	0.06	0.98	8	60	negative regulation of cell cycle G1/S phase transition	BP	0.80767	BCL2,MDM2,CDKN2B,JADE1,RBL2,DACT1,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0048514	0.06	0.96	47	508	blood vessel morphogenesis	BP	0.80767	CITED2,SASH1,ANGPT1,FAM19A5,SMOC2,ADGRB1,LEP,RECK,TGFBR1,CALD1,HIPK2,GATA2,COL4A1,COL4A2,CYP1B1,AMOTL2,CHD7,ADM,ABCC8,ANXA3,EDN1,JAM3,SEMA5A,LRP5,PRKCA,SEC24B,MFGE8,MYLK,LRP2,FGFR2,PRKD1,HSPB1,SERPINE1,UNC5B,HIF1A,NPPB,RORA,CDH2,ANGPTL4,FLNA,CDH13,F3,CYR61,LOX,TBX20,PIK3C2A,YAP1	darkgreen	VSMC_M4
GO:0002252	0.06	0.96	33	360	immune effector process	BP	0.80767	IRAK3,ANGPT1,C4A,LEP,DDX58,IL18R1,MAP3K7,GATA2,APBB1IP,FFAR3,CD180,CLU,APP,ANXA3,PTX3,LBP,PTPN22,ADA,CD47,CFI,TP53BP1,C1RL,WDR1,ADGRE2,RORA,TGFB3,LGALS9,VAMP7,PLCG2,CD59,MFAP4,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0045981	0.06	0.98	5	29	positive regulation of nucleotide metabolic process	BP	0.80767	APP,SLC25A12,HIF1A,PPARGC1A,PRKAA2	darkgreen	VSMC_M4
GO:1900544	0.06	0.98	5	29	positive regulation of purine nucleotide metabolic process	BP	0.80767	APP,SLC25A12,HIF1A,PPARGC1A,PRKAA2	darkgreen	VSMC_M4
GO:0032355	0.06	0.97	12	105	response to estradiol	BP	0.80767	GJA1,LEP,NCOR2,PAM,NCOA3,TXNIP,CFLAR,STRN3,CRYAB,IGFBP2,CYP19A1,PPARGC1A	darkgreen	VSMC_M4
GO:0006816	0.06	0.96	28	282	calcium ion transport	BP	0.80829	BCL2,PKDREJ,GJA1,TRDN,WFS1,TPT1,KCNE3,FGF14,TRPC4,ATP2C1,CHD7,MICU2,SLC35G1,JPH1,GPM6A,HTR2B,CAMK2D,MYLK,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A,SARAF,ICAM1	darkgreen	VSMC_M4
GO:0032613	0.06	0.98	5	32	interleukin-10 production	BP	0.80829	CD274,CD47,LGALS9,PLCG2,CD83	darkgreen	VSMC_M4
GO:0032653	0.06	0.98	5	32	regulation of interleukin-10 production	BP	0.80829	CD274,CD47,LGALS9,PLCG2,CD83	darkgreen	VSMC_M4
GO:0051402	0.06	0.97	20	198	neuron apoptotic process	BP	0.80829	BCL2,SOD2,OXR1,ANGPT1,WFS1,HIPK2,POLB,THRB,APP,NGF,LGMN,CTSZ,USP53,NCSTN,UNC5B,HIF1A,PPARGC1A,TGFB3,PAK3,BNIP3	darkgreen	VSMC_M4
GO:1904063	0.06	0.98	8	62	negative regulation of cation transmembrane transport	BP	0.80829	TRDN,KCNE3,RGS2,ACTN2,CAMK2D,SLC43A2,KCNE4,PLN	darkgreen	VSMC_M4
GO:0033135	0.06	0.97	12	104	regulation of peptidyl-serine phosphorylation	BP	0.80829	BCL2,ANGPT1,RASSF2,NCK1,APP,NGF,PLCL1,INPP5F,PRKD1,TERF2IP,BCAR3,DDIT4	darkgreen	VSMC_M4
GO:0032956	0.06	0.96	30	304	regulation of actin cytoskeleton organization	BP	0.80829	LIMCH1,KANK1,PPP1R9A,TGFBR1,CDC42EP3,WASF3,NCK1,PAM,JMY,EDN1,JAM3,CD47,SEMA5A,ACTN2,PREX1,SYNPO2,F11R,RDX,SYNPO2L,WDR1,TGFB3,SYNPO,PAK3,ARHGAP28,DAPK3,FLNA,SPTAN1,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0002455	0.06	0.99	4	24	humoral immune response mediated by circulating immunoglobulin	BP	0.80829	C4A,CLU,CFI,C1RL	darkgreen	VSMC_M4
GO:0006096	0.06	0.98	8	60	glycolytic process	BP	0.80829	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0006757	0.06	0.98	8	60	ATP generation from ADP	BP	0.80829	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0071312	0.06	0.98	5	29	cellular response to alkaloid	BP	0.80982	MDM2,PPARGC1A,SLC8A1,TMEM38A,ICAM1	darkgreen	VSMC_M4
GO:0070884	0.06	0.98	5	30	regulation of calcineurin-NFAT signaling cascade	BP	0.80982	LMCD1,RCAN1,AKAP6,PLCG2,C10orf71	darkgreen	VSMC_M4
GO:0060415	0.06	0.98	8	56	muscle tissue morphogenesis	BP	0.81203	TGFBR1,CHD7,ANKRD1,TNNT2,MYLK,LRP2,FGFR2,TBX20	darkgreen	VSMC_M4
GO:0008630	0.06	0.97	10	84	intrinsic apoptotic signaling pathway in response to DNA damage	BP	0.81397	BCL2,EP300,HIPK2,TPT1,POLB,CLU,MAEL,CDKN1A,NACC2,DDIT4	darkgreen	VSMC_M4
GO:0140115	0.06	0.98	7	49	export across plasma membrane	BP	0.81397	GJA1,ABCA1,KCNE3,FXYD1,SLC35G1,KCNE4,SLC8A1	darkgreen	VSMC_M4
GO:0032872	0.06	0.97	16	148	regulation of stress-activated MAPK cascade	BP	0.81397	SASH1,TPD52L1,LEP,SH3RF3,MDFIC,HIPK2,FOXO1,RASSF2,HIPK3,SH3RF1,APP,PTPN22,GDF6,MID1,NBR1,DACT1	darkgreen	VSMC_M4
GO:0071548	0.06	0.98	5	31	response to dexamethasone	BP	0.81397	FOXO1,EDN1,CFLAR,ICAM1,DDIT4	darkgreen	VSMC_M4
GO:0051345	0.06	0.96	40	440	positive regulation of hydrolase activity	BP	0.81397	MBP,DAPK1,GNAQ,DOCK8,RIC1,REST,SNX13,CHN2,ANTXR1,USP6NL,RALGAPA2,PTH,APP,PKP4,TNNT2,NPNT,PREX1,HTR2B,LGMN,CFLAR,FGFR2,PRKD1,NCSTN,F11R,PLXNB1,ITGA6,HIP1,TNFSF10,SIPA1L1,MAPRE2,EVI5L,LGALS9,TBC1D13,F3,ARHGAP29,BCAR3,CYR61,SYDE2,GABARAPL2,ICAM1	darkgreen	VSMC_M4
GO:0014033	0.06	0.97	10	77	neural crest cell differentiation	BP	0.81397	CITED2,SEMA3C,FAM172A,EDN1,SEMA5A,HTR2B,LRP6,HIF1A,CDH2,FRZB	darkgreen	VSMC_M4
GO:0042593	0.06	0.96	19	183	glucose homeostasis	BP	0.81445	LEP,WFS1,UNC13B,PDK4,FOXO1,ABCC8,HECTD4,PTPN11,HNF4A,BACE2,ABCG1,ADIPOR1,LRP5,SESN2,ADCY5,HIF1A,PPARGC1A,PRKAA2,ICAM1	darkgreen	VSMC_M4
GO:0050796	0.06	0.97	14	127	regulation of insulin secretion	BP	0.81445	GJA1,LEP,REST,ICA1,INHBB,ABCC8,PTPN11,HNF4A,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,HIF1A	darkgreen	VSMC_M4
GO:0009743	0.06	0.96	19	186	response to carbohydrate	BP	0.81445	SOD2,GJA1,LEP,UNC13B,HNF4A,LPL,ABCG1,PFKL,LRP5,TXNIP,SESN2,ADCY5,HIF1A,PPARGC1A,PRKAA2,SLC2A5,SLC8A1,ICAM1,MAFA	darkgreen	VSMC_M4
GO:0032958	0.06	0.98	4	21	inositol phosphate biosynthetic process	BP	0.81445	HRH1,PTH,PPIP5K1,PLCG2	darkgreen	VSMC_M4
GO:0090303	0.06	0.98	6	42	positive regulation of wound healing	BP	0.81445	SMOC2,KANK1,OCLN,MYLK,SERPINE1,F3	darkgreen	VSMC_M4
GO:1902893	0.06	0.98	7	47	regulation of pri-miRNA transcription by RNA polymerase II	BP	0.81445	MRTFA,REST,GATA2,ATOH8,TEAD1,HIF1A,SMAD6	darkgreen	VSMC_M4
GO:0034329	0.06	0.96	33	318	cell junction assembly	BP	0.81445	BCL2,GRHL2,GJA1,ADGRB1,LIMCH1,PPP1R9A,TESK2,PCDHB4,PCLO,OCLN,GPM6A,APP,PTPN11,PKP4,JAM3,RAB29,ACTN2,PRKCA,PARD6B,F11R,PLXNB1,ITGA6,ACHE,NLGN1,WDR1,ACTN1,NPTN,CDH2,PATJ,CDH18,DAPK3,PCDHB2,LRRC24	darkgreen	VSMC_M4

GO:0019216	0.06	0.96	24	251	regulation of lipid metabolic process	BP	0.81658	LEP,PDK4,REST,IGFBP7,FLT3,ADM,HNF4A,ABCG1,ADIPOR1,HTR2B,ARV1,WDTC1,PRKD1,ATG14,PPARGC1A,DISP3,RORA,LACTB,BBS4,MBTPS1,PLCG2,CYR61,ORMDL3,BMP6	darkgreen	VSMC_M4
GO:0051149	0.06	0.98	7	53	positive regulation of muscle cell differentiation	BP	0.81866	BCL2,MDM2,SOD2,SMARCD3,EDN1,AKAP6,HOPX	darkgreen	VSMC_M4
GO:0006812	0.06	0.95	67	796	cation transport	BP	0.82101	BCL2,PKDREJ,CALHM5,GJA1,TRDN,DAPK1,WFS1,SYT5,SLC17A5,PTPN3,TPT1,KCNE3,ACTN4,FGF14,TRPC4,ATP2C1,TF,TUSC3,FXYD1,HPN,CHD7,MICU2,SLC25A4,SCN8A,CLCN3,SLC35G1,JPH1,GPM6A,APP,ABCC8,SERINC3,ADA,EDN1,CNNM2,RGS2,ACTN2,HTR2B,CAMK2D,ABCC9,CTSS,MYLK,LRP2,PRKD1,CYBRD1,AKAP6,MAOB,LMTK2,NLGN1,CACNA1C,PPARGC1A,MAGT1,KCNK10,SLC43A2,SCNN1D,FLNA,VAMP7,HCN2,AHCYL1,PLCG2,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,SARAF,ICAM1,ATP6V0E1	darkgreen	VSMC_M4
GO:0031098	0.06	0.96	20	197	stress-activated protein kinase signaling cascade	BP	0.82101	SASH1,TPD52L1,LEP,SH3RF3,MAP3K7,MDFIC,HIPK2,FOXO1,RASSF2,HIPK3,SH3RF1,APP,PTPN22,GDF6,MID1,MAP3K13,CRYAB,NBR1,DACT1,LGALS9	darkgreen	VSMC_M4
GO:0071417	0.06	0.96	43	466	cellular response to organonitrogen compound	BP	0.82101	MDM2,GJA1,LEP,KANK1,PDK4,SESN1,INHBB,HRH1,FOXO1,COL4A1,APLP1,FFAR3,CPEB3,NCK1,APP,PDGFC,PTPN11,ADCY6,PTPN22,EDN1,LPL,ADIPOR1,ACTN2,ZNF106,HTR2B,LGMN,SESN2,ADCY5,CFLAR,WDTC1,CASTOR1,NCSTN,AKAP6,PPARGC1A,FLNA,HCN2,AHCYL1,VCAM1,BCAR3,SLC8A1,TMEM38A,ICAM1,PIK3C2A	darkgreen	VSMC_M4
GO:1903036	0.06	0.98	7	53	positive regulation of response to wounding	BP	0.82101	SMOC2,KANK1,OCLN,MYLK,SERPINE1,FLNA,F3	darkgreen	VSMC_M4
GO:0043462	0.06	0.98	5	37	regulation of ATPase activity	BP	0.82101	TPM2,TMEM64,TNNT2,PLN,GABARAPL2	darkgreen	VSMC_M4
GO:1902895	0.06	0.98	6	37	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	0.82118	MRTFA,GATA2,ATOH8,TEAD1,HIF1A,SMAD6	darkgreen	VSMC_M4
GO:0015748	0.06	0.97	12	102	organophosphate ester transport	BP	0.82261	GJA1,ABCA1,SLC25A4,SCARB2,CD47,ABCG1,ATP9A,EPG5,ABCA4,LRRC8C,PRELID2,SCP2	darkgreen	VSMC_M4
GO:0071621	0.06	0.97	9	76	granulocyte chemotaxis	BP	0.82261	EDN2,HRH1,LBP,EDN1,JAM3,RIPOR2,PREX1,ADGRE2,CSF1	darkgreen	VSMC_M4
GO:0003298	0.06	0.98	4	24	physiological muscle hypertrophy	BP	0.82261	SORBS2,EDN1,RGS2,AKAP6	darkgreen	VSMC_M4
GO:0003301	0.06	0.98	4	24	physiological cardiac muscle hypertrophy	BP	0.82261	SORBS2,EDN1,RGS2,AKAP6	darkgreen	VSMC_M4
GO:0061049	0.06	0.98	4	24	cell growth involved in cardiac muscle cell development	BP	0.82261	SORBS2,EDN1,RGS2,AKAP6	darkgreen	VSMC_M4
GO:0070229	0.06	0.98	4	22	negative regulation of lymphocyte apoptotic process	BP	0.82261	DOCK8,ADA,HIF1A,ORMDL3	darkgreen	VSMC_M4
GO:0036003	0.06	0.98	4	22	positive regulation of transcription from RNA polymerase II promoter in response to stress	BP	0.82261	CHD6,SESN2,ATF6,HIF1A	darkgreen	VSMC_M4
GO:0051271	0.06	0.96	24	241	negative regulation of cellular component movement	BP	0.82363	BCL2,RNF41,CITED2,FAM19A5,GJA1,ADGRB1,LIMCH1,KANK1,RECK,TCAF1,LRCH1,CYP1B1,PTPRG,MCTP1,ABCC8,ADA,ADIPOR1,RIPOR2,SERPINE1,PPARGC1A,ACTN1,MMP28,PLXNB3,PRKG1	darkgreen	VSMC_M4
GO:0007043	0.06	0.97	12	99	cell-cell junction assembly	BP	0.82363	GRHL2,GJA1,OCLN,PKP4,JAM3,PRKCA,PARD6B,F11R,WDR1,CDH2,PATJ,CDH18	darkgreen	VSMC_M4
GO:0001934	0.06	0.95	48	543	positive regulation of protein phosphorylation	BP	0.8268	GDF11,BCL2,SASH1,ANGPT1,TPD52L1,LEP,LIMCH1,VLDLR,PPP1R9A,TGFBR1,MAP3K7,HIPK2,INHBB,ADAM9,RASSF2,FLT3,CLU,APP,PDGFC,PTPN11,CCNT1,GDF6,AKTIP,NGF,EDN1,HTR2B,MST1R,AFAP1L2,PRKD1,DDR2,GPRC5A,MAP3K13,FAM129A,ATG14,TGFB3,TOM1L1,FAXDC2,NPTN,DAB2,CSF1,PLCG2,TERF2IP,BCAR3,CYR61,CDKN1A,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0099003	0.06	0.96	17	151	vesicle-mediated transport in synapse	BP	0.82762	STX11,GRIP1,SH3GL2,UNC13B,PREPL,SYT5,SNAP91,ITSN2,FGF14,PCLO,CLCN3,RAPGEF4,NLGN1,FBXL20,NUMB,CDH2,DNAJC6	darkgreen	VSMC_M4
GO:0061045	0.06	0.98	7	52	negative regulation of wound healing	BP	0.8307	FAM19A5,GJA1,ABCC8,PROS1,EDN1,SERPINE1,PRKG1	darkgreen	VSMC_M4
GO:0016055	0.06	0.96	35	373	Wnt signaling pathway	BP	0.8307	TLE4,GNAQ,MLLT3,KANK1,RECK,TBX18,MDFIC,FZD8,JADE1,NDRG2,AMOTL2,LATS2,TCF7L1,APP,TMEM64,SEMA5A,LRP5,FGFR2,ZRANB1,LRP6,ATP6AP2,IGFBP2,DACT1,CDH2,DAB2,PRKAA2,DAPK3,TLE2,PLCG2,WLS,FRZB,LYPD6,TMEM170B,EDA,YAP1	darkgreen	VSMC_M4
GO:0033500	0.06	0.96	19	184	carbohydrate homeostasis	BP	0.8307	LEP,WFS1,UNC13B,PDK4,FOXO1,ABCC8,HECTD4,PTPN11,HNF4A,BACE2,ABCG1,ADIPOR1,LRP5,SESN2,ADCY5,HIF1A,PPARGC1A,PRKAA2,ICAM1	darkgreen	VSMC_M4
GO:0051223	0.06	0.96	37	412	regulation of protein transport	BP	0.83081	SLC35D3,MDM2,ANGPT1,GJA1,LEP,UNC13B,REST,ICA1,MDFIC,TCAF1,INHBB,ADAM9,ATP2C1,ZDHHC2,ANKRD1,PAM,ABCC8,PTPN11,ATG13,HNF4A,RAB29,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,PTPN14,PRKD1,ACHE,EXPH5,HIF1A,TGFB3,ABLIM3,SH3TC2,FLNA,WLS,BMP6	darkgreen	VSMC_M4
GO:0007628	0.06	0.98	4	20	adult walking behavior	BP	0.83143	OXR1,HIPK2,ABHD12,CHD7	darkgreen	VSMC_M4
GO:0002065	0.06	0.97	8	61	columnar/cuboidal epithelial cell differentiation	BP	0.83238	HNF4A,FGFR2,SERPINE1,HIF1A,CDH2,CDKN1A,YAP1,BMP6	darkgreen	VSMC_M4
GO:0032368	0.07	0.97	11	95	regulation of lipid transport	BP	0.83614	LEP,ABCA1,PTPN11,EDN1,ABCG1,KDM5B,ARV1,CYP19A1,DISP3,BMP6,SCP2	darkgreen	VSMC_M4
GO:0010632	0.07	0.96	21	208	regulation of epithelial cell migration	BP	0.83614	SASH1,ANGPT1,SMOC2,ADGRB1,GATA2,ADAM9,PTPRG,ATOH8,ANXA3,EDN1,SEMA5A,ADIPOR1,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,MAPRE2,PLCG2,CCR6,PIK3C2A	darkgreen	VSMC_M4
GO:0061614	0.07	0.97	7	48	pri-miRNA transcription by RNA polymerase II	BP	0.83687	MRTFA,REST,GATA2,ATOH8,TEAD1,HIF1A,SMAD6	darkgreen	VSMC_M4
GO:0032414	0.07	0.97	10	80	positive regulation of ion transmembrane transporter activity	BP	0.83687	TRDN,TCAF1,KCNE3,ACTN4,FGF14,ABCC8,ACTN2,CTS,AKAP6,PLCG2	darkgreen	VSMC_M4
GO:0006109	0.07	0.96	15	139	regulation of carbohydrate metabolic process	BP	0.84639	EP300,LEP,PDK4,HRH1,PTH,APP,SCARB2,ADIPOR1,SESN2,SLC25A12,HIF1A,PPARGC1A,RORA,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:2000179	0.07	0.98	6	39	positive regulation of neural precursor cell proliferation	BP	0.84639	SMARCD3,LRP2,CTSZ,HIF1A,DISP3,FLNA	darkgreen	VSMC_M4
GO:0198738	0.07	0.95	35	374	cell-cell signaling by wnt	BP	0.84639	TLE4,GNAQ,MLLT3,KANK1,RECK,TBX18,MDFIC,FZD8,JADE1,NDRG2,AMOTL2,LATS2,TCF7L1,APP,TMEM64,SEMA5A,LRP5,FGFR2,ZRANB1,LRP6,ATP6AP2,IGFBP2,DACT1,CDH2,DAB2,PRKAA2,DAPK3,TLE2,PLCG2,WLS,FRZB,LYPD6,TMEM170B,EDA,YAP1	darkgreen	VSMC_M4
GO:0060191	0.07	0.97	8	63	regulation of lipase activity	BP	0.84639	GNAQ,PTH,RGS2,HTR2B,FGFR2,ANGPTL4,SORT1,CYR61	darkgreen	VSMC_M4

GO:1901342	0.07	0.96	23	232	regulation of vasculature development	BP	0.84844	SASH1,FAM19A5,SMOC2,ADGRB1,LEP,RECK,HIPK2,GATA2,COL4A2,CYP1B1,ADM,ABCC8,ANXA3,SEMA5A,PRKCA,PRKD1,HSPB1,SERPINE1,HIF1A,NPPB,ANGPTL7,ANGPTL4,F3	darkgreen	VSMC_M4
GO:0008360	0.07	0.96	15	134	regulation of cell shape	BP	0.84844	FMNL2,CDC42EP3,WASF3,HPN,SHROOM3,PLXNA2,F11R,PLXNB1,RDX,WDR1,MYO10,DAPK3,PLXNB3,ICAM1,MYL12B	darkgreen	VSMC_M4
GO:0030177	0.07	0.96	14	124	positive regulation of Wnt signaling pathway	BP	0.84844	MLLT3,KANK1,RECK,SEMA5A,FGFR2,ZRANB1,ATP6AP2,DACT1,DAB2,DAPK3,WLS,LYPD6,EDA,YAP1	darkgreen	VSMC_M4
GO:0051604	0.07	0.96	21	230	protein maturation	BP	0.84844	MDM2,EP300,WFS1,NAA16,LIPT2,HPN,CHAC1,BACE2,LGMN,CTSS,CTSZ,NCSTN,PRDX4,SERPINE1,C1RL,ATP6AP2,PCSK1N,TMEM59,PCSK4,F3,GLG1	darkgreen	VSMC_M4
GO:0086065	0.07	0.97	7	46	cell communication involved in cardiac conduction	BP	0.84844	GJA1,TRDN,TBX18,CAMK2D,CACNA1C,FLNA,SLC8A1	darkgreen	VSMC_M4
GO:0021517	0.07	0.98	5	31	ventral spinal cord development	BP	0.84844	VLDLR,GATA2,ZC4H2,LMO4,TBX20	darkgreen	VSMC_M4
GO:0046579	0.07	0.97	7	49	positive regulation of Ras protein signal transduction	BP	0.84844	ABRA,ARHGEF3,NGF,F11R,SYNPO2L,MAPRE2,CSF1	darkgreen	VSMC_M4
GO:0009749	0.07	0.96	16	153	response to glucose	BP	0.84844	GJA1,UNC13B,HNF4A,LPL,ABCG1,PFKL,LRP5,TXNIP,SESN2,ADCY5,HIF1A,PPARGC1A,PRKAA2,SLC8A1,ICAM1,MAFA	darkgreen	VSMC_M4
GO:0106056	0.07	0.98	5	31	regulation of calcineurin-mediated signaling	BP	0.84844	LMCD1,RCAN1,AKAP6,PLCG2,C10orf71	darkgreen	VSMC_M4
GO:0043536	0.07	0.97	7	53	positive regulation of blood vessel endothelial cell migration	BP	0.84844	ANGPT1,GATA2,PRKCA,PRKD1,HSPB1,HIF1A,PIK3C2A	darkgreen	VSMC_M4
GO:0046676	0.07	0.98	5	31	negative regulation of insulin secretion	BP	0.84844	REST,INHBB,ABCC8,PTPN11,PFKL	darkgreen	VSMC_M4
GO:0051251	0.07	0.96	18	186	positive regulation of lymphocyte activation	BP	0.84844	BCL2,LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,PTPN11,PTPN22,ADA,CD47,TP53BP1,IGFBP2,LGALS9,VCAM1,VNN1,CD83,CDKN1A	darkgreen	VSMC_M4
GO:0036294	0.07	0.96	14	129	cellular response to decreased oxygen levels	BP	0.84844	BCL2,CITED2,MDM2,HIPK2,ANKRD1,EDN1,CFLAR,HIF1A,PPARGC1A,RORA,SLC8A1,BNIP3,ICAM1,STC2	darkgreen	VSMC_M4
GO:0070302	0.07	0.96	16	151	regulation of stress-activated protein kinase signaling cascade	BP	0.84844	SASH1,TPD52L1,LEP,SH3RF3,MDFIC,HIPK2,FOXO1,RASSF2,HIPK3,SH3RF1,APP,PTPN22,GDF6,MID1,NBR1,DACT1	darkgreen	VSMC_M4
GO:0071526	0.07	0.98	6	38	semaphorin-plexin signaling pathway	BP	0.84844	SEMA3C,SEMA5A,PLXNA2,PLXNB1,PLXNB3,FLNA	darkgreen	VSMC_M4
GO:0014850	0.07	0.98	4	21	response to muscle activity	BP	0.84844	FNDC5,HIF1A,PPARGC1A,PRKAA2	darkgreen	VSMC_M4
GO:0051246	0.07	0.94	150	1953	regulation of protein metabolic process	BP	0.84844	MBP,GDF11,BCL2,RNF41,IFNGR1,SASH1,IRAK3,MDM2,LAPTM4B,RNF19A,OXR1,ANGPT1,C4A,GJA1,TPD52L1,EP300,ADGRB1,DAPK1,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,RIC1,REST,RECK,TGFBR1,PTPN3,MAP3K7,ANTXR1,HIPK2,GATA2,ITM2B,GGA3,INHBB,ITIH5,ADAM9,CRIM1,FOXO1,RASSF2,ANKLE2,FLT3,ZDHHC2,FXYD1,HPN,LATS2,HIPK3,CPEB3,NCK1,SH3RF1,OCLN,RNF34,CLU,APP,ATXN2,PDGFC,PTPN11,PTX3,CCNT1,HERPUD1,PROS1,PTPN22,CHAC1,GDF6,AKTIP,RCAN1,NGF,EDN1,N4BP1,BACE2,ABCG1,RGS2,LRP5,ARRDC4,PLCL1,HTR2B,MST1R,LGMN,AFAP1L2,SESN2,CAMK2D,NGRN,LRP2,CFLAR,CTSZ,INPP5F,RBM4B,PRKD1,NCSTN,DDR2,GPRC5A,MAP3K13,LRP6,HIP1,FAM129A,HSPB1,EIF4A2,SERPINE1,CRYAB,RDX,SECISBP2L,EIF4G3,ATG14,FBXL5,TNFSF10,DACT1,PCSK1N,HIF1A,FBXL20,PPARGC1A,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,DAB2,LGALS9,SKP2,PRKAA2,TMEM59,CTIF,DAPK3,FLNA,CSF1,PLCG2,TERF2IP,F3,GLG1,BCAR3,CYR61,SLC8A1,SPINK2,LOX,ITM2C,CST3,CDKN1A,FGF9,PPM1E,CNTD2,GABARAPL2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:1901653	0.07	0.96	26	270	cellular response to peptide	BP	0.84844	MDM2,GJA1,LEP,KANK1,PDK4,INHBB,FOXO1,FFAR3,NCK1,APP,PTPN11,ADCY6,PTPN22,EDN1,LPL,ADIPOR1,ACTN2,ZNF106,LGMN,CFLAR,WDTC1,AHCYL1,VCAM1,BCAR3,ICAM1,PIK3C2A	darkgreen	VSMC_M4
GO:0001568	0.07	0.95	52	576	blood vessel development	BP	0.84844	CITED2,SASH1,MDM2,ANGPT1,FAM19A5,SMOC2,ADGRB1,LEP,RECK,TGFBR1,CALD1,ANTXR1,HIPK2,GATA2,COL4A1,COL4A2,CYP1B1,SEMA3C,AMOTL2,CHD7,ADM,ABCC8,ANXA3,EDN1,JAM3,SEMA5A,LRP5,PRKCA,SEC24B,MFGE8,MYLK,LRP2,CFLAR,FGFR2,PRKD1,HSPB1,SERPINE1,UNC5B,HIF1A,NPPB,RORA,SMAD6,CDH2,ANGPTL4,FLNA,CDH13,F3,CYR61,LOX,TBX20,PIK3C2A,YAP1	darkgreen	VSMC_M4
GO:0062012	0.07	0.96	23	243	regulation of small molecule metabolic process	BP	0.84847	EP300,LEP,PDK4,REST,HRH1,NCOR2,ADM,PTH,APP,ABCG1,ADIPOR1,SESN2,ARV1,WDTC1,SLC25A12,HIF1A,PPARGC1A,RORA,PRKAA2,ATCAY,MBTPS1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0009791	0.07	0.97	9	68	post-embryonic development	BP	0.84847	BCL2,SCUBE1,TGFBR1,PPP1R13L,SEMA3C,KDM5B,FGFR2,ARID5B,ITPR1	darkgreen	VSMC_M4
GO:0048589	0.07	0.95	46	501	developmental growth	BP	0.84847	BCL2,CITED2,DDR1,GRHL2,GJA1,EP300,SH3GL2,LEP,TGFBR1,ITSN2,PPP1R13L,TENM4,SEMA3C,CHD7,LATS2,SORBS2,ADM,WWC2,APP,PTPN11,PTX3,CPQ,NGF,EDN1,SEMA5A,KDM5B,RGS2,LGMN,SHTN1,CFLAR,WDTC1,FGFR2,RAPH1,ARID5B,AKAP6,DDR2,MAP3K13,MAEL,SGCA,SLIT3,ULK2,CSF1,TBX20,CDKN1A,HOPX,YAP1	darkgreen	VSMC_M4
GO:0010942	0.07	0.95	40	470	positive regulation of cell death	BP	0.84916	SOD2,TPD52L1,DAPK1,LEP,UNC13B,CD274,REST,TGFBR1,INHBB,FOXO1,RASSF2,CYP1B1,LATS2,ANKRD1,NCK1,ADM,CLU,JMY,SERINC3,ZMAT3,TXNIP,CAMK2D,CTSZ,ITGA6,ATF6,ID3,TNFSF10,PPARGC1A,TGFB3,PAK3,LGALS9,DAPK3,SORT1,CYR61,BNIP3,FRZB,ITM2C,CDKN1A,NACC2,DDIT4	darkgreen	VSMC_M4
GO:0045668	0.07	0.97	6	41	negative regulation of osteoblast differentiation	BP	0.84916	CRIM1,TMEM64,LRP5,ID3,NBR1,SMAD6	darkgreen	VSMC_M4
GO:0051495	0.07	0.96	20	194	positive regulation of cytoskeleton organization	BP	0.85177	LIMCH1,TGFBR1,CDC42EP3,WASF3,NCK1,OCLN,JMY,EDN1,CD47,SEMA5A,ACTN2,SYNPO2,SYNPO2L,WDR1,TGFB3,SYNPO,FLNA,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0021762	0.07	0.98	5	35	substantia nigra development	BP	0.85279	MBP,NDRG2,GNB4,MAOB,FGF9	darkgreen	VSMC_M4
GO:0031638	0.07	0.98	5	38	zymogen activation	BP	0.85279	HPN,LGMN,CTSZ,SERPINE1,C1RL	darkgreen	VSMC_M4
GO:0051865	0.07	0.97	8	62	protein autoubiquitination	BP	0.85279	RNF41,SASH1,MDM2,SH3RF3,MARCH5,RNF141,SH3RF1,LRSAM1	darkgreen	VSMC_M4

GO:0016310	0.07	0.94	117	1440	phosphorylation	BP	0.85279	GDF11,BCL2,SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,EP300,DAPK1,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,PIP5K1B,VLDLR,PPP1R9A,PDK4,ZAP70,TGFBR1,MAP3K7,EPHB6,MAP3K8,HIPK2,SNRK,TESK2,INHBB,PFKFB3,ADAM9,RASSF2,ANKLE2,TF,FLT3,MAP3K1,LATS2,HIPK3,NCK1,GRK7,OCLN,CDKL2,CLU,APP,PDGFC,PTPN11,NEK4,CCNT1,PTPN22,GDF6,AKTIP,RBL2,NGF,EDN1,RGS2,PFKL,LRP5,PLCL1,HTR2B,MST1R,PRKCA,AFAP1L2,SESN2,CAMK2D,MYLK,INPP5F,FGFR2,PRKD1,PI4KB,PIP5K1,ITGA6,DDR2,GPRC5A,MAP3K13,LRP6,PRDX4,FAM129A,HSPB1,ENO2,ATG14,LMTK2,SPEG,HIF1A,PPARGC1A,NEK9,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,AK7,NPTN,NRK,ULK2,PAK3,DAB2,PRKAA2,DAPK3,PNCK,CSF1,PLCG2,TERF2IP,BCAR3,CDC7,LMO4,CYR61,AK5,SLC8A1,LOX,SRPK3,CDKN1A,FGF9,PPM1E,RFK,CNTD2,ICAM1,PIK3C2A,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0110148	0.07	0.96	14	127	biomineralization	BP	0.85279	LEP,FOXO1,FBLN7,PTH,FGFR2,DDR2,NBR1,HIF1A,TGFB3,CYR61,SLC8A1,LOX,BMP6,FAM83H	darkgreen	VSMC_M4
GO:0071453	0.07	0.96	15	142	cellular response to oxygen levels	BP	0.85299	BCL2,CITED2,MDM2,HIPK2,FOXO1,ANKRD1,EDN1,CFLAR,HIF1A,PPARGC1A,RORA,SLC8A1,BNIP3,ICAM1,STC2	darkgreen	VSMC_M4
GO:0014910	0.07	0.97	8	60	regulation of smooth muscle cell migration	BP	0.8538	BCL2,MDM2,FAM19A5,DOCK4,SERPINE1,PPARGC1A,FGF9,PRKG1	darkgreen	VSMC_M4
GO:0002718	0.07	0.97	8	63	regulation of cytokine production involved in immune response	BP	0.8538	IRAK3,ANGPT1,DDX58,IL18R1,MAP3K7,FFAR3,TGFB3,PLCG2	darkgreen	VSMC_M4
GO:1904659	0.07	0.97	10	80	glucose transmembrane transport	BP	0.85521	LEP,SLC2A1,OCLN,PTH,PTPN11,EDN1,SESN2,OPN3,SLC2A5,SORT1	darkgreen	VSMC_M4
GO:0033137	0.07	0.98	4	25	negative regulation of peptidyl-serine phosphorylation	BP	0.85542	RASSF2,NCK1,INPP5F,DDIT4	darkgreen	VSMC_M4
GO:0046058	0.07	0.98	4	19	cAMP metabolic process	BP	0.85566	PTH,ADCY6,ADCY5,ADCY9	darkgreen	VSMC_M4
GO:0033627	0.07	0.97	8	60	cell adhesion mediated by integrin	BP	0.85679	ADAM9,CYP1B1,PTPN11,ADA,JAM3,NPNT,SERPINE1,ICAM1	darkgreen	VSMC_M4
GO:1901135	0.07	0.94	63	791	carbohydrate derivative metabolic process	BP	0.85679	DSEL,BCL2,PIGN,UST,ANGPT1,EP300,LEP,PDK4,NT5C3A,HS6ST1,ITM2B,ITIH5,PFKFB3,STT3B,SUMF1,TUSC3,ST3GAL5,CHST2,PTH,EXTL3,APP,PTX3,ADCY6,DPY19L4,ADA,MARCH6,BACE2,NT5C2,PFKL,B3GNT7,GALNT3,B3GALNT2,TPST2,ADCY5,MAN2A2,NDST3,NCSTN,CHST15,SLC25A12,PDE1A,ENO2,FUT11,HIF1A,PPARGC1A,NPPB,RORA,PIGG,MAGT1,GALNT10,PIGS,PRKAA2,TMEM59,BGN,ADCY9,EXTL2,AK5,ST6GALNAC3,FBXO27,ITM2C,CST3,PIGK,RFK,DDIT4	darkgreen	VSMC_M4
GO:0008585	0.07	0.97	9	72	female gonad development	BP	0.85987	BCL2,LEP,INHBB,PTX3,ARID5B,CYP19A1,SLIT3,FST,ICAM1	darkgreen	VSMC_M4
GO:0090263	0.07	0.96	11	92	positive regulation of canonical Wnt signaling pathway	BP	0.86637	KANK1,RECK,SEMA5A,FGFR2,ATP6AP2,DACT1,DAPK3,WLS,LYPD6,EDA,YAP1	darkgreen	VSMC_M4
GO:0070527	0.07	0.97	7	51	platelet aggregation	BP	0.86637	MYL9,PRKCA,F11R,HSPB1,FLNA,CSRP1,PRKG1	darkgreen	VSMC_M4
GO:0001933	0.07	0.95	26	276	negative regulation of protein phosphorylation	BP	0.86637	IRAK3,ANGPT1,SH3GL2,GNAQ,CDKN2B,RASSF2,LATS2,HIPK3,NCK1,OCLN,PTPN22,RGS2,LRP5,INPP5F,GPRC5A,LRP6,FAM129A,HSPB1,ATG14,PPARGC1A,SMAD6,TERF2IP,SLC8A1,CDKN1A,PPM1E,DDIT4	darkgreen	VSMC_M4
GO:1902042	0.07	0.98	4	26	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	0.86651	RNF34,CFLAR,SERPINE1,ICAM1	darkgreen	VSMC_M4
GO:0030166	0.07	0.97	7	49	proteoglycan biosynthetic process	BP	0.86651	DSEL,UST,HS6ST1,EXTL3,NDST3,CHST15,EXTL2	darkgreen	VSMC_M4
GO:0050867	0.07	0.95	21	226	positive regulation of cell activation	BP	0.86651	BCL2,LEP,DOCK8,CD274,ZAP70,MAP3K8,GATA2,NCK1,PTPN11,LBP,PTPN22,ADA,CD47,TP53BP1,IGFBP2,LGALS9,VAMP7,VCAM1,VNN1,CD83,CDKN1A	darkgreen	VSMC_M4
GO:0003229	0.07	0.97	7	47	ventricular cardiac muscle tissue development	BP	0.86651	TGFBR1,PPP1R13L,CHD7,TNNT2,LRP2,FGFR2,HOPX	darkgreen	VSMC_M4
GO:0070231	0.07	0.98	5	36	T cell apoptotic process	BP	0.86651	DOCK8,CD274,ADA,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0110151	0.07	0.97	6	42	positive regulation of biomineralization	BP	0.86651	FBLN7,PTH,TGFB3,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:0046688	0.08	0.98	4	26	response to copper ion	BP	0.86651	MAP1LC3A,PAM,APP,ICAM1	darkgreen	VSMC_M4
GO:0001895	0.08	0.97	6	43	retina homeostasis	BP	0.86651	SLC2A1,TF,CLCN3,HSPB1,BBS4,ABCA4	darkgreen	VSMC_M4
GO:1903035	0.08	0.97	8	64	negative regulation of response to wounding	BP	0.86651	FAM19A5,GJA1,ABCC8,PROS1,EDN1,INPP5F,SERPINE1,PRKG1	darkgreen	VSMC_M4
GO:0002367	0.08	0.97	8	64	cytokine production involved in immune response	BP	0.86651	IRAK3,ANGPT1,DDX58,IL18R1,MAP3K7,FFAR3,TGFB3,PLCG2	darkgreen	VSMC_M4
GO:2000114	0.08	0.98	4	21	regulation of establishment of cell polarity	BP	0.86651	DOCK8,KANK1,RIPOR2,SHTN1	darkgreen	VSMC_M4
GO:0005975	0.08	0.95	39	458	carbohydrate metabolic process	BP	0.86651	EP300,LEP,CASD1,PDK4,SLC2A1,GYS1,HRH1,PFKFB3,GALM,ST3GAL5,CHST2,PTH,GYG1,APP,SCARB2,HECTD4,ADIPOR1,PFKL,LRP5,B3GNT7,GYG2,SIAE,GALNT3,SESN2,WDTC1,MAN2A2,NDST3,CHST15,SLC25A12,PPIP5K1,ENO2,HIF1A,PPARGC1A,RORA,OCRL,PRKAA2,SLC2A5,ST6GALNAC3,DDIT4	darkgreen	VSMC_M4
GO:0003014	0.08	0.97	9	74	renal system process	BP	0.86651	BCL2,GJA1,WFS1,ADM,ADCY6,EDN1,LGMN,NPPB,NPR3	darkgreen	VSMC_M4
GO:1903510	0.08	0.97	9	71	mucopolysaccharide metabolic process	BP	0.86651	DSEL,UST,ANGPT1,ITIH5,CHST2,B3GNT7,NDST3,CHST15,BGN	darkgreen	VSMC_M4
GO:0035637	0.08	0.96	14	114	multicellular organismal signaling	BP	0.86651	GJA1,TRDN,TBX18,KCNE3,SCN8A,JAM3,NFASC,CAMK2D,ABCC9,CACNA1C,FLNA,KCNE4,SLC8A1,PLN	darkgreen	VSMC_M4
GO:0018126	0.08	0.98	4	26	protein hydroxylation	BP	0.86651	P4HTM,PRDX4,P4HA1,PLOD1	darkgreen	VSMC_M4
GO:0043618	0.08	0.97	6	43	regulation of transcription from RNA polymerase II promoter in response to stress	BP	0.86651	CITED2,NCK1,CHD6,SESN2,ATF6,HIF1A	darkgreen	VSMC_M4
GO:0055023	0.08	0.98	5	31	positive regulation of cardiac muscle tissue growth	BP	0.86651	EDN1,FGFR2,AKAP6,TBX20,YAP1	darkgreen	VSMC_M4

GO:0009892	0.08	0.94	173	2254	negative regulation of metabolic process	BP	0.86651	BCL2,CITED2,IRAK3,MDM2,LAPTM4B,OXR1,ANGPT1,C4A,TRPS1,GJA1,ZHX1,EP300,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,CD274,RIC1,IL18R1,ZNF169,REST,RECK,PTPN3,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,INHBB,ITIH5,LBH,NDRG2,LMCD1,THRB,SATB1,CRIM1,FOXO1,RASSF2,ANKLE2,MIER3,NCOR2,FXYD1,ZC3H6,LATS2,HIPK3,ANKRD1,CPEB3,NCK1,SH3RF1,ATOH8,OCLN,WWC2,FAM172A,PTH,RNF34,CLU,MEIS2,APP,ATXN2,PTX3,LBP,CCNT1,HERPUD1,PROS1,PTPN22,HNF4A,CHAC1,NAB1,RBL2,NGF,EDN1,ETS2,N4BP1,BACE2,KDM5B,RGS2,MXI1,LRP5,FEZ1,PLCL1,HTR2B,LGMN,PRKCA,TXNIP,HELZ,SESN2,YEATS2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,TP53BP1,QSOX1,SLC25A12,STRN3,ARID5B,GPRC5A,ID3,LRP6,FAM129A,HSPB1,EIF4A2,CUX1,SERPINE1,CRYAB,EZH1,ATG14,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,OPN3,ZBTB18,APBB2,PPP1R36,ZBTB4,PPARGC1A,CHD3,SLIT3,TGFB3,SMAD6,NPTN,FST,DAB2,LGALS9,MARF1,NPR3,PRKAA2,TMEM59,CTIF,ATCAY,DAPK3,TLE2,FLNA,PPP1R26,TERF2IP,GLG1,ZFP90,MIR99A,MIR331,SLC8A1,SPINK2,BNIP3,ADAMTS5,CD83,TBX20,ITM2C,CST3,ZNF425,ZNF175,CDKN1A,ZNF572,PPM1E,NACC2,ZNF79,HOPX,GABARAPL2,ORMDL3,STC2,YAP1,HKR1,BMP6,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:2000146	0.08	0.95	23	234	negative regulation of cell motility	BP	0.86661	BCL2,RNF41,CITED2,FAM19A5,GJA1,ADGRB1,LIMCH1,KANK1,RECK,TCAF1,LRCH1,CYP1B1,PTPRG,MCTP1,ABCC8,ADA,ADIPOR1,RIPOR2,SERPINE1,PPARGC1A,MMP28,PLXNB3,PRKG1	darkgreen	VSMC_M4
GO:0060055	0.08	0.98	4	24	angiogenesis involved in wound healing	BP	0.86725	FAM19A5,SMOC2,GATA2,SERPINE1	darkgreen	VSMC_M4
GO:0006090	0.08	0.96	9	76	pyruvate metabolic process	BP	0.86725	EP300,PDK4,APP,PFKL,ENO2,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0035025	0.08	0.98	4	22	positive regulation of Rho protein signal transduction	BP	0.86964	ABRA,ARHGEF3,F11R,SYNPO2L	darkgreen	VSMC_M4
GO:0009584	0.08	0.98	4	25	detection of visible light	BP	0.87537	GNAQ,GRK7,OPN3,ABCA4	darkgreen	VSMC_M4
GO:0010927	0.08	0.96	11	87	cellular component assembly involved in morphogenesis	BP	0.87537	TENM4,ANKRD1,EDN1,TNNT2,ACTN2,CFLAR,SYNPO2L,WDR1,CCDC136,SPINK2,CSRP1	darkgreen	VSMC_M4
GO:0097191	0.08	0.95	17	173	extrinsic apoptotic signaling pathway	BP	0.87537	BCL2,RNF41,TGFBR1,SH3RF1,RNF34,NGF,EYA2,CFLAR,ITGA6,SERPINE1,UNC5B,TNFSF10,DAPK3,SORT1,ITM2C,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0045807	0.08	0.96	10	82	positive regulation of endocytosis	BP	0.87537	ANGPT1,GATA2,TF,CLU,HIP1,SERPINE1,NLGN1,DAB2,PLCG2,CD151	darkgreen	VSMC_M4
GO:0003151	0.08	0.97	8	59	outflow tract morphogenesis	BP	0.87537	CITED2,SEMA3C,SEC24B,LRP2,FGFR2,HIF1A,SMAD6,TBX20	darkgreen	VSMC_M4
GO:0007033	0.08	0.96	16	157	vacuole organization	BP	0.87537	LAPTM4B,ABCA1,MAP1LC3A,SCARB2,ATG13,AKTIP,FEZ1,SYNPO2,GABARAPL1,ATP6AP2,ATG14,ULK2,MAP1LC3B2,MBTPS1,LRSAM1,GABARAPL2	darkgreen	VSMC_M4
GO:0030595	0.08	0.96	15	150	leukocyte chemotaxis	BP	0.87537	CREB3,EDN2,HRH1,LBP,EDN1,JAM3,RIPOR2,PREX1,LGMN,SERPINE1,ADGRE2,MMP28,LGALS9,CSF1,CCR6	darkgreen	VSMC_M4
GO:0060324	0.08	0.97	6	40	face development	BP	0.87539	GRHL2,EP300,CHD7,PTPN11,ARID5B,TGFB3	darkgreen	VSMC_M4
GO:0071549	0.08	0.98	4	24	cellular response to dexamethasone stimulus	BP	0.87539	FOXO1,CFLAR,ICAM1,DDIT4	darkgreen	VSMC_M4
GO:0090659	0.08	0.98	4	21	walking behavior	BP	0.87539	OXR1,HIPK2,ABHD12,CHD7	darkgreen	VSMC_M4
GO:0032733	0.08	0.98	4	25	positive regulation of interleukin-10 production	BP	0.87539	CD274,LGALS9,PLCG2,CD83	darkgreen	VSMC_M4
GO:0046651	0.08	0.95	17	177	lymphocyte proliferation	BP	0.87539	BCL2,LEP,DOCK8,CD274,ZAP70,FLT3,NCK1,CD180,SH3RF1,PTPN22,ADA,NCSTN,IGFBP2,LGALS9,VCAM1,CD151,CDKN1A	darkgreen	VSMC_M4
GO:0010660	0.08	0.97	7	57	regulation of muscle cell apoptotic process	BP	0.87539	SOD2,EDN1,CAMK2D,CFLAR,LRP6,PDE1A,BNIP3	darkgreen	VSMC_M4
GO:0042127	0.08	0.94	97	1230	regulation of cell population proliferation	BP	0.87539	BCL2,RNF41,CITED2,MDM2,DDR1,SOD2,ANGPT1,FAM19A5,GJA1,ADGRB1,LEP,CDKN2B,C2orf40,CD274,REST,IGFBP7,ZAP70,TGFBR1,EDN2,HIPK2,GATA2,LIMS2,SMARCD3,FOSL2,LBH,NDRG2,CYP1B1,FLT3,HPN,NCK1,ADM,SH3RF1,ATOH8,PTH,CLU,MEIS2,APP,PDGFC,ABCC8,PTPN22,HNF4A,ADA,NGF,EDN1,CD47,SEMA5A,KDM5B,MARCKSL1,LRP5,HTR2B,MST1R,LGMN,PRKCA,TXNIP,LRP2,CFLAR,CTSZ,FGFR2,PTPN14,PRKD1,PLXNB1,DDR2,LRP6,PRDX4,PDE1A,IGFBP2,SPEG,HIF1A,CCPG1,PPARGC1A,DISP3,FGFRL1,SLIT3,TGFB3,CNN1,SMAD6,CDH2,LGALS9,SKP2,NPR3,PLXNB3,FLNA,CSF1,CDH13,VCAM1,F3,CDC7,CYR61,DNAJA2,FRZB,TBX20,CDKN1A,FGF9,NACC2,YAP1,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0048639	0.08	0.96	15	134	positive regulation of developmental growth	BP	0.87539	BCL2,LEP,ITSN2,CHD7,NGF,EDN1,SEMA5A,SHTN1,FGFR2,AKAP6,MAP3K13,CSF1,TBX20,HOPX,YAP1	darkgreen	VSMC_M4
GO:1904646	0.08	0.97	5	34	cellular response to amyloid-beta	BP	0.87539	GJA1,APP,LGMN,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:0018209	0.08	0.95	26	267	peptidyl-serine modification	BP	0.87669	BCL2,ANGPT1,TGFBR1,HIPK2,RASSF2,LATS2,HIPK3,NCK1,APP,NGF,PLCL1,GALNT3,PRKCA,CAMK2D,INPP5F,PRKD1,MAP3K13,LMTK2,ULK2,PRKAA2,BGN,PNCK,TERF2IP,BCAR3,CDC7,DDIT4	darkgreen	VSMC_M4
GO:0006622	0.08	0.98	4	22	protein targeting to lysosome	BP	0.87812	GGA3,CLU,SCARB2,SORT1	darkgreen	VSMC_M4
GO:0008037	0.08	0.96	11	97	cell recognition	BP	0.87812	ADGRB1,DOCK8,APP,PTX3,LBP,SEMA5A,ROBO3,MFGE8,NPTN,PCSK4,NEXN	darkgreen	VSMC_M4
GO:0044319	0.08	0.97	5	30	wound healing, spreading of cells	BP	0.87867	DDR1,MRTFA,FLNA,CYR61,CD151	darkgreen	VSMC_M4
GO:0090505	0.08	0.97	5	30	epiboly involved in wound healing	BP	0.87867	DDR1,MRTFA,FLNA,CYR61,CD151	darkgreen	VSMC_M4
GO:0072577	0.08	0.97	6	43	endothelial cell apoptotic process	BP	0.88111	ANGPT1,GATA2,SEMA5A,SERPINE1,ANGPTL4,ICAM1	darkgreen	VSMC_M4
GO:0007605	0.08	0.96	12	102	sensory perception of sound	BP	0.88173	MBP,WFS1,THRB,HPN,CHD7,SCARB2,PDZD7,RIPOR2,LRP2,USP53,WDR1,ICAM1	darkgreen	VSMC_M4
GO:0051093	0.08	0.94	58	676	negative regulation of developmental process	BP	0.88264	BCL2,CITED2,GRHL2,FAM19A5,GJA1,ADGRB1,LEP,KANK1,REST,TGFBR1,ABCA1,GATA2,TPT1,LBH,ACTN4,CRIM1,FOXO1,COL4A2,SEMA3C,TMEM178A,HPN,MARCH5,WWC2,PTH,MEIS2,APP,ABCC8,PTPN11,TMEM64,SEMA5A,ABCG1,ADIPOR1,RGS2,LRP5,LGMN,CFLAR,INPP5F,ID3,SERPINE1,NBR1,NLGN1,HIF1A,PPARGC1A,NPPB,DISP3,ANGPTL7,RORA,SMAD6,ULK2,FST,SORT1,BNIP3,FRZB,CST3,CDKN1A,FGF9,HOPX,YAP1	darkgreen	VSMC_M4
GO:0014912	0.08	0.98	4	24	negative regulation of smooth muscle cell migration	BP	0.88377	FAM19A5,SERPINE1,PPARGC1A,PRKG1	darkgreen	VSMC_M4
GO:0016052	0.08	0.96	12	113	carbohydrate catabolic process	BP	0.88418	EP300,GALM,APP,SCARB2,PFKL,LRP5,SLC25A12,ENO2,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4

GO:0035019	0.08	0.97	5	32	somatic stem cell population maintenance	BP	0.88677	REST,GATA2,LBH,LRP5,YAP1	darkgreen	VSMC_M4
GO:0046890	0.08	0.96	13	127	regulation of lipid biosynthetic process	BP	0.88768	LEP,PDK4,REST,IGFBP7,ADM,ABCG1,HTR2B,WDTC1,PPARGC1A,MBTPS1,CYR61,ORMDL3,BMP6	darkgreen	VSMC_M4
GO:0006941	0.08	0.95	14	128	striated muscle contraction	BP	0.88785	GJA1,PPP1R13L,KCNE3,RGS2,TNNT2,CAMK2D,CACNA1C,ADRA1B,FLNA,CCDC78,KCNE4,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0046427	0.08	0.98	4	24	positive regulation of receptor signaling pathway via JAK-STAT	BP	0.88785	LEP,CYP1B1,ADIPOR1,CRLF3	darkgreen	VSMC_M4
GO:0043304	0.08	0.98	4	24	regulation of mast cell degranulation	BP	0.89277	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0007162	0.08	0.95	21	215	negative regulation of cell adhesion	BP	0.89357	MBP,CDSN,ANGPT1,KANK1,CD274,ACTN4,CYP1B1,PTPN11,PTPN22,JAM3,SEMA5A,RIPOR2,PLXNA2,PLXNB1,SERPINE1,RDX,LGALS9,PLXNB3,CDH13,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0030500	0.08	0.96	8	62	regulation of bone mineralization	BP	0.89453	PTH,DDR2,NBR1,HIF1A,TGFB3,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:0006809	0.08	0.97	7	55	nitric oxide biosynthetic process	BP	0.89453	CYP1B1,CLU,PTX3,EDN1,CD47,RORA,ICAM1	darkgreen	VSMC_M4
GO:0003181	0.08	0.98	4	22	atrioventricular valve morphogenesis	BP	0.89453	MDM2,SLIT3,SMAD6,CYR61	darkgreen	VSMC_M4
GO:0055008	0.08	0.97	7	50	cardiac muscle tissue morphogenesis	BP	0.89831	TGFBR1,CHD7,ANKRD1,TNNT2,LRP2,FGFR2,TBX20	darkgreen	VSMC_M4
GO:0034097	0.08	0.94	54	659	response to cytokine	BP	0.9017	BCL2,IFNGR1,IRAK3,ANGPT1,DAPK1,TLE4,LEP,DDX58,DOCK8,CD274,IL18R1,EDN2,ABCA1,MAP3K7,LRCH1,MRC1,ACTN4,ADAM9,FLT3,ANKRD1,OCLN,APP,PTPN11,IFIT1,EDN1,CD47,MX1,ADIPOR1,KDM5B,RIPOR2,NPNT,MST1R,PRKCA,TRIM63,ARID5B,AKAP6,EIF4A2,HIF1A,PPARGC1A,RORA,CALCOCO2,SLIT3,BBS4,LGALS9,DAPK3,CSF1,VCAM1,F3,MIR99A,AFF3,LOX,CCR6,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0007029	0.09	0.96	9	80	endoplasmic reticulum organization	BP	0.90878	TRDN,LMAN2L,TMCC1,ESYT3,SHTN1,LNPK,EMC1,TMEM38A,REEP3	darkgreen	VSMC_M4
GO:1990000	0.09	0.98	4	26	amyloid fibril formation	BP	0.90885	MDM2,CLU,APP,CRYAB	darkgreen	VSMC_M4
GO:1901137	0.09	0.94	41	494	carbohydrate derivative biosynthetic process	BP	0.90885	DSEL,BCL2,PIGN,UST,ANGPT1,PDK4,HS6ST1,ITM2B,STT3B,TUSC3,ST3GAL5,CHST2,EXTL3,ADCY6,DPY19L4,ADA,BACE2,B3GNT7,GALNT3,B3GALNT2,ADCY5,MAN2A2,NDST3,NCSTN,CHST15,SLC25A12,FUT11,PPARGC1A,NPPB,PIGG,MAGT1,GALNT10,PIGS,TMEM59,ADCY9,EXTL2,AK5,ST6GALNAC3,ITM2C,PIGK,RFK	darkgreen	VSMC_M4
GO:0048333	0.09	0.98	4	23	mesodermal cell differentiation	BP	0.90885	GJA1,ITGA8,EYA2,FGFR2	darkgreen	VSMC_M4
GO:0008645	0.09	0.96	10	83	hexose transmembrane transport	BP	0.90885	LEP,SLC2A1,OCLN,PTH,PTPN11,EDN1,SESN2,OPN3,SLC2A5,SORT1	darkgreen	VSMC_M4
GO:0048015	0.09	0.95	15	133	phosphatidylinositol-mediated signaling	BP	0.90885	ANGPT1,LEP,PIP5K1B,PLCB4,FLT3,PDGFC,EDN1,PLCL1,HTR2B,INPP5F,PI4KB,PLXNB1,UNC5B,NPR3,PIK3C2A	darkgreen	VSMC_M4
GO:0045778	0.09	0.97	6	42	positive regulation of ossification	BP	0.91534	PTH,PTPN11,TGFB3,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:1901615	0.09	0.94	33	382	organic hydroxy compound metabolic process	BP	0.91534	BCL2,HSD17B6,LEP,VLDLR,REST,ABCA1,HRH1,CYP1B1,HPN,PTH,APP,CPQ,ABCG1,LRP5,LGMN,ARV1,LRP2,SLC25A12,PPIP5K1,MAOA,MAOB,CYP19A1,HIF1A,OPN3,DISP3,FAXDC2,OCRL,PRKAA2,MBTPS1,PLCG2,SLC27A5,BMP6,SCP2	darkgreen	VSMC_M4
GO:0071241	0.09	0.95	17	165	cellular response to inorganic substance	BP	0.91613	SYT5,FOXO1,CPNE4,TF,MAP1LC3A,APP,EDN1,LGMN,CAMK2D,CFLAR,NCSTN,NLGN1,PPARGC1A,PRKAA2,PLCG2,BNIP3,BMP6	darkgreen	VSMC_M4
GO:0009135	0.09	0.96	9	78	purine nucleoside diphosphate metabolic process	BP	0.91631	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0009179	0.09	0.96	9	78	purine ribonucleoside diphosphate metabolic process	BP	0.91631	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0019320	0.09	0.97	4	25	hexose catabolic process	BP	0.91996	GALM,PFKL,LRP5,SLC25A12	darkgreen	VSMC_M4
GO:0042771	0.09	0.97	5	34	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	BP	0.91996	BCL2,EP300,HIPK2,CDKN1A,DDIT4	darkgreen	VSMC_M4
GO:0032411	0.09	0.96	10	85	positive regulation of transporter activity	BP	0.91996	TRDN,TCAF1,KCNE3,ACTN4,FGF14,ABCC8,ACTN2,CTS5,AKAP6,PLCG2	darkgreen	VSMC_M4
GO:0007566	0.09	0.97	5	36	embryo implantation	BP	0.92016	DDR1,GJA1,RECK,IGFBP7,STC2	darkgreen	VSMC_M4
GO:0008286	0.09	0.96	11	93	insulin receptor signaling pathway	BP	0.92016	LEP,KANK1,PDK4,FOXO1,FFAR3,NCK1,PTPN11,ADIPOR1,ZNF106,BCAR3,PIK3C2A	darkgreen	VSMC_M4
GO:1901184	0.09	0.96	8	67	regulation of ERBB signaling pathway	BP	0.92016	PTPN3,LGMN,AFAP1L2,GPRC5A,HIP1,SH3TC2,CDH13,BCAR3	darkgreen	VSMC_M4
GO:0007179	0.09	0.95	17	156	transforming growth factor beta receptor signaling pathway	BP	0.92016	CITED2,EP300,CDKN2B,RASL11B,TGFBR1,MAP3K7,HIPK2,ADAM9,LATS2,FMOD,NPNT,TGFB3,SMAD6,DAB2,GLG1,ADAMTSL2,LOX	darkgreen	VSMC_M4
GO:0030282	0.09	0.95	11	97	bone mineralization	BP	0.92016	LEP,PTH,FGFR2,DDR2,NBR1,HIF1A,TGFB3,CYR61,SLC8A1,LOX,BMP6	darkgreen	VSMC_M4
GO:0071248	0.09	0.95	15	141	cellular response to metal ion	BP	0.92016	SYT5,CPNE4,TF,MAP1LC3A,APP,EDN1,LGMN,CAMK2D,NCSTN,NLGN1,PPARGC1A,PRKAA2,PLCG2,BNIP3,BMP6	darkgreen	VSMC_M4
GO:0046545	0.09	0.96	9	75	development of primary female sexual characteristics	BP	0.92016	BCL2,LEP,INHBB,PTX3,ARID5B,CYP19A1,SLIT3,FST,ICAM1	darkgreen	VSMC_M4
GO:0045927	0.09	0.94	20	199	positive regulation of growth	BP	0.92016	BCL2,LEP,WFS1,FAM122A,TGFBR1,ITSN2,HPN,CHD7,EXTL3,NGF,EDN1,SEMA5A,SHTN1,FGFR2,AKAP6,MAP3K13,CSF1,TBX20,HOPX,YAP1	darkgreen	VSMC_M4
GO:0040013	0.09	0.94	25	261	negative regulation of locomotion	BP	0.92051	BCL2,RNF41,CITED2,FAM19A5,GJA1,ADGRB1,LIMCH1,KANK1,RECK,TCAF1,LRCH1,CYP1B1,SEMA3C,PTPRG,MCTP1,ABCC8,ADA,SEMA5A,ADIPOR1,RIPOR2,SERPINE1,PPARGC1A,MMP28,PLXNB3,PRKG1	darkgreen	VSMC_M4
GO:0019933	0.09	0.97	6	40	cAMP-mediated signaling	BP	0.92051	PCLO,ADM,RGS2,RAPGEF4,AKAP6,GNAI1	darkgreen	VSMC_M4
GO:1903426	0.09	0.97	5	37	regulation of reactive oxygen species biosynthetic process	BP	0.92159	SOD2,ADGRB1,CLCN3,CFLAR,PLCG2	darkgreen	VSMC_M4
GO:0022604	0.09	0.94	26	261	regulation of cell morphogenesis	BP	0.92221	GRIP1,KANK1,ITSN2,LIMS2,ACTN4,FMNL2,CDC42EP3,WASF3,HPN,SHROOM3,PREX1,PLXNA2,F11R,PLXNB1,ZRANB1,MAP3K13,CUX1,RDX,WDR1,PAK3,MYO10,DAPK3,PLXNB3,FLNA,ICAM1,MYL12B	darkgreen	VSMC_M4
GO:0090022	0.09	0.97	4	27	regulation of neutrophil chemotaxis	BP	0.92229	LBP,EDN1,JAM3,RIPOR2	darkgreen	VSMC_M4
GO:0008406	0.09	0.95	17	166	gonad development	BP	0.92229	BCL2,CITED2,LEP,TGFBR1,INHBB,PTX3,LRP2,ARID5B,PRDX4,CYP19A1,TNFSF10,TEX11,SLIT3,FST,FLNA,FGF9,ICAM1	darkgreen	VSMC_M4
GO:0030219	0.09	0.97	6	44	megakaryocyte differentiation	BP	0.92229	EP300,CDKN2B,GATA2,PTPN11,FAXDC2,LOX	darkgreen	VSMC_M4
GO:0000045	0.09	0.96	10	88	autophagosome assembly	BP	0.92266	MAP1LC3A,ATG13,FEZ1,SYNPO2,GABARAPL1,ATG14,ULK2,MAP1LC3B2,LRSAM1,GABARAPL2	darkgreen	VSMC_M4
GO:0043542	0.09	0.94	19	195	endothelial cell migration	BP	0.9233	SASH1,ANGPT1,SMOC2,ADGRB1,TGFBR1,GATA2,CYP1B1,ATOH8,ANXA3,EDN1,SEMA5A,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,PLEKHG5,CDH13,PIK3C2A	darkgreen	VSMC_M4

GO:0034766	0.09	0.96	8	68	negative regulation of ion transmembrane transport	BP	0.9233	TRDN,KCNE3,RGS2,ACTN2,CAMK2D,SLC43A2,KCNE4,PLN	darkgreen	VSMC_M4
GO:0051172	0.09	0.92	137	1770	negative regulation of nitrogen compound metabolic process	BP	0.92433	CITED2,IRAK3,MDM2,LAPTM4B,OXR1,ANGPT1,C4A,TRPS1,GJA1,ZHX1,EP300,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,RIC1,ZNF169,REST,RECK,PTPN3,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,INHBB,ITIH5,LBH,LMCD1,THRB,SATB1,CRIM1,FOXO1,RASSF2,MIER3,NCOR2,FXYD1,ZC3H6,LATS2,HIPK3,ANKRD1,CPEB3,NCK1,SH3RF1,ATOH8,OCLN,WWC2,RNF34,CLU,MEIS2,APP,PTX3,CCNT1,HERPUD1,PROS1,PTPN22,HNF4A,CHAC1,NAB1,NGF,EDN1,ETS2,N4BP1,BACE2,KDM5B,RGS2,MXI1,LRP5,TXNIP,SESN2,YEATS2,CTSZ,WDTC1,INPP5F,FGFR2,TP53BP1,STRN3,ARID5B,GPRC5A,ID3,LRP6,FAM129A,HSPB1,EIF4A2,CUX1,SERPINE1,CRYAB,EZH1,ATG14,DACT1,MAEL,SIN3B,PCSK1N,ZBTB18,APBB2,ZBTB4,PPARGC1A,CHD3,SMAD6,FST,DAB2,PRKAA2,TMEM59,ATCAY,DAPK3,TLE2,FLNA,TERF2IP,GLG1,ZFP90,SLC8A1,SPINK2,TBX20,ITM2C,CST3,ZNF425,ZNF175,CDKN1A,ZNF572,PPM1E,NACC2,ZNF79,HOPX,GABARAPL2,ORMDL3,YAP1,HKR1,BMP6,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:0033006	0.09	0.97	4	25	regulation of mast cell activation involved in immune response	BP	0.92433	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0050892	0.09	0.97	4	24	intestinal absorption	BP	0.92433	LEP,FABP2,F11R,SLC2A5	darkgreen	VSMC_M4
GO:0016485	0.09	0.95	16	170	protein processing	BP	0.92433	MDM2,HPN,CHAC1,BACE2,LGMN,CTSS,CTSZ,NCSTN,SERPINE1,C1RL,ATP6AP2,PCSK1N,TMEM59,PCSK4,F3,GLG1	darkgreen	VSMC_M4
GO:0008544	0.09	0.94	20	201	epidermis development	BP	0.92433	BCL2,CDSN,GRHL2,SVEP1,FOSL2,ADAM9,ATP2C1,NAB1,PDZD7,NCOA3,TXNIP,SEC24B,FGFR2,EXPH5,OPN3,PLOD1,FST,MAFF,EDA,YAP1	darkgreen	VSMC_M4
GO:0007589	0.09	0.96	8	68	body fluid secretion	BP	0.92433	DDR1,NCOR2,PAM,ADA,EDN1,HIF1A,NPPB,NPR3	darkgreen	VSMC_M4
GO:0030324	0.09	0.95	15	141	lung development	BP	0.92433	GRHL2,EP300,EDN2,THRB,RXFP1,ADA,SEC24B,CTSZ,FGFR2,TGFB3,ADAMTSL2,LOX,FGF9,HOPX,YAP1	darkgreen	VSMC_M4
GO:1903008	0.09	0.95	11	101	organelle disassembly	BP	0.92444	MAP1LC3A,SLC25A4,ATG13,GABARAPL1,ATG14,HIF1A,PPARGC1A,ULK2,MAP1LC3B2,BNIP3,GABARAPL2	darkgreen	VSMC_M4
GO:1900027	0.09	0.97	4	26	regulation of ruffle assembly	BP	0.92444	KANK1,RDX,NLGN1,ICAM1	darkgreen	VSMC_M4
GO:0051222	0.09	0.94	23	241	positive regulation of protein transport	BP	0.92517	SLC35D3,MDM2,GJA1,LEP,UNC13B,TCAF1,ADAM9,ATP2C1,ZDHHC2,ANKRD1,ATG13,RAB29,ABCG1,TM7SF3,PRKD1,ACHE,EXPH5,HIF1A,TGFB3,ABLIM3,FLNA,WLS,BMP6	darkgreen	VSMC_M4
GO:0043393	0.09	0.95	16	162	regulation of protein binding	BP	0.9274	ANGPT1,EP300,TGFBR1,HIPK2,SMARCD3,APP,AKTIP,IFIT1,PLCL1,CTSZ,DACT1,DAB2,LOX,XIRP1,CDKN1A,HOPX	darkgreen	VSMC_M4
GO:0006468	0.09	0.92	100	1223	protein phosphorylation	BP	0.92744	GDF11,BCL2,SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,DAPK1,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,VLDLR,PPP1R9A,PDK4,ZAP70,TGFBR1,MAP3K7,EPHB6,MAP3K8,HIPK2,SNRK,TESK2,INHBB,ADAM9,RASSF2,FLT3,MAP3K1,LATS2,HIPK3,NCK1,GRK7,OCLN,CDKL2,CLU,APP,PDGFC,PTPN11,NEK4,CCNT1,PTPN22,GDF6,AKTIP,NGF,EDN1,RGS2,LRP5,PLCL1,HTR2B,MST1R,PRKCA,AFAP1L2,SESN2,CAMK2D,MYLK,INPP5F,FGFR2,PRKD1,DDR2,GPRC5A,MAP3K13,LRP6,PRDX4,FAM129A,HSPB1,ATG14,LMTK2,SPEG,PPARGC1A,NEK9,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,NRK,ULK2,PAK3,DAB2,PRKAA2,DAPK3,PNCK,CSF1,PLCG2,TERF2IP,BCAR3,CDC7,CYR61,SLC8A1,LOX,SRPK3,CDKN1A,FGF9,PPM1E,CNTD2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0022602	0.09	0.97	5	32	ovulation cycle process	BP	0.92744	LEP,PAM,PTX3,SLIT3,TGFB3	darkgreen	VSMC_M4
GO:0030048	0.09	0.95	12	97	actin filament-based movement	BP	0.92744	GJA1,LIMCH1,KCNE3,ACTN4,MYO1B,TNNT2,SHTN1,CAMK2D,CACNA1C,FLNA,KCNE4,PLN	darkgreen	VSMC_M4
GO:0015749	0.09	0.95	10	84	monosaccharide transmembrane transport	BP	0.92744	LEP,SLC2A1,OCLN,PTH,PTPN11,EDN1,SESN2,OPN3,SLC2A5,SORT1	darkgreen	VSMC_M4
GO:0071868	0.09	0.96	8	66	cellular response to monoamine stimulus	BP	0.92744	HRH1,APLP1,APP,ADCY6,HTR2B,ADCY5,NCSTN,FLNA	darkgreen	VSMC_M4
GO:0071870	0.09	0.96	8	66	cellular response to catecholamine stimulus	BP	0.92744	HRH1,APLP1,APP,ADCY6,HTR2B,ADCY5,NCSTN,FLNA	darkgreen	VSMC_M4
GO:2000378	0.09	0.97	5	37	negative regulation of reactive oxygen species metabolic process	BP	0.92744	BCL2,CFLAR,CRYAB,HIF1A,BNIP3	darkgreen	VSMC_M4
GO:0034103	0.09	0.96	7	57	regulation of tissue remodeling	BP	0.92926	LEP,PDK4,TF,TMEM64,PRKCA,DDR2,CST3	darkgreen	VSMC_M4
GO:0043270	0.09	0.94	18	182	positive regulation of ion transport	BP	0.93118	TRDN,LEP,WFS1,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,ABCC8,EDN1,ACTN2,CTSS,MYLK,AKAP6,FLNA,VAMP7,AHCYL1,PLCG2	darkgreen	VSMC_M4
GO:0099504	0.09	0.95	15	138	synaptic vesicle cycle	BP	0.93138	STX11,SH3GL2,UNC13B,PREPL,SYT5,SNAP91,ITSN2,FGF14,PCLO,CLCN3,RAPGEF4,NLGN1,FBXL20,CDH2,DNAJC6	darkgreen	VSMC_M4
GO:0060348	0.09	0.94	18	172	bone development	BP	0.93138	CITED2,GJA1,EP300,LEP,PTH,PDGFC,PTPN11,NAB1,LRP5,FGFR2,PLXNB1,PAPPA2,TGFB3,PLS3,BGN,GLG1,LOX,BMP6	darkgreen	VSMC_M4
GO:0090504	0.10	0.97	5	31	epiboly	BP	0.93138	DDR1,MRTFA,FLNA,CYR61,CD151	darkgreen	VSMC_M4
GO:0071260	0.10	0.96	8	69	cellular response to mechanical stimulus	BP	0.93138	GJA1,SLC2A1,MAP3K1,ANKRD1,PTPN11,F11R,BNIP3,BMP6	darkgreen	VSMC_M4
GO:0097009	0.10	0.97	5	32	energy homeostasis	BP	0.93138	SLC35D3,EDN2,FOXO1,PPARGC1A,PRKAA2	darkgreen	VSMC_M4
GO:0061082	0.10	0.97	4	24	myeloid leukocyte cytokine production	BP	0.93138	IRAK3,DDX58,TGFB3,PLCG2	darkgreen	VSMC_M4
GO:0120033	0.10	0.97	4	25	negative regulation of plasma membrane bounded cell projection assembly	BP	0.93186	KANK1,EVI5L,PLXNB3,YAP1	darkgreen	VSMC_M4
GO:0000904	0.10	0.93	52	562	cell morphogenesis involved in differentiation	BP	0.93186	BCL2,UST,GRHL2,LAMA2,EP300,ADGRB1,KANK1,VLDLR,PPP1R9A,ANTXR1,KIDINS220,EPHB6,LIMS2,ITGA8,ACTN4,SEMA3C,KIF13B,APP,PTPN11,NGF,PDZD7,NFASC,SEMA5A,FEZ1,PREX1,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,FGFR2,PLXNB1,RAPH1,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,WDR1,ACTN1,SIPA1L1,NUMB,SLIT3,NPTN,CDH2,ULK2,PAK3,PLXNB3,FLNA,NEXN,SDC2	darkgreen	VSMC_M4
GO:0030901	0.10	0.96	8	69	midbrain development	BP	0.93228	MBP,NDRG2,GNB4,FGFR2,LRP6,MAOB,WLS,FGF9	darkgreen	VSMC_M4
GO:1903409	0.10	0.96	6	47	reactive oxygen species biosynthetic process	BP	0.93228	SOD2,ADGRB1,CLCN3,CFLAR,MAOB,PLCG2	darkgreen	VSMC_M4
GO:1901019	0.10	0.96	8	67	regulation of calcium ion transmembrane transporter activity	BP	0.93228	TRDN,KCNE3,FGF14,JPH1,CAMK2D,AKAP6,PLCG2,PLN	darkgreen	VSMC_M4

GO:0045669	0.10	0.96	7	56	positive regulation of osteoblast differentiation	BP	0.93228	LRP5,NPNT,PRKD1,DDR2,CYR61,YAP1,BMP6	darkgreen	VSMC_M4
GO:2000379	0.10	0.96	7	57	positive regulation of reactive oxygen species metabolic process	BP	0.93228	RNF41,SOD2,ADGRB1,LEP,CLCN3,PLCG2,CDKN1A	darkgreen	VSMC_M4
GO:0045765	0.10	0.94	22	229	regulation of angiogenesis	BP	0.93328	SASH1,FAM19A5,SMOC2,ADGRB1,LEP,RECK,HIPK2,GATA2,COL4A2,CYP1B1,ADM,ABCC8,ANXA3,SEMA5A,PRKCA,PRKD1,HSPB1,SERPINE1,HIF1A,NPPB,ANGPTL4,F3	darkgreen	VSMC_M4
GO:0034764	0.10	0.94	16	155	positive regulation of transmembrane transport	BP	0.9388	TRDN,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,OCLN,PTH,ABCC8,PTPN11,ACTN2,CTSS,AKAP6,OPN3,FLNA,PLCG2	darkgreen	VSMC_M4
GO:0110149	0.10	0.95	9	75	regulation of biomineralization	BP	0.9388	FBLN7,PTH,DDR2,NBR1,HIF1A,TGFB3,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:0007568	0.10	0.94	23	252	aging	BP	0.94089	BCL2,CITED2,SOD2,LEP,CDKN2B,C2orf40,PPP1R9A,POLB,COL4A2,MARCH5,ADM,APP,NEK4,ADA,EDN1,SERPINE1,CRYAB,IGFBP2,PPARGC1A,TGFB3,VCAM1,CDKN1A,ICAM1	darkgreen	VSMC_M4
GO:0010675	0.10	0.95	12	114	regulation of cellular carbohydrate metabolic process	BP	0.9421	EP300,LEP,PDK4,HRH1,PTH,SCARB2,ADIPOR1,SESN2,SLC25A12,PPARGC1A,RORA,DDIT4	darkgreen	VSMC_M4
GO:0036296	0.10	0.97	4	27	response to increased oxygen levels	BP	0.94787	POLB,FOXO1,BNIP3,CDKN1A	darkgreen	VSMC_M4
GO:0007423	0.10	0.93	38	415	sensory organ development	BP	0.94799	BCL2,CITED2,DDR1,GRHL2,TGFBR1,TBX18,HIPK2,GATA2,PPP1R13L,SMARCD3,SALL2,THRB,COL4A1,CYP1B1,HPN,CHD7,GPM6A,MEIS2,PTPN11,PDZD7,EDN1,KDM5B,LRP5,SEC24B,FGFR2,ATF6,CRYGS,MFAP5,ACHE,CRYAB,HIF1A,CACNA1C,ANGPTL7,TGFB3,BBS4,BCAR3,FRZB,BMP6	darkgreen	VSMC_M4
GO:0010657	0.10	0.96	7	60	muscle cell apoptotic process	BP	0.94987	SOD2,EDN1,CAMK2D,CFLAR,LRP6,PDE1A,BNIP3	darkgreen	VSMC_M4
GO:0015012	0.10	0.97	4	24	heparan sulfate proteoglycan biosynthetic process	BP	0.95067	HS6ST1,EXTL3,NDST3,EXTL2	darkgreen	VSMC_M4
GO:0071402	0.10	0.97	4	26	cellular response to lipoprotein particle stimulus	BP	0.95317	ABCA1,LPL,ABCG1,CDH13	darkgreen	VSMC_M4
GO:0048709	0.10	0.95	8	67	oligodendrocyte differentiation	BP	0.95317	TENM4,TRPC4,WASF3,CLU,NCSTN,ZNF365,WDR1,BNIP3	darkgreen	VSMC_M4
GO:0045744	0.10	0.96	5	37	negative regulation of G protein-coupled receptor signaling pathway	BP	0.95317	APLP1,ADM,ADA,RGS2,HTR2B	darkgreen	VSMC_M4
GO:0034110	0.10	0.97	4	25	regulation of homotypic cell-cell adhesion	BP	0.95317	PRKCA,F11R,RDX,PRKG1	darkgreen	VSMC_M4
GO:0048017	0.10	0.94	15	137	inositol lipid-mediated signaling	BP	0.95317	ANGPT1,LEP,PIP5K1B,PLCB4,FLT3,PDGFC,EDN1,PLCL1,HTR2B,INPP5F,PI4KB,PLXNB1,UNC5B,NPR3,PIK3C2A	darkgreen	VSMC_M4
GO:0030042	0.10	0.96	7	51	actin filament depolymerization	BP	0.95324	SEMA5A,ACTN2,RDX,WDR1,MICAL3,SPTAN1,DSTN	darkgreen	VSMC_M4
GO:0032101	0.10	0.92	53	646	regulation of response to external stimulus	BP	0.95324	SASH1,IRAK3,FAM19A5,SMOC2,GJA1,EP300,LEP,DDX58,CREB3,EDN2,MAP3K7,ABHD12,SEMA3C,FFAR3,CD180,GRK7,APP,ABCC8,PTPN11,LBP,PROS1,PTPN22,ADA,IFIT1,EDN1,JAM3,CD47,N4BP1,SEMA5A,LPL,RIPOR2,LGMN,PRKCA,INPP5F,PRKD1,HSPB1,SERPINE1,RORA,BBS4,PAK3,MMP28,LGALS9,FLNA,VAMP7,CSF1,CDH13,PLCG2,F3,LRSAM1,CCR6,HOPX,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0008344	0.10	0.96	7	56	adult locomotory behavior	BP	0.95324	OXR1,HIPK2,ABHD12,CHD7,CLCN3,APP,INPP5F	darkgreen	VSMC_M4
GO:0030216	0.10	0.95	9	74	keratinocyte differentiation	BP	0.95342	CDSN,GRHL2,FOSL2,ADAM9,NCOA3,TXNIP,EXPH5,OPN3,YAP1	darkgreen	VSMC_M4
GO:0042552	0.10	0.94	12	109	myelination	BP	0.95491	MBP,TENM4,WASF3,SCN8A,CLU,NAB1,JAM3,NFASC,NCSTN,SLC25A12,SH3TC2,ORMDL3	darkgreen	VSMC_M4
GO:0038179	0.10	0.96	5	34	neurotrophin signaling pathway	BP	0.95701	KIDINS220,PTPN11,NGF,SORT1,DDIT4	darkgreen	VSMC_M4
GO:0070588	0.10	0.93	21	211	calcium ion transmembrane transport	BP	0.95778	PKDREJ,TRDN,KCNE3,FGF14,TRPC4,ATP2C1,CHD7,MICU2,SLC35G1,JPH1,GPM6A,HTR2B,CAMK2D,PRKD1,AKAP6,CACNA1C,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0008064	0.10	0.94	16	159	regulation of actin polymerization or depolymerization	BP	0.95778	KANK1,PPP1R9A,CDC42EP3,WASF3,NCK1,JMY,SEMA5A,ACTN2,PREX1,RDX,WDR1,PAK3,ARHGAP28,SPTAN1,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0120032	0.10	0.94	16	158	regulation of plasma membrane bounded cell projection assembly	BP	0.95778	KANK1,PPP1R9A,TGFBR1,CDC42EP3,OCLN,GPM6A,RIPOR2,RDX,NLGN1,TGFB3,BBS4,EVI5L,MYO10,PLXNB3,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0006810	0.10	0.91	246	3300	transport	BP	0.95778	BCL2,SLC35D3,STX11,GRIP1,MDM2,DDR1,LAPTM4B,IPCEF1,ABRA,ANGPT1,C4A,PKDREJ,CALHM5,GJA1,TRDN,ADGRB1,DAPK1,SH3GL2,LEP,WFS1,VLDLR,UNC13B,PPP1R9A,CD274,RIC1,DYNC1I1,REST,ICA1,LMAN2L,SNX13,SLC2A1,PREPL,LMBRD1,SYT5,SLC17A5,ABCA1,PTPN3,DOP1A,SNAP91,PEX13,ANTXR1,MDFIC,TCAF1,SLC37A3,ITSN2,GATA2,MRC1,TPT1,TMCC1,GGA3,INHBB,USP6NL,CD93,SYNGR2,KCNE3,RAB2B,ACTN4,ADAM9,FGF14,TRPC4,SLC16A3,ATP2C1,PCLO,TF,APLP1,TUSC3,ZDHHC2,NCOR2,FFAR3,FXYD1,HPN,DENND5A,CHD7,MICU2,ANKRD1,TRIM23,EXOC6,ADM,ESYT3,PAM,SLC25A4,SCN8A,CLCN3,OCLN,SLC35G1,MCTP1,JPH1,PTH,KIF13B,G3BP2,CLU,GPM6A,APP,ATXN2,SCARB2,ABCC8,ANXA3,PTPN11,PTX3,LBP,HERPUD1,SLC26A7,ATG13,HNF4A,SERINC3,ADA,AKTIP,IFIT1,EDN1,CD47,PLA2G4F,ANO5,MYO1B,RAB29,ABCG1,CNNM2,KDM5B,RGS2,EYA2,TNNT2,ACTN2,PFKL,LRP5,ARRDC4,FEZ1,HTR2B,MST1R,TINAGL1,ZMAT3,TM7SF3,SUN1,TXNIP,SEC24B,CFI,MFGE8,ATP9A,SESN2,ARV1,CAMK2D,ABCC9,ADCY5,CTSS,MYLK,LRP2,INPP5F,FABP2,PTPN14,PRKD1,PI4KB,F11R,CYBRD1,DYNC1I2,SLC25A12,RAPGEF4,AP3B2,AKAP6,LRP6,HIP1,HSPB1,CUX1,SERPINE1,ACHE,CRYAB,RDX,EXPH5,MAOB,GULP1,ATG14,CYP19A1,LMTK2,NLGN1,WDR1,RABEP1,HIF1A,SYT16,OPN3,CACNA1C,AP1S3,MICAL3,ADGRE2,FBXL20,PPARGC1A,NPPB,DISP3,FAF2,NUMB,TGFB3,IFT43,MAGT1,TOM1L1,KCNK10,KIAA0556,EPG5,SLC14A1,BBS4,STOML1,ATG4A,GP2,CDH2,EVI5L,ABLIM3,SH3TC2,RHOT1,MARCH2,DNAJC6,DAB2,LGALS9,NPR3,MYO10,RBFOX1,SLC43A2,SCNN1D,FLNA,VAMP7,SLC2A5,HCN2,AHCYL1,SORT1,FNBP1,MBTPS1,CDH13,PLCG2,TBC1D1	darkgreen	VSMC_M4
GO:0018105	0.10	0.93	24	249	peptidyl-serine phosphorylation	BP	0.95778	BCL2,ANGPT1,TGFBR1,HIPK2,RASSF2,LATS2,HIPK3,NCK1,APP,NGF,PLCL1,PRKCA,CAMK2D,INPP5F,PRKD1,MAP3K13,LMTK2,ULK2,PRKAA2,PNCK,TERF2IP,BCAR3,CDC7,DDIT4	darkgreen	VSMC_M4
GO:0010613	0.10	0.97	4	26	positive regulation of cardiac muscle hypertrophy	BP	0.95799	EDN1,PRKCA,CAMK2D,AKAP6	darkgreen	VSMC_M4
GO:0014742	0.10	0.97	4	26	positive regulation of muscle hypertrophy	BP	0.95799	EDN1,PRKCA,CAMK2D,AKAP6	darkgreen	VSMC_M4
GO:1990266	0.10	0.95	8	74	neutrophil migration	BP	0.96037	EDN2,LBP,EDN1,JAM3,RIPOR2,PREX1,WDR1,GP2	darkgreen	VSMC_M4
GO:0045137	0.11	0.94	17	170	development of primary sexual characteristics	BP	0.96037	BCL2,CITED2,LEP,TGFBR1,INHBB,PTX3,LRP2,ARID5B,PRDX4,CYP19A1,TNFSF10,TEX11,SLIT3,FST,FLNA,FGF9,ICAM1	darkgreen	VSMC_M4

GO:0032365	0.11	0.96	5	35	intracellular lipid transport	BP	0.96037	ABCA1,ABCG1,ARV1,LRP6,SCP2	darkgreen	VSMC_M4
GO:0051602	0.11	0.97	4	26	response to electrical stimulus	BP	0.96037	SOD2,REST,TRIM63,PPARGC1A	darkgreen	VSMC_M4
GO:0048608	0.11	0.93	30	330	reproductive structure development	BP	0.96037	BCL2,CITED2,GRHL2,GJA1,LEP,TGFBR1,GATA2,INHBB,CHD7,ADM,PTPN11,PTX3,ADA,KDM5B,LRP2,FGFR2,ARID5B,PRDX4,CYP19A1,TNFSF10,HIF1A,TEX11,SLIT3,FST,FLNA,CYR61,FGF9,ICAM1,STC2,BMP6	darkgreen	VSMC_M4
GO:0048598	0.11	0.92	42	469	embryonic morphogenesis	BP	0.96037	MBP,CITED2,GRHL2,GJA1,RECK,TGFBR1,LMBRD1,TBX18,HIPK2,GATA2,ITGA8,TENM4,COL4A2,HPN,CHD7,ADM,ATOH8,SHROOM3,HNF4A,PDZD7,EDN1,ETS2,EYA2,LRP5,HTR2B,SEC24B,LRP2,FGFR2,LNPK,MFAP5,DACT1,HIF1A,CACNA1C,TGFB3,BBS4,LMO4,CYR61,WLS,AFF3,FRZB,TBX20,YAP1	darkgreen	VSMC_M4
GO:0009185	0.11	0.95	9	81	ribonucleoside diphosphate metabolic process	BP	0.96037	EP300,APP,PFKL,ENO2,HIF1A,PPARGC1A,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0035904	0.11	0.95	7	50	aorta development	BP	0.96037	LEP,CHD7,SEC24B,MYLK,LRP2,SMAD6,LOX	darkgreen	VSMC_M4
GO:0086009	0.11	0.96	5	33	membrane repolarization	BP	0.96037	KCNE3,AKAP6,WDR1,FLNA,KCNE4	darkgreen	VSMC_M4
GO:0042149	0.11	0.96	6	44	cellular response to glucose starvation	BP	0.96037	BCL2,SLC2A1,SESN1,SESN2,ATG14,PRKAA2	darkgreen	VSMC_M4
GO:0043616	0.11	0.96	5	35	keratinocyte proliferation	BP	0.96073	FGFR2,PRKD1,FST,CDH13,YAP1	darkgreen	VSMC_M4
GO:0002682	0.11	0.92	72	915	regulation of immune system process	BP	0.96073	BCL2,IRAK3,ANGPT1,C4A,EP300,LEP,DDX58,DOCK8,CD274,IL18R1,CREB3,ZAP70,EDN2,MAP3K7,MAP3K8,GATA2,LRCH1,RASSF2,TMEM178A,MAP3K1,FFAR3,NCK1,SH3RF1,CHST2,CLU,BLNK,MEIS2,APP,PTPN11,LBP,TMEM64,PTPN22,ADA,IFIT1,EDN1,JAM3,CD47,N4BP1,RAB29,RIPOR2,LGMN,SIAE,PRKCA,CFI,P4HTM,CTSS,TP53BP1,SERPINE1,C1RL,IGFBP2,HIF1A,ADGRE2,RORA,TGFB3,FAXDC2,EPG5,PAK3,MMP28,LGALS9,VAMP7,CSF1,PLCG2,VCAM1,VNN1,TLR1,CD83,LOX,CD59,CDKN1A,MFAP4,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0048812	0.11	0.92	47	503	neuron projection morphogenesis	BP	0.96127	BCL2,UST,GRIP1,DDR1,GJA1,LAMA2,ADGRB1,SH3GL2,VLDLR,PPP1R9A,KIDINS220,EPHB6,ITSN2,SEMA3C,KIF13B,GPM6A,APP,PTPN11,NGF,NFASC,SEMA5A,FEZ1,ROBO3,PARD6B,PLXNA2,SHTN1,LRP2,FGFR2,PLXNB1,RAPH1,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,NPTN,NRK,CDH2,ULK2,PAK3,PLXNB3,NEXN,SDC2	darkgreen	VSMC_M4
GO:0007272	0.11	0.94	12	110	ensheathment of neurons	BP	0.96341	MBP,TENM4,WASF3,SCN8A,CLU,NAB1,JAM3,NFASC,NCSTN,SLC25A12,SH3TC2,ORMDL3	darkgreen	VSMC_M4
GO:0008366	0.11	0.94	12	110	axon ensheathment	BP	0.96341	MBP,TENM4,WASF3,SCN8A,CLU,NAB1,JAM3,NFASC,NCSTN,SLC25A12,SH3TC2,ORMDL3	darkgreen	VSMC_M4
GO:0072676	0.11	0.95	8	72	lymphocyte migration	BP	0.96452	DOCK8,ZAP70,LRCH1,APP,RIPOR2,F11R,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0001654	0.11	0.93	27	280	eye development	BP	0.96452	BCL2,CITED2,GRHL2,TGFBR1,HIPK2,PPP1R13L,SMARCD3,SALL2,THRB,COL4A1,CYP1B1,CHD7,GPM6A,MEIS2,KDM5B,LRP5,ATF6,CRYGS,MFAP5,ACHE,CRYAB,HIF1A,CACNA1C,ANGPTL7,BBS4,BCAR3,BMP6	darkgreen	VSMC_M4
GO:0060491	0.11	0.94	16	159	regulation of cell projection assembly	BP	0.96452	KANK1,PPP1R9A,TGFBR1,CDC42EP3,OCLN,GPM6A,RIPOR2,RDX,NLGN1,TGFB3,BBS4,EVI5L,MYO10,PLXNB3,ICAM1,YAP1	darkgreen	VSMC_M4
GO:1903573	0.11	0.96	5	39	negative regulation of response to endoplasmic reticulum stress	BP	0.96478	WFS1,CREB3,NCK1,CLU,HERPUD1	darkgreen	VSMC_M4
GO:0007498	0.11	0.94	10	89	mesoderm development	BP	0.96478	GDF11,CITED2,GJA1,ITGA8,ETS2,EYA2,FGFR2,WLS,TBX20,YAP1	darkgreen	VSMC_M4
GO:0010876	0.11	0.93	28	311	lipid localization	BP	0.96478	LEP,VLDLR,SLC2A1,ABCA1,ESYT3,CLU,SCARB2,PTPN11,LBP,EDN1,PLA2G4F,LPL,ABCG1,KDM5B,ATP9A,ARV1,FABP2,LRP6,GULP1,CYP19A1,DISP3,STOML1,VAMP7,ABCA4,SLC27A5,PRELID2,BMP6,SCP2	darkgreen	VSMC_M4
GO:0030832	0.11	0.93	16	160	regulation of actin filament length	BP	0.96478	KANK1,PPP1R9A,CDC42EP3,WASF3,NCK1,JMY,SEMA5A,ACTN2,PREX1,RDX,WDR1,PAK3,ARHGAP28,SPTAN1,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0035051	0.11	0.94	13	119	cardiocyte differentiation	BP	0.96545	CITED2,SGCB,REST,TBX18,TENM4,SEMA3C,SORBS2,EDN1,RGS2,ACTN2,AKAP6,VCAM1,SLC8A1	darkgreen	VSMC_M4
GO:0030323	0.11	0.94	15	145	respiratory tube development	BP	0.96545	GRHL2,EP300,EDN2,THRB,RXFP1,ADA,SEC24B,CTSZ,FGFR2,TGFB3,ADAMTSL2,LOX,FGF9,HOPX,YAP1	darkgreen	VSMC_M4
GO:0051353	0.11	0.96	6	50	positive regulation of oxidoreductase activity	BP	0.96545	EDN2,EDN1,HTR2B,HIF1A,NPR3,RFK	darkgreen	VSMC_M4
GO:0060325	0.11	0.97	4	25	face morphogenesis	BP	0.96796	EP300,PTPN11,ARID5B,TGFB3	darkgreen	VSMC_M4
GO:0015850	0.11	0.93	17	179	organic hydroxy compound transport	BP	0.96815	LEP,SYT5,ABCA1,SLC16A3,FFAR3,CLU,PTPN11,ABCG1,KDM5B,ARV1,LRP6,MAOB,CYP19A1,ABCA4,SLC27A5,BMP6,SCP2	darkgreen	VSMC_M4
GO:0035886	0.11	0.97	4	26	vascular associated smooth muscle cell differentiation	BP	0.9688	SOD2,SGCB,ADM,FGF9	darkgreen	VSMC_M4
GO:0043506	0.11	0.96	6	46	regulation of JUN kinase activity	BP	0.97143	SASH1,MAP3K7,HIPK3,PTPN22,EDN1,MAP3K13	darkgreen	VSMC_M4
GO:0043524	0.11	0.94	12	115	negative regulation of neuron apoptotic process	BP	0.97143	BCL2,SOD2,OXR1,ANGPT1,WFS1,HIPK2,NGF,LGMN,UNC5B,HIF1A,PPARGC1A,TGFB3	darkgreen	VSMC_M4
GO:0061564	0.11	0.92	36	380	axon development	BP	0.97349	BCL2,UST,DDR1,LAMA2,ADGRB1,EPHB6,SEMA3C,KIF13B,APP,PTPN11,NGF,JAM3,NFASC,SEMA5A,FEZ1,ROBO3,PARD6B,PLXNA2,SHTN1,INPP5F,FGFR2,PLXNB1,RAPH1,MAP3K13,UNC5B,LMTK2,SIPA1L1,NUMB,SLIT3,NPTN,CDH2,ULK2,PAK3,PLXNB3,FLNA,NEXN	darkgreen	VSMC_M4
GO:1901021	0.11	0.96	5	36	positive regulation of calcium ion transmembrane transporter activity	BP	0.97373	TRDN,KCNE3,FGF14,AKAP6,PLCG2	darkgreen	VSMC_M4
GO:0071901	0.11	0.94	10	93	negative regulation of protein serine/threonine kinase activity	BP	0.97394	IRAK3,CDKN2B,LATS2,HIPK3,PTPN22,RGS2,LRP5,LRP6,SLC8A1,CDKN1A	darkgreen	VSMC_M4
GO:0031032	0.11	0.93	18	172	actomyosin structure organization	BP	0.97423	LIMCH1,PPP1R9A,TGFBR1,ANKRD1,EPB41L4A,EDN1,CD47,TNNT2,ACTN2,CFLAR,F11R,SYNPO2L,WDR1,TGFB3,CNN1,ARHGAP28,CSRP1,PPM1E	darkgreen	VSMC_M4
GO:0001525	0.11	0.92	38	428	angiogenesis	BP	0.97533	SASH1,ANGPT1,FAM19A5,SMOC2,ADGRB1,LEP,RECK,TGFBR1,CALD1,HIPK2,GATA2,COL4A1,COL4A2,CYP1B1,AMOTL2,ADM,ABCC8,ANXA3,EDN1,JAM3,SEMA5A,PRKCA,MFGE8,FGFR2,PRKD1,HSPB1,SERPINE1,UNC5B,HIF1A,NPPB,RORA,ANGPTL4,FLNA,CDH13,F3,CYR61,TBX20,PIK3C2A	darkgreen	VSMC_M4

GO:0009893	0.11	0.90	212	2815	positive regulation of metabolic process	BP	0.97738	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,MDM2,DDR1,RNF19A,GRHL2,SOD2,ABRA,ANGPT1,SMOC2,GJA1,TPD52L1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,MLLT3,LEP,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,CD274,IL18R1,CREB3,REST,TGFBR1,MAP3K7,ANTXR1,MDFIC,EPHB6,SESN1,JADE1,HIPK2,GATA2,ZNF398,GGA3,NAA16,ELF1,INHBB,SMARCD3,HRH1,LMO7,BABAM2,FOSL2,LBH,LIPT2,SALL2,THRB,ACTN4,ADAM9,TACC1,FOXO1,RASSF2,ANKLE2,CYP1B1,TF,FLT3,NCOR2,FFAR3,HPN,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ADM,SLC25A4,ATOH8,CLCN3,OCLN,TEAD1,PTH,CLU,BLNK,MED12L,MEIS2,APP,PDGFC,ABCC8,ANXA3,PTPN11,PTX3,LBP,NEK4,CCNT1,HERPUD1,JMY,CHD6,PTPN22,HNF4A,GDF6,AKTIP,NGF,EDN1,ETS2,LPL,RAB29,ABCG1,ADIPOR1,KDM5B,EYA2,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,HTR2B,MST1R,LGMN,AFAP1L2,SESN2,NGRN,LRP2,CFLAR,INPP5F,FGFR2,RBM4B,TP53BP1,PRKD1,NCSTN,SLC25A12,ARID5B,ITGA6,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,FAM129A,HSPB1,SERPINE1,ACHE,ATP6AP2,RDX,MAOB,ZNF445,EZH1,ATG14,FBXL5,TNFSF10,DACT1,LMTK2,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,DISP3,RORA,CALCOCO2,TGFB3,SMAD6,TOM1L1,FAXDC2,NPTN,PAK3,ABLIM3,CRLF3,DAB2,LGALS9,SMARCA1,SKP2,PRKAA2,TMEM59,CTIF,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,LRSAM1,CDC7,LMO4,CYR61,ZFP90,TLR1,BNIP3,CD83,TBX20,ZNF175,MAFF,CDKN1A,FGF9,EDA,ZNF782,HLF,ICAM1,PIK3C2A,ORMDL3,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:1905037	0.11	0.94	10	92	autophagosome organization	BP	0.97738	MAP1LC3A,ATG13,FEZ1,SYNPO2,GABARAPL1,ATG14,ULK2,MAP1LC3B2,LRSAM1,GABARAPL2	darkgreen	VSMC_M4
GO:0046165	0.11	0.94	11	108	alcohol biosynthetic process	BP	0.9776	LEP,REST,HRH1,PTH,ABCG1,ARV1,PPIP5K1,PRKAA2,MBTPS1,PLCG2,BMP6	darkgreen	VSMC_M4
GO:0034767	0.11	0.94	12	114	positive regulation of ion transmembrane transport	BP	0.9779	TRDN,TCAF1,KCNE3,ACTN4,FGF14,FXYD1,ABCC8,ACTN2,CTSS,AKAP6,FLNA,PLCG2	darkgreen	VSMC_M4
GO:0048729	0.11	0.92	44	490	tissue morphogenesis	BP	0.98037	BCL2,CITED2,MDM2,DDR1,GRHL2,GJA1,MRTFA,MLLT3,TGFBR1,TBX18,ITGA8,COL4A1,SEMA3C,CHD7,ANKRD1,ADM,SHROOM3,EDN1,KDM5B,EYA2,TNNT2,LRP5,NPNT,SEC24B,MYLK,LRP2,CTSZ,FGFR2,CRYGS,DACT1,WDR1,HIF1A,BBS4,FST,DAB2,FLNA,CSF1,LMO4,CYR61,WLS,CD151,FRZB,TBX20,YAP1	darkgreen	VSMC_M4
GO:0006909	0.11	0.93	16	163	phagocytosis	BP	0.98044	C4A,ADGRB1,LEP,ABCA1,GATA2,CD93,CLCN3,ANXA3,PTX3,LBP,CD47,MST1R,MFGE8,GULP1,VAMP7,PLCG2	darkgreen	VSMC_M4
GO:0120039	0.11	0.91	48	517	plasma membrane bounded cell projection morphogenesis	BP	0.98049	BCL2,UST,GRIP1,DDR1,GJA1,LAMA2,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,KIDINS220,EPHB6,ITSN2,SEMA3C,KIF13B,GPM6A,APP,PTPN11,NGF,NFASC,SEMA5A,FEZ1,ROBO3,PARD6B,PLXNA2,SHTN1,LRP2,FGFR2,PLXNB1,RAPH1,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,NPTN,NRK,CDH2,ULK2,PAK3,PLXNB3,NEXN,SDC2	darkgreen	VSMC_M4
GO:0000122	0.11	0.91	57	694	negative regulation of transcription by RNA polymerase II	BP	0.98488	CITED2,MDM2,TRPS1,ZHX1,EP300,TLE4,LEP,WFS1,ZNF169,REST,TBX18,HIPK2,GATA2,ZNF398,PPP1R13L,LMCD1,THRB,SATB1,MIER3,NCOR2,ANKRD1,CPEB3,NCK1,WWC2,MEIS2,EDN1,ETS2,MXI1,TXNIP,YEATS2,WDTC1,FGFR2,ARID5B,ID3,CUX1,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,ZFP90,TBX20,ZNF425,ZNF175,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0046209	0.11	0.95	7	60	nitric oxide metabolic process	BP	0.98528	CYP1B1,CLU,PTX3,EDN1,CD47,RORA,ICAM1	darkgreen	VSMC_M4
GO:0006024	0.11	0.95	8	66	glycosaminoglycan biosynthetic process	BP	0.98528	DSEL,UST,ANGPT1,HS6ST1,CHST2,B3GNT7,NDST3,CHST15	darkgreen	VSMC_M4
GO:0002697	0.12	0.93	19	206	regulation of immune effector process	BP	0.98778	IRAK3,ANGPT1,LEP,DDX58,IL18R1,MAP3K7,GATA2,FFAR3,LBP,PTPN22,CD47,TP53BP1,ADGRE2,TGFB3,LGALS9,VAMP7,PLCG2,CD59,ICAM1	darkgreen	VSMC_M4
GO:0032269	0.12	0.91	61	760	negative regulation of cellular protein metabolic process	BP	0.98778	IRAK3,MDM2,LAPTM4B,OXR1,ANGPT1,C4A,ADGRB1,DAPK1,SH3GL2,GNAQ,CDKN2B,RIC1,RECK,PTPN3,HIPK2,ITIH5,CRIM1,RASSF2,FXYD1,LATS2,HIPK3,CPEB3,NCK1,SH3RF1,OCLN,RNF34,APP,HERPUD1,PROS1,PTPN22,CHAC1,NGF,EDN1,N4BP1,RGS2,LRP5,SESN2,CTSZ,INPP5F,GPRC5A,LRP6,FAM129A,HSPB1,SERPINE1,CRYAB,ATG14,PCSK1N,PPARGC1A,SMAD6,PRKAA2,TMEM59,DAPK3,TERF2IP,GLG1,SLC8A1,SPINK2,CST3,CDKN1A,PPM1E,GABARAPL2,DDIT4	darkgreen	VSMC_M4
GO:0060421	0.12	0.96	5	35	positive regulation of heart growth	BP	0.98778	EDN1,FGFR2,AKAP6,TBX20,YAP1	darkgreen	VSMC_M4
GO:0045913	0.12	0.95	7	57	positive regulation of carbohydrate metabolic process	BP	0.98778	HRH1,PTH,APP,SLC25A12,HIF1A,PPARGC1A,PRKAA2	darkgreen	VSMC_M4
GO:0061458	0.12	0.92	30	333	reproductive system development	BP	0.98778	BCL2,CITED2,GRHL2,GJA1,LEP,TGFBR1,GATA2,INHBB,CHD7,ADM,PTPN11,PTX3,ADA,KDM5B,LRP2,FGFR2,ARID5B,PRDX4,CYP19A1,TNFSF10,HIF1A,TEX11,SLIT3,FST,FLNA,CYR61,FGF9,ICAM1,STC2,BMP6	darkgreen	VSMC_M4
GO:0150063	0.12	0.92	27	282	visual system development	BP	0.98778	BCL2,CITED2,GRHL2,TGFBR1,HIPK2,PPP1R13L,SMARCD3,SALL2,THRB,COL4A1,CYP1B1,CHD7,GPM6A,MEIS2,KDM5B,LRP5,ATF6,CRYGS,MFAP5,ACHE,CRYAB,HIF1A,CACNA1C,ANGPTL7,BBS4,BCAR3,BMP6	darkgreen	VSMC_M4
GO:0032878	0.12	0.96	4	24	regulation of establishment or maintenance of cell polarity	BP	0.98914	DOCK8,KANK1,RIPOR2,SHTN1	darkgreen	VSMC_M4
GO:0045931	0.12	0.94	10	97	positive regulation of mitotic cell cycle	BP	0.98972	MDM2,SMOC2,SMARCD3,MEIS2,APP,PTPN11,LGMN,PRKCA,RDX,CDC7	darkgreen	VSMC_M4
GO:0042632	0.12	0.95	7	62	cholesterol homeostasis	BP	0.9911	ABCA1,HNF4A,LPL,ABCG1,LRP5,DISP3,RORA	darkgreen	VSMC_M4

GO:0035239	0.12	0.91	60	699	tube morphogenesis	BP	0.99285	BCL2,CITED2,SASH1,DDR1,GRHL2,ANGPT1,FAM19A5,SMOC2,ADGRB1,LEP,RECK,TGFBR1,CALD1,HIPK2,GATA2,COL4A1,COL4A2,CYP1B1,AMOTL2,CHD7,ADM,ATOH8,SHROOM3,ABCC8,ANXA3,EDN1,JAM3,SEMA5A,KDM5B,LRP5,NPNT,PRKCA,SEC24B,MFGE8,MYLK,LRP2,CTSZ,FGFR2,PRKD1,HSPB1,SERPINE1,UNC5B,DACT1,HIF1A,NPPB,RORA,BBS4,CDH2,ANGPTL4,FLNA,CSF1,CDH13,F3,LMO4,CYR61,LOX,TBX20,EDA,PIK3C2A,YAP1	darkgreen	VSMC_M4
GO:1905898	0.12	0.96	4	29	positive regulation of response to endoplasmic reticulum stress	BP	0.99285	NCK1,HERPUD1,SERINC3,ATF6	darkgreen	VSMC_M4
GO:0014888	0.12	0.96	5	37	striated muscle adaptation	BP	0.99422	FOXO1,CFLAR,INPP5F,TRIM63,PPARGC1A	darkgreen	VSMC_M4
GO:0045429	0.12	0.96	4	27	positive regulation of nitric oxide biosynthetic process	BP	0.99467	CLU,PTX3,EDN1,ICAM1	darkgreen	VSMC_M4
GO:0016043	0.12	0.89	346	4652	cellular component organization	BP	0.99467	MBP,BCL2,COL23A1,STX11,SHPRH,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,ANGPT1,SMOC2,GJA1,TRDN,LAMA2,EP300,MRTFA,ADGRB1,SH3GL2,MLLT3,LIMCH1,FAM122A,KANK1,VLDLR,UNC13B,TPM2,PPP1R9A,RIC1,REST,RECK,ECM2,IGFBP7,LMAN2L,SLC2A1,TGFBR1,ABCA1,SVEP1,SNAP91,PEX13,CALD1,ANTXR1,KIDINS220,EPHB6,JADE1,ITSN2,TUBE1,HIPK2,GATA2,LIMS2,TMEM135,TESK2,TMCC1,TENM4,SMARCD3,USP6NL,EXOG,BABAM2,SYNGR2,ARHGEF17,ACTN4,FMNL2,SATB1,ADAM9,TACC1,ATP2C1,COL4A1,COL4A2,ANKLE2,PCDHB4,CDC42EP3,CYP1B1,PCLO,SEMA3C,EML4,LMNTD2,TF,APLP1,AMOTL2,WASF3,ZDHHC2,RIC3,HPN,PTPRG,DENND5A,CHD7,CHPT1,ANKRD1,EPB41L4A,CPEB3,MARCH5,NCK1,SORBS2,EXOC6,ADM,ESYT3,MAP1LC3A,PAM,SLC25A4,CLCN3,OCLN,TCF7L1,TEAD1,MCTP1,FAM172A,KIF13B,LYSMD3,EXTL3,G3BP2,CLU,GPM6A,APP,ATXN2,SCARB2,PDGFC,PRPH,SHROOM3,RXFP1,ABCC8,PTPN11,PTX3,ADCY6,JMY,ATG13,DCBLD2,CHD6,PKP4,TANC1,LPCAT2,HNF4A,FMOD,AKTIP,RBL2,NGF,PDZD7,EDN1,JAM3,GPRIN3,CD47,NFASC,SMARCAD1,MYO1B,SEMA5A,LPL,RAB29,ABCG1,ADIPOR1,DNAH7,COL4A4,KDM5B,RIPOR2,CCDC80,MARCKSL1,RGS2,EYA2,TNNT2,PDE4DIP,ACTN2,LRP5,KCTD10,FEZ1,NPNT,PREX1,LGMN,ROBO3,NID1,SUN1,PRKCA,SEC24B,ABLIM1,MFGE8,PARD6B,MID1,ATP9A,PLXNA2,SESN2,ARV1,SHTN1,CAMK2D,CTSS,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,SYNPO2,TP53BP1,PRKD1,F11R,PLXNB1,QSOX1,LRCH3,ZRANB1,RAPH1,ITGA6,ZNF365,MAP7D2,AKAP6,DDR2,MAP3K13,HIP1,PRDX4,LNPK,COLGALT2,GABARAPL1,CUX1,MFAP5,SERPINE1,ACHE,CRYAB,ATP6AP2	darkgreen	VSMC_M4
GO:0009266	0.12	0.93	13	137	response to temperature stimulus	BP	0.99467	ZNF516,SOD2,EP300,IGFBP7,TMEM135,FOXO1,ADM,LPL,HTR2B,PCSK1N,PPARGC1A,DNAJA2,CDKN1A	darkgreen	VSMC_M4
GO:0031214	0.12	0.93	13	126	biomineral tissue development	BP	0.99467	LEP,FOXO1,PTH,FGFR2,DDR2,NBR1,HIF1A,TGFB3,CYR61,SLC8A1,LOX,BMP6,FAM83H	darkgreen	VSMC_M4
GO:1905952	0.12	0.93	12	118	regulation of lipid localization	BP	0.99467	LEP,ABCA1,PTPN11,EDN1,LPL,ABCG1,KDM5B,ARV1,CYP19A1,DISP3,BMP6,SCP2	darkgreen	VSMC_M4
GO:0099622	0.12	0.96	4	25	cardiac muscle cell membrane repolarization	BP	0.99467	KCNE3,WDR1,FLNA,KCNE4	darkgreen	VSMC_M4
GO:0014003	0.12	0.96	4	27	oligodendrocyte development	BP	0.99467	TENM4,WASF3,CLU,NCSTN	darkgreen	VSMC_M4
GO:0070201	0.12	0.91	37	436	regulation of establishment of protein localization	BP	0.99552	SLC35D3,MDM2,ANGPT1,GJA1,LEP,UNC13B,REST,ICA1,MDFIC,TCAF1,INHBB,ADAM9,ATP2C1,ZDHHC2,ANKRD1,PAM,ABCC8,PTPN11,ATG13,HNF4A,RAB29,ABCG1,PFKL,LRP5,TM7SF3,ADCY5,PTPN14,PRKD1,ACHE,EXPH5,HIF1A,TGFB3,ABLIM3,SH3TC2,FLNA,WLS,BMP6	darkgreen	VSMC_M4
GO:0097352	0.12	0.95	5	37	autophagosome maturation	BP	0.99552	MAP1LC3A,ATG14,CALCOCO2,EPG5,MAP1LC3B2	darkgreen	VSMC_M4
GO:0110020	0.12	0.94	10	86	regulation of actomyosin structure organization	BP	0.99552	LIMCH1,PPP1R9A,TGFBR1,EDN1,CD47,F11R,SYNPO2L,TGFB3,ARHGAP28,PPM1E	darkgreen	VSMC_M4
GO:0048858	0.12	0.91	48	520	cell projection morphogenesis	BP	0.99552	BCL2,UST,GRIP1,DDR1,GJA1,LAMA2,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,KIDINS220,EPHB6,ITSN2,SEMA3C,KIF13B,GPM6A,APP,PTPN11,NGF,NFASC,SEMA5A,FEZ1,ROBO3,PARD6B,PLXNA2,SHTN1,LRP2,FGFR2,PLXNB1,RAPH1,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,NPTN,NRK,CDH2,ULK2,PAK3,PLXNB3,NEXN,SDC2	darkgreen	VSMC_M4
GO:0055013	0.12	0.94	8	65	cardiac muscle cell development	BP	0.99552	SGCB,TBX18,SORBS2,EDN1,RGS2,ACTN2,AKAP6,SLC8A1	darkgreen	VSMC_M4
GO:2001057	0.12	0.95	7	61	reactive nitrogen species metabolic process	BP	0.99552	CYP1B1,CLU,PTX3,EDN1,CD47,RORA,ICAM1	darkgreen	VSMC_M4
GO:0062013	0.12	0.94	10	96	positive regulation of small molecule metabolic process	BP	0.99552	HRH1,ADM,PTH,APP,ABCG1,SLC25A12,HIF1A,PPARGC1A,PRKAA2,BMP6	darkgreen	VSMC_M4
GO:0042246	0.12	0.95	6	53	tissue regeneration	BP	0.99552	CPQ,CFLAR,SGCA,CDKN1A,HOPX,YAP1	darkgreen	VSMC_M4
GO:0032413	0.12	0.95	6	49	negative regulation of ion transmembrane transporter activity	BP	0.9958	TRDN,KCNE3,ACTN2,CAMK2D,KCNE4,PLN	darkgreen	VSMC_M4
GO:0001763	0.12	0.93	16	157	morphogenesis of a branching structure	BP	0.9958	BCL2,DDR1,GRHL2,COL4A1,SEMA3C,ADM,EDN1,KDM5B,LRP5,NPNT,CTSZ,FGFR2,MAP3K13,CSF1,TBX20,YAP1	darkgreen	VSMC_M4
GO:0051057	0.12	0.95	7	55	positive regulation of small GTPase mediated signal transduction	BP	0.99589	ABRA,ARHGEF3,NGF,F11R,SYNPO2L,MAPRE2,CSF1	darkgreen	VSMC_M4
GO:0038127	0.12	0.93	11	102	ERBB signaling pathway	BP	0.99871	PTPN3,RASSF2,PTPN11,LGMN,AFAP1L2,GPRC5A,HIP1,SH3TC2,CDH13,BCAR3,PIK3C2A	darkgreen	VSMC_M4
GO:0006506	0.12	0.96	4	31	GPI anchor biosynthetic process	BP	0.99871	PIGN,PIGG,PIGS,PIGK	darkgreen	VSMC_M4
GO:0036314	0.12	0.96	4	25	response to sterol	BP	0.99871	TGFBR1,ABCA1,LRP6,RORA	darkgreen	VSMC_M4
GO:0048286	0.12	0.95	5	35	lung alveolus development	BP	0.99871	EDN2,ADA,FGFR2,TGFB3,HOPX	darkgreen	VSMC_M4
GO:0070227	0.12	0.95	6	52	lymphocyte apoptotic process	BP	0.99871	DOCK8,CD274,ADA,HIF1A,LGALS9,ORMDL3	darkgreen	VSMC_M4
GO:0080134	0.12	0.90	76	970	regulation of response to stress	BP	0.99871	BCL2,SASH1,IRAK3,MDM2,SOD2,OXR1,FAM19A5,SMOC2,GJA1,TPD52L1,EP300,LEP,WFS1,DDX58,SH3RF3,KANK1,CREB3,REST,MAP3K7,MDFIC,SESN1,HIPK2,ABHD12,TPT1,BABAM2,FOXO1,RASSF2,FFAR3,HIPK3,ANKRD1,NCK1,SH3RF1,OCLN,MCTP1,CLU,APP,ABCC8,PTPN11,LBP,NEK4,HERPUD1,PROS1,PTPN22,GDF6,SERINC3,ADA,IFIT1,EDN1,CD47,N4BP1,LPL,EYA2,MID1,SESN2,MYLK,INPP5F,TP53BP1,ZNF365,ATF6,HSPB1,SERPINE1,NBR1,DACT1,HIF1A,RORA,PAK3,LGALS9,FLNA,VAMP7,PLCG2,TERF2IP,F3,LRSAM1,VNN1,NACC2,PRKG1	darkgreen	VSMC_M4
GO:1901016	0.12	0.95	5	35	regulation of potassium ion transmembrane transporter activity	BP	0.99871	KCNE3,ABCC8,ACTN2,AKAP6,KCNE4	darkgreen	VSMC_M4

GO:0014812	0.12	0.94	9	79	muscle cell migration	BP	0.99871	BCL2,MDM2,DDR1,FAM19A5,DOCK4,SERPINE1,PPARGC1A,FGF9,PRKG1	darkgreen	VSMC_M4
GO:0032615	0.12	0.95	5	38	interleukin-12 production	BP	0.99871	IRAK3,LEP,CD47,LGALS9,PLCG2	darkgreen	VSMC_M4
GO:0032655	0.12	0.95	5	38	regulation of interleukin-12 production	BP	0.99871	IRAK3,LEP,CD47,LGALS9,PLCG2	darkgreen	VSMC_M4
GO:0055092	0.12	0.94	7	63	sterol homeostasis	BP	0.99958	ABCA1,HNF4A,LPL,ABCG1,LRP5,DISP3,RORA	darkgreen	VSMC_M4
GO:0002275	0.12	0.94	7	62	myeloid cell activation involved in immune response	BP	1	GATA2,ANXA3,LBP,ADGRE2,LGALS9,VAMP7,PLCG2	darkgreen	VSMC_M4
GO:0030534	0.12	0.93	10	90	adult behavior	BP	1	OXR1,LEP,HIPK2,ABHD12,CHD7,CLCN3,APP,INPP5F,NCSTN,BBS4	darkgreen	VSMC_M4
GO:0031016	0.12	0.95	6	50	pancreas development	BP	1	WFS1,MEIS2,HNF4A,CDH2,WLS,BMP6	darkgreen	VSMC_M4
GO:0050435	0.12	0.95	6	50	amyloid-beta metabolic process	BP	1	IFNGR1,GGA3,CLU,BACE2,ABCG1,NCSTN	darkgreen	VSMC_M4
GO:2000036	0.12	0.96	4	26	regulation of stem cell population maintenance	BP	1	REST,LBH,NCOA3,YAP1	darkgreen	VSMC_M4
GO:0007200	0.12	0.95	6	53	phospholipase C-activating G protein-coupled receptor signaling pathway	BP	1	HRH1,EDN1,ACTN2,HTR2B,ADRA1B,NPR3	darkgreen	VSMC_M4
GO:0055117	0.12	0.94	7	58	regulation of cardiac muscle contraction	BP	1	RGS2,CAMK2D,CACNA1C,ADRA1B,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0043620	0.12	0.95	6	49	regulation of DNA-templated transcription in response to stress	BP	1	CITED2,NCK1,CHD6,SESN2,ATF6,HIF1A	darkgreen	VSMC_M4
GO:0061138	0.13	0.92	15	147	morphogenesis of a branching epithelium	BP	1	BCL2,DDR1,GRHL2,COL4A1,SEMA3C,ADM,EDN1,KDM5B,LRP5,NPNT,CTSZ,FGFR2,CSF1,TBX20,YAP1	darkgreen	VSMC_M4
GO:1904064	0.13	0.93	11	103	positive regulation of cation transmembrane transport	BP	1	TRDN,KCNE3,ACTN4,FGF14,FXYD1,ABCC8,ACTN2,CTSS,AKAP6,FLNA,PLCG2	darkgreen	VSMC_M4
GO:0030199	0.13	0.94	7	56	collagen fibril organization	BP	1	TGFBR1,CYP1B1,FMOD,DDR2,COLGALT2,P4HA1,LOX	darkgreen	VSMC_M4
GO:0071622	0.13	0.95	5	41	regulation of granulocyte chemotaxis	BP	1	LBP,EDN1,JAM3,RIPOR2,CSF1	darkgreen	VSMC_M4
GO:0046847	0.13	0.94	7	56	filopodium assembly	BP	1	PPP1R9A,TGFBR1,GPM6A,RIPOR2,NLGN1,TGFB3,MYO10	darkgreen	VSMC_M4
GO:0034198	0.13	0.95	5	39	cellular response to amino acid starvation	BP	1	SESN1,MAP1LC3A,SESN2,PRKD1,CDKN1A	darkgreen	VSMC_M4
GO:0030501	0.13	0.95	5	37	positive regulation of bone mineralization	BP	1	PTH,TGFB3,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:0032944	0.13	0.93	13	138	regulation of mononuclear cell proliferation	BP	1	BCL2,LEP,CD274,ZAP70,NCK1,SH3RF1,PTPN22,ADA,IGFBP2,LGALS9,CSF1,VCAM1,CDKN1A	darkgreen	VSMC_M4
GO:0008543	0.13	0.94	7	59	fibroblast growth factor receptor signaling pathway	BP	1	SMOC2,PTPN11,GALNT3,FGFR2,FGFRL1,NPTN,FGF9	darkgreen	VSMC_M4
GO:1904894	0.13	0.96	4	28	positive regulation of receptor signaling pathway via STAT	BP	1	LEP,CYP1B1,ADIPOR1,CRLF3	darkgreen	VSMC_M4
GO:0060135	0.13	0.95	6	49	maternal process involved in female pregnancy	BP	1	CITED2,GJA1,PAM,RGS2,LGALS9,STC2	darkgreen	VSMC_M4
GO:0046621	0.13	0.96	4	29	negative regulation of organ growth	BP	1	CITED2,GJA1,WWC2,RGS2	darkgreen	VSMC_M4
GO:0046634	0.13	0.94	7	63	regulation of alpha-beta T cell activation	BP	1	CD274,ZAP70,SH3RF1,PTPN22,ADA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0010574	0.13	0.96	4	27	regulation of vascular endothelial growth factor production	BP	1	NDRG2,CYP1B1,HIF1A,RORA	darkgreen	VSMC_M4
GO:0045022	0.13	0.95	5	37	early endosome to late endosome transport	BP	1	AKTIP,RDX,LMTK2,DAB2,FLNA	darkgreen	VSMC_M4
GO:0071480	0.13	0.96	4	29	cellular response to gamma radiation	BP	1	MDM2,CRYAB,CDKN1A,YAP1	darkgreen	VSMC_M4
GO:0051496	0.13	0.94	6	47	positive regulation of stress fiber assembly	BP	1	LIMCH1,TGFBR1,CD47,SYNPO2L,TGFB3,PPM1E	darkgreen	VSMC_M4
GO:0048880	0.13	0.91	27	286	sensory system development	BP	1	BCL2,CITED2,GRHL2,TGFBR1,HIPK2,PPP1R13L,SMARCD3,SALL2,THRB,COL4A1,CYP1B1,CHD7,GPM6A,MEIS2,KDM5B,LRP5,ATF6,CRYGS,MFAP5,ACHE,CRYAB,HIF1A,CACNA1C,ANGPTL7,BBS4,BCAR3,BMP6	darkgreen	VSMC_M4
GO:0010952	0.13	0.92	13	142	positive regulation of peptidase activity	BP	1	MBP,DAPK1,REST,ANTXR1,APP,LGMN,CFLAR,NCSTN,HIP1,TNFSF10,LGALS9,F3,CYR61	darkgreen	VSMC_M4
GO:1905114	0.13	0.90	39	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	TLE4,GNAQ,MLLT3,KANK1,UNC13B,PPP1R9A,RECK,TBX18,MDFIC,FZD8,JADE1,NDRG2,AMOTL2,LATS2,TCF7L1,APP,TMEM64,SEMA5A,LRP5,FGFR2,ZRANB1,INSYN2,LRP6,ATP6AP2,IGFBP2,DACT1,NLGN1,CDH2,DAB2,PRKAA2,DAPK3,TLE2,PLCG2,WLS,FRZB,LYPD6,TMEM170B,EDA,YAP1	darkgreen	VSMC_M4
GO:0061351	0.13	0.93	12	111	neural precursor cell proliferation	BP	1	GATA2,LIMS2,SMARCD3,LRP2,CTSZ,FGFR2,HIF1A,DISP3,RORA,NUMB,CDH2,FLNA	darkgreen	VSMC_M4
GO:1904407	0.13	0.96	4	28	positive regulation of nitric oxide metabolic process	BP	1	CLU,PTX3,EDN1,ICAM1	darkgreen	VSMC_M4
GO:0042098	0.13	0.93	12	127	T cell proliferation	BP	1	LEP,DOCK8,CD274,ZAP70,NCK1,SH3RF1,PTPN22,NCSTN,IGFBP2,LGALS9,VCAM1,CD151	darkgreen	VSMC_M4
GO:0006023	0.13	0.94	8	68	aminoglycan biosynthetic process	BP	1	DSEL,UST,ANGPT1,HS6ST1,CHST2,B3GNT7,NDST3,CHST15	darkgreen	VSMC_M4
GO:0030203	0.13	0.93	10	93	glycosaminoglycan metabolic process	BP	1	DSEL,UST,ANGPT1,HS6ST1,ITIH5,CHST2,B3GNT7,NDST3,CHST15,BGN	darkgreen	VSMC_M4
GO:0051241	0.13	0.90	60	743	negative regulation of multicellular organismal process	BP	1	BCL2,IFNGR1,CITED2,IRAK3,LAPTM4B,GRHL2,ANGPT1,FAM19A5,GJA1,ADGRB1,LEP,CD274,IL18R1,REST,TGFBR1,TBX18,DOCK4,GATA2,INHBB,NDRG2,FOXO1,COL4A2,SEMA3C,TMEM178A,HPN,PTPRG,ADM,WWC2,PTH,ABCC8,PTPN11,LBP,PROS1,PTPN22,ADA,EDN1,N4BP1,SEMA5A,ADIPOR1,RGS2,PLCL1,LGMN,TRIM63,PRDX4,SERPINE1,HIF1A,NPPB,ANGPTL7,TGFB3,SMAD6,NPTN,ULK2,LGALS9,NPR3,ADAMTS5,FRZB,CD83,CST3,PLN,PRKG1	darkgreen	VSMC_M4
GO:0046635	0.13	0.95	5	41	positive regulation of alpha-beta T cell activation	BP	1	ZAP70,PTPN22,ADA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0001774	0.13	0.96	4	29	microglial cell activation	BP	1	IFNGR1,CLU,APP,TLR1	darkgreen	VSMC_M4
GO:0006505	0.13	0.96	4	32	GPI anchor metabolic process	BP	1	PIGN,PIGG,PIGS,PIGK	darkgreen	VSMC_M4
GO:0005996	0.13	0.91	18	199	monosaccharide metabolic process	BP	1	EP300,LEP,PDK4,SLC2A1,PFKFB3,GALM,PTH,HECTD4,ADIPOR1,PFKL,LRP5,SESN2,WDTC1,MAN2A2,CHST15,SLC25A12,PPARGC1A,RORA	darkgreen	VSMC_M4
GO:0046365	0.13	0.96	4	30	monosaccharide catabolic process	BP	1	GALM,PFKL,LRP5,SLC25A12	darkgreen	VSMC_M4
GO:0042698	0.13	0.94	6	46	ovulation cycle	BP	1	LEP,NCOR2,PAM,PTX3,SLIT3,TGFB3	darkgreen	VSMC_M4
GO:0006029	0.13	0.93	8	67	proteoglycan metabolic process	BP	1	DSEL,UST,HS6ST1,EXTL3,NDST3,CHST15,BGN,EXTL2	darkgreen	VSMC_M4
GO:0019318	0.13	0.92	17	185	hexose metabolic process	BP	1	EP300,LEP,PDK4,PFKFB3,GALM,PTH,HECTD4,ADIPOR1,PFKL,LRP5,SESN2,WDTC1,MAN2A2,CHST15,SLC25A12,PPARGC1A,RORA	darkgreen	VSMC_M4
GO:0036473	0.13	0.93	8	76	cell death in response to oxidative stress	BP	1	BCL2,SOD2,OXR1,REST,CYP1B1,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0014032	0.13	0.93	8	69	neural crest cell development	BP	1	CITED2,SEMA3C,FAM172A,EDN1,SEMA5A,HTR2B,HIF1A,CDH2	darkgreen	VSMC_M4
GO:0046850	0.14	0.95	5	38	regulation of bone remodeling	BP	1	LEP,PDK4,TF,TMEM64,PRKCA	darkgreen	VSMC_M4
GO:0060538	0.14	0.92	13	132	skeletal muscle organ development	BP	1	BCL2,CITED2,EP300,ANKRD1,RCAN1,RIPOR2,CFLAR,ZBTB18,FGFRL1,RBFOX1,SRPK3,MAFF,HLF	darkgreen	VSMC_M4
GO:0086010	0.14	0.95	5	30	membrane depolarization during action potential	BP	1	PTPN3,SCN8A,CACNA1C,HCN2,SLC8A1	darkgreen	VSMC_M4
GO:0051781	0.14	0.94	7	63	positive regulation of cell division	BP	1	LBH,PDGFC,PKP4,HTR2B,FGFR2,TGFB3,FGF9	darkgreen	VSMC_M4

GO:0051606	0.14	0.92	13	135	detection of stimulus	BP	1	PKDREJ,GNAQ,HPN,GRK7,LBP,PDZD7,PPEF1,OPN3,TGFB3,CDH2,ABCA4,TLR1,YAP1	darkgreen	VSMC_M4
GO:0060443	0.14	0.95	5	37	mammary gland morphogenesis	BP	1	DDR1,KDM5B,LRP5,FGFR2,CSF1	darkgreen	VSMC_M4
GO:0060412	0.14	0.95	5	34	ventricular septum morphogenesis	BP	1	CITED2,TGFBR1,FGFR2,FGFRL1,SLIT3	darkgreen	VSMC_M4
GO:0031325	0.14	0.88	187	2483	positive regulation of cellular metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,MDM2,DDR1,RNF19A,GRHL2,SOD2,ABRA,ANGPT1,SMOC2,TPD52L1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,MLLT3,LEP,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,CREB3,REST,TGFBR1,MAP3K7,ANTXR1,MDFIC,EPHB6,SESN1,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,INHBB,SMARCD3,HRH1,LMO7,BABAM2,FOSL2,LBH,LIPT2,SALL2,THRB,ACTN4,ADAM9,TACC1,FOXO1,RASSF2,ANKLE2,TF,FLT3,HPN,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ADM,SLC25A4,ATOH8,CLCN3,TEAD1,PTH,CLU,MED12L,MEIS2,APP,PDGFC,ANXA3,PTPN11,PTX3,NEK4,CCNT1,HERPUD1,JMY,CHD6,PTPN22,HNF4A,GDF6,AKTIP,NGF,EDN1,ETS2,RAB29,ABCG1,EYA2,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,HTR2B,MST1R,LGMN,AFAP1L2,SESN2,NGRN,LRP2,CFLAR,INPP5F,FGFR2,TP53BP1,PRKD1,NCSTN,SLC25A12,ARID5B,ITGA6,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,LRP6,HIP1,FAM129A,RDX,MAOB,ZNF445,EZH1,ATG14,FBXL5,TNFSF10,DACT1,LMTK2,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,CALCOCO2,TGFB3,SMAD6,TOM1L1,FAXDC2,NPTN,PAK3,ABLIM3,CRLF3,DAB2,LGALS9,SMARCA1,SKP2,PRKAA2,TMEM59,CTIF,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,LRSAM1,CDC7,LMO4,CYR61,ZFP90,BNIP3,TBX20,ZNF175,MAFF,CDKN1A,FGF9,ZNF782,HLF,ICAM1,PIK3C2A,ORMDL3,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0008625	0.14	0.94	7	67	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	BCL2,RNF34,NGF,CFLAR,SERPINE1,SORT1,ICAM1	darkgreen	VSMC_M4
GO:0008277	0.14	0.93	10	96	regulation of G protein-coupled receptor signaling pathway	BP	1	FRMPD1,APLP1,ADM,GRK7,ADA,EDN1,RGS2,HTR2B,PRKCA,GAS2L2	darkgreen	VSMC_M4
GO:0070663	0.14	0.92	14	153	regulation of leukocyte proliferation	BP	1	BCL2,LEP,CD274,ZAP70,NCK1,SH3RF1,PTH,PTPN22,ADA,IGFBP2,LGALS9,CSF1,VCAM1,CDKN1A	darkgreen	VSMC_M4
GO:0010594	0.14	0.92	15	157	regulation of endothelial cell migration	BP	1	SASH1,ANGPT1,SMOC2,ADGRB1,GATA2,ATOH8,ANXA3,EDN1,SEMA5A,LGMN,PRKCA,PRKD1,HSPB1,HIF1A,PIK3C2A	darkgreen	VSMC_M4
GO:0008283	0.14	0.89	110	1442	cell population proliferation	BP	1	BCL2,RNF41,CITED2,MDM2,DDR1,GRHL2,SOD2,ANGPT1,FAM19A5,GJA1,ADGRB1,LEP,CDKN2B,DOCK8,KANK1,C2orf40,CD274,REST,IGFBP7,ZAP70,TGFBR1,EDN2,HIPK2,GATA2,LIMS2,TENM4,SMARCD3,FOSL2,LBH,NDRG2,TACC1,CYP1B1,FLT3,HPN,NCK1,ADM,CD180,SH3RF1,ATOH8,PTH,CLU,MEIS2,APP,PDGFC,ABCC8,PTPN11,PTPN22,HNF4A,ADA,NGF,EDN1,CD47,SEMA5A,KDM5B,MARCKSL1,LRP5,HTR2B,MST1R,LGMN,PRKCA,TXNIP,LRP2,CFLAR,CTSZ,FGFR2,PTPN14,PRKD1,NCSTN,PLXNB1,DDR2,LRP6,PRDX4,PDE1A,IGFBP2,SPEG,HIF1A,CCPG1,DDX41,PPARGC1A,DISP3,FGFRL1,RORA,NUMB,SLIT3,TGFB3,CNN1,SMAD6,CDH2,FST,LGALS9,SKP2,NPR3,PLXNB3,FLNA,CSF1,CDH13,VCAM1,F3,CDC7,CYR61,DNAJA2,CD151,FRZB,TBX20,CDKN1A,FGF9,NACC2,YAP1,PRKG1,BMP6	darkgreen	VSMC_M4
GO:0071347	0.14	0.93	8	75	cellular response to interleukin-1	BP	1	IRAK3,MAP3K7,ANKRD1,EDN1,CD47,HIF1A,RORA,ICAM1	darkgreen	VSMC_M4
GO:0048762	0.14	0.91	19	198	mesenchymal cell differentiation	BP	1	BCL2,CITED2,TGFBR1,SEMA3C,HPN,FAM172A,EDN1,SEMA5A,ADIPOR1,HTR2B,FGFR2,LRP6,HIF1A,TGFB3,CDH2,DAB2,FLNA,FRZB,TBX20	darkgreen	VSMC_M4
GO:0031099	0.14	0.92	14	150	regeneration	BP	1	BCL2,PTPN3,FLT3,ADM,ANXA3,CPQ,JAM3,CFLAR,INPP5F,SGCA,FLNA,CDKN1A,HOPX,YAP1	darkgreen	VSMC_M4
GO:0045494	0.14	0.95	4	26	photoreceptor cell maintenance	BP	1	SLC2A1,CLCN3,BBS4,ABCA4	darkgreen	VSMC_M4
GO:0001881	0.14	0.95	4	27	receptor recycling	BP	1	RAB29,INPP5F,ACHE,LMTK2	darkgreen	VSMC_M4
GO:0034763	0.14	0.93	9	88	negative regulation of transmembrane transport	BP	1	TRDN,LEP,KCNE3,RGS2,ACTN2,CAMK2D,SLC43A2,KCNE4,PLN	darkgreen	VSMC_M4
GO:0050877	0.14	0.89	57	678	nervous system process	BP	1	MBP,SOD2,EP300,WFS1,VLDLR,UNC13B,PPP1R9A,HIPK2,TENM4,HRH1,THRB,TUSC3,WASF3,HPN,CHD7,CPEB3,SCN8A,GRK7,MEIS2,APP,SCARB2,ABCC8,TANC1,RCAN1,NGF,PDZD7,EDN1,JAM3,NFASC,RIPOR2,LGMN,ABLIM1,ADCY5,LRP2,USP53,NCSTN,SLC25A12,PPEF1,ATF6,INSYN2,CRYGS,NLGN1,WDR1,HIF1A,MAGT1,KCNK10,KIAA0556,BBS4,NPTN,RBFOX1,SCNN1D,CCDC78,ABCA4,ITPR1,TMPRSS11E,ICAM1,NPAS1	darkgreen	VSMC_M4
GO:0090101	0.14	0.92	11	101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	RASL11B,HIPK2,CRIM1,LRP2,TGFB3,SMAD6,NOMO1,FST,GLG1,ADAMTSL2,TBX20	darkgreen	VSMC_M4
GO:0006796	0.14	0.88	162	2150	phosphate-containing compound metabolic process	BP	1	GDF11,BCL2,PIGN,SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,EP300,DAPK1,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,PIP5K1B,VLDLR,PPP1R9A,PDK4,ZAP70,TGFBR1,PTPN3,MAP3K7,NT5C3A,EPHB6,MAP3K8,HIPK2,ABHD12,SNRK,TESK2,INHBB,HRH1,ENTPD3,PFKFB3,POLB,ADAM9,RASSF2,ANKLE2,TF,FLT3,MAP3K1,PTPRG,LATS2,CHPT1,HIPK3,NCK1,GRK7,OCLN,PTH,CDKL2,CLU,ENTPD1,APP,PDGFC,PTPN11,ADCY6,NEK4,CCNT1,PTPN22,LPCAT2,GDF6,SERINC3,ADA,AKTIP,RCAN1,RBL2,NGF,EDN1,PLA2G4F,LPL,MTMR10,NT5C2,DAPP1,RGS2,AGPAT3,EYA2,PFKL,LRP5,NPNT,PLCL1,HTR2B,MST1R,SERINC2,PRKCA,AFAP1L2,TPST2,SESN2,CAMK2D,ADCY5,MYLK,INPP5F,FGFR2,PTPN14,PRKD1,PI4KB,SLC25A12,PPEF1,PPIP5K1,ITGA6,DDR2,GPRC5A,MAP3K13,LRP6,PRDX4,FAM129A,HSPB1,ACHE,PDE1A,ENO2,ATG14,LMTK2,SPEG,HIF1A,PPP1R36,PPARGC1A,NPPB,RORA,PIGG,NEK9,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,AK7,NPTN,NRK,ULK2,PAK3,DNAJC6,DAB2,OCRL,PIGS,PRKAA2,DAPK3,ADCY9,PNCK,PLPPR3,CSF1,PPP1R26,PLCG2,TERF2IP,BCAR3,CDC7,LMO4,CYR61,AK5,ACYP2,SLC8A1,LOX,SRPK3,PIGK,CDKN1A,FGF9,PPM1E,RFK,CNTD2,ICAM1,PIK3C2A,ORMDL3,BMP6,DDIT4	darkgreen	VSMC_M4

GO:2000401	0.14	0.94	5	41	regulation of lymphocyte migration	BP	1	DOCK8,LRCH1,APP,RIPOR2,CCR6	darkgreen	VSMC_M4
GO:0060425	0.14	0.94	5	39	lung morphogenesis	BP	1	GRHL2,SEC24B,CTSZ,FGFR2,YAP1	darkgreen	VSMC_M4
GO:1903037	0.14	0.91	18	206	regulation of leukocyte cell-cell adhesion	BP	1	LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,CHST2,PTPN11,PTPN22,ADA,CD47,RIPOR2,IGFBP2,LGALS9,VCAM1,VNN1,CD83,ICAM1	darkgreen	VSMC_M4
GO:0034394	0.14	0.93	7	59	protein localization to cell surface	BP	1	ANGPT1,GGA3,RIC3,JAM3,ACTN2,FLNA,PIGK	darkgreen	VSMC_M4
GO:0050829	0.14	0.95	4	32	defense response to Gram-negative bacterium	BP	1	ADGRB1,LBP,PRKD1,SERPINE1	darkgreen	VSMC_M4
GO:0060485	0.14	0.90	22	235	mesenchyme development	BP	1	BCL2,CITED2,MDM2,TGFBR1,SEMA3C,HPN,FAM172A,EDN1,SEMA5A,ADIPOR1,HTR2B,FGFR2,LRP6,HIF1A,TGFB3,CDH2,DAB2,FLNA,FRZB,TBX20,YAP1,CRELD1	darkgreen	VSMC_M4
GO:1902229	0.14	0.95	4	31	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	BCL2,TPT1,CLU,NACC2	darkgreen	VSMC_M4
GO:0051899	0.14	0.93	8	66	membrane depolarization	BP	1	BCL2,PTPN3,SCN8A,EDN1,CAMK2D,CACNA1C,HCN2,SLC8A1	darkgreen	VSMC_M4
GO:0032456	0.14	0.93	8	70	endocytic recycling	BP	1	GRIP1,GGA3,ZDHHC2,ACTN2,ATP9A,INPP5F,LMTK2,EPG5	darkgreen	VSMC_M4
GO:0010517	0.14	0.94	6	50	regulation of phospholipase activity	BP	1	GNAQ,PTH,RGS2,HTR2B,FGFR2,CYR61	darkgreen	VSMC_M4
GO:0046631	0.14	0.92	10	97	alpha-beta T cell activation	BP	1	BCL2,CD274,IL18R1,ZAP70,SH3RF1,PTPN22,ADA,RORA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0072332	0.14	0.93	7	63	intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	BCL2,MDM2,EP300,HIPK2,JMY,CDKN1A,DDIT4	darkgreen	VSMC_M4
GO:0001503	0.14	0.90	29	328	ossification	BP	1	BCL2,LEP,REST,CRIM1,RASSF2,PTH,PTPN11,TMEM64,NAB1,LRP5,NPNT,SUN1,FGFR2,PRKD1,PLXNB1,DDR2,ID3,ACHE,NBR1,HIF1A,TGFB3,SMAD6,CSF1,SORT1,CYR61,SLC8A1,LOX,YAP1,BMP6	darkgreen	VSMC_M4
GO:0043087	0.14	0.90	27	285	regulation of GTPase activity	BP	1	DOCK8,RIC1,SNX13,CHN2,LRCH1,USP6NL,RALGAPA2,PKP4,RIPOR2,PREX1,PLXNA2,F11R,PLXNB1,ITGA6,RDX,CCPG1,SIPA1L1,MAPRE2,EVI5L,OCRL,PLXNB3,TBC1D13,ARHGAP29,BCAR3,SYDE2,ICAM1,PRKG1	darkgreen	VSMC_M4
GO:0033173	0.14	0.94	5	38	calcineurin-NFAT signaling cascade	BP	1	LMCD1,RCAN1,AKAP6,PLCG2,C10orf71	darkgreen	VSMC_M4
GO:0034109	0.14	0.93	8	71	homotypic cell-cell adhesion	BP	1	MYL9,PRKCA,F11R,HSPB1,RDX,FLNA,CSRP1,PRKG1	darkgreen	VSMC_M4
GO:0007586	0.14	0.93	7	63	digestion	BP	1	LEP,SLC26A7,FABP2,F11R,PPARGC1A,NPR3,SLC2A5	darkgreen	VSMC_M4
GO:0050808	0.14	0.90	31	329	synapse organization	BP	1	ADGRB1,UNC13B,PPP1R9A,REST,COL4A1,PCDHB4,PCLO,WASF3,ZDHHC2,GPM6A,APP,TANC1,NFASC,RAB29,LGMN,PLXNB1,ZNF365,ACHE,NLGN1,APBB2,ADGRL1,ACTN1,ZC4H2,SIPA1L1,NPTN,SYNPO,CDH2,PAK3,FLNA,PCDHB2,LRRC24	darkgreen	VSMC_M4
GO:0090287	0.14	0.90	22	230	regulation of cellular response to growth factor stimulus	BP	1	CITED2,SMOC2,EP300,CDKN2B,RASL11B,HIPK2,CRIM1,LATS2,NPNT,LRP2,CFLAR,HIF1A,TGFB3,SMAD6,NPTN,FST,DAB2,GLG1,CYR61,ADAMTSL2,LOX,TBX20	darkgreen	VSMC_M4
GO:0033363	0.14	0.95	4	29	secretory granule organization	BP	1	ABCA1,ABCG1,CCDC136,SPINK2	darkgreen	VSMC_M4
GO:0002253	0.15	0.91	17	191	activation of immune response	BP	1	BCL2,C4A,EP300,ZAP70,MAP3K7,CLU,BLNK,PTPN22,ADA,CD47,RAB29,CFI,C1RL,PAK3,PLCG2,CD59,MFAP4	darkgreen	VSMC_M4
GO:0006793	0.15	0.87	163	2169	phosphorus metabolic process	BP	1	GDF11,BCL2,PIGN,SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,EP300,DAPK1,SH3GL2,GNAQ,LEP,CDKN2B,LIMCH1,PIP5K1B,VLDLR,PPP1R9A,PDK4,ZAP70,TGFBR1,PTPN3,MAP3K7,NT5C3A,EPHB6,MAP3K8,HIPK2,ABHD12,SNRK,TESK2,INHBB,HRH1,ENTPD3,PFKFB3,POLB,ADAM9,RASSF2,ANKLE2,TF,FLT3,MAP3K1,PTPRG,LATS2,CHPT1,HIPK3,NCK1,GRK7,OCLN,PTH,CDKL2,CLU,ENTPD1,APP,PDGFC,PTPN11,ADCY6,NEK4,CCNT1,PTPN22,LPCAT2,GDF6,SERINC3,ADA,AKTIP,RCAN1,RBL2,NGF,EDN1,PLA2G4F,LPL,MTMR10,NT5C2,DAPP1,RGS2,AGPAT3,EYA2,PFKL,LRP5,NPNT,PLCL1,HTR2B,MST1R,SERINC2,PRKCA,AFAP1L2,TPST2,SESN2,CAMK2D,ADCY5,MYLK,INPP5F,FGFR2,PTPN14,PRKD1,PI4KB,SLC25A12,PPEF1,PPIP5K1,ITGA6,DDR2,GPRC5A,MAP3K13,LRP6,PRDX4,FAM129A,HSPB1,ACHE,PDE1A,ENO2,ATG14,LMTK2,SPEG,HIF1A,PPP1R36,PPARGC1A,NPPB,RORA,PIGG,NEK9,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,AK7,NPTN,NRK,ULK2,PAK3,DNAJC6,DAB2,OCRL,PIGS,PRKAA2,DAPK3,ADCY9,PNCK,PLPPR3,CSF1,PPP1R26,PLCG2,EXTL2,TERF2IP,BCAR3,CDC7,LMO4,CYR61,AK5,ACYP2,SLC8A1,LOX,SRPK3,PIGK,CDKN1A,FGF9,PPM1E,RFK,CNTD2,ICAM1,PIK3C2A,ORMDL3,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0070997	0.15	0.90	25	288	neuron death	BP	1	BCL2,SOD2,OXR1,ANGPT1,WFS1,REST,HIPK2,POLB,THRB,CLU,APP,NGF,RAB29,LGMN,CTSZ,USP53,NCSTN,UNC5B,HIF1A,PPARGC1A,TGFB3,PAK3,CSF1,BNIP3,DDIT4	darkgreen	VSMC_M4
GO:0048667	0.15	0.89	41	446	cell morphogenesis involved in neuron differentiation	BP	1	BCL2,UST,LAMA2,ADGRB1,VLDLR,PPP1R9A,KIDINS220,EPHB6,SEMA3C,KIF13B,APP,PTPN11,NGF,PDZD7,NFASC,SEMA5A,FEZ1,ROBO3,SEC24B,PARD6B,PLXNA2,SHTN1,FGFR2,PLXNB1,RAPH1,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,NPTN,CDH2,ULK2,PAK3,PLXNB3,NEXN,SDC2	darkgreen	VSMC_M4
GO:0061180	0.15	0.93	7	58	mammary gland epithelium development	BP	1	DDR1,LBH,KDM5B,LRP5,FGFR2,HIF1A,CSF1	darkgreen	VSMC_M4
GO:1903556	0.15	0.94	5	43	negative regulation of tumor necrosis factor superfamily cytokine production	BP	1	IRAK3,CD274,LBP,PTPN22,LGALS9	darkgreen	VSMC_M4
GO:1904951	0.15	0.90	23	257	positive regulation of establishment of protein localization	BP	1	SLC35D3,MDM2,GJA1,LEP,UNC13B,TCAF1,ADAM9,ATP2C1,ZDHHC2,ANKRD1,ATG13,RAB29,ABCG1,TM7SF3,PRKD1,ACHE,EXPH5,HIF1A,TGFB3,ABLIM3,FLNA,WLS,BMP6	darkgreen	VSMC_M4
GO:0042326	0.15	0.90	27	311	negative regulation of phosphorylation	BP	1	IRAK3,ANGPT1,SH3GL2,GNAQ,CDKN2B,RASSF2,ANKLE2,LATS2,HIPK3,NCK1,OCLN,PTPN22,RGS2,LRP5,INPP5F,GPRC5A,LRP6,FAM129A,HSPB1,ATG14,PPARGC1A,SMAD6,TERF2IP,SLC8A1,CDKN1A,PPM1E,DDIT4	darkgreen	VSMC_M4
GO:0017157	0.15	0.91	14	147	regulation of exocytosis	BP	1	REST,PREPL,SYT5,GATA2,RAB2B,PCLO,ATP9A,RAPGEF4,EXPH5,NLGN1,ADGRE2,FBXL20,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0032874	0.15	0.92	10	97	positive regulation of stress-activated MAPK cascade	BP	1	SASH1,TPD52L1,LEP,SH3RF3,HIPK2,RASSF2,SH3RF1,APP,GDF6,MID1	darkgreen	VSMC_M4

GO:0030162	0.15	0.89	42	538	regulation of proteolysis	BP	1	MBP,MDM2,RNF19A,C4A,DAPK1,FAM122A,REST,RECK,PTPN3,ANTXR1,HIPK2,ITIH5,ADAM9,CRIM1,HPN,SH3RF1,RNF34,CLU,APP,HERPUD1,PROS1,CHAC1,NGF,N4BP1,LGMN,CFLAR,CTSZ,NCSTN,HIP1,SERPINE1,CRYAB,TNFSF10,PCSK1N,DAB2,LGALS9,TMEM59,F3,GLG1,CYR61,SPINK2,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:0046942	0.15	0.91	16	173	carboxylic acid transport	BP	1	SLC35D3,GJA1,LEP,SLC17A5,TRPC4,SLC16A3,SLC26A7,SERINC3,EDN1,PLA2G4F,RGS2,LRP2,SLC25A12,SLC43A2,LRRC8C,SLC27A5	darkgreen	VSMC_M4
GO:0030279	0.15	0.95	4	26	negative regulation of ossification	BP	1	BCL2,PTH,HIF1A,SMAD6	darkgreen	VSMC_M4
GO:0002886	0.15	0.94	5	41	regulation of myeloid leukocyte mediated immunity	BP	1	DDX58,GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0051651	0.15	0.91	16	163	maintenance of location in cell	BP	1	GJA1,TRDN,CHD7,JPH1,HTR2B,SUN1,CAMK2D,PRKD1,AKAP6,CACNA1C,BBS4,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0045598	0.15	0.92	11	109	regulation of fat cell differentiation	BP	1	LEP,GATA2,FOXO1,TMEM64,LPL,FNDC5,LRP5,RORA,SORT1,FRZB,YAP1	darkgreen	VSMC_M4
GO:0034637	0.15	0.93	7	63	cellular carbohydrate biosynthetic process	BP	1	LEP,GYS1,PTH,GYG1,B3GNT7,GYG2,NDST3	darkgreen	VSMC_M4
GO:0010171	0.15	0.94	5	38	body morphogenesis	BP	1	EP300,PTPN11,ARID5B,ATP6AP2,TGFB3	darkgreen	VSMC_M4
GO:0001836	0.15	0.94	5	48	release of cytochrome c from mitochondria	BP	1	BCL2,SOD2,CLU,TNFSF10,BNIP3	darkgreen	VSMC_M4
GO:0060429	0.15	0.88	67	810	epithelium development	BP	1	BCL2,CITED2,DDR1,CDSN,GRHL2,SCUBE1,GJA1,EP300,MRTFA,MLLT3,TBX18,FOSL2,LBH,THRB,ADAM9,COL4A1,SEMA3C,CHD7,ADM,ATOH8,SHROOM3,HNF4A,PDZD7,EDN1,KDM5B,NCOA3,LRP5,NPNT,TXNIP,SEC24B,PLXNA2,LRP2,CTSZ,FGFR2,F11R,TAGLN,ID3,LRP6,CRYGS,SERPINE1,ATP6AP2,RDX,EXPH5,DACT1,WDR1,HIF1A,OPN3,SMAD6,BBS4,CDH2,FST,DAB2,FLNA,CCDC78,CSF1,LMO4,CYR61,ADAMTSL2,CD151,FRZB,TBX20,MAFF,CDKN1A,EDA,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:0045471	0.15	0.92	9	87	response to ethanol	BP	1	SOD2,LEP,POLB,PTH,RGS2,FGFR2,MAOB,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:1901381	0.15	0.95	4	25	positive regulation of potassium ion transmembrane transport	BP	1	ABCC8,ACTN2,AKAP6,FLNA	darkgreen	VSMC_M4
GO:1904645	0.15	0.94	5	41	response to amyloid-beta	BP	1	GJA1,APP,LGMN,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:0046626	0.15	0.93	6	50	regulation of insulin receptor signaling pathway	BP	1	LEP,KANK1,FFAR3,NCK1,PTPN11,ADIPOR1	darkgreen	VSMC_M4
GO:0035329	0.15	0.94	5	35	hippo signaling	BP	1	AMOTL2,LATS2,WWC2,TEAD1,YAP1	darkgreen	VSMC_M4
GO:0043406	0.15	0.92	10	93	positive regulation of MAP kinase activity	BP	1	SASH1,TPD52L1,MAP3K7,ADAM9,FLT3,PDGFC,EDN1,HTR2B,MST1R,MAP3K13	darkgreen	VSMC_M4
GO:0030032	0.15	0.93	7	61	lamellipodium assembly	BP	1	WASF3,NCK1,OCLN,ABLIM1,ABLIM3,PLXNB3,CDH13	darkgreen	VSMC_M4
GO:0032602	0.15	0.93	7	64	chemokine production	BP	1	MBP,FFAR3,APP,LBP,LPL,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0032642	0.15	0.93	7	64	regulation of chemokine production	BP	1	MBP,FFAR3,APP,LBP,LPL,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0051341	0.15	0.92	8	79	regulation of oxidoreductase activity	BP	1	LEP,EDN2,EDN1,HTR2B,AOC3,HIF1A,NPR3,RFK	darkgreen	VSMC_M4
GO:1903649	0.15	0.95	4	28	regulation of cytoplasmic transport	BP	1	RAB29,ATP9A,RDX,DAB2	darkgreen	VSMC_M4
GO:0007422	0.15	0.92	8	69	peripheral nervous system development	BP	1	CITED2,LAMA2,ADGRB1,SCN8A,NAB1,NGF,NFASC,SH3TC2	darkgreen	VSMC_M4
GO:0051492	0.15	0.92	9	80	regulation of stress fiber assembly	BP	1	LIMCH1,PPP1R9A,TGFBR1,CD47,F11R,SYNPO2L,TGFB3,ARHGAP28,PPM1E	darkgreen	VSMC_M4
GO:0006811	0.15	0.88	80	1026	ion transport	BP	1	BCL2,SLC35D3,PKDREJ,CALHM5,GJA1,TRDN,DAPK1,LEP,WFS1,SLC2A1,SYT5,SLC17A5,PTPN3,TCAF1,TPT1,KCNE3,ACTN4,FGF14,TRPC4,SLC16A3,ATP2C1,TF,TUSC3,FXYD1,HPN,CHD7,MICU2,SLC25A4,SCN8A,CLCN3,SLC35G1,JPH1,GPM6A,APP,ABCC8,SLC26A7,SERINC3,ADA,EDN1,CD47,PLA2G4F,ANO5,CNNM2,RGS2,ACTN2,HTR2B,CAMK2D,ABCC9,CTSS,MYLK,LRP2,PRKD1,CYBRD1,SLC25A12,AKAP6,MAOB,LMTK2,NLGN1,WDR1,CACNA1C,PPARGC1A,MAGT1,KCNK10,SLC43A2,SCN1D,FLNA,VAMP7,HCN2,AHCYL1,PLCG2,LRRC8C,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,SLC27A5,SARAF,ICAM1,ATP6V0E1	darkgreen	VSMC_M4
GO:0051150	0.15	0.95	4	31	regulation of smooth muscle cell differentiation	BP	1	SOD2,SMARCD3,FGFR2,FGF9	darkgreen	VSMC_M4
GO:0032268	0.15	0.87	136	1819	regulation of cellular protein metabolic process	BP	1	MBP,GDF11,BCL2,SASH1,IRAK3,MDM2,LAPTM4B,RNF19A,OXR1,ANGPT1,C4A,TPD52L1,EP300,ADGRB1,DAPK1,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,FAM122A,DCUN1D4,VLDLR,PPP1R9A,RIC1,REST,RECK,TGFBR1,PTPN3,MAP3K7,ANTXR1,HIPK2,GATA2,INHBB,ITIH5,ADAM9,CRIM1,RASSF2,ANKLE2,FLT3,FXYD1,HPN,LATS2,HIPK3,CPEB3,NCK1,SH3RF1,OCLN,RNF34,CLU,APP,ATXN2,PDGFC,PTPN11,CCNT1,HERPUD1,PROS1,PTPN22,CHAC1,GDF6,AKTIP,RCAN1,NGF,EDN1,N4BP1,RGS2,LRP5,ARRDC4,PLCL1,HTR2B,MST1R,LGMN,AFAP1L2,SESN2,CAMK2D,NGRN,LRP2,CFLAR,CTSZ,INPP5F,RBM4B,PRKD1,NCSTN,DDR2,GPRC5A,MAP3K13,LRP6,HIP1,FAM129A,HSPB1,EIF4A2,SERPINE1,CRYAB,RDX,SECISBP2L,EIF4G3,ATG14,FBXL5,TNFSF10,DACT1,PCSK1N,HIF1A,PPARGC1A,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,DAB2,LGALS9,SKP2,PRKAA2,TMEM59,CTIF,DAPK3,CSF1,PLCG2,TERF2IP,F3,GLG1,BCAR3,CYR61,SLC8A1,SPINK2,LOX,CST3,CDKN1A,FGF9,PPM1E,CNTD2,GABARAPL2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0002931	0.15	0.93	6	51	response to ischemia	BP	1	BCL2,GJA1,REST,RCAN1,PPARGC1A,CSF1	darkgreen	VSMC_M4
GO:0048536	0.15	0.95	4	31	spleen development	BP	1	BCL2,CITED2,CDKN2B,POLB	darkgreen	VSMC_M4
GO:0050770	0.15	0.91	14	132	regulation of axonogenesis	BP	1	UST,SEMA3C,KIF13B,NGF,SEMA5A,PLXNA2,SHTN1,PLXNB1,MAP3K13,SIPA1L1,CDH2,ULK2,PAK3,PLXNB3	darkgreen	VSMC_M4
GO:0035023	0.15	0.92	8	69	regulation of Rho protein signal transduction	BP	1	ABRA,KANK1,ABCA1,ARHGEF3,RIPOR2,KCTD10,F11R,SYNPO2L	darkgreen	VSMC_M4
GO:0002833	0.15	0.92	10	101	positive regulation of response to biotic stimulus	BP	1	SASH1,EP300,CD274,MAP3K7,CD180,LBP,PRKCA,PAK3,PLCG2,BMP6	darkgreen	VSMC_M4
GO:0019748	0.15	0.95	4	30	secondary metabolic process	BP	1	BCL2,CYP1B1,PAM,OPN3	darkgreen	VSMC_M4
GO:0007409	0.15	0.89	32	341	axonogenesis	BP	1	BCL2,UST,LAMA2,ADGRB1,EPHB6,SEMA3C,KIF13B,APP,PTPN11,NGF,NFASC,SEMA5A,FEZ1,ROBO3,PARD6B,PLXNA2,SHTN1,FGFR2,PLXNB1,RAPH1,MAP3K13,UNC5B,LMTK2,SIPA1L1,NUMB,SLIT3,NPTN,CDH2,ULK2,PAK3,PLXNB3,NEXN	darkgreen	VSMC_M4
GO:0060291	0.15	0.93	7	62	long-term synaptic potentiation	BP	1	PPP1R9A,ZDHHC2,APP,LGMN,NCSTN,NLGN1,NPTN	darkgreen	VSMC_M4
GO:0033003	0.15	0.95	4	31	regulation of mast cell activation	BP	1	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4

GO:0042177	0.15	0.91	10	101	negative regulation of protein catabolic process	BP	1	IRAK3,LAPTM4B,ADGRB1,RIC1,PTPN3,HIPK2,N4BP1,FLNA,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:0086019	0.15	0.95	4	24	cell-cell signaling involved in cardiac conduction	BP	1	GJA1,TBX18,CACNA1C,FLNA	darkgreen	VSMC_M4
GO:0007369	0.15	0.91	14	138	gastrulation	BP	1	MBP,GJA1,LMBRD1,ITGA8,TENM4,COL4A2,ATOH8,HNF4A,ETS2,EYA2,LRP5,FGFR2,WLS,TBX20	darkgreen	VSMC_M4
GO:0001825	0.16	0.94	4	31	blastocyst formation	BP	1	CITED2,ADA,HOPX,YAP1	darkgreen	VSMC_M4
GO:0007519	0.16	0.91	12	122	skeletal muscle tissue development	BP	1	BCL2,CITED2,EP300,ANKRD1,RCAN1,RIPOR2,CFLAR,ZBTB18,RBFOX1,SRPK3,MAFF,HLF	darkgreen	VSMC_M4
GO:0030834	0.16	0.93	6	46	regulation of actin filament depolymerization	BP	1	SEMA5A,ACTN2,RDX,WDR1,SPTAN1,DSTN	darkgreen	VSMC_M4
GO:0050999	0.16	0.94	4	31	regulation of nitric-oxide synthase activity	BP	1	LEP,HTR2B,HIF1A,NPR3	darkgreen	VSMC_M4
GO:2001235	0.16	0.92	9	98	positive regulation of apoptotic signaling pathway	BP	1	TPD52L1,TGFBR1,INHBB,NCK1,SERINC3,TNFSF10,DAPK3,ITM2C,NACC2	darkgreen	VSMC_M4
GO:1903578	0.16	0.92	7	66	regulation of ATP metabolic process	BP	1	EP300,APP,SLC25A12,HIF1A,PPARGC1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0009583	0.16	0.94	4	32	detection of light stimulus	BP	1	GNAQ,GRK7,OPN3,ABCA4	darkgreen	VSMC_M4
GO:0046632	0.16	0.92	8	74	alpha-beta T cell differentiation	BP	1	BCL2,IL18R1,ZAP70,SH3RF1,ADA,RORA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0008203	0.16	0.91	10	103	cholesterol metabolic process	BP	1	LEP,VLDLR,ABCA1,APP,ABCG1,LRP5,ARV1,DISP3,PRKAA2,MBTPS1	darkgreen	VSMC_M4
GO:0030001	0.16	0.88	49	587	metal ion transport	BP	1	BCL2,PKDREJ,GJA1,TRDN,WFS1,PTPN3,TPT1,KCNE3,ACTN4,FGF14,TRPC4,ATP2C1,TF,TUSC3,FXYD1,HPN,CHD7,MICU2,SCN8A,SLC35G1,JPH1,GPM6A,ABCC8,CNNM2,ACTN2,HTR2B,CAMK2D,ABCC9,MYLK,LRP2,PRKD1,CYBRD1,AKAP6,LMTK2,CACNA1C,MAGT1,KCNK10,SCNN1D,FLNA,HCN2,AHCYL1,PLCG2,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,SARAF,ICAM1	darkgreen	VSMC_M4
GO:0031646	0.16	0.94	4	26	positive regulation of nervous system process	BP	1	UNC13B,TENM4,WASF3,SLC25A12	darkgreen	VSMC_M4
GO:1990928	0.16	0.93	5	42	response to amino acid starvation	BP	1	SESN1,MAP1LC3A,SESN2,PRKD1,CDKN1A	darkgreen	VSMC_M4
GO:0030968	0.16	0.92	7	69	endoplasmic reticulum unfolded protein response	BP	1	EP300,WFS1,CREB3,NCK1,HERPUD1,ATF6,MBTPS1	darkgreen	VSMC_M4
GO:0008154	0.16	0.90	17	183	actin polymerization or depolymerization	BP	1	KANK1,PPP1R9A,CDC42EP3,WASF3,NCK1,JMY,SEMA5A,ACTN2,PREX1,RDX,WDR1,MICAL3,PAK3,ARHGAP28,SPTAN1,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0070304	0.16	0.91	10	99	positive regulation of stress-activated protein kinase signaling cascade	BP	1	SASH1,TPD52L1,LEP,SH3RF3,HIPK2,RASSF2,SH3RF1,APP,GDF6,MID1	darkgreen	VSMC_M4
GO:0034976	0.16	0.89	19	222	response to endoplasmic reticulum stress	BP	1	BCL2,EP300,WFS1,CREB3,STT3B,NCK1,CLU,HERPUD1,CHAC1,SERINC3,MARCH6,SESN2,ATF6,FAM129A,JKAMP,FAF2,MBTPS1,ITPR1,FBXO27	darkgreen	VSMC_M4
GO:0021915	0.16	0.90	13	130	neural tube development	BP	1	CITED2,GRHL2,SEMA3C,ADM,SHROOM3,SEC24B,PLXNA2,LRP2,ATP6AP2,DACT1,HIF1A,BBS4,LMO4	darkgreen	VSMC_M4
GO:0061462	0.16	0.93	5	41	protein localization to lysosome	BP	1	LMBRD1,GGA3,CLU,SCARB2,SORT1	darkgreen	VSMC_M4
GO:0032990	0.16	0.87	48	536	cell part morphogenesis	BP	1	BCL2,UST,GRIP1,DDR1,GJA1,LAMA2,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,KIDINS220,EPHB6,ITSN2,SEMA3C,KIF13B,GPM6A,APP,PTPN11,NGF,NFASC,SEMA5A,FEZ1,ROBO3,PARD6B,PLXNA2,SHTN1,LRP2,FGFR2,PLXNB1,RAPH1,ZNF365,MAP3K13,CUX1,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,NPTN,NRK,CDH2,ULK2,PAK3,PLXNB3,NEXN,SDC2	darkgreen	VSMC_M4
GO:0002686	0.16	0.94	4	33	negative regulation of leukocyte migration	BP	1	LRCH1,ADA,RIPOR2,MMP28	darkgreen	VSMC_M4
GO:0071375	0.16	0.89	20	219	cellular response to peptide hormone stimulus	BP	1	MDM2,LEP,KANK1,PDK4,INHBB,FOXO1,FFAR3,NCK1,PTPN11,ADCY6,EDN1,LPL,ADIPOR1,ACTN2,ZNF106,CFLAR,WDTC1,AHCYL1,BCAR3,PIK3C2A	darkgreen	VSMC_M4
GO:0070374	0.16	0.90	13	145	positive regulation of ERK1 and ERK2 cascade	BP	1	ANGPT1,APP,PDGFC,PTPN11,PTPN22,NPNT,HTR2B,PRKCA,CFLAR,FGFR2,NPTN,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0030201	0.16	0.94	4	29	heparan sulfate proteoglycan metabolic process	BP	1	HS6ST1,EXTL3,NDST3,EXTL2	darkgreen	VSMC_M4
GO:0060390	0.16	0.94	4	28	regulation of SMAD protein signal transduction	BP	1	TGFBR1,TGFB3,DAB2,BMP6	darkgreen	VSMC_M4
GO:0033692	0.16	0.93	6	52	cellular polysaccharide biosynthetic process	BP	1	GYS1,PTH,GYG1,B3GNT7,GYG2,NDST3	darkgreen	VSMC_M4
GO:0035264	0.16	0.91	11	108	multicellular organism growth	BP	1	BCL2,GRHL2,EP300,PPP1R13L,CHD7,APP,PTPN11,LGMN,WDTC1,ARID5B,CSF1	darkgreen	VSMC_M4
GO:0048864	0.16	0.92	8	72	stem cell development	BP	1	CITED2,SEMA3C,FAM172A,EDN1,SEMA5A,HTR2B,HIF1A,CDH2	darkgreen	VSMC_M4
GO:1900076	0.16	0.93	6	51	regulation of cellular response to insulin stimulus	BP	1	LEP,KANK1,NCK1,PTPN11,LPL,ADIPOR1	darkgreen	VSMC_M4
GO:0033143	0.16	0.92	7	63	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	EP300,LBH,NCOR2,STRN3,DAB2,SKP2,YAP1	darkgreen	VSMC_M4
GO:0030225	0.16	0.94	4	32	macrophage differentiation	BP	1	GATA2,APP,PRKCA,CSF1	darkgreen	VSMC_M4
GO:0048661	0.17	0.91	8	78	positive regulation of smooth muscle cell proliferation	BP	1	MDM2,GJA1,EDN1,FGFR2,PPARGC1A,SKP2,CDH13,FGF9	darkgreen	VSMC_M4
GO:1902532	0.17	0.88	34	407	negative regulation of intracellular signal transduction	BP	1	BCL2,IRAK3,MDM2,SOD2,WFS1,KANK1,RNF149,CREB3,SESN1,TPT1,NDRG2,FOXO1,RASSF2,HIPK3,WWC2,RNF34,CLU,HERPUD1,PTPN22,RCAN1,ADIPOR1,RIPOR2,RGS2,KCTD10,SESN2,CASTOR1,HSPB1,DACT1,HIF1A,RORA,PRKAA2,ITPR1,VNN1,DDIT4	darkgreen	VSMC_M4
GO:0044262	0.17	0.89	20	229	cellular carbohydrate metabolic process	BP	1	EP300,LEP,PDK4,GYS1,HRH1,PFKFB3,PTH,GYG1,SCARB2,ADIPOR1,B3GNT7,GYG2,SESN2,NDST3,SLC25A12,PPIP5K1,PPARGC1A,RORA,OCRL,DDIT4	darkgreen	VSMC_M4
GO:0071346	0.17	0.91	8	80	cellular response to interferon-gamma	BP	1	IFNGR1,DAPK1,MRC1,EDN1,CD47,LGALS9,DAPK3,ICAM1	darkgreen	VSMC_M4
GO:0002088	0.17	0.92	7	63	lens development in camera-type eye	BP	1	CITED2,TGFBR1,HIPK2,KDM5B,CRYGS,CRYAB,BCAR3	darkgreen	VSMC_M4
GO:0070169	0.17	0.93	5	41	positive regulation of biomineral tissue development	BP	1	PTH,TGFB3,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:0010001	0.17	0.89	16	173	glial cell differentiation	BP	1	IFNGR1,LAMA2,TENM4,TRPC4,WASF3,CLU,APP,PTPN11,NAB1,BACE2,NCSTN,ZNF365,WDR1,CDH2,SH3TC2,BNIP3	darkgreen	VSMC_M4
GO:0002720	0.17	0.93	5	42	positive regulation of cytokine production involved in immune response	BP	1	DDX58,IL18R1,MAP3K7,FFAR3,PLCG2	darkgreen	VSMC_M4
GO:0035601	0.17	0.91	10	99	protein deacylation	BP	1	EP300,REST,ABHD12,SMARCAD1,CAMK2D,PRKD1,SIN3B,PRKAA2,FLNA,HOPX	darkgreen	VSMC_M4
GO:1902622	0.17	0.94	4	34	regulation of neutrophil migration	BP	1	LBP,EDN1,JAM3,RIPOR2	darkgreen	VSMC_M4
GO:0006022	0.17	0.91	10	98	aminoglycan metabolic process	BP	1	DSEL,UST,ANGPT1,HS6ST1,ITIH5,CHST2,B3GNT7,NDST3,CHST15,BGN	darkgreen	VSMC_M4
GO:0071711	0.17	0.94	4	30	basement membrane organization	BP	1	COL4A1,HPN,NID1,CTSS	darkgreen	VSMC_M4
GO:1905710	0.17	0.94	4	36	positive regulation of membrane permeability	BP	1	JAM3,EYA2,RHOT1,BNIP3	darkgreen	VSMC_M4
GO:0018210	0.17	0.90	11	104	peptidyl-threonine modification	BP	1	BCL2,TGFBR1,HIPK2,HIPK3,APP,GALNT3,PRKCA,CAMK2D,PRKD1,LMTK2,DDIT4	darkgreen	VSMC_M4
GO:1903201	0.17	0.92	6	56	regulation of oxidative stress-induced cell death	BP	1	SOD2,OXR1,REST,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0098927	0.17	0.93	5	40	vesicle-mediated transport between endosomal compartments	BP	1	AKTIP,RDX,LMTK2,DAB2,FLNA	darkgreen	VSMC_M4

GO:0097720	0.17	0.93	5	40	calcineurin-mediated signaling	BP	1	LMCD1,RCAN1,AKAP6,PLCG2,C10orf71	darkgreen	VSMC_M4
GO:0030574	0.17	0.94	4	31	collagen catabolic process	BP	1	CTSS,MMP1,MMP28,CST3	darkgreen	VSMC_M4
GO:2001239	0.17	0.94	4	33	regulation of extrinsic apoptotic signaling pathway in absence of ligand	BP	1	BCL2,EYA2,UNC5B,DAPK3	darkgreen	VSMC_M4
GO:0051247	0.17	0.86	87	1140	positive regulation of protein metabolic process	BP	1	MBP,GDF11,BCL2,RNF41,IFNGR1,SASH1,MDM2,RNF19A,ANGPT1,GJA1,TPD52L1,DAPK1,LEP,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,REST,TGFBR1,MAP3K7,ANTXR1,HIPK2,GGA3,INHBB,ADAM9,FOXO1,RASSF2,ANKLE2,FLT3,HPN,CPEB3,NCK1,CLU,APP,PDGFC,PTPN11,CCNT1,HERPUD1,PTPN22,GDF6,AKTIP,NGF,EDN1,ABCG1,ARRDC4,HTR2B,MST1R,LGMN,AFAP1L2,NGRN,LRP2,CFLAR,PRKD1,NCSTN,DDR2,GPRC5A,MAP3K13,HIP1,FAM129A,RDX,ATG14,FBXL5,TNFSF10,DACT1,PPARGC1A,TGFB3,TOM1L1,FAXDC2,NPTN,DAB2,LGALS9,SKP2,PRKAA2,CTIF,CSF1,PLCG2,TERF2IP,F3,BCAR3,CYR61,CDKN1A,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0007010	0.17	0.86	95	1177	cytoskeleton organization	BP	1	BCL2,RNF19A,GJA1,TRDN,MRTFA,LIMCH1,KANK1,TPM2,PPP1R9A,TGFBR1,CALD1,ANTXR1,TUBE1,TESK2,ARHGEF17,ACTN4,FMNL2,TACC1,ATP2C1,CDC42EP3,PCLO,EML4,TF,AMOTL2,WASF3,ANKRD1,EPB41L4A,NCK1,SORBS2,PAM,OCLN,PRPH,SHROOM3,JMY,EDN1,JAM3,CD47,MYO1B,SEMA5A,DNAH7,MARCKSL1,TNNT2,ACTN2,PREX1,SUN1,ABLIM1,PARD6B,MID1,SHTN1,CFLAR,SYNPO2,F11R,PLXNB1,LRCH3,ZRANB1,MAP7D2,HIP1,CRYAB,RDX,SYNPO2L,NLGN1,WDR1,IQSEC3,MICAL3,GNAI1,ACTN1,SIPA1L1,CHD3,TGFB3,CNN1,BBS4,NRK,MAPRE2,SPECC1,SYNPO,PAK3,GAS2L2,PLS3,ABLIM3,ARHGAP28,PATJ,PRKAA2,DAPK3,FLNA,CCDC78,SPTAN1,NEXN,XIRP1,PDLIM3,CSRP1,PPM1E,DSTN,ICAM1,PRKG1,FAM83H	darkgreen	VSMC_M4
GO:0003197	0.17	0.93	5	40	endocardial cushion development	BP	1	CITED2,MDM2,TGFBR1,TBX20,CRELD1	darkgreen	VSMC_M4
GO:0043405	0.17	0.89	14	146	regulation of MAP kinase activity	BP	1	SASH1,IRAK3,TPD52L1,MAP3K7,ADAM9,FLT3,HIPK3,PDGFC,PTPN22,EDN1,RGS2,HTR2B,MST1R,MAP3K13	darkgreen	VSMC_M4
GO:0090140	0.17	0.94	4	31	regulation of mitochondrial fission	BP	1	TMEM135,MARCH5,PPARGC1A,BNIP3	darkgreen	VSMC_M4
GO:0086003	0.17	0.92	7	57	cardiac muscle cell contraction	BP	1	GJA1,KCNE3,CAMK2D,CACNA1C,FLNA,KCNE4,PLN	darkgreen	VSMC_M4
GO:0051234	0.17	0.85	251	3429	establishment of localization	BP	1	BCL2,SLC35D3,STX11,GRIP1,MDM2,DDR1,LAPTM4B,IPCEF1,ABRA,ANGPT1,C4A,PKDREJ,CALHM5,GJA1,TRDN,ADGRB1,DAPK1,SH3GL2,LEP,WFS1,VLDLR,UNC13B,PPP1R9A,CD274,RIC1,DYNC1I1,REST,ICA1,FRMPD1,LMAN2L,SNX13,SLC2A1,PREPL,LMBRD1,SYT5,SLC17A5,ABCA1,PTPN3,DOP1A,SNAP91,PEX13,ANTXR1,MDFIC,TCAF1,SLC37A3,ITSN2,GATA2,MRC1,TPT1,TMCC1,GGA3,INHBB,USP6NL,CD93,SYNGR2,KCNE3,RAB2B,ACTN4,ADAM9,FGF14,TRPC4,SLC16A3,ATP2C1,PCLO,EML4,TF,APLP1,TUSC3,ZDHHC2,NCOR2,FFAR3,FXYD1,HPN,DENND5A,CHD7,MICU2,ANKRD1,TRIM23,EXOC6,ADM,ESYT3,PAM,SLC25A4,SCN8A,CLCN3,OCLN,SLC35G1,MCTP1,JPH1,PTH,KIF13B,G3BP2,CLU,GPM6A,APP,ATXN2,SCARB2,ABCC8,ANXA3,PTPN11,PTX3,LBP,HERPUD1,SLC26A7,ATG13,HNF4A,SERINC3,ADA,AKTIP,IFIT1,PDZD7,EDN1,CD47,PLA2G4F,ANO5,MYO1B,RAB29,ABCG1,CNNM2,KDM5B,RGS2,EYA2,TNNT2,ACTN2,PFKL,LRP5,ARRDC4,FEZ1,NPNT,HTR2B,MST1R,TINAGL1,ZMAT3,TM7SF3,SUN1,TXNIP,SEC24B,CFI,MFGE8,ATP9A,SESN2,ARV1,CAMK2D,ABCC9,ADCY5,CTSS,MYLK,LRP2,INPP5F,FABP2,PTPN14,PRKD1,PI4KB,F11R,CYBRD1,DYNC1I2,SLC25A12,RAPGEF4,AP3B2,AKAP6,LRP6,HIP1,HSPB1,CUX1,SERPINE1,ACHE,CRYAB,RDX,EXPH5,MAOB,GULP1,ATG14,EMC1,CYP19A1,LMTK2,NLGN1,WDR1,RABEP1,HIF1A,SYT16,OPN3,CACNA1C,AP1S3,MICAL3,ADGRE2,FBXL20,PPARGC1A,NPPB,DISP3,FAF2,NUMB,TGFB3,IFT43,MAGT1,TOM1L1,KCNK10,KIAA0556,EPG5,SLC14A1,BBS4,STOML1,ATG4A,GP2,CDH2,EVI5L,ABLIM3,SH3TC2,RHOT1,MARCH2,DNAJC6,DAB2,LGALS9,NPR3,MYO10,RBFOX1,SLC43A2,SCNN1D,FLNA,VAMP7,SLC2A5,HCN2,AHCYL1,SORT1,	darkgreen	VSMC_M4
GO:0007416	0.17	0.89	14	132	synapse assembly	BP	1	ADGRB1,PPP1R9A,PCDHB4,PCLO,GPM6A,APP,RAB29,PLXNB1,ACHE,NLGN1,NPTN,CDH2,PCDHB2,LRRC24	darkgreen	VSMC_M4
GO:0007212	0.17	0.94	4	31	dopamine receptor signaling pathway	BP	1	ADCY6,ADCY5,NCSTN,FLNA	darkgreen	VSMC_M4
GO:0042472	0.17	0.91	8	73	inner ear morphogenesis	BP	1	TBX18,GATA2,HPN,CHD7,PDZD7,SEC24B,FGFR2,FRZB	darkgreen	VSMC_M4
GO:0010332	0.17	0.92	6	53	response to gamma radiation	BP	1	BCL2,MDM2,POLB,CRYAB,CDKN1A,YAP1	darkgreen	VSMC_M4
GO:0009913	0.17	0.90	12	120	epidermal cell differentiation	BP	1	CDSN,GRHL2,FOSL2,ADAM9,PDZD7,NCOA3,TXNIP,SEC24B,EXPH5,OPN3,MAFF,YAP1	darkgreen	VSMC_M4
GO:0008637	0.17	0.91	8	87	apoptotic mitochondrial changes	BP	1	BCL2,SOD2,SLC25A4,CLU,EYA2,TNFSF10,RHOT1,BNIP3	darkgreen	VSMC_M4
GO:0046622	0.17	0.93	5	41	positive regulation of organ growth	BP	1	EDN1,FGFR2,AKAP6,TBX20,YAP1	darkgreen	VSMC_M4
GO:0030195	0.18	0.93	4	35	negative regulation of blood coagulation	BP	1	PROS1,EDN1,SERPINE1,PRKG1	darkgreen	VSMC_M4
GO:0051302	0.18	0.89	13	138	regulation of cell division	BP	1	MLLT3,LBH,PDGFC,PKP4,RBL2,NCOA3,HTR2B,TXNIP,FGFR2,ZFYVE26,TGFB3,BBS4,FGF9	darkgreen	VSMC_M4

GO:0010605	0.18	0.85	156	2090	negative regulation of macromolecule metabolic process	BP	1	CITED2,IRAK3,MDM2,LAPTM4B,OXR1,ANGPT1,C4A,TRPS1,GJA1,ZHX1,EP300,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,CD274,RIC1,ZNF169,REST,RECK,PTPN3,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,INHBB,ITIH5,LBH,NDRG2,LMCD1,THRB,SATB1,CRIM1,FOXO1,RASSF2,MIER3,NCOR2,FXYD1,ZC3H6,LATS2,HIPK3,ANKRD1,CPEB3,NCK1,SH3RF1,ATOH8,OCLN,WWC2,FAM172A,PTH,RNF34,CLU,MEIS2,APP,ATXN2,PTX3,LBP,CCNT1,HERPUD1,PROS1,PTPN22,HNF4A,CHAC1,NAB1,RBL2,NGF,EDN1,ETS2,N4BP1,BACE2,KDM5B,RGS2,MXI1,LRP5,LGMN,PRKCA,TXNIP,HELZ,SESN2,YEATS2,CTSZ,WDTC1,INPP5F,FGFR2,TP53BP1,STRN3,ARID5B,GPRC5A,ID3,LRP6,FAM129A,HSPB1,EIF4A2,CUX1,SERPINE1,CRYAB,EZH1,ATG14,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,ZBTB18,APBB2,ZBTB4,PPARGC1A,CHD3,SLIT3,TGFB3,SMAD6,NPTN,FST,DAB2,LGALS9,MARF1,PRKAA2,TMEM59,CTIF,DAPK3,TLE2,FLNA,TERF2IP,GLG1,ZFP90,MIR99A,MIR331,SLC8A1,SPINK2,CD83,TBX20,ITM2C,CST3,ZNF425,ZNF175,CDKN1A,ZNF572,PPM1E,NACC2,ZNF79,HOPX,GABARAPL2,STC2,YAP1,HKR1,BMP6,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:0002064	0.18	0.88	17	173	epithelial cell development	BP	1	CDSN,GRHL2,FOSL2,SHROOM3,HNF4A,PDZD7,SEC24B,F11R,RDX,EXPH5,HIF1A,CDH2,FLNA,CDKN1A,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:0071345	0.18	0.86	45	574	cellular response to cytokine stimulus	BP	1	IFNGR1,IRAK3,ANGPT1,DAPK1,TLE4,LEP,DOCK8,IL18R1,EDN2,ABCA1,MAP3K7,LRCH1,MRC1,ACTN4,FLT3,ANKRD1,OCLN,PTPN11,IFIT1,EDN1,CD47,MX1,ADIPOR1,KDM5B,RIPOR2,NPNT,MST1R,ARID5B,AKAP6,EIF4A2,HIF1A,PPARGC1A,RORA,SLIT3,BBS4,LGALS9,DAPK3,CSF1,VCAM1,F3,MIR99A,LOX,CCR6,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0006378	0.18	0.93	5	40	mRNA polyadenylation	BP	1	PAPOLG,CPEB3,APP,CCNT1,AHCYL1	darkgreen	VSMC_M4
GO:1905897	0.18	0.91	7	70	regulation of response to endoplasmic reticulum stress	BP	1	WFS1,CREB3,NCK1,CLU,HERPUD1,SERINC3,ATF6	darkgreen	VSMC_M4
GO:0070167	0.18	0.91	8	74	regulation of biomineral tissue development	BP	1	PTH,DDR2,NBR1,HIF1A,TGFB3,CYR61,SLC8A1,BMP6	darkgreen	VSMC_M4
GO:0055088	0.18	0.90	11	116	lipid homeostasis	BP	1	ABCA1,HNF4A,LPL,ABCG1,LRP5,SESN2,DISP3,RORA,ANGPTL4,PRKAA2,ORMDL3	darkgreen	VSMC_M4
GO:0010518	0.18	0.92	5	41	positive regulation of phospholipase activity	BP	1	GNAQ,PTH,HTR2B,FGFR2,CYR61	darkgreen	VSMC_M4
GO:0045428	0.18	0.92	5	43	regulation of nitric oxide biosynthetic process	BP	1	CLU,PTX3,EDN1,CD47,ICAM1	darkgreen	VSMC_M4
GO:0034341	0.18	0.90	9	95	response to interferon-gamma	BP	1	IFNGR1,DAPK1,MRC1,EDN1,CD47,CALCOCO2,LGALS9,DAPK3,ICAM1	darkgreen	VSMC_M4
GO:0055006	0.18	0.91	8	71	cardiac cell development	BP	1	SGCB,TBX18,SORBS2,EDN1,RGS2,ACTN2,AKAP6,SLC8A1	darkgreen	VSMC_M4
GO:0008584	0.18	0.90	11	111	male gonad development	BP	1	BCL2,CITED2,TGFBR1,LRP2,ARID5B,PRDX4,TNFSF10,TEX11,FLNA,FGF9,ICAM1	darkgreen	VSMC_M4
GO:0043467	0.18	0.90	10	104	regulation of generation of precursor metabolites and energy	BP	1	EP300,PTH,APP,SLC25A12,HIF1A,OPN3,PPARGC1A,PRKAA2,BNIP3,DDIT4	darkgreen	VSMC_M4
GO:0045124	0.18	0.93	4	32	regulation of bone resorption	BP	1	PDK4,TF,TMEM64,PRKCA	darkgreen	VSMC_M4
GO:0070839	0.18	0.92	5	40	metal ion export	BP	1	KCNE3,FXYD1,SLC35G1,KCNE4,SLC8A1	darkgreen	VSMC_M4
GO:0010573	0.18	0.93	4	30	vascular endothelial growth factor production	BP	1	NDRG2,CYP1B1,HIF1A,RORA	darkgreen	VSMC_M4
GO:0014020	0.18	0.90	9	86	primary neural tube formation	BP	1	CITED2,GRHL2,ADM,SHROOM3,SEC24B,LRP2,HIF1A,BBS4,LMO4	darkgreen	VSMC_M4
GO:0050890	0.18	0.88	20	214	cognition	BP	1	EP300,VLDLR,HRH1,TUSC3,CHD7,CPEB3,MEIS2,APP,ABCC8,TANC1,RCAN1,NGF,LGMN,NCSTN,HIF1A,MAGT1,KCNK10,BBS4,NPTN,TMPRSS11E	darkgreen	VSMC_M4
GO:0034205	0.18	0.92	5	44	amyloid-beta formation	BP	1	IFNGR1,GGA3,CLU,ABCG1,NCSTN	darkgreen	VSMC_M4
GO:0006643	0.18	0.89	14	164	membrane lipid metabolic process	BP	1	PIGN,SUMF1,CYP1B1,ST3GAL5,SERINC3,SERINC2,ARV1,PRKD1,PIGG,PIGS,CYR61,ST6GALNAC3,PIGK,ORMDL3	darkgreen	VSMC_M4
GO:0034260	0.18	0.93	4	31	negative regulation of GTPase activity	BP	1	LRCH1,F11R,RDX,PLXNB3	darkgreen	VSMC_M4
GO:0002526	0.18	0.91	6	58	acute inflammatory response	BP	1	FFAR3,LBP,VCAM1,F3,VNN1,ICAM1	darkgreen	VSMC_M4
GO:0002700	0.18	0.90	10	106	regulation of production of molecular mediator of immune response	BP	1	IRAK3,ANGPT1,DDX58,IL18R1,MAP3K7,FFAR3,PTPN22,TP53BP1,TGFB3,PLCG2	darkgreen	VSMC_M4
GO:0048863	0.18	0.88	16	171	stem cell differentiation	BP	1	CITED2,MLLT3,REST,LBH,SEMA3C,FAM172A,GPM6A,EDN1,SEMA5A,HTR2B,FGFR2,LRP6,HIF1A,CDH2,FRZB,YAP1	darkgreen	VSMC_M4
GO:0043300	0.18	0.93	4	32	regulation of leukocyte degranulation	BP	1	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0050954	0.18	0.89	12	120	sensory perception of mechanical stimulus	BP	1	MBP,WFS1,THRB,HPN,CHD7,SCARB2,PDZD7,RIPOR2,LRP2,USP53,WDR1,ICAM1	darkgreen	VSMC_M4
GO:0038066	0.18	0.92	5	44	p38MAPK cascade	BP	1	SASH1,LEP,PTPN22,GDF6,LGALS9	darkgreen	VSMC_M4
GO:0006954	0.18	0.86	39	497	inflammatory response	BP	1	C4A,SCUBE1,GJA1,LEP,IL18R1,ABHD12,HRH1,POLB,FFAR3,ADM,CD180,CHST2,BLNK,APP,PTX3,LBP,ADA,JAM3,CD47,LPL,AFAP1L2,PRKD1,F11R,SERPINE1,AOC3,HIF1A,ADGRE2,RORA,LGALS9,VAMP7,CSF1,PLCG2,VCAM1,F3,VNN1,TLR1,CCR6,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0098732	0.18	0.89	10	102	macromolecule deacylation	BP	1	EP300,REST,ABHD12,SMARCAD1,CAMK2D,PRKD1,SIN3B,PRKAA2,FLNA,HOPX	darkgreen	VSMC_M4
GO:0046637	0.18	0.92	5	44	regulation of alpha-beta T cell differentiation	BP	1	ZAP70,SH3RF1,ADA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0008610	0.19	0.86	42	544	lipid biosynthetic process	BP	1	PIGN,HSD17B6,LEP,PIP5K1B,PDK4,REST,IGFBP7,EDN2,CHPT1,ADM,PAM,ST3GAL5,LPCAT2,EDN1,PLA2G4F,LPL,ABCG1,AGPAT3,HTR2B,ARV1,WDTC1,INPP5F,PRKD1,PI4KB,ACHE,CYP19A1,PPARGC1A,PIGG,FAXDC2,OCRL,PIGS,PRKAA2,MBTPS1,PLCG2,CYR61,ST6GALNAC3,PIGK,SLC27A5,PIK3C2A,ORMDL3,BMP6,SCP2	darkgreen	VSMC_M4
GO:0021515	0.19	0.93	4	30	cell differentiation in spinal cord	BP	1	GATA2,ZC4H2,LMO4,TBX20	darkgreen	VSMC_M4
GO:0042752	0.19	0.90	9	89	regulation of circadian rhythm	BP	1	GNAQ,HNF4A,ADA,RBM4B,NLGN1,OPN3,PPARGC1A,RORA,PRKAA2	darkgreen	VSMC_M4
GO:0061912	0.19	0.91	7	63	selective autophagy	BP	1	SLC25A4,ATG13,SESN2,ATG14,CALCOCO2,ULK2,LRSAM1	darkgreen	VSMC_M4
GO:0006476	0.19	0.90	9	88	protein deacetylation	BP	1	EP300,REST,SMARCAD1,CAMK2D,PRKD1,SIN3B,PRKAA2,FLNA,HOPX	darkgreen	VSMC_M4
GO:0097306	0.19	0.90	8	71	cellular response to alcohol	BP	1	MDM2,SOD2,ABCA1,ADCY6,ADCY5,LRP6,GNAI1,PRKAA2	darkgreen	VSMC_M4
GO:0043627	0.19	0.91	6	57	response to estrogen	BP	1	CITED2,MDM2,EP300,IGFBP2,TGFB3,SMAD6	darkgreen	VSMC_M4
GO:0046546	0.19	0.89	11	112	development of primary male sexual characteristics	BP	1	BCL2,CITED2,TGFBR1,LRP2,ARID5B,PRDX4,TNFSF10,TEX11,FLNA,FGF9,ICAM1	darkgreen	VSMC_M4

GO:0001501	0.19	0.86	35	413	skeletal system development	BP	1	GDF11,CITED2,GRHL2,TRPS1,GJA1,EP300,LEP,TGFBR1,RASSF2,CHD7,PTH,PDGFC,PTPN11,GDF6,NAB1,EDN1,ETS2,LRP5,FGFR2,PLXNB1,ARID5B,LNPK,PAPPA2,HIF1A,FGFRL1,TGFB3,PLS3,FST,NPR3,BGN,GLG1,CYR61,FRZB,LOX,BMP6	darkgreen	VSMC_M4
GO:0060840	0.19	0.90	9	81	artery development	BP	1	CITED2,LEP,TGFBR1,CHD7,SEC24B,MYLK,LRP2,SMAD6,LOX	darkgreen	VSMC_M4
GO:0021987	0.19	0.90	9	87	cerebral cortex development	BP	1	SLC2A1,PEX13,TACC1,SUN1,HIF1A,BBS4,CDH2,FLNA,BNIP3	darkgreen	VSMC_M4
GO:0043547	0.19	0.87	19	202	positive regulation of GTPase activity	BP	1	DOCK8,RIC1,SNX13,CHN2,USP6NL,RALGAPA2,PKP4,PREX1,F11R,PLXNB1,ITGA6,SIPA1L1,MAPRE2,EVI5L,TBC1D13,ARHGAP29,BCAR3,SYDE2,ICAM1	darkgreen	VSMC_M4
GO:1900047	0.19	0.93	4	36	negative regulation of hemostasis	BP	1	PROS1,EDN1,SERPINE1,PRKG1	darkgreen	VSMC_M4
GO:0043647	0.19	0.92	5	42	inositol phosphate metabolic process	BP	1	HRH1,PTH,PPIP5K1,OCRL,PLCG2	darkgreen	VSMC_M4
GO:0001649	0.19	0.87	17	190	osteoblast differentiation	BP	1	REST,CRIM1,RASSF2,TMEM64,LRP5,NPNT,FGFR2,PRKD1,DDR2,ID3,ACHE,NBR1,SMAD6,CYR61,LOX,YAP1,BMP6	darkgreen	VSMC_M4
GO:0007610	0.19	0.86	35	406	behavior	BP	1	BCL2,OXR1,GJA1,EP300,LEP,WFS1,VLDLR,PEX13,HIPK2,ABHD12,HRH1,THRB,CHD7,CPEB3,CLCN3,MEIS2,APP,ABCC8,TANC1,ADA,RCAN1,NGF,HTR2B,LGMN,ADCY5,INPP5F,NCSTN,NLGN1,HIF1A,FBXL20,KCNK10,BBS4,NPTN,ORMDL3,NPAS1	darkgreen	VSMC_M4
GO:1903351	0.19	0.91	6	55	cellular response to dopamine	BP	1	HRH1,ADCY6,HTR2B,ADCY5,NCSTN,FLNA	darkgreen	VSMC_M4
GO:0033144	0.19	0.93	4	31	negative regulation of intracellular steroid hormone receptor signaling pathway	BP	1	LBH,NCOR2,STRN3,DAB2	darkgreen	VSMC_M4
GO:0032410	0.19	0.91	6	57	negative regulation of transporter activity	BP	1	TRDN,KCNE3,ACTN2,CAMK2D,KCNE4,PLN	darkgreen	VSMC_M4
GO:0048754	0.19	0.88	12	121	branching morphogenesis of an epithelial tube	BP	1	BCL2,DDR1,COL4A1,EDN1,KDM5B,LRP5,NPNT,CTSZ,FGFR2,CSF1,TBX20,YAP1	darkgreen	VSMC_M4
GO:0010822	0.19	0.91	6	59	positive regulation of mitochondrion organization	BP	1	MARCH5,SLC25A4,TNFSF10,HIF1A,PPARGC1A,BNIP3	darkgreen	VSMC_M4
GO:0001707	0.19	0.91	6	53	mesoderm formation	BP	1	GJA1,ITGA8,EYA2,FGFR2,WLS,TBX20	darkgreen	VSMC_M4
GO:0033146	0.19	0.93	4	32	regulation of intracellular estrogen receptor signaling pathway	BP	1	LBH,STRN3,SKP2,YAP1	darkgreen	VSMC_M4
GO:0010720	0.19	0.87	21	231	positive regulation of cell development	BP	1	BCL2,LIMS2,TENM4,SMARCD3,NGF,SEMA5A,PREX1,PLXNA2,SHTN1,LRP2,F11R,PLXNB1,ZNF365,MAP3K13,CUX1,HIF1A,NUMB,NPTN,PAK3,PLXNB3,FLNA	darkgreen	VSMC_M4
GO:0003179	0.19	0.91	6	50	heart valve morphogenesis	BP	1	MDM2,FGFRL1,SLIT3,SMAD6,CYR61,TBX20	darkgreen	VSMC_M4
GO:0009615	0.19	0.87	21	253	response to virus	BP	1	BCL2,IFNGR1,IRAK3,DDX58,NT5C3A,TPT1,CLU,PTPN22,SERINC3,IFIT1,MX1,MST1R,ABCC9,HSPB1,HIF1A,LGALS9,SKP2,IFI44,BNIP3,ZNF175,DDIT4	darkgreen	VSMC_M4
GO:0006006	0.19	0.88	14	155	glucose metabolic process	BP	1	EP300,LEP,PDK4,GALM,PTH,HECTD4,ADIPOR1,PFKL,LRP5,SESN2,WDTC1,SLC25A12,PPARGC1A,RORA	darkgreen	VSMC_M4
GO:0043631	0.19	0.92	5	41	RNA polyadenylation	BP	1	PAPOLG,CPEB3,APP,CCNT1,AHCYL1	darkgreen	VSMC_M4
GO:0034620	0.19	0.90	8	86	cellular response to unfolded protein	BP	1	EP300,WFS1,CREB3,NCK1,HERPUD1,TM7SF3,ATF6,MBTPS1	darkgreen	VSMC_M4
GO:0071774	0.19	0.89	9	91	response to fibroblast growth factor	BP	1	SMOC2,PTH,PTPN11,KDM5B,GALNT3,FGFR2,FGFRL1,NPTN,FGF9	darkgreen	VSMC_M4
GO:0034220	0.19	0.84	60	765	ion transmembrane transport	BP	1	SLC35D3,PKDREJ,CALHM5,GJA1,TRDN,DAPK1,SLC17A5,PTPN3,TCAF1,KCNE3,ACTN4,FGF14,TRPC4,SLC16A3,ATP2C1,TUSC3,FXYD1,HPN,CHD7,MICU2,SLC25A4,SCN8A,CLCN3,SLC35G1,JPH1,GPM6A,APP,ABCC8,SLC26A7,ANO5,CNNM2,RGS2,ACTN2,HTR2B,CAMK2D,ABCC9,CTSS,LRP2,PRKD1,SLC25A12,AKAP6,NLGN1,WDR1,CACNA1C,PPARGC1A,MAGT1,KCNK10,SLC43A2,SCNN1D,FLNA,HCN2,AHCYL1,PLCG2,LRRC8C,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,ATP6V0E1	darkgreen	VSMC_M4
GO:0046638	0.19	0.92	4	34	positive regulation of alpha-beta T cell differentiation	BP	1	ZAP70,ADA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0002831	0.19	0.87	19	224	regulation of response to biotic stimulus	BP	1	SASH1,IRAK3,EP300,LEP,DDX58,CD274,MAP3K7,CD180,PTPN11,LBP,PTPN22,IFIT1,N4BP1,PRKCA,PAK3,LGALS9,PLCG2,LRSAM1,BMP6	darkgreen	VSMC_M4
GO:0009247	0.19	0.91	6	61	glycolipid biosynthetic process	BP	1	PIGN,ST3GAL5,PIGG,PIGS,ST6GALNAC3,PIGK	darkgreen	VSMC_M4
GO:0030593	0.19	0.91	6	60	neutrophil chemotaxis	BP	1	EDN2,LBP,EDN1,JAM3,RIPOR2,PREX1	darkgreen	VSMC_M4
GO:0032731	0.19	0.92	4	33	positive regulation of interleukin-1 beta production	BP	1	APP,LPL,HSPB1,LGALS9	darkgreen	VSMC_M4
GO:0043122	0.19	0.87	17	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	ANGPT1,GJA1,MAP3K7,ATP2C1,HTR2B,CFLAR,PRKD1,HSPB1,TNFSF10,RORA,LGALS9,FLNA,PLEKHG5,PLCG2,TERF2IP,WLS,EDA	darkgreen	VSMC_M4
GO:0022600	0.19	0.91	6	56	digestive system process	BP	1	LEP,SLC26A7,FABP2,F11R,NPR3,SLC2A5	darkgreen	VSMC_M4
GO:0032370	0.20	0.91	6	55	positive regulation of lipid transport	BP	1	ABCA1,EDN1,ABCG1,CYP19A1,BMP6,SCP2	darkgreen	VSMC_M4
GO:0055010	0.20	0.91	5	39	ventricular cardiac muscle tissue morphogenesis	BP	1	TGFBR1,CHD7,TNNT2,LRP2,FGFR2	darkgreen	VSMC_M4
GO:0098900	0.20	0.91	5	39	regulation of action potential	BP	1	TBX18,KCNE3,CAMK2D,CACNA1C,FLNA	darkgreen	VSMC_M4
GO:0032869	0.20	0.87	15	161	cellular response to insulin stimulus	BP	1	LEP,KANK1,PDK4,INHBB,FOXO1,FFAR3,NCK1,PTPN11,LPL,ADIPOR1,ZNF106,CFLAR,WDTC1,BCAR3,PIK3C2A	darkgreen	VSMC_M4
GO:0080164	0.20	0.91	5	45	regulation of nitric oxide metabolic process	BP	1	CLU,PTX3,EDN1,CD47,ICAM1	darkgreen	VSMC_M4
GO:0042181	0.20	0.92	4	36	ketone biosynthetic process	BP	1	REST,ADM,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0055123	0.20	0.88	10	99	digestive system development	BP	1	BCL2,PDGFC,ADA,FGFR2,DACT1,HIF1A,TGFB3,WLS,CDKN1A,YAP1	darkgreen	VSMC_M4
GO:0002028	0.20	0.90	7	66	regulation of sodium ion transport	BP	1	PTPN3,ACTN4,FGF14,FXYD1,CAMK2D,AHCYL1,SLC8A1	darkgreen	VSMC_M4
GO:0002011	0.20	0.90	6	50	morphogenesis of an epithelial sheet	BP	1	DDR1,MRTFA,FLNA,CYR61,CD151,TBX20	darkgreen	VSMC_M4
GO:0050670	0.20	0.88	12	137	regulation of lymphocyte proliferation	BP	1	BCL2,LEP,CD274,ZAP70,NCK1,SH3RF1,PTPN22,ADA,IGFBP2,LGALS9,VCAM1,CDKN1A	darkgreen	VSMC_M4
GO:0042063	0.20	0.86	20	230	gliogenesis	BP	1	IFNGR1,LAMA2,TENM4,TRPC4,WASF3,CLU,APP,ABCC8,PTPN11,NAB1,BACE2,SUN1,LRP2,NCSTN,ZNF365,WDR1,CDH2,SH3TC2,CSF1,BNIP3	darkgreen	VSMC_M4
GO:0071825	0.20	0.92	4	35	protein-lipid complex subunit organization	BP	1	SH3GL2,ABCA1,LPL,ABCG1	darkgreen	VSMC_M4
GO:0006661	0.20	0.88	11	115	phosphatidylinositol biosynthetic process	BP	1	PIGN,PIP5K1B,HTR2B,INPP5F,PI4KB,PIGG,OCRL,PIGS,PLCG2,PIGK,PIK3C2A	darkgreen	VSMC_M4
GO:1903350	0.20	0.90	6	56	response to dopamine	BP	1	HRH1,ADCY6,HTR2B,ADCY5,NCSTN,FLNA	darkgreen	VSMC_M4
GO:2000649	0.20	0.91	5	43	regulation of sodium ion transmembrane transporter activity	BP	1	PTPN3,ACTN4,FGF14,FXYD1,CAMK2D	darkgreen	VSMC_M4
GO:0001659	0.20	0.87	13	141	temperature homeostasis	BP	1	ZNF516,GJA1,LEP,IL18R1,EDN2,FOXO1,PDGFC,ADIPOR1,PLCL1,ACHE,PPARGC1A,NPR3,ADAMTS5	darkgreen	VSMC_M4
GO:0042471	0.20	0.89	9	89	ear morphogenesis	BP	1	TBX18,GATA2,HPN,CHD7,PDZD7,EDN1,SEC24B,FGFR2,FRZB	darkgreen	VSMC_M4

GO:0051235	0.20	0.86	22	248	maintenance of location	BP	1	GJA1,TRDN,LEP,ABCA1,CHD7,JPH1,G3BP2,LPL,ABCG1,HTR2B,SUN1,CAMK2D,PRKD1,AKAP6,CACNA1C,BBS4,FLNA,PLCG2,ITPR1,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0046902	0.20	0.91	5	50	regulation of mitochondrial membrane permeability	BP	1	BCL2,SLC25A4,EYA2,RHOT1,BNIP3	darkgreen	VSMC_M4
GO:0030178	0.20	0.87	13	142	negative regulation of Wnt signaling pathway	BP	1	TLE4,MLLT3,TBX18,JADE1,LATS2,TMEM64,IGFBP2,DACT1,CDH2,DAB2,TLE2,FRZB,TMEM170B	darkgreen	VSMC_M4
GO:0061756	0.20	0.92	4	34	leukocyte adhesion to vascular endothelial cell	BP	1	LEP,CHST2,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:0019083	0.20	0.91	5	45	viral transcription	BP	1	EP300,REST,MDFIC,HPN,CCNT1	darkgreen	VSMC_M4
GO:2000116	0.20	0.87	14	167	regulation of cysteine-type endopeptidase activity	BP	1	MDM2,DAPK1,REST,SH3RF1,RNF34,HERPUD1,LGMN,CFLAR,HIP1,CRYAB,TNFSF10,LGALS9,F3,CYR61	darkgreen	VSMC_M4
GO:1904707	0.20	0.92	4	34	positive regulation of vascular associated smooth muscle cell proliferation	BP	1	MDM2,GJA1,EDN1,FGF9	darkgreen	VSMC_M4
GO:0043281	0.20	0.87	13	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MDM2,DAPK1,REST,SH3RF1,RNF34,HERPUD1,CFLAR,HIP1,CRYAB,TNFSF10,LGALS9,F3,CYR61	darkgreen	VSMC_M4
GO:0045599	0.20	0.91	5	43	negative regulation of fat cell differentiation	BP	1	GATA2,FOXO1,RORA,SORT1,YAP1	darkgreen	VSMC_M4
GO:0010950	0.20	0.88	11	127	positive regulation of endopeptidase activity	BP	1	MBP,DAPK1,REST,LGMN,CFLAR,NCSTN,HIP1,TNFSF10,LGALS9,F3,CYR61	darkgreen	VSMC_M4
GO:0032371	0.20	0.91	5	46	regulation of sterol transport	BP	1	LEP,ABCA1,ABCG1,ARV1,SCP2	darkgreen	VSMC_M4
GO:0032374	0.20	0.91	5	46	regulation of cholesterol transport	BP	1	LEP,ABCA1,ABCG1,ARV1,SCP2	darkgreen	VSMC_M4
GO:0030193	0.20	0.91	5	50	regulation of blood coagulation	BP	1	PROS1,EDN1,SERPINE1,F3,PRKG1	darkgreen	VSMC_M4
GO:0036465	0.20	0.89	7	64	synaptic vesicle recycling	BP	1	SH3GL2,SYT5,SNAP91,ITSN2,FGF14,NLGN1,DNAJC6	darkgreen	VSMC_M4
GO:0032880	0.20	0.84	55	693	regulation of protein localization	BP	1	BCL2,SLC35D3,MDM2,ANGPT1,GJA1,LEP,UNC13B,REST,ICA1,MDFIC,TCAF1,INHBB,ADAM9,ATP2C1,ZDHHC2,RIC3,LATS2,ANKRD1,PAM,ABCC8,PTPN11,ATG13,HNF4A,RAB29,ABCG1,RIPOR2,ACTN2,PFKL,LRP5,TM7SF3,SESN2,ADCY5,PTPN14,PRKD1,ACHE,RDX,EXPH5,NLGN1,HIF1A,GNAI1,NUMB,TGFB3,NPTN,CDH2,ABLIM3,SH3TC2,DAB2,PRKAA2,TMEM59,ATCAY,FLNA,WLS,ORMDL3,YAP1,BMP6	darkgreen	VSMC_M4
GO:0048488	0.20	0.90	6	52	synaptic vesicle endocytosis	BP	1	SH3GL2,SYT5,SNAP91,ITSN2,NLGN1,DNAJC6	darkgreen	VSMC_M4
GO:0140238	0.20	0.90	6	52	presynaptic endocytosis	BP	1	SH3GL2,SYT5,SNAP91,ITSN2,NLGN1,DNAJC6	darkgreen	VSMC_M4
GO:2000107	0.20	0.92	4	34	negative regulation of leukocyte apoptotic process	BP	1	DOCK8,ADA,HIF1A,ORMDL3	darkgreen	VSMC_M4
GO:0051493	0.20	0.84	39	457	regulation of cytoskeleton organization	BP	1	LIMCH1,KANK1,PPP1R9A,TGFBR1,CDC42EP3,WASF3,NCK1,PAM,OCLN,JMY,EDN1,JAM3,CD47,SEMA5A,ACTN2,PREX1,MID1,SYNPO2,F11R,PLXNB1,RDX,SYNPO2L,WDR1,GNAI1,TGFB3,MAPRE2,SYNPO,PAK3,GAS2L2,ARHGAP28,PATJ,PRKAA2,DAPK3,FLNA,SPTAN1,NEXN,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0002444	0.21	0.89	7	70	myeloid leukocyte mediated immunity	BP	1	DDX58,GATA2,ANXA3,WDR1,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0019395	0.21	0.89	8	87	fatty acid oxidation	BP	1	LEP,PDK4,PEX13,ADIPOR1,SESN2,PPARGC1A,ACAD11,SCP2	darkgreen	VSMC_M4
GO:1902742	0.21	0.92	4	32	apoptotic process involved in development	BP	1	LRP5,CRYAB,SLIT3,CYR61	darkgreen	VSMC_M4
GO:0001892	0.21	0.89	7	67	embryonic placenta development	BP	1	CITED2,GRHL2,GATA2,ADM,FGFR2,HIF1A,CYR61	darkgreen	VSMC_M4
GO:0007173	0.21	0.88	9	90	epidermal growth factor receptor signaling pathway	BP	1	PTPN3,RASSF2,PTPN11,AFAP1L2,GPRC5A,HIP1,CDH13,BCAR3,PIK3C2A	darkgreen	VSMC_M4
GO:0050863	0.21	0.86	17	206	regulation of T cell activation	BP	1	LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,SH3RF1,PTPN11,PTPN22,ADA,CD47,RIPOR2,IGFBP2,LGALS9,VCAM1,VNN1,CD83	darkgreen	VSMC_M4
GO:0034332	0.21	0.91	5	39	adherens junction organization	BP	1	JAM3,RDX,NUMB,CDH18,BMP6	darkgreen	VSMC_M4
GO:1901655	0.21	0.89	8	77	cellular response to ketone	BP	1	FOXO1,ADCY6,ADCY5,CFLAR,GNAI1,PRKAA2,ICAM1,DDIT4	darkgreen	VSMC_M4
GO:0043200	0.21	0.88	9	93	response to amino acid	BP	1	SESN1,COL4A1,CPEB3,PDGFC,EDN1,SESN2,CASTOR1,PPARGC1A,ICAM1	darkgreen	VSMC_M4
GO:0001890	0.21	0.87	11	117	placenta development	BP	1	CITED2,GRHL2,GJA1,LEP,GATA2,ADM,ADA,FGFR2,HIF1A,CYR61,STC2	darkgreen	VSMC_M4
GO:0006629	0.21	0.83	72	982	lipid metabolic process	BP	1	PIGN,HSD17B6,LEP,PIP5K1B,VLDLR,PDK4,REST,IGFBP7,EDN2,ABCA1,PEX13,ABHD12,PLCB4,SUMF1,CYP1B1,FLT3,CHPT1,ADM,PAM,ST3GAL5,CLU,APP,PTPN11,LPCAT2,HNF4A,SERINC3,EDN1,PLA2G4F,LPL,ABCG1,MTMR10,ADIPOR1,AGPAT3,LRP5,PLCL1,HTR2B,LGMN,SERINC2,SESN2,ARV1,LRP2,WDTC1,INPP5F,PRKD1,PI4KB,ACHE,ATG14,CYP19A1,PPARGC1A,DISP3,RORA,PIGG,LACTB,FAXDC2,BBS4,ANGPTL4,OCRL,PIGS,PRKAA2,PLPPR3,MBTPS1,PLCG2,ABCA4,CYR61,ST6GALNAC3,ACAD11,PIGK,SLC27A5,PIK3C2A,ORMDL3,BMP6,SCP2	darkgreen	VSMC_M4
GO:1902652	0.21	0.88	10	111	secondary alcohol metabolic process	BP	1	LEP,VLDLR,ABCA1,APP,ABCG1,LRP5,ARV1,DISP3,PRKAA2,MBTPS1	darkgreen	VSMC_M4
GO:0046649	0.21	0.84	37	470	lymphocyte activation	BP	1	BCL2,EP300,LEP,DOCK8,CD274,IL18R1,ZAP70,MAP3K8,APBB1IP,FLT3,CHD7,NCK1,CD180,SH3RF1,KIF13B,BLNK,PTPN11,PTPN22,ADA,CD47,RAB29,RIPOR2,PREX1,TP53BP1,NCSTN,IGFBP2,RORA,LGALS9,VAMP7,PLCG2,VCAM1,VNN1,CD151,CD83,CDKN1A,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0120254	0.21	0.88	8	86	olefinic compound metabolic process	BP	1	REST,ABHD12,CYP1B1,ADM,PPARGC1A,ABCA4,BMP6,SCP2	darkgreen	VSMC_M4
GO:0044070	0.21	0.90	6	57	regulation of anion transport	BP	1	LEP,TCAF1,EDN1,RGS2,SLC43A2,AHCYL1	darkgreen	VSMC_M4
GO:0007159	0.21	0.85	19	234	leukocyte cell-cell adhesion	BP	1	LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,CHST2,PTPN11,PTPN22,ADA,CD47,RIPOR2,F11R,IGFBP2,LGALS9,VCAM1,VNN1,CD83,ICAM1	darkgreen	VSMC_M4
GO:0050819	0.21	0.91	4	38	negative regulation of coagulation	BP	1	PROS1,EDN1,SERPINE1,PRKG1	darkgreen	VSMC_M4
GO:0002218	0.21	0.92	4	33	activation of innate immune response	BP	1	EP300,MAP3K7,PAK3,PLCG2	darkgreen	VSMC_M4
GO:0009314	0.21	0.84	29	359	response to radiation	BP	1	BCL2,MDM2,SOD2,EP300,GNAQ,HRH1,BABAM2,POLB,GRK7,MEIS2,APP,ABCC8,TANC1,N4BP1,LRP5,RBM4B,TP53BP1,F11R,CRYAB,MMP1,HIF1A,OPN3,NPTN,VCAM1,ABCA4,CDKN1A,MFAP4,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0043268	0.21	0.92	4	29	positive regulation of potassium ion transport	BP	1	ABCC8,ACTN2,AKAP6,FLNA	darkgreen	VSMC_M4
GO:0046661	0.21	0.87	12	128	male sex differentiation	BP	1	BCL2,CITED2,TGFBR1,LRP2,ARID5B,PRDX4,TNFSF10,TEX11,FLNA,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0097581	0.21	0.88	8	78	lamellipodium organization	BP	1	KANK1,WASF3,NCK1,OCLN,ABLIM1,ABLIM3,PLXNB3,CDH13	darkgreen	VSMC_M4
GO:0046889	0.21	0.90	6	61	positive regulation of lipid biosynthetic process	BP	1	ADM,ABCG1,HTR2B,PPARGC1A,CYR61,BMP6	darkgreen	VSMC_M4
GO:1900024	0.21	0.90	5	44	regulation of substrate adhesion-dependent cell spreading	BP	1	KANK1,LIMS2,ACTN4,PREX1,FLNA	darkgreen	VSMC_M4

GO:0046326	0.21	0.91	4	31	positive regulation of glucose import	BP	1	OCLN,PTH,PTPN11,OPN3	darkgreen	VSMC_M4
GO:0060349	0.21	0.88	8	76	bone morphogenesis	BP	1	CITED2,NAB1,LRP5,FGFR2,PAPPA2,TGFB3,GLG1,BMP6	darkgreen	VSMC_M4
GO:0050918	0.21	0.90	5	47	positive chemotaxis	BP	1	ANGPT1,SEMA5A,PLXNB3,CDH13,F3	darkgreen	VSMC_M4
GO:1900046	0.21	0.90	5	51	regulation of hemostasis	BP	1	PROS1,EDN1,SERPINE1,F3,PRKG1	darkgreen	VSMC_M4
GO:1901617	0.21	0.86	15	178	organic hydroxy compound biosynthetic process	BP	1	LEP,REST,HRH1,PTH,ABCG1,ARV1,PPIP5K1,OPN3,FAXDC2,PRKAA2,MBTPS1,PLCG2,SLC27A5,BMP6,SCP2	darkgreen	VSMC_M4
GO:0062014	0.21	0.89	7	73	negative regulation of small molecule metabolic process	BP	1	EP300,REST,WDTC1,SLC25A12,PPARGC1A,ATCAY,DDIT4	darkgreen	VSMC_M4
GO:0048511	0.22	0.85	20	223	rhythmic process	BP	1	EP300,GNAQ,LEP,NCOR2,PAM,PTX3,HNF4A,ADA,KDM5B,RBM4B,HEBP1,ID3,NLGN1,OPN3,PPARGC1A,RORA,SLIT3,TGFB3,PRKAA2,HLF	darkgreen	VSMC_M4
GO:1902003	0.22	0.91	4	35	regulation of amyloid-beta formation	BP	1	IFNGR1,GGA3,CLU,ABCG1	darkgreen	VSMC_M4
GO:0030879	0.22	0.87	11	114	mammary gland development	BP	1	DDR1,LBH,NCOR2,PAM,RXFP1,KDM5B,LRP5,FGFR2,HIF1A,TGFB3,CSF1	darkgreen	VSMC_M4
GO:0016241	0.22	0.86	12	128	regulation of macroautophagy	BP	1	MAP3K7,SESN1,SLC25A4,FEZ1,SESN2,QSOX1,HIF1A,CALCOCO2,PRKAA2,LRSAM1,BNIP3,ATP6V0E1	darkgreen	VSMC_M4
GO:0060041	0.22	0.87	11	108	retina development in camera-type eye	BP	1	HIPK2,SMARCD3,THRB,COL4A1,CYP1B1,CHD7,GPM6A,LRP5,ACHE,HIF1A,BBS4	darkgreen	VSMC_M4
GO:0048640	0.22	0.88	9	90	negative regulation of developmental growth	BP	1	CITED2,GJA1,SEMA3C,WWC2,SEMA5A,RGS2,LGMN,ULK2,CDKN1A	darkgreen	VSMC_M4
GO:0080135	0.22	0.83	43	553	regulation of cellular response to stress	BP	1	BCL2,SASH1,MDM2,SOD2,OXR1,TPD52L1,EP300,LEP,WFS1,SH3RF3,CREB3,REST,MDFIC,HIPK2,TPT1,BABAM2,FOXO1,RASSF2,HIPK3,ANKRD1,NCK1,SH3RF1,CLU,APP,NEK4,HERPUD1,PTPN22,GDF6,SERINC3,EYA2,MID1,INPP5F,TP53BP1,ZNF365,ATF6,HSPB1,NBR1,DACT1,HIF1A,FLNA,TERF2IP,VNN1,NACC2	darkgreen	VSMC_M4
GO:0009395	0.22	0.91	4	36	phospholipid catabolic process	BP	1	ABHD12,PLA2G4F,INPP5F,PLCG2	darkgreen	VSMC_M4
GO:0010563	0.22	0.84	29	356	negative regulation of phosphorus metabolic process	BP	1	IRAK3,ANGPT1,SH3GL2,GNAQ,CDKN2B,RASSF2,ANKLE2,LATS2,HIPK3,NCK1,OCLN,PTPN22,RGS2,LRP5,INPP5F,GPRC5A,LRP6,FAM129A,HSPB1,ATG14,PPP1R36,PPARGC1A,SMAD6,PPP1R26,TERF2IP,SLC8A1,CDKN1A,PPM1E,DDIT4	darkgreen	VSMC_M4
GO:0045936	0.22	0.84	29	356	negative regulation of phosphate metabolic process	BP	1	IRAK3,ANGPT1,SH3GL2,GNAQ,CDKN2B,RASSF2,ANKLE2,LATS2,HIPK3,NCK1,OCLN,PTPN22,RGS2,LRP5,INPP5F,GPRC5A,LRP6,FAM129A,HSPB1,ATG14,PPP1R36,PPARGC1A,SMAD6,PPP1R26,TERF2IP,SLC8A1,CDKN1A,PPM1E,DDIT4	darkgreen	VSMC_M4
GO:1904892	0.22	0.89	6	59	regulation of receptor signaling pathway via STAT	BP	1	LEP,CYP1B1,ADIPOR1,INPP5F,CRLF3,MIR99A	darkgreen	VSMC_M4
GO:0003161	0.22	0.91	4	31	cardiac conduction system development	BP	1	GJA1,TBX18,NPPB,HOPX	darkgreen	VSMC_M4
GO:2000106	0.22	0.89	6	59	regulation of leukocyte apoptotic process	BP	1	DOCK8,CD274,ADA,HIF1A,LGALS9,ORMDL3	darkgreen	VSMC_M4
GO:0016126	0.22	0.90	5	49	sterol biosynthetic process	BP	1	ABCG1,ARV1,FAXDC2,PRKAA2,MBTPS1	darkgreen	VSMC_M4
GO:0002440	0.22	0.86	12	138	production of molecular mediator of immune response	BP	1	IRAK3,ANGPT1,DDX58,IL18R1,MAP3K7,POLB,FFAR3,PTPN22,TP53BP1,TGFB3,PLCG2,CCR6	darkgreen	VSMC_M4
GO:0002263	0.22	0.85	16	185	cell activation involved in immune response	BP	1	IL18R1,GATA2,APBB1IP,CD180,APP,ANXA3,LBP,ADA,TP53BP1,ADGRE2,RORA,LGALS9,VAMP7,PLCG2,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0120036	0.22	0.81	96	1193	plasma membrane bounded cell projection organization	BP	1	BCL2,UST,GRIP1,MDM2,DDR1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,TGFBR1,KIDINS220,EPHB6,ITSN2,CDC42EP3,SEMA3C,WASF3,PTPRG,DENND5A,ANKRD1,CPEB3,NCK1,ADM,OCLN,KIF13B,GPM6A,APP,SCARB2,PTPN11,ADCY6,TANC1,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,RAB29,DNAH7,RIPOR2,RGS2,ACTN2,FEZ1,PREX1,LGMN,ROBO3,SEC24B,ABLIM1,PARD6B,PLXNA2,SHTN1,MYLK,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,PLXNB1,RAPH1,ITGA6,ZNF365,MAP3K13,CUX1,RDX,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,TGFB3,IFT43,BBS4,NPTN,NRK,CDH2,ULK2,PAK3,EVI5L,ABLIM3,OCRL,MYO10,ATCAY,PLXNB3,FLNA,CDH13,NEXN,ITM2C,ICAM1,SDC2,YAP1,PRKG1	darkgreen	VSMC_M4
GO:0098655	0.22	0.82	49	623	cation transmembrane transport	BP	1	PKDREJ,CALHM5,TRDN,DAPK1,SLC17A5,PTPN3,KCNE3,ACTN4,FGF14,TRPC4,ATP2C1,TUSC3,FXYD1,HPN,CHD7,MICU2,SLC25A4,SCN8A,CLCN3,SLC35G1,JPH1,GPM6A,APP,ABCC8,CNNM2,RGS2,ACTN2,HTR2B,CAMK2D,ABCC9,CTSS,PRKD1,AKAP6,NLGN1,CACNA1C,PPARGC1A,MAGT1,KCNK10,SLC43A2,SCNN1D,FLNA,HCN2,PLCG2,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,ATP6V0E1	darkgreen	VSMC_M4
GO:0051216	0.22	0.86	14	154	cartilage development	BP	1	TRPS1,LEP,TGFBR1,PTH,PTPN11,GDF6,EDN1,LNPK,HIF1A,BGN,GLG1,CYR61,FRZB,BMP6	darkgreen	VSMC_M4
GO:0019319	0.22	0.89	6	61	hexose biosynthetic process	BP	1	EP300,LEP,SESN2,CHST15,SLC25A12,PPARGC1A	darkgreen	VSMC_M4
GO:0090596	0.22	0.85	18	198	sensory organ morphogenesis	BP	1	BCL2,CITED2,TBX18,HIPK2,GATA2,THRB,HPN,CHD7,PDZD7,EDN1,LRP5,SEC24B,FGFR2,MFAP5,HIF1A,BBS4,BCAR3,FRZB	darkgreen	VSMC_M4
GO:0015711	0.22	0.85	19	228	organic anion transport	BP	1	SLC35D3,GJA1,LEP,SLC2A1,SLC17A5,TRPC4,SLC16A3,SLC25A4,SLC26A7,SERINC3,EDN1,CD47,PLA2G4F,RGS2,LRP2,SLC25A12,SLC43A2,LRRC8C,SLC27A5	darkgreen	VSMC_M4
GO:0048332	0.22	0.89	6	55	mesoderm morphogenesis	BP	1	GJA1,ITGA8,EYA2,FGFR2,WLS,TBX20	darkgreen	VSMC_M4
GO:0048732	0.22	0.84	28	335	gland development	BP	1	BCL2,CITED2,DDR1,TGFBR1,PTPN3,GATA2,LIMS2,LBH,POLB,SEMA3C,NCOR2,HPN,PAM,RXFP1,HNF4A,ADA,KDM5B,LRP5,CFLAR,FGFR2,ARID5B,HIF1A,TGFB3,CSF1,LMO4,WLS,FRZB,EDA	darkgreen	VSMC_M4
GO:0046328	0.22	0.87	10	104	regulation of JNK cascade	BP	1	TPD52L1,SH3RF3,MDFIC,HIPK2,RASSF2,HIPK3,SH3RF1,APP,PTPN22,DACT1	darkgreen	VSMC_M4

GO:0030030	0.22	0.81	98	1226	cell projection organization	BP	1	BCL2,UST,GRIP1,MDM2,DDR1,GJA1,LAMA2,EP300,ADGRB1,SH3GL2,KANK1,VLDLR,PPP1R9A,TGFBR1,KIDINS220,EPHB6,ITSN2,CDC42EP3,SEMA3C,WASF3,PTPRG,DENND5A,ANKRD1,CPEB3,NCK1,ADM,OCLN,KIF13B,GPM6A,APP,SCARB2,PTPN11,ADCY6,TANC1,NGF,PDZD7,JAM3,GPRIN3,NFASC,SEMA5A,RAB29,DNAH7,RIPOR2,RGS2,ACTN2,FEZ1,PREX1,LGMN,ROBO3,SEC24B,ABLIM1,PARD6B,PLXNA2,SHTN1,MYLK,LRP2,CFLAR,CTSZ,INPP5F,FGFR2,PRKD1,PLXNB1,RAPH1,ITGA6,ZNF365,MAP3K13,CUX1,RDX,UNC5B,LMTK2,NLGN1,SIPA1L1,NUMB,SLIT3,TGFB3,IFT43,BBS4,AK7,NPTN,NRK,CDH2,ULK2,PAK3,EVI5L,ABLIM3,OCRL,MYO10,ATCAY,PLXNB3,FLNA,CCDC78,CDH13,NEXN,ITM2C,ICAM1,SDC2,YAP1,PRKG1	darkgreen	VSMC_M4
GO:0007218	0.22	0.91	4	36	neuropeptide signaling pathway	BP	1	NXPH2,PCSK1N,NPPB,SORT1	darkgreen	VSMC_M4
GO:0032270	0.22	0.81	80	1066	positive regulation of cellular protein metabolic process	BP	1	MBP,GDF11,BCL2,SASH1,MDM2,RNF19A,ANGPT1,TPD52L1,DAPK1,LEP,WFS1,LIMCH1,FAM122A,DCUN1D4,VLDLR,PPP1R9A,REST,TGFBR1,MAP3K7,ANTXR1,HIPK2,INHBB,ADAM9,RASSF2,ANKLE2,FLT3,HPN,CPEB3,NCK1,CLU,APP,PDGFC,PTPN11,CCNT1,HERPUD1,PTPN22,GDF6,AKTIP,NGF,EDN1,ARRDC4,HTR2B,MST1R,LGMN,AFAP1L2,NGRN,LRP2,CFLAR,PRKD1,NCSTN,DDR2,GPRC5A,MAP3K13,HIP1,FAM129A,RDX,ATG14,FBXL5,TNFSF10,DACT1,PPARGC1A,TGFB3,TOM1L1,FAXDC2,NPTN,DAB2,LGALS9,SKP2,PRKAA2,CTIF,CSF1,PLCG2,TERF2IP,F3,BCAR3,CYR61,CDKN1A,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0018107	0.22	0.87	10	98	peptidyl-threonine phosphorylation	BP	1	BCL2,TGFBR1,HIPK2,HIPK3,APP,PRKCA,CAMK2D,PRKD1,LMTK2,DDIT4	darkgreen	VSMC_M4
GO:0060193	0.22	0.90	5	46	positive regulation of lipase activity	BP	1	GNAQ,PTH,HTR2B,FGFR2,CYR61	darkgreen	VSMC_M4
GO:1905953	0.22	0.91	4	37	negative regulation of lipid localization	BP	1	LEP,ABCA1,PTPN11,ABCG1	darkgreen	VSMC_M4
GO:0032984	0.22	0.85	18	195	protein-containing complex disassembly	BP	1	IRAK3,SMARCD3,MAP1LC3A,SEMA5A,ACTN2,MID1,RDX,ATG14,WDR1,MICAL3,CALCOCO2,EPG5,DNAJC6,MAP1LC3B2,SPTAN1,BNIP3,DSTN,DDIT4	darkgreen	VSMC_M4
GO:0021543	0.22	0.86	12	127	pallium development	BP	1	SLC2A1,PEX13,TACC1,ANXA3,FEZ1,SUN1,EZH1,HIF1A,BBS4,CDH2,FLNA,BNIP3	darkgreen	VSMC_M4
GO:0008206	0.22	0.91	4	36	bile acid metabolic process	BP	1	LEP,ARV1,SLC27A5,SCP2	darkgreen	VSMC_M4
GO:0045834	0.22	0.87	10	109	positive regulation of lipid metabolic process	BP	1	FLT3,ADM,ABCG1,HTR2B,PRKD1,ATG14,PPARGC1A,DISP3,CYR61,BMP6	darkgreen	VSMC_M4
GO:0051129	0.22	0.82	46	569	negative regulation of cellular component organization	BP	1	IRAK3,MDM2,EP300,KANK1,PPP1R9A,ANTXR1,SEMA3C,PTPRG,DENND5A,MCTP1,CLU,ATXN2,ADCY6,JAM3,SEMA5A,RAB29,FEZ1,MID1,CFLAR,CTSZ,INPP5F,PRKD1,F11R,ZNF365,CRYAB,RDX,DACT1,NLGN1,PPARGC1A,SMAD6,TOM1L1,ULK2,EVI5L,ARHGAP28,PLXNB3,FLNA,SPTAN1,TERF2IP,LRSAM1,LMO4,BNIP3,TBX20,ITM2C,CST3,YAP1,BMP6	darkgreen	VSMC_M4
GO:0042129	0.22	0.87	9	102	regulation of T cell proliferation	BP	1	LEP,CD274,ZAP70,NCK1,SH3RF1,PTPN22,IGFBP2,LGALS9,VCAM1	darkgreen	VSMC_M4
GO:0015804	0.22	0.91	4	36	neutral amino acid transport	BP	1	LEP,SERINC3,RGS2,SLC43A2	darkgreen	VSMC_M4
GO:0071354	0.23	0.91	4	33	cellular response to interleukin-6	BP	1	PPARGC1A,MIR99A,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0071214	0.23	0.84	22	267	cellular response to abiotic stimulus	BP	1	MDM2,GJA1,EP300,REST,SLC2A1,MAP3K1,ANKRD1,GRK7,PTPN11,N4BP1,MYLK,TP53BP1,F11R,CRYAB,MMP1,OPN3,LRRC8C,BNIP3,CDKN1A,MFAP4,YAP1,BMP6	darkgreen	VSMC_M4
GO:0104004	0.23	0.84	22	267	cellular response to environmental stimulus	BP	1	MDM2,GJA1,EP300,REST,SLC2A1,MAP3K1,ANKRD1,GRK7,PTPN11,N4BP1,MYLK,TP53BP1,F11R,CRYAB,MMP1,OPN3,LRRC8C,BNIP3,CDKN1A,MFAP4,YAP1,BMP6	darkgreen	VSMC_M4
GO:0046173	0.23	0.89	5	49	polyol biosynthetic process	BP	1	LEP,HRH1,PTH,PPIP5K1,PLCG2	darkgreen	VSMC_M4
GO:0008038	0.23	0.90	5	42	neuron recognition	BP	1	APP,SEMA5A,ROBO3,NPTN,NEXN	darkgreen	VSMC_M4
GO:0031333	0.23	0.86	11	115	negative regulation of protein-containing complex assembly	BP	1	EP300,KANK1,CLU,JAM3,CRYAB,RDX,DACT1,SMAD6,SPTAN1,LMO4,TBX20	darkgreen	VSMC_M4
GO:0006942	0.23	0.88	7	68	regulation of striated muscle contraction	BP	1	RGS2,CAMK2D,CACNA1C,ADRA1B,SLC8A1,PLN,TMEM38A	darkgreen	VSMC_M4
GO:0034440	0.23	0.87	8	90	lipid oxidation	BP	1	LEP,PDK4,PEX13,ADIPOR1,SESN2,PPARGC1A,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0086091	0.23	0.91	4	30	regulation of heart rate by cardiac conduction	BP	1	KCNE3,CAMK2D,CACNA1C,KCNE4	darkgreen	VSMC_M4
GO:0007584	0.23	0.86	12	137	response to nutrient	BP	1	MDM2,SOD2,LEP,CDKN2B,ABCA1,PTH,ADA,LPL,IGFBP2,VCAM1,SLC8A1,STC2	darkgreen	VSMC_M4
GO:0002009	0.23	0.82	35	412	morphogenesis of an epithelium	BP	1	BCL2,CITED2,DDR1,GRHL2,GJA1,MRTFA,MLLT3,TBX18,COL4A1,SEMA3C,ADM,SHROOM3,EDN1,KDM5B,LRP5,NPNT,SEC24B,LRP2,CTSZ,FGFR2,CRYGS,DACT1,WDR1,HIF1A,BBS4,FST,DAB2,FLNA,CSF1,LMO4,CYR61,CD151,FRZB,TBX20,YAP1	darkgreen	VSMC_M4
GO:0048806	0.23	0.90	4	34	genitalia development	BP	1	CHD7,PTPN11,LRP2,BMP6	darkgreen	VSMC_M4
GO:0097479	0.23	0.89	5	46	synaptic vesicle localization	BP	1	SNAP91,PCLO,AP3B2,NLGN1,CDH2	darkgreen	VSMC_M4

GO:0031323	0.23	0.79	316	4391	regulation of cellular metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,SMOC2,GJA1,ZHX1,TPD52L1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,RIC1,PDK4,IL18R1,CREB3,ZNF169,REST,RECK,TGFBR1,ZNF331,PTPN3,TBX18,MAP3K7,ANTXR1,MDFIC,EPHB6,SESN1,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,NAA16,ELF1,INHBB,SMARCD3,HRH1,LMO7,ITIH5,BABAM2,FOSL2,LBH,LIPT2,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,FOXO1,RASSF2,ANKLE2,CYP1B1,TF,EBF4,FLT3,MIER3,NCOR2,FFAR3,FXYD1,HPN,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,SLC25A4,SH3RF1,ATOH8,CLCN3,OCLN,TCF7L1,WWC2,TEAD1,FAM172A,PTH,RNF34,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ANXA3,PTPN11,PTX3,NEK4,CCNT1,HERPUD1,PROS1,JMY,CHD6,PTPN22,HNF4A,CHAC1,GDF6,NAB1,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,SMARCAD1,BACE2,RAB29,ABCG1,ADIPOR1,KDM5B,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,FEZ1,NPNT,PLCL1,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,QSOX1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,SERPINE1,ACHE,CRYAB,RDX,MAOB,ZNF445,SECISBP2L,EZH1,EIF4G3,ATG14,FBXL5,TNFSF10,DACT1,LMTK2,MAEL,SIN3B,PCSK1N,HIF1A,OPN3,ZBT	darkgreen	VSMC_M4
GO:0010906	0.23	0.86	9	96	regulation of glucose metabolic process	BP	1	EP300,LEP,PDK4,PTH,ADIPOR1,SESN2,SLC25A12,PPARGC1A,RORA	darkgreen	VSMC_M4
GO:0045055	0.23	0.85	15	167	regulated exocytosis	BP	1	STX11,UNC13B,REST,PREPL,SYT5,GATA2,SYNGR2,PCLO,ANXA3,RAPGEF4,NLGN1,ADGRE2,FBXL20,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0033559	0.23	0.88	6	64	unsaturated fatty acid metabolic process	BP	1	EDN2,ABHD12,CYP1B1,EDN1,PLA2G4F,SCP2	darkgreen	VSMC_M4
GO:0002520	0.23	0.81	54	694	immune system development	BP	1	BCL2,CITED2,IRAK3,ANGPT1,EP300,MLLT3,LEP,CDKN2B,CD274,IL18R1,REST,ZAP70,TGFBR1,HIPK2,GATA2,SNRK,POLB,RASSF2,TMEM178A,TF,FLT3,CHD7,SH3RF1,BLNK,MEIS2,APP,PTPN11,TMEM64,PTPN22,ADAJAM3,LRP5,PREX1,PRKCA,P4HTM,FGFR2,TP53BP1,MFAP5,WDR1,HIF1A,CACNA1C,ACTN1,RORA,FAXDC2,FST,LGALS9,CSF1,PLCG2,VCAM1,LMO4,VNN1,CD83,LOX,CCR6	darkgreen	VSMC_M4
GO:0002443	0.23	0.84	18	221	leukocyte mediated immunity	BP	1	C4A,LEP,DDX58,IL18R1,MAP3K7,GATA2,CLU,ANXA3,CFI,TP53BP1,C1RL,WDR1,ADGRE2,LGALS9,VAMP7,PLCG2,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0051452	0.23	0.90	4	36	intracellular pH reduction	BP	1	BCL2,CLCN3,ATP6AP2,ATP6V0E1	darkgreen	VSMC_M4
GO:0009755	0.23	0.85	13	142	hormone-mediated signaling pathway	BP	1	EP300,LBH,THRB,NCOR2,LATS2,PTH,RXFP1,PTPN11,ADIPOR1,STRN3,DAB2,SKP2,YAP1	darkgreen	VSMC_M4
GO:2000045	0.23	0.86	9	97	regulation of G1/S transition of mitotic cell cycle	BP	1	BCL2,MDM2,CDKN2B,JADE1,RBL2,RDX,DACT1,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0046324	0.23	0.89	5	44	regulation of glucose import	BP	1	LEP,OCLN,PTH,PTPN11,OPN3	darkgreen	VSMC_M4
GO:0071634	0.23	0.90	4	33	regulation of transforming growth factor beta production	BP	1	LAPTM4B,ATP6AP2,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0034599	0.23	0.83	19	234	cellular response to oxidative stress	BP	1	BCL2,MDM2,SOD2,OXR1,DAPK1,REST,FOXO1,CYP1B1,MAP1LC3A,PTPN11,CHD6,SESN2,PRKD1,HSPB1,HIF1A,PPARGC1A,PRKAA2,VNN1,BNIP3	darkgreen	VSMC_M4
GO:0035148	0.23	0.85	12	129	tube formation	BP	1	CITED2,GRHL2,ADM,ATOH8,SHROOM3,SEC24B,LRP2,FGFR2,HIF1A,BBS4,LMO4,EDA	darkgreen	VSMC_M4
GO:0009582	0.23	0.87	8	83	detection of abiotic stimulus	BP	1	PKDREJ,GNAQ,HPN,GRK7,PDZD7,OPN3,CDH2,ABCA4	darkgreen	VSMC_M4
GO:0043112	0.23	0.85	12	131	receptor metabolic process	BP	1	ANGPT1,LMBRD1,ADM,ATXN2,RAB29,HTR2B,LGMN,INPP5F,ACHE,LMTK2,NUMB,PLCG2	darkgreen	VSMC_M4
GO:1990845	0.23	0.85	12	132	adaptive thermogenesis	BP	1	ZNF516,GJA1,LEP,IL18R1,SLC25A4,PDGFC,ADIPOR1,PLCL1,ACHE,PPARGC1A,NPR3,ADAMTS5	darkgreen	VSMC_M4
GO:0008285	0.23	0.81	42	548	negative regulation of cell population proliferation	BP	1	BCL2,RNF41,CITED2,DDR1,SOD2,FAM19A5,GJA1,ADGRB1,CDKN2B,CD274,REST,IGFBP7,TGFBR1,GATA2,LIMS2,NDRG2,CYP1B1,HPN,ADM,ATOH8,APP,ABCC8,HNF4A,NGF,FGFR2,PTPN14,PLXNB1,PRDX4,SPEG,PPARGC1A,FGFRL1,SLIT3,TGFB3,CNN1,SMAD6,LGALS9,NPR3,CDH13,FRZB,CDKN1A,NACC2,PRKG1	darkgreen	VSMC_M4
GO:0070741	0.24	0.90	4	34	response to interleukin-6	BP	1	PPARGC1A,MIR99A,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0001841	0.24	0.86	9	92	neural tube formation	BP	1	CITED2,GRHL2,ADM,SHROOM3,SEC24B,LRP2,HIF1A,BBS4,LMO4	darkgreen	VSMC_M4
GO:0050795	0.24	0.90	4	33	regulation of behavior	BP	1	GJA1,ADA,HTR2B,NLGN1	darkgreen	VSMC_M4
GO:0098876	0.24	0.85	12	129	vesicle-mediated transport to the plasma membrane	BP	1	GRIP1,PREPL,GGA3,ATP2C1,ZDHHC2,EXOC6,ACTN2,ATP9A,INPP5F,LMTK2,RABEP1,EPG5	darkgreen	VSMC_M4
GO:0097035	0.24	0.89	5	43	regulation of membrane lipid distribution	BP	1	ABCA1,ABCG1,ATP9A,ARV1,ABCA4	darkgreen	VSMC_M4
GO:0043123	0.24	0.85	13	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	GJA1,MAP3K7,ATP2C1,HTR2B,CFLAR,PRKD1,TNFSF10,LGALS9,FLNA,PLEKHG5,TERF2IP,WLS,EDA	darkgreen	VSMC_M4
GO:0086002	0.24	0.89	5	41	cardiac muscle cell action potential involved in contraction	BP	1	GJA1,KCNE3,CACNA1C,FLNA,KCNE4	darkgreen	VSMC_M4
GO:0000271	0.24	0.88	6	58	polysaccharide biosynthetic process	BP	1	GYS1,PTH,GYG1,B3GNT7,GYG2,NDST3	darkgreen	VSMC_M4
GO:0002067	0.24	0.90	4	35	glandular epithelial cell differentiation	BP	1	HNF4A,FGFR2,CDH2,BMP6	darkgreen	VSMC_M4
GO:0002702	0.24	0.87	7	75	positive regulation of production of molecular mediator of immune response	BP	1	DDX58,IL18R1,MAP3K7,FFAR3,PTPN22,TP53BP1,PLCG2	darkgreen	VSMC_M4
GO:0050764	0.24	0.88	6	59	regulation of phagocytosis	BP	1	C4A,GATA2,PTX3,CD47,MFGE8,PLCG2	darkgreen	VSMC_M4
GO:0050778	0.24	0.82	24	306	positive regulation of immune response	BP	1	BCL2,C4A,EP300,CD274,IL18R1,ZAP70,MAP3K7,GATA2,CLU,BLNK,LBP,PTPN22,ADA,CD47,RAB29,CFI,TP53BP1,C1RL,PAK3,LGALS9,VAMP7,PLCG2,CD59,MFAP4	darkgreen	VSMC_M4
GO:1901379	0.24	0.88	6	56	regulation of potassium ion transmembrane transport	BP	1	KCNE3,ABCC8,ACTN2,AKAP6,FLNA,KCNE4	darkgreen	VSMC_M4
GO:0016236	0.24	0.82	22	265	macroautophagy	BP	1	MAP3K7,SESN1,MAP1LC3A,SLC25A4,ATG13,FEZ1,SESN2,SYNPO2,QSOX1,GABARAPL1,NBR1,ATG14,HIF1A,CALCOCO2,EPG5,ULK2,PRKAA2,MAP1LC3B2,LRSAM1,BNIP3,GABARAPL2,ATP6V0E1	darkgreen	VSMC_M4

GO:0033674	0.24	0.81	31	373	positive regulation of kinase activity	BP	1	SASH1,DDR1,ANGPT1,TPD52L1,LEP,VLDLR,PPP1R9A,MAP3K7,EPHB6,ADAM9,RASSF2,FLT3,CLU,PDGFC,CCNT1,EDN1,HTR2B,MST1R,AFAP1L2,FGFR2,PRKD1,DDR2,GPRC5A,MAP3K13,ATG14,LMTK2,TOM1L1,CSF1,LMO4,CYR61,CDKN1A	darkgreen	VSMC_M4
GO:1903305	0.24	0.86	9	95	regulation of regulated secretory pathway	BP	1	REST,PREPL,SYT5,GATA2,NLGN1,ADGRE2,FBXL20,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0006486	0.24	0.84	15	182	protein glycosylation	BP	1	STT3B,TUSC3,ST3GAL5,EXTL3,DPY19L4,B3GNT7,GALNT3,B3GALNT2,MAN2A2,FUT11,MAGT1,GALNT10,TMEM59,EXTL2,ST6GALNAC3	darkgreen	VSMC_M4
GO:0043413	0.24	0.84	15	182	macromolecule glycosylation	BP	1	STT3B,TUSC3,ST3GAL5,EXTL3,DPY19L4,B3GNT7,GALNT3,B3GALNT2,MAN2A2,FUT11,MAGT1,GALNT10,TMEM59,EXTL2,ST6GALNAC3	darkgreen	VSMC_M4
GO:0017156	0.24	0.88	5	44	calcium-ion regulated exocytosis	BP	1	UNC13B,REST,SYT5,RAPGEF4,VAMP7	darkgreen	VSMC_M4
GO:0097006	0.24	0.88	5	53	regulation of plasma lipoprotein particle levels	BP	1	VLDLR,ABCA1,ABCC8,LPL,ABCG1	darkgreen	VSMC_M4
GO:0048167	0.24	0.84	13	143	regulation of synaptic plasticity	BP	1	ADGRB1,PPP1R9A,HRH1,FGF14,ZDHHC2,CPEB3,MCTP1,APP,LGMN,NCSTN,NLGN1,SIPA1L1,NPTN	darkgreen	VSMC_M4
GO:0009581	0.24	0.86	8	84	detection of external stimulus	BP	1	PKDREJ,GNAQ,HPN,GRK7,PDZD7,OPN3,CDH2,ABCA4	darkgreen	VSMC_M4
GO:0033619	0.24	0.88	5	48	membrane protein proteolysis	BP	1	PTPN3,ADAM9,BACE2,NCSTN,MBTPS1	darkgreen	VSMC_M4
GO:0045453	0.25	0.88	5	50	bone resorption	BP	1	PDK4,TF,PTH,TMEM64,PRKCA	darkgreen	VSMC_M4
GO:1901215	0.25	0.84	14	161	negative regulation of neuron death	BP	1	BCL2,SOD2,OXR1,ANGPT1,WFS1,REST,HIPK2,NGF,LGMN,UNC5B,HIF1A,PPARGC1A,TGFB3,CSF1	darkgreen	VSMC_M4
GO:0007040	0.25	0.87	6	61	lysosome organization	BP	1	LAPTM4B,ABCA1,SCARB2,AKTIP,ATP6AP2,MBTPS1	darkgreen	VSMC_M4
GO:0080171	0.25	0.87	6	61	lytic vacuole organization	BP	1	LAPTM4B,ABCA1,SCARB2,AKTIP,ATP6AP2,MBTPS1	darkgreen	VSMC_M4
GO:0033138	0.25	0.86	7	74	positive regulation of peptidyl-serine phosphorylation	BP	1	BCL2,ANGPT1,APP,NGF,PRKD1,TERF2IP,BCAR3	darkgreen	VSMC_M4
GO:1900744	0.25	0.89	4	37	regulation of p38MAPK cascade	BP	1	SASH1,LEP,PTPN22,GDF6	darkgreen	VSMC_M4
GO:0050818	0.25	0.88	5	54	regulation of coagulation	BP	1	PROS1,EDN1,SERPINE1,F3,PRKG1	darkgreen	VSMC_M4
GO:0002698	0.25	0.87	6	62	negative regulation of immune effector process	BP	1	IRAK3,ANGPT1,CD47,TGFB3,LGALS9,CD59	darkgreen	VSMC_M4
GO:0031399	0.25	0.79	89	1182	regulation of protein modification process	BP	1	GDF11,BCL2,SASH1,IRAK3,OXR1,ANGPT1,TPD52L1,EP300,ADGRB1,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,DCUN1D4,VLDLR,PPP1R9A,TGFBR1,MAP3K7,HIPK2,GATA2,INHBB,ADAM9,RASSF2,ANKLE2,FLT3,FXYD1,LATS2,HIPK3,NCK1,OCLN,CLU,APP,PDGFC,PTPN11,CCNT1,HERPUD1,PTPN22,GDF6,AKTIP,RCAN1,NGF,EDN1,N4BP1,RGS2,LRP5,ARRDC4,PLCL1,HTR2B,MST1R,AFAP1L2,SESN2,CAMK2D,INPP5F,PRKD1,DDR2,GPRC5A,MAP3K13,LRP6,FAM129A,HSPB1,ATG14,HIF1A,PPARGC1A,TGFB3,CCNG1,SMAD6,TOM1L1,FAXDC2,NPTN,DAB2,SKP2,PRKAA2,TMEM59,CSF1,PLCG2,TERF2IP,BCAR3,CYR61,SLC8A1,LOX,CDKN1A,FGF9,PPM1E,CNTD2,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0042176	0.25	0.81	27	342	regulation of protein catabolic process	BP	1	RNF41,IRAK3,MDM2,LAPTM4B,RNF19A,GJA1,ADGRB1,FAM122A,RIC1,PTPN3,HIPK2,GGA3,ADAM9,FOXO1,ZDHHC2,CLU,HERPUD1,N4BP1,LRP2,RDX,FBXL5,DACT1,FBXL20,DAB2,FLNA,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:0030855	0.25	0.80	35	430	epithelial cell differentiation	BP	1	CDSN,GRHL2,SCUBE1,FOSL2,LBH,THRB,ADAM9,COL4A1,ATOH8,SHROOM3,HNF4A,PDZD7,KDM5B,NCOA3,TXNIP,SEC24B,FGFR2,F11R,TAGLN,ID3,SERPINE1,RDX,EXPH5,HIF1A,OPN3,CDH2,DAB2,FLNA,CCDC78,FRZB,MAFF,CDKN1A,ICAM1,YAP1,BMP6	darkgreen	VSMC_M4
GO:0034113	0.25	0.89	4	36	heterotypic cell-cell adhesion	BP	1	MBP,JAM3,CD47,VCAM1	darkgreen	VSMC_M4
GO:1903115	0.25	0.89	4	32	regulation of actin filament-based movement	BP	1	TNNT2,CAMK2D,CACNA1C,PLN	darkgreen	VSMC_M4
GO:0001817	0.25	0.80	38	492	regulation of cytokine production	BP	1	MBP,IFNGR1,IRAK3,LAPTM4B,ANGPT1,LEP,DDX58,CD274,IL18R1,MAP3K7,INHBB,NDRG2,CYP1B1,FFAR3,CLU,APP,ABCC8,PTPN11,LBP,PTPN22,CD47,N4BP1,LPL,HTR2B,AFAP1L2,F11R,HSPB1,SERPINE1,ATP6AP2,HIF1A,RORA,TGFB3,NPTN,LGALS9,PLCG2,F3,TLR1,CD83	darkgreen	VSMC_M4
GO:0001505	0.25	0.83	13	147	regulation of neurotransmitter levels	BP	1	STX11,UNC13B,PPP1R9A,PREPL,SYT5,PCLO,MCTP1,ACHE,MAOA,MAOB,NLGN1,FBXL20,RHOT1	darkgreen	VSMC_M4
GO:0031623	0.25	0.85	8	85	receptor internalization	BP	1	ANGPT1,LMBRD1,ADM,ATXN2,HTR2B,ACHE,NUMB,PLCG2	darkgreen	VSMC_M4
GO:0106106	0.25	0.84	11	123	cold-induced thermogenesis	BP	1	ZNF516,GJA1,LEP,IL18R1,PDGFC,ADIPOR1,PLCL1,ACHE,PPARGC1A,NPR3,ADAMTS5	darkgreen	VSMC_M4
GO:0120161	0.25	0.84	11	123	regulation of cold-induced thermogenesis	BP	1	ZNF516,GJA1,LEP,IL18R1,PDGFC,ADIPOR1,PLCL1,ACHE,PPARGC1A,NPR3,ADAMTS5	darkgreen	VSMC_M4
GO:0043457	0.25	0.89	4	39	regulation of cellular respiration	BP	1	HIF1A,OPN3,PPARGC1A,BNIP3	darkgreen	VSMC_M4
GO:0007249	0.25	0.82	18	222	I-kappaB kinase/NF-kappaB signaling	BP	1	ANGPT1,GJA1,MAP3K7,ATP2C1,HTR2B,CFLAR,PRKD1,PRDX4,HSPB1,TNFSF10,RORA,LGALS9,FLNA,PLEKHG5,PLCG2,TERF2IP,WLS,EDA	darkgreen	VSMC_M4
GO:0048565	0.25	0.85	9	92	digestive tract development	BP	1	BCL2,PDGFC,ADA,FGFR2,DACT1,HIF1A,TGFB3,CDKN1A,YAP1	darkgreen	VSMC_M4
GO:0034754	0.25	0.86	7	79	cellular hormone metabolic process	BP	1	HSD17B6,REST,CYP1B1,ADM,CYP19A1,PPARGC1A,BMP6	darkgreen	VSMC_M4
GO:0042058	0.25	0.87	6	62	regulation of epidermal growth factor receptor signaling pathway	BP	1	PTPN3,AFAP1L2,GPRC5A,HIP1,CDH13,BCAR3	darkgreen	VSMC_M4
GO:0051056	0.25	0.81	24	259	regulation of small GTPase mediated signal transduction	BP	1	ABRA,DOCK8,KANK1,ABCA1,CHN2,RALGAPA2,ARHGEF17,ARHGEF3,NGF,RIPOR2,KCTD10,PREX1,F11R,ARHGAP20,RDX,SYNPO2L,IQSEC3,SIPA1L1,MAPRE2,ARHGAP28,PLEKHG5,CSF1,ARHGAP29,SYDE2	darkgreen	VSMC_M4
GO:2001056	0.25	0.85	9	105	positive regulation of cysteine-type endopeptidase activity	BP	1	DAPK1,REST,LGMN,CFLAR,HIP1,TNFSF10,LGALS9,F3,CYR61	darkgreen	VSMC_M4
GO:0007569	0.25	0.85	9	98	cell aging	BP	1	BCL2,CITED2,CDKN2B,C2orf40,MARCH5,NEK4,SERPINE1,CDKN1A,ICAM1	darkgreen	VSMC_M4
GO:0046364	0.26	0.87	6	65	monosaccharide biosynthetic process	BP	1	EP300,LEP,SESN2,CHST15,SLC25A12,PPARGC1A	darkgreen	VSMC_M4
GO:0106027	0.26	0.85	8	78	neuron projection organization	BP	1	PPP1R9A,APP,TANC1,LGMN,ZNF365,NLGN1,SIPA1L1,PAK3	darkgreen	VSMC_M4
GO:0031331	0.26	0.80	29	366	positive regulation of cellular catabolic process	BP	1	MDM2,RNF19A,DAPK1,FAM122A,MAP3K7,SESN1,ADAM9,FOXO1,CPEB3,SLC25A4,CLU,APP,HERPUD1,SESN2,LRP2,PRKD1,ATF6,RDX,FBXL5,DACT1,HIF1A,CALCOCO2,DAB2,PRKAA2,TMEM59,LRSAM1,BNIP3,PIK3C2A,ORMDL3	darkgreen	VSMC_M4
GO:0043507	0.26	0.89	4	35	positive regulation of JUN kinase activity	BP	1	SASH1,MAP3K7,EDN1,MAP3K13	darkgreen	VSMC_M4
GO:0005978	0.26	0.89	4	36	glycogen biosynthetic process	BP	1	GYS1,PTH,GYG1,GYG2	darkgreen	VSMC_M4
GO:0009250	0.26	0.89	4	36	glucan biosynthetic process	BP	1	GYS1,PTH,GYG1,GYG2	darkgreen	VSMC_M4

GO:0045851	0.26	0.89	4	38	pH reduction	BP	1	BCL2,CLCN3,ATP6AP2,ATP6V0E1	darkgreen	VSMC_M4
GO:0001843	0.26	0.85	8	82	neural tube closure	BP	1	CITED2,GRHL2,ADM,SHROOM3,SEC24B,LRP2,BBS4,LMO4	darkgreen	VSMC_M4
GO:0016051	0.26	0.83	13	155	carbohydrate biosynthetic process	BP	1	EP300,LEP,GYS1,HRH1,PTH,GYG1,B3GNT7,GYG2,SESN2,NDST3,CHST15,SLC25A12,PPARGC1A	darkgreen	VSMC_M4
GO:0048168	0.26	0.89	4	38	regulation of neuronal synaptic plasticity	BP	1	ZDHHC2,MCTP1,APP,NPTN	darkgreen	VSMC_M4
GO:0006509	0.26	0.89	4	36	membrane protein ectodomain proteolysis	BP	1	PTPN3,ADAM9,BACE2,NCSTN	darkgreen	VSMC_M4
GO:0060711	0.26	0.89	4	37	labyrinthine layer development	BP	1	GRHL2,ADM,FGFR2,CYR61	darkgreen	VSMC_M4
GO:0040014	0.26	0.87	5	47	regulation of multicellular organism growth	BP	1	BCL2,CHD7,APP,LGMN,CSF1	darkgreen	VSMC_M4
GO:0060322	0.26	0.79	51	624	head development	BP	1	MBP,BCL2,GRHL2,EP300,SLC2A1,PEX13,GATA2,ITGA8,PCDH9,PFKFB3,NDRG2,TACC1,COL4A1,APLP1,PTPRG,CHD7,MEIS2,APP,ANXA3,PTPN11,SEMA5A,RGS2,FEZ1,SUN1,GNB4,SEC24B,PLXNA2,LRP2,FGFR2,NCSTN,ARID5B,ZNF365,LRP6,ATP6AP2,MAOB,EZH1,HIF1A,PPARGC1A,RORA,NUMB,TGFB3,BBS4,CDH2,SMARCA1,FLNA,WLS,SLC8A1,BNIP3,FGF9,PRKG1,DDIT4	darkgreen	VSMC_M4
GO:0030902	0.26	0.84	11	116	hindbrain development	BP	1	BCL2,GATA2,PTPN11,SEC24B,PLXNA2,NCSTN,ZNF365,PPARGC1A,RORA,FLNA,WLS	darkgreen	VSMC_M4
GO:0006865	0.26	0.84	9	99	amino acid transport	BP	1	GJA1,LEP,SLC17A5,TRPC4,SERINC3,RGS2,SLC25A12,SLC43A2,LRRC8C	darkgreen	VSMC_M4
GO:0007254	0.26	0.83	12	134	JNK cascade	BP	1	TPD52L1,SH3RF3,MAP3K7,MDFIC,HIPK2,RASSF2,HIPK3,SH3RF1,APP,PTPN22,MAP3K13,DACT1	darkgreen	VSMC_M4
GO:0006805	0.26	0.89	4	41	xenobiotic metabolic process	BP	1	CYP1B1,HNF4A,FMO4,RORA	darkgreen	VSMC_M4
GO:0030307	0.26	0.83	12	134	positive regulation of cell growth	BP	1	BCL2,FAM122A,TGFBR1,ITSN2,HPN,EXTL3,NGF,EDN1,SEMA5A,SHTN1,AKAP6,MAP3K13	darkgreen	VSMC_M4
GO:0051926	0.26	0.89	4	39	negative regulation of calcium ion transport	BP	1	BCL2,TRDN,PLN,ICAM1	darkgreen	VSMC_M4
GO:0010827	0.26	0.86	6	58	regulation of glucose transmembrane transport	BP	1	LEP,OCLN,PTH,PTPN11,EDN1,OPN3	darkgreen	VSMC_M4
GO:0035914	0.26	0.87	5	48	skeletal muscle cell differentiation	BP	1	CITED2,ANKRD1,RBFOX1,MAFF,HLF	darkgreen	VSMC_M4
GO:0045859	0.26	0.79	40	513	regulation of protein kinase activity	BP	1	SASH1,IRAK3,ANGPT1,TPD52L1,GNAQ,LEP,CDKN2B,VLDLR,PPP1R9A,MAP3K7,ADAM9,RASSF2,FLT3,LATS2,HIPK3,CLU,APP,PDGFC,CCNT1,PTPN22,EDN1,RGS2,LRP5,HTR2B,MST1R,AFAP1L2,SESN2,DDR2,GPRC5A,MAP3K13,LRP6,HSPB1,CCNG1,TOM1L1,CSF1,CYR61,SLC8A1,CDKN1A,PPM1E,CNTD2	darkgreen	VSMC_M4
GO:0006887	0.26	0.81	22	266	exocytosis	BP	1	STX11,UNC13B,REST,PREPL,SYT5,GATA2,SYNGR2,RAB2B,PCLO,EXOC6,ANXA3,ATP9A,RAPGEF4,EXPH5,NLGN1,SYT16,MICAL3,ADGRE2,FBXL20,LGALS9,VAMP7,PIK3C2A	darkgreen	VSMC_M4
GO:0050709	0.26	0.87	5	51	negative regulation of protein secretion	BP	1	REST,INHBB,ABCC8,PTPN11,PFKL	darkgreen	VSMC_M4
GO:0009636	0.26	0.82	14	174	response to toxic substance	BP	1	MBP,BCL2,MDM2,IPCEF1,SOD2,PPP1R9A,PON2,SESN1,CYP1B1,KDM5B,SESN2,PRDX4,MAOB,CDKN1A	darkgreen	VSMC_M4
GO:0060606	0.26	0.85	8	83	tube closure	BP	1	CITED2,GRHL2,ADM,SHROOM3,SEC24B,LRP2,BBS4,LMO4	darkgreen	VSMC_M4
GO:0051155	0.26	0.88	4	37	positive regulation of striated muscle cell differentiation	BP	1	BCL2,EDN1,AKAP6,HOPX	darkgreen	VSMC_M4
GO:0002699	0.26	0.83	12	142	positive regulation of immune effector process	BP	1	DDX58,IL18R1,MAP3K7,GATA2,FFAR3,LBP,PTPN22,TP53BP1,ADGRE2,LGALS9,VAMP7,PLCG2	darkgreen	VSMC_M4
GO:0045666	0.26	0.86	6	61	positive regulation of neuron differentiation	BP	1	REST,GATA2,NGF,FEZ1,ZC4H2,BMP6	darkgreen	VSMC_M4
GO:0014911	0.26	0.88	4	35	positive regulation of smooth muscle cell migration	BP	1	BCL2,MDM2,DOCK4,FGF9	darkgreen	VSMC_M4
GO:0032388	0.26	0.82	15	173	positive regulation of intracellular transport	BP	1	SLC35D3,MDM2,LEP,TCAF1,ZDHHC2,ATG13,RAB29,ACTN2,FEZ1,PRKD1,RDX,ABLIM3,DAB2,FLNA,SCP2	darkgreen	VSMC_M4
GO:0044344	0.27	0.84	8	86	cellular response to fibroblast growth factor stimulus	BP	1	SMOC2,PTPN11,KDM5B,GALNT3,FGFR2,FGFRL1,NPTN,FGF9	darkgreen	VSMC_M4
GO:0048534	0.27	0.78	50	649	hematopoietic or lymphoid organ development	BP	1	BCL2,CITED2,ANGPT1,EP300,MLLT3,LEP,CDKN2B,IL18R1,REST,ZAP70,TGFBR1,HIPK2,GATA2,SNRK,POLB,RASSF2,TMEM178A,TF,FLT3,CHD7,SH3RF1,BLNK,MEIS2,APP,PTPN11,TMEM64,PTPN22,ADA,JAM3,LRP5,PREX1,PRKCA,P4HTM,FGFR2,MFAP5,WDR1,HIF1A,ACTN1,RORA,FAXDC2,FST,LGALS9,CSF1,PLCG2,VCAM1,LMO4,VNN1,CD83,LOX,CCR6	darkgreen	VSMC_M4
GO:1902991	0.27	0.88	4	39	regulation of amyloid precursor protein catabolic process	BP	1	IFNGR1,GGA3,CLU,ABCG1	darkgreen	VSMC_M4
GO:0070098	0.27	0.88	4	40	chemokine-mediated signaling pathway	BP	1	EDN1,HIF1A,SLIT3,CCR6	darkgreen	VSMC_M4
GO:0120192	0.27	0.87	5	48	tight junction assembly	BP	1	GRHL2,GJA1,OCLN,F11R,PATJ	darkgreen	VSMC_M4
GO:0043549	0.27	0.78	48	612	regulation of kinase activity	BP	1	SASH1,IRAK3,DDR1,ANGPT1,TPD52L1,GNAQ,LEP,CDKN2B,VLDLR,PPP1R9A,MAP3K7,EPHB6,ADAM9,RASSF2,FLT3,LATS2,HIPK3,CLU,APP,PDGFC,CCNT1,PTPN22,RBL2,EDN1,RGS2,LRP5,HTR2B,MST1R,AFAP1L2,SESN2,FGFR2,PRKD1,DDR2,GPRC5A,MAP3K13,LRP6,HSPB1,ATG14,LMTK2,CCNG1,TOM1L1,CSF1,LMO4,CYR61,SLC8A1,CDKN1A,PPM1E,CNTD2	darkgreen	VSMC_M4
GO:1905954	0.27	0.85	7	73	positive regulation of lipid localization	BP	1	ABCA1,EDN1,LPL,ABCG1,CYP19A1,BMP6,SCP2	darkgreen	VSMC_M4
GO:0010469	0.27	0.83	10	112	regulation of signaling receptor activity	BP	1	DAPK1,APP,EDN1,NCOA3,GPRC5A,SERPINE1,NLGN1,HIF1A,PPARGC1A,LYPD6	darkgreen	VSMC_M4
GO:0016197	0.27	0.81	18	209	endosomal transport	BP	1	GRIP1,LAPTM4B,RIC1,PREPL,ABCA1,ITSN2,TMCC1,GGA3,ZDHHC2,DENND5A,RAB29,ACTN2,TINAGL1,ATP9A,INPP5F,LMTK2,EPG5,SORT1	darkgreen	VSMC_M4
GO:0071604	0.27	0.88	4	35	transforming growth factor beta production	BP	1	LAPTM4B,ATP6AP2,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0042306	0.27	0.87	5	52	regulation of protein import into nucleus	BP	1	ANGPT1,LEP,MDFIC,PRKD1,FLNA	darkgreen	VSMC_M4
GO:0048013	0.27	0.87	5	45	ephrin receptor signaling pathway	BP	1	EPHB6,NCK1,PTPN11,SIPA1L1,PAK3	darkgreen	VSMC_M4
GO:0034644	0.27	0.85	7	77	cellular response to UV	BP	1	MDM2,EP300,N4BP1,MMP1,OPN3,CDKN1A,MFAP4	darkgreen	VSMC_M4
GO:0051962	0.27	0.81	19	216	positive regulation of nervous system development	BP	1	ADGRB1,TENM4,SMARCD3,NGF,SEMA5A,PLXNA2,SHTN1,LRP2,PLXNB1,ZNF365,MAP3K13,CUX1,NLGN1,HIF1A,NUMB,NPTN,PAK3,PLXNB3,LRRC24	darkgreen	VSMC_M4
GO:1990090	0.27	0.87	5	46	cellular response to nerve growth factor stimulus	BP	1	SH3GL2,KIDINS220,APP,NGF,SORT1	darkgreen	VSMC_M4
GO:0031102	0.27	0.87	5	49	neuron projection regeneration	BP	1	BCL2,ADM,JAM3,INPP5F,FLNA	darkgreen	VSMC_M4
GO:0015914	0.27	0.85	7	70	phospholipid transport	BP	1	ABCA1,SCARB2,ABCG1,ATP9A,ABCA4,PRELID2,SCP2	darkgreen	VSMC_M4
GO:0043010	0.27	0.80	21	242	camera-type eye development	BP	1	CITED2,GRHL2,TGFBR1,HIPK2,PPP1R13L,SMARCD3,THRB,COL4A1,CYP1B1,CHD7,GPM6A,KDM5B,LRP5,CRYGS,ACHE,CRYAB,HIF1A,CACNA1C,ANGPTL7,BBS4,BCAR3	darkgreen	VSMC_M4
GO:0051147	0.27	0.83	10	115	regulation of muscle cell differentiation	BP	1	BCL2,MDM2,SOD2,SMARCD3,EDN1,RGS2,FGFR2,AKAP6,FGF9,HOPX	darkgreen	VSMC_M4
GO:0071230	0.27	0.86	6	59	cellular response to amino acid stimulus	BP	1	SESN1,COL4A1,CPEB3,PDGFC,SESN2,CASTOR1	darkgreen	VSMC_M4

GO:0042475	0.27	0.85	6	63	odontogenesis of dentin-containing tooth	BP	1	FOXO1,ADM,SERPINE1,FST,CSF1,EDA	darkgreen	VSMC_M4
GO:0071840	0.27	0.75	349	4827	cellular component organization or biogenesis	BP	1	MBP,BCL2,COL23A1,STX11,SHPRH,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,ANGPT1,SMOC2,GJA1,TRDN,LAMA2,EP300,MRTFA,ADGRB1,SH3GL2,MLLT3,LIMCH1,FAM122A,KANK1,VLDLR,UNC13B,TPM2,PPP1R9A,RIC1,REST,RECK,ECM2,IGFBP7,LMAN2L,SLC2A1,TGFBR1,ABCA1,SVEP1,SNAP91,PEX13,CALD1,ANTXR1,KIDINS220,EPHB6,JADE1,ITSN2,TUBE1,HIPK2,GATA2,LIMS2,TMEM135,TESK2,TMCC1,TENM4,SMARCD3,USP6NL,EXOG,BABAM2,SYNGR2,ARHGEF17,ACTN4,FMNL2,SATB1,ADAM9,TACC1,ATP2C1,COL4A1,COL4A2,ANKLE2,PCDHB4,CDC42EP3,CYP1B1,PCLO,SEMA3C,EML4,LMNTD2,TF,APLP1,AMOTL2,WASF3,ZDHHC2,RIC3,HPN,PTPRG,DENND5A,CHD7,CHPT1,ANKRD1,EPB41L4A,CPEB3,MARCH5,NCK1,SORBS2,EXOC6,ADM,ESYT3,MAP1LC3A,PAM,SLC25A4,CLCN3,OCLN,TCF7L1,TEAD1,MCTP1,FAM172A,KIF13B,LYSMD3,EXTL3,G3BP2,CLU,GPM6A,APP,ATXN2,SCARB2,PDGFC,PRPH,SHROOM3,RXFP1,ABCC8,PTPN11,PTX3,ADCY6,JMY,ATG13,DCBLD2,CHD6,PKP4,TANC1,LPCAT2,HNF4A,FMOD,AKTIP,RBL2,NGF,PDZD7,EDN1,JAM3,GPRIN3,CD47,NFASC,SMARCAD1,MYO1B,SEMA5A,LPL,RAB29,ABCG1,ADIPOR1,DNAH7,COL4A4,KDM5B,RIPOR2,CCDC80,MARCKSL1,RGS2,EYA2,TNNT2,PDE4DIP,ACTN2,LRP5,KCTD10,ARRDC4,FEZ1,NPNT,PREX1,LGMN,ROBO3,NID1,SUN1,PRKCA,SEC24B,ABLIM1,MFGE8,PARD6B,MID1,ATP9A,PLXNA2,SESN2,ARV1,SHTN1,CAMK2D,CTSS,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,SYNPO2,TP53BP1,PRKD1,F11R,PLXNB1,QSOX1,LRCH3,ZRANB1,RAPH1,ITGA6,ZNF365,MAP7D2,AKAP6,DDR2,MAP3K13,HIP1,PRDX4,LNPK,COLGALT2,GABARAPL1,CUX1,MFAP5,SERPINE1,ACHE,CRYAB,	darkgreen	VSMC_M4
GO:0051338	0.27	0.78	54	706	regulation of transferase activity	BP	1	SASH1,IRAK3,DDR1,GRHL2,ANGPT1,TPD52L1,GNAQ,LEP,CDKN2B,DCUN1D4,VLDLR,PPP1R9A,MAP3K7,EPHB6,ADAM9,RASSF2,FLT3,LATS2,HIPK3,CLU,APP,PDGFC,CCNT1,PTPN22,RBL2,EDN1,RGS2,LRP5,ARRDC4,HTR2B,MST1R,SERINC2,AFAP1L2,SESN2,FGFR2,PRKD1,DDR2,GPRC5A,MAP3K13,LRP6,HSPB1,EIF4A2,ATG14,LMTK2,CCNG1,TOM1L1,CSF1,LMO4,CYR61,SLC8A1,CDKN1A,PPM1E,CNTD2,ORMDL3	darkgreen	VSMC_M4
GO:0097178	0.27	0.88	4	38	ruffle assembly	BP	1	KANK1,RDX,NLGN1,ICAM1	darkgreen	VSMC_M4
GO:0048562	0.27	0.80	19	225	embryonic organ morphogenesis	BP	1	CITED2,GRHL2,TGFBR1,TBX18,HIPK2,GATA2,HPN,CHD7,PDZD7,EDN1,SEC24B,FGFR2,MFAP5,HIF1A,TGFB3,BBS4,FRZB,TBX20,YAP1	darkgreen	VSMC_M4
GO:1902414	0.27	0.84	8	82	protein localization to cell junction	BP	1	GRIP1,PCLO,ZDHHC2,JAM3,F11R,HSPB1,NLGN1,FLNA	darkgreen	VSMC_M4
GO:0048546	0.27	0.88	4	36	digestive tract morphogenesis	BP	1	BCL2,FGFR2,DACT1,HIF1A	darkgreen	VSMC_M4
GO:0007269	0.27	0.83	10	110	neurotransmitter secretion	BP	1	STX11,UNC13B,PPP1R9A,PREPL,SYT5,PCLO,MCTP1,NLGN1,FBXL20,RHOT1	darkgreen	VSMC_M4
GO:0099643	0.27	0.83	10	110	signal release from synapse	BP	1	STX11,UNC13B,PPP1R9A,PREPL,SYT5,PCLO,MCTP1,NLGN1,FBXL20,RHOT1	darkgreen	VSMC_M4
GO:0043154	0.27	0.86	5	55	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MDM2,SH3RF1,RNF34,HERPUD1,CRYAB	darkgreen	VSMC_M4
GO:0043299	0.27	0.86	5	51	leukocyte degranulation	BP	1	GATA2,ANXA3,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:1900407	0.27	0.85	6	66	regulation of cellular response to oxidative stress	BP	1	SOD2,OXR1,REST,HSPB1,HIF1A,VNN1	darkgreen	VSMC_M4
GO:0030433	0.27	0.84	7	78	ubiquitin-dependent ERAD pathway	BP	1	WFS1,STT3B,HERPUD1,MARCH6,JKAMP,FAF2,FBXO27	darkgreen	VSMC_M4
GO:0043303	0.27	0.88	4	38	mast cell degranulation	BP	1	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0007595	0.27	0.88	4	37	lactation	BP	1	DDR1,NCOR2,PAM,HIF1A	darkgreen	VSMC_M4
GO:0001704	0.27	0.83	9	93	formation of primary germ layer	BP	1	GJA1,ITGA8,COL4A2,ATOH8,ETS2,EYA2,FGFR2,WLS,TBX20	darkgreen	VSMC_M4
GO:0051347	0.28	0.78	35	441	positive regulation of transferase activity	BP	1	SASH1,DDR1,GRHL2,ANGPT1,TPD52L1,LEP,DCUN1D4,VLDLR,PPP1R9A,MAP3K7,EPHB6,ADAM9,RASSF2,FLT3,CLU,PDGFC,CCNT1,EDN1,ARRDC4,HTR2B,MST1R,SERINC2,AFAP1L2,FGFR2,PRKD1,DDR2,GPRC5A,MAP3K13,ATG14,LMTK2,TOM1L1,CSF1,LMO4,CYR61,CDKN1A	darkgreen	VSMC_M4
GO:0050729	0.28	0.84	8	93	positive regulation of inflammatory response	BP	1	FFAR3,APP,LBP,CD47,LPL,SERPINE1,VAMP7,PLCG2	darkgreen	VSMC_M4
GO:0051851	0.28	0.86	5	51	modulation by host of symbiont process	BP	1	EP300,REST,HPN,PTX3,CCNT1	darkgreen	VSMC_M4
GO:0071900	0.28	0.79	24	300	regulation of protein serine/threonine kinase activity	BP	1	SASH1,IRAK3,TPD52L1,CDKN2B,MAP3K7,ADAM9,FLT3,LATS2,HIPK3,PDGFC,CCNT1,PTPN22,EDN1,RGS2,LRP5,HTR2B,MST1R,SESN2,MAP3K13,LRP6,CCNG1,SLC8A1,CDKN1A,CNTD2	darkgreen	VSMC_M4
GO:0042987	0.28	0.86	5	52	amyloid precursor protein catabolic process	BP	1	IFNGR1,GGA3,CLU,ABCG1,NCSTN	darkgreen	VSMC_M4
GO:0002366	0.28	0.81	15	181	leukocyte activation involved in immune response	BP	1	IL18R1,GATA2,APBB1IP,CD180,ANXA3,LBP,ADA,TP53BP1,ADGRE2,RORA,LGALS9,VAMP7,PLCG2,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0007229	0.28	0.83	9	92	integrin-mediated signaling pathway	BP	1	LIMS2,ITGA8,ITGA9,ADAM9,PTPN11,CD47,PRKD1,ITGA6,FLNA	darkgreen	VSMC_M4
GO:0055085	0.28	0.76	78	1047	transmembrane transport	BP	1	BCL2,SLC35D3,PKDREJ,CALHM5,GJA1,TRDN,DAPK1,LEP,SLC2A1,SLC17A5,ABCA1,PTPN3,PEX13,TCAF1,KCNE3,ACTN4,FGF14,TRPC4,SLC16A3,ATP2C1,TUSC3,FXYD1,HPN,CHD7,MICU2,SLC25A4,SCN8A,CLCN3,OCLN,SLC35G1,JPH1,PTH,GPM6A,APP,ABCC8,PTPN11,SLC26A7,EDN1,ANO5,ABCG1,CNNM2,RGS2,ACTN2,HTR2B,SESN2,CAMK2D,ABCC9,CTSS,LRP2,PRKD1,CYBRD1,SLC25A12,AKAP6,NLGN1,WDR1,OPN3,CACNA1C,PPARGC1A,MAGT1,KCNK10,SLC14A1,SLC43A2,SCNN1D,FLNA,SLC2A5,HCN2,AHCYL1,SORT1,PLCG2,ABCA4,LRRC8C,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,SLC27A5,ATP6V0E1	darkgreen	VSMC_M4
GO:1902806	0.28	0.82	10	115	regulation of cell cycle G1/S phase transition	BP	1	BCL2,MDM2,CDKN2B,JADE1,RBL2,RDX,DACT1,PLCG2,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0048538	0.28	0.87	4	38	thymus development	BP	1	BCL2,CITED2,TGFBR1,LMO4	darkgreen	VSMC_M4
GO:0050769	0.28	0.80	16	181	positive regulation of neurogenesis	BP	1	TENM4,SMARCD3,NGF,SEMA5A,PLXNA2,SHTN1,LRP2,PLXNB1,ZNF365,MAP3K13,CUX1,HIF1A,NUMB,NPTN,PAK3,PLXNB3	darkgreen	VSMC_M4
GO:1990089	0.28	0.86	5	47	response to nerve growth factor	BP	1	SH3GL2,KIDINS220,APP,NGF,SORT1	darkgreen	VSMC_M4
GO:0048844	0.28	0.85	6	57	artery morphogenesis	BP	1	CITED2,TGFBR1,CHD7,SEC24B,MYLK,LRP2	darkgreen	VSMC_M4
GO:0002285	0.28	0.82	11	127	lymphocyte activation involved in immune response	BP	1	IL18R1,APBB1IP,CD180,ADA,TP53BP1,RORA,LGALS9,VAMP7,PLCG2,CCR6,ICAM1	darkgreen	VSMC_M4

GO:0032720	0.28	0.87	4	41	negative regulation of tumor necrosis factor production	BP	1	IRAK3,LBP,PTPN22,LGALS9	darkgreen	VSMC_M4
GO:0010828	0.28	0.87	4	35	positive regulation of glucose transmembrane transport	BP	1	OCLN,PTH,PTPN11,OPN3	darkgreen	VSMC_M4
GO:0032526	0.28	0.83	8	84	response to retinoic acid	BP	1	GJA1,LEP,IGFBP7,ABCA1,FGFR2,IGFBP2,YAP1,BMP6	darkgreen	VSMC_M4
GO:0050865	0.29	0.78	29	385	regulation of cell activation	BP	1	BCL2,LEP,DOCK8,CD274,ZAP70,MAP3K8,GATA2,NCK1,SH3RF1,PTPN11,LBP,PTPN22,ADA,CD47,RIPOR2,PRKCA,TP53BP1,F11R,IGFBP2,ADGRE2,RORA,LGALS9,VAMP7,VCAM1,LMO4,VNN1,CD83,CDKN1A,PRKG1	darkgreen	VSMC_M4
GO:0032963	0.29	0.84	7	78	collagen metabolic process	BP	1	CTSS,MMP1,HIF1A,TGFB3,MMP28,CST3,MFAP4	darkgreen	VSMC_M4
GO:0043266	0.29	0.84	6	59	regulation of potassium ion transport	BP	1	KCNE3,ABCC8,ACTN2,AKAP6,FLNA,KCNE4	darkgreen	VSMC_M4
GO:0030301	0.29	0.84	7	77	cholesterol transport	BP	1	LEP,ABCA1,CLU,ABCG1,ARV1,LRP6,SCP2	darkgreen	VSMC_M4
GO:0030038	0.29	0.82	9	95	contractile actin filament bundle assembly	BP	1	LIMCH1,PPP1R9A,TGFBR1,CD47,F11R,SYNPO2L,TGFB3,ARHGAP28,PPM1E	darkgreen	VSMC_M4
GO:0043149	0.29	0.82	9	95	stress fiber assembly	BP	1	LIMCH1,PPP1R9A,TGFBR1,CD47,F11R,SYNPO2L,TGFB3,ARHGAP28,PPM1E	darkgreen	VSMC_M4
GO:0002279	0.29	0.87	4	39	mast cell activation involved in immune response	BP	1	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0010604	0.29	0.74	188	2586	positive regulation of macromolecule metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,MDM2,RNF19A,GRHL2,ABRA,ANGPT1,SMOC2,GJA1,TPD52L1,EP300,MRTFA,BRD8,DAPK1,BRPF3,MLLT3,LEP,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,CD274,IL18R1,CREB3,REST,TGFBR1,MAP3K7,ANTXR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,GGA3,NAA16,ELF1,INHBB,SMARCD3,LMO7,BABAM2,FOSL2,LBH,SALL2,THRB,ACTN4,ADAM9,TACC1,FOXO1,RASSF2,ANKLE2,CYP1B1,TF,FLT3,NCOR2,FFAR3,HPN,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ATOH8,OCLN,TEAD1,PTH,CLU,BLNK,MED12L,MEIS2,APP,PDGFC,ABCC8,ANXA3,PTPN11,LBP,NEK4,CCNT1,HERPUD1,JMY,CHD6,PTPN22,HNF4A,GDF6,AKTIP,NGF,EDN1,ETS2,LPL,RAB29,ABCG1,KDM5B,EYA2,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,HTR2B,MST1R,LGMN,AFAP1L2,SESN2,NGRN,LRP2,CFLAR,INPP5F,FGFR2,RBM4B,TP53BP1,PRKD1,NCSTN,ARID5B,ITGA6,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,FAM129A,HSPB1,SERPINE1,ATP6AP2,RDX,ZNF445,EZH1,ATG14,FBXL5,TNFSF10,DACT1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,TOM1L1,FAXDC2,NPTN,PAK3,ABLIM3,CRLF3,DAB2,LGALS9,SMARCA1,SKP2,PRKAA2,CTIF,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,CDC7,LMO4,CYR61,ZFP90,TLR1,CD83,TBX20,ZNF175,MAFF,CDKN1A,FGF9,EDA,ZNF782,HLF,ICAM1,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0003170	0.29	0.84	6	58	heart valve development	BP	1	MDM2,FGFRL1,SLIT3,SMAD6,CYR61,TBX20	darkgreen	VSMC_M4
GO:1902041	0.29	0.87	4	42	regulation of extrinsic apoptotic signaling pathway via death domain receptors	BP	1	RNF34,CFLAR,SERPINE1,ICAM1	darkgreen	VSMC_M4
GO:0018958	0.29	0.84	6	65	phenol-containing compound metabolic process	BP	1	BCL2,HPN,CPQ,MAOA,MAOB,OPN3	darkgreen	VSMC_M4
GO:0071326	0.29	0.82	10	113	cellular response to monosaccharide stimulus	BP	1	LEP,UNC13B,ABCG1,LRP5,ADCY5,HIF1A,PPARGC1A,PRKAA2,SLC2A5,ICAM1	darkgreen	VSMC_M4
GO:0032873	0.29	0.87	4	38	negative regulation of stress-activated MAPK cascade	BP	1	FOXO1,HIPK3,PTPN22,DACT1	darkgreen	VSMC_M4
GO:0070303	0.29	0.87	4	38	negative regulation of stress-activated protein kinase signaling cascade	BP	1	FOXO1,HIPK3,PTPN22,DACT1	darkgreen	VSMC_M4
GO:0001541	0.29	0.87	4	39	ovarian follicle development	BP	1	BCL2,INHBB,PTX3,ICAM1	darkgreen	VSMC_M4
GO:0071383	0.29	0.80	14	163	cellular response to steroid hormone stimulus	BP	1	EP300,REST,LBH,FOXO1,FLT3,NCOR2,EDN1,CFLAR,STRN3,DAB2,SKP2,ICAM1,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0046474	0.29	0.80	15	185	glycerophospholipid biosynthetic process	BP	1	PIGN,PIP5K1B,CHPT1,LPCAT2,AGPAT3,HTR2B,INPP5F,PI4KB,ACHE,PIGG,OCRL,PIGS,PLCG2,PIGK,PIK3C2A	darkgreen	VSMC_M4
GO:0048678	0.29	0.84	6	65	response to axon injury	BP	1	BCL2,JAM3,INPP5F,FLNA,PLCG2,BNIP3	darkgreen	VSMC_M4
GO:0043523	0.29	0.80	14	169	regulation of neuron apoptotic process	BP	1	BCL2,SOD2,OXR1,ANGPT1,WFS1,HIPK2,NGF,LGMN,CTSZ,UNC5B,HIF1A,PPARGC1A,TGFB3,PAK3	darkgreen	VSMC_M4
GO:0006111	0.29	0.87	4	40	regulation of gluconeogenesis	BP	1	EP300,LEP,SESN2,PPARGC1A	darkgreen	VSMC_M4
GO:0062197	0.29	0.78	22	282	cellular response to chemical stress	BP	1	BCL2,MDM2,SOD2,OXR1,DAPK1,REST,SLC2A1,FOXO1,CYP1B1,MAP1LC3A,PTPN11,CHD6,SESN2,MYLK,PRKD1,HSPB1,HIF1A,PPARGC1A,PRKAA2,LRRC8C,VNN1,BNIP3	darkgreen	VSMC_M4
GO:0050772	0.29	0.83	7	68	positive regulation of axonogenesis	BP	1	NGF,SEMA5A,PLXNA2,SHTN1,PLXNB1,MAP3K13,PLXNB3	darkgreen	VSMC_M4
GO:0014902	0.29	0.82	8	86	myotube differentiation	BP	1	BCL2,ADGRB1,TANC1,RCAN1,RIPOR2,CFLAR,SORT1,ADAMTS5	darkgreen	VSMC_M4
GO:0001756	0.29	0.85	5	48	somitogenesis	BP	1	EP300,TBX18,SEMA3C,PLXNA2,LRP6	darkgreen	VSMC_M4
GO:0009416	0.29	0.79	19	239	response to light stimulus	BP	1	BCL2,MDM2,EP300,GNAQ,HRH1,GRK7,MEIS2,APP,ABCC8,TANC1,N4BP1,RBM4B,MMP1,HIF1A,OPN3,NPTN,ABCA4,CDKN1A,MFAP4	darkgreen	VSMC_M4
GO:0002224	0.29	0.82	8	92	toll-like receptor signaling pathway	BP	1	IRAK3,MAP3K7,LBP,PTPN22,CTSS,EPG5,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0022406	0.29	0.83	7	76	membrane docking	BP	1	STX11,UNC13B,ESYT3,ATG14,AHCYL1,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:0008333	0.29	0.85	5	50	endosome to lysosome transport	BP	1	AKTIP,ATG14,EPG5,VAMP7,SORT1	darkgreen	VSMC_M4
GO:0006820	0.29	0.77	25	319	anion transport	BP	1	SLC35D3,GJA1,LEP,SLC2A1,SLC17A5,TCAF1,TRPC4,SLC16A3,FXYD1,SLC25A4,CLCN3,SLC26A7,SERINC3,EDN1,CD47,PLA2G4F,ANO5,RGS2,ABCC9,LRP2,SLC25A12,SLC43A2,AHCYL1,LRRC8C,SLC27A5	darkgreen	VSMC_M4
GO:0021782	0.29	0.82	8	86	glial cell development	BP	1	IFNGR1,TENM4,WASF3,CLU,APP,BACE2,NCSTN,SH3TC2	darkgreen	VSMC_M4
GO:0097061	0.30	0.83	7	70	dendritic spine organization	BP	1	PPP1R9A,TANC1,LGMN,ZNF365,NLGN1,SIPA1L1,PAK3	darkgreen	VSMC_M4
GO:0006623	0.30	0.86	4	35	protein targeting to vacuole	BP	1	GGA3,CLU,SCARB2,SORT1	darkgreen	VSMC_M4
GO:0046822	0.30	0.82	8	94	regulation of nucleocytoplasmic transport	BP	1	MDM2,ANGPT1,LEP,MDFIC,PTPN11,PTPN14,PRKD1,FLNA	darkgreen	VSMC_M4
GO:0046488	0.30	0.80	12	138	phosphatidylinositol metabolic process	BP	1	PIGN,PIP5K1B,MTMR10,HTR2B,INPP5F,PI4KB,PIGG,OCRL,PIGS,PLCG2,PIGK,PIK3C2A	darkgreen	VSMC_M4
GO:0051952	0.30	0.85	5	55	regulation of amine transport	BP	1	LEP,SYT5,FFAR3,RGS2,SLC43A2	darkgreen	VSMC_M4
GO:0045912	0.30	0.86	4	39	negative regulation of carbohydrate metabolic process	BP	1	EP300,SLC25A12,PPARGC1A,DDIT4	darkgreen	VSMC_M4
GO:0046425	0.30	0.85	5	52	regulation of receptor signaling pathway via JAK-STAT	BP	1	LEP,CYP1B1,ADIPOR1,INPP5F,CRLF3	darkgreen	VSMC_M4

GO:0030522	0.30	0.78	18	217	intracellular receptor signaling pathway	BP	1	CITED2,EP300,LEP,DDX58,MAP3K7,LBH,THRB,ACTN4,NCOR2,RNF34,DCBLD2,PTPN22,HNF4A,STRN3,RORA,DAB2,SKP2,YAP1	darkgreen	VSMC_M4
GO:2000514	0.30	0.86	4	41	regulation of CD4-positive, alpha-beta T cell activation	BP	1	CD274,SH3RF1,LGALS9,CD83	darkgreen	VSMC_M4
GO:0043280	0.30	0.82	8	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	DAPK1,REST,CFLAR,HIP1,TNFSF10,LGALS9,F3,CYR61	darkgreen	VSMC_M4
GO:0000266	0.30	0.86	4	40	mitochondrial fission	BP	1	TMEM135,MARCH5,PPARGC1A,BNIP3	darkgreen	VSMC_M4
GO:0120162	0.30	0.82	7	78	positive regulation of cold-induced thermogenesis	BP	1	ZNF516,GJA1,LEP,PDGFC,ADIPOR1,ACHE,PPARGC1A	darkgreen	VSMC_M4
GO:1902305	0.30	0.84	5	50	regulation of sodium ion transmembrane transport	BP	1	PTPN3,ACTN4,FGF14,FXYD1,CAMK2D	darkgreen	VSMC_M4
GO:0032732	0.30	0.86	4	40	positive regulation of interleukin-1 production	BP	1	APP,LPL,HSPB1,LGALS9	darkgreen	VSMC_M4
GO:0045806	0.30	0.86	4	41	negative regulation of endocytosis	BP	1	MCTP1,ATXN2,PRKD1,LRSAM1	darkgreen	VSMC_M4
GO:0085029	0.31	0.86	4	39	extracellular matrix assembly	BP	1	ANTXR1,QSOX1,LOX,MFAP4	darkgreen	VSMC_M4
GO:0051897	0.31	0.81	8	88	positive regulation of protein kinase B signaling	BP	1	ANGPT1,LEP,TGFBR1,SEMA5A,MST1R,LRP2,HIP1,F3	darkgreen	VSMC_M4
GO:0006457	0.31	0.79	12	166	protein folding	BP	1	WFS1,LMAN2L,RIC3,CLU,ERO1B,QSOX1,ATF6,PRDX4,HSPB1,CRYAB,NPPB,DNAJA2	darkgreen	VSMC_M4
GO:0002448	0.31	0.85	4	40	mast cell mediated immunity	BP	1	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:1904589	0.31	0.84	5	55	regulation of protein import	BP	1	ANGPT1,LEP,MDFIC,PRKD1,FLNA	darkgreen	VSMC_M4
GO:0010676	0.31	0.85	4	40	positive regulation of cellular carbohydrate metabolic process	BP	1	HRH1,PTH,SLC25A12,PPARGC1A	darkgreen	VSMC_M4
GO:0071482	0.31	0.81	8	94	cellular response to light stimulus	BP	1	MDM2,EP300,GRK7,N4BP1,MMP1,OPN3,CDKN1A,MFAP4	darkgreen	VSMC_M4
GO:0048146	0.31	0.85	4	41	positive regulation of fibroblast proliferation	BP	1	FOSL2,PDGFC,DDR2,CDKN1A	darkgreen	VSMC_M4
GO:0071702	0.31	0.72	136	1891	organic substance transport	BP	1	SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,VLDLR,UNC13B,RIC1,REST,ICA1,LMAN2L,SNX13,SLC2A1,PREPL,LMBRD1,SYT5,SLC17A5,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,SLC37A3,GGA3,INHBB,USP6NL,RAB2B,ACTN4,ADAM9,TRPC4,SLC16A3,ATP2C1,PCLO,ZDHHC2,FFAR3,CHD7,ANKRD1,TRIM23,EXOC6,ESYT3,PAM,SLC25A4,OCLN,PTH,KIF13B,G3BP2,CLU,ATXN2,SCARB2,ABCC8,PTPN11,LBP,HERPUD1,SLC26A7,ATG13,HNF4A,SERINC3,ADA,AKTIP,IFIT1,EDN1,CD47,PLA2G4F,RAB29,ABCG1,KDM5B,RGS2,PFKL,LRP5,ARRDC4,ZMAT3,TM7SF3,TXNIP,SEC24B,ATP9A,SESN2,ARV1,ADCY5,LRP2,FABP2,PTPN14,PRKD1,SLC25A12,RAPGEF4,AP3B2,AKAP6,LRP6,HIP1,HSPB1,ACHE,EXPH5,MAOB,GULP1,CYP19A1,LMTK2,NLGN1,RABEP1,HIF1A,OPN3,AP1S3,DISP3,FAF2,TGFB3,TOM1L1,EPG5,SLC14A1,BBS4,STOML1,ATG4A,EVI5L,ABLIM3,SH3TC2,DAB2,RBFOX1,SLC43A2,FLNA,VAMP7,SLC2A5,AHCYL1,SORT1,TBC1D13,ABCA4,LRSAM1,LRRC8C,WLS,CDKN1A,SLC27A5,GABARAPL2,PRELID2,BMP6,SCP2,MAFA	darkgreen	VSMC_M4
GO:0010883	0.31	0.85	4	41	regulation of lipid storage	BP	1	LEP,ABCA1,LPL,ABCG1	darkgreen	VSMC_M4
GO:0050678	0.31	0.76	22	275	regulation of epithelial cell proliferation	BP	1	GJA1,LEP,CDKN2B,TGFBR1,GATA2,LIMS2,HPN,ATOH8,SEMA5A,KDM5B,HTR2B,PRKCA,CFLAR,FGFR2,PRKD1,HIF1A,PLXNB3,CDH13,F3,FGF9,YAP1,BMP6	darkgreen	VSMC_M4
GO:0001816	0.31	0.75	38	504	cytokine production	BP	1	MBP,IFNGR1,IRAK3,LAPTM4B,ANGPT1,LEP,DDX58,CD274,IL18R1,MAP3K7,INHBB,NDRG2,CYP1B1,FFAR3,CLU,APP,ABCC8,PTPN11,LBP,PTPN22,CD47,N4BP1,LPL,HTR2B,AFAP1L2,F11R,HSPB1,SERPINE1,ATP6AP2,HIF1A,RORA,TGFB3,NPTN,LGALS9,PLCG2,F3,TLR1,CD83	darkgreen	VSMC_M4
GO:0006650	0.31	0.77	20	257	glycerophospholipid metabolic process	BP	1	PIGN,PIP5K1B,ABHD12,CHPT1,LPCAT2,SERINC3,PLA2G4F,MTMR10,AGPAT3,HTR2B,SERINC2,INPP5F,PI4KB,ACHE,PIGG,OCRL,PIGS,PLCG2,PIGK,PIK3C2A	darkgreen	VSMC_M4
GO:0035710	0.31	0.82	6	65	CD4-positive, alpha-beta T cell activation	BP	1	CD274,IL18R1,SH3RF1,RORA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0006695	0.31	0.85	4	43	cholesterol biosynthetic process	BP	1	ABCG1,ARV1,PRKAA2,MBTPS1	darkgreen	VSMC_M4
GO:1902653	0.31	0.85	4	43	secondary alcohol biosynthetic process	BP	1	ABCG1,ARV1,PRKAA2,MBTPS1	darkgreen	VSMC_M4
GO:0009894	0.31	0.74	60	806	regulation of catabolic process	BP	1	BCL2,RNF41,IRAK3,MDM2,LAPTM4B,RNF19A,GJA1,EP300,ADGRB1,DAPK1,LEP,FAM122A,RIC1,PTPN3,MAP3K7,SESN1,HIPK2,GGA3,ADAM9,FOXO1,ZDHHC2,CPEB3,SLC25A4,CLU,APP,SCARB2,HERPUD1,PTPN22,N4BP1,FEZ1,HTR2B,PRKCA,SESN2,LRP2,PRKD1,QSOX1,SLC25A12,ATF6,HSPB1,RDX,FBXL5,DACT1,HIF1A,FBXL20,PPARGC1A,CALCOCO2,DAB2,PRKAA2,TMEM59,DAPK3,FLNA,LRSAM1,ITPR1,BNIP3,CST3,GABARAPL2,PIK3C2A,ORMDL3,ATP6V0E1,DDIT4	darkgreen	VSMC_M4
GO:0046839	0.31	0.85	4	40	phospholipid dephosphorylation	BP	1	MTMR10,INPP5F,OCRL,PLPPR3	darkgreen	VSMC_M4
GO:0050853	0.31	0.85	4	41	B cell receptor signaling pathway	BP	1	BCL2,BLNK,PTPN22,PLCG2	darkgreen	VSMC_M4
GO:0044088	0.31	0.85	4	42	regulation of vacuole organization	BP	1	LAPTM4B,SCARB2,FEZ1,LRSAM1	darkgreen	VSMC_M4
GO:0030900	0.31	0.76	24	282	forebrain development	BP	1	SLC2A1,PEX13,GATA2,PCDH9,TACC1,APLP1,CHD7,APP,ANXA3,SEMA5A,FEZ1,SUN1,LRP2,FGFR2,EZH1,HIF1A,PPARGC1A,NUMB,BBS4,CDH2,FLNA,SLC8A1,BNIP3,PRKG1	darkgreen	VSMC_M4
GO:0006469	0.31	0.78	14	172	negative regulation of protein kinase activity	BP	1	IRAK3,GNAQ,CDKN2B,LATS2,HIPK3,PTPN22,RGS2,LRP5,GPRC5A,LRP6,HSPB1,SLC8A1,CDKN1A,PPM1E	darkgreen	VSMC_M4
GO:0043297	0.32	0.83	5	52	apical junction assembly	BP	1	GRHL2,GJA1,OCLN,F11R,WDR1	darkgreen	VSMC_M4
GO:0051817	0.32	0.82	6	67	modulation of process of other organism involved in symbiotic interaction	BP	1	EP300,REST,HPN,PTX3,CCNT1,ULK2	darkgreen	VSMC_M4
GO:0045600	0.32	0.83	5	53	positive regulation of fat cell differentiation	BP	1	TMEM64,LPL,FNDC5,LRP5,FRZB	darkgreen	VSMC_M4
GO:0015849	0.32	0.77	16	203	organic acid transport	BP	1	GJA1,LEP,SLC2A1,SLC17A5,TRPC4,SLC16A3,SLC26A7,SERINC3,EDN1,PLA2G4F,RGS2,LRP2,SLC25A12,SLC43A2,LRRC8C,SLC27A5	darkgreen	VSMC_M4
GO:0000082	0.32	0.78	13	160	G1/S transition of mitotic cell cycle	BP	1	BCL2,MDM2,CDKN2B,JADE1,LATS2,RBL2,RDX,DACT1,CRLF3,SKP2,CDC7,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0030101	0.32	0.85	4	43	natural killer cell activation	BP	1	LEP,IL18R1,PTPN22,VAMP7	darkgreen	VSMC_M4
GO:0071709	0.32	0.85	4	39	membrane assembly	BP	1	ANKLE2,NLGN1,CDH2,REEP3	darkgreen	VSMC_M4

GO:0007264	0.32	0.74	36	437	small GTPase mediated signal transduction	BP	1	ABRA,DOCK8,KANK1,ABCA1,CHN2,DOCK4,RALGAPA2,ARHGEF17,CDC42EP3,KIAA0355,ARHGEF3,PTH,G3BP2,NGF,RIPOR2,KCTD10,PREX1,SHTN1,PRKD1,F11R,RAPGEF4,ARHGAP20,RDX,SYNPO2L,IQSEC3,SIPA1L1,MAPRE2,RHOT1,ARHGAP28,PLEKHG5,CSF1,CDH13,ARHGAP29,BCAR3,SYDE2,CDKN1A	darkgreen	VSMC_M4
GO:0003143	0.32	0.83	5	50	embryonic heart tube morphogenesis	BP	1	CITED2,HIF1A,BBS4,TBX20,YAP1	darkgreen	VSMC_M4
GO:0019222	0.32	0.71	344	4858	regulation of metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,SMOC2,AFF4,GJA1,ZHX1,TPD52L1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,CD274,RIC1,PDK4,IL18R1,CREB3,ZNF169,REST,RECK,IGFBP7,TGFBR1,ZNF331,PTPN3,TBX18,MAP3K7,ANTXR1,MDFIC,EPHB6,SESN1,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,NAA16,ELF1,INHBB,SMARCD3,HRH1,LMO7,ITIH5,BABAM2,FOSL2,LBH,NDRG2,LIPT2,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,FOXO1,RASSF2,ANKLE2,CYP1B1,TF,EBF4,FLT3,ZDHHC2,MIER3,NCOR2,FFAR3,FXYD1,HPN,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,SLC25A4,SH3RF1,ATOH8,CLCN3,OCLN,TCF7L1,WWC2,TEAD1,FAM172A,PTH,RNF34,G3BP2,CLU,BLNK,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ABCC8,ANXA3,PTPN11,PTX3,LBP,NEK4,CCNT1,HERPUD1,PROS1,JMY,CHD6,PTPN22,HNF4A,CHAC1,GDF6,NAB1,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,SMARCAD1,BACE2,LPL,RAB29,ABCG1,ADIPOR1,KDM5B,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,FEZ1,NPNT,PLCL1,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,TXNIP,HELZ,SESN2,ARV1,YEATS2,ZNF710,CAMK2D,NGRN,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,F11R,QSOX1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,SERPINE1,ACHE,CRYAB,ATP6AP2,RDX,MAOB,ZNF445,SECISBP2L,	darkgreen	VSMC_M4
GO:0007420	0.32	0.73	47	587	brain development	BP	1	MBP,BCL2,GRHL2,SLC2A1,PEX13,GATA2,ITGA8,PCDH9,PFKFB3,NDRG2,TACC1,COL4A1,APLP1,PTPRG,CHD7,MEIS2,APP,ANXA3,PTPN11,SEMA5A,RGS2,FEZ1,SUN1,GNB4,SEC24B,PLXNA2,LRP2,FGFR2,NCSTN,ZNF365,LRP6,MAOB,EZH1,HIF1A,PPARGC1A,RORA,NUMB,BBS4,CDH2,SMARCA1,FLNA,WLS,SLC8A1,BNIP3,FGF9,PRKG1,DDIT4	darkgreen	VSMC_M4
GO:0010821	0.32	0.79	10	124	regulation of mitochondrion organization	BP	1	EP300,TMEM135,MARCH5,SLC25A4,CLU,TNFSF10,HIF1A,PPARGC1A,RHOT1,BNIP3	darkgreen	VSMC_M4
GO:0010565	0.32	0.80	8	95	regulation of cellular ketone metabolic process	BP	1	PDK4,REST,NCOR2,ADM,WDTC1,PPARGC1A,ATCAY,BMP6	darkgreen	VSMC_M4
GO:0021700	0.32	0.77	17	204	developmental maturation	BP	1	BCL2,LEP,UNC13B,RECK,GATA2,ZDHHC2,CLCN3,PTH,APP,PLXNB1,MAP3K13,ATP6AP2,HIF1A,ADGRL1,PCSK4,CDKN1A,CCR6	darkgreen	VSMC_M4
GO:0070085	0.32	0.77	15	194	glycosylation	BP	1	STT3B,TUSC3,ST3GAL5,EXTL3,DPY19L4,B3GNT7,GALNT3,B3GALNT2,MAN2A2,FUT11,MAGT1,GALNT10,TMEM59,EXTL2,ST6GALNAC3	darkgreen	VSMC_M4
GO:0045860	0.32	0.75	24	305	positive regulation of protein kinase activity	BP	1	SASH1,ANGPT1,TPD52L1,LEP,VLDLR,PPP1R9A,MAP3K7,ADAM9,RASSF2,FLT3,CLU,PDGFC,CCNT1,EDN1,HTR2B,MST1R,AFAP1L2,DDR2,GPRC5A,MAP3K13,TOM1L1,CSF1,CYR61,CDKN1A	darkgreen	VSMC_M4
GO:0003407	0.32	0.83	5	49	neural retina development	BP	1	HIPK2,SMARCD3,THRB,GPM6A,BBS4	darkgreen	VSMC_M4
GO:0090102	0.32	0.84	4	40	cochlea development	BP	1	TBX18,GATA2,HPN,FRZB	darkgreen	VSMC_M4
GO:0046677	0.32	0.84	4	41	response to antibiotic	BP	1	MDM2,PLA2G4F,KDM5B,AOC3	darkgreen	VSMC_M4
GO:0030833	0.33	0.78	12	145	regulation of actin filament polymerization	BP	1	KANK1,PPP1R9A,CDC42EP3,WASF3,NCK1,JMY,PREX1,RDX,PAK3,ARHGAP28,SPTAN1,ICAM1	darkgreen	VSMC_M4
GO:0070265	0.33	0.84	4	45	necrotic cell death	BP	1	SLC25A4,CFLAR,BNIP3,TMEM123	darkgreen	VSMC_M4
GO:0006998	0.33	0.84	4	43	nuclear envelope organization	BP	1	ANKLE2,SUN1,PRKCA,REEP3	darkgreen	VSMC_M4
GO:0007389	0.33	0.75	26	329	pattern specification process	BP	1	CITED2,EP300,MLLT3,TGFBR1,TBX18,HIPK2,ENKUR,SMARCD3,SEMA3C,MEIS2,SHROOM3,EDN1,ETS2,LRP5,MID1,PLXNA2,LRP2,FGFR2,LRP6,ATP6AP2,HIF1A,SMAD6,BBS4,FST,WLS,TBX20	darkgreen	VSMC_M4
GO:0046434	0.33	0.78	10	126	organophosphate catabolic process	BP	1	ABHD12,ENTPD3,ENTPD1,ADA,PLA2G4F,NT5C2,INPP5F,PDE1A,OCRL,PLCG2	darkgreen	VSMC_M4
GO:0002703	0.33	0.78	11	136	regulation of leukocyte mediated immunity	BP	1	LEP,DDX58,IL18R1,MAP3K7,GATA2,TP53BP1,ADGRE2,LGALS9,VAMP7,PLCG2,ICAM1	darkgreen	VSMC_M4
GO:1903507	0.33	0.72	70	945	negative regulation of nucleic acid-templated transcription	BP	1	CITED2,MDM2,TRPS1,ZHX1,EP300,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,HNF4A,NAB1,EDN1,ETS2,KDM5B,MXI1,TXNIP,YEATS2,WDTC1,FGFR2,STRN3,ARID5B,ID3,EIF4A2,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TLE2,FLNA,ZFP90,TBX20,ZNF425,ZNF175,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0031670	0.33	0.84	4	40	cellular response to nutrient	BP	1	MDM2,LEP,CDKN2B,LPL	darkgreen	VSMC_M4
GO:0009896	0.33	0.74	32	420	positive regulation of catabolic process	BP	1	RNF41,MDM2,RNF19A,GJA1,DAPK1,FAM122A,MAP3K7,SESN1,GGA3,ADAM9,FOXO1,CPEB3,SLC25A4,CLU,APP,HERPUD1,SESN2,LRP2,PRKD1,ATF6,RDX,FBXL5,DACT1,HIF1A,CALCOCO2,DAB2,PRKAA2,TMEM59,LRSAM1,BNIP3,PIK3C2A,ORMDL3	darkgreen	VSMC_M4
GO:0098662	0.33	0.73	41	541	inorganic cation transmembrane transport	BP	1	PKDREJ,TRDN,SLC17A5,PTPN3,KCNE3,ACTN4,FGF14,TRPC4,ATP2C1,TUSC3,FXYD1,HPN,CHD7,MICU2,SLC25A4,SCN8A,CLCN3,SLC35G1,JPH1,GPM6A,ABCC8,CNNM2,ACTN2,HTR2B,CAMK2D,ABCC9,PRKD1,AKAP6,CACNA1C,MAGT1,KCNK10,SCNN1D,FLNA,HCN2,PLCG2,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,ATP6V0E1	darkgreen	VSMC_M4
GO:0006664	0.33	0.80	7	87	glycolipid metabolic process	BP	1	PIGN,SUMF1,ST3GAL5,PIGG,PIGS,ST6GALNAC3,PIGK	darkgreen	VSMC_M4
GO:1903509	0.33	0.80	7	87	liposaccharide metabolic process	BP	1	PIGN,SUMF1,ST3GAL5,PIGG,PIGS,ST6GALNAC3,PIGK	darkgreen	VSMC_M4
GO:0015837	0.33	0.82	5	58	amine transport	BP	1	LEP,SYT5,FFAR3,RGS2,SLC43A2	darkgreen	VSMC_M4

GO:1902679	0.33	0.72	70	946	negative regulation of RNA biosynthetic process	BP	1	CITED2,MDM2,TRPS1,ZHX1,EP300,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,HNF4A,NAB1,EDN1,ETS2,KDM5B,MXI1,TXNIP,YEATS2,WDTC1,FGFR2,STRN3,ARID5B,ID3,EIF4A2,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TLE2,FLNA,ZFP90,TBX20,ZNF425,ZNF175,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0045670	0.33	0.84	4	42	regulation of osteoclast differentiation	BP	1	RASSF2,TMEM178A,TMEM64,CSF1	darkgreen	VSMC_M4
GO:0002532	0.33	0.82	5	59	production of molecular mediator involved in inflammatory response	BP	1	LEP,LBP,SERPINE1,HIF1A,VAMP7	darkgreen	VSMC_M4
GO:0035967	0.33	0.79	8	103	cellular response to topologically incorrect protein	BP	1	EP300,WFS1,CREB3,NCK1,HERPUD1,TM7SF3,ATF6,MBTPS1	darkgreen	VSMC_M4
GO:0016331	0.33	0.77	11	127	morphogenesis of embryonic epithelium	BP	1	CITED2,GRHL2,TBX18,ADM,SHROOM3,SEC24B,LRP2,FGFR2,HIF1A,BBS4,LMO4	darkgreen	VSMC_M4
GO:0072384	0.34	0.80	7	78	organelle transport along microtubule	BP	1	DYNC1I1,FEZ1,SUN1,AP3B2,HIF1A,RHOT1,VAMP7	darkgreen	VSMC_M4
GO:2000117	0.34	0.82	5	60	negative regulation of cysteine-type endopeptidase activity	BP	1	MDM2,SH3RF1,RNF34,HERPUD1,CRYAB	darkgreen	VSMC_M4
GO:0061053	0.34	0.81	6	63	somite development	BP	1	EP300,TBX18,SEMA3C,PLXNA2,LRP6,FRZB	darkgreen	VSMC_M4
GO:0043966	0.34	0.82	5	54	histone H3 acetylation	BP	1	EP300,BRPF3,MAP3K7,JADE1,YEATS2	darkgreen	VSMC_M4
GO:0032768	0.34	0.83	4	43	regulation of monooxygenase activity	BP	1	LEP,HTR2B,HIF1A,NPR3	darkgreen	VSMC_M4
GO:0045787	0.34	0.75	19	243	positive regulation of cell cycle	BP	1	CITED2,MDM2,SMOC2,SMARCD3,MEIS2,APP,PTPN11,CCNT1,PKP4,EDN1,LRP5,LGMN,PRKCA,FGFR2,LRP6,RDX,CCPG1,PLCG2,CDC7	darkgreen	VSMC_M4
GO:0050982	0.34	0.83	4	40	detection of mechanical stimulus	BP	1	PKDREJ,HPN,PDZD7,CDH2	darkgreen	VSMC_M4
GO:0046928	0.34	0.81	6	66	regulation of neurotransmitter secretion	BP	1	PPP1R9A,PREPL,MCTP1,NLGN1,FBXL20,RHOT1	darkgreen	VSMC_M4
GO:0038093	0.34	0.83	4	39	Fc receptor signaling pathway	BP	1	MAP3K7,MAP3K1,CD47,PLCG2	darkgreen	VSMC_M4
GO:0032387	0.34	0.83	4	46	negative regulation of intracellular transport	BP	1	ANGPT1,MDFIC,CRYAB,PLN	darkgreen	VSMC_M4
GO:0031401	0.34	0.71	56	747	positive regulation of protein modification process	BP	1	GDF11,BCL2,SASH1,ANGPT1,TPD52L1,LEP,WFS1,LIMCH1,DCUN1D4,VLDLR,PPP1R9A,TGFBR1,MAP3K7,HIPK2,INHBB,ADAM9,RASSF2,ANKLE2,FLT3,CLU,APP,PDGFC,PTPN11,CCNT1,PTPN22,GDF6,AKTIP,NGF,EDN1,ARRDC4,HTR2B,MST1R,AFAP1L2,PRKD1,DDR2,GPRC5A,MAP3K13,FAM129A,ATG14,PPARGC1A,TGFB3,TOM1L1,FAXDC2,NPTN,DAB2,SKP2,PRKAA2,CSF1,PLCG2,TERF2IP,BCAR3,CYR61,CDKN1A,FGF9,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0014065	0.34	0.78	10	111	phosphatidylinositol 3-kinase signaling	BP	1	ANGPT1,LEP,PIP5K1B,FLT3,PDGFC,EDN1,HTR2B,PLXNB1,UNC5B,PIK3C2A	darkgreen	VSMC_M4
GO:0006766	0.34	0.80	6	71	vitamin metabolic process	BP	1	SLC2A1,LMBRD1,LGMN,LRP2,VNN1,RFK	darkgreen	VSMC_M4
GO:0035335	0.34	0.80	7	77	peptidyl-tyrosine dephosphorylation	BP	1	PTPN3,PTPRG,PTPN11,PTPN22,EYA2,PTPN14,DNAJC6	darkgreen	VSMC_M4
GO:0007613	0.34	0.79	8	86	memory	BP	1	VLDLR,HRH1,CPEB3,ABCC8,RCAN1,NGF,LGMN,KCNK10	darkgreen	VSMC_M4
GO:0030258	0.34	0.76	13	171	lipid modification	BP	1	LEP,PDK4,PEX13,ABCG1,MTMR10,ADIPOR1,SESN2,INPP5F,PPARGC1A,OCRL,PLPPR3,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0010638	0.34	0.73	33	428	positive regulation of organelle organization	BP	1	LIMCH1,TGFBR1,CDC42EP3,WASF3,MARCH5,NCK1,SLC25A4,OCLN,G3BP2,JMY,EDN1,CD47,SEMA5A,ABCG1,ACTN2,LRP5,SYNPO2,LNPK,SYNPO2L,TNFSF10,WDR1,HIF1A,PPARGC1A,CALCOCO2,TGFB3,BBS4,SYNPO,FLNA,LRSAM1,BNIP3,PPM1E,DSTN,ICAM1	darkgreen	VSMC_M4
GO:0009566	0.34	0.78	9	113	fertilization	BP	1	PKDREJ,UNC13B,KDM5B,MST1R,MFGE8,MAEL,TEX11,PCSK4,CCDC136	darkgreen	VSMC_M4
GO:0006813	0.34	0.76	12	140	potassium ion transport	BP	1	KCNE3,FXYD1,HPN,ABCC8,ACTN2,ABCC9,AKAP6,KCNK10,FLNA,HCN2,KCNE4,TMEM38A	darkgreen	VSMC_M4
GO:0006094	0.34	0.81	5	58	gluconeogenesis	BP	1	EP300,LEP,SESN2,SLC25A12,PPARGC1A	darkgreen	VSMC_M4
GO:1904427	0.34	0.81	5	55	positive regulation of calcium ion transmembrane transport	BP	1	TRDN,KCNE3,FGF14,AKAP6,PLCG2	darkgreen	VSMC_M4
GO:0060284	0.34	0.73	31	384	regulation of cell development	BP	1	BCL2,KANK1,REST,RECK,LIMS2,TENM4,SMARCD3,ACTN4,SEMA3C,CHD7,ABCC8,NGF,SEMA5A,PREX1,PLXNA2,SHTN1,LRP2,F11R,PLXNB1,ZNF365,MAP3K13,CUX1,HIF1A,NUMB,NPTN,ULK2,PAK3,PLXNB3,FLNA,FRZB,YAP1	darkgreen	VSMC_M4
GO:0019538	0.34	0.68	287	4113	protein metabolic process	BP	1	MBP,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,IFNGR1,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,OXR1,ANGPT1,C4A,GJA1,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,SH3RF3,DCUN1D4,VLDLR,C2orf40,PPP1R9A,RIC1,PDK4,RNF149,REST,RECK,ZAP70,TGFBR1,PREPL,ABCA1,KLHL7,PTPN3,MAP3K7,ANTXR1,PAPPA,PREP,EPHB6,JADE1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ITM2B,SNRK,TESK2,GGA3,NAA16,INHBB,MKRN2,LMO7,ITIH5,BABAM2,STT3B,LIPT2,ADAM9,CRIM1,SUMF1,FOXO1,RASSF2,ANKLE2,QPCT,FLT3,TUSC3,ZDHHC2,MAP3K1,FXYD1,HPN,FBXO3,PTPRG,LATS2,HIPK3,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,RNF141,PAM,SH3RF1,ST3GAL5,GRK7,OCLN,EXTL3,RNF34,CDKL2,CLU,APP,ATXN2,PDGFC,HECTD4,PTPN11,PTX3,NEK4,CCNT1,HERPUD1,PROS1,PTPN22,DPY19L4,CHAC1,GDF6,CPQ,AKTIP,RCAN1,NGF,EDN1,N4BP1,SMARCAD1,MARCH6,BACE2,ABCG1,TMPRSS7,KDM5B,TARSL2,DAPP1,RGS2,EYA2,NCOA3,UBE3B,LRP5,KCTD10,ARRDC4,PLCL1,HTR2B,MST1R,LGMN,B3GNT7,AMZ2,GALNT3,B3GALNT2,PRKCA,AFAP1L2,CFI,TPST2,SESN2,YEATS2,P4HTM,CAMK2D,CTSS,NGRN,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,MAN2A2,NDST3,FGFR2,RBM4B,SYNPO2,CTSF,USP53,PTPN14,PRKD1,NCSTN,TRIM63,CHST15,ZRANB1,PPEF1,DDR2,GPRC5A,MAP3K13,PCMTD2,LRP6,HIP1,PRDX4,FAM129A,HSPB1,EIF4A2,RIMKLB,SERPINE1,ACHE,CRYAB,C1RL,ATP6AP2,PAPPA2,RDX,P4HA1,SECISBP2L,EZH1,FUT11,EIF4G3,USP11,ATG14,MMP1,LAP3,FBXL5,TNFSF10,DACT1,LMTK2,SPEG,JKAMP,SIN3B,PCSK1N,HIF1A,OPN3,FBXL20,PPARGC1A,PLOD1,DCAF5,FAF2,PIG	darkgreen	VSMC_M4
GO:0002062	0.34	0.78	8	91	chondrocyte differentiation	BP	1	TRPS1,TGFBR1,PTH,PTPN11,GDF6,LNPK,GLG1,BMP6	darkgreen	VSMC_M4
GO:0043491	0.35	0.76	12	147	protein kinase B signaling	BP	1	RNF41,ANGPT1,LEP,TGFBR1,SEMA5A,MST1R,SESN2,LRP2,INPP5F,HIP1,F3,LOX	darkgreen	VSMC_M4
GO:0071320	0.35	0.83	4	37	cellular response to cAMP	BP	1	APP,AKAP6,HCN2,SLC8A1	darkgreen	VSMC_M4

GO:0098656	0.35	0.75	13	161	anion transmembrane transport	BP	1	SLC35D3,GJA1,TCAF1,SLC16A3,SLC25A4,CLCN3,SLC26A7,ANO5,RGS2,LRP2,SLC25A12,SLC43A2,LRRC8C	darkgreen	VSMC_M4
GO:0007338	0.35	0.79	7	86	single fertilization	BP	1	PKDREJ,UNC13B,KDM5B,MST1R,MFGE8,PCSK4,CCDC136	darkgreen	VSMC_M4
GO:0006081	0.35	0.83	4	46	cellular aldehyde metabolic process	BP	1	REST,CYP1B1,ABCA4,BMP6	darkgreen	VSMC_M4
GO:0033059	0.35	0.83	4	43	cellular pigmentation	BP	1	BCL2,SHROOM3,RAB29,BBS4	darkgreen	VSMC_M4
GO:0001776	0.35	0.80	6	70	leukocyte homeostasis	BP	1	BCL2,FLT3,ADA,JAM3,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0080090	0.35	0.68	298	4206	regulation of primary metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,MDM2,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,SMOC2,GJA1,ZHX1,TPD52L1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,RIC1,PDK4,IL18R1,CREB3,ZNF169,REST,RECK,IGFBP7,TGFBR1,ZNF331,PTPN3,TBX18,MAP3K7,ANTXR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,NAA16,ELF1,INHBB,SMARCD3,HRH1,LMO7,ITIH5,BABAM2,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,FOXO1,RASSF2,ANKLE2,CYP1B1,TF,EBF4,FLT3,ZDHHC2,MIER3,NCOR2,FXYD1,HPN,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,SH3RF1,ATOH8,OCLN,TCF7L1,WWC2,TEAD1,FAM172A,PTH,RNF34,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ANXA3,PTPN11,PTX3,NEK4,CCNT1,HERPUD1,PROS1,JMY,CHD6,PTPN22,HNF4A,CHAC1,GDF6,NAB1,AKTIP,RCAN1,RBL2,NGF,EDN1,ETS2,N4BP1,SMARCAD1,BACE2,ABCG1,ADIPOR1,KDM5B,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,PLCL1,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,TXNIP,SESN2,ARV1,YEATS2,ZNF710,CAMK2D,NGRN,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,SERPINE1,CRYAB,RDX,MAOB,ZNF445,SECISBP2L,EZH1,EIF4G3,ATG14,FBXL5,TNFSF10,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,FBXL20,PPARGC1A,ACTN1,DISP3,RORA	darkgreen	VSMC_M4
GO:0030510	0.35	0.79	7	74	regulation of BMP signaling pathway	BP	1	HIPK2,CRIM1,LRP2,SMAD6,FST,CYR61,TBX20	darkgreen	VSMC_M4
GO:0046486	0.35	0.73	24	317	glycerolipid metabolic process	BP	1	PIGN,PIP5K1B,ABHD12,CHPT1,PTPN11,LPCAT2,SERINC3,PLA2G4F,LPL,MTMR10,AGPAT3,HTR2B,SERINC2,INPP5F,PI4KB,ACHE,ATG14,PIGG,OCRL,PIGS,PLCG2,PIGK,SLC27A5,PIK3C2A	darkgreen	VSMC_M4
GO:0061951	0.35	0.81	5	55	establishment of protein localization to plasma membrane	BP	1	GRIP1,PREPL,GGA3,ATP2C1,ZDHHC2	darkgreen	VSMC_M4
GO:0043279	0.35	0.79	7	81	response to alkaloid	BP	1	MDM2,MAP1LC3A,ADA,PPARGC1A,SLC8A1,TMEM38A,ICAM1	darkgreen	VSMC_M4
GO:0031400	0.35	0.72	32	426	negative regulation of protein modification process	BP	1	IRAK3,OXR1,ANGPT1,ADGRB1,SH3GL2,GNAQ,CDKN2B,RASSF2,FXYD1,LATS2,HIPK3,NCK1,OCLN,PTPN22,N4BP1,RGS2,LRP5,INPP5F,GPRC5A,LRP6,FAM129A,HSPB1,ATG14,PPARGC1A,SMAD6,PRKAA2,TMEM59,TERF2IP,SLC8A1,CDKN1A,PPM1E,DDIT4	darkgreen	VSMC_M4
GO:0031100	0.35	0.81	5	58	animal organ regeneration	BP	1	PTPN3,FLT3,ADM,ANXA3,CDKN1A	darkgreen	VSMC_M4
GO:0060999	0.35	0.82	4	38	positive regulation of dendritic spine development	BP	1	PPP1R9A,CPEB3,NLGN1,PAK3	darkgreen	VSMC_M4
GO:0072175	0.35	0.76	10	116	epithelial tube formation	BP	1	CITED2,GRHL2,ADM,SHROOM3,SEC24B,LRP2,FGFR2,HIF1A,BBS4,LMO4	darkgreen	VSMC_M4
GO:0009259	0.35	0.73	22	302	ribonucleotide metabolic process	BP	1	EP300,PDK4,PTH,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,PRKAA2,ADCY9,AK5,RFK,DDIT4	darkgreen	VSMC_M4
GO:0030514	0.35	0.82	4	39	negative regulation of BMP signaling pathway	BP	1	HIPK2,CRIM1,LRP2,SMAD6	darkgreen	VSMC_M4
GO:0030856	0.35	0.77	9	106	regulation of epithelial cell differentiation	BP	1	GRHL2,ATOH8,NCOA3,F11R,SERPINE1,FRZB,MAFF,YAP1,BMP6	darkgreen	VSMC_M4
GO:0009150	0.35	0.73	21	286	purine ribonucleotide metabolic process	BP	1	EP300,PDK4,PTH,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,PRKAA2,ADCY9,AK5,DDIT4	darkgreen	VSMC_M4
GO:0031103	0.36	0.82	4	42	axon regeneration	BP	1	BCL2,JAM3,INPP5F,FLNA	darkgreen	VSMC_M4
GO:0120034	0.36	0.77	8	92	positive regulation of plasma membrane bounded cell projection assembly	BP	1	TGFBR1,CDC42EP3,OCLN,GPM6A,RIPOR2,NLGN1,TGFB3,BBS4	darkgreen	VSMC_M4
GO:0051171	0.36	0.67	289	4082	regulation of nitrogen compound metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,MDM2,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,SMOC2,GJA1,ZHX1,TPD52L1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,RIC1,PDK4,IL18R1,CREB3,ZNF169,REST,RECK,TGFBR1,ZNF331,PTPN3,TBX18,MAP3K7,ANTXR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,NAA16,ELF1,INHBB,SMARCD3,LMO7,ITIH5,BABAM2,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,FOXO1,RASSF2,ANKLE2,CYP1B1,TF,EBF4,FLT3,ZDHHC2,MIER3,NCOR2,FXYD1,HPN,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,SH3RF1,ATOH8,OCLN,TCF7L1,WWC2,TEAD1,FAM172A,PTH,RNF34,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,PDGFC,ANXA3,PTPN11,PTX3,NEK4,CCNT1,HERPUD1,PROS1,JMY,CHD6,PTPN22,HNF4A,CHAC1,GDF6,NAB1,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,SMARCAD1,BACE2,ABCG1,KDM5B,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,PLCL1,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,SERPINE1,CRYAB,RDX,MAOB,ZNF445,SECISBP2L,EZH1,EIF4G3,ATG14,FBXL5,TNFSF10,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,FBXL20,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,CCNG1,SMAD6,TOM1L1,ZKSCAN	darkgreen	VSMC_M4
GO:0001101	0.36	0.76	9	107	response to acid chemical	BP	1	SESN1,COL4A1,CPEB3,PDGFC,EDN1,SESN2,CASTOR1,PPARGC1A,ICAM1	darkgreen	VSMC_M4

GO:0098660	0.36	0.70	43	574	inorganic ion transmembrane transport	BP	1	PKDREJ,TRDN,SLC17A5,PTPN3,KCNE3,ACTN4,FGF14,TRPC4,ATP2C1,TUSC3,FXYD1,HPN,CHD7,MICU2,SLC25A4,SCN8A,CLCN3,SLC35G1,JPH1,GPM6A,ABCC8,SLC26A7,ANO5,CNNM2,ACTN2,HTR2B,CAMK2D,ABCC9,PRKD1,AKAP6,CACNA1C,MAGT1,KCNK10,SCNN1D,FLNA,HCN2,PLCG2,KCNE4,ITPR1,SLC8A1,PLN,TMEM38A,ATP6V0E1	darkgreen	VSMC_M4
GO:0031341	0.36	0.82	4	46	regulation of cell killing	BP	1	LEP,LGALS9,CD59,ICAM1	darkgreen	VSMC_M4
GO:0150115	0.36	0.76	9	95	cell-substrate junction organization	BP	1	BCL2,LIMCH1,TESK2,PTPN11,ACTN2,ITGA6,ACTN1,MAPRE2,DAPK3	darkgreen	VSMC_M4
GO:0043244	0.36	0.76	10	107	regulation of protein-containing complex disassembly	BP	1	IRAK3,SEMA5A,ACTN2,MID1,RDX,WDR1,CALCOCO2,SPTAN1,BNIP3,DSTN	darkgreen	VSMC_M4
GO:0009123	0.36	0.80	5	65	nucleoside monophosphate metabolic process	BP	1	ADA,NT5C2,AK7,AK5,RFK	darkgreen	VSMC_M4
GO:0019637	0.36	0.69	52	743	organophosphate metabolic process	BP	1	PIGN,EP300,PIP5K1B,PDK4,NT5C3A,ABHD12,HRH1,ENTPD3,PFKFB3,CHPT1,PTH,ENTPD1,APP,ADCY6,LPCAT2,SERINC3,ADA,PLA2G4F,LPL,MTMR10,NT5C2,AGPAT3,PFKL,HTR2B,SERINC2,TPST2,ADCY5,INPP5F,PI4KB,SLC25A12,PPIP5K1,ACHE,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,PIGG,AK7,OCRL,PIGS,PRKAA2,ADCY9,PLPPR3,PLCG2,AK5,PIGK,RFK,PIK3C2A,ORMDL3,DDIT4	darkgreen	VSMC_M4
GO:0071322	0.36	0.76	10	121	cellular response to carbohydrate stimulus	BP	1	LEP,UNC13B,ABCG1,LRP5,ADCY5,HIF1A,PPARGC1A,PRKAA2,SLC2A5,ICAM1	darkgreen	VSMC_M4
GO:0048736	0.36	0.75	12	140	appendage development	BP	1	GRHL2,RECK,SEMA3C,CHD7,PAM,LRP5,PLXNA2,FGFR2,ITGA6,LNPK,CACNA1C,AFF3	darkgreen	VSMC_M4
GO:0060173	0.36	0.75	12	140	limb development	BP	1	GRHL2,RECK,SEMA3C,CHD7,PAM,LRP5,PLXNA2,FGFR2,ITGA6,LNPK,CACNA1C,AFF3	darkgreen	VSMC_M4
GO:0046330	0.36	0.79	6	68	positive regulation of JNK cascade	BP	1	TPD52L1,SH3RF3,HIPK2,RASSF2,SH3RF1,APP	darkgreen	VSMC_M4
GO:0010256	0.36	0.71	32	422	endomembrane system organization	BP	1	STX11,LAPTM4B,TRDN,SH3GL2,LMAN2L,ABCA1,TMCC1,USP6NL,SYNGR2,ANKLE2,ESYT3,CLCN3,LYSMD3,CLU,SCARB2,AKTIP,RAB29,ABCG1,PDE4DIP,SUN1,PRKCA,ARV1,SHTN1,PRKD1,LNPK,EMC1,SH3TC2,VAMP7,CCDC136,SPINK2,TMEM38A,REEP3	darkgreen	VSMC_M4
GO:0007268	0.36	0.70	37	471	chemical synaptic transmission	BP	1	MBP,STX11,RNF19A,LAMA2,ADGRB1,UNC13B,PPP1R9A,PREPL,SYT5,HRH1,PLCB4,FGF14,PCDHB4,PCLO,ZDHHC2,RIC3,CPEB3,CLCN3,MCTP1,APP,NGF,EDN1,PLCL1,HTR2B,LGMN,NCSTN,INSYN2,LRP6,ACHE,NLGN1,GNAI1,FBXL20,SIPA1L1,NPTN,CDH2,RHOT1,PCDHB2	darkgreen	VSMC_M4
GO:0098916	0.36	0.70	37	471	anterograde trans-synaptic signaling	BP	1	MBP,STX11,RNF19A,LAMA2,ADGRB1,UNC13B,PPP1R9A,PREPL,SYT5,HRH1,PLCB4,FGF14,PCDHB4,PCLO,ZDHHC2,RIC3,CPEB3,CLCN3,MCTP1,APP,NGF,EDN1,PLCL1,HTR2B,LGMN,NCSTN,INSYN2,LRP6,ACHE,NLGN1,GNAI1,FBXL20,SIPA1L1,NPTN,CDH2,RHOT1,PCDHB2	darkgreen	VSMC_M4
GO:0030097	0.36	0.69	46	618	hemopoiesis	BP	1	BCL2,CITED2,ANGPT1,EP300,MLLT3,LEP,CDKN2B,IL18R1,REST,ZAP70,HIPK2,GATA2,SNRK,RASSF2,TMEM178A,TF,FLT3,CHD7,SH3RF1,BLNK,MEIS2,APP,PTPN11,TMEM64,PTPN22,ADA,JAM3,PREX1,PRKCA,P4HTM,FGFR2,MFAP5,WDR1,HIF1A,ACTN1,RORA,FAXDC2,FST,LGALS9,CSF1,PLCG2,VCAM1,VNN1,CD83,LOX,CCR6	darkgreen	VSMC_M4
GO:0006984	0.36	0.81	4	44	ER-nucleus signaling pathway	BP	1	WFS1,NCK1,ATF6,MBTPS1	darkgreen	VSMC_M4
GO:0002449	0.36	0.74	12	159	lymphocyte mediated immunity	BP	1	C4A,LEP,IL18R1,MAP3K7,CLU,CFI,TP53BP1,C1RL,LGALS9,VAMP7,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0010628	0.36	0.69	58	803	positive regulation of gene expression	BP	1	MBP,IFNGR1,CITED2,IRAK3,MDM2,ANGPT1,GJA1,EP300,LEP,DDX58,CD274,IL18R1,TGFBR1,MAP3K7,GATA2,CYP1B1,NCOR2,FFAR3,HPN,CPEB3,NCK1,OCLN,CLU,BLNK,APP,ABCC8,PTPN11,LBP,PTPN22,NGF,LPL,KDM5B,RBM20,HTR2B,AFAP1L2,NGRN,RBM4B,TP53BP1,ID3,FAM129A,HSPB1,SERPINE1,ATP6AP2,RDX,HIF1A,PPARGC1A,RORA,LGALS9,CTIF,CSF1,PLCG2,F3,TLR1,CD83,FGF9,EDA,YAP1,BMP6	darkgreen	VSMC_M4
GO:0007528	0.36	0.81	4	39	neuromuscular junction development	BP	1	UNC13B,COL4A1,APP,ZC4H2	darkgreen	VSMC_M4
GO:0016079	0.37	0.77	7	79	synaptic vesicle exocytosis	BP	1	STX11,UNC13B,PREPL,SYT5,PCLO,NLGN1,FBXL20	darkgreen	VSMC_M4
GO:0032609	0.37	0.79	5	59	interferon-gamma production	BP	1	CD274,IL18R1,PTPN22,CD47,LGALS9	darkgreen	VSMC_M4
GO:0032649	0.37	0.79	5	59	regulation of interferon-gamma production	BP	1	CD274,IL18R1,PTPN22,CD47,LGALS9	darkgreen	VSMC_M4
GO:0051098	0.37	0.72	22	296	regulation of binding	BP	1	ANGPT1,EP300,TGFBR1,HIPK2,SMARCD3,APP,AKTIP,IFIT1,NGF,RIPOR2,PLCL1,CTSZ,DACT1,CCPG1,ARHGAP28,DAB2,ZFP90,LOX,XIRP1,PLN,CDKN1A,HOPX	darkgreen	VSMC_M4
GO:0048701	0.37	0.81	4	40	embryonic cranial skeleton morphogenesis	BP	1	GRHL2,TGFBR1,FGFR2,TGFB3	darkgreen	VSMC_M4
GO:0006464	0.37	0.66	205	2859	cellular protein modification process	BP	1	TMX3,GDF11,BCL2,PIGN,RNF41,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,RNF19A,OXR1,ANGPT1,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,SH3RF3,DCUN1D4,VLDLR,PPP1R9A,PDK4,RNF149,REST,ZAP70,TGFBR1,ABCA1,KLHL7,PTPN3,MAP3K7,EPHB6,JADE1,MAP3K8,HIPK2,GATA2,ABHD12,SNRK,TESK2,NAA16,INHBB,MKRN2,LMO7,BABAM2,STT3B,LIPT2,ADAM9,SUMF1,FOXO1,RASSF2,ANKLE2,QPCT,FLT3,TUSC3,ZDHHC2,MAP3K1,FXYD1,FBXO3,PTPRG,LATS2,HIPK3,PCGF5,MARCH5,TRIM23,RMND5A,NCK1,RNF141,PAM,SH3RF1,ST3GAL5,GRK7,OCLN,EXTL3,RNF34,CDKL2,CLU,APP,PDGFC,HECTD4,PTPN11,NEK4,CCNT1,HERPUD1,PTPN22,DPY19L4,GDF6,AKTIP,RCAN1,NGF,EDN1,N4BP1,SMARCAD1,MARCH6,KDM5B,DAPP1,RGS2,EYA2,NCOA3,UBE3B,LRP5,KCTD10,ARRDC4,PLCL1,HTR2B,MST1R,B3GNT7,GALNT3,B3GALNT2,PRKCA,AFAP1L2,TPST2,SESN2,YEATS2,P4HTM,CAMK2D,MYLK,WDTC1,INPP5F,MAN2A2,FGFR2,USP53,PTPN14,PRKD1,TRIM63,ZRANB1,PPEF1,DDR2,GPRC5A,MAP3K13,PCMTD2,LRP6,PRDX4,FAM129A,HSPB1,RIMKLB,P4HA1,EZH1,FUT11,USP11,ATG14,FBXL5,LMTK2,SPEG,SIN3B,HIF1A,OPN3,PPARGC1A,PLOD1,DCAF5,PIGG,NEK9,TGFB3,CCNG1,MAGT1,SMAD6,TOM1L1,FAXDC2,GALNT10,USP32,NPTN,NRK,ULK2,PAK3,MARCH2,DNAJC6,DAB2,PIGS,SKP2,PRKAA2,TMEM59,DAPK3,BGN,PNCK,FLNA,CSF1,PLCG2,EXTL2,TERF2IP,BCAR3,LRSAM1,CDC7,CYR61,ST6GALNAC3,SLC8A1,FBXO27,LOX,FBXO28,SRPK3,PIGK,CDKN1A,FGF9,PPM1E,CNTD2,HOPX,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4

GO:0036211	0.37	0.66	205	2859	protein modification process	BP	1	TMX3,GDF11,BCL2,PIGN,RNF41,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,RNF19A,OXR1,ANGPT1,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,SH3RF3,DCUN1D4,VLDLR,PPP1R9A,PDK4,RNF149,REST,ZAP70,TGFBR1,ABCA1,KLHL7,PTPN3,MAP3K7,EPHB6,JADE1,MAP3K8,HIPK2,GATA2,ABHD12,SNRK,TESK2,NAA16,INHBB,MKRN2,LMO7,BABAM2,STT3B,LIPT2,ADAM9,SUMF1,FOXO1,RASSF2,ANKLE2,QPCT,FLT3,TUSC3,ZDHHC2,MAP3K1,FXYD1,FBXO3,PTPRG,LATS2,HIPK3,PCGF5,MARCH5,TRIM23,RMND5A,NCK1,RNF141,PAM,SH3RF1,ST3GAL5,GRK7,OCLN,EXTL3,RNF34,CDKL2,CLU,APP,PDGFC,HECTD4,PTPN11,NEK4,CCNT1,HERPUD1,PTPN22,DPY19L4,GDF6,AKTIP,RCAN1,NGF,EDN1,N4BP1,SMARCAD1,MARCH6,KDM5B,DAPP1,RGS2,EYA2,NCOA3,UBE3B,LRP5,KCTD10,ARRDC4,PLCL1,HTR2B,MST1R,B3GNT7,GALNT3,B3GALNT2,PRKCA,AFAP1L2,TPST2,SESN2,YEATS2,P4HTM,CAMK2D,MYLK,WDTC1,INPP5F,MAN2A2,FGFR2,USP53,PTPN14,PRKD1,TRIM63,ZRANB1,PPEF1,DDR2,GPRC5A,MAP3K13,PCMTD2,LRP6,PRDX4,FAM129A,HSPB1,RIMKLB,P4HA1,EZH1,FUT11,USP11,ATG14,FBXL5,LMTK2,SPEG,SIN3B,HIF1A,OPN3,PPARGC1A,PLOD1,DCAF5,PIGG,NEK9,TGFB3,CCNG1,MAGT1,SMAD6,TOM1L1,FAXDC2,GALNT10,USP32,NPTN,NRK,ULK2,PAK3,MARCH2,DNAJC6,DAB2,PIGS,SKP2,PRKAA2,TMEM59,DAPK3,BGN,PNCK,FLNA,CSF1,PLCG2,EXTL2,TERF2IP,BCAR3,LRSAM1,CDC7,CYR61,ST6GALNAC3,SLC8A1,FBXO27,LOX,FBXO28,SRPK3,PIGK,CDKN1A,FGF9,PPM1E,CNTD2,HOPX,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0006690	0.37	0.79	5	62	icosanoid metabolic process	BP	1	EDN2,ABHD12,CYP1B1,EDN1,PLA2G4F	darkgreen	VSMC_M4
GO:0044843	0.37	0.73	14	180	cell cycle G1/S phase transition	BP	1	BCL2,MDM2,CDKN2B,JADE1,LATS2,RBL2,RDX,DACT1,CRLF3,SKP2,PLCG2,CDC7,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0035107	0.37	0.75	10	115	appendage morphogenesis	BP	1	GRHL2,RECK,SEMA3C,CHD7,LRP5,PLXNA2,FGFR2,LNPK,CACNA1C,AFF3	darkgreen	VSMC_M4
GO:0035108	0.37	0.75	10	115	limb morphogenesis	BP	1	GRHL2,RECK,SEMA3C,CHD7,LRP5,PLXNA2,FGFR2,LNPK,CACNA1C,AFF3	darkgreen	VSMC_M4
GO:0045892	0.37	0.68	69	943	negative regulation of transcription, DNA-templated	BP	1	CITED2,MDM2,TRPS1,ZHX1,EP300,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,HNF4A,NAB1,EDN1,ETS2,KDM5B,MXI1,TXNIP,YEATS2,WDTC1,FGFR2,STRN3,ARID5B,ID3,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TLE2,FLNA,ZFP90,TBX20,ZNF425,ZNF175,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0071229	0.37	0.78	6	65	cellular response to acid chemical	BP	1	SESN1,COL4A1,CPEB3,PDGFC,SESN2,CASTOR1	darkgreen	VSMC_M4
GO:0010507	0.37	0.78	6	67	negative regulation of autophagy	BP	1	BCL2,LEP,PTPN22,FEZ1,HTR2B,QSOX1	darkgreen	VSMC_M4
GO:0007623	0.37	0.73	13	160	circadian rhythm	BP	1	EP300,GNAQ,LEP,HNF4A,ADA,RBM4B,HEBP1,ID3,NLGN1,OPN3,PPARGC1A,RORA,PRKAA2	darkgreen	VSMC_M4
GO:0046467	0.37	0.75	9	120	membrane lipid biosynthetic process	BP	1	PIGN,ST3GAL5,PRKD1,PIGG,PIGS,CYR61,ST6GALNAC3,PIGK,ORMDL3	darkgreen	VSMC_M4
GO:0038084	0.37	0.81	4	41	vascular endothelial growth factor signaling pathway	BP	1	SMOC2,FLT3,PRKD1,HSPB1	darkgreen	VSMC_M4
GO:0051173	0.37	0.66	167	2331	positive regulation of nitrogen compound metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,MDM2,RNF19A,GRHL2,ABRA,ANGPT1,SMOC2,GJA1,TPD52L1,EP300,MRTFA,BRD8,DAPK1,MLLT3,LEP,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,CREB3,REST,TGFBR1,MAP3K7,ANTXR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,GGA3,NAA16,ELF1,INHBB,SMARCD3,LMO7,BABAM2,FOSL2,LBH,SALL2,THRB,ACTN4,ADAM9,TACC1,FOXO1,RASSF2,ANKLE2,TF,FLT3,HPN,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ATOH8,TEAD1,PTH,CLU,MED12L,MEIS2,APP,PDGFC,ANXA3,PTPN11,PTX3,NEK4,CCNT1,HERPUD1,JMY,CHD6,PTPN22,HNF4A,GDF6,AKTIP,NGF,EDN1,ETS2,ABCG1,EYA2,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,HTR2B,MST1R,LGMN,AFAP1L2,SESN2,NGRN,LRP2,CFLAR,FGFR2,TP53BP1,PRKD1,NCSTN,SLC25A12,ARID5B,ITGA6,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,LRP6,HIP1,FAM129A,RDX,MAOB,ZNF445,EZH1,ATG14,FBXL5,TNFSF10,DACT1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,TOM1L1,FAXDC2,NPTN,PAK3,ABLIM3,CRLF3,DAB2,LGALS9,SMARCA1,SKP2,PRKAA2,CTIF,CSF1,CDH13,PLCG2,TERF2IP,F3,BCAR3,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,CDKN1A,FGF9,ZNF782,HLF,ICAM1,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:1901343	0.37	0.77	7	84	negative regulation of vasculature development	BP	1	FAM19A5,ADGRB1,COL4A2,ABCC8,SERPINE1,NPPB,ANGPTL7	darkgreen	VSMC_M4
GO:0071805	0.37	0.74	11	131	potassium ion transmembrane transport	BP	1	KCNE3,HPN,ABCC8,ACTN2,ABCC9,AKAP6,KCNK10,FLNA,HCN2,KCNE4,TMEM38A	darkgreen	VSMC_M4
GO:0009952	0.37	0.74	12	150	anterior/posterior pattern specification	BP	1	EP300,MLLT3,TGFBR1,TBX18,HIPK2,SEMA3C,ETS2,LRP5,PLXNA2,LRP6,ATP6AP2,WLS	darkgreen	VSMC_M4
GO:0031146	0.37	0.81	4	44	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	BP	1	FBXL5,FBXL20,SKP2,FBXO27	darkgreen	VSMC_M4
GO:0044272	0.37	0.75	10	127	sulfur compound biosynthetic process	BP	1	DSEL,UST,ANGPT1,PDK4,CHST2,CHAC1,B3GNT7,NDST3,CHST15,MAT2B	darkgreen	VSMC_M4
GO:0030858	0.37	0.81	4	45	positive regulation of epithelial cell differentiation	BP	1	ATOH8,NCOA3,SERPINE1,BMP6	darkgreen	VSMC_M4
GO:0006767	0.37	0.81	4	47	water-soluble vitamin metabolic process	BP	1	SLC2A1,LMBRD1,VNN1,RFK	darkgreen	VSMC_M4
GO:0034204	0.38	0.80	4	39	lipid translocation	BP	1	ABCA1,ABCG1,ATP9A,ABCA4	darkgreen	VSMC_M4
GO:0035418	0.38	0.79	5	54	protein localization to synapse	BP	1	GRIP1,PCLO,ZDHHC2,HSPB1,NLGN1	darkgreen	VSMC_M4

GO:0009891	0.38	0.66	111	1533	positive regulation of biosynthetic process	BP	1	ZNF516,CITED2,GRHL2,SOD2,ABRA,SMOC2,EP300,MRTFA,BRD8,ADGRB1,BRPF3,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,HRH1,LMO7,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ADM,ATOH8,CLCN3,TEAD1,PTH,CLU,MED12L,MEIS2,APP,PTX3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,EDN1,ETS2,ABCG1,NCOA3,ACTN2,LRP5,NPNT,HTR2B,AFAP1L2,SESN2,NGRN,FGFR2,TP53BP1,PRKD1,NCSTN,SLC25A12,ARID5B,ITGA6,ATF6,NPAS3,LRP6,FAM129A,ZNF445,EZH1,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,PAK3,ABLIM3,CRLF3,DAB2,SMARCA1,CTIF,CDH13,PLCG2,BCAR3,CDC7,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,ICAM1,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0043367	0.38	0.79	5	56	CD4-positive, alpha-beta T cell differentiation	BP	1	IL18R1,SH3RF1,RORA,LGALS9,CD83	darkgreen	VSMC_M4
GO:0030217	0.38	0.72	14	179	T cell differentiation	BP	1	BCL2,LEP,IL18R1,ZAP70,CHD7,SH3RF1,PTPN22,ADA,PREX1,RORA,LGALS9,VNN1,CD83,CCR6	darkgreen	VSMC_M4
GO:0031124	0.38	0.78	5	56	mRNA 3'-end processing	BP	1	PAPOLG,CPEB3,APP,CCNT1,AHCYL1	darkgreen	VSMC_M4
GO:0001838	0.38	0.74	9	107	embryonic epithelial tube formation	BP	1	CITED2,GRHL2,ADM,SHROOM3,SEC24B,LRP2,HIF1A,BBS4,LMO4	darkgreen	VSMC_M4
GO:0006885	0.38	0.77	6	70	regulation of pH	BP	1	BCL2,PDK4,CLCN3,EDN1,ATP6AP2,ATP6V0E1	darkgreen	VSMC_M4
GO:0032006	0.38	0.76	7	84	regulation of TOR signaling	BP	1	LEP,SESN1,SESN2,CASTOR1,HIF1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:0019221	0.38	0.70	22	306	cytokine-mediated signaling pathway	BP	1	IFNGR1,IRAK3,ANGPT1,LEP,IL18R1,EDN2,MAP3K7,ACTN4,FLT3,PTPN11,EDN1,MX1,ADIPOR1,MST1R,HIF1A,SLIT3,BBS4,CSF1,F3,MIR99A,CCR6,YAP1	darkgreen	VSMC_M4
GO:0046777	0.38	0.71	17	204	protein autophosphorylation	BP	1	IRAK3,DDR1,DAPK1,ZAP70,RASSF2,FLT3,GRK7,PDGFC,CAMK2D,FGFR2,PRKD1,DDR2,MAP3K13,LMTK2,TOM1L1,ULK2,DAPK3	darkgreen	VSMC_M4
GO:0033157	0.38	0.72	15	196	regulation of intracellular protein transport	BP	1	SLC35D3,MDM2,ANGPT1,LEP,MDFIC,TCAF1,ZDHHC2,PTPN11,ATG13,RAB29,PTPN14,PRKD1,ABLIM3,SH3TC2,FLNA	darkgreen	VSMC_M4
GO:0016575	0.38	0.77	6	71	histone deacetylation	BP	1	REST,SMARCAD1,CAMK2D,PRKD1,SIN3B,HOPX	darkgreen	VSMC_M4
GO:0072666	0.39	0.80	4	42	establishment of protein localization to vacuole	BP	1	GGA3,CLU,SCARB2,SORT1	darkgreen	VSMC_M4
GO:0051261	0.39	0.74	9	99	protein depolymerization	BP	1	SEMA5A,ACTN2,MID1,RDX,WDR1,MICAL3,DNAJC6,SPTAN1,DSTN	darkgreen	VSMC_M4
GO:0006644	0.39	0.70	23	314	phospholipid metabolic process	BP	1	PIGN,PIP5K1B,ABHD12,CHPT1,LPCAT2,SERINC3,PLA2G4F,LPL,MTMR10,AGPAT3,HTR2B,SERINC2,INPP5F,PI4KB,ACHE,PIGG,OCRL,PIGS,PLPPR3,PLCG2,PIGK,PIK3C2A,ORMDL3	darkgreen	VSMC_M4
GO:1903828	0.39	0.75	8	99	negative regulation of cellular protein localization	BP	1	ANGPT1,MDFIC,LATS2,RIPOR2,ACTN2,NUMB,DAB2,TMEM59	darkgreen	VSMC_M4
GO:0050673	0.39	0.69	24	316	epithelial cell proliferation	BP	1	GJA1,LEP,CDKN2B,TGFBR1,GATA2,LIMS2,HPN,ATOH8,SEMA5A,KDM5B,HTR2B,PRKCA,CFLAR,FGFR2,PRKD1,NCSTN,HIF1A,FST,PLXNB3,CDH13,F3,FGF9,YAP1,BMP6	darkgreen	VSMC_M4
GO:0099537	0.39	0.68	37	477	trans-synaptic signaling	BP	1	MBP,STX11,RNF19A,LAMA2,ADGRB1,UNC13B,PPP1R9A,PREPL,SYT5,HRH1,PLCB4,FGF14,PCDHB4,PCLO,ZDHHC2,RIC3,CPEB3,CLCN3,MCTP1,APP,NGF,EDN1,PLCL1,HTR2B,LGMN,NCSTN,INSYN2,LRP6,ACHE,NLGN1,GNAI1,FBXL20,SIPA1L1,NPTN,CDH2,RHOT1,PCDHB2	darkgreen	VSMC_M4
GO:0000209	0.39	0.71	16	203	protein polyubiquitination	BP	1	BCL2,RNF41,SHPRH,SASH1,MDM2,RNF19A,MARCH5,RMND5A,RNF34,PTPN22,AKTIP,MARCH6,UBE3B,SKP2,LRSAM1,FBXO28	darkgreen	VSMC_M4
GO:0002090	0.39	0.80	4	43	regulation of receptor internalization	BP	1	ANGPT1,ATXN2,NUMB,PLCG2	darkgreen	VSMC_M4
GO:0045582	0.39	0.78	5	60	positive regulation of T cell differentiation	BP	1	ZAP70,ADA,LGALS9,VNN1,CD83	darkgreen	VSMC_M4
GO:0014068	0.39	0.76	6	66	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	ANGPT1,LEP,FLT3,PDGFC,PLXNB1,UNC5B	darkgreen	VSMC_M4
GO:0070830	0.39	0.79	4	44	bicellular tight junction assembly	BP	1	GRHL2,GJA1,OCLN,F11R	darkgreen	VSMC_M4
GO:0098869	0.39	0.78	5	67	cellular oxidant detoxification	BP	1	IPCEF1,SOD2,SESN1,SESN2,PRDX4	darkgreen	VSMC_M4
GO:0044091	0.39	0.79	4	44	membrane biogenesis	BP	1	ANKLE2,NLGN1,CDH2,REEP3	darkgreen	VSMC_M4
GO:0035050	0.39	0.78	5	55	embryonic heart tube development	BP	1	CITED2,HIF1A,BBS4,TBX20,YAP1	darkgreen	VSMC_M4
GO:1901214	0.39	0.70	19	251	regulation of neuron death	BP	1	BCL2,SOD2,OXR1,ANGPT1,WFS1,REST,HIPK2,CLU,NGF,RAB29,LGMN,CTSZ,UNC5B,HIF1A,PPARGC1A,TGFB3,PAK3,CSF1,DDIT4	darkgreen	VSMC_M4
GO:1903363	0.39	0.77	5	60	negative regulation of cellular protein catabolic process	BP	1	LAPTM4B,RIC1,HIPK2,N4BP1,GABARAPL2	darkgreen	VSMC_M4
GO:0001952	0.39	0.74	9	105	regulation of cell-matrix adhesion	BP	1	BCL2,DDR1,LIMCH1,PTPN11,SERPINE1,DAPK3,CSF1,CDH13,PLEKHA2	darkgreen	VSMC_M4
GO:0006893	0.39	0.77	5	56	Golgi to plasma membrane transport	BP	1	PREPL,GGA3,ATP2C1,EXOC6,RABEP1	darkgreen	VSMC_M4
GO:0032092	0.39	0.76	6	73	positive regulation of protein binding	BP	1	EP300,HIPK2,APP,AKTIP,PLCL1,DACT1	darkgreen	VSMC_M4
GO:0030509	0.39	0.73	10	116	BMP signaling pathway	BP	1	HIPK2,CRIM1,GDF6,LRP2,TGFB3,SMAD6,FST,CYR61,TBX20,BMP6	darkgreen	VSMC_M4
GO:1904888	0.39	0.77	5	54	cranial skeletal system development	BP	1	GRHL2,RIC1,TGFBR1,FGFR2,TGFB3	darkgreen	VSMC_M4
GO:0120163	0.39	0.79	4	44	negative regulation of cold-induced thermogenesis	BP	1	IL18R1,PLCL1,NPR3,ADAMTS5	darkgreen	VSMC_M4
GO:0051896	0.39	0.73	10	125	regulation of protein kinase B signaling	BP	1	RNF41,ANGPT1,LEP,TGFBR1,SEMA5A,MST1R,LRP2,INPP5F,HIP1,F3	darkgreen	VSMC_M4
GO:0030168	0.40	0.74	8	96	platelet activation	BP	1	MYL9,PRKCA,F11R,HSPB1,FLNA,PLCG2,CSRP1,PRKG1	darkgreen	VSMC_M4
GO:0099536	0.40	0.67	38	494	synaptic signaling	BP	1	MBP,STX11,RNF19A,LAMA2,ADGRB1,GNAQ,UNC13B,PPP1R9A,PREPL,SYT5,HRH1,PLCB4,FGF14,PCDHB4,PCLO,ZDHHC2,RIC3,CPEB3,CLCN3,MCTP1,APP,NGF,EDN1,PLCL1,HTR2B,LGMN,NCSTN,INSYN2,LRP6,ACHE,NLGN1,GNAI1,FBXL20,SIPA1L1,NPTN,CDH2,RHOT1,PCDHB2	darkgreen	VSMC_M4
GO:0060042	0.40	0.79	4	42	retina morphogenesis in camera-type eye	BP	1	HIPK2,THRB,LRP5,BBS4	darkgreen	VSMC_M4
GO:0006835	0.40	0.77	5	56	dicarboxylic acid transport	BP	1	GJA1,SLC26A7,LRP2,SLC25A12,LRRC8C	darkgreen	VSMC_M4
GO:0051928	0.40	0.75	7	86	positive regulation of calcium ion transport	BP	1	TRDN,WFS1,KCNE3,FGF14,MYLK,AKAP6,PLCG2	darkgreen	VSMC_M4
GO:0032890	0.40	0.79	4	47	regulation of organic acid transport	BP	1	LEP,EDN1,RGS2,SLC43A2	darkgreen	VSMC_M4
GO:0006665	0.40	0.73	9	120	sphingolipid metabolic process	BP	1	SUMF1,ST3GAL5,SERINC3,SERINC2,ARV1,PRKD1,CYR61,ST6GALNAC3,ORMDL3	darkgreen	VSMC_M4
GO:0043588	0.40	0.70	14	171	skin development	BP	1	BCL2,CDSN,GRHL2,FOSL2,ADAM9,NCOA3,TXNIP,FGFR2,ITGA6,EXPH5,OPN3,FST,EDA,YAP1	darkgreen	VSMC_M4
GO:1900180	0.40	0.73	9	116	regulation of protein localization to nucleus	BP	1	ANGPT1,LEP,MDFIC,LATS2,SESN2,PRKD1,FLNA,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0019693	0.40	0.68	22	312	ribose phosphate metabolic process	BP	1	EP300,PDK4,PTH,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,PRKAA2,ADCY9,AK5,RFK,DDIT4	darkgreen	VSMC_M4

GO:0048568	0.40	0.68	26	341	embryonic organ development	BP	1	CITED2,GRHL2,TGFBR1,TBX18,HIPK2,GATA2,PPP1R13L,HPN,CHD7,ADM,TEAD1,PDGFC,ADA,PDZD7,EDN1,SEC24B,FGFR2,ID3,MFAP5,HIF1A,TGFB3,BBS4,CYR61,FRZB,TBX20,YAP1	darkgreen	VSMC_M4
GO:0002768	0.40	0.71	12	158	immune response-regulating cell surface receptor signaling pathway	BP	1	BCL2,EP300,ZAP70,MAP3K7,MAP3K1,BLNK,PTPN22,ADA,CD47,RAB29,PAK3,PLCG2	darkgreen	VSMC_M4
GO:0010769	0.40	0.74	7	80	regulation of cell morphogenesis involved in differentiation	BP	1	KANK1,LIMS2,ACTN4,PREX1,CUX1,PAK3,FLNA	darkgreen	VSMC_M4
GO:0045017	0.40	0.70	16	214	glycerolipid biosynthetic process	BP	1	PIGN,PIP5K1B,CHPT1,LPCAT2,LPL,AGPAT3,HTR2B,INPP5F,PI4KB,ACHE,PIGG,OCRL,PIGS,PLCG2,PIGK,PIK3C2A	darkgreen	VSMC_M4
GO:0090311	0.40	0.78	4	42	regulation of protein deacetylation	BP	1	EP300,CAMK2D,PRKD1,PRKAA2	darkgreen	VSMC_M4
GO:0002694	0.40	0.68	25	352	regulation of leukocyte activation	BP	1	BCL2,LEP,DOCK8,CD274,ZAP70,MAP3K8,GATA2,NCK1,SH3RF1,PTPN11,LBP,PTPN22,ADA,CD47,RIPOR2,TP53BP1,IGFBP2,ADGRE2,RORA,LGALS9,VAMP7,VCAM1,VNN1,CD83,CDKN1A	darkgreen	VSMC_M4
GO:0060976	0.40	0.78	4	39	coronary vasculature development	BP	1	TGFBR1,SEC24B,LRP2,SMAD6	darkgreen	VSMC_M4
GO:0071695	0.40	0.70	13	163	anatomical structure maturation	BP	1	BCL2,LEP,RECK,GATA2,PTH,APP,PLXNB1,MAP3K13,ATP6AP2,HIF1A,PCSK4,CDKN1A,CCR6	darkgreen	VSMC_M4
GO:0048588	0.40	0.69	16	195	developmental cell growth	BP	1	DDR1,SH3GL2,ITSN2,SEMA3C,SORBS2,APP,NGF,EDN1,SEMA5A,RGS2,SHTN1,RAPH1,AKAP6,MAP3K13,SLIT3,ULK2	darkgreen	VSMC_M4
GO:0043583	0.40	0.70	13	162	ear development	BP	1	BCL2,DDR1,TBX18,GATA2,HPN,CHD7,PTPN11,PDZD7,EDN1,SEC24B,FGFR2,TGFB3,FRZB	darkgreen	VSMC_M4
GO:0032835	0.41	0.76	5	52	glomerulus development	BP	1	BCL2,ANGPT1,COL4A4,NID1,CFLAR	darkgreen	VSMC_M4
GO:0043535	0.41	0.74	7	87	regulation of blood vessel endothelial cell migration	BP	1	ANGPT1,GATA2,PRKCA,PRKD1,HSPB1,HIF1A,PIK3C2A	darkgreen	VSMC_M4
GO:0038034	0.41	0.78	4	49	signal transduction in absence of ligand	BP	1	BCL2,EYA2,UNC5B,DAPK3	darkgreen	VSMC_M4
GO:0097192	0.41	0.78	4	49	extrinsic apoptotic signaling pathway in absence of ligand	BP	1	BCL2,EYA2,UNC5B,DAPK3	darkgreen	VSMC_M4
GO:0032091	0.41	0.75	6	76	negative regulation of protein binding	BP	1	IFIT1,CTSZ,DACT1,DAB2,XIRP1,CDKN1A	darkgreen	VSMC_M4
GO:0021537	0.41	0.70	15	184	telencephalon development	BP	1	SLC2A1,PEX13,TACC1,CHD7,ANXA3,FEZ1,SUN1,EZH1,HIF1A,NUMB,BBS4,CDH2,FLNA,SLC8A1,BNIP3	darkgreen	VSMC_M4
GO:0001678	0.41	0.72	10	124	cellular glucose homeostasis	BP	1	UNC13B,FOXO1,ABCC8,ABCG1,LRP5,ADCY5,HIF1A,PPARGC1A,PRKAA2,ICAM1	darkgreen	VSMC_M4
GO:1901879	0.41	0.74	7	75	regulation of protein depolymerization	BP	1	SEMA5A,ACTN2,MID1,RDX,WDR1,SPTAN1,DSTN	darkgreen	VSMC_M4
GO:0071331	0.41	0.72	9	112	cellular response to hexose stimulus	BP	1	UNC13B,ABCG1,LRP5,ADCY5,HIF1A,PPARGC1A,PRKAA2,SLC2A5,ICAM1	darkgreen	VSMC_M4
GO:0051702	0.41	0.76	5	61	biological process involved in interaction with symbiont	BP	1	EP300,REST,HPN,PTX3,CCNT1	darkgreen	VSMC_M4
GO:0060997	0.41	0.76	5	54	dendritic spine morphogenesis	BP	1	PPP1R9A,ZNF365,NLGN1,SIPA1L1,PAK3	darkgreen	VSMC_M4
GO:0031349	0.41	0.70	13	177	positive regulation of defense response	BP	1	GJA1,EP300,MAP3K7,FFAR3,APP,LBP,CD47,LPL,SERPINE1,PAK3,VAMP7,PLCG2,LRSAM1	darkgreen	VSMC_M4
GO:0043113	0.41	0.78	4	43	receptor clustering	BP	1	ZDHHC2,NLGN1,CDH2,FLNA	darkgreen	VSMC_M4
GO:0033077	0.41	0.76	5	61	T cell differentiation in thymus	BP	1	BCL2,ZAP70,ADA,VNN1,CCR6	darkgreen	VSMC_M4
GO:0003002	0.41	0.68	19	251	regionalization	BP	1	CITED2,EP300,MLLT3,TGFBR1,TBX18,HIPK2,SMARCD3,SEMA3C,EDN1,ETS2,LRP5,PLXNA2,LRP2,FGFR2,LRP6,ATP6AP2,SMAD6,WLS,TBX20	darkgreen	VSMC_M4
GO:0035821	0.41	0.74	6	75	modulation of process of other organism	BP	1	EP300,REST,HPN,PTX3,CCNT1,ULK2	darkgreen	VSMC_M4
GO:0001889	0.41	0.72	9	116	liver development	BP	1	CITED2,PTPN3,LIMS2,HPN,HNF4A,ADA,CFLAR,ARID5B,FRZB	darkgreen	VSMC_M4
GO:0061001	0.41	0.78	4	42	regulation of dendritic spine morphogenesis	BP	1	PPP1R9A,NLGN1,SIPA1L1,PAK3	darkgreen	VSMC_M4
GO:0045576	0.41	0.78	4	48	mast cell activation	BP	1	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0050804	0.41	0.67	25	317	modulation of chemical synaptic transmission	BP	1	RNF19A,LAMA2,ADGRB1,PPP1R9A,PREPL,HRH1,PLCB4,FGF14,ZDHHC2,CPEB3,MCTP1,APP,NGF,EDN1,PLCL1,LGMN,NCSTN,ACHE,NLGN1,GNAI1,FBXL20,SIPA1L1,NPTN,CDH2,RHOT1	darkgreen	VSMC_M4
GO:0070301	0.41	0.74	6	79	cellular response to hydrogen peroxide	BP	1	MDM2,FOXO1,CYP1B1,MAP1LC3A,PTPN11,BNIP3	darkgreen	VSMC_M4
GO:0000079	0.41	0.74	6	80	regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	CDKN2B,LATS2,CCNT1,CCNG1,CDKN1A,CNTD2	darkgreen	VSMC_M4
GO:0009790	0.41	0.64	63	841	embryo development	BP	1	MBP,CITED2,GRHL2,ANGPT1,GJA1,LAMA2,EP300,RECK,TGFBR1,LMBRD1,TBX18,KIDINS220,HIPK2,GATA2,PPP1R13L,ITGA8,TENM4,POLB,COL4A2,SEMA3C,HPN,CHD7,ADM,ATOH8,TEAD1,MEIS2,PDGFC,SHROOM3,HNF4A,ADA,PDZD7,EDN1,ETS2,EYA2,LRP5,HTR2B,SEC24B,PLXNA2,LRP2,WDTC1,FGFR2,ID3,LRP6,LNPK,MFAP5,ATP6AP2,DACT1,HIF1A,CACNA1C,TGFB3,SMAD6,BBS4,ADCY9,CMIP,LMO4,CYR61,WLS,AFF3,FRZB,TBX20,MAFF,HOPX,YAP1	darkgreen	VSMC_M4
GO:0098739	0.41	0.71	10	123	import across plasma membrane	BP	1	SLC2A1,RGS2,ABCC9,LRP2,SLC43A2,SLC2A5,HCN2,LRRC8C,SLC8A1,SLC27A5	darkgreen	VSMC_M4
GO:0051588	0.41	0.74	6	73	regulation of neurotransmitter transport	BP	1	PPP1R9A,PREPL,MCTP1,NLGN1,FBXL20,RHOT1	darkgreen	VSMC_M4
GO:0035270	0.42	0.73	7	87	endocrine system development	BP	1	CITED2,TGFBR1,GATA2,HNF4A,ARID5B,CDH2,BMP6	darkgreen	VSMC_M4
GO:0045088	0.42	0.70	11	148	regulation of innate immune response	BP	1	IRAK3,EP300,LEP,MAP3K7,PTPN11,LBP,PTPN22,N4BP1,PAK3,LGALS9,PLCG2	darkgreen	VSMC_M4
GO:0099177	0.42	0.66	25	318	regulation of trans-synaptic signaling	BP	1	RNF19A,LAMA2,ADGRB1,PPP1R9A,PREPL,HRH1,PLCB4,FGF14,ZDHHC2,CPEB3,MCTP1,APP,NGF,EDN1,PLCL1,LGMN,NCSTN,ACHE,NLGN1,GNAI1,FBXL20,SIPA1L1,NPTN,CDH2,RHOT1	darkgreen	VSMC_M4
GO:0002824	0.42	0.75	5	64	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	CD274,IL18R1,MAP3K7,ADA,TP53BP1	darkgreen	VSMC_M4
GO:0097237	0.42	0.74	6	85	cellular response to toxic substance	BP	1	IPCEF1,SOD2,PPP1R9A,SESN1,SESN2,PRDX4	darkgreen	VSMC_M4
GO:0046503	0.42	0.77	4	47	glycerolipid catabolic process	BP	1	ABHD12,PLA2G4F,LPL,INPP5F	darkgreen	VSMC_M4
GO:0006836	0.42	0.70	11	139	neurotransmitter transport	BP	1	STX11,UNC13B,PPP1R9A,ICA1,PREPL,SYT5,PCLO,MCTP1,NLGN1,FBXL20,RHOT1	darkgreen	VSMC_M4
GO:0048872	0.42	0.68	17	229	homeostasis of number of cells	BP	1	BCL2,CITED2,HIPK2,GATA2,POLB,RASSF2,FLT3,PTH,PTPN11,ADA,JAM3,P4HTM,NCSTN,HIF1A,CDH2,LGALS9,CSF1	darkgreen	VSMC_M4
GO:0006497	0.42	0.74	6	81	protein lipidation	BP	1	PIGN,ABCA1,ZDHHC2,PIGG,PIGS,PIGK	darkgreen	VSMC_M4
GO:0010761	0.42	0.77	4	46	fibroblast migration	BP	1	ARID5B,DDR2,PAK3,SLC8A1	darkgreen	VSMC_M4
GO:0043407	0.42	0.77	4	47	negative regulation of MAP kinase activity	BP	1	IRAK3,HIPK3,PTPN22,RGS2	darkgreen	VSMC_M4
GO:0032535	0.42	0.66	25	325	regulation of cellular component size	BP	1	KANK1,PPP1R9A,CDC42EP3,SEMA3C,WASF3,NCK1,CLCN3,JMY,NGF,EDN1,SEMA5A,ACTN2,PREX1,SHTN1,WDTC1,MAP3K13,RDX,WDR1,ULK2,PAK3,ARHGAP28,SPTAN1,DSTN,TMEM123,ICAM1	darkgreen	VSMC_M4

GO:0010718	0.42	0.77	4	45	positive regulation of epithelial to mesenchymal transition	BP	1	TGFBR1,TGFB3,DAB2,TBX20	darkgreen	VSMC_M4
GO:0001947	0.42	0.77	4	45	heart looping	BP	1	CITED2,HIF1A,BBS4,TBX20	darkgreen	VSMC_M4
GO:0045862	0.42	0.67	21	297	positive regulation of proteolysis	BP	1	MBP,MDM2,RNF19A,DAPK1,FAM122A,REST,ANTXR1,ADAM9,HPN,CLU,APP,HERPUD1,LGMN,CFLAR,NCSTN,HIP1,TNFSF10,DAB2,LGALS9,F3,CYR61	darkgreen	VSMC_M4
GO:0030520	0.42	0.77	4	46	intracellular estrogen receptor signaling pathway	BP	1	LBH,STRN3,SKP2,YAP1	darkgreen	VSMC_M4
GO:0007405	0.42	0.77	4	42	neuroblast proliferation	BP	1	SMARCD3,FGFR2,HIF1A,NUMB	darkgreen	VSMC_M4
GO:0006473	0.42	0.69	13	168	protein acetylation	BP	1	EP300,BRD8,BRPF3,MAP3K7,JADE1,GATA2,NAA16,FOXO1,NCOA3,YEATS2,PPARGC1A,PRKAA2,TERF2IP	darkgreen	VSMC_M4
GO:0051646	0.42	0.77	4	46	mitochondrion localization	BP	1	FEZ1,HIF1A,RHOT1,ATCAY	darkgreen	VSMC_M4
GO:0001676	0.42	0.75	5	66	long-chain fatty acid metabolic process	BP	1	ABHD12,CYP1B1,PAM,SLC27A5,SCP2	darkgreen	VSMC_M4
GO:0033273	0.42	0.74	6	75	response to vitamin	BP	1	MDM2,SOD2,LEP,PTH,ADA,STC2	darkgreen	VSMC_M4
GO:0099601	0.42	0.77	4	44	regulation of neurotransmitter receptor activity	BP	1	DAPK1,APP,NLGN1,PPARGC1A	darkgreen	VSMC_M4
GO:0007611	0.42	0.68	15	183	learning or memory	BP	1	EP300,VLDLR,HRH1,CPEB3,MEIS2,APP,ABCC8,TANC1,RCAN1,NGF,LGMN,NCSTN,HIF1A,KCNK10,NPTN	darkgreen	VSMC_M4
GO:0042157	0.42	0.71	8	111	lipoprotein metabolic process	BP	1	PIGN,LEP,ABCA1,ABHD12,ZDHHC2,PIGG,PIGS,PIGK	darkgreen	VSMC_M4
GO:0002260	0.42	0.77	4	50	lymphocyte homeostasis	BP	1	BCL2,ADA,HIF1A,LGALS9	darkgreen	VSMC_M4
GO:0030705	0.42	0.68	14	173	cytoskeleton-dependent intracellular transport	BP	1	DYNC1I1,ACTN4,APP,MYO1B,FEZ1,SUN1,DYNC1I2,AP3B2,HSPB1,HIF1A,IFT43,RHOT1,MYO10,VAMP7	darkgreen	VSMC_M4
GO:0007346	0.43	0.65	26	360	regulation of mitotic cell cycle	BP	1	BCL2,MDM2,SMOC2,CDKN2B,FAM122A,TMEM8B,PTPN3,JADE1,SMARCD3,BABAM2,MEIS2,APP,PTPN11,RBL2,EDN1,LRP5,LGMN,PRKCA,AFAP1L2,RDX,DACT1,TOM1L1,DAPK3,CDC7,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0006611	0.43	0.76	4	49	protein export from nucleus	BP	1	MDM2,PTPN11,PTPN14,AHCYL1	darkgreen	VSMC_M4
GO:0002429	0.43	0.69	11	148	immune response-activating cell surface receptor signaling pathway	BP	1	BCL2,EP300,ZAP70,MAP3K7,BLNK,PTPN22,ADA,CD47,RAB29,PAK3,PLCG2	darkgreen	VSMC_M4
GO:0002757	0.43	0.69	11	148	immune response-activating signal transduction	BP	1	BCL2,EP300,ZAP70,MAP3K7,BLNK,PTPN22,ADA,CD47,RAB29,PAK3,PLCG2	darkgreen	VSMC_M4
GO:0045639	0.43	0.73	6	77	positive regulation of myeloid cell differentiation	BP	1	GATA2,TMEM64,PRKCA,HIF1A,FAXDC2,CSF1	darkgreen	VSMC_M4
GO:0098657	0.43	0.69	12	155	import into cell	BP	1	SLC2A1,RGS2,ABCC9,LRP2,CYBRD1,SLC43A2,SLC2A5,HCN2,LRSAM1,LRRC8C,SLC8A1,SLC27A5	darkgreen	VSMC_M4
GO:0002521	0.43	0.65	28	383	leukocyte differentiation	BP	1	BCL2,CITED2,EP300,LEP,IL18R1,ZAP70,GATA2,RASSF2,TMEM178A,TF,FLT3,CHD7,SH3RF1,BLNK,APP,TMEM64,PTPN22,ADA,PREX1,PRKCA,RORA,LGALS9,CSF1,PLCG2,VCAM1,VNN1,CD83,CCR6	darkgreen	VSMC_M4
GO:0009895	0.43	0.66	19	254	negative regulation of catabolic process	BP	1	BCL2,IRAK3,LAPTM4B,ADGRB1,LEP,RIC1,PTPN3,HIPK2,PTPN22,N4BP1,FEZ1,HTR2B,QSOX1,SLC25A12,PPARGC1A,FLNA,CST3,GABARAPL2,DDIT4	darkgreen	VSMC_M4
GO:0009141	0.43	0.73	6	86	nucleoside triphosphate metabolic process	BP	1	ENTPD3,ADA,SLC25A12,PPARGC1A,AK7,AK5	darkgreen	VSMC_M4
GO:1900182	0.43	0.73	6	76	positive regulation of protein localization to nucleus	BP	1	LEP,SESN2,PRKD1,FLNA,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0060078	0.43	0.72	7	85	regulation of postsynaptic membrane potential	BP	1	UNC13B,PPP1R9A,FGF14,APP,GABBR1,INSYN2,NLGN1	darkgreen	VSMC_M4
GO:0007265	0.43	0.65	23	296	Ras protein signal transduction	BP	1	ABRA,KANK1,ABCA1,CDC42EP3,KIAA0355,ARHGEF3,PTH,G3BP2,NGF,RIPOR2,KCTD10,SHTN1,PRKD1,F11R,RDX,SYNPO2L,IQSEC3,MAPRE2,PLEKHG5,CSF1,CDH13,ARHGAP29,CDKN1A	darkgreen	VSMC_M4
GO:0060562	0.43	0.66	21	269	epithelial tube morphogenesis	BP	1	BCL2,CITED2,DDR1,GRHL2,COL4A1,ADM,SHROOM3,EDN1,KDM5B,LRP5,NPNT,SEC24B,LRP2,CTSZ,FGFR2,HIF1A,BBS4,CSF1,LMO4,TBX20,YAP1	darkgreen	VSMC_M4
GO:0055007	0.43	0.71	8	96	cardiac muscle cell differentiation	BP	1	SGCB,TBX18,SORBS2,EDN1,RGS2,ACTN2,AKAP6,SLC8A1	darkgreen	VSMC_M4
GO:0022037	0.43	0.72	7	84	metencephalon development	BP	1	BCL2,PTPN11,SEC24B,NCSTN,ZNF365,PPARGC1A,RORA	darkgreen	VSMC_M4
GO:0051960	0.43	0.65	27	344	regulation of nervous system development	BP	1	ADGRB1,REST,TENM4,SMARCD3,SEMA3C,WASF3,CHD7,ABCC8,NGF,SEMA5A,PLXNA2,SHTN1,LRP2,PLXNB1,SLC25A12,ZNF365,MAP3K13,CUX1,NLGN1,HIF1A,NUMB,NPTN,ULK2,PAK3,PLXNB3,LRRC24,YAP1	darkgreen	VSMC_M4
GO:0007044	0.43	0.71	8	89	cell-substrate junction assembly	BP	1	BCL2,LIMCH1,TESK2,PTPN11,ACTN2,ITGA6,ACTN1,DAPK3	darkgreen	VSMC_M4
GO:0044283	0.43	0.64	28	414	small molecule biosynthetic process	BP	1	EP300,LEP,PDK4,REST,EDN2,HRH1,ADM,PTH,SERINC3,ADA,EDN1,PLA2G4F,LPL,ABCG1,SESN2,ARV1,WDTC1,CHST15,SLC25A12,PPIP5K1,PPARGC1A,PRKAA2,MBTPS1,PLCG2,RFK,SLC27A5,BMP6,SCP2	darkgreen	VSMC_M4
GO:0018212	0.43	0.65	22	290	peptidyl-tyrosine modification	BP	1	DDR1,ANGPT1,LEP,ZAP70,EPHB6,HIPK2,TESK2,FLT3,HIPK3,APP,PDGFC,PTPN11,MST1R,AFAP1L2,TPST2,INPP5F,FGFR2,DDR2,GPRC5A,PLCG2,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0060760	0.43	0.76	4	49	positive regulation of response to cytokine stimulus	BP	1	DDX58,EDN1,HIF1A,CSF1	darkgreen	VSMC_M4
GO:0071887	0.43	0.72	6	79	leukocyte apoptotic process	BP	1	DOCK8,CD274,ADA,HIF1A,LGALS9,ORMDL3	darkgreen	VSMC_M4
GO:0045732	0.44	0.67	15	203	positive regulation of protein catabolic process	BP	1	RNF41,MDM2,RNF19A,GJA1,FAM122A,GGA3,ADAM9,FOXO1,CLU,HERPUD1,LRP2,RDX,FBXL5,DACT1,DAB2	darkgreen	VSMC_M4
GO:0046513	0.44	0.75	4	51	ceramide biosynthetic process	BP	1	ST3GAL5,CYR61,ST6GALNAC3,ORMDL3	darkgreen	VSMC_M4
GO:1903364	0.44	0.69	10	137	positive regulation of cellular protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,CLU,HERPUD1,LRP2,RDX,FBXL5,DACT1,DAB2	darkgreen	VSMC_M4
GO:0072665	0.44	0.74	5	60	protein localization to vacuole	BP	1	LMBRD1,GGA3,CLU,SCARB2,SORT1	darkgreen	VSMC_M4
GO:0032481	0.44	0.75	4	48	positive regulation of type I interferon production	BP	1	DDX58,PTPN11,PTPN22,PLCG2	darkgreen	VSMC_M4
GO:0051348	0.44	0.66	16	219	negative regulation of transferase activity	BP	1	IRAK3,GNAQ,CDKN2B,LATS2,HIPK3,PTPN22,RGS2,LRP5,GPRC5A,LRP6,HSPB1,EIF4A2,SLC8A1,CDKN1A,PPM1E,ORMDL3	darkgreen	VSMC_M4
GO:0015918	0.44	0.71	7	89	sterol transport	BP	1	LEP,ABCA1,CLU,ABCG1,ARV1,LRP6,SCP2	darkgreen	VSMC_M4
GO:0044380	0.44	0.73	5	55	protein localization to cytoskeleton	BP	1	MID1,BBS4,MAPRE2,GAS2L2,FAM83H	darkgreen	VSMC_M4
GO:1904029	0.44	0.72	6	83	regulation of cyclin-dependent protein kinase activity	BP	1	CDKN2B,LATS2,CCNT1,CCNG1,CDKN1A,CNTD2	darkgreen	VSMC_M4
GO:0071478	0.45	0.68	11	150	cellular response to radiation	BP	1	MDM2,EP300,GRK7,N4BP1,TP53BP1,CRYAB,MMP1,OPN3,CDKN1A,MFAP4,YAP1	darkgreen	VSMC_M4
GO:0010970	0.45	0.68	11	139	transport along microtubule	BP	1	DYNC1I1,APP,FEZ1,SUN1,DYNC1I2,AP3B2,HSPB1,HIF1A,IFT43,RHOT1,VAMP7	darkgreen	VSMC_M4
GO:0043473	0.45	0.72	6	75	pigmentation	BP	1	BCL2,SHROOM3,RAB29,ATP6AP2,BBS4,EDA	darkgreen	VSMC_M4
GO:0061008	0.45	0.69	9	119	hepaticobiliary system development	BP	1	CITED2,PTPN3,LIMS2,HPN,HNF4A,ADA,CFLAR,ARID5B,FRZB	darkgreen	VSMC_M4

GO:0006163	0.45	0.64	21	302	purine nucleotide metabolic process	BP	1	EP300,PDK4,PTH,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,PRKAA2,ADCY9,AK5,DDIT4	darkgreen	VSMC_M4
GO:0071479	0.45	0.73	5	64	cellular response to ionizing radiation	BP	1	MDM2,TP53BP1,CRYAB,CDKN1A,YAP1	darkgreen	VSMC_M4
GO:0016311	0.45	0.63	25	342	dephosphorylation	BP	1	BCL2,PTPN3,NT5C3A,PFKFB3,POLB,ANKLE2,PTPRG,NCK1,PTPN11,PTPN22,RCAN1,MTMR10,NT5C2,DAPP1,EYA2,NPNT,INPP5F,PTPN14,PPEF1,PPP1R36,DNAJC6,OCRL,PLPPR3,PPP1R26,PPM1E	darkgreen	VSMC_M4
GO:1905039	0.45	0.69	8	105	carboxylic acid transmembrane transport	BP	1	SLC2A1,SLC16A3,RGS2,LRP2,SLC25A12,SLC43A2,LRRC8C,SLC27A5	darkgreen	VSMC_M4
GO:0070509	0.45	0.73	5	58	calcium ion import	BP	1	TRPC4,MICU2,CACNA1C,SLC8A1,PLN	darkgreen	VSMC_M4
GO:0006508	0.45	0.60	89	1295	proteolysis	BP	1	MBP,RNF41,MDM2,RNF19A,C4A,DAPK1,WFS1,FAM122A,C2orf40,RNF149,REST,RECK,PREPL,PTPN3,ANTXR1,PAPPA,PREP,HIPK2,ITIH5,BABAM2,STT3B,ADAM9,CRIM1,QPCT,HPN,FBXO3,RMND5A,SH3RF1,RNF34,CLU,APP,HERPUD1,PROS1,CHAC1,CPQ,NGF,N4BP1,MARCH6,BACE2,TMPRSS7,UBE3B,KCTD10,LGMN,AMZ2,CFI,CTSS,CFLAR,CTSZ,CTSF,USP53,NCSTN,ZRANB1,HIP1,SERPINE1,CRYAB,C1RL,ATP6AP2,PAPPA2,USP11,MMP1,LAP3,FBXL5,TNFSF10,JKAMP,PCSK1N,FBXL20,FAF2,LACTB,TOM1L1,USP32,ATG4A,MMP28,DAB2,LGALS9,SKP2,TMEM59,PCSK4,MBTPS1,F3,GLG1,CYR61,PRSS48,SPINK2,FBXO27,ADAMTS5,TMPRSS11E,CST3,PIGK,GABARAPL2	darkgreen	VSMC_M4
GO:0007041	0.45	0.69	8	100	lysosomal transport	BP	1	GGA3,CLU,SCARB2,AKTIP,ATG14,EPG5,VAMP7,SORT1	darkgreen	VSMC_M4
GO:0035282	0.45	0.71	6	74	segmentation	BP	1	EP300,MLLT3,TBX18,SEMA3C,PLXNA2,LRP6	darkgreen	VSMC_M4
GO:0008654	0.45	0.65	16	222	phospholipid biosynthetic process	BP	1	PIGN,PIP5K1B,CHPT1,LPCAT2,AGPAT3,HTR2B,INPP5F,PI4KB,ACHE,PIGG,OCRL,PIGS,PLCG2,PIGK,PIK3C2A,ORMDL3	darkgreen	VSMC_M4
GO:0031529	0.45	0.74	4	49	ruffle organization	BP	1	KANK1,RDX,NLGN1,ICAM1	darkgreen	VSMC_M4
GO:0048041	0.45	0.70	7	81	focal adhesion assembly	BP	1	BCL2,LIMCH1,TESK2,PTPN11,ACTN2,ACTN1,DAPK3	darkgreen	VSMC_M4
GO:0051249	0.45	0.64	20	287	regulation of lymphocyte activation	BP	1	BCL2,LEP,DOCK8,CD274,ZAP70,MAP3K8,NCK1,SH3RF1,PTPN11,PTPN22,ADA,CD47,RIPOR2,TP53BP1,IGFBP2,LGALS9,VCAM1,VNN1,CD83,CDKN1A	darkgreen	VSMC_M4
GO:0030330	0.45	0.72	5	63	DNA damage response, signal transduction by p53 class mediator	BP	1	MDM2,HIPK2,ANKRD1,SESN2,CDKN1A	darkgreen	VSMC_M4
GO:0002821	0.45	0.72	5	66	positive regulation of adaptive immune response	BP	1	CD274,IL18R1,MAP3K7,ADA,TP53BP1	darkgreen	VSMC_M4
GO:0002312	0.45	0.72	5	64	B cell activation involved in immune response	BP	1	CD180,ADA,TP53BP1,PLCG2,CCR6	darkgreen	VSMC_M4
GO:0031328	0.45	0.59	107	1503	positive regulation of cellular biosynthetic process	BP	1	ZNF516,CITED2,GRHL2,SOD2,ABRA,SMOC2,EP300,MRTFA,BRD8,BRPF3,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,HRH1,LMO7,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ADM,ATOH8,TEAD1,PTH,CLU,MED12L,MEIS2,APP,PTX3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,EDN1,ETS2,NCOA3,ACTN2,LRP5,NPNT,HTR2B,AFAP1L2,SESN2,NGRN,FGFR2,TP53BP1,PRKD1,NCSTN,SLC25A12,ARID5B,ITGA6,ATF6,NPAS3,LRP6,FAM129A,ZNF445,EZH1,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,PAK3,ABLIM3,CRLF3,DAB2,SMARCA1,CTIF,CDH13,BCAR3,CDC7,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,ICAM1,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0042158	0.45	0.71	6	84	lipoprotein biosynthetic process	BP	1	PIGN,ABCA1,ZDHHC2,PIGG,PIGS,PIGK	darkgreen	VSMC_M4
GO:0000086	0.46	0.68	9	124	G2/M transition of mitotic cell cycle	BP	1	TPD52L1,CDKN2B,FAM122A,SMARCD3,BABAM2,APP,SKP2,CDC7,CDKN1A	darkgreen	VSMC_M4
GO:0030098	0.46	0.64	19	259	lymphocyte differentiation	BP	1	BCL2,EP300,LEP,IL18R1,ZAP70,FLT3,CHD7,SH3RF1,BLNK,PTPN22,ADA,PREX1,RORA,LGALS9,PLCG2,VCAM1,VNN1,CD83,CCR6	darkgreen	VSMC_M4
GO:0045921	0.46	0.72	5	63	positive regulation of exocytosis	BP	1	GATA2,RAB2B,EXPH5,NLGN1,VAMP7	darkgreen	VSMC_M4
GO:0007411	0.46	0.65	15	181	axon guidance	BP	1	LAMA2,EPHB6,SEMA3C,APP,NFASC,SEMA5A,FEZ1,ROBO3,PLXNA2,PLXNB1,UNC5B,SLIT3,NPTN,PLXNB3,NEXN	darkgreen	VSMC_M4
GO:0051224	0.46	0.69	7	96	negative regulation of protein transport	BP	1	ANGPT1,REST,MDFIC,INHBB,ABCC8,PTPN11,PFKL	darkgreen	VSMC_M4
GO:0042440	0.46	0.72	5	65	pigment metabolic process	BP	1	BCL2,ADA,OPN3,PPARGC1A,PGRMC1	darkgreen	VSMC_M4
GO:0006446	0.46	0.72	5	66	regulation of translational initiation	BP	1	NCK1,HSPB1,EIF4A2,EIF4G3,CTIF	darkgreen	VSMC_M4
GO:0061371	0.46	0.74	4	47	determination of heart left/right asymmetry	BP	1	CITED2,HIF1A,BBS4,TBX20	darkgreen	VSMC_M4
GO:1901292	0.46	0.72	5	69	nucleoside phosphate catabolic process	BP	1	ENTPD3,ENTPD1,ADA,NT5C2,PDE1A	darkgreen	VSMC_M4
GO:0006753	0.46	0.62	26	387	nucleoside phosphate metabolic process	BP	1	EP300,PDK4,NT5C3A,ENTPD3,PTH,ENTPD1,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,AK7,PRKAA2,ADCY9,AK5,RFK,DDIT4	darkgreen	VSMC_M4
GO:1903825	0.46	0.68	8	106	organic acid transmembrane transport	BP	1	SLC2A1,SLC16A3,RGS2,LRP2,SLC25A12,SLC43A2,LRRC8C,SLC27A5	darkgreen	VSMC_M4
GO:0044264	0.46	0.70	6	75	cellular polysaccharide metabolic process	BP	1	GYS1,PTH,GYG1,B3GNT7,GYG2,NDST3	darkgreen	VSMC_M4
GO:0006892	0.46	0.68	8	99	post-Golgi vesicle-mediated transport	BP	1	PREPL,DOP1A,GGA3,ATP2C1,EXOC6,MYO1B,RABEP1,SORT1	darkgreen	VSMC_M4
GO:0061178	0.46	0.73	4	50	regulation of insulin secretion involved in cellular response to glucose stimulus	BP	1	ABCG1,LRP5,ADCY5,HIF1A	darkgreen	VSMC_M4
GO:0001954	0.46	0.73	4	49	positive regulation of cell-matrix adhesion	BP	1	PTPN11,CSF1,CDH13,PLEKHA2	darkgreen	VSMC_M4
GO:0001755	0.46	0.73	4	47	neural crest cell migration	BP	1	SEMA3C,SEMA5A,HTR2B,HIF1A	darkgreen	VSMC_M4
GO:0030041	0.46	0.65	12	160	actin filament polymerization	BP	1	KANK1,PPP1R9A,CDC42EP3,WASF3,NCK1,JMY,PREX1,RDX,PAK3,ARHGAP28,SPTAN1,ICAM1	darkgreen	VSMC_M4
GO:0070372	0.46	0.64	15	211	regulation of ERK1 and ERK2 cascade	BP	1	ANGPT1,NDRG2,APP,PDGFC,PTPN11,PTPN22,NPNT,HTR2B,PRKCA,CFLAR,FGFR2,NPTN,LGALS9,CYR61,ICAM1	darkgreen	VSMC_M4
GO:0001708	0.46	0.71	5	62	cell fate specification	BP	1	TBX18,TENM4,EYA2,LMO4,TBX20	darkgreen	VSMC_M4
GO:0097485	0.47	0.64	15	182	neuron projection guidance	BP	1	LAMA2,EPHB6,SEMA3C,APP,NFASC,SEMA5A,FEZ1,ROBO3,PLXNA2,PLXNB1,UNC5B,SLIT3,NPTN,PLXNB3,NEXN	darkgreen	VSMC_M4
GO:1902107	0.47	0.68	8	110	positive regulation of leukocyte differentiation	BP	1	ZAP70,TMEM64,ADA,PRKCA,LGALS9,CSF1,VNN1,CD83	darkgreen	VSMC_M4
GO:1903708	0.47	0.68	8	110	positive regulation of hemopoiesis	BP	1	ZAP70,TMEM64,ADA,PRKCA,LGALS9,CSF1,VNN1,CD83	darkgreen	VSMC_M4

GO:0022414	0.47	0.58	72	1029	reproductive process	BP	1	BCL2,CITED2,DDR1,GRHL2,PKDREJ,AFF4,GJA1,LEP,UNC13B,SPATA6L,RECK,IGFBP7,SLC2A1,TGFBR1,ANTXR1,PAPPA,GATA2,ENKUR,TESK2,INHBB,THRB,GTSF1,NCOR2,CHD7,ADM,PAM,CDKL2,APP,RXFP1,ABCC8,PTPN11,PTX3,HNF4A,ADA,EDN1,JAM3,KDM5B,RGS2,MST1R,SUN1,MFGE8,LRP2,FGFR2,ARID5B,PRDX4,IGFBP2,CYP19A1,TNFSF10,MAEL,HIF1A,TEX11,SLIT3,TGFB3,BBS4,FST,LGALS9,MARF1,PCSK4,FLNA,CSF1,HFM1,CYR61,CCDC136,SPINK2,OSGIN2,MAFF,FGF9,CCR6,ICAM1,STC2,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0045596	0.47	0.60	36	489	negative regulation of cell differentiation	BP	1	GRHL2,KANK1,REST,TGFBR1,ABCA1,GATA2,LBH,ACTN4,CRIM1,FOXO1,SEMA3C,TMEM178A,HPN,PTH,MEIS2,APP,ABCC8,PTPN11,TMEM64,SEMA5A,ABCG1,ADIPOR1,RGS2,LRP5,ID3,NBR1,DISP3,RORA,SMAD6,ULK2,FST,SORT1,FRZB,FGF9,HOPX,YAP1	darkgreen	VSMC_M4
GO:0016064	0.47	0.70	6	85	immunoglobulin mediated immune response	BP	1	C4A,CLU,CFI,TP53BP1,C1RL,CCR6	darkgreen	VSMC_M4
GO:0006066	0.47	0.63	18	258	alcohol metabolic process	BP	1	LEP,VLDLR,REST,ABCA1,HRH1,CYP1B1,PTH,APP,ABCG1,LRP5,ARV1,PPIP5K1,DISP3,OCRL,PRKAA2,MBTPS1,PLCG2,BMP6	darkgreen	VSMC_M4
GO:0015718	0.47	0.71	5	66	monocarboxylic acid transport	BP	1	LEP,SLC16A3,EDN1,PLA2G4F,SLC27A5	darkgreen	VSMC_M4
GO:0032611	0.47	0.73	4	52	interleukin-1 beta production	BP	1	APP,LPL,HSPB1,LGALS9	darkgreen	VSMC_M4
GO:0032651	0.47	0.73	4	52	regulation of interleukin-1 beta production	BP	1	APP,LPL,HSPB1,LGALS9	darkgreen	VSMC_M4
GO:0050806	0.47	0.67	8	104	positive regulation of synaptic transmission	BP	1	LAMA2,PPP1R9A,ZDHHC2,APP,LGMN,NCSTN,NLGN1,NPTN	darkgreen	VSMC_M4
GO:0031329	0.47	0.59	49	689	regulation of cellular catabolic process	BP	1	BCL2,MDM2,LAPTM4B,RNF19A,EP300,DAPK1,LEP,FAM122A,RIC1,PTPN3,MAP3K7,SESN1,HIPK2,ADAM9,FOXO1,CPEB3,SLC25A4,CLU,APP,SCARB2,HERPUD1,PTPN22,N4BP1,FEZ1,HTR2B,PRKCA,SESN2,LRP2,PRKD1,QSOX1,ATF6,HSPB1,RDX,FBXL5,DACT1,HIF1A,CALCOCO2,DAB2,PRKAA2,TMEM59,DAPK3,LRSAM1,ITPR1,BNIP3,CST3,GABARAPL2,PIK3C2A,ORMDL3,ATP6V0E1	darkgreen	VSMC_M4
GO:0033673	0.47	0.64	14	191	negative regulation of kinase activity	BP	1	IRAK3,GNAQ,CDKN2B,LATS2,HIPK3,PTPN22,RGS2,LRP5,GPRC5A,LRP6,HSPB1,SLC8A1,CDKN1A,PPM1E	darkgreen	VSMC_M4
GO:0014066	0.47	0.68	7	86	regulation of phosphatidylinositol 3-kinase signaling	BP	1	ANGPT1,LEP,PIP5K1B,FLT3,PDGFC,PLXNB1,UNC5B	darkgreen	VSMC_M4
GO:0000003	0.47	0.58	72	1031	reproduction	BP	1	BCL2,CITED2,DDR1,GRHL2,PKDREJ,AFF4,GJA1,LEP,UNC13B,SPATA6L,RECK,IGFBP7,SLC2A1,TGFBR1,ANTXR1,PAPPA,GATA2,ENKUR,TESK2,INHBB,THRB,GTSF1,NCOR2,CHD7,ADM,PAM,CDKL2,APP,RXFP1,ABCC8,PTPN11,PTX3,HNF4A,ADA,EDN1,JAM3,KDM5B,RGS2,MST1R,SUN1,MFGE8,LRP2,FGFR2,ARID5B,PRDX4,IGFBP2,CYP19A1,TNFSF10,MAEL,HIF1A,TEX11,SLIT3,TGFB3,BBS4,FST,LGALS9,MARF1,PCSK4,FLNA,CSF1,HFM1,CYR61,CCDC136,SPINK2,OSGIN2,MAFF,FGF9,CCR6,ICAM1,STC2,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0032787	0.47	0.61	27	404	monocarboxylic acid metabolic process	BP	1	EP300,LEP,PDK4,EDN2,PEX13,ABHD12,CYP1B1,PAM,APP,EDN1,PLA2G4F,LPL,ADIPOR1,PFKL,SESN2,ARV1,WDTC1,SLC25A12,ENO2,HIF1A,PPARGC1A,PRKAA2,VNN1,ACAD11,SLC27A5,SCP2,DDIT4	darkgreen	VSMC_M4
GO:0060759	0.48	0.66	9	128	regulation of response to cytokine stimulus	BP	1	IRAK3,ANGPT1,DDX58,PTPN11,EDN1,HIF1A,SLIT3,CSF1,MIR99A	darkgreen	VSMC_M4
GO:0032436	0.48	0.69	6	83	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,CLU,HERPUD1,DAB2	darkgreen	VSMC_M4
GO:0034250	0.48	0.66	9	130	positive regulation of cellular amide metabolic process	BP	1	IFNGR1,CPEB3,NCK1,CLU,ABCG1,NGRN,FAM129A,CTIF,CYR61	darkgreen	VSMC_M4
GO:0060560	0.48	0.63	16	200	developmental growth involved in morphogenesis	BP	1	DDR1,SH3GL2,ITSN2,SEMA3C,APP,NGF,SEMA5A,KDM5B,SHTN1,FGFR2,RAPH1,MAP3K13,SLIT3,ULK2,CSF1,YAP1	darkgreen	VSMC_M4
GO:0050767	0.48	0.61	22	285	regulation of neurogenesis	BP	1	REST,TENM4,SMARCD3,SEMA3C,CHD7,ABCC8,NGF,SEMA5A,PLXNA2,SHTN1,LRP2,PLXNB1,ZNF365,MAP3K13,CUX1,HIF1A,NUMB,NPTN,ULK2,PAK3,PLXNB3,YAP1	darkgreen	VSMC_M4
GO:0140029	0.48	0.70	5	66	exocytic process	BP	1	STX11,UNC13B,EXOC6,NLGN1,VAMP7	darkgreen	VSMC_M4
GO:0035924	0.48	0.70	5	62	cellular response to vascular endothelial growth factor stimulus	BP	1	SMOC2,FLT3,PRKD1,HSPB1,VCAM1	darkgreen	VSMC_M4
GO:0045637	0.48	0.64	11	152	regulation of myeloid cell differentiation	BP	1	GATA2,RASSF2,TMEM178A,MEIS2,TMEM64,PRKCA,P4HTM,HIF1A,FAXDC2,CSF1,LOX	darkgreen	VSMC_M4
GO:0046578	0.48	0.63	13	161	regulation of Ras protein signal transduction	BP	1	ABRA,KANK1,ABCA1,ARHGEF3,NGF,RIPOR2,KCTD10,F11R,RDX,SYNPO2L,IQSEC3,MAPRE2,CSF1	darkgreen	VSMC_M4
GO:0061024	0.48	0.58	42	599	membrane organization	BP	1	MBP,BCL2,STX11,LAPTM4B,TRDN,ADGRB1,SH3GL2,ABCA1,SNAP91,GATA2,TMCC1,SYNGR2,ATP2C1,ANKLE2,ZDHHC2,SLC25A4,CLCN3,CLU,LPCAT2,ABCG1,EYA2,SUN1,PRKCA,SEC24B,MFGE8,ATP9A,ARV1,GULP1,EMC1,NLGN1,RABEP1,CDH2,SH3TC2,RHOT1,OCRL,VAMP7,PLCG2,ABCA4,BNIP3,PRELID2,PIK3C2A,REEP3	darkgreen	VSMC_M4
GO:0044087	0.48	0.57	59	801	regulation of cellular component biogenesis	BP	1	GJA1,EP300,ADGRB1,LIMCH1,KANK1,UNC13B,PPP1R9A,REST,TGFBR1,ABCA1,ANTXR1,CDC42EP3,LMNTD2,WASF3,NCK1,OCLN,G3BP2,CLU,GPM6A,APP,PTPN11,JMY,JAM3,CD47,RIPOR2,FEZ1,PREX1,PRKCA,SYNPO2,F11R,CRYAB,RDX,SYNPO2L,MMP1,DACT1,NLGN1,TGFB3,SMAD6,BBS4,SYNPO,PAK3,EVI5L,ARHGAP28,PRKAA2,MYO10,DAPK3,PLXNB3,FLNA,PLCG2,SPTAN1,LRSAM1,LMO4,CYR61,TBX20,LRRC24,PPM1E,ICAM1,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0006631	0.48	0.61	18	271	fatty acid metabolic process	BP	1	LEP,PDK4,EDN2,PEX13,ABHD12,CYP1B1,PAM,EDN1,PLA2G4F,LPL,ADIPOR1,SESN2,WDTC1,PPARGC1A,PRKAA2,ACAD11,SLC27A5,SCP2	darkgreen	VSMC_M4
GO:0070371	0.48	0.62	16	227	ERK1 and ERK2 cascade	BP	1	ANGPT1,NDRG2,TF,APP,PDGFC,PTPN11,PTPN22,NPNT,HTR2B,PRKCA,CFLAR,FGFR2,NPTN,LGALS9,CYR61,ICAM1	darkgreen	VSMC_M4
GO:0016482	0.48	0.64	12	153	cytosolic transport	BP	1	RIC1,PREPL,DOP1A,DENND5A,AKTIP,RAB29,ATP9A,RDX,LMTK2,DAB2,FLNA,SORT1	darkgreen	VSMC_M4
GO:1901796	0.48	0.68	6	83	regulation of signal transduction by p53 class mediator	BP	1	BCL2,MDM2,EP300,HIPK2,ANKRD1,RNF34	darkgreen	VSMC_M4
GO:0043255	0.48	0.68	6	78	regulation of carbohydrate biosynthetic process	BP	1	EP300,LEP,HRH1,PTH,SESN2,PPARGC1A	darkgreen	VSMC_M4

GO:0043254	0.48	0.60	26	361	regulation of protein-containing complex assembly	BP	1	EP300,KANK1,UNC13B,PPP1R9A,ABCA1,CDC42EP3,WASF3,NCK1,OCLN,CLU,PTPN11,JMY,JAM3,PREX1,CRYAB,RDX,MMP1,DACT1,SMAD6,PAK3,ARHGAP28,PLCG2,SPTAN1,LMO4,TBX20,ICAM1	darkgreen	VSMC_M4
GO:0010212	0.48	0.64	10	137	response to ionizing radiation	BP	1	BCL2,MDM2,BABAM2,POLB,TP53BP1,CRYAB,VCAM1,CDKN1A,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0045682	0.48	0.71	4	50	regulation of epidermis development	BP	1	GRHL2,NAB1,NCOA3,MAFF	darkgreen	VSMC_M4
GO:0051649	0.49	0.55	119	1679	establishment of localization in cell	BP	1	BCL2,SLC35D3,STX11,GRIP1,MDM2,LAPTM4B,ABRA,ANGPT1,GJA1,TRDN,SH3GL2,LEP,UNC13B,PPP1R9A,RIC1,DYNC1I1,LMAN2L,SNX13,PREPL,SYT5,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,ITSN2,GATA2,TMCC1,GGA3,USP6NL,KCNE3,ACTN4,FGF14,PCLO,EML4,ZDHHC2,DENND5A,CHD7,TRIM23,EXOC6,CLCN3,MCTP1,JPH1,KIF13B,CLU,APP,SCARB2,ANXA3,PTPN11,HERPUD1,ATG13,AKTIP,MYO1B,RAB29,ABCG1,TNNT2,ACTN2,LRP5,FEZ1,HTR2B,TINAGL1,SUN1,TXNIP,SEC24B,ATP9A,ARV1,CAMK2D,ADCY5,INPP5F,PTPN14,PRKD1,CYBRD1,DYNC1I2,RAPGEF4,AP3B2,AKAP6,LRP6,HSPB1,CRYAB,RDX,EXPH5,ATG14,LMTK2,NLGN1,WDR1,HIF1A,CACNA1C,AP1S3,ADGRE2,FBXL20,FAF2,NUMB,IFT43,EPG5,BBS4,CDH2,EVI5L,ABLIM3,SH3TC2,RHOT1,DNAJC6,DAB2,LGALS9,MYO10,FLNA,VAMP7,AHCYL1,SORT1,PLCG2,TBC1D13,WLS,KCNE4,ITPR1,SLC8A1,PLN,CDKN1A,TMEM38A,SCP2	darkgreen	VSMC_M4
GO:0019724	0.49	0.68	6	87	B cell mediated immunity	BP	1	C4A,CLU,CFI,TP53BP1,C1RL,CCR6	darkgreen	VSMC_M4
GO:0001837	0.49	0.64	10	131	epithelial to mesenchymal transition	BP	1	TGFBR1,HPN,ADIPOR1,FGFR2,LRP6,HIF1A,TGFB3,DAB2,FLNA,TBX20	darkgreen	VSMC_M4
GO:0009142	0.49	0.71	4	62	nucleoside triphosphate biosynthetic process	BP	1	SLC25A12,PPARGC1A,AK7,AK5	darkgreen	VSMC_M4
GO:0002286	0.49	0.69	5	65	T cell activation involved in immune response	BP	1	IL18R1,APBB1IP,RORA,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0002460	0.49	0.63	12	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	C4A,CD274,IL18R1,MAP3K7,CLU,ADA,CFI,TP53BP1,C1RL,RORA,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0072331	0.49	0.64	10	139	signal transduction by p53 class mediator	BP	1	BCL2,MDM2,EP300,HIPK2,ANKRD1,RNF34,JMY,SESN2,CDKN1A,DDIT4	darkgreen	VSMC_M4
GO:0071772	0.49	0.64	10	126	response to BMP	BP	1	HIPK2,CRIM1,GDF6,LRP2,TGFB3,SMAD6,FST,CYR61,TBX20,BMP6	darkgreen	VSMC_M4
GO:0071773	0.49	0.64	10	126	cellular response to BMP stimulus	BP	1	HIPK2,CRIM1,GDF6,LRP2,TGFB3,SMAD6,FST,CYR61,TBX20,BMP6	darkgreen	VSMC_M4
GO:0030099	0.49	0.60	21	293	myeloid cell differentiation	BP	1	CITED2,EP300,CDKN2B,HIPK2,GATA2,SNRK,RASSF2,TMEM178A,TF,MEIS2,APP,PTPN11,TMEM64,PRKCA,P4HTM,WDR1,HIF1A,ACTN1,FAXDC2,CSF1,LOX	darkgreen	VSMC_M4
GO:0036503	0.49	0.66	7	99	ERAD pathway	BP	1	WFS1,STT3B,HERPUD1,MARCH6,JKAMP,FAF2,FBXO27	darkgreen	VSMC_M4
GO:0045664	0.50	0.63	11	145	regulation of neuron differentiation	BP	1	BCL2,REST,GATA2,APP,NGF,FEZ1,MAP3K13,NLGN1,ZC4H2,DISP3,BMP6	darkgreen	VSMC_M4
GO:0071705	0.50	0.55	111	1609	nitrogen compound transport	BP	1	SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,VLDLR,UNC13B,RIC1,REST,ICA1,LMAN2L,SNX13,PREPL,LMBRD1,SYT5,SLC17A5,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,GGA3,INHBB,USP6NL,RAB2B,ACTN4,ADAM9,TRPC4,ATP2C1,PCLO,ZDHHC2,FFAR3,CHD7,ANKRD1,TRIM23,EXOC6,PAM,SLC25A4,KIF13B,G3BP2,CLU,ATXN2,SCARB2,ABCC8,PTPN11,HERPUD1,ATG13,HNF4A,SERINC3,ADA,AKTIP,IFIT1,EDN1,CD47,RAB29,ABCG1,RGS2,PFKL,LRP5,ARRDC4,ZMAT3,TM7SF3,TXNIP,SEC24B,ADCY5,LRP2,PTPN14,PRKD1,SLC25A12,RAPGEF4,AP3B2,AKAP6,HIP1,HSPB1,ACHE,EXPH5,MAOB,LMTK2,NLGN1,RABEP1,HIF1A,AP1S3,FAF2,TGFB3,TOM1L1,EPG5,SLC14A1,BBS4,ATG4A,EVI5L,ABLIM3,SH3TC2,DAB2,RBFOX1,SLC43A2,FLNA,VAMP7,AHCYL1,SORT1,TBC1D13,LRSAM1,LRRC8C,WLS,CDKN1A,GABARAPL2,BMP6,MAFA	darkgreen	VSMC_M4
GO:0010389	0.50	0.67	6	82	regulation of G2/M transition of mitotic cell cycle	BP	1	FAM122A,SMARCD3,BABAM2,APP,CDC7,CDKN1A	darkgreen	VSMC_M4
GO:0045944	0.50	0.55	65	904	positive regulation of transcription by RNA polymerase II	BP	1	CITED2,GRHL2,ABRA,EP300,MRTFA,BRD8,DDX58,CREB3,REST,HIPK2,GATA2,ELF1,LMO7,FOSL2,SALL2,THRB,FOXO1,CHD7,PCGF5,NCK1,ATOH8,TEAD1,PTH,MEIS2,APP,CCNT1,CHD6,HNF4A,EDN1,ETS2,NCOA3,LRP5,NPNT,SESN2,FGFR2,TP53BP1,PRKD1,ITGA6,ATF6,LRP6,ZNF445,EZH1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,RORA,TGFB3,SMAD6,ABLIM3,CRLF3,DAB2,SMARCA1,CDH13,LMO4,CYR61,TBX20,ZNF175,MAFF,ZNF782,HLF,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0090316	0.50	0.63	10	136	positive regulation of intracellular protein transport	BP	1	SLC35D3,MDM2,LEP,TCAF1,ZDHHC2,ATG13,RAB29,PRKD1,ABLIM3,FLNA	darkgreen	VSMC_M4
GO:0044242	0.50	0.62	11	164	cellular lipid catabolic process	BP	1	LEP,PEX13,ABHD12,CYP1B1,PLA2G4F,LPL,SESN2,INPP5F,PLCG2,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0030010	0.51	0.62	10	123	establishment of cell polarity	BP	1	UST,GJA1,DOCK8,KANK1,AMOTL2,JAM3,RIPOR2,FEZ1,SHTN1,PATJ	darkgreen	VSMC_M4
GO:0007626	0.51	0.62	10	132	locomotory behavior	BP	1	OXR1,PEX13,HIPK2,ABHD12,CHD7,CLCN3,APP,RCAN1,ADCY5,INPP5F	darkgreen	VSMC_M4
GO:0015031	0.51	0.54	90	1301	protein transport	BP	1	SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,VLDLR,UNC13B,RIC1,REST,ICA1,LMAN2L,SNX13,PREPL,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,GGA3,INHBB,USP6NL,RAB2B,ACTN4,ADAM9,ATP2C1,PCLO,ZDHHC2,ANKRD1,TRIM23,EXOC6,PAM,KIF13B,CLU,SCARB2,ABCC8,PTPN11,HERPUD1,ATG13,HNF4A,AKTIP,IFIT1,RAB29,ABCG1,PFKL,LRP5,ARRDC4,ZMAT3,TM7SF3,TXNIP,SEC24B,ADCY5,LRP2,PTPN14,PRKD1,RAPGEF4,AP3B2,AKAP6,HIP1,HSPB1,ACHE,EXPH5,LMTK2,NLGN1,RABEP1,HIF1A,AP1S3,FAF2,TGFB3,TOM1L1,BBS4,ATG4A,EVI5L,ABLIM3,SH3TC2,DAB2,FLNA,VAMP7,AHCYL1,SORT1,TBC1D13,LRSAM1,WLS,CDKN1A,GABARAPL2,BMP6,MAFA	darkgreen	VSMC_M4
GO:1901616	0.51	0.69	4	56	organic hydroxy compound catabolic process	BP	1	HSD17B6,MAOA,MAOB,OCRL	darkgreen	VSMC_M4
GO:1904950	0.51	0.65	7	100	negative regulation of establishment of protein localization	BP	1	ANGPT1,REST,MDFIC,INHBB,ABCC8,PTPN11,PFKL	darkgreen	VSMC_M4

GO:0018108	0.51	0.58	21	287	peptidyl-tyrosine phosphorylation	BP	1	DDR1,ANGPT1,LEP,ZAP70,EPHB6,HIPK2,TESK2,FLT3,HIPK3,APP,PDGFC,PTPN11,MST1R,AFAP1L2,INPP5F,FGFR2,DDR2,GPRC5A,PLCG2,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0050852	0.51	0.66	6	85	T cell receptor signaling pathway	BP	1	ZAP70,MAP3K7,PTPN22,ADA,RAB29,PLCG2	darkgreen	VSMC_M4
GO:1901991	0.51	0.62	10	142	negative regulation of mitotic cell cycle phase transition	BP	1	BCL2,MDM2,CDKN2B,FAM122A,JADE1,BABAM2,RBL2,DACT1,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0044267	0.51	0.52	255	3725	cellular protein metabolic process	BP	1	MBP,TMX3,GDF11,BCL2,PIGN,RNF41,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,OXR1,ANGPT1,C4A,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,FAM122A,SH3RF3,DCUN1D4,VLDLR,C2orf40,PPP1R9A,RIC1,PDK4,RNF149,REST,RECK,ZAP70,TGFBR1,ABCA1,KLHL7,PTPN3,MAP3K7,ANTXR1,PAPPA,EPHB6,JADE1,MAP3K8,HIPK2,GATA2,ABHD12,SNRK,TESK2,NAA16,INHBB,MKRN2,LMO7,ITIH5,BABAM2,STT3B,LIPT2,ADAM9,CRIM1,SUMF1,FOXO1,RASSF2,ANKLE2,QPCT,FLT3,TUSC3,ZDHHC2,MAP3K1,FXYD1,HPN,FBXO3,PTPRG,LATS2,HIPK3,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,RNF141,PAM,SH3RF1,ST3GAL5,GRK7,OCLN,EXTL3,RNF34,CDKL2,CLU,APP,ATXN2,PDGFC,HECTD4,PTPN11,NEK4,CCNT1,HERPUD1,PROS1,PTPN22,DPY19L4,CHAC1,GDF6,AKTIP,RCAN1,NGF,EDN1,N4BP1,SMARCAD1,MARCH6,KDM5B,TARSL2,DAPP1,RGS2,EYA2,NCOA3,UBE3B,LRP5,KCTD10,ARRDC4,PLCL1,HTR2B,MST1R,LGMN,B3GNT7,GALNT3,B3GALNT2,PRKCA,AFAP1L2,TPST2,SESN2,YEATS2,P4HTM,CAMK2D,CTSS,NGRN,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,MAN2A2,FGFR2,RBM4B,CTSF,USP53,PTPN14,PRKD1,NCSTN,TRIM63,ZRANB1,PPEF1,DDR2,GPRC5A,MAP3K13,PCMTD2,LRP6,HIP1,PRDX4,FAM129A,HSPB1,EIF4A2,RIMKLB,SERPINE1,CRYAB,PAPPA2,RDX,P4HA1,SECISBP2L,EZH1,FUT11,EIF4G3,USP11,ATG14,MMP1,FBXL5,TNFSF10,DACT1,LMTK2,SPEG,JKAMP,SIN3B,PCSK1N,HIF1A,OPN3,FBXL20,PPARGC1A,PLOD1,DCAF5,FAF2,PIGG,NEK9,TGFB3,CCNG1,MAGT1,SMAD6,TOM1L1,FAXDC2,GALNT10,USP32,NPTN,NRK,ULK2,PAK3,MARCH2,DNAJC6,DAB2,LGALS9,PIGS,SKP2,PRKAA2,TMEM59,CTIF	darkgreen	VSMC_M4
GO:0030183	0.51	0.64	7	96	B cell differentiation	BP	1	BCL2,EP300,FLT3,BLNK,ADA,PLCG2,VCAM1	darkgreen	VSMC_M4
GO:0034121	0.51	0.69	4	54	regulation of toll-like receptor signaling pathway	BP	1	IRAK3,LBP,PTPN22,TLR1	darkgreen	VSMC_M4
GO:0007286	0.51	0.64	7	100	spermatid development	BP	1	AFF4,JAM3,BBS4,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0034446	0.51	0.64	7	89	substrate adhesion-dependent cell spreading	BP	1	KANK1,ANTXR1,LIMS2,ITGA8,ACTN4,PREX1,FLNA	darkgreen	VSMC_M4
GO:0055067	0.52	0.63	8	108	monovalent inorganic cation homeostasis	BP	1	BCL2,PDK4,CLCN3,EDN1,ATP6AP2,NPPB,SLC8A1,ATP6V0E1	darkgreen	VSMC_M4
GO:0051100	0.52	0.62	9	129	negative regulation of binding	BP	1	IFIT1,CTSZ,DACT1,ARHGAP28,DAB2,ZFP90,XIRP1,PLN,CDKN1A	darkgreen	VSMC_M4
GO:0044703	0.52	0.54	47	688	multi-organism reproductive process	BP	1	BCL2,CITED2,DDR1,PKDREJ,AFF4,GJA1,LEP,UNC13B,SPATA6L,RECK,IGFBP7,SLC2A1,TGFBR1,PAPPA,TESK2,INHBB,THRB,GTSF1,ADM,PAM,APP,RXFP1,ABCC8,PTX3,ADA,EDN1,JAM3,KDM5B,RGS2,MST1R,SUN1,MFGE8,PRDX4,IGFBP2,MAEL,TEX11,TGFB3,BBS4,FST,LGALS9,MARF1,PCSK4,CCDC136,SPINK2,MAFF,CCR6,STC2	darkgreen	VSMC_M4
GO:0055072	0.52	0.66	5	72	iron ion homeostasis	BP	1	TF,CYBRD1,FBXL5,HIF1A,BMP6	darkgreen	VSMC_M4
GO:0016525	0.52	0.65	6	82	negative regulation of angiogenesis	BP	1	FAM19A5,ADGRB1,COL4A2,ABCC8,SERPINE1,NPPB	darkgreen	VSMC_M4
GO:0140056	0.52	0.66	5	67	organelle localization by membrane tethering	BP	1	STX11,UNC13B,ESYT3,ATG14,AHCYL1	darkgreen	VSMC_M4
GO:0006112	0.52	0.66	5	65	energy reserve metabolic process	BP	1	LEP,GYS1,PTH,GYG1,GYG2	darkgreen	VSMC_M4
GO:0051607	0.52	0.60	12	174	defense response to virus	BP	1	BCL2,DDX58,NT5C3A,PTPN22,SERINC3,IFIT1,MX1,ABCC9,SKP2,BNIP3,ZNF175,DDIT4	darkgreen	VSMC_M4
GO:0140546	0.52	0.60	12	174	defense response to symbiont	BP	1	BCL2,DDX58,NT5C3A,PTPN22,SERINC3,IFIT1,MX1,ABCC9,SKP2,BNIP3,ZNF175,DDIT4	darkgreen	VSMC_M4
GO:0046824	0.52	0.68	4	54	positive regulation of nucleocytoplasmic transport	BP	1	MDM2,LEP,PRKD1,FLNA	darkgreen	VSMC_M4
GO:0016050	0.52	0.57	18	255	vesicle organization	BP	1	BCL2,STX11,LAPTM4B,UNC13B,ABCA1,SNAP91,TMCC1,ZDHHC2,CLCN3,SCARB2,AKTIP,RAB29,ABCG1,SEC24B,VAMP7,SORT1,CCDC136,SPINK2	darkgreen	VSMC_M4
GO:1901992	0.52	0.66	5	73	positive regulation of mitotic cell cycle phase transition	BP	1	MDM2,SMARCD3,APP,RDX,CDC7	darkgreen	VSMC_M4
GO:0090407	0.52	0.55	30	452	organophosphate biosynthetic process	BP	1	PIGN,PIP5K1B,PDK4,HRH1,CHPT1,PTH,ADCY6,LPCAT2,ADA,AGPAT3,HTR2B,ADCY5,INPP5F,PI4KB,SLC25A12,PPIP5K1,ACHE,PPARGC1A,NPPB,PIGG,AK7,OCRL,PIGS,ADCY9,PLCG2,AK5,PIGK,RFK,PIK3C2A,ORMDL3	darkgreen	VSMC_M4
GO:0001959	0.53	0.62	8	119	regulation of cytokine-mediated signaling pathway	BP	1	IRAK3,ANGPT1,PTPN11,EDN1,HIF1A,SLIT3,CSF1,MIR99A	darkgreen	VSMC_M4
GO:0001764	0.53	0.61	9	113	neuron migration	BP	1	PEX13,GATA2,SH3RF1,GPM6A,SHTN1,FLNA,TBX20,PRKG1,DDIT4	darkgreen	VSMC_M4
GO:0045995	0.53	0.68	4	50	regulation of embryonic development	BP	1	LAMA2,TBX18,TENM4,HNF4A	darkgreen	VSMC_M4
GO:0006879	0.53	0.67	4	56	cellular iron ion homeostasis	BP	1	TF,CYBRD1,HIF1A,BMP6	darkgreen	VSMC_M4
GO:2001021	0.53	0.65	5	72	negative regulation of response to DNA damage stimulus	BP	1	BCL2,MDM2,TPT1,CLU,TP53BP1	darkgreen	VSMC_M4
GO:0010717	0.53	0.64	6	80	regulation of epithelial to mesenchymal transition	BP	1	TGFBR1,HPN,ADIPOR1,TGFB3,DAB2,TBX20	darkgreen	VSMC_M4
GO:0022408	0.53	0.61	9	130	negative regulation of cell-cell adhesion	BP	1	MBP,CDSN,CD274,PTPN22,RIPOR2,RDX,LGALS9,PRKG1,BMP6	darkgreen	VSMC_M4
GO:2000181	0.53	0.64	6	83	negative regulation of blood vessel morphogenesis	BP	1	FAM19A5,ADGRB1,COL4A2,ABCC8,SERPINE1,NPPB	darkgreen	VSMC_M4
GO:1990748	0.53	0.65	5	79	cellular detoxification	BP	1	IPCEF1,SOD2,SESN1,SESN2,PRDX4	darkgreen	VSMC_M4
GO:0001736	0.53	0.65	5	64	establishment of planar polarity	BP	1	MLLT3,SEC24B,DACT1,WDR1,DAB2	darkgreen	VSMC_M4
GO:0007164	0.53	0.65	5	64	establishment of tissue polarity	BP	1	MLLT3,SEC24B,DACT1,WDR1,DAB2	darkgreen	VSMC_M4
GO:0044839	0.53	0.60	9	132	cell cycle G2/M phase transition	BP	1	TPD52L1,CDKN2B,FAM122A,SMARCD3,BABAM2,APP,SKP2,CDC7,CDKN1A	darkgreen	VSMC_M4
GO:1903362	0.53	0.57	15	222	regulation of cellular protein catabolic process	BP	1	MDM2,LAPTM4B,RNF19A,FAM122A,RIC1,HIPK2,CLU,HERPUD1,N4BP1,LRP2,RDX,FBXL5,DACT1,DAB2,GABARAPL2	darkgreen	VSMC_M4
GO:0071333	0.53	0.61	8	110	cellular response to glucose stimulus	BP	1	UNC13B,ABCG1,LRP5,ADCY5,HIF1A,PPARGC1A,PRKAA2,ICAM1	darkgreen	VSMC_M4
GO:0042100	0.54	0.67	4	56	B cell proliferation	BP	1	BCL2,CD180,ADA,CDKN1A	darkgreen	VSMC_M4

GO:0044255	0.54	0.52	49	743	cellular lipid metabolic process	BP	1	PIGN,LEP,PIP5K1B,PDK4,EDN2,PEX13,ABHD12,SUMF1,CYP1B1,CHPT1,PAM,ST3GAL5,PTPN11,LPCAT2,SERINC3,EDN1,PLA2G4F,LPL,ABCG1,MTMR10,ADIPOR1,AGPAT3,HTR2B,SERINC2,SESN2,ARV1,LRP2,WDTC1,INPP5F,PRKD1,PI4KB,ACHE,ATG14,PPARGC1A,PIGG,OCRL,PIGS,PRKAA2,PLPPR3,PLCG2,ABCA4,CYR61,ST6GALNAC3,ACAD11,PIGK,SLC27A5,PIK3C2A,ORMDL3,SCP2	darkgreen	VSMC_M4
GO:0010629	0.54	0.52	53	766	negative regulation of gene expression	BP	1	CITED2,IRAK3,MDM2,LAPTM4B,ANGPT1,DAPK1,SH3GL2,CD274,REST,GATA2,INHBB,NDRG2,NCOR2,CPEB3,ATOH8,OCLN,FAM172A,PTH,APP,LBP,PTPN22,CHAC1,RBL2,EDN1,N4BP1,RGS2,LGMN,PRKCA,HELZ,SESN2,CTSZ,ID3,SERPINE1,CRYAB,EZH1,MAEL,HIF1A,SLIT3,TGFB3,NPTN,LGALS9,MARF1,PRKAA2,TMEM59,CTIF,DAPK3,GLG1,MIR99A,MIR331,CD83,CDKN1A,STC2,YAP1	darkgreen	VSMC_M4
GO:0050851	0.54	0.61	8	117	antigen receptor-mediated signaling pathway	BP	1	BCL2,ZAP70,MAP3K7,BLNK,PTPN22,ADA,RAB29,PLCG2	darkgreen	VSMC_M4
GO:0015908	0.54	0.66	4	60	fatty acid transport	BP	1	SLC2A1,EDN1,PLA2G4F,SLC27A5	darkgreen	VSMC_M4
GO:0072521	0.54	0.55	21	319	purine-containing compound metabolic process	BP	1	EP300,PDK4,PTH,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,PRKAA2,ADCY9,AK5,DDIT4	darkgreen	VSMC_M4
GO:0060255	0.54	0.49	310	4468	regulation of macromolecule metabolic process	BP	1	MBP,ZNF516,GDF11,BCL2,RNF41,IFNGR1,CITED2,SASH1,IRAK3,MDM2,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,SMOC2,AFF4,GJA1,ZHX1,TPD52L1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,DCUN1D4,VLDLR,PPP1R9A,CD274,RIC1,IL18R1,CREB3,ZNF169,REST,RECK,TGFBR1,ZNF331,PTPN3,TBX18,MAP3K7,ANTXR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,GGA3,NAA16,ELF1,INHBB,SMARCD3,LMO7,ITIH5,BABAM2,FOSL2,LBH,NDRG2,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,FOXO1,RASSF2,ANKLE2,CYP1B1,TF,EBF4,FLT3,ZDHHC2,MIER3,NCOR2,FFAR3,FXYD1,HPN,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,SH3RF1,ATOH8,OCLN,TCF7L1,WWC2,TEAD1,FAM172A,PTH,RNF34,G3BP2,CLU,BLNK,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ABCC8,ANXA3,PTPN11,PTX3,LBP,NEK4,CCNT1,HERPUD1,PROS1,JMY,CHD6,PTPN22,HNF4A,CHAC1,GDF6,NAB1,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,SMARCAD1,BACE2,LPL,RAB29,ABCG1,KDM5B,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,LRP5,ARRDC4,NPNT,PLCL1,HTR2B,MST1R,LGMN,PRKCA,AFAP1L2,TXNIP,HELZ,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,F11R,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,GPRC5A,MAP3K13,ID3,LRP6,HIP1,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,SERPINE1,ACHE,CRYAB,ATP6AP2,RDX,ZNF445,SECISBP2L,EZH1,EIF4G3,ATG14,FBXL5,TNFSF10,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,F	darkgreen	VSMC_M4
GO:0031647	0.54	0.56	17	249	regulation of protein stability	BP	1	BCL2,MDM2,EP300,GNAQ,WFS1,RNF149,GGA3,NAA16,RASSF2,TF,CLU,PRKD1,HIP1,CRYAB,DACT1,PPARGC1A,FLNA	darkgreen	VSMC_M4
GO:0030512	0.54	0.64	5	64	negative regulation of transforming growth factor beta receptor signaling pathway	BP	1	RASL11B,TGFB3,SMAD6,GLG1,ADAMTSL2	darkgreen	VSMC_M4
GO:0001818	0.54	0.57	13	195	negative regulation of cytokine production	BP	1	IRAK3,LAPTM4B,ANGPT1,CD274,INHBB,NDRG2,LBP,PTPN22,N4BP1,TGFB3,NPTN,LGALS9,CD83	darkgreen	VSMC_M4
GO:0045893	0.54	0.50	88	1244	positive regulation of transcription, DNA-templated	BP	1	ZNF516,CITED2,GRHL2,ABRA,EP300,MRTFA,BRD8,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,NCK1,ATOH8,TEAD1,PTH,MED12L,MEIS2,APP,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,EDN1,ETS2,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,SESN2,FGFR2,TP53BP1,PRKD1,ARID5B,ITGA6,ATF6,NPAS3,LRP6,ZNF445,EZH1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,ABLIM3,CRLF3,DAB2,SMARCA1,CDH13,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:1903508	0.54	0.50	88	1244	positive regulation of nucleic acid-templated transcription	BP	1	ZNF516,CITED2,GRHL2,ABRA,EP300,MRTFA,BRD8,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,NCK1,ATOH8,TEAD1,PTH,MED12L,MEIS2,APP,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,EDN1,ETS2,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,SESN2,FGFR2,TP53BP1,PRKD1,ARID5B,ITGA6,ATF6,NPAS3,LRP6,ZNF445,EZH1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,ABLIM3,CRLF3,DAB2,SMARCA1,CDH13,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0099111	0.54	0.58	12	165	microtubule-based transport	BP	1	DYNC1I1,APP,FEZ1,SUN1,DYNC1I2,AP3B2,HSPB1,HIF1A,IFT43,KIAA0556,RHOT1,VAMP7	darkgreen	VSMC_M4
GO:0002761	0.54	0.62	6	86	regulation of myeloid leukocyte differentiation	BP	1	GATA2,RASSF2,TMEM178A,TMEM64,PRKCA,CSF1	darkgreen	VSMC_M4
GO:0045621	0.54	0.64	5	72	positive regulation of lymphocyte differentiation	BP	1	ZAP70,ADA,LGALS9,VNN1,CD83	darkgreen	VSMC_M4
GO:0030316	0.54	0.64	5	68	osteoclast differentiation	BP	1	RASSF2,TMEM178A,TF,TMEM64,CSF1	darkgreen	VSMC_M4
GO:0090175	0.55	0.66	4	51	regulation of establishment of planar polarity	BP	1	MLLT3,SEC24B,DACT1,DAB2	darkgreen	VSMC_M4
GO:0003341	0.55	0.61	7	103	cilium movement	BP	1	ENKUR,DNHD1,DNAH7,KIAA0556,BBS4,GAS2L2,CCR6	darkgreen	VSMC_M4
GO:0051704	0.55	0.51	48	709	multi-organism process	BP	1	BCL2,CITED2,DDR1,PKDREJ,AFF4,GJA1,LEP,UNC13B,SPATA6L,RECK,IGFBP7,SLC2A1,TGFBR1,PAPPA,TESK2,INHBB,THRB,GTSF1,ADM,PAM,APP,RXFP1,ABCC8,PTX3,ADA,IFIT1,EDN1,JAM3,KDM5B,RGS2,MST1R,SUN1,MFGE8,PRDX4,IGFBP2,MAEL,TEX11,TGFB3,BBS4,FST,LGALS9,MARF1,PCSK4,CCDC136,SPINK2,MAFF,CCR6,STC2	darkgreen	VSMC_M4

GO:1902680	0.55	0.50	88	1246	positive regulation of RNA biosynthetic process	BP	1	ZNF516,CITED2,GRHL2,ABRA,EP300,MRTFA,BRD8,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,NCK1,ATOH8,TEAD1,PTH,MED12L,MEIS2,APP,NEK4,CCNT1,IMY,CHD6,HNF4A,GDF6,EDN1,ETS2,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,SESN2,FGFR2,TP53BP1,PRKD1,ARID5B,ITGA6,ATF6,NPAS3,LRP6,ZNF445,EZH1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,ABLIM3,CRLF3,DAB2,SMARCA1,CDH13,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0071300	0.55	0.65	4	52	cellular response to retinoic acid	BP	1	LEP,ABCA1,FGFR2,YAP1	darkgreen	VSMC_M4
GO:0031532	0.55	0.61	7	94	actin cytoskeleton reorganization	BP	1	ANTXR1,ATP2C1,F11R,SIPA1L1,NRK,DAPK3,FLNA	darkgreen	VSMC_M4
GO:0010770	0.55	0.63	5	65	positive regulation of cell morphogenesis involved in differentiation	BP	1	LIMS2,PREX1,CUX1,PAK3,FLNA	darkgreen	VSMC_M4
GO:0010558	0.55	0.50	80	1150	negative regulation of macromolecule biosynthetic process	BP	1	CITED2,MDM2,TRPS1,GJA1,ZHX1,EP300,DAPK1,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,HNF4A,NAB1,EDN1,ETS2,BACE2,KDM5B,RGS2,MXI1,TXNIP,SESN2,YEATS2,WDTC1,FGFR2,STRN3,ARID5B,ID3,EIF4A2,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TMEM59,DAPK3,TLE2,FLNA,ZFP90,TBX20,ITM2C,ZNF425,ZNF175,CDKN1A,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0018193	0.55	0.50	69	997	peptidyl-amino acid modification	BP	1	TMX3,BCL2,MDM2,DDR1,OXR1,ANGPT1,EP300,BRD8,BRPF3,LEP,ZAP70,TGFBR1,MAP3K7,EPHB6,JADE1,HIPK2,GATA2,TESK2,NAA16,STT3B,LIPT2,RASSF2,QPCT,FLT3,TUSC3,ZDHHC2,LATS2,HIPK3,NCK1,APP,PDGFC,PTPN11,DPY19L4,NGF,NCOA3,PLCL1,MST1R,GALNT3,PRKCA,AFAP1L2,TPST2,YEATS2,P4HTM,CAMK2D,INPP5F,FGFR2,PRKD1,DDR2,GPRC5A,MAP3K13,PRDX4,P4HA1,EZH1,LMTK2,PPARGC1A,PLOD1,MAGT1,ULK2,PRKAA2,BGN,PNCK,PLCG2,TERF2IP,BCAR3,CDC7,LOX,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0019751	0.55	0.61	6	88	polyol metabolic process	BP	1	LEP,HRH1,PTH,PPIP5K1,OCRL,PLCG2	darkgreen	VSMC_M4
GO:0048592	0.55	0.58	9	118	eye morphogenesis	BP	1	BCL2,CITED2,HIPK2,THRB,LRP5,MFAP5,HIF1A,BBS4,BCAR3	darkgreen	VSMC_M4
GO:0032024	0.55	0.65	4	56	positive regulation of insulin secretion	BP	1	GJA1,ABCG1,TM7SF3,HIF1A	darkgreen	VSMC_M4
GO:0019827	0.55	0.59	8	106	stem cell population maintenance	BP	1	REST,GATA2,TPT1,LBH,NCOA3,LRP5,CDH2,YAP1	darkgreen	VSMC_M4
GO:0007612	0.56	0.59	8	104	learning	BP	1	HRH1,MEIS2,APP,ABCC8,TANC1,LGMN,HIF1A,NPTN	darkgreen	VSMC_M4
GO:0003006	0.56	0.51	47	685	developmental process involved in reproduction	BP	1	BCL2,CITED2,GRHL2,AFF4,GJA1,LEP,SPATA6L,TGFBR1,GATA2,TESK2,INHBB,GTSF1,CHD7,ADM,CDKL2,PTPN11,PTX3,HNF4A,ADA,JAM3,KDM5B,RGS2,SUN1,LRP2,FGFR2,ARID5B,PRDX4,CYP19A1,TNFSF10,MAEL,HIF1A,TEX11,SLIT3,BBS4,FST,MARF1,PCSK4,FLNA,CSF1,CYR61,CCDC136,SPINK2,FGF9,CCR6,ICAM1,STC2,BMP6	darkgreen	VSMC_M4
GO:0072001	0.56	0.54	19	256	renal system development	BP	1	BCL2,ANGPT1,WFS1,TGFBR1,TBX18,ITGA8,COL4A1,GDF6,COL4A4,NPNT,NID1,LRP2,CFLAR,FGFR2,ARID5B,ID3,SMAD6,YAP1,BMP6	darkgreen	VSMC_M4
GO:1901989	0.56	0.61	6	91	positive regulation of cell cycle phase transition	BP	1	MDM2,SMARCD3,APP,RDX,PLCG2,CDC7	darkgreen	VSMC_M4
GO:0019882	0.56	0.64	4	61	antigen processing and presentation	BP	1	LGMN,CTSS,CTSF,ICAM1	darkgreen	VSMC_M4
GO:1902749	0.56	0.61	6	87	regulation of cell cycle G2/M phase transition	BP	1	FAM122A,SMARCD3,BABAM2,APP,CDC7,CDKN1A	darkgreen	VSMC_M4
GO:0007032	0.56	0.62	5	71	endosome organization	BP	1	LAPTM4B,TMCC1,CLCN3,SCARB2,AKTIP	darkgreen	VSMC_M4
GO:0043543	0.56	0.55	14	202	protein acylation	BP	1	EP300,BRD8,BRPF3,MAP3K7,JADE1,GATA2,NAA16,FOXO1,ZDHHC2,NCOA3,YEATS2,PPARGC1A,PRKAA2,TERF2IP	darkgreen	VSMC_M4
GO:0009308	0.56	0.62	5	77	amine metabolic process	BP	1	MAOA,MAOB,AOC3,ATCAY,VCAM1	darkgreen	VSMC_M4
GO:0002244	0.56	0.59	7	96	hematopoietic progenitor cell differentiation	BP	1	BCL2,CITED2,MLLT3,REST,FLT3,JAM3,FST	darkgreen	VSMC_M4
GO:0019080	0.56	0.60	6	86	viral gene expression	BP	1	EP300,REST,MDFIC,HPN,CCNT1,ST6GALNAC3	darkgreen	VSMC_M4
GO:0005976	0.56	0.60	6	83	polysaccharide metabolic process	BP	1	GYS1,PTH,GYG1,B3GNT7,GYG2,NDST3	darkgreen	VSMC_M4
GO:0048645	0.57	0.64	4	56	animal organ formation	BP	1	CITED2,SMARCD3,LRP2,FGFR2	darkgreen	VSMC_M4
GO:0018394	0.57	0.56	10	143	peptidyl-lysine acetylation	BP	1	EP300,BRD8,BRPF3,MAP3K7,JADE1,GATA2,NCOA3,YEATS2,PPARGC1A,PRKAA2	darkgreen	VSMC_M4
GO:0098727	0.57	0.57	8	108	maintenance of cell number	BP	1	REST,GATA2,TPT1,LBH,NCOA3,LRP5,CDH2,YAP1	darkgreen	VSMC_M4
GO:0030518	0.57	0.58	7	96	intracellular steroid hormone receptor signaling pathway	BP	1	EP300,LBH,NCOR2,STRN3,DAB2,SKP2,YAP1	darkgreen	VSMC_M4
GO:0006633	0.57	0.58	7	107	fatty acid biosynthetic process	BP	1	PDK4,EDN2,EDN1,PLA2G4F,LPL,WDTC1,PRKAA2	darkgreen	VSMC_M4
GO:0051153	0.57	0.61	5	72	regulation of striated muscle cell differentiation	BP	1	BCL2,EDN1,RGS2,AKAP6,HOPX	darkgreen	VSMC_M4
GO:0048839	0.57	0.56	10	139	inner ear development	BP	1	TBX18,GATA2,HPN,CHD7,PTPN11,PDZD7,SEC24B,FGFR2,TGFB3,FRZB	darkgreen	VSMC_M4
GO:0048515	0.57	0.58	7	106	spermatid differentiation	BP	1	AFF4,JAM3,BBS4,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0042742	0.57	0.58	7	109	defense response to bacterium	BP	1	ADGRB1,TF,ANXA3,LBP,PRKD1,SERPINE1,ADAMTS5	darkgreen	VSMC_M4
GO:0051648	0.57	0.55	11	154	vesicle localization	BP	1	DYNC1I1,SNAP91,ACTN4,PCLO,EXOC6,MYO1B,AP3B2,NLGN1,BBS4,CDH2,VAMP7	darkgreen	VSMC_M4
GO:0035773	0.57	0.63	4	58	insulin secretion involved in cellular response to glucose stimulus	BP	1	ABCG1,LRP5,ADCY5,HIF1A	darkgreen	VSMC_M4

GO:0008150	0.58	0.48	828	12183	biological_process	BP	1	MBP,ZNF516,DOK6,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,HSD17B6,COL23A1,SLC35D3,IFNGR1,CITED2,STX11,SHPRH,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,CDSN,RGS22,RNF19A,IPCEF1,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,FAM19A5,PKDREJ,TRPS1,RNASET2,SMOC2,CALHM5,SCUBE1,AFF4,GJA1,ZHX1,TRDN,TPD52L1,TATDN1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,AHCYL2,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,DCUN1D4,SGCB,RASL11B,VLDLR,UNC13B,RUSC2,SPATA6L,TPM2,CASD1,C2orf40,PPP1R9A,CD274,PON2,RIC1,PDK4,IL18R1,DYNC1I1,RNF149,CREB3,ZNF169,TMEM8B,REST,ICA1,RECK,ECM2,IGFBP7,ZAP70,FRMPD1,LMAN2L,SNX13,SLC2A1,C1orf50,TGFBR1,PREPL,LMBRD1,EDN2,SYT5,SLC17A5,ABCA1,ZNF331,KLHL7,TMEM245,PTPN3,DOP1A,SVEP1,SNAP91,PAPOLG,TBX18,PEX13,CHN2,MAP3K7,NT5C3A,CALD1,ANTXR1,DOCK4,KIDINS220,MDFIC,GPR63,PAPPA,TCAF1,PREP,FZD8,EPHB6,SESN1,JADE1,GYS1,METTL24,SLC37A3,MAP3K8,ITSN2,TUBE1,HIPK2,JRKL,GATA2,PLEKHB2,HS6ST1,ENKUR,THNSL1,APBB1IP,LIMS2,ABHD12,TMEM135,ZNF398,RCBTB2,ITM2B,PPP1R13L,LRCH1,SNRK,MRC1,TPT1,TESK2,TMCC1,ITGA8,TENM4,GGA3,NAA16,ELF1,ITGA9,INHBB,SMARCD3,USP6NL,PCDH9,MKRN2,GPR39,HRH1,EXOG,LMO7,ITIH5,ENTPD3,CD93,PFKFB3,NXPH2,BABAM2,FOSL2,ANKRD16,RALGAPA2,SYNGR2,LBH,STT3B,RNASE4,NDRG2,LIPT2,KCNE3,POLB,LMCD1,ARHGEF17,RAB2B,SALL2,THRB,PLCB4,ACTN4,TM9SF2,FMNL2,SATB1,ADAM9,TACC1,CRIM1,FGF14,SUMF1,FOXO1,TRPC4,RASSF2,SLC16A3,ATP2C1,COL4A1,COL4A2,ANKLE2,PC	darkgreen	VSMC_M4
GO:0099518	0.58	0.61	5	65	vesicle cytoskeletal trafficking	BP	1	DYNC1I1,ACTN4,MYO1B,AP3B2,VAMP7	darkgreen	VSMC_M4
GO:0045184	0.58	0.47	95	1395	establishment of protein localization	BP	1	SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,VLDLR,UNC13B,RIC1,REST,ICA1,FRMPD1,LMAN2L,SNX13,PREPL,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,GGA3,INHBB,USP6NL,RAB2B,ACTN4,ADAM9,ATP2C1,PCLO,ZDHHC2,ANKRD1,TRIM23,EXOC6,PAM,KIF13B,CLU,SCARB2,ABCC8,PTPN11,HERPUD1,ATG13,HNF4A,AKTIP,IFIT1,PDZD7,RAB29,ABCG1,PFKL,LRP5,ARRDC4,NPNT,ZMAT3,TM7SF3,TXNIP,SEC24B,ADCY5,LRP2,PTPN14,PRKD1,RAPGEF4,AP3B2,AKAP6,HIP1,HSPB1,ACHE,RDX,EXPH5,EMC1,LMTK2,NLGN1,RABEP1,HIF1A,AP1S3,FAF2,TGFB3,TOM1L1,BBS4,ATG4A,EVI5L,ABLIM3,SH3TC2,DAB2,FLNA,VAMP7,AHCYL1,SORT1,TBC1D13,LRSAM1,WLS,CDKN1A,GABARAPL2,BMP6,MAFA	darkgreen	VSMC_M4
GO:0045934	0.58	0.47	77	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	CITED2,MDM2,TRPS1,GJA1,ZHX1,EP300,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,CCNT1,HNF4A,NAB1,EDN1,ETS2,KDM5B,MXI1,TXNIP,YEATS2,WDTC1,FGFR2,TP53BP1,STRN3,ARID5B,ID3,EIF4A2,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,PPARGC1A,CHD3,FST,DAB2,TLE2,FLNA,TERF2IP,ZFP90,TBX20,ZNF425,ZNF175,CDKN1A,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1,DDIT4	darkgreen	VSMC_M4
GO:2000113	0.58	0.47	79	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	CITED2,MDM2,TRPS1,GJA1,ZHX1,EP300,DAPK1,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,HNF4A,NAB1,EDN1,ETS2,BACE2,KDM5B,RGS2,MXI1,TXNIP,SESN2,YEATS2,WDTC1,FGFR2,STRN3,ARID5B,ID3,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TMEM59,DAPK3,TLE2,FLNA,ZFP90,TBX20,ITM2C,ZNF425,ZNF175,CDKN1A,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0001906	0.58	0.60	5	78	cell killing	BP	1	LEP,LGALS9,VAMP7,CD59,ICAM1	darkgreen	VSMC_M4
GO:0008088	0.58	0.60	5	68	axo-dendritic transport	BP	1	APP,FEZ1,AP3B2,HSPB1,HIF1A	darkgreen	VSMC_M4
GO:0048593	0.58	0.57	7	96	camera-type eye morphogenesis	BP	1	CITED2,HIPK2,THRB,LRP5,HIF1A,BBS4,BCAR3	darkgreen	VSMC_M4
GO:0043412	0.58	0.45	209	3029	macromolecule modification	BP	1	TMX3,GDF11,BCL2,PIGN,RNF41,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,RNF19A,GRHL2,OXR1,ANGPT1,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,SH3RF3,DCUN1D4,VLDLR,PPP1R9A,PDK4,RNF149,REST,ZAP70,TGFBR1,ABCA1,KLHL7,PTPN3,MAP3K7,EPHB6,JADE1,MAP3K8,HIPK2,GATA2,ABHD12,SNRK,TESK2,NAA16,INHBB,MKRN2,LMO7,BABAM2,ANKRD16,STT3B,LIPT2,ADAM9,SUMF1,FOXO1,RASSF2,ANKLE2,QPCT,FLT3,TUSC3,ZDHHC2,MAP3K1,FXYD1,FBXO3,PTPRG,LATS2,HIPK3,PCGF5,MARCH5,TRIM23,RMND5A,NCK1,RNF141,PAM,SH3RF1,ST3GAL5,GRK7,OCLN,EXTL3,RNF34,CDKL2,CLU,APP,PDGFC,HECTD4,PTPN11,NEK4,CCNT1,HERPUD1,PTPN22,DPY19L4,GDF6,AKTIP,RCAN1,NGF,EDN1,N4BP1,SMARCAD1,MARCH6,KDM5B,DAPP1,RGS2,EYA2,NCOA3,UBE3B,LRP5,KCTD10,ARRDC4,PLCL1,HTR2B,MST1R,B3GNT7,GALNT3,B3GALNT2,PRKCA,AFAP1L2,TPST2,SESN2,YEATS2,P4HTM,CAMK2D,MYLK,WDTC1,INPP5F,MAN2A2,FGFR2,USP53,PTPN14,PRKD1,TRIM63,ZRANB1,PPEF1,DDR2,GPRC5A,MAP3K13,PCMTD2,LRP6,PRDX4,FAM129A,HSPB1,RIMKLB,P4HA1,EZH1,FUT11,USP11,ATG14,FBXL5,LMTK2,SPEG,MAEL,SIN3B,HIF1A,OPN3,PPARGC1A,PLOD1,DCAF5,PIGG,NEK9,TGFB3,CCNG1,MAGT1,SMAD6,TOM1L1,FAXDC2,GALNT10,USP32,NPTN,MRM1,NRK,ULK2,PAK3,MARCH2,DNAJC6,DAB2,PIGS,SKP2,PRKAA2,TMEM59,DAPK3,BGN,PNCK,FLNA,CSF1,PLCG2,EXTL2,TERF2IP,BCAR3,LRSAM1,CDC7,CYR61,ST6GALNAC3,SLC8A1,FBXO27,LOX,FBXO28,SRPK3,PIGK,CDKN1A,FGF9,PPM1E,CNTD2,HOPX,ICAM1,BMP6,DDIT4	darkgreen	VSMC_M4
GO:0035567	0.58	0.60	5	68	non-canonical Wnt signaling pathway	BP	1	MLLT3,FZD8,DACT1,DAB2,FRZB	darkgreen	VSMC_M4

GO:0051253	0.58	0.47	71	1032	negative regulation of RNA metabolic process	BP	1	CITED2,MDM2,TRPS1,ZHX1,EP300,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,CCNT1,HNF4A,NAB1,EDN1,ETS2,KDM5B,MXI1,TXNIP,YEATS2,WDTC1,FGFR2,STRN3,ARID5B,ID3,EIF4A2,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TLE2,FLNA,ZFP90,TBX20,ZNF425,ZNF175,ZNF572,NACC2,ZNF79,HOPX,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0090630	0.58	0.57	7	93	activation of GTPase activity	BP	1	USP6NL,RALGAPA2,SIPA1L1,EVI5L,TBC1D13,ARHGAP29,SYDE2	darkgreen	VSMC_M4
GO:0097696	0.58	0.57	7	105	receptor signaling pathway via STAT	BP	1	LEP,CYP1B1,FLT3,ADIPOR1,INPP5F,CRLF3,MIR99A	darkgreen	VSMC_M4
GO:0016573	0.59	0.55	9	131	histone acetylation	BP	1	EP300,BRD8,BRPF3,MAP3K7,JADE1,GATA2,NCOA3,YEATS2,PPARGC1A	darkgreen	VSMC_M4
GO:0001909	0.59	0.62	4	61	leukocyte mediated cytotoxicity	BP	1	LEP,LGALS9,VAMP7,ICAM1	darkgreen	VSMC_M4
GO:0002250	0.59	0.51	16	244	adaptive immune response	BP	1	C4A,CD274,IL18R1,ZAP70,MAP3K7,CLU,ADA,JAM3,CFI,CTSS,TP53BP1,RAPGEF4,C1RL,RORA,CCR6,ICAM1	darkgreen	VSMC_M4
GO:0043624	0.59	0.55	9	119	cellular protein complex disassembly	BP	1	SEMA5A,ACTN2,MID1,RDX,WDR1,MICAL3,DNAJC6,SPTAN1,DSTN	darkgreen	VSMC_M4
GO:0002221	0.59	0.55	9	134	pattern recognition receptor signaling pathway	BP	1	IRAK3,DDX58,MAP3K7,LBP,PTPN22,CTSS,EPG5,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0048469	0.59	0.56	8	116	cell maturation	BP	1	BCL2,GATA2,APP,MAP3K13,HIF1A,PCSK4,CDKN1A,CCR6	darkgreen	VSMC_M4
GO:0072698	0.59	0.61	4	52	protein localization to microtubule cytoskeleton	BP	1	MID1,BBS4,MAPRE2,GAS2L2	darkgreen	VSMC_M4
GO:0046854	0.59	0.61	4	54	phosphatidylinositol phosphate biosynthetic process	BP	1	PIP5K1B,PI4KB,OCRL,PIK3C2A	darkgreen	VSMC_M4
GO:0009117	0.60	0.49	24	381	nucleotide metabolic process	BP	1	EP300,PDK4,NT5C3A,PTH,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,AK7,PRKAA2,ADCY9,AK5,RFK,DDIT4	darkgreen	VSMC_M4
GO:0050871	0.60	0.61	4	61	positive regulation of B cell activation	BP	1	BCL2,ADA,TP53BP1,CDKN1A	darkgreen	VSMC_M4
GO:0016042	0.60	0.51	14	225	lipid catabolic process	BP	1	HSD17B6,LEP,PEX13,ABHD12,PLCB4,CYP1B1,PLA2G4F,LPL,SESN2,INPP5F,CYP19A1,PLCG2,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0030326	0.60	0.56	7	96	embryonic limb morphogenesis	BP	1	GRHL2,RECK,CHD7,LRP5,LNPK,CACNA1C,AFF3	darkgreen	VSMC_M4
GO:0035113	0.60	0.56	7	96	embryonic appendage morphogenesis	BP	1	GRHL2,RECK,CHD7,LRP5,LNPK,CACNA1C,AFF3	darkgreen	VSMC_M4
GO:0002705	0.60	0.58	5	76	positive regulation of leukocyte mediated immunity	BP	1	DDX58,IL18R1,MAP3K7,TP53BP1,PLCG2	darkgreen	VSMC_M4
GO:0099173	0.60	0.53	10	137	postsynapse organization	BP	1	PPP1R9A,ZDHHC2,TANC1,LGMN,ZNF365,NLGN1,ACTN1,SIPA1L1,CDH2,PAK3	darkgreen	VSMC_M4
GO:0006635	0.60	0.60	4	64	fatty acid beta-oxidation	BP	1	LEP,SESN2,ACAD11,SCP2	darkgreen	VSMC_M4
GO:1903706	0.60	0.50	17	258	regulation of hemopoiesis	BP	1	ZAP70,GATA2,RASSF2,TMEM178A,SH3RF1,MEIS2,TMEM64,ADA,PRKCA,P4HTM,HIF1A,FAXDC2,LGALS9,CSF1,VNN1,CD83,LOX	darkgreen	VSMC_M4
GO:0006357	0.60	0.44	124	1784	regulation of transcription by RNA polymerase II	BP	1	ZNF516,CITED2,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,LEP,WFS1,DDX58,CREB3,ZNF169,REST,ZNF331,TBX18,HIPK2,GATA2,ZNF398,PPP1R13L,ELF1,SMARCD3,LMO7,FOSL2,LMCD1,SALL2,THRB,SATB1,FOXO1,EBF4,MIER3,NCOR2,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,PAM,ATOH8,TCF7L1,WWC2,TEAD1,PTH,MED12L,MEIS2,APP,CCNT1,JMY,CHD6,HNF4A,RBL2,EDN1,ETS2,MXI1,NCOA3,LRP5,NPNT,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,WDTC1,FGFR2,TP53BP1,PRKD1,ARID5B,ITGA6,ATF6,NPAS3,ID3,LRP6,ZNF280B,CUX1,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,SMARCA1,CDH13,ZNF821,LMO4,CYR61,ZFP90,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0031327	0.60	0.45	82	1198	negative regulation of cellular biosynthetic process	BP	1	CITED2,MDM2,TRPS1,GJA1,ZHX1,EP300,DAPK1,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,HNF4A,NAB1,EDN1,ETS2,BACE2,KDM5B,RGS2,MXI1,TXNIP,SESN2,YEATS2,WDTC1,FGFR2,STRN3,ARID5B,ID3,EIF4A2,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,OPN3,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TMEM59,DAPK3,TLE2,FLNA,ZFP90,TBX20,ITM2C,ZNF425,ZNF175,CDKN1A,ZNF572,NACC2,ZNF79,HOPX,ORMDL3,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0051453	0.60	0.60	4	58	regulation of intracellular pH	BP	1	BCL2,CLCN3,ATP6AP2,ATP6V0E1	darkgreen	VSMC_M4
GO:0016358	0.60	0.50	15	204	dendrite development	BP	1	GRIP1,VLDLR,PPP1R9A,KIDINS220,CPEB3,APP,PREX1,ZNF365,CUX1,NLGN1,SIPA1L1,BBS4,PAK3,SDC2,PRKG1	darkgreen	VSMC_M4
GO:0035725	0.60	0.53	9	120	sodium ion transmembrane transport	BP	1	PTPN3,ACTN4,FGF14,FXYD1,SCN8A,CAMK2D,SCNN1D,HCN2,SLC8A1	darkgreen	VSMC_M4
GO:0032922	0.60	0.60	4	55	circadian regulation of gene expression	BP	1	RBM4B,ID3,PPARGC1A,RORA	darkgreen	VSMC_M4
GO:0005977	0.60	0.60	4	57	glycogen metabolic process	BP	1	GYS1,PTH,GYG1,GYG2	darkgreen	VSMC_M4
GO:0048525	0.61	0.60	4	61	negative regulation of viral process	BP	1	PTX3,IFIT1,N4BP1,MX1	darkgreen	VSMC_M4
GO:0018393	0.61	0.53	9	134	internal peptidyl-lysine acetylation	BP	1	EP300,BRD8,BRPF3,MAP3K7,JADE1,GATA2,NCOA3,YEATS2,PPARGC1A	darkgreen	VSMC_M4
GO:1903131	0.61	0.49	20	297	mononuclear cell differentiation	BP	1	BCL2,EP300,LEP,IL18R1,ZAP70,FLT3,CHD7,SH3RF1,BLNK,PTPN22,ADA,PREX1,RORA,LGALS9,CSF1,PLCG2,VCAM1,VNN1,CD83,CCR6	darkgreen	VSMC_M4
GO:0032612	0.61	0.59	4	62	interleukin-1 production	BP	1	APP,LPL,HSPB1,LGALS9	darkgreen	VSMC_M4
GO:0032652	0.61	0.59	4	62	regulation of interleukin-1 production	BP	1	APP,LPL,HSPB1,LGALS9	darkgreen	VSMC_M4
GO:1903827	0.61	0.46	31	454	regulation of cellular protein localization	BP	1	SLC35D3,MDM2,ANGPT1,LEP,MDFIC,TCAF1,ATP2C1,ZDHHC2,RIC3,LATS2,PTPN11,ATG13,RAB29,RIPOR2,ACTN2,SESN2,PTPN14,PRKD1,RDX,GNAI1,NUMB,NPTN,CDH2,ABLIM3,SH3TC2,DAB2,PRKAA2,TMEM59,FLNA,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0050821	0.61	0.52	10	154	protein stabilization	BP	1	EP300,GNAQ,WFS1,NAA16,RASSF2,CLU,HIP1,CRYAB,PPARGC1A,FLNA	darkgreen	VSMC_M4
GO:0021510	0.61	0.57	5	70	spinal cord development	BP	1	VLDLR,GATA2,ZC4H2,LMO4,TBX20	darkgreen	VSMC_M4
GO:0032418	0.61	0.59	4	62	lysosome localization	BP	1	GATA2,ADGRE2,LGALS9,VAMP7	darkgreen	VSMC_M4

GO:0072330	0.61	0.52	9	144	monocarboxylic acid biosynthetic process	BP	1	PDK4,EDN2,EDN1,PLA2G4F,LPL,WDTC1,PRKAA2,SLC27A5,SCP2	darkgreen	VSMC_M4
GO:0035249	0.62	0.59	4	57	synaptic transmission, glutamatergic	BP	1	UNC13B,CLCN3,NLGN1,CDH2	darkgreen	VSMC_M4
GO:0006073	0.62	0.59	4	58	cellular glucan metabolic process	BP	1	GYS1,PTH,GYG1,GYG2	darkgreen	VSMC_M4
GO:0044042	0.62	0.59	4	58	glucan metabolic process	BP	1	GYS1,PTH,GYG1,GYG2	darkgreen	VSMC_M4
GO:0031644	0.62	0.53	7	100	regulation of nervous system process	BP	1	UNC13B,TENM4,WASF3,APP,EDN1,SLC25A12,NLGN1	darkgreen	VSMC_M4
GO:1901216	0.62	0.56	5	78	positive regulation of neuron death	BP	1	REST,CLU,CTSZ,PAK3,DDIT4	darkgreen	VSMC_M4
GO:0006475	0.62	0.51	9	136	internal protein amino acid acetylation	BP	1	EP300,BRD8,BRPF3,MAP3K7,JADE1,GATA2,NCOA3,YEATS2,PPARGC1A	darkgreen	VSMC_M4
GO:0009890	0.62	0.42	83	1222	negative regulation of biosynthetic process	BP	1	CITED2,MDM2,TRPS1,GJA1,ZHX1,EP300,DAPK1,TLE4,LEP,WFS1,ZNF169,REST,TBX18,MDFIC,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,LBH,LMCD1,THRB,SATB1,FOXO1,MIER3,NCOR2,ZC3H6,ANKRD1,CPEB3,NCK1,ATOH8,WWC2,MEIS2,HNF4A,NAB1,EDN1,ETS2,BACE2,KDM5B,RGS2,MXI1,TXNIP,SESN2,YEATS2,CFLAR,WDTC1,FGFR2,STRN3,ARID5B,ID3,EIF4A2,CUX1,CRYAB,EZH1,DACT1,MAEL,SIN3B,OPN3,ZBTB18,APBB2,ZBTB4,CHD3,FST,DAB2,TMEM59,DAPK3,TLE2,FLNA,ZFP90,TBX20,ITM2C,ZNF425,ZNF175,CDKN1A,ZNF572,NACC2,ZNF79,HOPX,ORMDL3,YAP1,HKR1,BMP6,NPAS1	darkgreen	VSMC_M4
GO:0009260	0.62	0.51	9	149	ribonucleotide biosynthetic process	BP	1	PDK4,ADCY6,ADCY5,SLC25A12,PPARGC1A,NPPB,ADCY9,AK5,RFK	darkgreen	VSMC_M4
GO:0031929	0.63	0.53	7	105	TOR signaling	BP	1	LEP,SESN1,SESN2,CASTOR1,HIF1A,PRKAA2,DDIT4	darkgreen	VSMC_M4
GO:1901988	0.63	0.49	13	201	negative regulation of cell cycle phase transition	BP	1	BCL2,MDM2,CDKN2B,FAM122A,JADE1,BABAM2,PTPN11,RBL2,TP53BP1,DACT1,APBB2,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0006164	0.63	0.51	9	149	purine nucleotide biosynthetic process	BP	1	PDK4,ADCY6,ADA,ADCY5,SLC25A12,PPARGC1A,NPPB,ADCY9,AK5	darkgreen	VSMC_M4
GO:0033043	0.63	0.42	66	950	regulation of organelle organization	BP	1	LAPTM4B,EP300,LIMCH1,KANK1,PPP1R9A,TGFBR1,TMEM135,USP6NL,CDC42EP3,WASF3,MARCH5,NCK1,PAM,SLC25A4,OCLN,G3BP2,CLU,SCARB2,JMY,EDN1,JAM3,CD47,SEMA5A,ABCG1,PDE4DIP,ACTN2,LRP5,FEZ1,PREX1,MID1,SYNPO2,F11R,PLXNB1,LNPK,RDX,SYNPO2L,TNFSF10,WDR1,HIF1A,GNAI1,PPARGC1A,CALCOCO2,TGFB3,TOM1L1,BBS4,MAPRE2,SYNPO,CDH2,PAK3,GAS2L2,EVI5L,RHOT1,ARHGAP28,PATJ,PRKAA2,DAPK3,FLNA,SPTAN1,TERF2IP,LRSAM1,NEXN,BNIP3,PPM1E,DSTN,ICAM1,YAP1	darkgreen	VSMC_M4
GO:2000060	0.63	0.53	6	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,CLU,HERPUD1,DAB2	darkgreen	VSMC_M4
GO:0008361	0.63	0.49	11	157	regulation of cell size	BP	1	SEMA3C,CLCN3,NGF,EDN1,SEMA5A,SHTN1,WDTC1,MAP3K13,RDX,ULK2,TMEM123	darkgreen	VSMC_M4
GO:0045930	0.63	0.48	12	186	negative regulation of mitotic cell cycle	BP	1	BCL2,MDM2,CDKN2B,FAM122A,PTPN3,JADE1,BABAM2,RBL2,DACT1,TOM1L1,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0048708	0.63	0.57	4	60	astrocyte differentiation	BP	1	IFNGR1,APP,PTPN11,BACE2	darkgreen	VSMC_M4
GO:0055086	0.63	0.44	27	439	nucleobase-containing small molecule metabolic process	BP	1	EP300,PDK4,NT5C3A,ENTPD3,PTH,ENTPD1,APP,ADCY6,ADA,NT5C2,PFKL,TPST2,ADCY5,SLC25A12,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,RORA,AK7,PRKAA2,ADCY9,EXTL2,AK5,RFK,DDIT4	darkgreen	VSMC_M4
GO:0001655	0.63	0.46	20	283	urogenital system development	BP	1	BCL2,ANGPT1,WFS1,TGFBR1,TBX18,GATA2,ITGA8,COL4A1,GDF6,COL4A4,NPNT,NID1,LRP2,CFLAR,FGFR2,ARID5B,ID3,SMAD6,YAP1,BMP6	darkgreen	VSMC_M4
GO:0031123	0.63	0.53	6	94	RNA 3'-end processing	BP	1	PAPOLG,CPEB3,APP,CCNT1,INTS6L,AHCYL1	darkgreen	VSMC_M4
GO:0007005	0.63	0.44	26	436	mitochondrion organization	BP	1	BCL2,SOD2,EP300,TMEM135,MARCH5,MAP1LC3A,SLC25A4,CLU,ATG13,RAB29,EYA2,FEZ1,SESN2,GABARAPL1,ATG14,TNFSF10,HIF1A,PPARGC1A,TTC19,ULK2,ABLIM3,RHOT1,ATCAY,MAP1LC3B2,BNIP3,GABARAPL2	darkgreen	VSMC_M4
GO:0098930	0.64	0.57	4	58	axonal transport	BP	1	FEZ1,AP3B2,HSPB1,HIF1A	darkgreen	VSMC_M4
GO:0048477	0.64	0.56	4	62	oogenesis	BP	1	BCL2,INHBB,PTX3,MARF1	darkgreen	VSMC_M4
GO:0009798	0.64	0.56	4	59	axis specification	BP	1	CITED2,ETS2,SMAD6,WLS	darkgreen	VSMC_M4
GO:0061515	0.64	0.56	4	59	myeloid cell development	BP	1	CITED2,EP300,APP,PTPN11	darkgreen	VSMC_M4
GO:0060998	0.64	0.56	4	54	regulation of dendritic spine development	BP	1	PPP1R9A,CPEB3,NLGN1,PAK3	darkgreen	VSMC_M4
GO:0099565	0.64	0.54	5	74	chemical synaptic transmission, postsynaptic	BP	1	UNC13B,PPP1R9A,APP,INSYN2,NLGN1	darkgreen	VSMC_M4
GO:0048813	0.64	0.49	9	126	dendrite morphogenesis	BP	1	VLDLR,PPP1R9A,KIDINS220,ZNF365,CUX1,NLGN1,SIPA1L1,PAK3,SDC2	darkgreen	VSMC_M4
GO:0009062	0.64	0.54	5	86	fatty acid catabolic process	BP	1	LEP,PEX13,SESN2,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0030148	0.64	0.54	5	83	sphingolipid biosynthetic process	BP	1	ST3GAL5,PRKD1,CYR61,ST6GALNAC3,ORMDL3	darkgreen	VSMC_M4
GO:1990830	0.64	0.54	5	77	cellular response to leukemia inhibitory factor	BP	1	TLE4,KDM5B,ARID5B,EIF4A2,ICAM1	darkgreen	VSMC_M4
GO:0045069	0.64	0.56	4	62	regulation of viral genome replication	BP	1	BCL2,IFIT1,N4BP1,MX1	darkgreen	VSMC_M4
GO:2000278	0.64	0.52	6	95	regulation of DNA biosynthetic process	BP	1	GRHL2,SMOC2,GJA1,ANKRD1,PAK3,CDKN1A	darkgreen	VSMC_M4
GO:0042303	0.65	0.53	5	75	molting cycle	BP	1	BCL2,PPP1R13L,FGFR2,FST,EDA	darkgreen	VSMC_M4
GO:0042633	0.65	0.53	5	75	hair cycle	BP	1	BCL2,PPP1R13L,FGFR2,FST,EDA	darkgreen	VSMC_M4
GO:0099175	0.65	0.53	5	73	regulation of postsynapse organization	BP	1	PPP1R9A,NLGN1,SIPA1L1,CDH2,PAK3	darkgreen	VSMC_M4
GO:0009411	0.65	0.49	8	127	response to UV	BP	1	BCL2,MDM2,EP300,N4BP1,MMP1,OPN3,CDKN1A,MFAP4	darkgreen	VSMC_M4
GO:0043534	0.65	0.50	7	108	blood vessel endothelial cell migration	BP	1	ANGPT1,GATA2,PRKCA,PRKD1,HSPB1,HIF1A,PIK3C2A	darkgreen	VSMC_M4
GO:0050680	0.65	0.50	7	108	negative regulation of epithelial cell proliferation	BP	1	GJA1,CDKN2B,TGFBR1,LIMS2,HPN,ATOH8,FGFR2	darkgreen	VSMC_M4
GO:0050776	0.65	0.42	35	538	regulation of immune response	BP	1	BCL2,IRAK3,C4A,EP300,LEP,DDX58,CD274,IL18R1,ZAP70,MAP3K7,GATA2,MAP3K1,CLU,BLNK,PTPN11,LBP,PTPN22,ADA,IFIT1,CD47,N4BP1,RAB29,CFI,CTSS,TP53BP1,C1RL,ADGRE2,EPG5,PAK3,LGALS9,VAMP7,PLCG2,TLR1,CD59,MFAP4	darkgreen	VSMC_M4
GO:0010557	0.65	0.39	98	1433	positive regulation of macromolecule biosynthetic process	BP	1	ZNF516,CITED2,GRHL2,ABRA,SMOC2,EP300,MRTFA,BRD8,BRPF3,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ATOH8,TEAD1,PTH,MED12L,MEIS2,APP,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,EDN1,ETS2,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,SESN2,NGRN,FGFR2,TP53BP1,PRKD1,NCSTN,ARID5B,ITGA6,ATF6,NPAS3,LRP6,FAM129A,ZNF445,EZH1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,PAK3,ABLIM3,CRLF3,DAB2,SMARCA1,CTIF,CDH13,BCAR3,CDC7,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,YAP1,BMP6,MAFA	darkgreen	VSMC_M4

GO:1990823	0.65	0.53	5	78	response to leukemia inhibitory factor	BP	1	TLE4,KDM5B,ARID5B,EIF4A2,ICAM1	darkgreen	VSMC_M4
GO:0022412	0.65	0.45	16	247	cellular process involved in reproduction in multicellular organism	BP	1	BCL2,AFF4,TGFBR1,INHBB,PTX3,JAM3,PRDX4,MAEL,TEX11,SLIT3,BBS4,MARF1,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0042180	0.65	0.48	9	150	cellular ketone metabolic process	BP	1	HSD17B6,PDK4,REST,NCOR2,ADM,WDTC1,PPARGC1A,ATCAY,BMP6	darkgreen	VSMC_M4
GO:0002764	0.65	0.44	18	278	immune response-regulating signaling pathway	BP	1	BCL2,IRAK3,EP300,DDX58,ZAP70,MAP3K7,MAP3K1,BLNK,LBP,PTPN22,ADA,CD47,RAB29,CTSS,EPG5,PAK3,PLCG2,TLR1	darkgreen	VSMC_M4
GO:0021675	0.65	0.55	4	59	nerve development	BP	1	CITED2,CHD7,NGF,VCAM1	darkgreen	VSMC_M4
GO:0098754	0.65	0.52	5	90	detoxification	BP	1	IPCEF1,SOD2,SESN1,SESN2,PRDX4	darkgreen	VSMC_M4
GO:0007018	0.65	0.44	19	283	microtubule-based movement	BP	1	DYNC1I1,ENKUR,DNHD1,KIF13B,APP,DNAH7,FEZ1,SUN1,DYNC1I2,AP3B2,HSPB1,HIF1A,IFT43,KIAA0556,BBS4,GAS2L2,RHOT1,VAMP7,CCR6	darkgreen	VSMC_M4
GO:0001539	0.66	0.52	5	79	cilium or flagellum-dependent cell motility	BP	1	ENKUR,DNAH7,BBS4,GAS2L2,CCR6	darkgreen	VSMC_M4
GO:0060285	0.66	0.52	5	79	cilium-dependent cell motility	BP	1	ENKUR,DNAH7,BBS4,GAS2L2,CCR6	darkgreen	VSMC_M4
GO:1901983	0.66	0.54	4	63	regulation of protein acetylation	BP	1	GATA2,PPARGC1A,PRKAA2,TERF2IP	darkgreen	VSMC_M4
GO:0090277	0.66	0.54	4	65	positive regulation of peptide hormone secretion	BP	1	GJA1,ABCG1,TM7SF3,HIF1A	darkgreen	VSMC_M4
GO:0001942	0.66	0.54	4	61	hair follicle development	BP	1	BCL2,FGFR2,FST,EDA	darkgreen	VSMC_M4
GO:0031396	0.66	0.46	11	180	regulation of protein ubiquitination	BP	1	SASH1,ANGPT1,ADGRB1,WFS1,DCUN1D4,TGFBR1,HERPUD1,PTPN22,N4BP1,ARRDC4,SKP2	darkgreen	VSMC_M4
GO:0043550	0.66	0.54	4	58	regulation of lipid kinase activity	BP	1	FLT3,RBL2,PRKD1,ATG14	darkgreen	VSMC_M4
GO:0006821	0.66	0.54	4	60	chloride transport	BP	1	FXYD1,CLCN3,SLC26A7,ANO5	darkgreen	VSMC_M4
GO:0021766	0.66	0.54	4	59	hippocampus development	BP	1	ANXA3,FEZ1,EZH1,BBS4	darkgreen	VSMC_M4
GO:0001701	0.66	0.42	21	314	in utero embryonic development	BP	1	CITED2,GRHL2,ANGPT1,TGFBR1,KIDINS220,GATA2,POLB,CHD7,ADM,ADA,EDN1,WDTC1,FGFR2,HIF1A,TGFB3,ADCY9,CMIP,CYR61,MAFF,HOPX,YAP1	darkgreen	VSMC_M4
GO:0002793	0.66	0.53	4	66	positive regulation of peptide secretion	BP	1	GJA1,ABCG1,TM7SF3,HIF1A	darkgreen	VSMC_M4
GO:0030838	0.66	0.51	5	82	positive regulation of actin filament polymerization	BP	1	CDC42EP3,WASF3,NCK1,JMY,ICAM1	darkgreen	VSMC_M4
GO:0009152	0.67	0.47	8	137	purine ribonucleotide biosynthetic process	BP	1	PDK4,ADCY6,ADCY5,SLC25A12,PPARGC1A,NPPB,ADCY9,AK5	darkgreen	VSMC_M4
GO:0007600	0.67	0.42	21	320	sensory perception	BP	1	MBP,WFS1,THRB,HPN,CHD7,GRK7,SCARB2,PDZD7,EDN1,RIPOR2,ABLIM1,LRP2,USP53,PPEF1,ATF6,CRYGS,WDR1,BBS4,SCNN1D,ABCA4,ICAM1	darkgreen	VSMC_M4
GO:0021761	0.67	0.51	5	75	limbic system development	BP	1	ANXA3,FEZ1,FGFR2,EZH1,BBS4	darkgreen	VSMC_M4
GO:1903506	0.67	0.36	165	2412	regulation of nucleic acid-templated transcription	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0045580	0.67	0.49	6	98	regulation of T cell differentiation	BP	1	ZAP70,SH3RF1,ADA,LGALS9,VNN1,CD83	darkgreen	VSMC_M4
GO:0048144	0.67	0.53	4	66	fibroblast proliferation	BP	1	FOSL2,PDGFC,DDR2,CDKN1A	darkgreen	VSMC_M4
GO:0048145	0.67	0.53	4	66	regulation of fibroblast proliferation	BP	1	FOSL2,PDGFC,DDR2,CDKN1A	darkgreen	VSMC_M4
GO:0050773	0.67	0.49	6	87	regulation of dendrite development	BP	1	VLDLR,PREX1,CUX1,SIPA1L1,PAK3,SDC2	darkgreen	VSMC_M4
GO:0060996	0.67	0.49	6	87	dendritic spine development	BP	1	PPP1R9A,CPEB3,ZNF365,NLGN1,SIPA1L1,PAK3	darkgreen	VSMC_M4
GO:0019915	0.67	0.52	4	65	lipid storage	BP	1	LEP,ABCA1,LPL,ABCG1	darkgreen	VSMC_M4
GO:0046390	0.67	0.46	9	156	ribose phosphate biosynthetic process	BP	1	PDK4,ADCY6,ADCY5,SLC25A12,PPARGC1A,NPPB,ADCY9,AK5,RFK	darkgreen	VSMC_M4
GO:0032271	0.67	0.43	13	199	regulation of protein polymerization	BP	1	KANK1,PPP1R9A,CDC42EP3,WASF3,NCK1,OCLN,JMY,PREX1,RDX,PAK3,ARHGAP28,SPTAN1,ICAM1	darkgreen	VSMC_M4
GO:0044403	0.67	0.43	13	206	biological process involved in symbiotic interaction	BP	1	EP300,REST,MRC1,INHBB,HPN,SCARB2,PTX3,CCNT1,IFIT1,F11R,ULK2,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0021953	0.67	0.46	8	116	central nervous system neuron differentiation	BP	1	LEP,EPHB6,GATA2,FGFR2,ZC4H2,RORA,LMO4,TBX20	darkgreen	VSMC_M4
GO:0048814	0.68	0.52	4	57	regulation of dendrite morphogenesis	BP	1	CUX1,SIPA1L1,PAK3,SDC2	darkgreen	VSMC_M4
GO:1902105	0.68	0.44	12	193	regulation of leukocyte differentiation	BP	1	ZAP70,GATA2,RASSF2,TMEM178A,SH3RF1,TMEM64,ADA,PRKCA,LGALS9,CSF1,VNN1,CD83	darkgreen	VSMC_M4
GO:2000027	0.68	0.47	7	108	regulation of animal organ morphogenesis	BP	1	CITED2,MLLT3,EDN1,SEC24B,DACT1,DAB2,CSF1	darkgreen	VSMC_M4
GO:2001141	0.68	0.36	165	2416	regulation of RNA biosynthetic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4

GO:1903829	0.68	0.42	16	241	positive regulation of cellular protein localization	BP	1	LEP,TCAF1,ATP2C1,ZDHHC2,RIC3,ATG13,SESN2,PRKD1,RDX,GNAI1,NPTN,ABLIM3,PRKAA2,FLNA,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:0001824	0.68	0.49	5	86	blastocyst development	BP	1	CITED2,TGFBR1,ADA,HOPX,YAP1	darkgreen	VSMC_M4
GO:0007281	0.68	0.44	11	177	germ cell development	BP	1	BCL2,AFF4,INHBB,PTX3,JAM3,BBS4,MARF1,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0071902	0.68	0.44	11	170	positive regulation of protein serine/threonine kinase activity	BP	1	SASH1,TPD52L1,MAP3K7,ADAM9,FLT3,PDGFC,CCNT1,EDN1,HTR2B,MST1R,MAP3K13	darkgreen	VSMC_M4
GO:0007259	0.68	0.48	6	98	receptor signaling pathway via JAK-STAT	BP	1	LEP,CYP1B1,FLT3,ADIPOR1,INPP5F,CRLF3	darkgreen	VSMC_M4
GO:0006814	0.68	0.44	11	161	sodium ion transport	BP	1	PTPN3,KCNE3,ACTN4,FGF14,FXYD1,SCN8A,CAMK2D,SCNN1D,HCN2,AHCYL1,SLC8A1	darkgreen	VSMC_M4
GO:0050905	0.68	0.47	7	103	neuromuscular process	BP	1	HIPK2,APP,ADCY5,RBFOX1,CCDC78,ITPR1,NPAS1	darkgreen	VSMC_M4
GO:0022404	0.68	0.51	4	63	molting cycle process	BP	1	BCL2,FGFR2,FST,EDA	darkgreen	VSMC_M4
GO:0022405	0.68	0.51	4	63	hair cycle process	BP	1	BCL2,FGFR2,FST,EDA	darkgreen	VSMC_M4
GO:0042113	0.68	0.43	12	193	B cell activation	BP	1	BCL2,EP300,ZAP70,FLT3,CD180,BLNK,ADA,TP53BP1,PLCG2,VCAM1,CDKN1A,CCR6	darkgreen	VSMC_M4
GO:0030641	0.68	0.51	4	64	regulation of cellular pH	BP	1	BCL2,CLCN3,ATP6AP2,ATP6V0E1	darkgreen	VSMC_M4
GO:0072522	0.68	0.45	9	157	purine-containing compound biosynthetic process	BP	1	PDK4,ADCY6,ADA,ADCY5,SLC25A12,PPARGC1A,NPPB,ADCY9,AK5	darkgreen	VSMC_M4
GO:0045089	0.68	0.49	5	83	positive regulation of innate immune response	BP	1	EP300,MAP3K7,LBP,PAK3,PLCG2	darkgreen	VSMC_M4
GO:1901564	0.68	0.34	318	4789	organonitrogen compound metabolic process	BP	1	MBP,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,IFNGR1,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,OXR1,ANGPT1,C4A,GJA1,TPD52L1,EP300,BRD8,ADGRB1,DAPK1,BRPF3,SH3GL2,GNAQ,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,SH3RF3,DCUN1D4,VLDLR,C2orf40,PPP1R9A,RIC1,PDK4,RNF149,REST,RECK,ZAP70,TGFBR1,PREPL,LMBRD1,ABCA1,KLHL7,PTPN3,MAP3K7,NT5C3A,ANTXR1,PAPPA,PREP,EPHB6,JADE1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ITM2B,SNRK,TESK2,GGA3,NAA16,INHBB,MKRN2,LMO7,ITIH5,BABAM2,STT3B,LIPT2,ADAM9,CRIM1,SUMF1,FOXO1,RASSF2,ANKLE2,QPCT,FLT3,TUSC3,ZDHHC2,MAP3K1,FXYD1,HPN,FBXO3,PTPRG,LATS2,CHPT1,HIPK3,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,RNF141,PAM,SH3RF1,ST3GAL5,GRK7,OCLN,CHST2,PTH,EXTL3,RNF34,CDKL2,CLU,APP,ATXN2,PDGFC,HECTD4,PTPN11,PTX3,ADCY6,NEK4,CCNT1,HERPUD1,PROS1,PTPN22,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,CPQ,ADA,AKTIP,RCAN1,NGF,EDN1,N4BP1,SMARCAD1,MARCH6,BACE2,ABCG1,NT5C2,TMPRSS7,KDM5B,TARSL2,DAPP1,RGS2,EYA2,NCOA3,PFKL,UBE3B,LRP5,KCTD10,ARRDC4,PLCL1,HTR2B,MST1R,LGMN,B3GNT7,SERINC2,AMZ2,GALNT3,B3GALNT2,PRKCA,AFAP1L2,CFI,TPST2,SESN2,ARV1,YEATS2,P4HTM,CAMK2D,ADCY5,CTSS,NGRN,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,MAN2A2,NDST3,FGFR2,RBM4B,SYNPO2,CTSF,USP53,PTPN14,PRKD1,NCSTN,TRIM63,CHST15,ZRANB1,SLC25A12,PPEF1,DDR2,GPRC5A,MAP3K13,PCMTD2,LRP6,HIP1,PRDX4,FAM129A,HSPB1,EIF4A2,RIMKLB,SERPINE1,ACHE,CRYAB,C1RL,ATP6AP2,PAPPA2,PDE1A,RDX,MAOA,MAOB,ENO2,P4HA1,AOC3,SECISBP2L,EZH1,FUT	darkgreen	VSMC_M4
GO:0021549	0.68	0.49	5	77	cerebellum development	BP	1	PTPN11,NCSTN,ZNF365,PPARGC1A,RORA	darkgreen	VSMC_M4
GO:0032508	0.69	0.49	5	75	DNA duplex unwinding	BP	1	CHD7,CHD6,SMARCAD1,CHD3,HFM1	darkgreen	VSMC_M4
GO:0034612	0.69	0.43	11	181	response to tumor necrosis factor	BP	1	ACTN4,ADAM9,ANKRD1,OCLN,EDN1,NPNT,PPARGC1A,RORA,VCAM1,AFF3,ICAM1	darkgreen	VSMC_M4
GO:0060294	0.69	0.51	4	68	cilium movement involved in cell motility	BP	1	ENKUR,BBS4,GAS2L2,CCR6	darkgreen	VSMC_M4
GO:0032102	0.69	0.41	17	266	negative regulation of response to external stimulus	BP	1	IRAK3,FAM19A5,GJA1,LEP,SEMA3C,ABCC8,PROS1,ADA,EDN1,SEMA5A,INPP5F,SERPINE1,RORA,BBS4,MMP28,LGALS9,PRKG1	darkgreen	VSMC_M4
GO:0006606	0.69	0.45	8	129	protein import into nucleus	BP	1	ABRA,ANGPT1,LEP,MDFIC,TXNIP,PRKD1,FLNA,CDKN1A	darkgreen	VSMC_M4
GO:0003333	0.69	0.50	4	66	amino acid transmembrane transport	BP	1	RGS2,SLC25A12,SLC43A2,LRRC8C	darkgreen	VSMC_M4
GO:0001822	0.69	0.40	17	248	kidney development	BP	1	BCL2,ANGPT1,WFS1,TGFBR1,ITGA8,GDF6,COL4A4,NPNT,NID1,LRP2,CFLAR,FGFR2,ARID5B,ID3,SMAD6,YAP1,BMP6	darkgreen	VSMC_M4
GO:1901800	0.69	0.46	6	104	positive regulation of proteasomal protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,CLU,HERPUD1,DAB2	darkgreen	VSMC_M4
GO:0033554	0.69	0.35	103	1561	cellular response to stress	BP	1	BCL2,CITED2,SHPRH,SASH1,MDM2,SOD2,OXR1,TPD52L1,EP300,DAPK1,LEP,CDKN2B,WFS1,SH3RF3,C2orf40,PDK4,CREB3,REST,SLC2A1,MAP3K7,MDFIC,SESN1,HIPK2,TPT1,INHBB,BABAM2,STT3B,POLB,FOXO1,RASSF2,CYP1B1,HIPK3,ANKRD1,NCK1,ADM,MAP1LC3A,SH3RF1,CLU,APP,PTPN11,NEK4,HERPUD1,JMY,CHD6,PTPN22,CHAC1,GDF6,SERINC3,EDN1,JAM3,SMARCAD1,MARCH6,EYA2,ZMAT3,TM7SF3,MID1,SESN2,MYLK,CFLAR,INPP5F,TP53BP1,PRKD1,ZNF365,ATF6,MAP3K13,PRDX4,GABARAPL1,FAM129A,HSPB1,CRYAB,NBR1,ATG14,DACT1,JKAMP,MAEL,HIF1A,ZBTB4,ZFYVE26,PPARGC1A,FAF2,RORA,LGALS9,MARF1,PRKAA2,FLNA,MAP1LC3B2,MBTPS1,TERF2IP,CDC7,LRRC8C,ITPR1,VNN1,SLC8A1,FBXO27,BNIP3,EXO5,CDKN1A,NACC2,GABARAPL2,ICAM1,STC2,YAP1,DDIT4	darkgreen	VSMC_M4
GO:2000241	0.70	0.46	6	105	regulation of reproductive process	BP	1	CITED2,GJA1,INHBB,ADA,PRDX4,CCR6	darkgreen	VSMC_M4
GO:0044089	0.70	0.37	30	441	positive regulation of cellular component biogenesis	BP	1	ADGRB1,LIMCH1,UNC13B,TGFBR1,ABCA1,CDC42EP3,WASF3,NCK1,OCLN,G3BP2,CLU,GPM6A,PTPN11,JMY,CD47,RIPOR2,PRKCA,SYNPO2,SYNPO2L,MMP1,NLGN1,TGFB3,BBS4,SYNPO,FLNA,PLCG2,LRSAM1,LRRC24,PPM1E,ICAM1	darkgreen	VSMC_M4

GO:0009889	0.70	0.33	204	3010	regulation of biosynthetic process	BP	1	ZNF516,BCL2,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,IGFBP7,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,HRH1,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,FFAR3,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,ATOH8,CLCN3,TCF7L1,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,PTX3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,CD47,ETS2,BACE2,ABCG1,KDM5B,RGS2,MXI1,NCOA3,ACTN2,LRP5,NPNT,HTR2B,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,SECISBP2L,EZH1,EIF4G3,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,TMEM59,CTIF,DAPK3,TLE2,FLNA,MBTPS1,CDH13,PLCG2,TERF2IP,BCAR3,CDC7,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ITM2C,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,ORMDL3,STC2,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0046916	0.70	0.47	5	86	cellular transition metal ion homeostasis	BP	1	TF,APP,CYBRD1,HIF1A,BMP6	darkgreen	VSMC_M4
GO:0045185	0.70	0.47	5	80	maintenance of protein location	BP	1	GJA1,G3BP2,SUN1,BBS4,FLNA	darkgreen	VSMC_M4
GO:0090398	0.70	0.49	4	68	cellular senescence	BP	1	CDKN2B,C2orf40,NEK4,CDKN1A	darkgreen	VSMC_M4
GO:0006355	0.70	0.33	164	2411	regulation of transcription, DNA-templated	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0050730	0.70	0.41	12	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	ANGPT1,LEP,FLT3,APP,PDGFC,PTPN11,AFAP1L2,INPP5F,GPRC5A,PLCG2,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0048609	0.70	0.36	36	563	multicellular organismal reproductive process	BP	1	BCL2,CITED2,AFF4,GJA1,LEP,SPATA6L,TGFBR1,TESK2,INHBB,THRB,GTSF1,NCOR2,PAM,APP,PTPN11,PTX3,ADA,EDN1,JAM3,RGS2,SUN1,PRDX4,MAEL,TEX11,SLIT3,TGFB3,BBS4,FST,LGALS9,MARF1,PCSK4,CCDC136,SPINK2,CCR6,STC2,NPAS1	darkgreen	VSMC_M4
GO:0032434	0.70	0.44	7	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,CLU,HERPUD1,N4BP1,DAB2	darkgreen	VSMC_M4
GO:0098773	0.70	0.49	4	65	skin epidermis development	BP	1	BCL2,FGFR2,FST,EDA	darkgreen	VSMC_M4
GO:0000041	0.71	0.46	5	86	transition metal ion transport	BP	1	TRPC4,ATP2C1,TF,CYBRD1,LMTK2	darkgreen	VSMC_M4
GO:0090288	0.71	0.46	5	78	negative regulation of cellular response to growth factor stimulus	BP	1	HIPK2,CRIM1,LRP2,CFLAR,SMAD6	darkgreen	VSMC_M4
GO:0003158	0.71	0.44	7	107	endothelium development	BP	1	SCUBE1,GJA1,ATOH8,F11R,RDX,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0021954	0.71	0.48	4	61	central nervous system neuron development	BP	1	LEP,EPHB6,GATA2,FGFR2	darkgreen	VSMC_M4
GO:0043409	0.71	0.42	8	131	negative regulation of MAPK cascade	BP	1	IRAK3,RNF149,NDRG2,FOXO1,HIPK3,PTPN22,RGS2,DACT1	darkgreen	VSMC_M4
GO:0051170	0.71	0.42	8	132	import into nucleus	BP	1	ABRA,ANGPT1,LEP,MDFIC,TXNIP,PRKD1,FLNA,CDKN1A	darkgreen	VSMC_M4
GO:0046718	0.71	0.44	6	100	viral entry into host cell	BP	1	MRC1,SCARB2,PTX3,F11R,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0034614	0.71	0.43	7	124	cellular response to reactive oxygen species	BP	1	MDM2,SOD2,FOXO1,CYP1B1,MAP1LC3A,PTPN11,BNIP3	darkgreen	VSMC_M4
GO:0031398	0.71	0.44	6	102	positive regulation of protein ubiquitination	BP	1	ANGPT1,WFS1,DCUN1D4,PTPN22,ARRDC4,SKP2	darkgreen	VSMC_M4
GO:0042147	0.71	0.46	5	80	retrograde transport, endosome to Golgi	BP	1	RIC1,PREPL,DENND5A,RAB29,ATP9A	darkgreen	VSMC_M4
GO:0031330	0.71	0.39	13	207	negative regulation of cellular catabolic process	BP	1	BCL2,LAPTM4B,LEP,RIC1,PTPN3,HIPK2,PTPN22,N4BP1,FEZ1,HTR2B,QSOX1,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:2001020	0.71	0.39	12	200	regulation of response to DNA damage stimulus	BP	1	BCL2,MDM2,TPT1,BABAM2,ANKRD1,CLU,NEK4,EYA2,TP53BP1,ZNF365,TERF2IP,NACC2	darkgreen	VSMC_M4
GO:0045446	0.71	0.44	6	91	endothelial cell differentiation	BP	1	SCUBE1,ATOH8,F11R,RDX,ICAM1,BMP6	darkgreen	VSMC_M4
GO:1990778	0.71	0.37	18	279	protein localization to cell periphery	BP	1	GRIP1,PREPL,GGA3,ATP2C1,ZDHHC2,NFASC,RAB29,ACTN2,F11R,LRP6,RDX,RABEP1,GNAI1,NUMB,CDH2,DAB2,TMEM59,FLNA	darkgreen	VSMC_M4

GO:0006366	0.72	0.32	126	1862	transcription by RNA polymerase II	BP	1	ZNF516,CITED2,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,LEP,WFS1,DDX58,CREB3,ZNF169,REST,ZNF331,TBX18,HIPK2,GATA2,ZNF398,PPP1R13L,ELF1,SMARCD3,LMO7,FOSL2,LMCD1,SALL2,THRB,SATB1,FOXO1,EBF4,MIER3,NCOR2,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,MED12L,MEIS2,APP,CCNT1,JMY,CHD6,HNF4A,RBL2,EDN1,ETS2,MXI1,NCOA3,LRP5,NPNT,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,WDTC1,FGFR2,TP53BP1,PRKD1,ARID5B,ITGA6,ATF6,NPAS3,ID3,LRP6,ZNF280B,CUX1,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,SMARCA1,FLNA,CDH13,ZNF821,LMO4,CYR61,ZFP90,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0043401	0.72	0.42	7	111	steroid hormone mediated signaling pathway	BP	1	EP300,LBH,NCOR2,STRN3,DAB2,SKP2,YAP1	darkgreen	VSMC_M4
GO:0007292	0.72	0.44	6	101	female gamete generation	BP	1	BCL2,LEP,INHBB,PTX3,RGS2,MARF1	darkgreen	VSMC_M4
GO:0030004	0.72	0.45	5	81	cellular monovalent inorganic cation homeostasis	BP	1	BCL2,CLCN3,ATP6AP2,SLC8A1,ATP6V0E1	darkgreen	VSMC_M4
GO:1990138	0.72	0.40	10	147	neuron projection extension	BP	1	DDR1,SH3GL2,ITSN2,SEMA3C,SEMA5A,SHTN1,RAPH1,MAP3K13,SLIT3,ULK2	darkgreen	VSMC_M4
GO:0050684	0.72	0.42	7	118	regulation of mRNA processing	BP	1	REST,CPEB3,FAM172A,CCNT1,RBFOX1,AHCYL1,SRPK3	darkgreen	VSMC_M4
GO:0050792	0.72	0.42	7	119	regulation of viral process	BP	1	BCL2,MDFIC,PTX3,IFIT1,N4BP1,MX1,LGALS9	darkgreen	VSMC_M4
GO:0055076	0.72	0.43	6	107	transition metal ion homeostasis	BP	1	TF,APP,CYBRD1,FBXL5,HIF1A,BMP6	darkgreen	VSMC_M4
GO:0051650	0.72	0.40	9	143	establishment of vesicle localization	BP	1	DYNC1I1,SNAP91,ACTN4,EXOC6,MYO1B,AP3B2,NLGN1,BBS4,VAMP7	darkgreen	VSMC_M4
GO:0048675	0.72	0.42	7	106	axon extension	BP	1	SEMA3C,SEMA5A,SHTN1,RAPH1,MAP3K13,SLIT3,ULK2	darkgreen	VSMC_M4
GO:0072329	0.72	0.44	5	95	monocarboxylic acid catabolic process	BP	1	LEP,PEX13,SESN2,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0006641	0.72	0.46	4	70	triglyceride metabolic process	BP	1	PTPN11,LPL,ATG14,SLC27A5	darkgreen	VSMC_M4
GO:0014074	0.72	0.42	7	109	response to purine-containing compound	BP	1	APP,ABCC9,AKAP6,PPARGC1A,HCN2,SLC8A1,TMEM38A	darkgreen	VSMC_M4
GO:0034504	0.72	0.37	15	244	protein localization to nucleus	BP	1	MDM2,ABRA,ANGPT1,LEP,MDFIC,LATS2,SUN1,TXNIP,SESN2,PRKD1,BBS4,FLNA,CDKN1A,ORMDL3,YAP1	darkgreen	VSMC_M4
GO:1902904	0.72	0.40	9	139	negative regulation of supramolecular fiber organization	BP	1	KANK1,PPP1R9A,CLU,MID1,F11R,CRYAB,RDX,ARHGAP28,SPTAN1	darkgreen	VSMC_M4
GO:0032392	0.73	0.44	5	80	DNA geometric change	BP	1	CHD7,CHD6,SMARCAD1,CHD3,HFM1	darkgreen	VSMC_M4
GO:0009165	0.73	0.38	11	198	nucleotide biosynthetic process	BP	1	PDK4,ADCY6,ADA,ADCY5,SLC25A12,PPARGC1A,NPPB,AK7,ADCY9,AK5,RFK	darkgreen	VSMC_M4
GO:0007006	0.73	0.44	5	99	mitochondrial membrane organization	BP	1	BCL2,SLC25A4,EYA2,RHOT1,BNIP3	darkgreen	VSMC_M4
GO:0032504	0.73	0.33	36	571	multicellular organism reproduction	BP	1	BCL2,CITED2,AFF4,GJA1,LEP,SPATA6L,TGFBR1,TESK2,INHBB,THRB,GTSF1,NCOR2,PAM,APP,PTPN11,PTX3,ADA,EDN1,JAM3,RGS2,SUN1,PRDX4,MAEL,TEX11,SLIT3,TGFB3,BBS4,FST,LGALS9,MARF1,PCSK4,CCDC136,SPINK2,CCR6,STC2,NPAS1	darkgreen	VSMC_M4
GO:0051099	0.73	0.40	8	141	positive regulation of binding	BP	1	EP300,HIPK2,APP,AKTIP,NGF,RIPOR2,PLCL1,DACT1	darkgreen	VSMC_M4
GO:0045132	0.73	0.45	4	73	meiotic chromosome segregation	BP	1	SUN1,MAEL,TEX11,HFM1	darkgreen	VSMC_M4
GO:1901293	0.73	0.38	11	199	nucleoside phosphate biosynthetic process	BP	1	PDK4,ADCY6,ADA,ADCY5,SLC25A12,PPARGC1A,NPPB,AK7,ADCY9,AK5,RFK	darkgreen	VSMC_M4
GO:0031326	0.73	0.30	199	2955	regulation of cellular biosynthetic process	BP	1	ZNF516,BCL2,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,HRH1,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,FFAR3,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,PTX3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,CD47,ETS2,BACE2,KDM5B,RGS2,MXI1,NCOA3,ACTN2,LRP5,NPNT,HTR2B,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,SECISBP2L,EZH1,EIF4G3,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,TMEM59,CTIF,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,BCAR3,CDC7,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ITM2C,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,ORMDL3,STC2,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:1901990	0.74	0.36	14	237	regulation of mitotic cell cycle phase transition	BP	1	BCL2,MDM2,CDKN2B,FAM122A,JADE1,SMARCD3,BABAM2,APP,RBL2,RDX,DACT1,CDC7,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0061387	0.74	0.41	6	95	regulation of extent of cell growth	BP	1	SEMA3C,NGF,SEMA5A,SHTN1,MAP3K13,ULK2	darkgreen	VSMC_M4
GO:1903900	0.74	0.41	6	104	regulation of viral life cycle	BP	1	BCL2,PTX3,IFIT1,N4BP1,MX1,LGALS9	darkgreen	VSMC_M4
GO:0030163	0.74	0.31	52	815	protein catabolic process	BP	1	RNF41,IRAK3,MDM2,LAPTM4B,RNF19A,GJA1,ADGRB1,WFS1,FAM122A,C2orf40,RIC1,RNF149,PTPN3,HIPK2,ABHD12,GGA3,STT3B,ADAM9,FOXO1,ZDHHC2,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,LGMN,CTSS,LRP2,CTSZ,SYNPO2,CTSF,ZRANB1,RDX,USP11,FBXL5,DACT1,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,FLNA,LRSAM1,FBXO27,BNIP3,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:0071897	0.74	0.38	9	150	DNA biosynthetic process	BP	1	GRHL2,SMOC2,GJA1,POLB,ANKRD1,PAK3,TERF2IP,LOX,CDKN1A	darkgreen	VSMC_M4
GO:0010921	0.75	0.43	4	68	regulation of phosphatase activity	BP	1	RCAN1,NPNT,PPP1R36,PPP1R26	darkgreen	VSMC_M4

GO:0016567	0.75	0.31	42	656	protein ubiquitination	BP	1	BCL2,RNF41,SHPRH,SASH1,MDM2,RNF19A,ANGPT1,ADGRB1,WFS1,SH3RF3,DCUN1D4,RNF149,TGFBR1,KLHL7,MKRN2,LMO7,FBXO3,PCGF5,MARCH5,TRIM23,RMND5A,RNF141,SH3RF1,RNF34,HECTD4,HERPUD1,PTPN22,AKTIP,N4BP1,MARCH6,UBE3B,KCTD10,ARRDC4,WDTC1,TRIM63,FBXL5,DCAF5,MARCH2,SKP2,LRSAM1,FBXO27,FBXO28	darkgreen	VSMC_M4
GO:0006575	0.75	0.39	7	136	cellular modified amino acid metabolic process	BP	1	ABHD12,HPN,CHAC1,SERINC3,CPQ,SERINC2,VNN1	darkgreen	VSMC_M4
GO:0017038	0.75	0.36	10	174	protein import	BP	1	ABRA,ANGPT1,LEP,PEX13,MDFIC,CLU,TXNIP,PRKD1,FLNA,CDKN1A	darkgreen	VSMC_M4
GO:0044281	0.75	0.29	79	1301	small molecule metabolic process	BP	1	HSD17B6,EP300,AHCYL2,LEP,VLDLR,PDK4,REST,SLC2A1,LMBRD1,EDN2,ABCA1,PEX13,NT5C3A,ABHD12,HRH1,ENTPD3,PFKFB3,LIPT2,CYP1B1,GALM,NCOR2,CHPT1,ADM,PAM,PTH,ENTPD1,APP,HECTD4,ADCY6,LPCAT2,HNF4A,SERINC3,ADA,EDN1,PLA2G4F,LPL,ABCG1,NT5C2,ADIPOR1,TARSL2,PFKL,LRP5,LGMN,TPST2,SESN2,ARV1,ADCY5,LRP2,WDTC1,MAN2A2,CHST15,SLC25A12,PPIP5K1,RIMKLB,PDE1A,ENO2,HIF1A,PPARGC1A,NPPB,DISP3,RORA,MAT2B,AK7,OCRL,PRKAA2,ATCAY,ADCY9,AHCYL1,MBTPS1,PLCG2,EXTL2,AK5,VNN1,ACAD11,RFK,SLC27A5,BMP6,SCP2,DDIT4	darkgreen	VSMC_M4
GO:0050868	0.75	0.43	4	76	negative regulation of T cell activation	BP	1	CD274,PTPN22,RIPOR2,LGALS9	darkgreen	VSMC_M4
GO:0016032	0.75	0.33	20	325	viral process	BP	1	BCL2,EP300,REST,MDFIC,MRC1,USP6NL,HPN,SCARB2,PTX3,CCNT1,IFIT1,N4BP1,MX1,RAB29,F11R,CALCOCO2,LGALS9,LRSAM1,ST6GALNAC3,ICAM1	darkgreen	VSMC_M4
GO:0002706	0.75	0.41	5	92	regulation of lymphocyte mediated immunity	BP	1	LEP,IL18R1,MAP3K7,TP53BP1,LGALS9	darkgreen	VSMC_M4
GO:0072659	0.75	0.34	15	239	protein localization to plasma membrane	BP	1	GRIP1,PREPL,GGA3,ATP2C1,ZDHHC2,NFASC,ACTN2,F11R,LRP6,RDX,NUMB,CDH2,DAB2,TMEM59,FLNA	darkgreen	VSMC_M4
GO:1903320	0.75	0.35	12	211	regulation of protein modification by small protein conjugation or removal	BP	1	SASH1,ANGPT1,ADGRB1,WFS1,DCUN1D4,TGFBR1,HERPUD1,PTPN22,N4BP1,ARRDC4,HIF1A,SKP2	darkgreen	VSMC_M4
GO:0150116	0.75	0.42	4	65	regulation of cell-substrate junction organization	BP	1	LIMCH1,PTPN11,MAPRE2,DAPK3	darkgreen	VSMC_M4
GO:0002573	0.76	0.36	9	154	myeloid leukocyte differentiation	BP	1	CITED2,GATA2,RASSF2,TMEM178A,TF,APP,TMEM64,PRKCA,CSF1	darkgreen	VSMC_M4
GO:0010948	0.76	0.34	14	237	negative regulation of cell cycle process	BP	1	BCL2,MDM2,CDKN2B,FAM122A,JADE1,BABAM2,PTPN11,RBL2,TP53BP1,DACT1,APBB2,TOM1L1,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0050731	0.76	0.37	8	136	positive regulation of peptidyl-tyrosine phosphorylation	BP	1	ANGPT1,LEP,FLT3,PTPN11,AFAP1L2,PLCG2,ICAM1,BMP6	darkgreen	VSMC_M4
GO:0032147	0.76	0.39	6	105	activation of protein kinase activity	BP	1	ANGPT1,LEP,MAP3K7,PDGFC,GPRC5A,TOM1L1	darkgreen	VSMC_M4
GO:0031347	0.76	0.31	24	397	regulation of defense response	BP	1	IRAK3,GJA1,EP300,LEP,DDX58,MAP3K7,ABHD12,FFAR3,APP,PTPN11,LBP,PTPN22,ADA,IFIT1,CD47,N4BP1,LPL,SERPINE1,RORA,PAK3,LGALS9,VAMP7,PLCG2,LRSAM1	darkgreen	VSMC_M4
GO:2000058	0.76	0.37	8	143	regulation of ubiquitin-dependent protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,HIPK2,CLU,HERPUD1,N4BP1,DAB2	darkgreen	VSMC_M4
GO:0006970	0.76	0.42	4	71	response to osmotic stress	BP	1	SLC2A1,MYLK,PAPPA2,LRRC8C	darkgreen	VSMC_M4
GO:0006493	0.76	0.42	4	74	protein O-linked glycosylation	BP	1	B3GNT7,GALNT3,B3GALNT2,GALNT10	darkgreen	VSMC_M4
GO:0051591	0.76	0.42	4	68	response to cAMP	BP	1	APP,AKAP6,HCN2,SLC8A1	darkgreen	VSMC_M4
GO:0014013	0.76	0.41	4	73	regulation of gliogenesis	BP	1	TENM4,ABCC8,LRP2,ZNF365	darkgreen	VSMC_M4
GO:0097659	0.76	0.27	169	2522	nucleic acid-templated transcription	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0044409	0.76	0.38	6	106	entry into host	BP	1	MRC1,SCARB2,PTX3,F11R,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0051963	0.77	0.39	5	79	regulation of synapse assembly	BP	1	ADGRB1,PPP1R9A,APP,NLGN1,LRRC24	darkgreen	VSMC_M4
GO:0016441	0.77	0.37	6	115	posttranscriptional gene silencing	BP	1	NCOR2,HELZ,MAEL,MARF1,MIR99A,MIR331	darkgreen	VSMC_M4
GO:0120031	0.77	0.30	28	435	plasma membrane bounded cell projection assembly	BP	1	KANK1,PPP1R9A,TGFBR1,CDC42EP3,WASF3,NCK1,OCLN,GPM6A,DNAH7,RIPOR2,ACTN2,ABLIM1,SHTN1,MYLK,RDX,NLGN1,TGFB3,IFT43,BBS4,EVI5L,ABLIM3,OCRL,MYO10,PLXNB3,FLNA,CDH13,ICAM1,YAP1	darkgreen	VSMC_M4
GO:0006470	0.77	0.32	14	228	protein dephosphorylation	BP	1	BCL2,PTPN3,ANKLE2,PTPRG,NCK1,PTPN11,PTPN22,RCAN1,DAPP1,EYA2,PTPN14,PPEF1,DNAJC6,PPM1E	darkgreen	VSMC_M4
GO:1904375	0.77	0.37	6	107	regulation of protein localization to cell periphery	BP	1	ATP2C1,ZDHHC2,GNAI1,NUMB,DAB2,TMEM59	darkgreen	VSMC_M4
GO:1903076	0.77	0.38	5	90	regulation of protein localization to plasma membrane	BP	1	ATP2C1,ZDHHC2,NUMB,DAB2,TMEM59	darkgreen	VSMC_M4

GO:0051254	0.77	0.26	90	1357	positive regulation of RNA metabolic process	BP	1	ZNF516,CITED2,GRHL2,ABRA,EP300,MRTFA,BRD8,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ATOH8,TEAD1,PTH,MED12L,MEIS2,APP,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,EDN1,ETS2,RBM20,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,SESN2,FGFR2,TP53BP1,PRKD1,ARID5B,ITGA6,ATF6,NPAS3,LRP6,ZNF445,EZH1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,ABLIM3,CRLF3,DAB2,SMARCA1,CDH13,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0007034	0.78	0.34	8	137	vacuolar transport	BP	1	GGA3,CLU,SCARB2,AKTIP,ATG14,EPG5,VAMP7,SORT1	darkgreen	VSMC_M4
GO:0046907	0.78	0.26	82	1261	intracellular transport	BP	1	SLC35D3,STX11,GRIP1,MDM2,LAPTM4B,ABRA,ANGPT1,LEP,RIC1,DYNC1I1,LMAN2L,SNX13,PREPL,ABCA1,DOP1A,PEX13,MDFIC,TCAF1,ITSN2,TMCC1,GGA3,USP6NL,ACTN4,ZDHHC2,DENND5A,TRIM23,EXOC6,KIF13B,CLU,APP,SCARB2,PTPN11,HERPUD1,ATG13,AKTIP,MYO1B,RAB29,ABCG1,TNNT2,ACTN2,FEZ1,TINAGL1,SUN1,TXNIP,SEC24B,ATP9A,ARV1,INPP5F,PTPN14,PRKD1,DYNC1I2,AP3B2,AKAP6,LRP6,HSPB1,CRYAB,RDX,EXPH5,ATG14,LMTK2,NLGN1,HIF1A,AP1S3,FAF2,IFT43,EPG5,BBS4,EVI5L,ABLIM3,SH3TC2,RHOT1,DAB2,MYO10,FLNA,VAMP7,AHCYL1,SORT1,TBC1D13,WLS,PLN,CDKN1A,SCP2	darkgreen	VSMC_M4
GO:0006672	0.78	0.39	4	78	ceramide metabolic process	BP	1	ST3GAL5,CYR61,ST6GALNAC3,ORMDL3	darkgreen	VSMC_M4
GO:0007163	0.78	0.32	12	189	establishment or maintenance of cell polarity	BP	1	UST,GJA1,DOCK8,KANK1,AMOTL2,JAM3,RIPOR2,FEZ1,PARD6B,SHTN1,WDR1,PATJ	darkgreen	VSMC_M4
GO:0010468	0.78	0.25	230	3428	regulation of gene expression	BP	1	MBP,ZNF516,BCL2,IFNGR1,CITED2,IRAK3,MDM2,LAPTM4B,GRHL2,SOD2,ABRA,ANGPT1,TRPS1,AFF4,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,TLE4,SH3GL2,MLLT3,LEP,WFS1,DDX58,CD274,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,INHBB,SMARCD3,LMO7,FOSL2,LBH,NDRG2,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,FFAR3,HPN,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,OCLN,TCF7L1,WWC2,TEAD1,FAM172A,PTH,G3BP2,CLU,BLNK,MED12L,MEIS2,APP,ATXN2,ABCC8,ANXA3,PTPN11,LBP,NEK4,CCNT1,JMY,CHD6,PTPN22,HNF4A,CHAC1,GDF6,NAB1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,LPL,KDM5B,RGS2,MXI1,RBM20,NCOA3,ACTN2,LRP5,NPNT,HTR2B,LGMN,PRKCA,AFAP1L2,TXNIP,HELZ,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,CFLAR,CTSZ,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,F11R,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,SERPINE1,CRYAB,ATP6AP2,RDX,ZNF445,SECISBP2L,EZH1,EIF4G3,ATG14,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,SLIT3,TGFB3,SMAD6,ZKSCAN2,NPTN,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,PRKAA2,TMEM59,CTIF,RBFOX1,DAPK3,TLE2,FLNA,CSF1,SORT1,CDH13,PLCG2,TERF2IP,F3,GLG1,ZNF821,LMO4,CYR61,ZFP90,MIR99A,MIR331,AFF3,SLC8A1,ZSCAN30,TLR1,CD83,LOX,TBX20,ZNF425,ZNF175,MAFF,CDKN1A,FGF9,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,STC2,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0010721	0.78	0.34	8	130	negative regulation of cell development	BP	1	KANK1,REST,ACTN4,SEMA3C,ABCC8,SEMA5A,ULK2,FRZB	darkgreen	VSMC_M4
GO:0060021	0.78	0.39	4	71	roof of mouth development	BP	1	TGFBR1,CHD7,ARID5B,TGFB3	darkgreen	VSMC_M4
GO:0032774	0.78	0.24	169	2534	RNA biosynthetic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0006413	0.78	0.36	5	99	translational initiation	BP	1	NCK1,HSPB1,EIF4A2,EIF4G3,CTIF	darkgreen	VSMC_M4
GO:0006790	0.78	0.30	15	270	sulfur compound metabolic process	BP	1	DSEL,UST,ANGPT1,AHCYL2,PDK4,CHST2,CHAC1,B3GNT7,TPST2,NDST3,TSTD1,CHST15,MAT2B,BGN,AHCYL1	darkgreen	VSMC_M4
GO:0006639	0.79	0.36	5	92	acylglycerol metabolic process	BP	1	ABHD12,PTPN11,LPL,ATG14,SLC27A5	darkgreen	VSMC_M4

GO:0006351	0.79	0.24	168	2521	transcription, DNA-templated	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0071356	0.79	0.32	9	163	cellular response to tumor necrosis factor	BP	1	ACTN4,ANKRD1,OCLN,EDN1,NPNT,PPARGC1A,RORA,VCAM1,ICAM1	darkgreen	VSMC_M4
GO:0048705	0.79	0.31	11	186	skeletal system morphogenesis	BP	1	CITED2,GRHL2,TGFBR1,NAB1,LRP5,FGFR2,ARID5B,PAPPA2,TGFB3,GLG1,BMP6	darkgreen	VSMC_M4
GO:0001738	0.79	0.36	5	84	morphogenesis of a polarized epithelium	BP	1	MLLT3,SEC24B,DACT1,WDR1,DAB2	darkgreen	VSMC_M4
GO:0006638	0.79	0.35	5	93	neutral lipid metabolic process	BP	1	ABHD12,PTPN11,LPL,ATG14,SLC27A5	darkgreen	VSMC_M4
GO:0032479	0.79	0.37	4	75	regulation of type I interferon production	BP	1	DDX58,PTPN11,PTPN22,PLCG2	darkgreen	VSMC_M4
GO:0032606	0.79	0.37	4	75	type I interferon production	BP	1	DDX58,PTPN11,PTPN22,PLCG2	darkgreen	VSMC_M4
GO:0062207	0.79	0.37	4	77	regulation of pattern recognition receptor signaling pathway	BP	1	IRAK3,LBP,PTPN22,TLR1	darkgreen	VSMC_M4
GO:0007368	0.79	0.35	5	90	determination of left/right symmetry	BP	1	CITED2,ENKUR,HIF1A,BBS4,TBX20	darkgreen	VSMC_M4
GO:0007601	0.80	0.33	7	123	visual perception	BP	1	WFS1,GRK7,ABLIM1,ATF6,CRYGS,BBS4,ABCA4	darkgreen	VSMC_M4
GO:0030031	0.80	0.26	28	443	cell projection assembly	BP	1	KANK1,PPP1R9A,TGFBR1,CDC42EP3,WASF3,NCK1,OCLN,GPM6A,DNAH7,RIPOR2,ACTN2,ABLIM1,SHTN1,MYLK,RDX,NLGN1,TGFB3,IFT43,BBS4,EVI5L,ABLIM3,OCRL,MYO10,PLXNB3,FLNA,CDH13,ICAM1,YAP1	darkgreen	VSMC_M4
GO:2000112	0.80	0.23	188	2822	regulation of cellular macromolecule biosynthetic process	BP	1	ZNF516,BCL2,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,BACE2,KDM5B,RGS2,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,SECISBP2L,EZH1,EIF4G3,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,TMEM59,CTIF,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,BCAR3,CDC7,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ITM2C,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0001570	0.80	0.36	4	71	vasculogenesis	BP	1	CITED2,ADM,TBX20,YAP1	darkgreen	VSMC_M4
GO:1901987	0.80	0.27	18	311	regulation of cell cycle phase transition	BP	1	BCL2,MDM2,CDKN2B,FAM122A,JADE1,SMARCD3,BABAM2,APP,PTPN11,RBL2,TP53BP1,RDX,DACT1,APBB2,PLCG2,CDC7,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0006091	0.80	0.27	21	392	generation of precursor metabolites and energy	BP	1	HSD17B6,EP300,LEP,GYS1,SLC25A4,PTH,GYG1,APP,PFKL,GYG2,SLC25A12,MAOB,ENO2,CYP19A1,HIF1A,OPN3,PPARGC1A,PRKAA2,BNIP3,SLC27A5,DDIT4	darkgreen	VSMC_M4
GO:0001656	0.80	0.36	4	74	metanephros development	BP	1	BCL2,GDF6,ID3,YAP1	darkgreen	VSMC_M4
GO:0051641	0.80	0.22	153	2295	cellular localization	BP	1	BCL2,SLC35D3,STX11,GRIP1,MDM2,LAPTM4B,ABRA,ANGPT1,GJA1,TRDN,SH3GL2,LEP,UNC13B,PPP1R9A,RIC1,DYNC1I1,FRMPD1,LMAN2L,SNX13,PREPL,LMBRD1,SYT5,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,ITSN2,GATA2,TMCC1,GGA3,USP6NL,KCNE3,ACTN4,TM9SF2,FGF14,ATP2C1,PCLO,EML4,ZDHHC2,RIC3,DEND5A,CHD7,LATS2,MARCH5,TRIM23,EXOC6,ESYT3,CLCN3,OCLN,MCTP1,JPH1,KIF13B,CLU,APP,SCARB2,ANXA3,PTPN11,HERPUD1,ATG13,AKTIP,JAM3,NFASC,MYO1B,RAB29,ABCG1,RIPOR2,TNNT2,ACTN2,LRP5,FEZ1,HTR2B,TINAGL1,SUN1,TXNIP,SEC24B,PARD6B,MID1,ATP9A,SESN2,ARV1,CAMK2D,ADCY5,INPP5F,PTPN14,PRKD1,F11R,CYBRD1,DYNC1I2,RAPGEF4,AP3B2,AKAP6,LRP6,HSPB1,CRYAB,RDX,EXPH5,ATG14,EMC1,LMTK2,NLGN1,WDR1,RABEP1,HIF1A,CACNA1C,AP1S3,ADGRE2,GNAI1,FBXL20,FAF2,NUMB,IFT43,EPG5,BBS4,NPTN,MAPRE2,CDH2,GAS2L2,EVI5L,ABLIM3,SH3TC2,RHOT1,DNAJC6,DAB2,LGALS9,PRKAA2,TMEM59,MYO10,ATCAY,FLNA,VAMP7,AHCYL1,SORT1,CDH13,PLCG2,TBC1D13,TERF2IP,LRSAM1,WLS,KCNE4,ITPR1,SLC8A1,PLN,PIGK,CDKN1A,NACC2,TMEM38A,GABARAPL2,ORMDL3,YAP1,FAM83H,SCP2	darkgreen	VSMC_M4
GO:0010232	0.80	0.36	4	71	vascular transport	BP	1	GJA1,SLC2A1,ABCC9,LRP2	darkgreen	VSMC_M4

GO:0043009	0.80	0.25	33	522	chordate embryonic development	BP	1	CITED2,GRHL2,ANGPT1,EP300,TGFBR1,TBX18,KIDINS220,GATA2,POLB,SEMA3C,CHD7,ADM,SHROOM3,ADA,EDN1,SEC24B,PLXNA2,LRP2,WDTC1,FGFR2,LRP6,ATP6AP2,DACT1,HIF1A,TGFB3,BBS4,ADCY9,CMIP,LMO4,CYR61,MAFF,HOPX,YAP1	darkgreen	VSMC_M4
GO:0034248	0.81	0.26	23	395	regulation of cellular amide metabolic process	BP	1	IFNGR1,DAPK1,PDK4,GGA3,CPEB3,NCK1,CLU,APP,ATXN2,ABCG1,RGS2,SESN2,NGRN,RBM4B,FAM129A,HSPB1,EIF4A2,SECISBP2L,EIF4G3,CTIF,DAPK3,CYR61,ORMDL3	darkgreen	VSMC_M4
GO:1903052	0.81	0.32	6	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,CLU,HERPUD1,DAB2	darkgreen	VSMC_M4
GO:0072006	0.81	0.31	7	118	nephron development	BP	1	BCL2,ANGPT1,COL4A4,NPNT,NID1,CFLAR,YAP1	darkgreen	VSMC_M4
GO:0009408	0.81	0.35	4	84	response to heat	BP	1	EP300,IGFBP7,DNAJA2,CDKN1A	darkgreen	VSMC_M4
GO:0010556	0.81	0.21	189	2846	regulation of macromolecule biosynthetic process	BP	1	ZNF516,BCL2,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,BACE2,KDM5B,RGS2,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,SECISBP2L,EZH1,EIF4G3,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,TMEM59,CTIF,DAPK3,TLE2,FLNA,CDH13,PLCG2,TERF2IP,BCAR3,CDC7,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,ITM2C,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,ORMDL3,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0007030	0.81	0.30	7	122	Golgi organization	BP	1	LMAN2L,USP6NL,LYSMD3,RAB29,PDE4DIP,PRKD1,VAMP7	darkgreen	VSMC_M4
GO:0051053	0.81	0.32	5	94	negative regulation of DNA metabolic process	BP	1	GJA1,ANKRD1,TP53BP1,TERF2IP,CDKN1A	darkgreen	VSMC_M4
GO:0050807	0.81	0.28	10	165	regulation of synapse organization	BP	1	ADGRB1,PPP1R9A,GPM6A,APP,NLGN1,ADGRL1,SIPA1L1,CDH2,PAK3,LRRC24	darkgreen	VSMC_M4
GO:0050953	0.81	0.30	7	126	sensory perception of light stimulus	BP	1	WFS1,GRK7,ABLIM1,ATF6,CRYGS,BBS4,ABCA4	darkgreen	VSMC_M4
GO:0045165	0.81	0.28	10	172	cell fate commitment	BP	1	BCL2,TGFBR1,TBX18,GATA2,TENM4,ETS2,EYA2,FGFR2,LMO4,TBX20	darkgreen	VSMC_M4
GO:0019079	0.82	0.32	5	99	viral genome replication	BP	1	BCL2,IFIT1,N4BP1,MX1,RAB29	darkgreen	VSMC_M4
GO:0045619	0.82	0.31	6	117	regulation of lymphocyte differentiation	BP	1	ZAP70,SH3RF1,ADA,LGALS9,VNN1,CD83	darkgreen	VSMC_M4
GO:0002822	0.82	0.32	5	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	CD274,IL18R1,MAP3K7,ADA,TP53BP1	darkgreen	VSMC_M4
GO:0044772	0.82	0.25	20	350	mitotic cell cycle phase transition	BP	1	BCL2,MDM2,TPD52L1,CDKN2B,FAM122A,JADE1,SMARCD3,BABAM2,LATS2,APP,RBL2,RDX,DACT1,CCNG1,CRLF3,SKP2,CDC7,CDKN1A,CNTD2,NACC2	darkgreen	VSMC_M4
GO:1901136	0.82	0.30	6	126	carbohydrate derivative catabolic process	BP	1	STT3B,ADA,NT5C2,PDE1A,FBXO27,CST3	darkgreen	VSMC_M4
GO:0045935	0.82	0.21	97	1489	positive regulation of nucleobase-containing compound metabolic process	BP	1	ZNF516,CITED2,GRHL2,ABRA,SMOC2,EP300,MRTFA,BRD8,MLLT3,DDX58,CREB3,REST,TGFBR1,MDFIC,JADE1,HIPK2,GATA2,ZNF398,NAA16,ELF1,SMARCD3,LMO7,BABAM2,FOSL2,LBH,SALL2,THRB,ACTN4,TACC1,FOXO1,TF,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,ATOH8,TEAD1,PTH,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,EDN1,ETS2,EYA2,RBM20,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,SESN2,FGFR2,TP53BP1,PRKD1,SLC25A12,ARID5B,ITGA6,ATF6,NPAS3,LRP6,ZNF445,EZH1,HIF1A,ZBTB18,APBB2,CCPG1,PPARGC1A,ACTN1,RORA,TGFB3,SMAD6,PAK3,ABLIM3,CRLF3,DAB2,SMARCA1,PRKAA2,CDH13,LMO4,CYR61,ZFP90,TBX20,ZNF175,MAFF,ZNF782,HLF,YAP1,BMP6,MAFA	darkgreen	VSMC_M4
GO:0000278	0.82	0.22	45	729	mitotic cell cycle	BP	1	BCL2,MDM2,SMOC2,GJA1,TPD52L1,CDKN2B,FAM122A,TMEM8B,PTPN3,JADE1,TUBE1,SMARCD3,BABAM2,TACC1,ANKLE2,EML4,LATS2,MEIS2,APP,PTPN11,NEK4,RBL2,EDN1,LRP5,LGMN,PRKCA,AFAP1L2,RDX,DACT1,GNAI1,ZFYVE26,CCNG1,TOM1L1,BBS4,TTC19,CRLF3,SKP2,DAPK3,FLNA,CDH13,CDC7,CDKN1A,CNTD2,NACC2,REEP3	darkgreen	VSMC_M4
GO:0046394	0.82	0.27	11	213	carboxylic acid biosynthetic process	BP	1	PDK4,EDN2,SERINC3,EDN1,PLA2G4F,LPL,WDTC1,SLC25A12,PRKAA2,SLC27A5,SCP2	darkgreen	VSMC_M4

GO:1901362	0.82	0.20	198	3012	organic cyclic compound biosynthetic process	BP	1	ZNF516,HSD17B6,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,IGFBP7,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,ADCY6,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,ADA,RBL2,EDN1,ETS2,ABCG1,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,ARV1,YEATS2,ZNF710,CAMK2D,ADCY5,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,CYP19A1,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,FAXDC2,AK7,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,PRKAA2,DAPK3,ADCY9,TLE2,FLNA,MBTPS1,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AK5,AFF3,ZSCAN30,LOX,TBX20,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZNF782,SLC27A5,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,SCP2,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0001657	0.82	0.33	4	78	ureteric bud development	BP	1	BCL2,NPNT,FGFR2,SMAD6	darkgreen	VSMC_M4
GO:0051701	0.83	0.28	8	150	biological process involved in interaction with host	BP	1	MRC1,SCARB2,PTX3,IFIT1,F11R,ULK2,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0048193	0.83	0.25	15	259	Golgi vesicle transport	BP	1	LMAN2L,PREPL,DOP1A,GGA3,ATP2C1,EXOC6,MYO1B,SEC24B,ATP9A,PRKD1,CUX1,RABEP1,VAMP7,SORT1,GABARAPL2	darkgreen	VSMC_M4
GO:0032446	0.83	0.22	43	703	protein modification by small protein conjugation	BP	1	BCL2,RNF41,SHPRH,SASH1,MDM2,RNF19A,ANGPT1,ADGRB1,WFS1,SH3RF3,DCUN1D4,RNF149,TGFBR1,KLHL7,MKRN2,LMO7,FBXO3,PCGF5,MARCH5,TRIM23,RMND5A,RNF141,SH3RF1,RNF34,HECTD4,HERPUD1,PTPN22,AKTIP,N4BP1,MARCH6,UBE3B,KCTD10,ARRDC4,WDTC1,TRIM63,FBXL5,HIF1A,DCAF5,MARCH2,SKP2,LRSAM1,FBXO27,FBXO28	darkgreen	VSMC_M4
GO:1903038	0.83	0.32	4	87	negative regulation of leukocyte cell-cell adhesion	BP	1	CD274,PTPN22,RIPOR2,LGALS9	darkgreen	VSMC_M4
GO:0016053	0.83	0.26	11	215	organic acid biosynthetic process	BP	1	PDK4,EDN2,SERINC3,EDN1,PLA2G4F,LPL,WDTC1,SLC25A12,PRKAA2,SLC27A5,SCP2	darkgreen	VSMC_M4
GO:1902600	0.83	0.30	5	115	proton transmembrane transport	BP	1	SLC17A5,ACTN4,SLC25A4,CLCN3,ATP6V0E1	darkgreen	VSMC_M4
GO:0000018	0.83	0.32	4	83	regulation of DNA recombination	BP	1	SMARCAD1,TP53BP1,ZNF365,TERF2IP	darkgreen	VSMC_M4
GO:0043242	0.83	0.31	4	70	negative regulation of protein-containing complex disassembly	BP	1	IRAK3,MID1,RDX,SPTAN1	darkgreen	VSMC_M4
GO:0002040	0.83	0.28	6	114	sprouting angiogenesis	BP	1	ANGPT1,RECK,GATA2,SEMA5A,CDH13,PIK3C2A	darkgreen	VSMC_M4
GO:1903322	0.84	0.28	6	121	positive regulation of protein modification by small protein conjugation or removal	BP	1	ANGPT1,WFS1,DCUN1D4,PTPN22,ARRDC4,SKP2	darkgreen	VSMC_M4
GO:0072163	0.84	0.31	4	79	mesonephric epithelium development	BP	1	BCL2,NPNT,FGFR2,SMAD6	darkgreen	VSMC_M4
GO:0072164	0.84	0.31	4	79	mesonephric tubule development	BP	1	BCL2,NPNT,FGFR2,SMAD6	darkgreen	VSMC_M4
GO:0061326	0.84	0.31	4	77	renal tubule development	BP	1	BCL2,COL4A1,NPNT,YAP1	darkgreen	VSMC_M4
GO:0046683	0.84	0.29	5	94	response to organophosphorus	BP	1	APP,ABCC9,AKAP6,HCN2,SLC8A1	darkgreen	VSMC_M4
GO:0031334	0.84	0.25	11	199	positive regulation of protein-containing complex assembly	BP	1	UNC13B,ABCA1,CDC42EP3,WASF3,NCK1,OCLN,CLU,JMY,MMP1,PLCG2,ICAM1	darkgreen	VSMC_M4
GO:0044260	0.84	0.18	393	5916	cellular macromolecule metabolic process	BP	1	MBP,ZNF516,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,CITED2,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TPD52L1,TATDN1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,SH3RF3,DCUN1D4,VLDLR,C2orf40,PPP1R9A,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,ZAP70,TGFBR1,LMBRD1,ABCA1,ZNF331,KLHL7,PTPN3,TBX18,MAP3K7,ANTXR1,MDFIC,PAPPA,EPHB6,JADE1,GYS1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ZNF398,ITM2B,PPP1R13L,SNRK,TESK2,NAA16,ELF1,INHBB,SMARCD3,MKRN2,EXOG,LMO7,ITIH5,BABAM2,FOSL2,LBH,STT3B,LIPT2,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,SUMF1,FOXO1,RASSF2,COL4A2,ANKLE2,QPCT,CYP1B1,TF,EBF4,FLT3,TUSC3,ZDHHC2,MAP3K1,MIER3,NCOR2,FXYD1,HPN,FBXO3,PTPRG,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,ADM,RNF141,PAM,SH3RF1,ST3GAL5,ATOH8,GRK7,OCLN,TCF7L1,ELL2,WWC2,TEAD1,PTH,GYG1,EXTL3,RNF34,CDKL2,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,PDGFC,ANXA3,HECTD4,PTPN11,PTX3,NEK4,CCNT1,HERPUD1,PROS1,JMY,CHD6,PTPN22,DPY19L4,HNF4A,CHAC1,GDF6,NAB1,AKTIP,RCAN1,RBL2,NGF,EDN1,ETS2,N4BP1,SMARCAD1,MARCH6,BACE2,RAB29,KDM5B,TARSL2,DAPP1,RGS2,EYA2,MXI1,NCOA3,ACTN2,UBE3B,LRP5,KCTD10,ARRDC4,NPNT,PLCL1,HTR2B,MST1R,LGMN,B3GNT7,GYG2,GALNT3,B3GALNT2,PRKCA,AFAP1L2,TXNIP,TPST2,SESN2,YEATS2,P4HTM,ZNF710,CAMK2D,CTSS,NGRN,MYLK,LRP2,CFLAR,CTSZ,WDTC1,INPP5F,MAN	darkgreen	VSMC_M4
GO:0032273	0.84	0.28	6	116	positive regulation of protein polymerization	BP	1	CDC42EP3,WASF3,NCK1,OCLN,JMY,ICAM1	darkgreen	VSMC_M4
GO:0009855	0.84	0.29	5	97	determination of bilateral symmetry	BP	1	CITED2,ENKUR,HIF1A,BBS4,TBX20	darkgreen	VSMC_M4
GO:1901888	0.84	0.25	10	165	regulation of cell junction assembly	BP	1	GJA1,ADGRB1,LIMCH1,PPP1R9A,APP,PTPN11,F11R,NLGN1,DAPK3,LRRC24	darkgreen	VSMC_M4
GO:0048704	0.84	0.30	4	83	embryonic skeletal system morphogenesis	BP	1	GRHL2,TGFBR1,FGFR2,TGFB3	darkgreen	VSMC_M4
GO:0050803	0.84	0.25	10	170	regulation of synapse structure or activity	BP	1	ADGRB1,PPP1R9A,GPM6A,APP,NLGN1,ADGRL1,SIPA1L1,CDH2,PAK3,LRRC24	darkgreen	VSMC_M4
GO:0002262	0.84	0.27	7	134	myeloid cell homeostasis	BP	1	CITED2,HIPK2,GATA2,JAM3,P4HTM,NCSTN,HIF1A	darkgreen	VSMC_M4
GO:0046034	0.84	0.24	10	219	ATP metabolic process	BP	1	EP300,APP,PFKL,SLC25A12,ENO2,HIF1A,PPARGC1A,PRKAA2,AK5,DDIT4	darkgreen	VSMC_M4
GO:0006605	0.84	0.23	14	262	protein targeting	BP	1	PEX13,TCAF1,GGA3,ZDHHC2,KIF13B,CLU,SCARB2,HERPUD1,ATG13,AKAP6,NLGN1,AP1S3,ABLIM3,SORT1	darkgreen	VSMC_M4
GO:0009799	0.84	0.28	5	98	specification of symmetry	BP	1	CITED2,ENKUR,HIF1A,BBS4,TBX20	darkgreen	VSMC_M4

GO:0009056	0.84	0.18	126	2000	catabolic process	BP	1	BCL2,RNF41,HSD17B6,IRAK3,MDM2,LAPTM4B,RNF19A,RNASET2,GJA1,EP300,ADGRB1,DAPK1,LEP,WFS1,FAM122A,C2orf40,PON2,RIC1,RNF149,PTPN3,PEX13,MAP3K7,SESN1,HIPK2,ABHD12,GGA3,EXOG,ENTPD3,STT3B,PLCB4,ADAM9,FOXO1,CYP1B1,GALM,ZDHHC2,CPEB3,RMND5A,MAP1LC3A,SLC25A4,RNF34,CLU,ENTPD1,APP,SCARB2,HERPUD1,ATG13,PTPN22,CHAC1,CPQ,ADA,PLA2G4F,N4BP1,MARCH6,LPL,NT5C2,PFKL,UBE3B,LRP5,KCTD10,FEZ1,HTR2B,LGMN,PRKCA,SESN2,CTSS,LRP2,CTSZ,INPP5F,SYNPO2,CTSF,PRKD1,QSOX1,ZRANB1,SLC25A12,ATF6,PRDX4,GABARAPL1,HSPB1,ACHE,PDE1A,RDX,MAOA,MAOB,ENO2,NBR1,FMO4,USP11,ATG14,MMP1,FBXL5,CYP19A1,DACT1,JKAMP,HIF1A,FBXL20,PPARGC1A,FAF2,CALCOCO2,TOM1L1,EPG5,USP32,ATG4A,ULK2,MMP28,DAB2,OCRL,SKP2,PRKAA2,TMEM59,CTIF,DAPK3,FLNA,MAP1LC3B2,PLCG2,LRSAM1,ITPR1,ACAD11,FBXO27,BNIP3,CST3,GABARAPL2,PIK3C2A,ORMDL3,ATP6V0E1,SCP2,DDIT4	darkgreen	VSMC_M4
GO:0042770	0.85	0.25	8	155	signal transduction in response to DNA damage	BP	1	MDM2,HIPK2,BABAM2,ANKRD1,PTPN11,SESN2,TP53BP1,CDKN1A	darkgreen	VSMC_M4
GO:0001823	0.85	0.29	4	81	mesonephros development	BP	1	BCL2,NPNT,FGFR2,SMAD6	darkgreen	VSMC_M4
GO:0051640	0.85	0.20	27	447	organelle localization	BP	1	STX11,GJA1,UNC13B,DYNC1I1,SNAP91,PEX13,GATA2,ACTN4,PCLO,EML4,EXOC6,ESYT3,MYO1B,FEZ1,SUN1,AP3B2,ATG14,NLGN1,HIF1A,ADGRE2,BBS4,CDH2,RHOT1,LGALS9,ATCAY,VAMP7,AHCYL1	darkgreen	VSMC_M4
GO:0015698	0.85	0.26	6	113	inorganic anion transport	BP	1	FXYD1,CLCN3,SLC26A7,ANO5,ABCC9,LRRC8C	darkgreen	VSMC_M4
GO:0045727	0.85	0.27	5	109	positive regulation of translation	BP	1	CPEB3,NCK1,NGRN,FAM129A,CTIF	darkgreen	VSMC_M4
GO:0019058	0.85	0.22	13	239	viral life cycle	BP	1	BCL2,MRC1,USP6NL,SCARB2,PTX3,IFIT1,N4BP1,MX1,RAB29,F11R,LGALS9,LRSAM1,ICAM1	darkgreen	VSMC_M4
GO:0009792	0.85	0.19	33	537	embryo development ending in birth or egg hatching	BP	1	CITED2,GRHL2,ANGPT1,EP300,TGFBR1,TBX18,KIDINS220,GATA2,POLB,SEMA3C,CHD7,ADM,SHROOM3,ADA,EDN1,SEC24B,PLXNA2,LRP2,WDTC1,FGFR2,LRP6,ATP6AP2,DACT1,HIF1A,TGFB3,BBS4,ADCY9,CMIP,LMO4,CYR61,MAFF,HOPX,YAP1	darkgreen	VSMC_M4
GO:0000077	0.86	0.26	5	105	DNA damage checkpoint signaling	BP	1	MDM2,BABAM2,PTPN11,TP53BP1,CDKN1A	darkgreen	VSMC_M4
GO:0031110	0.86	0.27	4	79	regulation of microtubule polymerization or depolymerization	BP	1	OCLN,MID1,MAPRE2,GAS2L2	darkgreen	VSMC_M4
GO:0035194	0.86	0.26	5	112	post-transcriptional gene silencing by RNA	BP	1	NCOR2,HELZ,MAEL,MIR99A,MIR331	darkgreen	VSMC_M4
GO:0007219	0.86	0.24	7	138	Notch signaling pathway	BP	1	GATA2,SORBS2,APP,CHAC1,NCSTN,PLN,YAP1	darkgreen	VSMC_M4
GO:0015931	0.86	0.22	9	181	nucleobase-containing compound transport	BP	1	SLC35D3,GJA1,SLC25A4,G3BP2,ATXN2,CD47,EPG5,RBFOX1,LRRC8C	darkgreen	VSMC_M4
GO:0030218	0.86	0.25	5	102	erythrocyte differentiation	BP	1	CITED2,HIPK2,GATA2,P4HTM,HIF1A	darkgreen	VSMC_M4
GO:0006886	0.87	0.17	44	739	intracellular protein transport	BP	1	SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,LEP,RIC1,SNX13,PEX13,MDFIC,TCAF1,GGA3,USP6NL,ZDHHC2,TRIM23,EXOC6,KIF13B,CLU,SCARB2,PTPN11,HERPUD1,ATG13,RAB29,TXNIP,SEC24B,PTPN14,PRKD1,AP3B2,AKAP6,HSPB1,EXPH5,NLGN1,AP1S3,FAF2,EVI5L,ABLIM3,SH3TC2,FLNA,AHCYL1,SORT1,TBC1D13,WLS,CDKN1A	darkgreen	VSMC_M4
GO:0034654	0.87	0.15	185	2841	nucleobase-containing compound biosynthetic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,ADCY6,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,ADA,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,AK7,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,ADCY9,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AK5,AFF3,ZSCAN30,LOX,TBX20,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0044770	0.87	0.18	24	426	cell cycle phase transition	BP	1	BCL2,MDM2,TPD52L1,CDKN2B,FAM122A,JADE1,SMARCD3,BABAM2,LATS2,APP,PTPN11,RBL2,TP53BP1,RDX,DACT1,APBB2,CCNG1,CRLF3,SKP2,PLCG2,CDC7,CDKN1A,CNTD2,NACC2	darkgreen	VSMC_M4
GO:0061136	0.87	0.22	8	166	regulation of proteasomal protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,CLU,HERPUD1,N4BP1,DAB2,GABARAPL2	darkgreen	VSMC_M4
GO:0043433	0.87	0.23	6	126	negative regulation of DNA-binding transcription factor activity	BP	1	IRAK3,WFS1,CYP1B1,G3BP2,ID3,FLNA	darkgreen	VSMC_M4
GO:0002819	0.87	0.24	5	111	regulation of adaptive immune response	BP	1	CD274,IL18R1,MAP3K7,ADA,TP53BP1	darkgreen	VSMC_M4
GO:0051101	0.87	0.25	4	91	regulation of DNA binding	BP	1	EP300,HIPK2,NGF,ZFP90	darkgreen	VSMC_M4

GO:0044248	0.87	0.15	109	1755	cellular catabolic process	BP	1	BCL2,RNF41,HSD17B6,MDM2,LAPTM4B,RNF19A,RNASET2,EP300,DAPK1,LEP,WFS1,FAM122A,C2orf40,PON2,RIC1,RNF149,PTPN3,PEX13,MAP3K7,SESN1,HIPK2,ABHD12,EXOG,ENTPD3,STT3B,ADAM9,FOXO1,CYP1B1,CPEB3,RMND5A,MAP1LC3A,SLC25A44,RNF34,CLU,ENTPD1,APP,SCARB2,HERPUD1,ATG13,PTPN22,CHAC1,CPQ,ADA,PLA2G4F,N4BP1,MARCH6,LPL,NT5C2,UBE3B,KCTD10,FEZ1,HTR2B,LGMN,PRKCA,SESN2,CTSS,LRP2,CTSZ,INPP5F,SYNPO2,CTSF,PRKD1,QSOX1,ZRANB1,ATF6,PRDX4,GABARAPL1,HSPB1,ACHE,PDE1A,RDX,MAOA,MAOB,NBR1,FMO4,USP11,ATG14,FBXL5,DACT1,JKAMP,HIF1A,FBXL20,PPARGC1A,FAF2,CALCOCO2,TOM1L1,EPG5,USP32,ATG4A,ULK2,DAB2,SKP2,PRKAA2,TMEM59,CTIF,DAPK3,MAP1LC3B2,PLCG2,LRSAM1,ITPR1,ACAD11,FBXO27,BNIP3,CST3,GABARAPL2,PIK3C2A,ORMDL3,ATP6V0E1,SCP2	darkgreen	VSMC_M4
GO:0090068	0.88	0.20	9	180	positive regulation of cell cycle process	BP	1	MDM2,SMARCD3,APP,PKP4,EDN1,LRP5,RDX,PLCG2,CDC7	darkgreen	VSMC_M4
GO:0040029	0.88	0.24	4	86	regulation of gene expression, epigenetic	BP	1	EP300,PCGF5,FAM172A,EZH1	darkgreen	VSMC_M4
GO:0050864	0.88	0.24	4	93	regulation of B cell activation	BP	1	BCL2,ADA,TP53BP1,CDKN1A	darkgreen	VSMC_M4
GO:0007127	0.88	0.24	4	94	meiosis I	BP	1	SUN1,MAEL,TEX11,HFM1	darkgreen	VSMC_M4
GO:0030516	0.88	0.24	4	83	regulation of axon extension	BP	1	SEMA3C,SEMA5A,SHTN1,MAP3K13	darkgreen	VSMC_M4
GO:0043161	0.89	0.16	20	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	MDM2,RNF19A,WFS1,FAM122A,C2orf40,STT3B,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,KCTD10,FBXL5,JKAMP,FBXL20,FAF2,DAB2,SKP2,FBXO27	darkgreen	VSMC_M4
GO:0031570	0.89	0.22	5	111	DNA integrity checkpoint signaling	BP	1	MDM2,BABAM2,PTPN11,TP53BP1,CDKN1A	darkgreen	VSMC_M4
GO:0006325	0.89	0.16	17	301	chromatin organization	BP	1	SHPRH,MLLT3,SMARCD3,BABAM2,SATB1,LMNTD2,CHD7,TCF7L1,FAM172A,CHD6,RBL2,SMARCAD1,KDM5B,EZH1,CHD3,SMARCA1,DAPK3	darkgreen	VSMC_M4
GO:1901890	0.89	0.23	4	82	positive regulation of cell junction assembly	BP	1	ADGRB1,PTPN11,NLGN1,LRRC24	darkgreen	VSMC_M4
GO:0006338	0.89	0.18	9	175	chromatin remodeling	BP	1	SHPRH,SMARCD3,SATB1,CHD7,SMARCAD1,KDM5B,EZH1,CHD3,SMARCA1	darkgreen	VSMC_M4
GO:0052126	0.89	0.20	6	127	movement in host environment	BP	1	MRC1,SCARB2,PTX3,F11R,LGALS9,ICAM1	darkgreen	VSMC_M4
GO:0051726	0.89	0.14	49	827	regulation of cell cycle	BP	1	BCL2,CITED2,MDM2,SMOC2,LEP,CDKN2B,FAM122A,TMEM8B,TGFBR1,PTPN3,JADE1,HIPK2,SMARCD3,BABAM2,LATS2,CDKL2,MEIS2,APP,PTPN11,CCNT1,JMY,PKP4,RBL2,EDN1,LRP5,LGMN,PRKCA,AFAP1L2,FGFR2,TP53BP1,ID3,LRP6,RDX,DACT1,APBB2,CCPG1,GNAI1,ZFYVE26,CCNG1,TOM1L1,BBS4,CRLF3,SKP2,DAPK3,PLCG2,CDC7,CDKN1A,CNTD2,NACC2	darkgreen	VSMC_M4
GO:0070647	0.89	0.14	48	806	protein modification by small protein conjugation or removal	BP	1	BCL2,RNF41,SHPRH,SASH1,MDM2,RNF19A,ANGPT1,ADGRB1,WFS1,SH3RF3,DCUN1D4,RNF149,TGFBR1,KLHL7,MKRN2,LMO7,BABAM2,FBXO3,PCGF5,MARCH5,TRIM23,RMND5A,RNF141,SH3RF1,RNF34,HECTD4,HERPUD1,PTPN22,AKTIP,N4BP1,MARCH6,UBE3B,KCTD10,ARRDC4,WDTC1,USP53,TRIM63,ZRANB1,USP11,FBXL5,HIF1A,DCAF5,USP32,MARCH2,SKP2,LRSAM1,FBXO27,FBXO28	darkgreen	VSMC_M4
GO:0016458	0.90	0.18	8	169	gene silencing	BP	1	NCOR2,FAM172A,HELZ,EZH1,MAEL,MARF1,MIR99A,MIR331	darkgreen	VSMC_M4
GO:0032886	0.90	0.17	11	202	regulation of microtubule-based process	BP	1	OCLN,FEZ1,MID1,GNAI1,BBS4,MAPRE2,GAS2L2,RHOT1,PATJ,PRKAA2,CCR6	darkgreen	VSMC_M4
GO:1903047	0.90	0.14	35	608	mitotic cell cycle process	BP	1	BCL2,MDM2,GJA1,TPD52L1,CDKN2B,FAM122A,JADE1,SMARCD3,BABAM2,TACC1,ANKLE2,EML4,LATS2,APP,RBL2,EDN1,LRP5,PRKCA,RDX,DACT1,GNAI1,ZFYVE26,CCNG1,TOM1L1,BBS4,TTC19,CRLF3,SKP2,DAPK3,FLNA,CDC7,CDKN1A,CNTD2,NACC2,REEP3	darkgreen	VSMC_M4
GO:0019438	0.90	0.12	187	2902	aromatic compound biosynthetic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,ADCY6,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,ADA,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,AK7,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,ADCY9,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AK5,AFF3,ZSCAN30,LOX,TBX20,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:2001022	0.90	0.21	4	95	positive regulation of response to DNA damage stimulus	BP	1	BABAM2,ANKRD1,EYA2,NACC2	darkgreen	VSMC_M4
GO:0070507	0.90	0.18	7	135	regulation of microtubule cytoskeleton organization	BP	1	OCLN,MID1,GNAI1,MAPRE2,GAS2L2,PATJ,PRKAA2	darkgreen	VSMC_M4
GO:0051250	0.90	0.21	4	99	negative regulation of lymphocyte activation	BP	1	CD274,PTPN22,RIPOR2,LGALS9	darkgreen	VSMC_M4
GO:0045786	0.90	0.15	16	306	negative regulation of cell cycle	BP	1	BCL2,MDM2,CDKN2B,FAM122A,PTPN3,JADE1,BABAM2,LATS2,PTPN11,RBL2,TP53BP1,DACT1,APBB2,TOM1L1,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0035303	0.90	0.20	5	106	regulation of dephosphorylation	BP	1	ANKLE2,RCAN1,NPNT,PPP1R36,PPP1R26	darkgreen	VSMC_M4
GO:0050768	0.90	0.20	5	102	negative regulation of neurogenesis	BP	1	REST,SEMA3C,ABCC8,SEMA5A,ULK2	darkgreen	VSMC_M4
GO:1903050	0.90	0.17	9	192	regulation of proteolysis involved in cellular protein catabolic process	BP	1	MDM2,RNF19A,FAM122A,HIPK2,CLU,HERPUD1,N4BP1,DAB2,GABARAPL2	darkgreen	VSMC_M4
GO:0061982	0.90	0.21	4	99	meiosis I cell cycle process	BP	1	SUN1,MAEL,TEX11,HFM1	darkgreen	VSMC_M4
GO:0007088	0.90	0.21	4	96	regulation of mitotic nuclear division	BP	1	EDN1,LRP5,TOM1L1,DAPK3	darkgreen	VSMC_M4
GO:0034101	0.90	0.19	5	111	erythrocyte homeostasis	BP	1	CITED2,HIPK2,GATA2,P4HTM,HIF1A	darkgreen	VSMC_M4

GO:1905475	0.90	0.17	7	147	regulation of protein localization to membrane	BP	1	TCAF1,ATP2C1,ZDHHC2,NUMB,CDH2,DAB2,TMEM59	darkgreen	VSMC_M4
GO:0006839	0.91	0.16	9	210	mitochondrial transport	BP	1	BCL2,MICU2,SLC25A4,ATG13,EYA2,SLC25A12,ABLIM3,RHOT1,BNIP3	darkgreen	VSMC_M4
GO:0051301	0.91	0.13	30	525	cell division	BP	1	MLLT3,BABAM2,LBH,TACC1,ANKLE2,EML4,LATS2,PDGFC,NEK4,CCNT1,PKP4,RBL2,NCOA3,HTR2B,TXNIP,PARD6B,FGFR2,MICAL3,GNAI1,ZFYVE26,NUMB,NEK9,TGFB3,CCNG1,BBS4,MAPRE2,TTC19,CDC7,FGF9,REEP3	darkgreen	VSMC_M4
GO:0018130	0.91	0.11	186	2900	heterocycle biosynthetic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,ADCY6,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,ADA,RBL2,EDN1,ETS2,KDM5B,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,AK7,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,DAPK3,ADCY9,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AK5,AFF3,ZSCAN30,LOX,TBX20,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0006275	0.91	0.19	4	92	regulation of DNA replication	BP	1	BRPF3,ID3,BCAR3,CDC7	darkgreen	VSMC_M4
GO:0051258	0.91	0.14	13	250	protein polymerization	BP	1	KANK1,PPP1R9A,CDC42EP3,WASF3,NCK1,OCLN,JMY,PREX1,RDX,PAK3,ARHGAP28,SPTAN1,ICAM1	darkgreen	VSMC_M4
GO:0016579	0.91	0.18	5	108	protein deubiquitination	BP	1	BABAM2,USP53,ZRANB1,USP11,USP32	darkgreen	VSMC_M4
GO:1902115	0.91	0.16	8	161	regulation of organelle assembly	BP	1	G3BP2,FEZ1,RDX,BBS4,EVI5L,PRKAA2,LRSAM1,YAP1	darkgreen	VSMC_M4
GO:0008104	0.91	0.11	129	2028	protein localization	BP	1	BCL2,SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,VLDLR,UNC13B,RIC1,REST,ICA1,FRMPD1,LMAN2L,SNX13,PREPL,LMBRD1,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,GGA3,INHBB,USP6NL,RAB2B,ACTN4,TM9SF2,ADAM9,ATP2C1,PCLO,ZDHHC2,RIC3,LATS2,ANKRD1,MARCH5,TRIM23,EXOC6,PAM,OCLN,KIF13B,G3BP2,CLU,SCARB2,SHROOM3,ABCC8,PTPN11,HERPUD1,ATG13,HNF4A,AKTIP,IFIT1,PDZD7,JAM3,NFASC,RAB29,ABCG1,RIPOR2,ACTN2,PFKL,LRP5,ARRDC4,NPNT,ZMAT3,TM7SF3,SUN1,TXNIP,SEC24B,MID1,SESN2,ADCY5,LRP2,PTPN14,PRKD1,NBEAL1,F11R,RAPGEF4,AP3B2,AKAP6,LRP6,HIP1,HSPB1,ACHE,RDX,EXPH5,EMC1,LMTK2,NLGN1,RABEP1,HIF1A,AP1S3,GNAI1,FAF2,NUMB,TGFB3,TOM1L1,BBS4,NPTN,MAPRE2,ATG4A,CDH2,GAS2L2,EVI5L,ABLIM3,SH3TC2,DAB2,PRKAA2,TMEM59,ATCAY,FLNA,VAMP7,AHCYL1,SORT1,TBC1D13,TERF2IP,LRSAM1,WLS,PIGK,CDKN1A,NACC2,GABARAPL2,ORMDL3,YAP1,BMP6,FAM83H,MAFA	darkgreen	VSMC_M4
GO:0044257	0.91	0.12	39	685	cellular protein catabolic process	BP	1	RNF41,MDM2,LAPTM4B,RNF19A,WFS1,FAM122A,C2orf40,RIC1,RNF149,HIPK2,STT3B,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,LGMN,CTSS,LRP2,CTSZ,CTSF,ZRANB1,RDX,USP11,FBXL5,DACT1,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,FBXO27,BNIP3,GABARAPL2	darkgreen	VSMC_M4
GO:0006282	0.91	0.18	5	118	regulation of DNA repair	BP	1	BABAM2,EYA2,TP53BP1,ZNF365,TERF2IP	darkgreen	VSMC_M4
GO:0051494	0.91	0.16	7	138	negative regulation of cytoskeleton organization	BP	1	KANK1,PPP1R9A,MID1,F11R,RDX,ARHGAP28,SPTAN1	darkgreen	VSMC_M4
GO:0051252	0.91	0.10	171	2654	regulation of RNA metabolic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,FAM172A,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,KDM5B,MXI1,RBM20,NCOA3,ACTN2,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,RBFOX1,DAPK3,TLE2,FLNA,AHCYL1,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,SRPK3,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0051054	0.91	0.15	8	176	positive regulation of DNA metabolic process	BP	1	GRHL2,SMOC2,BABAM2,ANXA3,EYA2,TP53BP1,PPARGC1A,PAK3	darkgreen	VSMC_M4
GO:0031109	0.92	0.17	5	109	microtubule polymerization or depolymerization	BP	1	OCLN,MID1,CRYAB,MAPRE2,GAS2L2	darkgreen	VSMC_M4
GO:0006997	0.92	0.17	5	112	nucleus organization	BP	1	HIPK2,ANKLE2,SUN1,PRKCA,REEP3	darkgreen	VSMC_M4
GO:0051961	0.92	0.17	5	106	negative regulation of nervous system development	BP	1	REST,SEMA3C,ABCC8,SEMA5A,ULK2	darkgreen	VSMC_M4

GO:0051656	0.92	0.12	18	334	establishment of organelle localization	BP	1	GJA1,DYNC1I1,SNAP91,GATA2,ACTN4,EML4,EXOC6,MYO1B,FEZ1,SUN1,AP3B2,NLGN1,HIF1A,ADGRE2,BBS4,RHOT1,LGALS9,VAMP7	darkgreen	VSMC_M4
GO:0007009	0.92	0.17	4	94	plasma membrane organization	BP	1	SH3GL2,CLU,ARV1,SH3TC2	darkgreen	VSMC_M4
GO:0019953	0.92	0.11	31	565	sexual reproduction	BP	1	BCL2,PKDREJ,AFF4,GJA1,LEP,UNC13B,SPATA6L,TGFBR1,TESK2,INHBB,THRB,GTSF1,APP,PTX3,ADA,JAM3,KDM5B,RGS2,MST1R,SUN1,MFGE8,PRDX4,MAEL,TEX11,BBS4,FST,MARF1,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0035195	0.92	0.17	4	107	gene silencing by miRNA	BP	1	NCOR2,MAEL,MIR99A,MIR331	darkgreen	VSMC_M4
GO:0031023	0.92	0.15	6	127	microtubule organizing center organization	BP	1	TUBE1,PARD6B,CHD3,BBS4,PATJ,CCDC78	darkgreen	VSMC_M4
GO:0022900	0.92	0.16	5	149	electron transport chain	BP	1	HSD17B6,SLC25A12,MAOB,CYP19A1,PPARGC1A	darkgreen	VSMC_M4
GO:0019219	0.93	0.09	183	2852	regulation of nucleobase-containing compound metabolic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,BABAM2,FOSL2,LBH,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,WWC2,TEAD1,FAM172A,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ANXA3,NEK4,CCNT1,JMY,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,SMARCAD1,KDM5B,EYA2,MXI1,RBM20,NCOA3,ACTN2,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,ZKSCAN2,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,PRKAA2,RBFOX1,DAPK3,TLE2,FLNA,AHCYL1,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AFF3,ZSCAN30,TBX20,SRPK3,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,DDIT4,VGLL3	darkgreen	VSMC_M4
GO:0019752	0.93	0.10	34	659	carboxylic acid metabolic process	BP	1	EP300,LEP,PDK4,SLC2A1,EDN2,PEX13,ABHD12,LIPT2,CYP1B1,PAM,APP,HNF4A,SERINC3,EDN1,PLA2G4F,LPL,ADIPOR1,TARSL2,PFKL,SESN2,ARV1,WDTC1,SLC25A12,RIMKLB,ENO2,HIF1A,PPARGC1A,PRKAA2,ATCAY,VNN1,ACAD11,SLC27A5,SCP2,DDIT4	darkgreen	VSMC_M4
GO:0043436	0.93	0.10	35	677	oxoacid metabolic process	BP	1	EP300,LEP,PDK4,SLC2A1,EDN2,PEX13,ABHD12,LIPT2,CYP1B1,PAM,APP,HNF4A,SERINC3,EDN1,PLA2G4F,LPL,ADIPOR1,TARSL2,PFKL,TPST2,SESN2,ARV1,WDTC1,SLC25A12,RIMKLB,ENO2,HIF1A,PPARGC1A,PRKAA2,ATCAY,VNN1,ACAD11,SLC27A5,SCP2,DDIT4	darkgreen	VSMC_M4
GO:0002683	0.93	0.11	14	290	negative regulation of immune system process	BP	1	IRAK3,ANGPT1,CD274,GATA2,LRCH1,TMEM178A,PTPN22,ADA,CD47,RIPOR2,TGFB3,MMP28,LGALS9,CD59	darkgreen	VSMC_M4
GO:0031047	0.93	0.14	5	129	gene silencing by RNA	BP	1	NCOR2,HELZ,MAEL,MIR99A,MIR331	darkgreen	VSMC_M4
GO:0009059	0.93	0.08	227	3569	macromolecule biosynthetic process	BP	1	ZNF516,DSEL,BCL2,PIGN,CITED2,UST,IRAK3,MDM2,GRHL2,SOD2,ABRA,ANGPT1,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ABCA1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,GYS1,HIPK2,GATA2,HS6ST1,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,STT3B,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,TUSC3,ZDHHC2,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ST3GAL5,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,CHST2,PTH,GYG1,EXTL3,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,NEK4,CCNT1,JMY,CHD6,DPY19L4,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,BACE2,KDM5B,TARSL2,RGS2,MXI1,NCOA3,ACTN2,LRP5,NPNT,B3GNT7,GYG2,GALNT3,B3GALNT2,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,CFLAR,WDTC1,MAN2A2,NDST3,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,CHST15,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,SECISBP2L,EZH1,FUT11,EIF4G3,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,PIGG,CHD3,TGFB3,MAGT1,SMAD6,GTF3C1,ZKSCAN2,GALNT10,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,PIGS,TMEM59,CTIF,DAPK3,TLE2,FLNA,CDH13,PLCG2,EXTL2,TERF2IP,BCAR3,CDC7,ZNF821,LMO4,CYR61,ZFP90,ST6GALNAC3,AFF3,ZSCAN30,LOX,TBX20,ITM2C,ZNF425,PIGK,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,ORMDL3,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0050727	0.93	0.11	11	239	regulation of inflammatory response	BP	1	ABHD12,FFAR3,APP,LBP,ADA,CD47,LPL,SERPINE1,RORA,VAMP7,PLCG2	darkgreen	VSMC_M4

GO:0033036	0.94	0.08	149	2356	macromolecule localization	BP	1	BCL2,SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,VLDLR,UNC13B,RIC1,REST,ICA1,FRMPD1,LMAN2L,SNX13,SLC2A1,PREPL,LMBRD1,ABCA1,DOP1A,SNAP91,PEX13,MDFIC,TCAF1,GGA3,INHBB,USP6NL,RAB2B,ACTN4,TM9SF2,ADAM9,ATP2C1,PCLO,ZDHHC2,RIC3,LATS2,ANKRD1,MARCH5,TRIM23,EXOC6,ESYT3,PAM,OCLN,KIF13B,G3BP2,CLU,ATXN2,SCARB2,SHROOM3,ABCC8,PTPN11,LBP,HERPUD1,ATG13,HNF4A,AKTIP,IFIT1,PDZD7,EDN1,JAM3,NFASC,PLA2G4F,LPL,RAB29,ABCG1,KDM5B,RIPOR2,ACTN2,PFKL,LRP5,ARRDC4,NPNT,ZMAT3,TM7SF3,SUN1,TXNIP,SEC24B,MID1,ATP9A,SESN2,ARV1,ADCY5,LRP2,FABP2,PTPN14,PRKD1,NBEAL1,F11R,RAPGEF4,AP3B2,AKAP6,LRP6,HIP1,HSPB1,ACHE,RDX,EXPH5,GULP1,EMC1,CYP19A1,LMTK2,NLGN1,RABEP1,HIF1A,AP1S3,GNAI1,DISP3,FAF2,NUMB,TGFB3,TOM1L1,BBS4,NPTN,STOML1,MAPRE2,ATG4A,CDH2,GAS2L2,EVI5L,ABLIM3,SH3TC2,DAB2,PRKAA2,TMEM59,RBFOX1,ATCAY,FLNA,VAMP7,AHCYL1,SORT1,TBC1D13,TERF2IP,ABCA4,LRSAM1,WLS,PIGK,CDKN1A,NACC2,SLC27A5,GABARAPL2,PRELID2,ORMDL3,YAP1,BMP6,FAM83H,SCP2,MAFA	darkgreen	VSMC_M4
GO:0072073	0.94	0.13	5	115	kidney epithelium development	BP	1	BCL2,NPNT,FGFR2,SMAD6,YAP1	darkgreen	VSMC_M4
GO:0034645	0.94	0.07	224	3533	cellular macromolecule biosynthetic process	BP	1	ZNF516,DSEL,BCL2,PIGN,CITED2,UST,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ABCA1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,GYS1,HIPK2,GATA2,HS6ST1,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,STT3B,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,TUSC3,ZDHHC2,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ST3GAL5,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,GYG1,EXTL3,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,NEK4,CCNT1,JMY,CHD6,DPY19L4,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,BACE2,KDM5B,TARSL2,RGS2,MXI1,NCOA3,ACTN2,LRP5,NPNT,B3GNT7,GYG2,GALNT3,B3GALNT2,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,NGRN,CFLAR,WDTC1,MAN2A2,NDST3,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,CHST15,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,SECISBP2L,EZH1,FUT11,EIF4G3,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,RORA,PIGG,CHD3,TGFB3,MAGT1,SMAD6,GTF3C1,ZKSCAN2,GALNT10,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,PIGS,TMEM59,CTIF,DAPK3,TLE2,FLNA,CDH13,PLCG2,EXTL2,TERF2IP,BCAR3,CDC7,ZNF821,LMO4,CYR61,ZFP90,ST6GALNAC3,AFF3,ZSCAN30,LOX,TBX20,ITM2C,ZNF425,PIGK,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0006333	0.94	0.14	4	106	chromatin assembly or disassembly	BP	1	SHPRH,SMARCD3,LMNTD2,CHD3	darkgreen	VSMC_M4
GO:0009987	0.94	0.07	783	11676	cellular process	BP	1	MBP,ZNF516,DOK6,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,HSD17B6,COL23A1,SLC35D3,IFNGR1,CITED2,STX11,SHPRH,SASH1,UST,IRAK3,GRIP1,MDM2,DDR1,LAPTM4B,CDSN,RGS22,RNF19A,IPCEF1,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,FAM19A5,PKDREJ,TRPS1,RNASET2,SMOC2,CALHM5,SCUBE1,AFF4,GJA1,ZHX1,TRDN,TPD52L1,TATDN1,LAMA2,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,AHCYL2,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,DOCK8,SH3RF3,KANK1,DCUN1D4,SGCB,RASL11B,VLDLR,UNC13B,TPM2,C2orf40,PPP1R9A,CD274,PON2,RIC1,PDK4,IL18R1,DYNC1I1,RNF149,CREB3,ZNF169,TMEM8B,REST,ICA1,RECK,ECM2,IGFBP7,ZAP70,FRMPD1,LMAN2L,SNX13,SLC2A1,TGFBR1,PREPL,LMBRD1,EDN2,SYT5,SLC17A5,ABCA1,ZNF331,KLHL7,PTPN3,DOP1A,SVEP1,SNAP91,PAPOLG,TBX18,PEX13,CHN2,MAP3K7,NT5C3A,CALD1,ANTXR1,DOCK4,KIDINS220,MDFIC,GPR63,PAPPA,TCAF1,FZD8,EPHB6,SESN1,JADE1,GYS1,MAP3K8,ITSN2,TUBE1,HIPK2,GATA2,PLEKHB2,HS6ST1,ENKUR,APBB1IP,LIMS2,ABHD12,TMEM135,ZNF398,ITM2B,PPP1R13L,LRCH1,SNRK,MRC1,TPT1,TESK2,TMCC1,ITGA8,TENM4,GGA3,NAA16,ELF1,ITGA9,INHBB,SMARCD3,USP6NL,PCDH9,MKRN2,GPR39,HRH1,EXOG,LMO7,ITIH5,ENTPD3,CD93,PFKFB3,NXPH2,BABAM2,FOSL2,ANKRD16,RALGAPA2,SYNGR2,LBH,STT3B,RNASE4,NDRG2,LIPT2,KCNE3,POLB,LMCD1,ARHGEF17,RAB2B,SALL2,THRB,PLCB4,ACTN4,TM9SF2,FMNL2,SATB1,ADAM9,TACC1,CRIM1,FGF14,SUMF1,FOXO1,TRPC4,RASSF2,SLC16A3,ATP2C1,COL4A1,COL4A2,ANKLE2,PCDHB4,QPCT,CDC42EP3,CYP1B1,CPNE4,PCLO,VEZT,SEMA3C,GTSF1,TMEM178A,DNHD1,EML4,L	darkgreen	VSMC_M4
GO:0010498	0.94	0.09	22	434	proteasomal protein catabolic process	BP	1	RNF41,MDM2,RNF19A,WFS1,FAM122A,C2orf40,STT3B,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,KCTD10,FBXL5,JKAMP,FBXL20,FAF2,DAB2,SKP2,FBXO27,GABARAPL2	darkgreen	VSMC_M4
GO:0000724	0.94	0.12	5	124	double-strand break repair via homologous recombination	BP	1	TP53BP1,ZNF365,ZFYVE26,TERF2IP,CDC7	darkgreen	VSMC_M4
GO:0006913	0.94	0.10	12	257	nucleocytoplasmic transport	BP	1	MDM2,ABRA,ANGPT1,LEP,MDFIC,PTPN11,TXNIP,PTPN14,PRKD1,FLNA,AHCYL1,CDKN1A	darkgreen	VSMC_M4
GO:0051169	0.94	0.10	12	257	nuclear transport	BP	1	MDM2,ABRA,ANGPT1,LEP,MDFIC,PTPN11,TXNIP,PTPN14,PRKD1,FLNA,AHCYL1,CDKN1A	darkgreen	VSMC_M4
GO:0007224	0.94	0.12	5	119	smoothened signaling pathway	BP	1	SCUBE1,HIPK2,FGFR2,DISP3,RORA	darkgreen	VSMC_M4
GO:0006082	0.94	0.08	35	689	organic acid metabolic process	BP	1	EP300,LEP,PDK4,SLC2A1,EDN2,PEX13,ABHD12,LIPT2,CYP1B1,PAM,APP,HNF4A,SERINC3,EDN1,PLA2G4F,LPL,ADIPOR1,TARSL2,PFKL,TPST2,SESN2,ARV1,WDTC1,SLC25A12,RIMKLB,ENO2,HIF1A,PPARGC1A,PRKAA2,ATCAY,VNN1,ACAD11,SLC27A5,SCP2,DDIT4	darkgreen	VSMC_M4
GO:0048706	0.94	0.13	4	105	embryonic skeletal system development	BP	1	GRHL2,TGFBR1,FGFR2,TGFB3	darkgreen	VSMC_M4
GO:0000725	0.95	0.11	5	126	recombinational repair	BP	1	TP53BP1,ZNF365,ZFYVE26,TERF2IP,CDC7	darkgreen	VSMC_M4

GO:0034249	0.95	0.10	8	183	negative regulation of cellular amide metabolic process	BP	1	DAPK1,GGA3,CPEB3,CLU,RGS2,SESN2,DAPK3,ORMDL3	darkgreen	VSMC_M4
GO:0044282	0.95	0.09	12	284	small molecule catabolic process	BP	1	HSD17B6,LEP,PEX13,GALM,ADA,PFKL,LRP5,SESN2,SLC25A12,OCRL,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0010639	0.95	0.08	15	297	negative regulation of organelle organization	BP	1	KANK1,PPP1R9A,CLU,FEZ1,MID1,F11R,RDX,PPARGC1A,TOM1L1,EVI5L,ARHGAP28,SPTAN1,TERF2IP,BNIP3,YAP1	darkgreen	VSMC_M4
GO:0051260	0.95	0.11	5	128	protein homooligomerization	BP	1	SOD2,G3BP2,KCTD10,TP53BP1,NACC2	darkgreen	VSMC_M4
GO:1901605	0.95	0.11	5	146	alpha-amino acid metabolic process	BP	1	HNF4A,SERINC3,SLC25A12,RIMKLB,ATCAY	darkgreen	VSMC_M4
GO:0072594	0.95	0.08	17	355	establishment of protein localization to organelle	BP	1	ABRA,ANGPT1,LEP,PEX13,MDFIC,GGA3,CLU,SCARB2,HERPUD1,ATG13,TXNIP,PRKD1,ABLIM3,FLNA,SORT1,LRSAM1,CDKN1A	darkgreen	VSMC_M4
GO:0050866	0.95	0.11	5	136	negative regulation of cell activation	BP	1	CD274,PTPN22,RIPOR2,LGALS9,PRKG1	darkgreen	VSMC_M4
GO:0051783	0.95	0.11	4	114	regulation of nuclear division	BP	1	EDN1,LRP5,TOM1L1,DAPK3	darkgreen	VSMC_M4
GO:0018205	0.95	0.08	15	313	peptidyl-lysine modification	BP	1	MDM2,EP300,BRD8,BRPF3,MAP3K7,JADE1,GATA2,LIPT2,NCOA3,YEATS2,EZH1,PPARGC1A,PLOD1,PRKAA2,LOX	darkgreen	VSMC_M4
GO:0070646	0.95	0.10	5	125	protein modification by small protein removal	BP	1	BABAM2,USP53,ZRANB1,USP11,USP32	darkgreen	VSMC_M4
GO:0002695	0.95	0.11	4	118	negative regulation of leukocyte activation	BP	1	CD274,PTPN22,RIPOR2,LGALS9	darkgreen	VSMC_M4
GO:0051052	0.95	0.08	14	297	regulation of DNA metabolic process	BP	1	GRHL2,SMOC2,GJA1,BABAM2,ANKRD1,ANXA3,SMARCAD1,EYA2,TP53BP1,ZNF365,PPARGC1A,PAK3,TERF2IP,CDKN1A	darkgreen	VSMC_M4
GO:0010608	0.96	0.07	24	480	posttranscriptional regulation of gene expression	BP	1	DAPK1,NCOR2,CPEB3,NCK1,APP,ATXN2,RGS2,PRKCA,HELZ,SESN2,NGRN,RBM4B,FAM129A,HSPB1,EIF4A2,SECISBP2L,EIF4G3,ATG14,MAEL,MARF1,CTIF,DAPK3,MIR99A,MIR331	darkgreen	VSMC_M4
GO:0000075	0.96	0.09	6	155	cell cycle checkpoint signaling	BP	1	MDM2,FAM122A,BABAM2,PTPN11,TP53BP1,CDKN1A	darkgreen	VSMC_M4
GO:0016570	0.96	0.07	21	399	histone modification	BP	1	EP300,BRD8,BRPF3,REST,MAP3K7,JADE1,GATA2,PCGF5,SMARCAD1,KDM5B,EYA2,NCOA3,PRKCA,YEATS2,CAMK2D,PRKD1,EZH1,SIN3B,PPARGC1A,PRKAA2,HOPX	darkgreen	VSMC_M4
GO:0007093	0.96	0.10	4	117	mitotic cell cycle checkpoint signaling	BP	1	MDM2,FAM122A,BABAM2,CDKN1A	darkgreen	VSMC_M4
GO:0006417	0.96	0.07	16	341	regulation of translation	BP	1	DAPK1,CPEB3,NCK1,APP,ATXN2,RGS2,SESN2,NGRN,RBM4B,FAM129A,HSPB1,EIF4A2,SECISBP2L,EIF4G3,CTIF,DAPK3	darkgreen	VSMC_M4
GO:1901566	0.96	0.05	71	1317	organonitrogen compound biosynthetic process	BP	1	DSEL,BCL2,PIGN,UST,ANGPT1,DAPK1,PDK4,ABCA1,HS6ST1,ITM2B,STT3B,TUSC3,ZDHHC2,CHPT1,CPEB3,NCK1,PAM,ST3GAL5,CHST2,EXTL3,APP,ATXN2,ADCY6,DPY19L4,LPCAT2,CHAC1,SERINC3,ADA,BACE2,TARSL2,RGS2,B3GNT7,GALNT3,B3GALNT2,SESN2,ADCY5,NGRN,MAN2A2,NDST3,RBM4B,PRKD1,NCSTN,CHST15,SLC25A12,FAM129A,HSPB1,EIF4A2,ACHE,SECISBP2L,FUT11,EIF4G3,HIF1A,PPARGC1A,NPPB,PIGG,MAGT1,GALNT10,PGRMC1,PIGS,TMEM59,CTIF,DAPK3,ADCY9,EXTL2,CYR61,AK5,ST6GALNAC3,ITM2C,PIGK,RFK,ORMDL3	darkgreen	VSMC_M4
GO:0015980	0.96	0.07	10	259	energy derivation by oxidation of organic compounds	BP	1	LEP,GYS1,PTH,GYG1,GYG2,SLC25A12,HIF1A,OPN3,PPARGC1A,BNIP3	darkgreen	VSMC_M4
GO:1901565	0.96	0.05	59	1069	organonitrogen compound catabolic process	BP	1	RNF41,IRAK3,MDM2,LAPTM4B,RNF19A,GJA1,ADGRB1,WFS1,FAM122A,C2orf40,RIC1,RNF149,PTPN3,HIPK2,ABHD12,GGA3,STT3B,ADAM9,FOXO1,ZDHHC2,RMND5A,RNF34,CLU,HERPUD1,CHAC1,CPQ,ADA,N4BP1,MARCH6,NT5C2,UBE3B,KCTD10,LGMN,CTSS,LRP2,CTSZ,SYNPO2,CTSF,ZRANB1,PDE1A,RDX,MAOA,MAOB,USP11,FBXL5,DACT1,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,FLNA,LRSAM1,FBXO27,BNIP3,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:0140013	0.96	0.08	5	139	meiotic nuclear division	BP	1	SUN1,MAEL,TEX11,MARF1,HFM1	darkgreen	VSMC_M4
GO:0051668	0.97	0.05	28	537	localization within membrane	BP	1	GRIP1,FRMPD1,PREPL,TCAF1,GGA3,TM9SF2,ATP2C1,ZDHHC2,EXOC6,NFASC,RAB29,ACTN2,ATP9A,INPP5F,F11R,LRP6,RDX,EMC1,LMTK2,NLGN1,RABEP1,NUMB,EPG5,CDH2,DAB2,TMEM59,FLNA,CDH13	darkgreen	VSMC_M4
GO:0044249	0.97	0.04	267	4271	cellular biosynthetic process	BP	1	ZNF516,DSEL,BCL2,PIGN,HSD17B6,CITED2,UST,IRAK3,MDM2,GRHL2,SOD2,ABRA,ANGPT1,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,PIP5K1B,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,EDN2,ABCA1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,GYS1,HIPK2,GATA2,HS6ST1,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,HRH1,LMO7,FOSL2,LBH,STT3B,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,TUSC3,ZDHHC2,MIER3,NCOR2,FFAR3,ZC3H6,CHD7,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,ST3GAL5,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,CHST2,PTH,GYG1,EXTL3,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,PTX3,ADCY6,NEK4,CCNT1,JMY,CHD6,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,NAB1,ADA,RBL2,EDN1,CD47,PLA2G4F,ETS2,BACE2,LPL,KDM5B,TARSL2,RGS2,AGPAT3,MXI1,NCOA3,ACTN2,LRP5,NPNT,HTR2B,B3GNT7,GYG2,GALNT3,B3GALNT2,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,NGRN,CFLAR,WDTC1,INPP5F,MAN2A2,NDST3,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,PI4KB,CHST15,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,ACHE,CRYAB,MAOB,ZNF445,SECISBP2L,EZH1,FUT11,EIF4G3,CYP19A1,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,PIGG,CHD3,TGFB3,MAT2B,MAGT1,SMAD6,GTF3C1,ZKSCAN2,GALNT10,AK7,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,OCRL,PIGS,PRKAA2,TMEM59,CTIF,DAPK3,ADCY9,TLE2,FLNA,CDH13,PLCG2,EXTL2,TERF2	darkgreen	VSMC_M4

GO:0009058	0.97	0.04	275	4393	biosynthetic process	BP	1	ZNF516,DSEL,BCL2,PIGN,HSD17B6,CITED2,UST,JRAK3,MDM2,GRHL2,SOD2,ABRA,ANGPT1,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,PIP5K1B,PDK4,IL18R1,CREB3,ZNF169,REST,IGFBP7,TGFBR1,EDN2,ABCA1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,GYS1,HIPK2,GATA2,HS6ST1,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,HRH1,LMO7,FOSL2,LBH,STT3B,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,TUSC3,ZDHHC2,MIER3,NCOR2,FFAR3,ZC3H6,CHD7,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,ST3GAL5,ATOH8,CLCN3,TCF7L1,ELL2,WWC2,TEAD1,CHST2,PTH,GYG1,EXTL3,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,PTX3,ADCY6,NEK4,CCNT1,JMY,CHD6,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,NAB1,ADA,RBL2,EDN1,CD47,PLA2G4F,ETS2,BACE2,LPL,ABCG1,KDM5B,TARSL2,RGS2,AGPAT3,MXI1,NCOA3,ACTN2,LRP5,NPNT,HTR2B,B3GNT7,GYG2,GALNT3,B3GALNT2,AFAP1L2,TXNIP,SESN2,ARV1,YEATS2,ZNF710,CAMK2D,ADCY5,NGRN,CFLAR,WDTC1,INPP5F,MAN2A2,NDST3,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,PI4KB,CHST15,SLC25A12,STRN3,ARID5B,PPIP5K1,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,ACHE,CRYAB,MAOB,ZNF445,SECISBP2L,EZH1,FUT11,EIF4G3,CYP19A1,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,PIGG,CHD3,TGFB3,MAT2B,MAGT1,SMAD6,GTF3C1,ZKSCAN2,FAXDC2,GALNT10,AK7,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,OCRL,PIGS,PRKAA2,TMEM59,CTIF,	darkgreen	VSMC_M4
GO:0007276	0.97	0.05	23	469	gamete generation	BP	1	BCL2,AFF4,GJA1,LEP,SPATA6L,TGFBR1,TESK2,INHBB,GTSF1,PTX3,JAM3,RGS2,SUN1,PRDX4,MAEL,TEX11,BBS4,FST,MARF1,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0006996	0.97	0.04	185	2943	organelle organization	BP	1	BCL2,STX11,SHPRH,LAPTM4B,RNF19A,SOD2,GJA1,TRDN,EP300,MRTFA,MLLT3,LIMCH1,KANK1,UNC13B,TPM2,PPP1R9A,LMAN2L,TGFBR1,ABCA1,SNAP91,PEX13,CALD1,ANTXR1,TUBE1,HIPK2,TMEM135,TESK2,TMCC1,SMARCD3,USP6NL,BABAM2,ARHGEF17,ACTN4,FMNL2,SATB1,TACC1,ATP2C1,ANKLE2,CDC42EP3,PCLO,EML4,LMNTD2,TF,AMOTL2,WASF3,ZDHHC2,CHD7,ANKRD1,EPB41L4A,MARCH5,NCK1,SORBS2,ESYT3,MAP1LC3A,PAM,SLC25A4,CLCN3,OCLN,TCF7L1,FAM172A,LYSMD3,G3BP2,CLU,ATXN2,SCARB2,PRPH,SHROOM3,JMY,ATG13,CHD6,AKTIP,RBL2,EDN1,JAM3,CD47,SMARCAD1,MYO1B,SEMA5A,RAB29,ABCG1,DNAH7,KDM5B,MARCKSL1,EYA2,TNNT2,PDE4DIP,ACTN2,LRP5,FEZ1,PREX1,SUN1,PRKCA,SEC24B,ABLIM1,PARD6B,MID1,SESN2,SHTN1,CFLAR,SYNPO2,PRKD1,F11R,PLXNB1,LRCH3,ZRANB1,ZNF365,MAP7D2,HIP1,LNPK,GABARAPL1,CRYAB,ATP6AP2,RDX,EZH1,SYNPO2L,ATG14,EMC1,TNFSF10,NLGN1,WDR1,MAEL,HIF1A,IQSEC3,MICAL3,GNAI1,PPARGC1A,ACTN1,FAF2,SIPA1L1,CHD3,CALCOCO2,TEX11,TGFB3,IFT43,CNN1,TOM1L1,BBS4,NRK,MAPRE2,TTC19,SPECC1,SYNPO,CDH2,ULK2,PAK3,GAS2L2,PLS3,EVI5L,ABLIM3,RHOT1,ARHGAP28,SMARCA1,OCRL,MARF1,PATJ,PRKAA2,ATCAY,DAPK3,FLNA,CCDC78,VAMP7,SORT1,MAP1LC3B2,MBTPS1,SPTAN1,TERF2IP,LRSAM1,HFM1,NEXN,CCDC136,SPINK2,BNIP3,XIRP1,PDLIM3,CSRP1,PPM1E,DSTN,TMEM38A,GABARAPL2,ICAM1,YAP1,PRKG1,FAM83H,SCP2,REEP3	darkgreen	VSMC_M4
GO:0051603	0.97	0.04	33	639	proteolysis involved in cellular protein catabolic process	BP	1	RNF41,MDM2,RNF19A,WFS1,FAM122A,C2orf40,RNF149,HIPK2,STT3B,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,LGMN,CTSS,CTSZ,CTSF,ZRANB1,USP11,FBXL5,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,FBXO27,GABARAPL2	darkgreen	VSMC_M4
GO:1901575	0.97	0.04	93	1628	organic substance catabolic process	BP	1	RNF41,HSD17B6,IRAK3,MDM2,LAPTM4B,RNF19A,RNASET2,GJA1,EP300,ADGRB1,LEP,WFS1,FAM122A,C2orf40,RIC1,RNF149,PTPN3,PEX13,HIPK2,ABHD12,GGA3,EXOG,ENTPD3,STT3B,PLCB4,ADAM9,FOXO1,CYP1B1,GALM,ZDHHC2,CPEB3,RMND5A,RNF34,CLU,ENTPD1,APP,SCARB2,HERPUD1,CHAC1,CPQ,ADA,PLA2G4F,N4BP1,MARCH6,LPL,NT5C2,PFKL,UBE3B,LRP5,KCTD10,LGMN,PRKCA,SESN2,CTSS,LRP2,CTSZ,INPP5F,SYNPO2,CTSF,ZRANB1,SLC25A12,ACHE,PDE1A,RDX,MAOA,MAOB,ENO2,USP11,FBXL5,CYP19A1,DACT1,JKAMP,HIF1A,FBXL20,PPARGC1A,FAF2,TOM1L1,USP32,DAB2,OCRL,SKP2,PRKAA2,CTIF,FLNA,PLCG2,LRSAM1,ACAD11,FBXO27,BNIP3,CST3,GABARAPL2,SCP2,DDIT4	darkgreen	VSMC_M4
GO:0090150	0.97	0.06	8	210	establishment of protein localization to membrane	BP	1	GRIP1,FRMPD1,PREPL,TCAF1,GGA3,ATP2C1,ZDHHC2,EMC1	darkgreen	VSMC_M4
GO:0010564	0.97	0.04	26	515	regulation of cell cycle process	BP	1	BCL2,MDM2,CDKN2B,FAM122A,JADE1,SMARCD3,BABAM2,APP,PTPN11,PKP4,RBL2,EDN1,LRP5,TP53BP1,RDX,DACT1,APBB2,GNAI1,ZFYVE26,TOM1L1,BBS4,DAPK3,PLCG2,CDC7,CDKN1A,NACC2	darkgreen	VSMC_M4
GO:0090501	0.97	0.07	4	124	RNA phosphodiester bond hydrolysis	BP	1	RNASET2,EXOG,RNASE4,N4BP1	darkgreen	VSMC_M4
GO:0007098	0.98	0.06	4	115	centrosome cycle	BP	1	TUBE1,PARD6B,CHD3,BBS4	darkgreen	VSMC_M4
GO:0140694	0.98	0.04	14	305	non-membrane-bounded organelle assembly	BP	1	ANKRD1,G3BP2,ATXN2,EDN1,TNNT2,ACTN2,CFLAR,SYNPO2L,WDR1,MAPRE2,PRKAA2,FLNA,CCDC78,CSRP1	darkgreen	VSMC_M4
GO:0006310	0.98	0.05	10	245	DNA recombination	BP	1	POLB,SMARCAD1,TP53BP1,ZNF365,ZFYVE26,TEX11,TERF2IP,CDC7,HFM1,CCR6	darkgreen	VSMC_M4
GO:0006511	0.98	0.03	27	542	ubiquitin-dependent protein catabolic process	BP	1	MDM2,RNF19A,WFS1,FAM122A,C2orf40,RNF149,HIPK2,STT3B,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,ZRANB1,USP11,FBXL5,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,FBXO27	darkgreen	VSMC_M4
GO:0006302	0.98	0.04	9	225	double-strand break repair	BP	1	BABAM2,POLB,SMARCAD1,TP53BP1,ZNF365,ZFYVE26,MARF1,TERF2IP,CDC7	darkgreen	VSMC_M4

GO:0043170	0.98	0.03	449	7034	macromolecule metabolic process	BP	1	MBP,ZNF516,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,IFNGR1,CITED2,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,RNASET2,SMOC2,AFF4,GJA1,ZHX1,TPD52L1,TATDN1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,SH3RF3,DCUN1D4,VLDLR,C2orf40,PPP1R9A,CD274,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,ZAP70,TGFBR1,PREPL,LMBRD1,ABCA1,ZNF331,KLHL7,PTPN3,SVEP1,PAPOLG,TBX18,MAP3K7,ANTXR1,MDFIC,PAPPA,PREP,EPHB6,JADE1,GYS1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ZNF398,ITM2B,PPP1R13L,SNRK,TESK2,GGA3,NAA16,ELF1,INHBB,SMARCD3,MKRN2,EXOG,LMO7,ITIH5,BABAM2,FOSL2,ANKRD16,LBH,STT3B,RNASE4,NDRG2,LIPT2,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,SUMF1,FOXO1,RASSF2,COL4A2,ANKLE2,QPCT,CYP1B1,TF,EBF4,FLT3,TUSC3,ZDHHC2,MAP3K1,MIER3,NCOR2,FFAR3,FXYD1,HPN,FBXO3,PTPRG,ZC3H6,CHD7,LATS2,HIPK3,ANKRD1,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,ADM,RNF141,PAM,SH3RF1,ST3GAL5,ATOH8,GRK7,OCLN,TCF7L1,ELL2,WWC2,TEAD1,CHST2,FAM172A,PTH,GYG1,INTS9,EXTL3,RNF34,CDKL2,G3BP2,CLU,BLNK,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ABCC8,ANXA3,HECTD4,PTPN11,PTX3,LBP,NEK4,CCNT1,HERPUD1,PROS1,JMY,ZNF638,CHD6,PTPN22,DPY19L4,HNF4A,CHAC1,GDF6,CPQ,NAB1,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,SMARCAD1,MARCH6,BACE2,LPL,RAB29,ABCG1,TMPRSS7,KDM5B,TARSL2,DAPP1,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,UBE3B,LRP5,KCTD10,ARRDC4,NPNT,PLCL1	darkgreen	VSMC_M4
GO:1901576	0.98	0.03	268	4324	organic substance biosynthetic process	BP	1	ZNF516,DSEL,BCL2,PIGN,HSD17B6,CITED2,UST,IRAK3,MDM2,GRHL2,SOD2,ABRA,ANGPT1,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,BRPF3,TLE4,MLLT3,LEP,WFS1,DDX58,PIP5K1B,PDK4,IL18R1,CREB3,ZNF169,REST,IGFBP7,TGFBR1,EDN2,ABCA1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,GYS1,HIPK2,GATA2,HS6ST1,ZNF398,ITM2B,PPP1R13L,NAA16,ELF1,SMARCD3,HRH1,LMO7,FOSL2,LBH,STT3B,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,TUSC3,ZDHHC2,MIER3,NCOR2,ZC3H6,CHD7,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,ST3GAL5,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,CHST2,PTH,GYG1,EXTL3,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,ADCY6,NEK4,CCNT1,JMY,CHD6,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,NAB1,ADA,RBL2,EDN1,PLA2G4F,ETS2,BACE2,LPL,ABCG1,KDM5B,TARSL2,RGS2,AGPAT3,MXI1,NCOA3,ACTN2,LRP5,NPNT,HTR2B,B3GNT7,GYG2,GALNT3,B3GALNT2,AFAP1L2,TXNIP,SESN2,ARV1,YEATS2,ZNF710,CAMK2D,ADCY5,NGRN,CFLAR,WDTC1,INPP5F,MAN2A2,NDST3,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,PI4KB,CHST15,SLC25A12,STRN3,ARID5B,PPIP5K1,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,ACHE,CRYAB,ZNF445,SECISBP2L,EZH1,FUT11,EIF4G3,CYP19A1,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,PIGG,CHD3,TGFB3,MAT2B,MAGT1,SMAD6,GTF3C1,ZKSCAN2,FAXDC2,GALNT10,AK7,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,OCRL,PIGS,PRKAA2,TMEM59,CTIF,DAPK3,ADCY9,TLE2,FLNA,MBTPS1,CD	darkgreen	VSMC_M4
GO:0034613	0.98	0.03	84	1451	cellular protein localization	BP	1	SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,RIC1,FRMPD1,SNX13,PREPL,LMBRD1,PEX13,MDFIC,TCAF1,GGA3,USP6NL,TM9SF2,ATP2C1,ZDHHC2,RIC3,LATS2,MARCH5,TRIM23,EXOC6,OCLN,KIF13B,CLU,SCARB2,PTPN11,HERPUD1,ATG13,JAM3,NFASC,RAB29,RIPOR2,ACTN2,SUN1,TXNIP,SEC24B,MID1,SESN2,PTPN14,PRKD1,F11R,AP3B2,AKAP6,LRP6,HSPB1,RDX,EXPH5,EMC1,NLGN1,RABEP1,AP1S3,GNAI1,FAF2,NUMB,BBS4,NPTN,MAPRE2,CDH2,GAS2L2,EVI5L,ABLIM3,SH3TC2,DAB2,PRKAA2,TMEM59,FLNA,AHCYL1,SORT1,TBC1D13,TERF2IP,LRSAM1,WLS,PIGK,CDKN1A,NACC2,GABARAPL2,ORMDL3,YAP1,FAM83H	darkgreen	VSMC_M4
GO:0043484	0.98	0.05	4	126	regulation of RNA splicing	BP	1	REST,FAM172A,RBM20,RBFOX1	darkgreen	VSMC_M4
GO:0031056	0.98	0.05	4	124	regulation of histone modification	BP	1	GATA2,CAMK2D,PRKD1,PPARGC1A	darkgreen	VSMC_M4
GO:1903046	0.98	0.05	5	153	meiotic cell cycle process	BP	1	SUN1,MAEL,TEX11,MARF1,HFM1	darkgreen	VSMC_M4
GO:0019941	0.98	0.03	27	550	modification-dependent protein catabolic process	BP	1	MDM2,RNF19A,WFS1,FAM122A,C2orf40,RNF149,HIPK2,STT3B,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,ZRANB1,USP11,FBXL5,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,FBXO27	darkgreen	VSMC_M4
GO:0007017	0.98	0.03	38	715	microtubule-based process	BP	1	RNF19A,GJA1,TRDN,DYNC1I1,PEX13,TUBE1,ENKUR,TACC1,DNHD1,EML4,OCLN,KIF13B,APP,DNAH7,FEZ1,SUN1,PARD6B,MID1,DYNC1I2,MAP7D2,AP3B2,HSPB1,CRYAB,HIF1A,GNAI1,CHD3,IFT43,KIAA0556,BBS4,MAPRE2,GAS2L2,RHOT1,PATJ,PRKAA2,FLNA,CCDC78,VAMP7,CCR6	darkgreen	VSMC_M4
GO:0048232	0.98	0.03	16	371	male gamete generation	BP	1	AFF4,GJA1,SPATA6L,TESK2,GTSF1,JAM3,RGS2,SUN1,PRDX4,MAEL,TEX11,BBS4,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0051168	0.98	0.05	4	131	nuclear export	BP	1	MDM2,PTPN11,PTPN14,AHCYL1	darkgreen	VSMC_M4
GO:0070727	0.98	0.02	84	1462	cellular macromolecule localization	BP	1	SLC35D3,STX11,GRIP1,MDM2,ABRA,ANGPT1,GJA1,LEP,RIC1,FRMPD1,SNX13,PREPL,LMBRD1,PEX13,MDFIC,TCAF1,GGA3,USP6NL,TM9SF2,ATP2C1,ZDHHC2,RIC3,LATS2,MARCH5,TRIM23,EXOC6,OCLN,KIF13B,CLU,SCARB2,PTPN11,HERPUD1,ATG13,JAM3,NFASC,RAB29,RIPOR2,ACTN2,SUN1,TXNIP,SEC24B,MID1,SESN2,PTPN14,PRKD1,F11R,AP3B2,AKAP6,LRP6,HSPB1,RDX,EXPH5,EMC1,NLGN1,RABEP1,AP1S3,GNAI1,FAF2,NUMB,BBS4,NPTN,MAPRE2,CDH2,GAS2L2,EVI5L,ABLIM3,SH3TC2,DAB2,PRKAA2,TMEM59,FLNA,AHCYL1,SORT1,TBC1D13,TERF2IP,LRSAM1,WLS,PIGK,CDKN1A,NACC2,GABARAPL2,ORMDL3,YAP1,FAM83H	darkgreen	VSMC_M4
GO:0031503	0.98	0.04	7	186	protein-containing complex localization	BP	1	GRIP1,HIP1,NLGN1,NUMB,IFT43,NPTN,NACC2	darkgreen	VSMC_M4

GO:0070925	0.98	0.02	37	705	organelle assembly	BP	1	ANKRD1,MAP1LC3A,G3BP2,ATXN2,ATG13,EDN1,DNAH7,TNNT2,ACTN2,FEZ1,ABLIM1,CFLAR,SYNPO2,GABARAPL1,RDX,SYNPO2L,ATG14,NLGN1,WDR1,IFT43,BBS4,MAPRE2,SYNPO,ULK2,EVI5L,ABLIM3,OCRL,PRKAA2,FLNA,CCDC78,MAP1LC3B2,LRSAM1,CCDC136,SPINK2,CSRP1,GABARAPL2,YAP1	darkgreen	VSMC_M4
GO:0048285	0.98	0.03	18	401	organelle fission	BP	1	TMEM135,TMCC1,ANKLE2,EML4,MARCH5,EDN1,LRP5,SUN1,MAEL,PPARGC1A,TEX11,TOM1L1,MARF1,DAPK3,FLNA,HFM1,BNIP3,REEP3	darkgreen	VSMC_M4
GO:0072657	0.98	0.03	22	466	protein localization to membrane	BP	1	GRIP1,FRMPD1,PREPL,TCAF1,GGA3,TM9SF2,ATP2C1,ZDHHC2,NFASC,RAB29,ACTN2,F11R,LRP6,RDX,EMC1,NLGN1,RABEP1,NUMB,CDH2,DAB2,TMEM59,FLNA	darkgreen	VSMC_M4
GO:0007283	0.98	0.03	15	357	spermatogenesis	BP	1	AFF4,GJA1,SPATA6L,TESK2,GTSF1,JAM3,RGS2,SUN1,PRDX4,MAEL,BBS4,PCSK4,CCDC136,SPINK2,CCR6	darkgreen	VSMC_M4
GO:0022402	0.99	0.02	51	951	cell cycle process	BP	1	BCL2,MDM2,GJA1,TPD52L1,CDKN2B,FAM122A,C2orf40,JADE1,TUBE1,SMARCD3,BABAM2,TACC1,ANKLE2,EML4,LATS2,APP,PTPN11,PKP4,RBL2,EDN1,SMARCAD1,LRP5,SUN1,PRKCA,PARD6B,TP53BP1,RDX,DACT1,MAEL,APBB2,GNAI1,ZFYVE26,CHD3,TEX11,CCNG1,TOM1L1,BBS4,MAPRE2,TTC19,CRLF3,SKP2,MARF1,DAPK3,FLNA,PLCG2,CDC7,HFM1,CDKN1A,CNTD2,NACC2,REEP3	darkgreen	VSMC_M4
GO:0051259	0.99	0.03	6	174	protein complex oligomerization	BP	1	SOD2,G3BP2,KCTD10,TP53BP1,LRRC8C,NACC2	darkgreen	VSMC_M4
GO:0043632	0.99	0.02	27	561	modification-dependent macromolecule catabolic process	BP	1	MDM2,RNF19A,WFS1,FAM122A,C2orf40,RNF149,HIPK2,STT3B,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,ZRANB1,USP11,FBXL5,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,FBXO27	darkgreen	VSMC_M4
GO:0045333	0.99	0.03	5	191	cellular respiration	BP	1	SLC25A12,HIF1A,OPN3,PPARGC1A,BNIP3	darkgreen	VSMC_M4
GO:1902850	0.99	0.04	4	133	microtubule cytoskeleton organization involved in mitosis	BP	1	GJA1,TACC1,GNAI1,FLNA	darkgreen	VSMC_M4
GO:0017148	0.99	0.03	5	158	negative regulation of translation	BP	1	DAPK1,CPEB3,RGS2,SESN2,DAPK3	darkgreen	VSMC_M4
GO:0033365	0.99	0.02	37	737	protein localization to organelle	BP	1	MDM2,ABRA,ANGPT1,GJA1,LEP,LMBRD1,PEX13,MDFIC,GGA3,LATS2,MARCH5,CLU,SCARB2,HERPUD1,ATG13,RAB29,SUN1,TXNIP,MID1,SESN2,PRKD1,RDX,EMC1,RABEP1,BBS4,MAPRE2,GAS2L2,ABLIM3,FLNA,SORT1,TERF2IP,LRSAM1,CDKN1A,GABARAPL2,ORMDL3,YAP1,FAM83H	darkgreen	VSMC_M4
GO:0022607	0.99	0.01	132	2230	cellular component assembly	BP	1	BCL2,SHPRH,MDM2,GRHL2,SOD2,ANGPT1,GJA1,EP300,ADGRB1,SH3GL2,LIMCH1,KANK1,UNC13B,PPP1R9A,SLC2A1,TGFBR1,ABCA1,SNAP91,CALD1,ANTXR1,TESK2,TENM4,ANKLE2,PCDHB4,CDC42EP3,PCLO,LMNTD2,WASF3,RIC3,ANKRD1,NCK1,MAP1LC3A,OCLN,TEAD1,G3BP2,CLU,GPM6A,APP,ATXN2,PDGFC,PTPN11,JMY,ATG13,PKP4,FMOD,EDN1,JAM3,CD47,MYO1B,RAB29,DNAH7,RIPOR2,TNNT2,PDE4DIP,ACTN2,KCTD10,FEZ1,PREX1,PRKCA,ABLIM1,PARD6B,SHTN1,MYLK,CFLAR,SYNPO2,TP53BP1,F11R,PLXNB1,QSOX1,ITGA6,HIP1,GABARAPL1,ACHE,CRYAB,RDX,SYNPO2L,ATG14,MMP1,DACT1,NLGN1,WDR1,PPARGC1A,ACTN1,TEX11,TGFB3,IFT43,SMAD6,BBS4,NPTN,MAPRE2,TTC19,SYNPO,CDH2,ULK2,PAK3,PLS3,EVI5L,ABLIM3,ARHGAP28,OCRL,PATJ,PRKAA2,CDH18,MYO10,DAPK3,PLXNB3,FLNA,CCDC78,MAP1LC3B2,CDH13,PLCG2,SPTAN1,LRSAM1,LRRC8C,LMO4,CCDC136,SPINK2,PCDHB2,LOX,TBX20,LRRC24,CSRP1,SRPK3,PPM1E,MFAP4,NACC2,HOPX,GABARAPL2,ICAM1,PIK3C2A,YAP1,REEP3	darkgreen	VSMC_M4
GO:0007049	0.99	0.01	78	1405	cell cycle	BP	1	BCL2,CITED2,MDM2,SMOC2,GJA1,TPD52L1,EP300,LEP,CDKN2B,FAM122A,C2orf40,TMEM8B,TGFBR1,PTPN3,JADE1,MAP3K8,TUBE1,HIPK2,SMARCD3,BABAM2,TACC1,RASSF2,ANKLE2,EML4,LATS2,CDKL2,MEIS2,APP,PTPN11,NEK4,CCNT1,JMY,PKP4,RBL2,EDN1,SMARCAD1,RGS2,LRP5,LGMN,SUN1,PRKCA,AFAP1L2,TXNIP,PARD6B,FGFR2,TP53BP1,ID3,LRP6,RDX,DACT1,MAEL,APBB2,CCPG1,MICAL3,GNAI1,ZFYVE26,CHD3,TEX11,NEK9,CCNG1,TOM1L1,BBS4,MAPRE2,TTC19,CRLF3,SKP2,MARF1,DAPK3,FLNA,CDH13,PLCG2,CDC7,HFM1,OSGIN2,CDKN1A,CNTD2,NACC2,REEP3	darkgreen	VSMC_M4
GO:0046395	0.99	0.03	5	182	carboxylic acid catabolic process	BP	1	LEP,PEX13,SESN2,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0071103	0.99	0.02	7	200	DNA conformation change	BP	1	SHPRH,LMNTD2,CHD7,CHD6,SMARCAD1,CHD3,HFM1	darkgreen	VSMC_M4
GO:0016054	0.99	0.02	5	186	organic acid catabolic process	BP	1	LEP,PEX13,SESN2,ACAD11,SCP2	darkgreen	VSMC_M4
GO:0007051	0.99	0.02	5	165	spindle organization	BP	1	TACC1,GNAI1,CHD3,MAPRE2,FLNA	darkgreen	VSMC_M4
GO:0051321	0.99	0.02	6	192	meiotic cell cycle	BP	1	SUN1,MAEL,TEX11,MARF1,HFM1,OSGIN2	darkgreen	VSMC_M4

GO:0044238	0.99	0.01	481	7641	primary metabolic process	BP	1	MBP,ZNF516,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,HSD17B6,IFNGR1,CITED2,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TPD52L1,TATDN1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,SH3RF3,DCUN1D4,VLDLR,CASD1,C2orf40,PPP1R9A,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,IGFBP7,ZAP70,SLC2A1,TGFBR1,PREPL,EDN2,ABCA1,ZNF331,KLHL7,PTPN3,PAPOLG,TBX18,PEX13,MAP3K7,NT5C3A,ANTXR1,MDFIC,PAPPA,PREP,EPHB6,JADE1,GYS1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ZNF398,ITM2B,PPP1R13L,SNRK,TESK2,GGA3,NAA16,ELF1,INHBB,SMARCD3,MKRN2,HRH1,EXOG,LMO7,ITIH5,ENTPD3,PFKFB3,BABAM2,FOSL2,ANKRD16,LBH,STT3B,RNASE4,LIPT2,POLB,LMCD1,SALL2,THRB,PLCB4,ACTN4,SATB1,ADAM9,TACC1,CRIM1,SUMF1,FOXO1,RASSF2,COL4A2,ANKLE2,QPCT,CYP1B1,GALM,TF,EBF4,FLT3,TUSC3,ZDHHC2,MAP3K1,MIER3,NCOR2,FXYD1,HPN,FBXO3,PTPRG,ZC3H6,CHD7,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,ADM,RNF141,PAM,SH3RF1,ST3GAL5,ATOH8,GRK7,OCLN,TCF7L1,ELL2,WWC2,TEAD1,CHST2,FAM172A,PTH,GYG1,INTS9,EXTL3,RNF34,CDKL2,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ANXA3,HECTD4,PTPN11,PTX3,ADCY6,NEK4,CCNT1,HERPUD1,PROS1,JMY,ZNF638,CHD6,PTPN22,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,CPQ,NAB1,ADA,AKTIP,RCAN1,RBL2,NGF,EDN1,PLA2G4F,ETS2,N4BP1,SMARCAD1,MARCH6,BACE2,LPL,ABCG1,MTMR10,NT5C2,ADIPOR1,TMP	darkgreen	VSMC_M4
GO:0006518	0.99	0.01	30	688	peptide metabolic process	BP	1	IFNGR1,DAPK1,GGA3,CPEB3,NCK1,PAM,CLU,APP,ATXN2,CHAC1,CPQ,BACE2,ABCG1,TARSL2,RGS2,SESN2,NGRN,CTSZ,RBM4B,NCSTN,FAM129A,HSPB1,EIF4A2,ATP6AP2,SECISBP2L,EIF4G3,PCSK1N,CTIF,DAPK3,PCSK4	darkgreen	VSMC_M4
GO:0031348	0.99	0.02	4	149	negative regulation of defense response	BP	1	IRAK3,ADA,RORA,LGALS9	darkgreen	VSMC_M4
GO:0000910	0.99	0.02	4	141	cytokinesis	BP	1	PKP4,ZFYVE26,BBS4,TTC19	darkgreen	VSMC_M4
GO:0009057	0.99	0.01	57	1102	macromolecule catabolic process	BP	1	RNF41,IRAK3,MDM2,LAPTM4B,RNF19A,RNASET2,GJA1,ADGRB1,WFS1,FAM122A,C2orf40,RIC1,RNF149,PTPN3,HIPK2,ABHD12,GGA3,EXOG,STT3B,ADAM9,FOXO1,ZDHHC2,CPEB3,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,LGMN,PRKCA,CTSS,LRP2,CTSZ,SYNPO2,CTSF,ZRANB1,RDX,USP11,FBXL5,DACT1,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,CTIF,FLNA,LRSAM1,FBXO27,BNIP3,CST3,GABARAPL2	darkgreen	VSMC_M4
GO:0071704	0.99	0.01	509	8083	organic substance metabolic process	BP	1	MBP,ZNF516,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,HSD17B6,IFNGR1,CITED2,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,RNASET2,SMOC2,AFF4,GJA1,ZHX1,TPD52L1,TATDN1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,AHCYL2,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,SH3RF3,DCUN1D4,VLDLR,CASD1,C2orf40,PPP1R9A,CD274,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,IGFBP7,ZAP70,SLC2A1,TGFBR1,PREPL,LMBRD1,EDN2,ABCA1,ZNF331,KLHL7,PTPN3,SVEP1,PAPOLG,TBX18,PEX13,MAP3K7,NT5C3A,ANTXR1,MDFIC,PAPPA,PREP,EPHB6,JADE1,GYS1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ZNF398,ITM2B,PPP1R13L,SNRK,TESK2,GGA3,NAA16,ELF1,INHBB,SMARCD3,MKRN2,HRH1,EXOG,LMO7,ITIH5,ENTPD3,PFKFB3,BABAM2,FOSL2,ANKRD16,LBH,STT3B,RNASE4,NDRG2,LIPT2,POLB,LMCD1,SALL2,THRB,PLCB4,ACTN4,SATB1,ADAM9,TACC1,CRIM1,SUMF1,FOXO1,RASSF2,COL4A2,ANKLE2,QPCT,CYP1B1,GALM,TF,EBF4,FLT3,TUSC3,ZDHHC2,MAP3K1,MIER3,NCOR2,FFAR3,FXYD1,HPN,FBXO3,PTPRG,ZC3H6,CHD7,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,ADM,RNF141,PAM,SH3RF1,ST3GAL5,ATOH8,GRK7,OCLN,TCF7L1,ELL2,WWC2,TEAD1,CHST2,FAM172A,PTH,GYG1,INTS9,EXTL3,RNF34,CDKL2,G3BP2,CLU,ENTPD1,BLNK,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ABCC8,ANXA3,HECTD4,PTPN11,PTX3,ADCY6,LBP,NEK4,CCNT1,HERPUD1,PROS1,JMY,ZNF638,CHD6,PTPN22,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,CPQ,NAB1,ADA,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,PLA2G4F,ETS2,N4BP	darkgreen	VSMC_M4
GO:0044271	1.00	0.01	203	3436	cellular nitrogen compound biosynthetic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,SMOC2,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,LMO7,FOSL2,LBH,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ST3GAL5,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,PTH,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,PTX3,ADCY6,NEK4,CCNT1,JMY,CHD6,HNF4A,CHAC1,GDF6,NAB1,ADA,RBL2,EDN1,CD47,ETS2,KDM5B,TARSL2,RGS2,MXI1,NCOA3,ACTN2,LRP5,NPNT,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,NGRN,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,JD3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,SECISBP2L,EZH1,EIF4G3,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,ZBTB4,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,AK7,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,CTIF,DAPK3,ADCY9,TLE2,FLNA,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,AK5,ST6GALNAC3,AFF3,ZSCAN30,LOX,TBX20,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,ORMDL3,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4

GO:0006520	1.00	0.01	6	224	cellular amino acid metabolic process	BP	1	HNF4A,SERINC3,TARSL2,SLC25A12,RIMKLB,ATCAY	darkgreen	VSMC_M4
GO:0008152	1.00	0.01	533	8467	metabolic process	BP	1	MBP,ZNF516,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,HSD17B6,IFNGR1,CITED2,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,RNASET2,SMOC2,AFF4,GJA1,ZHX1,TPD52L1,TATDN1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,AHCYL2,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,SH3RF3,DCUN1D4,VLDLR,CASD1,C2orf40,PPP1R9A,CD274,PON2,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,IGFBP7,ZAP70,SLC2A1,TGFBR1,PREPL,LMBRD1,EDN2,ABCA1,ZNF331,KLHL7,PTPN3,SVEP1,PAPOLG,TBX18,PEX13,MAP3K7,NT5C3A,ANTXR1,MDFIC,PAPPA,PREP,EPHB6,SESN1,JADE1,GYS1,METTL24,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ZNF398,ITM2B,PPP1R13L,SNRK,TESK2,GGA3,NAA16,ELF1,INHBB,SMARCD3,MKRN2,HRH1,EXOG,LMO7,ITIH5,ENTPD3,PFKFB3,BABAM2,FOSL2,ANKRD16,LBH,STT3B,RNASE4,NDRG2,LIPT2,POLB,LMCD1,SALL2,THRB,PLCB4,ACTN4,SATB1,ADAM9,TACC1,CRIM1,SUMF1,FOXO1,RASSF2,COL4A2,ANKLE2,QPCT,CYP1B1,GALM,TF,EBF4,FLT3,TUSC3,ZDHHC2,MAP3K1,MIER3,NCOR2,FFAR3,FXYD1,HPN,FBXO3,PTPRG,ZC3H6,CHD7,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,ADM,MAP1LC3A,RNF141,PAM,SLC25A4,SH3RF1,ST3GAL5,ATOH8,CLCN3,GRK7,OCLN,TCF7L1,ELL2,WWC2,TEAD1,CHST2,FAM172A,PTH,GYG1,INTS9,EXTL3,RNF34,CDKL2,G3BP2,CLU,ENTPD1,BLNK,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ABCC8,ANXA3,HECTD4,PTPN11,PTX3,ADCY6,LBP,NEK4,CCNT1,HERPUD1,PROS1,JMY,ZNF638,ATG13,CHD6,PTPN22,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,CPQ,NAB1,ADA,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,SMARCAD1,MARCH6,BACE2,ABCG1,NT5C2,TMPRSS7,KDM5B,TARSL2,DAPP1,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,PFKL,UBE3B,LRP5,KCTD10,ARRDC4,NPNT,PLCL1,HTR2B,MST1R,	darkgreen	VSMC_M4
GO:0140014	1.00	0.01	8	244	mitotic nuclear division	BP	1	ANKLE2,EML4,EDN1,LRP5,TOM1L1,DAPK3,FLNA,REEP3	darkgreen	VSMC_M4
GO:1903311	1.00	0.01	8	247	regulation of mRNA metabolic process	BP	1	REST,CPEB3,FAM172A,CCNT1,PRKCA,RBFOX1,AHCYL1,SRPK3	darkgreen	VSMC_M4
GO:0090305	1.00	0.01	6	213	nucleic acid phosphodiester bond hydrolysis	BP	1	RNASET2,TATDN1,EXOG,RNASE4,N4BP1,EXO5	darkgreen	VSMC_M4
GO:0000280	1.00	0.01	13	355	nuclear division	BP	1	ANKLE2,EML4,EDN1,LRP5,SUN1,MAEL,TEX11,TOM1L1,MARF1,DAPK3,FLNA,HFM1,REEP3	darkgreen	VSMC_M4
GO:0060271	1.00	0.01	9	266	cilium assembly	BP	1	DNAH7,ABLIM1,IFT43,BBS4,EVI5L,ABLIM3,OCRL,FLNA,YAP1	darkgreen	VSMC_M4
GO:0006807	1.00	0.00	452	7284	nitrogen compound metabolic process	BP	1	MBP,ZNF516,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,IFNGR1,CITED2,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TPD52L1,TATDN1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,FAM122A,SH3RF3,DCUN1D4,VLDLR,C2orf40,PPP1R9A,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,ZAP70,TGFBR1,PREPL,LMBRD1,ABCA1,ZNF331,KLHL7,PTPN3,PAPOLG,TBX18,MAP3K7,NT5C3A,ANTXR1,MDFIC,PAPPA,PREP,EPHB6,JADE1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ZNF398,ITM2B,PPP1R13L,SNRK,TESK2,GGA3,NAA16,ELF1,INHBB,SMARCD3,MKRN2,EXOG,LMO7,ITIH5,ENTPD3,BABAM2,FOSL2,ANKRD16,LBH,STT3B,RNASE4,LIPT2,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,SUMF1,FOXO1,RASSF2,COL4A2,ANKLE2,QPCT,CYP1B1,TF,EBF4,FLT3,TUSC3,ZDHHC2,MAP3K1,MIER3,NCOR2,FXYD1,HPN,FBXO3,PTPRG,ZC3H6,CHD7,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,RNF141,PAM,SH3RF1,ST3GAL5,ATOH8,GRK7,OCLN,TCF7L1,ELL2,WWC2,TEAD1,CHST2,FAM172A,PTH,INTS9,EXTL3,RNF34,CDKL2,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,PDGFC,ANXA3,HECTD4,PTPN11,PTX3,ADCY6,NEK4,CCNT1,HERPUD1,PROS1,JMY,ZNF638,CHD6,PTPN22,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,CPQ,NAB1,ADA,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,SMARCAD1,MARCH6,BACE2,ABCG1,NT5C2,TMPRSS7,KDM5B,TARSL2,DAPP1,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,PFKL,UBE3B,LRP5,KCTD10,ARRDC4,NPNT,PLCL1,HTR2B,MST1R,	darkgreen	VSMC_M4
GO:0043933	1.00	0.00	70	1370	protein-containing complex subunit organization	BP	1	SHPRH,IRAK3,MDM2,SOD2,ANGPT1,EP300,SH3GL2,KANK1,UNC13B,PPP1R9A,SLC2A1,ABCA1,SNAP91,SMARCD3,CDC42EP3,WASF3,RIC3,NCK1,MAP1LC3A,OCLN,TEAD1,G3BP2,CLU,PDGFC,PTPN11,JMY,FMOD,JAM3,SEMA5A,LPL,ABCG1,DNAH7,PDE4DIP,ACTN2,KCTD10,PREX1,PARD6B,MID1,TP53BP1,HIP1,CRYAB,RDX,ATG14,MMP1,DACT1,WDR1,MICAL3,PPARGC1A,CALCOCO2,SMAD6,EPG5,TTC19,PAK3,ARHGAP28,DNAJC6,MAP1LC3B2,PLCG2,SPTAN1,LRRC8C,LMO4,BNIP3,TBX20,SRPK3,NACC2,DSTN,HOPX,ICAM1,PIK3C2A,YAP1,DDIT4	darkgreen	VSMC_M4
GO:0006974	1.00	0.00	31	699	cellular response to DNA damage stimulus	BP	1	BCL2,SHPRH,MDM2,EP300,HIPK2,TPT1,BABAM2,POLB,FOXO1,ANKRD1,CLU,PTPN11,NEK4,JMY,SMARCAD1,EYA2,ZMAT3,SESN2,TP53BP1,ZNF365,MAEL,ZBTB4,ZFYVE26,MARF1,TERF2IP,CDC7,EXO5,CDKN1A,NACC2,YAP1,DDIT4	darkgreen	VSMC_M4
GO:1901361	1.00	0.00	14	395	organic cyclic compound catabolic process	BP	1	HSD17B6,RNASET2,EXOG,ENTPD3,CPEB3,ENTPD1,ADA,NT5C2,PRKCA,PDE1A,MAOA,MAOB,CYP19A1,CTIF	darkgreen	VSMC_M4
GO:0044265	1.00	0.00	45	947	cellular macromolecule catabolic process	BP	1	RNF41,MDM2,LAPTM4B,RNF19A,RNASET2,WFS1,FAM122A,C2orf40,RIC1,RNF149,HIPK2,EXOG,STT3B,CPEB3,RMND5A,RNF34,CLU,HERPUD1,N4BP1,MARCH6,UBE3B,KCTD10,LGMN,PRKCA,CTSS,LRP2,CTSZ,CTSF,ZRANB1,RDX,USP11,FBXL5,DACT1,JKAMP,FBXL20,FAF2,TOM1L1,USP32,DAB2,SKP2,CTIF,FBXO27,BNIP3,CST3,GABARAPL2	darkgreen	VSMC_M4

GO:0044085	1.00	0.00	139	2454	cellular component biogenesis	BP	1	BCL2,SHPRH,MDM2,GRHL2,SOD2,ANGPT1,GJA1,EP300,ADGRB1,SH3GL2,LIMCH1,KANK1,UNC13B,PPP1R9A,REST,SLC2A1,TGFBR1,ABCA1,SNAP91,CALD1,ANTXR1,TESK2,TENM4,ANKLE2,PCDHB4,CDC42EP3,PCLO,LMNTD2,WASF3,RIC3,CHD7,ANKRD1,NCK1,MAP1LC3A,OCLN,TEAD1,G3BP2,CLU,GPM6A,APP,ATXN2,PDGFC,PTPN11,JMY,ATG13,PKP4,FMOD,EDN1,JAM3,CD47,MYO1B,RAB29,DNAH7,RIPOR2,TNNT2,PDE4DIP,ACTN2,KCTD10,ARRDC4,FEZ1,PREX1,PRKCA,ABLIM1,PARD6B,ATP9A,SHTN1,MYLK,CFLAR,SYNPO2,TP53BP1,F11R,PLXNB1,QSOX1,ITGA6,HIP1,GABARAPL1,ACHE,CRYAB,RDX,SYNPO2L,ATG14,MMP1,DACT1,NLGN1,WDR1,PPARGC1A,ACTN1,TEX11,TGFB3,IFT43,SMAD6,BBS4,NPTN,MRM1,MAPRE2,TTC19,SYNPO,CDH2,ULK2,PAK3,PLS3,EVI5L,ABLIM3,ARHGAP28,OCRL,PATJ,PRKAA2,CDH18,MYO10,DAPK3,PLXNB3,FLNA,CCDC78,MAP1LC3B2,CDH13,PLCG2,SPTAN1,LRSAM1,LRRC8C,LMO4,CYR61,CCDC136,SPINK2,PCDHB2,LOX,TBX20,LRRC24,CSRP1,SRPK3,PPM1E,MFAP4,NACC2,HOPX,GABARAPL2,ICAM1,PIK3C2A,ORMDL3,YAP1,REEP3	darkgreen	VSMC_M4
GO:0019439	1.00	0.00	13	375	aromatic compound catabolic process	BP	1	RNASET2,PON2,EXOG,ENTPD3,CPEB3,ENTPD1,ADA,NT5C2,PRKCA,PDE1A,MAOA,MAOB,CTIF	darkgreen	VSMC_M4
GO:0000226	1.00	0.00	22	522	microtubule cytoskeleton organization	BP	1	RNF19A,GJA1,TRDN,TUBE1,TACC1,EML4,OCLN,DNAH7,SUN1,PARD6B,MID1,MAP7D2,CRYAB,GNAI1,CHD3,BBS4,MAPRE2,GAS2L2,PATJ,PRKAA2,FLNA,CCDC78	darkgreen	VSMC_M4
GO:0044237	1.00	0.00	491	7918	cellular metabolic process	BP	1	MBP,ZNF516,TMX3,DSEL,GDF11,BCL2,PIGN,RNF41,HSD17B6,IFNGR1,CITED2,SHPRH,SASH1,UST,IRAK3,MDM2,DDR1,LAPTM4B,RNF19A,GRHL2,SOD2,OXR1,ABRA,ANGPT1,C4A,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TPD52L1,TATDN1,EP300,MRTFA,BRD8,ADGRB1,DAPK1,BRPF3,AHCYL2,TLE4,SH3GL2,GNAQ,MLLT3,LEP,CDKN2B,WFS1,LIMCH1,DDX58,PIP5K1B,FAM122A,SH3RF3,DCUN1D4,VLDLR,C2orf40,PPP1R9A,PON2,RIC1,PDK4,IL18R1,RNF149,CREB3,ZNF169,REST,RECK,ZAP70,SLC2A1,TGFBR1,LMBRD1,EDN2,ABCA1,ZNF331,KLHL7,PTPN3,PAPOLG,TBX18,PEX13,MAP3K7,NT5C3A,ANTXR1,MDFIC,PAPPA,EPHB6,SESN1,JADE1,GYS1,MAP3K8,HIPK2,GATA2,HS6ST1,ABHD12,ZNF398,ITM2B,PPP1R13L,SNRK,TESK2,GGA3,NAA16,ELF1,INHBB,SMARCD3,MKRN2,HRH1,EXOG,LMO7,ITIH5,ENTPD3,PFKFB3,BABAM2,FOSL2,ANKRD16,LBH,STT3B,RNASE4,LIPT2,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,ADAM9,TACC1,CRIM1,SUMF1,FOXO1,RASSF2,COL4A2,ANKLE2,QPCT,CYP1B1,TF,EBF4,FLT3,TUSC3,ZDHHC2,MAP3K1,MIER3,NCOR2,FFAR3,FXYD1,HPN,FBXO3,PTPRG,ZC3H6,CHD7,LATS2,CHPT1,HIPK3,ANKRD1,PCGF5,CPEB3,MARCH5,TRIM23,RMND5A,NCK1,ADM,MAP1LC3A,RNF141,PAM,SLC25A4,SH3RF1,ST3GAL5,ATOH8,CLCN3,GRK7,OCLN,TCF7L1,ELL2,WWC2,TEAD1,CHST2,FAM172A,PTH,GYG1,INTS9,EXTL3,RNF34,CDKL2,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,SCARB2,PDGFC,ANXA3,HECTD4,PTPN11,PTX3,ADCY6,NEK4,CCNT1,HERPUD1,PROS1,JMY,ZNF638,ATG13,CHD6,PTPN22,DPY19L4,LPCAT2,HNF4A,CHAC1,GDF6,SERINC3,CPQ,NAB1,ADA,AKTIP,RCAN1,RBL2,NGF,EDN1,CD47,PLA2G4F,ETS2,N4BP1,SMARCAD1,MARCH6,BACE2,LPL	darkgreen	VSMC_M4
GO:0043603	1.00	0.00	38	897	cellular amide metabolic process	BP	1	IFNGR1,DAPK1,PDK4,GGA3,CPEB3,NCK1,PAM,ST3GAL5,CLU,APP,ATXN2,CHAC1,CPQ,ADA,BACE2,ABCG1,NT5C2,TARSL2,RGS2,SESN2,NGRN,CTSZ,RBM4B,NCSTN,FAM129A,HSPB1,EIF4A2,ATP6AP2,SECISBP2L,EIF4G3,PCSK1N,CTIF,DAPK3,PCSK4,CYR61,ST6GALNAC3,VNN1,ORMDL3	darkgreen	VSMC_M4
GO:0044782	1.00	0.00	9	288	cilium organization	BP	1	DNAH7,ABLIM1,IFT43,BBS4,EVI5L,ABLIM3,OCRL,FLNA,YAP1	darkgreen	VSMC_M4
GO:0000377	1.00	0.00	6	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1	REST,FAM172A,RBM4B,DDX41,RBFOX1,SRPK3	darkgreen	VSMC_M4
GO:0000398	1.00	0.00	6	255	mRNA splicing, via spliceosome	BP	1	REST,FAM172A,RBM4B,DDX41,RBFOX1,SRPK3	darkgreen	VSMC_M4
GO:0006260	1.00	0.00	6	230	DNA replication	BP	1	BRPF3,POLB,ZNF365,ID3,BCAR3,CDC7	darkgreen	VSMC_M4
GO:0006397	1.00	0.00	13	407	mRNA processing	BP	1	REST,PAPOLG,CPEB3,FAM172A,APP,CCNT1,RBM20,RBM4B,DDX41,PPARGC1A,RBFOX1,AHCYL1,SRPK3	darkgreen	VSMC_M4
GO:0000375	1.00	0.00	6	259	RNA splicing, via transesterification reactions	BP	1	REST,FAM172A,RBM4B,DDX41,RBFOX1,SRPK3	darkgreen	VSMC_M4
GO:0034655	1.00	0.00	10	335	nucleobase-containing compound catabolic process	BP	1	RNASET2,EXOG,ENTPD3,CPEB3,ENTPD1,ADA,NT5C2,PRKCA,PDE1A,CTIF	darkgreen	VSMC_M4

GO:0010467	1.00	0.00	257	4455	gene expression	BP	1	MBP,ZNF516,BCL2,IFNGR1,CITED2,IRAK3,MDM2,LAPTM4B,GRHL2,SOD2,ABRA,ANGPT1,TRPS1,AFF4,GJA1,ZHX1,EP300,MRTFA,BRD8,DAPK1,TLE4,SH3GL2,MLLT3,LEP,WFS1,DDX58,CD274,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,SVEP1,PAPOLG,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,INHBB,SMARCD3,LMO7,FOSL2,ANKRD16,LBH,NDRG2,LIPT2,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,FFAR3,HPN,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,OCLN,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,BLNK,MED12L,MEIS2,APP,ATXN2,SCARB2,ABCC8,ANXA3,PTPN11,LBP,NEK4,CCNT1,JMY,ZNF638,CHD6,PTPN22,HNF4A,CHAC1,GDF6,NAB1,RBL2,NGF,EDN1,CD47,ETS2,N4BP1,BACE2,LPL,KDM5B,TARSL2,RGS2,MXI1,RBM20,NCOA3,ACTN2,LRP5,NPNT,HTR2B,LGMN,PRKCA,AFAP1L2,TXNIP,HELZ,SESN2,YEATS2,ZNF710,CAMK2D,CTSS,NGRN,CFLAR,CTSZ,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,F11R,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,PRDX4,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,SERPINE1,CRYAB,C1RL,ATP6AP2,RDX,ZNF445,SECISBP2L,EZH1,EIF4G3,ATG14,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,SLIT3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,NPTN,MRM1,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,INTS6L,PRKAA2,TMEM59,CTIF,RBFOX1,DAPK3,TLE2,PCSK4,FLNA,AHCYL1,CSF1,SORT1,CDH13,PLCG2,TERF2IP,F3,GLG1,ZNF821,LMO4,CYR61,ZFP90,MIR99A,MIR331,SNORA27,AFF3,SLC8A1,ZS	darkgreen	VSMC_M4
GO:0006259	1.00	0.00	30	741	DNA metabolic process	BP	1	SHPRH,GRHL2,SMOC2,GJA1,TATDN1,EXOG,BABAM2,POLB,ANKRD1,ANXA3,JMY,SMARCAD1,EYA2,SESN2,TP53BP1,ZNF365,ZNF445,MAEL,ZFYVE26,PPARGC1A,TEX11,PAK3,MARF1,TERF2IP,CDC7,HFM1,EXO5,LOX,CDKN1A,CCR6	darkgreen	VSMC_M4
GO:0043604	1.00	0.00	24	672	amide biosynthetic process	BP	1	DAPK1,PDK4,CPEB3,NCK1,PAM,ST3GAL5,APP,ATXN2,CHAC1,TARSL2,RGS2,SESN2,NGRN,RBM4B,FAM129A,HSPB1,EIF4A2,SECISBP2L,EIF4G3,CTIF,DAPK3,CYR61,ST6GALNAC3,ORMDL3	darkgreen	VSMC_M4
GO:0098813	1.00	0.00	5	230	nuclear chromosome segregation	BP	1	EML4,SUN1,MAEL,TEX11,HFM1	darkgreen	VSMC_M4
GO:0034622	1.00	0.00	33	830	cellular protein-containing complex assembly	BP	1	SHPRH,ANGPT1,SH3GL2,KANK1,UNC13B,PPP1R9A,SNAP91,CDC42EP3,WASF3,RIC3,NCK1,OCLN,CLU,PDGFC,JMY,FMOD,DNAH7,PDE4DIP,PREX1,HIP1,CRYAB,RDX,SMAD6,TTC19,PAK3,ARHGAP28,PLCG2,SPTAN1,TBX20,SRPK3,HOPX,ICAM1,PIK3C2A	darkgreen	VSMC_M4
GO:0046700	1.00	0.00	10	357	heterocycle catabolic process	BP	1	RNASET2,EXOG,ENTPD3,CPEB3,ENTPD1,ADA,NT5C2,PRKCA,PDE1A,CTIF	darkgreen	VSMC_M4
GO:0044270	1.00	0.00	10	361	cellular nitrogen compound catabolic process	BP	1	RNASET2,EXOG,ENTPD3,CPEB3,ENTPD1,ADA,NT5C2,PRKCA,PDE1A,CTIF	darkgreen	VSMC_M4
GO:0043043	1.00	0.00	18	566	peptide biosynthetic process	BP	1	DAPK1,CPEB3,NCK1,APP,ATXN2,CHAC1,TARSL2,RGS2,SESN2,NGRN,RBM4B,FAM129A,HSPB1,EIF4A2,SECISBP2L,EIF4G3,CTIF,DAPK3	darkgreen	VSMC_M4
GO:0008380	1.00	0.00	9	356	RNA splicing	BP	1	REST,FAM172A,ZNF638,RBM20,RBM4B,DDX41,PPARGC1A,RBFOX1,SRPK3	darkgreen	VSMC_M4
GO:0006412	1.00	0.00	17	548	translation	BP	1	DAPK1,CPEB3,NCK1,APP,ATXN2,TARSL2,RGS2,SESN2,NGRN,RBM4B,FAM129A,HSPB1,EIF4A2,SECISBP2L,EIF4G3,CTIF,DAPK3	darkgreen	VSMC_M4
GO:0016070	1.00	0.00	192	3480	RNA metabolic process	BP	1	ZNF516,CITED2,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,RNASET2,ZHX1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,PAPOLG,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,EXOG,LMO7,FOSL2,ANKRD16,LBH,RNASE4,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,NEK4,CCNT1,JMY,ZNF638,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,N4BP1,KDM5B,TARSL2,MXI1,RBM20,NCOA3,ACTN2,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,PPARGC1A,ACTN1,RORA,CHD3,TGFB3,SMAD6,GTF3C1,ZKSCAN2,DDX24,MRM1,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,INTS6L,CTIF,RBFOX1,DAPK3,TLE2,FLNA,AHCYL1,CDH13,PLCG2,TERF2IP,ZNF821,LMO4,CYR61,ZFP90,SNORA27,AFF3,ZSCAN30,TBX20,SRPK3,ZNF425,ZNF175,MAFF,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4
GO:0043414	1.00	0.00	5	254	macromolecule methylation	BP	1	GRHL2,PCMTD2,EZH1,MAEL,MRM1	darkgreen	VSMC_M4
GO:0065003	1.00	0.00	52	1210	protein-containing complex assembly	BP	1	SHPRH,MDM2,SOD2,ANGPT1,EP300,SH3GL2,KANK1,UNC13B,PPP1R9A,SLC2A1,ABCA1,SNAP91,CDC42EP3,WASF3,RIC3,NCK1,OCLN,TEAD1,G3BP2,CLU,PDGFC,PTPN11,JMY,FMOD,JAM3,DNAH7,PDE4DIP,KCTD10,PREX1,PARD6B,TP53BP1,HIP1,CRYAB,RDX,MMP1,DACT1,PPARGC1A,SMAD6,TTC19,PAK3,ARHGAP28,PLCG2,SPTAN1,LRRC8C,LMO4,TBX20,SRPK3,NACC2,HOPX,ICAM1,PIK3C2A,YAP1	darkgreen	VSMC_M4
GO:0032259	1.00	0.00	6	290	methylation	BP	1	GRHL2,METTL24,PCMTD2,EZH1,MAEL,MRM1	darkgreen	VSMC_M4

GO:1901360	1.00	0.00	256	4575	organic cyclic compound metabolic process	BP	1	ZNF516,BCL2,HSD17B6,CITED2,SHPRH,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TATDN1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,VLDLR,PDK4,IL18R1,CREB3,ZNF169,REST,IGFBP7,SLC2A1,TGFBR1,LMBRD1,ABCA1,ZNF331,PAPOLG,TBX18,MAP3K7,NT5C3A,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,EXOG,LMO7,ENTPD3,BABAM2,FOSL2,ANKRD16,LBH,RNASE4,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,HPN,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,ADM,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,ANXA3,ADCY6,NEK4,CCNT1,JMY,ZNF638,CHD6,HNF4A,GDF6,CPQ,NAB1,ADA,RBL2,EDN1,ETS2,N4BP1,SMARCAD1,ABCG1,NT5C2,KDM5B,TARSL2,EYA2,MXI1,RBM20,NCOA3,ACTN2,PFKL,LRP5,NPNT,LGMN,PRKCA,AFAP1L2,TXNIP,TPST2,SESN2,ARV1,YEATS2,ZNF710,CAMK2D,ADCY5,LRP2,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,PDE1A,MAOA,MAOB,ZNF445,ENO2,EZH1,CYP19A1,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,ZFYVE26,PPARGC1A,ACTN1,NPPB,DISP3,RORA,CHD3,TEX11,TGFB3,SMAD6,GTF3C1,ZKSCAN2,DDX24,FAXDC2,AK7,MRM1,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,INTS6L,PRKAA2,CTIF,RBFOX1,DAPK3,ADCY9,TLE2,FLNA,AHCYL1,MBTPS1,CDH13,PLCG2,EXTL2,TERF2IP,CDC7,HFM1,ZNF821,LMO4,CYR61,ZFP90,AK5,SNORA27,AFF	darkgreen	VSMC_M4
GO:0007059	1.00	0.00	6	288	chromosome segregation	BP	1	EML4,SMARCAD1,SUN1,MAEL,TEX11,HFM1	darkgreen	VSMC_M4
GO:0006281	1.00	0.00	13	455	DNA repair	BP	1	SHPRH,BABAM2,POLB,JMY,SMARCAD1,EYA2,TP53BP1,ZNF365,ZFYVE26,MARF1,TERF2IP,CDC7,EXO5	darkgreen	VSMC_M4
GO:0006401	1.00	0.00	4	237	RNA catabolic process	BP	1	RNASET2,CPEB3,PRKCA,CTIF	darkgreen	VSMC_M4
GO:0016071	1.00	0.00	18	586	mRNA metabolic process	BP	1	REST,PAPOLG,RNASE4,HIPK3,CPEB3,FAM172A,APP,CCNT1,RBM20,PRKCA,RBM4B,DDX41,PPARGC1A,CTIF,RBFOX1,FLNA,AHCYL1,SRPK3	darkgreen	VSMC_M4
GO:0051276	1.00	0.00	24	682	chromosome organization	BP	1	SHPRH,MLLT3,SMARCD3,BABAM2,SATB1,EML4,LMNTD2,CHD7,TCF7L1,FAM172A,CHD6,RBL2,SMARCAD1,KDM5B,SUN1,ZNF365,EZH1,MAEL,CHD3,TEX11,SMARCA1,DAPK3,TERF2IP,HFM1	darkgreen	VSMC_M4
GO:0006725	1.00	0.00	241	4410	cellular aromatic compound metabolic process	BP	1	ZNF516,BCL2,CITED2,SHPRH,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TATDN1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PON2,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,LMBRD1,ZNF331,PAPOLG,TBX18,MAP3K7,NT5C3A,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,EXOG,LMO7,ENTPD3,BABAM2,FOSL2,ANKRD16,LBH,RNASE4,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,HPN,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,ANXA3,ADCY6,NEK4,CCNT1,JMY,ZNF638,CHD6,HNF4A,GDF6,CPQ,NAB1,ADA,RBL2,EDN1,ETS2,N4BP1,SMARCAD1,KDM5B,TARSL2,EYA2,MXI1,RBM20,NCOA3,ACTN2,PFKL,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,TPST2,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,PDE1A,MAOA,MAOB,ZNF445,ENO2,EZH1,DACT1,MAEL,SIN3B,HIF1A,OPN3,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,ZFYVE26,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TEX11,TGFB3,SMAD6,GTF3C1,ZKSCAN2,DDX24,AK7,MRM1,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,INTS6L,PRKAA2,CTIF,RBFOX1,DAPK3,ADCY9,TLE2,FLNA,AHCYL1,CDH13,PLCG2,EXTL2,TERF2IP,CDC7,HFM1,ZNF821,LMO4,CYR61,ZFP90,AK5,SNORA27,AFF3,ZSCAN30,EXO5,LOX,TBX20,SRPK3,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZN	darkgreen	VSMC_M4
GO:0090304	1.00	0.00	211	3916	nucleic acid metabolic process	BP	1	ZNF516,CITED2,SHPRH,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TATDN1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,PAPOLG,TBX18,MAP3K7,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,EXOG,LMO7,BABAM2,FOSL2,ANKRD16,LBH,RNASE4,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,MED12L,MEIS2,APP,ATXN2,ANXA3,NEK4,CCNT1,JMY,ZNF638,CHD6,HNF4A,GDF6,NAB1,RBL2,EDN1,ETS2,N4BP1,SMARCAD1,KDM5B,TARSL2,EYA2,MXI1,RBM20,NCOA3,ACTN2,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,SESN2,YEATS2,ZNF710,CAMK2D,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,ZNF445,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,ZFYVE26,PPARGC1A,ACTN1,RORA,CHD3,TEX11,TGFB3,SMAD6,GTF3C1,ZKSCAN2,DDX24,MRM1,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,INTS6L,CTIF,RBFOX1,DAPK3,TLE2,FLNA,AHCYL1,CDH13,PLCG2,TERF2IP,CDC7,HFM1,ZNF821,LMO4,CYR61,ZFP90,SNORA27,AFF3,ZSCAN30,EXO5,LOX,TBX20,SRPK3,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,NACC2,ZNF782,HLF,CCR6,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,BMP6,NPAS1,MAFA,VGLL3	darkgreen	VSMC_M4

GO:0006139	1.00	0.00	232	4274	nucleobase-containing compound metabolic process	BP	1	ZNF516,CITED2,SHPRH,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TATDN1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,PAPOLG,TBX18,MAP3K7,NT5C3A,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,EXOG,LMO7,ENTPD3,BABAM2,FOSL2,ANKRD16,LBH,RNASE4,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,ANXA3,ADCY6,NEK4,CCNT1,JMY,ZNF638,CHD6,HNF4A,GDF6,NAB1,ADA,RBL2,EDN1,ETS2,N4BP1,SMARCAD1,NT5C2,KDM5B,TARSL2,EYA2,MXI1,RBM20,NCOA3,ACTN2,PFKL,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,TPST2,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,PDE1A,ZNF445,ENO2,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,ZFYVE26,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TEX11,TGFB3,SMAD6,GTF3C1,ZKSCAN2,DDX24,AK7,MRM1,PAK3,ABLIM3,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,INTS6L,PRKAA2,CTIF,RBFOX1,DAPK3,ADCY9,TLE2,FLNA,AHCYL1,CDH13,PLCG2,EXTL2,TERF2IP,CDC7,HFM1,ZNF821,LMO4,CYR61,ZFP90,AK5,SNORA27,AFF3,ZSCAN30,EXO5,LOX,TBX20,SRPK3,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZNF782,HLF,CCR6,ZNF79,HOPX,ICAM1,ZNF853,YAP1,HKR1,B	darkgreen	VSMC_M4
GO:0046483	1.00	0.00	235	4376	heterocycle metabolic process	BP	1	ZNF516,CITED2,SHPRH,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TATDN1,EP300,MRTFA,BRD8,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,SLC2A1,TGFBR1,LMBRD1,ZNF331,PAPOLG,TBX18,MAP3K7,NT5C3A,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,NAA16,ELF1,SMARCD3,EXOG,LMO7,ENTPD3,BABAM2,FOSL2,ANKRD16,LBH,RNASE4,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,ANXA3,ADCY6,NEK4,CCNT1,JMY,ZNF638,CHD6,HNF4A,GDF6,NAB1,ADA,RBL2,EDN1,ETS2,N4BP1,SMARCAD1,NT5C2,KDM5B,TARSL2,EYA2,MXI1,RBM20,NCOA3,ACTN2,PFKL,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,TPST2,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,CFLAR,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,ZNF280B,EIF4A2,CUX1,CRYAB,PDE1A,ZNF445,ENO2,EZH1,DACT1,MAEL,SIN3B,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,ZFYVE26,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TEX11,TGFB3,SMAD6,GTF3C1,ZKSCAN2,DDX24,AK7,MRM1,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,INTS6L,PRKAA2,CTIF,RBFOX1,DAPK3,ADCY9,TLE2,FLNA,AHCYL1,CDH13,PLCG2,EXTL2,TERF2IP,CDC7,HFM1,ZNF821,LMO4,CYR61,ZFP90,AK5,SNORA27,AFF3,ZSCAN30,EXO5,LOX,TBX20,SRPK3,ZNF425,ZNF175,MAFF,CDKN1A,EDA,ZFP14,ZNF572,RFK,NACC2,ZNF782,HLF,CCR6,ZNF79,HOPX,I	darkgreen	VSMC_M4
GO:0034470	1.00	0.00	5	345	ncRNA processing	BP	1	ANKRD16,CHD7,INTS9,MRM1,INTS6L	darkgreen	VSMC_M4
GO:0034660	1.00	0.00	7	412	ncRNA metabolic process	BP	1	ANKRD16,CHD7,INTS9,TARSL2,MAEL,MRM1,INTS6L	darkgreen	VSMC_M4
GO:0034641	1.00	0.00	260	4878	cellular nitrogen compound metabolic process	BP	1	ZNF516,IFNGR1,CITED2,SHPRH,IRAK3,MDM2,GRHL2,SOD2,ABRA,TRPS1,RNASET2,SMOC2,GJA1,ZHX1,TATDN1,EP300,MRTFA,BRD8,DAPK1,TLE4,MLLT3,LEP,WFS1,DDX58,PDK4,IL18R1,CREB3,ZNF169,REST,TGFBR1,ZNF331,PAPOLG,TBX18,MAP3K7,NT5C3A,MDFIC,JADE1,HIPK2,GATA2,ZNF398,PPP1R13L,GGA3,NAA16,ELF1,SMARCD3,EXOG,LMO7,ENTPD3,BABAM2,FOSL2,ANKRD16,LBH,RNASE4,POLB,LMCD1,SALL2,THRB,ACTN4,SATB1,TACC1,FOXO1,COL4A2,CYP1B1,TF,EBF4,MIER3,NCOR2,ZC3H6,CHD7,HIPK3,ANKRD1,PCGF5,CPEB3,NCK1,RNF141,PAM,ST3GAL5,ATOH8,TCF7L1,ELL2,WWC2,TEAD1,FAM172A,PTH,INTS9,G3BP2,CLU,ENTPD1,MED12L,MEIS2,APP,ATXN2,ANXA3,PTX3,ADCY6,NEK4,CCNT1,JMY,ZNF638,CHD6,HNF4A,CHAC1,GDF6,CPQ,NAB1,ADA,RBL2,EDN1,CD47,ETS2,N4BP1,SMARCAD1,BACE2,ABCG1,NT5C2,KDM5B,TARSL2,RGS2,EYA2,MXI1,RBM20,NCOA3,ACTN2,PFKL,LRP5,NPNT,PRKCA,AFAP1L2,TXNIP,TPST2,SESN2,YEATS2,ZNF710,CAMK2D,ADCY5,NGRN,CFLAR,CTSZ,WDTC1,FGFR2,RBM4B,TP53BP1,PTPN14,PRKD1,NCSTN,SLC25A12,STRN3,ARID5B,ITGA6,ZNF365,ATF6,NPAS3,DDR2,MAP3K13,ID3,LRP6,FAM129A,HSPB1,ZNF280B,EIF4A2,CUX1,CRYAB,ATP6AP2,PDE1A,MAOA,MAOB,ZNF445,ENO2,SECISBP2L,EZH1,EIF4G3,DACT1,MAEL,SIN3B,PCSK1N,HIF1A,ZBTB18,APBB2,CCPG1,AC090517.4,DDX41,ZBTB4,ZFYVE26,PPARGC1A,ACTN1,NPPB,RORA,CHD3,TEX11,TGFB3,SMAD6,GTF3C1,ZKSCAN2,DDX24,AK7,MRM1,PAK3,ABLIM3,PGRMC1,FST,CRLF3,DAB2,LGALS9,SMARCA1,MARF1,INTS6L,PRKAA2,CTIF,RBFOX1,ATCAY,DAPK3,ADCY9,TLE2,PCSK4,FLNA,AHCYL1,CDH13,PLCG2,EXTL2,TERF2IP,CDC7,HFM1,ZNF821,LMO4,CYR6	darkgreen	VSMC_M4
GO:0006396	1.00	0.00	21	950	RNA processing	BP	1	REST,PAPOLG,ANKRD16,NCOR2,CHD7,CPEB3,FAM172A,INTS9,APP,CCNT1,ZNF638,RBM20,RBM4B,DDX41,PPARGC1A,MRM1,INTS6L,RBFOX1,AHCYL1,SNORA27,SRPK3	darkgreen	VSMC_M4
GO:0048731	0.00	1.00	47	3556	system development	BP	0.02101	CCBE1,AVPR1A,PTPRB,DMRT2,CAV1,SVIL,STIM1,VIT,POSTN,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,DPPA4,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,DSCAML1,LMX1A,HOXD11,PCYT1B,SSTR1,CYBB,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,IGF2BP1,COL5A3,ADRB2,TNFRSF13B,EGFLAM,NTNG1,ARSE,POPDC3,HAPLN1,FGF16,LMX1B,SPOCK1	violet	VSMC_M7

GO:0032501	0.00	1.00	58	5003	multicellular organismal process	BP	0.02101	NETO1,CCBE1,AVPR1A,PTPRB,DMRT2,ERMAP,CAV1,GJB4,SVIL,STIM1,VIT,POSTN,SIGIRR,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,LGR4,DYNLL1,DPPA4,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,DSCAML1,ADGRG2,LMX1A,HOXD11,PCYT1B,PTH2R,SSTR1,CYBB,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,SLC6A13,JAKMIP1,IGF2BP1,COL5A3,ADRB2,TNFRSF13B,EGFLAM,NTNG1,ARSE,POPDC3,HAPLN1,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0030198	0.00	1.00	10	250	extracellular matrix organization	BP	0.0416	CAV1,VIT,POSTN,SPINK5,CMA1,COMP,COL5A3,EGFLAM,NTNG1,OLFML2A	violet	VSMC_M7
GO:0045229	0.00	1.00	10	251	external encapsulating structure organization	BP	0.0416	CAV1,VIT,POSTN,SPINK5,CMA1,COMP,COL5A3,EGFLAM,NTNG1,OLFML2A	violet	VSMC_M7
GO:0043062	0.00	1.00	10	251	extracellular structure organization	BP	0.0416	CAV1,VIT,POSTN,SPINK5,CMA1,COMP,COL5A3,EGFLAM,NTNG1,OLFML2A	violet	VSMC_M7
GO:0007275	0.00	1.00	47	3815	multicellular organism development	BP	0.0416	CCBE1,AVPR1A,PTPRB,DMRT2,CAV1,SVIL,STIM1,VIT,POSTN,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,DPPA4,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,DSCAML1,LMX1A,HOXD11,PCYT1B,SSTR1,CYBB,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,IGF2BP1,COL5A3,ADRB2,TNFRSF13B,EGFLAM,NTNG1,ARSE,POPDC3,HAPLN1,FGF16,LMX1B,SPOCK1	violet	VSMC_M7
GO:0007166	0.00	1.00	30	1935	cell surface receptor signaling pathway	BP	0.0416	NETO1,CCBE1,ERMAP,CAV1,POSTN,SIGIRR,FZD10,SH2B3,SAMHD1,DHH,LGR4,FGF19,PTPRU,ACKR3,ADGRG2,STYK1,PTH2R,SSTR1,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,ADRB2,TNFRSF13B,GRIA3,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0007186	0.00	1.00	13	458	G protein-coupled receptor signaling pathway	BP	0.0416	AVPR1A,CAV1,FZD10,RGS9BP,F2RL2,LGR4,ACKR3,ADGRG2,PTH2R,SSTR1,ADRB2,DNM1,CCL8	violet	VSMC_M7
GO:0032502	0.00	1.00	52	4589	developmental process	BP	0.06456	CCBE1,AVPR1A,PTPRB,DMRT2,CAV1,SVIL,STIM1,VIT,POSTN,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,DPPA4,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,DSCAML1,ADGRG2,LMX1A,STYK1,HOXD11,PCYT1B,SSTR1,CYBB,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,IGF2BP1,COL5A3,OLFM2,ADRB2,TNFRSF13B,EGFLAM,NTNG1,ARSE,POPDC3,HAPLN1,FGF16,SPAG8,LMX1B,EMP1,SPOCK1	violet	VSMC_M7
GO:0048856	0.00	1.00	49	4193	anatomical structure development	BP	0.06456	CCBE1,AVPR1A,PTPRB,DMRT2,CAV1,SVIL,STIM1,VIT,POSTN,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,DPPA4,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,DSCAML1,LMX1A,HOXD11,PCYT1B,SSTR1,CYBB,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,IGF2BP1,COL5A3,OLFM2,ADRB2,TNFRSF13B,EGFLAM,NTNG1,ARSE,POPDC3,HAPLN1,FGF16,LMX1B,EMP1,SPOCK1	violet	VSMC_M7
GO:0048513	0.00	1.00	33	2529	animal organ development	BP	0.32988	CCBE1,AVPR1A,CAV1,SVIL,STIM1,VIT,SPINK5,SH2B3,DHH,LGR4,DYNLL1,DPPA4,FGF19,PTPRU,EMX2,CMA1,DSCAML1,LMX1A,HOXD11,PCYT1B,SSTR1,COMP,CRLF1,FGF7,MYOC,IGF2BP1,COL5A3,ADRB2,TNFRSF13B,EGFLAM,NTNG1,POPDC3,FGF16	violet	VSMC_M7
GO:0007267	0.00	1.00	19	1146	cell-cell signaling	BP	0.60645	NETO1,CAV1,GJB4,FZD10,DHH,SV2C,LGR4,DYNLL1,PTPRU,TFR2,TNN,FGF7,MYOC,NTF3,ADRB2,NTNG1,DNM1,CCL8,FGF16	violet	VSMC_M7
GO:0007155	0.00	1.00	18	1044	cell adhesion	BP	0.62882	CAV1,VIT,POSTN,SPINK5,SH2B3,PTPRU,ACAN,CADM3,ACKR3,DSCAML1,TNN,COMP,MYOC,COL5A3,EGFLAM,NTNG1,HAPLN1,SPOCK1	violet	VSMC_M7
GO:0022610	0.00	1.00	18	1050	biological adhesion	BP	0.62882	CAV1,VIT,POSTN,SPINK5,SH2B3,PTPRU,ACAN,CADM3,ACKR3,DSCAML1,TNN,COMP,MYOC,COL5A3,EGFLAM,NTNG1,HAPLN1,SPOCK1	violet	VSMC_M7
GO:0001960	0.00	1.00	4	58	negative regulation of cytokine-mediated signaling pathway	BP	0.63696	CAV1,SIGIRR,SH2B3,SAMHD1	violet	VSMC_M7
GO:0060761	0.00	1.00	4	61	negative regulation of response to cytokine stimulus	BP	0.7212	CAV1,SIGIRR,SH2B3,SAMHD1	violet	VSMC_M7
GO:0003073	0.00	1.00	4	60	regulation of systemic arterial blood pressure	BP	0.7212	AVPR1A,POSTN,CMA1,ADRB2	violet	VSMC_M7
GO:0035295	0.00	1.00	15	849	tube development	BP	0.77222	CCBE1,PTPRB,CAV1,STIM1,SPINK5,LGR4,DPPA4,EMX2,ACKR3,CMA1,HOXD11,CYBB,COMP,CRLF1,FGF7	violet	VSMC_M7
GO:0042221	0.00	1.00	34	2921	response to chemical	BP	0.77222	CCBE1,AVPR1A,FBP1,CAV1,GJB4,STIM1,POSTN,SIGIRR,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,FGF19,PDZK1,PTPRU,EMX2,ACKR3,CMA1,DSCAML1,LMX1A,SSTR1,CYBB,TFR2,COMP,CRLF1,FGF7,NTF3,ADRB2,DNM1,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0019221	0.00	1.00	8	306	cytokine-mediated signaling pathway	BP	0.77222	CAV1,SIGIRR,SH2B3,SAMHD1,ACKR3,CRLF1,ZBP1,CCL8	violet	VSMC_M7
GO:0001959	0.00	1.00	5	119	regulation of cytokine-mediated signaling pathway	BP	0.80502	CAV1,SIGIRR,SH2B3,SAMHD1,ZBP1	violet	VSMC_M7
GO:0031589	0.00	1.00	8	294	cell-substrate adhesion	BP	0.87301	VIT,POSTN,TNN,MYOC,COL5A3,EGFLAM,NTNG1,SPOCK1	violet	VSMC_M7
GO:0060759	0.00	1.00	5	128	regulation of response to cytokine stimulus	BP	0.9895	CAV1,SIGIRR,SH2B3,SAMHD1,ZBP1	violet	VSMC_M7
GO:0030334	0.00	1.00	13	735	regulation of cell migration	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,ACKR3,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16	violet	VSMC_M7
GO:0009605	0.00	1.00	23	1770	response to external stimulus	BP	1	AVPR1A,CAV1,POSTN,SIGIRR,SPINK5,RGS9BP,SH2B3,SAMHD1,LGR4,ACKR3,CMA1,DSCAML1,LMX1A,STYK1,SSTR1,MASP1,CYBB,FGF7,NTF3,ADRB2,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0006898	0.00	1.00	6	192	receptor-mediated endocytosis	BP	1	CAV1,ACKR3,TFR2,NTF3,ADRB2,DNM1	violet	VSMC_M7
GO:0031623	0.00	1.00	4	85	receptor internalization	BP	1	CAV1,ACKR3,NTF3,DNM1	violet	VSMC_M7
GO:2000145	0.00	1.00	13	772	regulation of cell motility	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,ACKR3,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16	violet	VSMC_M7
GO:0044344	0.00	1.00	4	86	cellular response to fibroblast growth factor stimulus	BP	1	POSTN,FGF19,FGF7,FGF16	violet	VSMC_M7
GO:0071774	0.00	1.00	4	91	response to fibroblast growth factor	BP	1	POSTN,FGF19,FGF7,FGF16	violet	VSMC_M7
GO:0030335	0.00	1.00	9	443	positive regulation of cell migration	BP	1	CCBE1,CAV1,POSTN,ACKR3,FGF7,MYOC,NTF3,CCL8,FGF16	violet	VSMC_M7
GO:0040012	0.00	1.00	13	796	regulation of locomotion	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,ACKR3,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16	violet	VSMC_M7
GO:0035239	0.00	1.00	12	699	tube morphogenesis	BP	1	CCBE1,PTPRB,CAV1,STIM1,SPINK5,LGR4,EMX2,ACKR3,CMA1,HOXD11,CYBB,COMP	violet	VSMC_M7
GO:0007417	0.00	1.00	13	795	central nervous system development	BP	1	AVPR1A,VIT,SPINK5,DYNLL1,ACAN,EMX2,CMA1,DSCAML1,LMX1A,SSTR1,IGF2BP1,HAPLN1,SPOCK1	violet	VSMC_M7
GO:2000147	0.01	1.00	9	455	positive regulation of cell motility	BP	1	CCBE1,CAV1,POSTN,ACKR3,FGF7,MYOC,NTF3,CCL8,FGF16	violet	VSMC_M7

GO:0035150	0.01	1.00	4	100	regulation of tube size	BP	1	AVPR1A,CAV1,COMP,ADRB2	violet	VSMC_M7
GO:0035296	0.01	1.00	4	100	regulation of tube diameter	BP	1	AVPR1A,CAV1,COMP,ADRB2	violet	VSMC_M7
GO:0097746	0.01	1.00	4	100	blood vessel diameter maintenance	BP	1	AVPR1A,CAV1,COMP,ADRB2	violet	VSMC_M7
GO:0040017	0.01	1.00	9	462	positive regulation of locomotion	BP	1	CCBE1,CAV1,POSTN,ACKR3,FGF7,MYOC,NTF3,CCL8,FGF16	violet	VSMC_M7
GO:0009653	0.01	1.00	25	2050	anatomical structure morphogenesis	BP	1	CCBE1,PTPRB,DMRT2,CAV1,STIM1,POSTN,SPINK5,LGR4,FGF19,EMX2,ACKR3,CMA1,DSCAML1,LMX1A,HOXD11,CYBB,TNN,COMP,FGF7,MYOC,NTF3,IGF2BP1,EGFLAM,NTNG1,FGF16	violet	VSMC_M7
GO:0051272	0.01	1.00	9	466	positive regulation of cellular component movement	BP	1	CCBE1,CAV1,POSTN,ACKR3,FGF7,MYOC,NTF3,CCL8,FGF16	violet	VSMC_M7
GO:0051270	0.01	1.00	13	830	regulation of cellular component movement	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,ACKR3,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16	violet	VSMC_M7
GO:0071310	0.01	1.00	22	1784	cellular response to organic substance	BP	1	CCBE1,CAV1,POSTN,SIGIRR,FZD10,SH2B3,SAMHD1,LGR4,DYNLL1,FGF19,ACKR3,CMA1,SSTR1,CYBB,COMP,CRLF1,FGF7,NTF3,ADRB2,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0071345	0.01	1.00	10	574	cellular response to cytokine stimulus	BP	1	CAV1,POSTN,SIGIRR,SH2B3,SAMHD1,ACKR3,SSTR1,CRLF1,ZBP1,CCL8	violet	VSMC_M7
GO:0010033	0.01	1.00	26	2273	response to organic substance	BP	1	CCBE1,AVPR1A,CAV1,POSTN,SIGIRR,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,CMA1,SSTR1,CYBB,COMP,CRLF1,FGF7,NTF3,ADRB2,DNM1,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0043588	0.01	1.00	5	171	skin development	BP	1	SPINK5,LGR4,COMP,FGF7,COL5A3	violet	VSMC_M7
GO:0007167	0.01	1.00	12	752	enzyme linked receptor protein signaling pathway	BP	1	CCBE1,CAV1,SH2B3,FGF19,PTPRU,STYK1,COMP,FGF7,MYOC,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0032412	0.01	1.00	5	178	regulation of ion transmembrane transporter activity	BP	1	NETO1,CAV1,STIM1,PDZK1,ADRB2	violet	VSMC_M7
GO:0023052	0.01	0.99	42	4258	signaling	BP	1	NETO1,CCBE1,AVPR1A,FBP1,ERMAP,RASSF6,CAV1,GJB4,POSTN,SIGIRR,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,SV2C,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,ADGRG2,STYK1,PTH2R,SSTR1,CYBB,TFR2,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,ADRB2,TNFRSF13B,GRIA3,NTNG1,DNM1,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0043408	0.01	1.00	9	502	regulation of MAPK cascade	BP	1	CAV1,FZD10,SH2B3,FGF19,ACKR3,MYOC,NTF3,ADRB2,CCL8	violet	VSMC_M7
GO:0010810	0.01	1.00	5	175	regulation of cell-substrate adhesion	BP	1	VIT,POSTN,MYOC,EGFLAM,SPOCK1	violet	VSMC_M7
GO:2001257	0.01	1.00	4	116	regulation of cation channel activity	BP	1	NETO1,CAV1,STIM1,ADRB2	violet	VSMC_M7
GO:0043270	0.01	1.00	5	182	positive regulation of ion transport	BP	1	AVPR1A,CAV1,STIM1,PDZK1,ADRB2	violet	VSMC_M7
GO:0001501	0.01	1.00	8	413	skeletal system development	BP	1	DMRT2,SH2B3,ACAN,DSCAML1,COMP,MYOC,ARSE,HAPLN1	violet	VSMC_M7
GO:0008217	0.01	1.00	4	122	regulation of blood pressure	BP	1	AVPR1A,POSTN,CMA1,ADRB2	violet	VSMC_M7
GO:0007154	0.01	0.99	42	4300	cell communication	BP	1	NETO1,CCBE1,AVPR1A,FBP1,ERMAP,RASSF6,CAV1,GJB4,POSTN,SIGIRR,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,SV2C,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,ADGRG2,STYK1,PTH2R,SSTR1,CYBB,TFR2,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,ADRB2,TNFRSF13B,GRIA3,NTNG1,DNM1,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0022898	0.01	1.00	5	186	regulation of transmembrane transporter activity	BP	1	NETO1,CAV1,STIM1,PDZK1,ADRB2	violet	VSMC_M7
GO:0007169	0.01	1.00	9	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	CCBE1,SH2B3,FGF19,STYK1,FGF7,MYOC,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0106106	0.01	1.00	4	123	cold-induced thermogenesis	BP	1	CAV1,LGR4,PTH2R,ADRB2	violet	VSMC_M7
GO:0120161	0.01	1.00	4	123	regulation of cold-induced thermogenesis	BP	1	CAV1,LGR4,PTH2R,ADRB2	violet	VSMC_M7
GO:0048514	0.01	1.00	9	508	blood vessel morphogenesis	BP	1	CCBE1,PTPRB,CAV1,STIM1,SPINK5,ACKR3,CMA1,CYBB,COMP	violet	VSMC_M7
GO:0070887	0.01	0.99	25	2230	cellular response to chemical stimulus	BP	1	CCBE1,AVPR1A,FBP1,CAV1,POSTN,SIGIRR,FZD10,SH2B3,SAMHD1,LGR4,DYNLL1,FGF19,ACKR3,CMA1,SSTR1,CYBB,TFR2,COMP,CRLF1,FGF7,NTF3,ADRB2,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0009887	0.01	1.00	12	784	animal organ morphogenesis	BP	1	CAV1,STIM1,LGR4,FGF19,EMX2,DSCAML1,HOXD11,COMP,FGF7,EGFLAM,NTNG1,FGF16	violet	VSMC_M7
GO:0008283	0.01	0.99	18	1442	cell population proliferation	BP	1	AVPR1A,CAV1,SH2B3,LGR4,FGF19,PTPRU,EMX2,ACKR3,SSTR1,TNN,COMP,CRLF1,FGF7,NTF3,IGF2BP1,TNFRSF13B,CCL8,FGF16	violet	VSMC_M7
GO:0007283	0.01	1.00	7	357	spermatogenesis	BP	1	DHH,LGR4,DYNLL1,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0001525	0.01	1.00	8	428	angiogenesis	BP	1	CCBE1,PTPRB,CAV1,STIM1,SPINK5,ACKR3,CMA1,CYBB	violet	VSMC_M7
GO:0050730	0.01	1.00	5	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	CAV1,SH2B3,CRLF1,FGF7,NTF3	violet	VSMC_M7
GO:0006811	0.01	0.99	14	1026	ion transport	BP	1	NETO1,AVPR1A,CAV1,STIM1,PDZK1,CYBB,TFR2,ANO2,SLC6A13,GRAMD2A,ADRB2,GRIA3,CALHM6,CCL8	violet	VSMC_M7
GO:0031214	0.01	1.00	4	126	biomineral tissue development	BP	1	STIM1,LGR4,COMP,ADRB2	violet	VSMC_M7
GO:0032409	0.01	1.00	5	198	regulation of transporter activity	BP	1	NETO1,CAV1,STIM1,PDZK1,ADRB2	violet	VSMC_M7
GO:0110148	0.01	1.00	4	127	biomineralization	BP	1	STIM1,LGR4,COMP,ADRB2	violet	VSMC_M7
GO:0007188	0.01	1.00	4	129	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	BP	1	LGR4,ADGRG2,PTH2R,ADRB2	violet	VSMC_M7
GO:0043269	0.01	1.00	8	444	regulation of ion transport	BP	1	NETO1,AVPR1A,CAV1,STIM1,PDZK1,CYBB,GRAMD2A,ADRB2	violet	VSMC_M7
GO:0007399	0.01	0.99	22	1867	nervous system development	BP	1	AVPR1A,VIT,POSTN,SPINK5,FZD10,DHH,DYNLL1,FGF19,ACAN,EMX2,CMA1,DSCAML1,LMX1A,SSTR1,TNN,MYOC,NTF3,IGF2BP1,NTNG1,HAPLN1,LMX1B,SPOCK1	violet	VSMC_M7
GO:1990845	0.01	1.00	4	132	adaptive thermogenesis	BP	1	CAV1,LGR4,PTH2R,ADRB2	violet	VSMC_M7
GO:0043112	0.01	1.00	4	131	receptor metabolic process	BP	1	CAV1,ACKR3,NTF3,DNM1	violet	VSMC_M7
GO:0016477	0.01	0.99	15	1120	cell migration	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,EMX2,ACKR3,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0048232	0.02	1.00	7	371	male gamete generation	BP	1	DHH,LGR4,DYNLL1,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0045766	0.02	1.00	4	133	positive regulation of angiogenesis	BP	1	CCBE1,STIM1,CMA1,CYBB	violet	VSMC_M7
GO:1904018	0.02	1.00	4	133	positive regulation of vasculature development	BP	1	CCBE1,STIM1,CMA1,CYBB	violet	VSMC_M7
GO:0030154	0.02	0.99	31	2966	cell differentiation	BP	1	AVPR1A,CAV1,POSTN,SPINK5,FZD10,SH2B3,DHH,LGR4,DYNLL1,FGF19,PTPRU,EMX2,ACKR3,DSCAML1,LMX1A,STYK1,TNN,COMP,FGF7,MYOC,NTF3,IGF2BP1,OLFM2,ADRB2,TNFRSF13B,NTNG1,POPDC3,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0050801	0.02	0.99	9	542	ion homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,TFR2,MYOC,CA12,CCL8	violet	VSMC_M7
GO:0003018	0.02	1.00	5	200	vascular process in circulatory system	BP	1	AVPR1A,CAV1,COMP,SLC6A13,ADRB2	violet	VSMC_M7

GO:0040011	0.02	0.99	17	1349	locomotion	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,EMX2,ACKR3,DSCAML1,LMX1A,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0006874	0.02	1.00	6	283	cellular calcium ion homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,CCL8	violet	VSMC_M7
GO:0010648	0.02	0.99	14	1047	negative regulation of cell communication	BP	1	AVPR1A,FBP1,CAV1,SIGIRR,RGS9BP,SH2B3,SAMHD1,LGR4,PTPRU,ACKR3,TNN,MYOC,ADRB2,DNM1	violet	VSMC_M7
GO:1905114	0.02	0.99	8	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	NETO1,CAV1,FZD10,LGR4,PTPRU,TNN,MYOC,ADRB2	violet	VSMC_M7
GO:0023057	0.02	0.99	14	1048	negative regulation of signaling	BP	1	AVPR1A,FBP1,CAV1,SIGIRR,RGS9BP,SH2B3,SAMHD1,LGR4,PTPRU,ACKR3,TNN,MYOC,ADRB2,DNM1	violet	VSMC_M7
GO:0030155	0.02	0.99	9	541	regulation of cell adhesion	BP	1	CAV1,VIT,POSTN,SPINK5,SH2B3,PTPRU,MYOC,EGFLAM,SPOCK1	violet	VSMC_M7
GO:0034097	0.02	0.99	10	659	response to cytokine	BP	1	CAV1,POSTN,SIGIRR,SH2B3,SAMHD1,ACKR3,SSTR1,CRLF1,ZBP1,CCL8	violet	VSMC_M7
GO:0019953	0.02	0.99	9	565	sexual reproduction	BP	1	AVPR1A,DHH,LGR4,DYNLL1,LRMP,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0001659	0.02	1.00	4	141	temperature homeostasis	BP	1	CAV1,LGR4,PTH2R,ADRB2	violet	VSMC_M7
GO:0055074	0.02	1.00	6	291	calcium ion homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,CCL8	violet	VSMC_M7
GO:0018108	0.02	1.00	6	287	peptidyl-tyrosine phosphorylation	BP	1	CAV1,SH2B3,STYK1,CRLF1,FGF7,NTF3	violet	VSMC_M7
GO:0018212	0.02	0.99	6	290	peptidyl-tyrosine modification	BP	1	CAV1,SH2B3,STYK1,CRLF1,FGF7,NTF3	violet	VSMC_M7
GO:0032879	0.02	0.99	23	2074	regulation of localization	BP	1	NETO1,CCBE1,AVPR1A,CAV1,STIM1,POSTN,DYNLL1,FGF19,PDZK1,PTPRU,ACKR3,CYBB,TFR2,TNN,FGF7,MYOC,NTF3,GRAMD2A,ADRB2,NTNG1,DNM1,CCL8,FGF16	violet	VSMC_M7
GO:0051050	0.02	0.99	10	660	positive regulation of transport	BP	1	AVPR1A,CAV1,STIM1,DYNLL1,FGF19,PDZK1,TFR2,NTF3,ADRB2,DNM1	violet	VSMC_M7
GO:0006875	0.02	0.99	7	381	cellular metal ion homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,TFR2,CCL8	violet	VSMC_M7
GO:0051604	0.02	1.00	5	230	protein maturation	BP	1	CCBE1,DHH,CMA1,TFR2,COMP	violet	VSMC_M7
GO:0055082	0.02	0.99	9	564	cellular chemical homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,DYNLL1,ACKR3,CMA1,TFR2,CCL8	violet	VSMC_M7
GO:0009968	0.02	0.99	13	973	negative regulation of signal transduction	BP	1	FBP1,CAV1,SIGIRR,RGS9BP,SH2B3,SAMHD1,LGR4,PTPRU,ACKR3,TNN,MYOC,ADRB2,DNM1	violet	VSMC_M7
GO:0048869	0.02	0.99	31	3033	cellular developmental process	BP	1	AVPR1A,CAV1,POSTN,SPINK5,FZD10,SH2B3,DHH,LGR4,DYNLL1,FGF19,PTPRU,EMX2,ACKR3,DSCAML1,LMX1A,STYK1,TNN,COMP,FGF7,MYOC,NTF3,IGF2BP1,OLFM2,ADRB2,TNFRSF13B,NTNG1,POPDC3,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0042592	0.02	0.99	16	1295	homeostatic process	BP	1	AVPR1A,CAV1,STIM1,SH2B3,F2RL2,LGR4,DYNLL1,ACKR3,CMA1,PTH2R,TFR2,MYOC,CA12,ADRB2,TNFRSF13B,CCL8	violet	VSMC_M7
GO:0009888	0.02	0.99	17	1389	tissue development	BP	1	DMRT2,CAV1,SVIL,STIM1,POSTN,SPINK5,LGR4,DPPA4,HOXD11,COMP,CRLF1,FGF7,ADRB2,EGFLAM,NTNG1,POPDC3,EMP1	violet	VSMC_M7
GO:0043405	0.02	1.00	4	146	regulation of MAP kinase activity	BP	1	CAV1,FZD10,SH2B3,NTF3	violet	VSMC_M7
GO:0000165	0.02	0.99	9	579	MAPK cascade	BP	1	CAV1,FZD10,SH2B3,FGF19,ACKR3,MYOC,NTF3,ADRB2,CCL8	violet	VSMC_M7
GO:1901654	0.02	1.00	4	151	response to ketone	BP	1	AVPR1A,CAV1,POSTN,CYBB	violet	VSMC_M7
GO:0072503	0.02	0.99	6	306	cellular divalent inorganic cation homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,CCL8	violet	VSMC_M7
GO:0022603	0.02	0.99	11	761	regulation of anatomical structure morphogenesis	BP	1	CCBE1,DMRT2,STIM1,POSTN,SPINK5,LGR4,CMA1,CYBB,FGF7,MYOC,NTNG1	violet	VSMC_M7
GO:0042326	0.02	0.99	6	311	negative regulation of phosphorylation	BP	1	PTPRB,FBP1,CAV1,SH2B3,DYNLL1,NTF3	violet	VSMC_M7
GO:0034762	0.02	0.99	7	396	regulation of transmembrane transport	BP	1	NETO1,CAV1,STIM1,FGF19,PDZK1,CYBB,ADRB2	violet	VSMC_M7
GO:0001568	0.02	0.99	9	576	blood vessel development	BP	1	CCBE1,PTPRB,CAV1,STIM1,SPINK5,ACKR3,CMA1,CYBB,COMP	violet	VSMC_M7
GO:0045765	0.02	0.99	5	229	regulation of angiogenesis	BP	1	CCBE1,STIM1,SPINK5,CMA1,CYBB	violet	VSMC_M7
GO:0042127	0.03	0.99	15	1230	regulation of cell population proliferation	BP	1	AVPR1A,CAV1,SH2B3,FGF19,PTPRU,ACKR3,SSTR1,TNN,COMP,CRLF1,FGF7,NTF3,TNFRSF13B,CCL8,FGF16	violet	VSMC_M7
GO:1901342	0.03	0.99	5	232	regulation of vasculature development	BP	1	CCBE1,STIM1,SPINK5,CMA1,CYBB	violet	VSMC_M7
GO:0034764	0.03	0.99	4	155	positive regulation of transmembrane transport	BP	1	STIM1,FGF19,PDZK1,ADRB2	violet	VSMC_M7
GO:0051704	0.03	0.99	10	709	multi-organism process	BP	1	AVPR1A,CAV1,DHH,LGR4,DYNLL1,LRMP,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0098771	0.03	0.99	8	502	inorganic ion homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,TFR2,CA12,CCL8	violet	VSMC_M7
GO:0001816	0.03	0.99	8	504	cytokine production	BP	1	CCBE1,ERMAP,POSTN,SIGIRR,LGR4,CMA1,CYBB,IGF2BP1	violet	VSMC_M7
GO:1904062	0.03	0.99	5	241	regulation of cation transmembrane transport	BP	1	NETO1,CAV1,STIM1,PDZK1,ADRB2	violet	VSMC_M7
GO:0007596	0.03	0.99	4	164	blood coagulation	BP	1	CAV1,SH2B3,F2RL2,COMP	violet	VSMC_M7
GO:0072507	0.03	0.99	6	323	divalent inorganic cation homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,CCL8	violet	VSMC_M7
GO:0034765	0.03	0.99	6	323	regulation of ion transmembrane transport	BP	1	NETO1,CAV1,STIM1,PDZK1,CYBB,ADRB2	violet	VSMC_M7
GO:0016485	0.03	0.99	4	170	protein processing	BP	1	CCBE1,DHH,CMA1,COMP	violet	VSMC_M7
GO:0010646	0.03	0.98	26	2513	regulation of cell communication	BP	1	NETO1,CCBE1,AVPR1A,FBP1,CAV1,POSTN,SIGIRR,FZD10,RGS9BP,SH2B3,SAMHD1,F2RL2,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,TFR2,TNN,MYOC,NTF3,ADRB2,NTNG1,DNM1,ZBP1,CCL8	violet	VSMC_M7
GO:0007599	0.03	0.99	4	166	hemostasis	BP	1	CAV1,SH2B3,F2RL2,COMP	violet	VSMC_M7
GO:0050817	0.03	0.99	4	166	coagulation	BP	1	CAV1,SH2B3,F2RL2,COMP	violet	VSMC_M7
GO:0007165	0.03	0.98	37	3919	signal transduction	BP	1	NETO1,CCBE1,AVPR1A,FBP1,ERMAP,RASSF6,CAV1,POSTN,SIGIRR,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,LGR4,FGF19,PTPRU,ACKR3,ADGRG2,STYK1,PTH2R,SSTR1,CYBB,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,ADRB2,TNFRSF13B,GRIA3,DNM1,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0048870	0.03	0.98	15	1234	cell motility	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,EMX2,ACKR3,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0051674	0.03	0.98	15	1234	localization of cell	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,EMX2,ACKR3,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0010647	0.03	0.98	15	1251	positive regulation of cell communication	BP	1	NETO1,CCBE1,CAV1,FZD10,F2RL2,LGR4,DYNLL1,FGF19,ACKR3,TFR2,MYOC,NTF3,ADRB2,ZBP1,CCL8	violet	VSMC_M7
GO:0023051	0.03	0.98	26	2524	regulation of signaling	BP	1	NETO1,CCBE1,AVPR1A,FBP1,CAV1,POSTN,SIGIRR,FZD10,RGS9BP,SH2B3,SAMHD1,F2RL2,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,TFR2,TNN,MYOC,NTF3,ADRB2,NTNG1,DNM1,ZBP1,CCL8	violet	VSMC_M7
GO:0001503	0.03	0.99	6	328	ossification	BP	1	DHH,LGR4,TNN,COMP,MYOC,ADRB2	violet	VSMC_M7
GO:0001944	0.03	0.99	9	607	vasculature development	BP	1	CCBE1,PTPRB,CAV1,STIM1,SPINK5,ACKR3,CMA1,CYBB,COMP	violet	VSMC_M7

GO:0003008	0.03	0.98	15	1240	system process	BP	1	NETO1,CCBE1,AVPR1A,CAV1,GJB4,POSTN,RGS9BP,CMA1,LMX1A,COMP,MYOC,NTF3,SLC6A13,JAKMIP1,ADRB2	violet	VSMC_M7
GO:0023056	0.03	0.98	15	1258	positive regulation of signaling	BP	1	NETO1,CCBE1,CAV1,FZD10,F2RL2,LGR4,DYNLL1,FGF19,ACKR3,TFR2,MYOC,NTF3,ADRB2,ZBP1,CCL8	violet	VSMC_M7
GO:0006935	0.03	0.99	7	426	chemotaxis	BP	1	ACKR3,DSCAML1,LMX1A,FGF7,NTF3,CCL8,FGF16	violet	VSMC_M7
GO:0055085	0.03	0.98	13	1047	transmembrane transport	BP	1	NETO1,CAV1,GJB4,STIM1,SV2C,FGF19,PDZK1,CYBB,ANO2,SLC6A13,ADRB2,GRIA3,CALHM6	violet	VSMC_M7
GO:0042330	0.03	0.99	7	427	taxis	BP	1	ACKR3,DSCAML1,LMX1A,FGF7,NTF3,CCL8,FGF16	violet	VSMC_M7
GO:0006952	0.03	0.98	12	949	defense response	BP	1	SIGIRR,SPINK5,SAMHD1,LGR4,CMA1,STYK1,MASP1,CYBB,TFR2,ZBP1,CCL8,CD300C	violet	VSMC_M7
GO:0003002	0.03	0.99	5	251	regionalization	BP	1	DMRT2,EMX2,DSCAML1,HOXD11,LMX1B	violet	VSMC_M7
GO:0060070	0.03	0.99	5	250	canonical Wnt signaling pathway	BP	1	CAV1,FZD10,LGR4,PTPRU,TNN	violet	VSMC_M7
GO:0048878	0.04	0.98	11	832	chemical homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,DYNLL1,ACKR3,CMA1,TFR2,MYOC,CA12,CCL8	violet	VSMC_M7
GO:0030003	0.04	0.99	7	434	cellular cation homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,TFR2,CCL8	violet	VSMC_M7
GO:0030100	0.04	0.99	4	174	regulation of endocytosis	BP	1	CAV1,TFR2,NTF3,DNM1	violet	VSMC_M7
GO:0055065	0.04	0.99	7	438	metal ion homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,TFR2,CCL8	violet	VSMC_M7
GO:0032101	0.04	0.98	9	646	regulation of response to external stimulus	BP	1	CAV1,SIGIRR,SPINK5,SH2B3,SAMHD1,CMA1,NTF3,ZBP1,FGF16	violet	VSMC_M7
GO:0008285	0.04	0.98	8	548	negative regulation of cell population proliferation	BP	1	CAV1,SH2B3,PTPRU,ACKR3,SSTR1,TNN,TNFRSF13B,CCL8	violet	VSMC_M7
GO:0010959	0.04	0.99	5	263	regulation of metal ion transport	BP	1	NETO1,CAV1,STIM1,GRAMD2A,ADRB2	violet	VSMC_M7
GO:0003013	0.04	0.99	7	437	circulatory system process	BP	1	AVPR1A,CAV1,POSTN,CMA1,COMP,SLC6A13,ADRB2	violet	VSMC_M7
GO:0019725	0.04	0.98	9	638	cellular homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,DYNLL1,ACKR3,CMA1,TFR2,CCL8	violet	VSMC_M7
GO:0006873	0.04	0.99	7	444	cellular ion homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,TFR2,CCL8	violet	VSMC_M7
GO:0010563	0.04	0.99	6	356	negative regulation of phosphorus metabolic process	BP	1	PTPRB,FBP1,CAV1,SH2B3,DYNLL1,NTF3	violet	VSMC_M7
GO:0045936	0.04	0.99	6	356	negative regulation of phosphate metabolic process	BP	1	PTPRB,FBP1,CAV1,SH2B3,DYNLL1,NTF3	violet	VSMC_M7
GO:0043410	0.04	0.99	6	356	positive regulation of MAPK cascade	BP	1	FZD10,FGF19,ACKR3,NTF3,ADRB2,CCL8	violet	VSMC_M7
GO:0001934	0.04	0.98	8	543	positive regulation of protein phosphorylation	BP	1	CAV1,FZD10,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0045087	0.04	0.98	7	459	innate immune response	BP	1	SAMHD1,LGR4,STYK1,MASP1,CYBB,ZBP1,CCL8	violet	VSMC_M7
GO:0042325	0.04	0.98	12	967	regulation of phosphorylation	BP	1	PTPRB,FBP1,CAV1,FZD10,SH2B3,DYNLL1,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0048609	0.05	0.98	8	563	multicellular organismal reproductive process	BP	1	AVPR1A,DHH,LGR4,DYNLL1,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0033993	0.05	0.98	9	657	response to lipid	BP	1	AVPR1A,CAV1,POSTN,SIGIRR,FZD10,DHH,PTPRU,SSTR1,CYBB	violet	VSMC_M7
GO:0034220	0.05	0.98	10	765	ion transmembrane transport	BP	1	NETO1,CAV1,STIM1,PDZK1,CYBB,ANO2,SLC6A13,ADRB2,GRIA3,CALHM6	violet	VSMC_M7
GO:0071363	0.05	0.98	8	545	cellular response to growth factor stimulus	BP	1	CCBE1,CAV1,POSTN,FGF19,COMP,FGF7,NTF3,FGF16	violet	VSMC_M7
GO:0007276	0.05	0.98	7	469	gamete generation	BP	1	DHH,LGR4,DYNLL1,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0021537	0.05	0.99	4	184	telencephalon development	BP	1	AVPR1A,EMX2,LMX1A,IGF2BP1	violet	VSMC_M7
GO:0001649	0.05	0.99	4	190	osteoblast differentiation	BP	1	DHH,LGR4,TNN,MYOC	violet	VSMC_M7
GO:0010038	0.05	0.99	5	279	response to metal ion	BP	1	FBP1,CAV1,STIM1,CYBB,TFR2	violet	VSMC_M7
GO:0032504	0.05	0.98	8	571	multicellular organism reproduction	BP	1	AVPR1A,DHH,LGR4,DYNLL1,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0098542	0.05	0.98	8	574	defense response to other organism	BP	1	SPINK5,SAMHD1,LGR4,STYK1,MASP1,CYBB,ZBP1,CCL8	violet	VSMC_M7
GO:0030182	0.05	0.98	13	1067	neuron differentiation	BP	1	POSTN,SPINK5,FZD10,EMX2,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1,LMX1B,SPOCK1	violet	VSMC_M7
GO:0009719	0.05	0.97	14	1202	response to endogenous stimulus	BP	1	AVPR1A,CAV1,POSTN,DHH,LGR4,FGF19,PTPRU,SSTR1,CYBB,COMP,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0007204	0.05	0.99	4	194	positive regulation of cytosolic calcium ion concentration	BP	1	AVPR1A,CAV1,F2RL2,ACKR3	violet	VSMC_M7
GO:0008015	0.05	0.98	6	369	blood circulation	BP	1	AVPR1A,CAV1,POSTN,CMA1,COMP,ADRB2	violet	VSMC_M7
GO:0006955	0.05	0.98	12	1012	immune response	BP	1	ERMAP,CAV1,SPINK5,SAMHD1,LGR4,ACKR3,STYK1,MASP1,CYBB,TNFRSF13B,ZBP1,CCL8	violet	VSMC_M7
GO:0044703	0.05	0.98	9	688	multi-organism reproductive process	BP	1	AVPR1A,DHH,LGR4,DYNLL1,LRMP,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0048585	0.05	0.97	14	1229	negative regulation of response to stimulus	BP	1	FBP1,CAV1,SIGIRR,SPINK5,RGS9BP,SH2B3,SAMHD1,LGR4,PTPRU,ACKR3,TNN,MYOC,ADRB2,DNM1	violet	VSMC_M7
GO:0016055	0.05	0.98	6	373	Wnt signaling pathway	BP	1	CAV1,FZD10,LGR4,PTPRU,TNN,MYOC	violet	VSMC_M7
GO:0198738	0.05	0.98	6	374	cell-cell signaling by wnt	BP	1	CAV1,FZD10,LGR4,PTPRU,TNN,MYOC	violet	VSMC_M7
GO:0050896	0.06	0.96	50	5876	response to stimulus	BP	1	NETO1,CCBE1,AVPR1A,FBP1,ERMAP,RASSF6,CAV1,GJB4,STIM1,POSTN,SIGIRR,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,LGR4,DYNLL1,FGF19,PDZK1,PTPRU,EMX2,ACKR3,CMA1,DSCAML1,ADGRG2,LMX1A,STYK1,PTH2R,SSTR1,MASP1,CYBB,TFR2,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,IGF2BP1,ADRB2,TNFRSF13B,GRIA3,DNM1,ZBP1,CCL8,CD300C,FGF16	violet	VSMC_M7
GO:0006812	0.06	0.97	10	796	cation transport	BP	1	NETO1,CAV1,STIM1,PDZK1,TFR2,SLC6A13,GRAMD2A,ADRB2,CALHM6,CCL8	violet	VSMC_M7
GO:0007160	0.06	0.99	4	192	cell-matrix adhesion	BP	1	POSTN,TNN,MYOC,COL5A3	violet	VSMC_M7
GO:0009967	0.06	0.97	13	1127	positive regulation of signal transduction	BP	1	NETO1,CCBE1,CAV1,FZD10,F2RL2,LGR4,FGF19,ACKR3,MYOC,NTF3,ADRB2,ZBP1,CCL8	violet	VSMC_M7
GO:0070848	0.06	0.98	8	570	response to growth factor	BP	1	CCBE1,CAV1,POSTN,FGF19,COMP,FGF7,NTF3,FGF16	violet	VSMC_M7
GO:0050877	0.06	0.97	9	678	nervous system process	BP	1	NETO1,AVPR1A,GJB4,RGS9BP,LMX1A,COMP,NTF3,JAKMIP1,ADRB2	violet	VSMC_M7
GO:0006928	0.06	0.97	17	1565	movement of cell or subcellular component	BP	1	CCBE1,CAV1,POSTN,FGF19,PTPRU,EMX2,ACKR3,DSCAML1,LMX1A,TNN,FGF7,MYOC,NTF3,NTNG1,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0051239	0.06	0.97	20	1937	regulation of multicellular organismal process	BP	1	NETO1,CCBE1,AVPR1A,DMRT2,ERMAP,CAV1,STIM1,POSTN,SIGIRR,SPINK5,SH2B3,LGR4,CMA1,PTH2R,CYBB,COMP,FGF7,IGF2BP1,ADRB2,FGF16	violet	VSMC_M7
GO:0008544	0.06	0.98	4	201	epidermis development	BP	1	SPINK5,LGR4,FGF7,EMP1	violet	VSMC_M7
GO:0030900	0.06	0.98	5	282	forebrain development	BP	1	AVPR1A,EMX2,LMX1A,SSTR1,IGF2BP1	violet	VSMC_M7
GO:0048584	0.06	0.97	16	1488	positive regulation of response to stimulus	BP	1	NETO1,CCBE1,ERMAP,CAV1,FZD10,F2RL2,LGR4,FGF19,ACKR3,MASP1,MYOC,NTF3,ADRB2,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0043207	0.06	0.97	10	820	response to external biotic stimulus	BP	1	CAV1,SIGIRR,SPINK5,SAMHD1,LGR4,STYK1,MASP1,CYBB,ZBP1,CCL8	violet	VSMC_M7
GO:0051707	0.06	0.97	10	820	response to other organism	BP	1	CAV1,SIGIRR,SPINK5,SAMHD1,LGR4,STYK1,MASP1,CYBB,ZBP1,CCL8	violet	VSMC_M7

GO:0007548	0.06	0.98	4	206	sex differentiation	BP	1	DMRT2,DHH,LGR4,PCYT1B	violet	VSMC_M7
GO:0048518	0.06	0.96	40	4533	positive regulation of biological process	BP	1	NETO1,CCBE1,AVPR1A,DMRT2,ERMAP,CAV1,SVIL,STIM1,VIT,POSTN,FZD10,F2RL2,LGR4,DYNLL1,FGF19,PDZK1,PTPRU,ACKR3,CMA1,LMX1A,PTH2R,MASP1,CYBB,TFR2,COMP,CRLF1,FGF7,MYOC,NTF3,SLC6A13,IGF2BP1,OLFM2,ADRB2,EGFLAM,DNM1,ZBP1,CCL8,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0048583	0.06	0.96	27	2834	regulation of response to stimulus	BP	1	NETO1,CCBE1,FBP1,ERMAP,CAV1,POSTN,SIGIRR,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,F2RL2,LGR4,FGF19,PTPRU,ACKR3,CMA1,MASP1,TNN,MYOC,NTF3,ADRB2,DNM1,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0001817	0.06	0.98	7	492	regulation of cytokine production	BP	1	CCBE1,ERMAP,POSTN,SIGIRR,LGR4,CYBB,IGF2BP1	violet	VSMC_M7
GO:0030001	0.06	0.97	8	587	metal ion transport	BP	1	NETO1,CAV1,STIM1,TFR2,SLC6A13,GRAMD2A,ADRB2,CCL8	violet	VSMC_M7
GO:0071900	0.06	0.98	5	300	regulation of protein serine/threonine kinase activity	BP	1	CAV1,FZD10,SH2B3,NTF3,ADRB2	violet	VSMC_M7
GO:0055080	0.06	0.97	7	494	cation homeostasis	BP	1	AVPR1A,CAV1,STIM1,F2RL2,ACKR3,TFR2,CCL8	violet	VSMC_M7
GO:0007420	0.07	0.97	8	587	brain development	BP	1	AVPR1A,DYNLL1,EMX2,CMA1,DSCAML1,LMX1A,SSTR1,IGF2BP1	violet	VSMC_M7
GO:0060828	0.07	0.98	4	210	regulation of canonical Wnt signaling pathway	BP	1	CAV1,LGR4,PTPRU,TNN	violet	VSMC_M7
GO:0051480	0.07	0.98	4	212	regulation of cytosolic calcium ion concentration	BP	1	AVPR1A,CAV1,F2RL2,ACKR3	violet	VSMC_M7
GO:0042391	0.07	0.98	5	302	regulation of membrane potential	BP	1	NETO1,CAV1,MYOC,ADRB2,POPDC3	violet	VSMC_M7
GO:0016049	0.07	0.97	6	399	cell growth	BP	1	AVPR1A,FBP1,POSTN,LMX1A,TNN,SPOCK1	violet	VSMC_M7
GO:0007162	0.07	0.98	4	215	negative regulation of cell adhesion	BP	1	POSTN,SH2B3,MYOC,SPOCK1	violet	VSMC_M7
GO:0045785	0.07	0.98	5	306	positive regulation of cell adhesion	BP	1	CAV1,VIT,PTPRU,MYOC,EGFLAM	violet	VSMC_M7
GO:0009966	0.07	0.96	22	2237	regulation of signal transduction	BP	1	NETO1,CCBE1,FBP1,CAV1,POSTN,SIGIRR,FZD10,RGS9BP,SH2B3,SAMHD1,F2RL2,LGR4,FGF19,PTPRU,ACKR3,TNN,MYOC,NTF3,ADRB2,DNM1,ZBP1,CCL8	violet	VSMC_M7
GO:0050890	0.07	0.98	4	214	cognition	BP	1	NETO1,LMX1A,NTF3,JAKMIP1	violet	VSMC_M7
GO:1902533	0.07	0.97	9	731	positive regulation of intracellular signal transduction	BP	1	CAV1,FZD10,F2RL2,FGF19,ACKR3,MYOC,NTF3,ADRB2,CCL8	violet	VSMC_M7
GO:0002831	0.07	0.98	4	224	regulation of response to biotic stimulus	BP	1	SIGIRR,SPINK5,SAMHD1,ZBP1	violet	VSMC_M7
GO:0140352	0.08	0.97	8	618	export from cell	BP	1	AVPR1A,DYNLL1,PDZK1,TFR2,COMP,FGF7,OLFM2,CCL8	violet	VSMC_M7
GO:0042327	0.08	0.97	8	612	positive regulation of phosphorylation	BP	1	CAV1,FZD10,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0009607	0.08	0.96	10	856	response to biotic stimulus	BP	1	CAV1,SIGIRR,SPINK5,SAMHD1,LGR4,STYK1,MASP1,CYBB,ZBP1,CCL8	violet	VSMC_M7
GO:0001932	0.08	0.96	10	845	regulation of protein phosphorylation	BP	1	PTPRB,CAV1,FZD10,SH2B3,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0019220	0.08	0.96	12	1074	regulation of phosphate metabolic process	BP	1	PTPRB,FBP1,CAV1,FZD10,SH2B3,DYNLL1,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0051174	0.08	0.96	12	1074	regulation of phosphorus metabolic process	BP	1	PTPRB,FBP1,CAV1,FZD10,SH2B3,DYNLL1,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0009611	0.08	0.97	6	422	response to wounding	BP	1	CAV1,POSTN,SH2B3,F2RL2,COMP,FGF7	violet	VSMC_M7
GO:0048812	0.08	0.96	7	503	neuron projection morphogenesis	BP	1	POSTN,DSCAML1,LMX1A,TNN,NTF3,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0050804	0.09	0.97	5	317	modulation of chemical synaptic transmission	BP	1	NETO1,NTF3,ADRB2,NTNG1,DNM1	violet	VSMC_M7
GO:0010035	0.09	0.97	6	435	response to inorganic substance	BP	1	AVPR1A,FBP1,CAV1,STIM1,CYBB,TFR2	violet	VSMC_M7
GO:0099177	0.09	0.97	5	318	regulation of trans-synaptic signaling	BP	1	NETO1,NTF3,ADRB2,NTNG1,DNM1	violet	VSMC_M7
GO:0060322	0.09	0.96	8	624	head development	BP	1	AVPR1A,DYNLL1,EMX2,CMA1,DSCAML1,LMX1A,SSTR1,IGF2BP1	violet	VSMC_M7
GO:0040007	0.09	0.96	9	742	growth	BP	1	AVPR1A,FBP1,POSTN,LMX1A,TNN,COMP,FGF7,ADRB2,SPOCK1	violet	VSMC_M7
GO:0050776	0.09	0.96	7	538	regulation of immune response	BP	1	ERMAP,CAV1,SPINK5,SAMHD1,LGR4,MASP1,ZBP1	violet	VSMC_M7
GO:0007389	0.09	0.97	5	329	pattern specification process	BP	1	DMRT2,EMX2,DSCAML1,HOXD11,LMX1B	violet	VSMC_M7
GO:0042060	0.09	0.97	5	329	wound healing	BP	1	CAV1,POSTN,SH2B3,F2RL2,COMP	violet	VSMC_M7
GO:0043086	0.09	0.96	7	555	negative regulation of catalytic activity	BP	1	PTPRB,CAV1,SPINK5,FZD10,SH2B3,DYNLL1,SPOCK1	violet	VSMC_M7
GO:0048699	0.09	0.95	13	1177	generation of neurons	BP	1	POSTN,SPINK5,FZD10,EMX2,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1,LMX1B,SPOCK1	violet	VSMC_M7
GO:0016310	0.09	0.95	15	1440	phosphorylation	BP	1	PTPRB,FBP1,CAV1,FZD10,SH2B3,DYNLL1,FGF19,STYK1,CRLF1,GALK2,FGF7,NTF3,ADRB2,CCL8,FGF16	violet	VSMC_M7
GO:0120039	0.09	0.96	7	517	plasma membrane bounded cell projection morphogenesis	BP	1	POSTN,DSCAML1,LMX1A,TNN,NTF3,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0062012	0.09	0.97	4	243	regulation of small molecule metabolic process	BP	1	AVPR1A,FBP1,CAV1,FGF19	violet	VSMC_M7
GO:0048858	0.10	0.96	7	520	cell projection morphogenesis	BP	1	POSTN,DSCAML1,LMX1A,TNN,NTF3,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0032970	0.10	0.96	5	337	regulation of actin filament-based process	BP	1	CAV1,SVIL,FZD10,MYOC,NTF3	violet	VSMC_M7
GO:0019216	0.10	0.97	4	251	regulation of lipid metabolic process	BP	1	AVPR1A,CAV1,DHH,FGF19	violet	VSMC_M7
GO:1901701	0.10	0.95	10	887	cellular response to oxygen-containing compound	BP	1	AVPR1A,CAV1,POSTN,SIGIRR,FZD10,DYNLL1,CMA1,SSTR1,CYBB,ADRB2	violet	VSMC_M7
GO:0032990	0.11	0.95	7	536	cell part morphogenesis	BP	1	POSTN,DSCAML1,LMX1A,TNN,NTF3,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0006897	0.11	0.96	6	444	endocytosis	BP	1	CAV1,ACKR3,TFR2,NTF3,ADRB2,DNM1	violet	VSMC_M7
GO:0046903	0.11	0.95	8	673	secretion	BP	1	AVPR1A,CAV1,DYNLL1,TFR2,COMP,FGF7,OLFM2,CCL8	violet	VSMC_M7
GO:0044092	0.11	0.95	9	806	negative regulation of molecular function	BP	1	PTPRB,CAV1,SIGIRR,SPINK5,FZD10,SH2B3,DYNLL1,ADRB2,SPOCK1	violet	VSMC_M7
GO:0003006	0.11	0.95	8	685	developmental process involved in reproduction	BP	1	DMRT2,DHH,LGR4,DYNLL1,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0048545	0.11	0.96	4	258	response to steroid hormone	BP	1	AVPR1A,CAV1,PTPRU,CYBB	violet	VSMC_M7
GO:0010562	0.11	0.95	8	669	positive regulation of phosphorus metabolic process	BP	1	CAV1,FZD10,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0045937	0.11	0.95	8	669	positive regulation of phosphate metabolic process	BP	1	CAV1,FZD10,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0010628	0.12	0.94	9	803	positive regulation of gene expression	BP	1	CCBE1,CAV1,POSTN,FGF19,CYBB,TFR2,FGF7,IGF2BP1,FGF16	violet	VSMC_M7
GO:0050793	0.12	0.93	18	1852	regulation of developmental process	BP	1	CCBE1,DMRT2,CAV1,STIM1,POSTN,SPINK5,LGR4,CMA1,LMX1A,CYBB,TNN,COMP,FGF7,MYOC,NTF3,OLFM2,ADRB2,NTNG1	violet	VSMC_M7
GO:0032940	0.12	0.95	7	574	secretion by cell	BP	1	AVPR1A,DYNLL1,TFR2,COMP,FGF7,OLFM2,CCL8	violet	VSMC_M7
GO:0032102	0.12	0.96	4	266	negative regulation of response to external stimulus	BP	1	SIGIRR,SPINK5,SH2B3,SAMHD1	violet	VSMC_M7
GO:0072001	0.12	0.96	4	256	renal system development	BP	1	LGR4,EMX2,HOXD11,CRLF1	violet	VSMC_M7
GO:0051049	0.12	0.93	13	1276	regulation of transport	BP	1	NETO1,AVPR1A,CAV1,STIM1,DYNLL1,FGF19,PDZK1,CYBB,TFR2,NTF3,GRAMD2A,ADRB2,DNM1	violet	VSMC_M7

GO:0071495	0.12	0.93	11	1018	cellular response to endogenous stimulus	BP	1	CAV1,POSTN,LGR4,FGF19,SSTR1,CYBB,COMP,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0072359	0.12	0.93	10	902	circulatory system development	BP	1	CCBE1,PTPRB,CAV1,STIM1,SPINK5,ACKR3,CMA1,CYBB,COMP,POPDC3	violet	VSMC_M7
GO:0031175	0.13	0.94	9	784	neuron projection development	BP	1	POSTN,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1,SPOCK1	violet	VSMC_M7
GO:0000904	0.13	0.94	7	562	cell morphogenesis involved in differentiation	BP	1	POSTN,DSCAML1,LMX1A,TNN,MYOC,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0044419	0.13	0.93	10	948	biological process involved in interspecies interaction between organisms	BP	1	CAV1,SIGIRR,SPINK5,SAMHD1,LGR4,STYK1,MASP1,CYBB,ZBP1,CCL8	violet	VSMC_M7
GO:0050878	0.13	0.95	4	273	regulation of body fluid levels	BP	1	CAV1,SH2B3,F2RL2,COMP	violet	VSMC_M7
GO:0006950	0.14	0.91	24	2715	response to stress	BP	1	AVPR1A,CAV1,POSTN,SIGIRR,SPINK5,SH2B3,SAMHD1,F2RL2,LGR4,FGF19,ACKR3,CMA1,STYK1,SSTR1,MASP1,CYBB,TFR2,COMP,FGF7,IGF2BP1,ADRB2,ZBP1,CCL8,CD300C	violet	VSMC_M7
GO:0007268	0.14	0.94	6	471	chemical synaptic transmission	BP	1	NETO1,SV2C,NTF3,ADRB2,NTNG1,DNM1	violet	VSMC_M7
GO:0098916	0.14	0.94	6	471	anterograde trans-synaptic signaling	BP	1	NETO1,SV2C,NTF3,ADRB2,NTNG1,DNM1	violet	VSMC_M7
GO:0001933	0.14	0.95	4	276	negative regulation of protein phosphorylation	BP	1	PTPRB,CAV1,SH2B3,NTF3	violet	VSMC_M7
GO:0009991	0.14	0.94	5	385	response to extracellular stimulus	BP	1	AVPR1A,POSTN,SSTR1,CYBB,ADRB2	violet	VSMC_M7
GO:0006954	0.14	0.94	6	497	inflammatory response	BP	1	SIGIRR,CMA1,CYBB,TFR2,ZBP1,CCL8	violet	VSMC_M7
GO:0030111	0.14	0.95	4	277	regulation of Wnt signaling pathway	BP	1	CAV1,LGR4,PTPRU,TNN	violet	VSMC_M7
GO:0099537	0.14	0.94	6	477	trans-synaptic signaling	BP	1	NETO1,SV2C,NTF3,ADRB2,NTNG1,DNM1	violet	VSMC_M7
GO:0022008	0.14	0.92	13	1272	neurogenesis	BP	1	POSTN,SPINK5,FZD10,EMX2,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1,LMX1B,SPOCK1	violet	VSMC_M7
GO:0098609	0.15	0.93	7	592	cell-cell adhesion	BP	1	CAV1,SH2B3,PTPRU,CADM3,DSCAML1,COMP,NTNG1	violet	VSMC_M7
GO:0006816	0.15	0.95	4	282	calcium ion transport	BP	1	CAV1,STIM1,GRAMD2A,CCL8	violet	VSMC_M7
GO:0061061	0.15	0.93	6	504	muscle structure development	BP	1	AVPR1A,CAV1,SVIL,COMP,OLFM2,POPDC3	violet	VSMC_M7
GO:0098655	0.16	0.92	7	623	cation transmembrane transport	BP	1	NETO1,CAV1,STIM1,PDZK1,SLC6A13,ADRB2,CALHM6	violet	VSMC_M7
GO:0099536	0.16	0.93	6	494	synaptic signaling	BP	1	NETO1,SV2C,NTF3,ADRB2,NTNG1,DNM1	violet	VSMC_M7
GO:0001655	0.16	0.94	4	283	urogenital system development	BP	1	LGR4,EMX2,HOXD11,CRLF1	violet	VSMC_M7
GO:0045859	0.16	0.93	6	513	regulation of protein kinase activity	BP	1	PTPRB,CAV1,FZD10,SH2B3,NTF3,ADRB2	violet	VSMC_M7
GO:0032269	0.17	0.91	8	760	negative regulation of cellular protein metabolic process	BP	1	PTPRB,CAV1,SPINK5,SH2B3,FSCB,NTF3,IGF2BP1,SPOCK1	violet	VSMC_M7
GO:0120036	0.17	0.90	12	1193	plasma membrane bounded cell projection organization	BP	1	CAV1,POSTN,DYNLL1,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1,EMP1,SPOCK1	violet	VSMC_M7
GO:1901700	0.17	0.90	12	1234	response to oxygen-containing compound	BP	1	AVPR1A,CAV1,POSTN,SIGIRR,FZD10,DHH,DYNLL1,CMA1,SSTR1,CYBB,ADRB2,DNM1	violet	VSMC_M7
GO:1902532	0.17	0.93	5	407	negative regulation of intracellular signal transduction	BP	1	FBP1,CAV1,SH2B3,ACKR3,MYOC	violet	VSMC_M7
GO:0031401	0.17	0.91	8	747	positive regulation of protein modification process	BP	1	CAV1,FZD10,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0032989	0.17	0.92	7	609	cellular component morphogenesis	BP	1	POSTN,DSCAML1,LMX1A,TNN,NTF3,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0051716	0.17	0.88	41	5042	cellular response to stimulus	BP	1	NETO1,CCBE1,AVPR1A,FBP1,ERMAP,RASSF6,CAV1,POSTN,SIGIRR,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,CMA1,ADGRG2,STYK1,PTH2R,SSTR1,CYBB,TFR2,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,IGF2BP1,ADRB2,TNFRSF13B,GRIA3,DNM1,ZBP1,CCL8,FGF16	violet	VSMC_M7
GO:0006468	0.17	0.90	12	1223	protein phosphorylation	BP	1	PTPRB,CAV1,FZD10,SH2B3,FGF19,STYK1,CRLF1,FGF7,NTF3,ADRB2,CCL8,FGF16	violet	VSMC_M7
GO:0042692	0.17	0.93	4	303	muscle cell differentiation	BP	1	AVPR1A,COMP,OLFM2,POPDC3	violet	VSMC_M7
GO:0007610	0.18	0.92	5	406	behavior	BP	1	NETO1,AVPR1A,GJB4,LMX1A,NTF3	violet	VSMC_M7
GO:0032956	0.18	0.93	4	304	regulation of actin cytoskeleton organization	BP	1	SVIL,FZD10,MYOC,NTF3	violet	VSMC_M7
GO:0006796	0.18	0.88	19	2150	phosphate-containing compound metabolic process	BP	1	PTPRB,FBP1,CAV1,PPP2R2B,FZD10,SH2B3,SAMHD1,DYNLL1,FGF19,PTPRU,STYK1,PCYT1B,CRLF1,GALK2,FGF7,NTF3,ADRB2,CCL8,FGF16	violet	VSMC_M7
GO:0031400	0.19	0.92	5	426	negative regulation of protein modification process	BP	1	PTPRB,CAV1,SH2B3,FSCB,NTF3	violet	VSMC_M7
GO:0030030	0.19	0.89	12	1226	cell projection organization	BP	1	CAV1,POSTN,DYNLL1,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1,EMP1,SPOCK1	violet	VSMC_M7
GO:0009725	0.19	0.90	7	652	response to hormone	BP	1	AVPR1A,CAV1,DHH,LGR4,PTPRU,SSTR1,CYBB	violet	VSMC_M7
GO:0090066	0.19	0.92	5	418	regulation of anatomical structure size	BP	1	AVPR1A,CAV1,SVIL,COMP,ADRB2	violet	VSMC_M7
GO:0002376	0.19	0.88	15	1656	immune system process	BP	1	ERMAP,CAV1,SPINK5,SH2B3,SAMHD1,LGR4,LRMP,ACKR3,STYK1,MASP1,CYBB,TNFRSF13B,ZBP1,CCL8,CD300C	violet	VSMC_M7
GO:0022414	0.19	0.89	10	1029	reproductive process	BP	1	AVPR1A,DMRT2,DHH,LGR4,DYNLL1,LRMP,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0000003	0.19	0.89	10	1031	reproduction	BP	1	AVPR1A,DMRT2,DHH,LGR4,DYNLL1,LRMP,ADGRG2,PCYT1B,SSTR1,SPAG8	violet	VSMC_M7
GO:0048646	0.19	0.89	9	877	anatomical structure formation involved in morphogenesis	BP	1	CCBE1,PTPRB,DMRT2,CAV1,STIM1,SPINK5,ACKR3,CMA1,CYBB	violet	VSMC_M7
GO:0006793	0.19	0.87	19	2169	phosphorus metabolic process	BP	1	PTPRB,FBP1,CAV1,PPP2R2B,FZD10,SH2B3,SAMHD1,DYNLL1,FGF19,PTPRU,STYK1,PCYT1B,CRLF1,GALK2,FGF7,NTF3,ADRB2,CCL8,FGF16	violet	VSMC_M7
GO:0050789	0.19	0.86	61	7907	regulation of biological process	BP	1	NETO1,CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,RASSF6,CAV1,SVIL,STIM1,VIT,POSTN,SIGIRR,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,LGR4,DYNLL1,FGF19,PDZK1,PTPRU,EMX2,ACKR3,CMA1,ADGRG2,LMX1A,STYK1,HOXD11,PTH2R,SSTR1,MASP1,CYBB,FSCB,TFR2,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,SLC6A13,IGF2BP1,GRAMD2A,OLFM2,ADRB2,TNFRSF13B,GRIA3,EGFLAM,NTNG1,DNM1,ZBP1,CCL8,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0006820	0.20	0.92	4	319	anion transport	BP	1	AVPR1A,PDZK1,ANO2,SLC6A13	violet	VSMC_M7
GO:0002682	0.20	0.89	9	915	regulation of immune system process	BP	1	ERMAP,CAV1,SPINK5,SAMHD1,LGR4,MASP1,TNFRSF13B,ZBP1,CCL8	violet	VSMC_M7
GO:0048666	0.20	0.89	9	877	neuron development	BP	1	POSTN,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1,SPOCK1	violet	VSMC_M7
GO:0051179	0.21	0.85	37	4586	localization	BP	1	NETO1,CCBE1,AVPR1A,CAV1,GJB4,STIM1,POSTN,SV2C,DYNLL1,FGF19,PDZK1,LRMP,PTPRU,EMX2,ACKR3,CYBB,TFR2,TNN,COMP,FGF7,MYOC,ANO2,NTF3,SLC6A13,JAKMIP1,TNS4,IGF2BP1,GRAMD2A,OLFM2,ADRB2,GRIA3,NTNG1,DNM1,CALHM6,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0008284	0.21	0.89	7	681	positive regulation of cell population proliferation	BP	1	AVPR1A,FGF19,COMP,CRLF1,FGF7,NTF3,FGF16	violet	VSMC_M7
GO:0051345	0.21	0.90	5	440	positive regulation of hydrolase activity	BP	1	AVPR1A,CAV1,FZD10,NTF3,CCL8	violet	VSMC_M7

GO:0065007	0.21	0.85	64	8375	biological regulation	BP	1	NETO1,CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,RASSF6,CAV1,SVIL,STIM1,VIT,POSTN,SIGIRR,PPP2R2B,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,LGR4,DYNLL1,FGF19,PDZK1,PTPRU,EMX2,ACKR3,CMA1,ADGRG2,LMX1A,STYK1,HOXD11,PTH2R,SSTR1,MASP1,CYBB,FSCB,TFR2,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,SLC6A13,IGF2BP1,CA12,GRAMD2A,OLFM2,ADRB2,TNFRSF13B,GRIA3,EGFLAM,NTNG1,DNM1,ZBP1,CCL8,POPDC3,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0051248	0.21	0.88	8	813	negative regulation of protein metabolic process	BP	1	PTPRB,CAV1,SPINK5,SH2B3,FSCB,NTF3,IGF2BP1,SPOCK1	violet	VSMC_M7
GO:0048523	0.21	0.85	30	3647	negative regulation of cellular process	BP	1	AVPR1A,PTPRB,FBP1,CAV1,SVIL,POSTN,SIGIRR,SPINK5,RGS9BP,SH2B3,SAMHD1,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,LMX1A,SSTR1,FSCB,TNN,COMP,CRLF1,MYOC,NTF3,IGF2BP1,ADRB2,TNFRSF13B,DNM1,CCL8,SPOCK1	violet	VSMC_M7
GO:0003012	0.22	0.91	4	332	muscle system process	BP	1	CAV1,COMP,MYOC,ADRB2	violet	VSMC_M7
GO:0031399	0.22	0.86	11	1182	regulation of protein modification process	BP	1	PTPRB,CAV1,FZD10,SH2B3,FGF19,FSCB,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0051240	0.22	0.87	10	1050	positive regulation of multicellular organismal process	BP	1	CCBE1,AVPR1A,CAV1,STIM1,POSTN,LGR4,CMA1,PTH2R,CYBB,ADRB2	violet	VSMC_M7
GO:0048522	0.23	0.83	34	4212	positive regulation of cellular process	BP	1	NETO1,CCBE1,AVPR1A,DMRT2,CAV1,SVIL,STIM1,VIT,POSTN,FZD10,F2RL2,LGR4,DYNLL1,FGF19,PDZK1,PTPRU,ACKR3,LMX1A,TFR2,COMP,CRLF1,FGF7,MYOC,NTF3,SLC6A13,OLFM2,ADRB2,EGFLAM,DNM1,ZBP1,CCL8,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0001558	0.23	0.90	4	339	regulation of cell growth	BP	1	AVPR1A,FBP1,LMX1A,SPOCK1	violet	VSMC_M7
GO:0016311	0.23	0.90	4	342	dephosphorylation	BP	1	PTPRB,FBP1,PPP2R2B,PTPRU	violet	VSMC_M7
GO:0006810	0.23	0.83	27	3300	transport	BP	1	NETO1,AVPR1A,CAV1,GJB4,STIM1,SV2C,DYNLL1,FGF19,PDZK1,LRMP,ACKR3,CYBB,TFR2,COMP,FGF7,ANO2,NTF3,SLC6A13,JAKMIP1,IGF2BP1,GRAMD2A,OLFM2,ADRB2,GRIA3,DNM1,CALHM6,CCL8	violet	VSMC_M7
GO:0014070	0.24	0.87	7	703	response to organic cyclic compound	BP	1	AVPR1A,CAV1,POSTN,DHH,PTPRU,SSTR1,CYBB	violet	VSMC_M7
GO:0048667	0.24	0.88	5	446	cell morphogenesis involved in neuron differentiation	BP	1	DSCAML1,LMX1A,TNN,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0050794	0.24	0.82	58	7581	regulation of cellular process	BP	1	NETO1,CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,RASSF6,CAV1,SVIL,STIM1,VIT,POSTN,SIGIRR,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,LGR4,DYNLL1,FGF19,PDZK1,PTPRU,EMX2,ACKR3,ADGRG2,LMX1A,STYK1,HOXD11,PTH2R,SSTR1,CYBB,FSCB,TFR2,TNN,COMP,CRLF1,FGF7,MYOC,NTF3,SLC6A13,IGF2BP1,OLFM2,ADRB2,TNFRSF13B,GRIA3,EGFLAM,NTNG1,DNM1,ZBP1,CCL8,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0000902	0.25	0.86	8	799	cell morphogenesis	BP	1	POSTN,DSCAML1,LMX1A,TNN,MYOC,NTF3,IGF2BP1,NTNG1	violet	VSMC_M7
GO:0065008	0.25	0.82	23	2770	regulation of biological quality	BP	1	NETO1,AVPR1A,CAV1,SVIL,STIM1,POSTN,SH2B3,F2RL2,LGR4,DYNLL1,ACKR3,CMA1,PTH2R,TFR2,COMP,MYOC,SLC6A13,IGF2BP1,CA12,ADRB2,TNFRSF13B,CCL8,POPDC3	violet	VSMC_M7
GO:0031667	0.25	0.89	4	362	response to nutrient levels	BP	1	POSTN,SSTR1,CYBB,ADRB2	violet	VSMC_M7
GO:0007409	0.25	0.89	4	341	axonogenesis	BP	1	DSCAML1,LMX1A,TNN,NTNG1	violet	VSMC_M7
GO:1901652	0.28	0.87	4	375	response to peptide	BP	1	CAV1,CYBB,ADRB2,DNM1	violet	VSMC_M7
GO:0051094	0.28	0.83	9	982	positive regulation of developmental process	BP	1	CCBE1,DMRT2,STIM1,LGR4,CMA1,CYBB,MYOC,OLFM2,ADRB2	violet	VSMC_M7
GO:0043549	0.28	0.85	6	612	regulation of kinase activity	BP	1	PTPRB,CAV1,FZD10,SH2B3,NTF3,ADRB2	violet	VSMC_M7
GO:0051247	0.29	0.82	10	1140	positive regulation of protein metabolic process	BP	1	CCBE1,CAV1,FZD10,FGF19,TFR2,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0050865	0.29	0.86	4	385	regulation of cell activation	BP	1	CAV1,SPINK5,SH2B3,TNFRSF13B	violet	VSMC_M7
GO:0051336	0.29	0.83	7	754	regulation of hydrolase activity	BP	1	AVPR1A,CAV1,SPINK5,FZD10,NTF3,CCL8,SPOCK1	violet	VSMC_M7
GO:0048871	0.29	0.86	4	378	multicellular organismal homeostasis	BP	1	CAV1,LGR4,PTH2R,ADRB2	violet	VSMC_M7
GO:0051246	0.30	0.79	16	1953	regulation of protein metabolic process	BP	1	CCBE1,PTPRB,CAV1,SPINK5,FZD10,SH2B3,FGF19,FSCB,TFR2,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPOCK1	violet	VSMC_M7
GO:0032268	0.30	0.79	15	1819	regulation of cellular protein metabolic process	BP	1	CCBE1,PTPRB,CAV1,SPINK5,FZD10,SH2B3,FGF19,FSCB,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPOCK1	violet	VSMC_M7
GO:0009628	0.30	0.82	8	891	response to abiotic stimulus	BP	1	NETO1,AVPR1A,CAV1,POSTN,RGS9BP,CYBB,ADRB2,FGF16	violet	VSMC_M7
GO:0051234	0.30	0.77	27	3429	establishment of localization	BP	1	NETO1,AVPR1A,CAV1,GJB4,STIM1,SV2C,DYNLL1,FGF19,PDZK1,LRMP,ACKR3,CYBB,TFR2,COMP,FGF7,ANO2,NTF3,SLC6A13,JAKMIP1,IGF2BP1,GRAMD2A,OLFM2,ADRB2,GRIA3,DNM1,CALHM6,CCL8	violet	VSMC_M7
GO:0048589	0.31	0.84	5	501	developmental growth	BP	1	POSTN,TNN,COMP,FGF7,ADRB2	violet	VSMC_M7
GO:0031347	0.31	0.85	4	397	regulation of defense response	BP	1	SPINK5,SAMHD1,CMA1,ZBP1	violet	VSMC_M7
GO:0032787	0.31	0.85	4	404	monocarboxylic acid metabolic process	BP	1	AVPR1A,FBP1,CAV1,FGF19	violet	VSMC_M7
GO:0048519	0.31	0.76	31	3961	negative regulation of biological process	BP	1	AVPR1A,PTPRB,FBP1,CAV1,SVIL,POSTN,SIGIRR,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,LGR4,DYNLL1,FGF19,PTPRU,ACKR3,LMX1A,SSTR1,FSCB,TNN,COMP,CRLF1,MYOC,NTF3,IGF2BP1,ADRB2,TNFRSF13B,DNM1,CCL8,SPOCK1	violet	VSMC_M7
GO:0061564	0.32	0.85	4	380	axon development	BP	1	DSCAML1,LMX1A,TNN,NTNG1	violet	VSMC_M7
GO:0040008	0.32	0.83	5	518	regulation of growth	BP	1	AVPR1A,FBP1,LMX1A,ADRB2,SPOCK1	violet	VSMC_M7
GO:0044057	0.33	0.84	4	398	regulation of system process	BP	1	NETO1,AVPR1A,CAV1,ADRB2	violet	VSMC_M7
GO:0060627	0.33	0.83	4	403	regulation of vesicle-mediated transport	BP	1	CAV1,TFR2,NTF3,DNM1	violet	VSMC_M7
GO:0002684	0.33	0.82	5	542	positive regulation of immune system process	BP	1	ERMAP,CAV1,MASP1,ZBP1,CCL8	violet	VSMC_M7
GO:1902531	0.34	0.77	11	1309	regulation of intracellular signal transduction	BP	1	FBP1,CAV1,FZD10,SH2B3,F2RL2,FGF19,ACKR3,MYOC,NTF3,ADRB2,CCL8	violet	VSMC_M7
GO:0032270	0.34	0.78	9	1066	positive regulation of cellular protein metabolic process	BP	1	CCBE1,CAV1,FZD10,FGF19,CRLF1,FGF7,NTF3,ADRB2,FGF16	violet	VSMC_M7
GO:0051093	0.36	0.78	6	676	negative regulation of developmental process	BP	1	CAV1,POSTN,SPINK5,LMX1A,TNN,ADRB2	violet	VSMC_M7
GO:0030029	0.36	0.78	6	662	actin filament-based process	BP	1	CAV1,SVIL,FZD10,FGF7,MYOC,NTF3	violet	VSMC_M7
GO:0001775	0.37	0.78	6	692	cell activation	BP	1	CAV1,SPINK5,SH2B3,F2RL2,COMP,TNFRSF13B	violet	VSMC_M7
GO:0060429	0.38	0.76	7	810	epithelium development	BP	1	DMRT2,CAV1,SPINK5,LGR4,HOXD11,CRLF1,FGF7	violet	VSMC_M7
GO:0065009	0.38	0.72	18	2307	regulation of molecular function	BP	1	NETO1,AVPR1A,PTPRB,CAV1,STIM1,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,LGR4,DYNLL1,PDZK1,NTF3,ADRB2,CCL8,SPAG8,SPOCK1	violet	VSMC_M7

GO:0048468	0.38	0.73	13	1587	cell development	BP	1	POSTN,SH2B3,DHH,DYNLL1,DSCAML1,LMX1A,TNN,COMP,MYOC,NTF3,IGF2BP1,NTNG1,SPOCK1	violet	VSMC_M7
GO:0080134	0.38	0.75	8	970	regulation of response to stress	BP	1	CAV1,SPINK5,SH2B3,SAMHD1,FGF19,ACKR3,CMA1,ZBP1	violet	VSMC_M7
GO:0098660	0.39	0.77	5	574	inorganic ion transmembrane transport	BP	1	NETO1,CAV1,STIM1,ANO2,SLC6A13	violet	VSMC_M7
GO:0051338	0.40	0.76	6	706	regulation of transferase activity	BP	1	PTPRB,CAV1,FZD10,SH2B3,NTF3,ADRB2	violet	VSMC_M7
GO:0018193	0.42	0.72	8	997	peptidyl-amino acid modification	BP	1	CAV1,SH2B3,STYK1,FSCB,CRLF1,FGF7,NTF3,EGFLAM	violet	VSMC_M7
GO:0006508	0.42	0.70	10	1295	proteolysis	BP	1	CCBE1,CAV1,SPINK5,DHH,ACAN,CMA1,MASP1,TFR2,COMP,SPOCK1	violet	VSMC_M7
GO:0050790	0.43	0.68	14	1823	regulation of catalytic activity	BP	1	AVPR1A,PTPRB,CAV1,STIM1,PPP2R2B,SPINK5,FZD10,SH2B3,LGR4,DYNLL1,NTF3,ADRB2,CCL8,SPOCK1	violet	VSMC_M7
GO:0051493	0.43	0.76	4	457	regulation of cytoskeleton organization	BP	1	SVIL,FZD10,MYOC,NTF3	violet	VSMC_M7
GO:0043085	0.44	0.71	7	875	positive regulation of catalytic activity	BP	1	AVPR1A,CAV1,STIM1,FZD10,NTF3,ADRB2,CCL8	violet	VSMC_M7
GO:0051241	0.44	0.72	6	743	negative regulation of multicellular organismal process	BP	1	AVPR1A,SIGIRR,SPINK5,SH2B3,LGR4,ADRB2	violet	VSMC_M7
GO:0008219	0.44	0.67	12	1587	cell death	BP	1	RASSF6,CAV1,PPP2R2B,DYNLL1,ACKR3,COMP,CRLF1,NTF3,SLC6A13,TNS4,ZBP1,EMP1	violet	VSMC_M7
GO:0044093	0.45	0.69	9	1151	positive regulation of molecular function	BP	1	AVPR1A,CAV1,STIM1,FZD10,PDZK1,NTF3,ADRB2,CCL8,SPAG8	violet	VSMC_M7
GO:0030036	0.46	0.72	5	600	actin cytoskeleton organization	BP	1	SVIL,FZD10,FGF7,MYOC,NTF3	violet	VSMC_M7
GO:2000026	0.46	0.68	8	1014	regulation of multicellular organismal development	BP	1	CCBE1,CAV1,STIM1,SPINK5,CMA1,CYBB,COMP,ADRB2	violet	VSMC_M7
GO:0045596	0.47	0.72	4	489	negative regulation of cell differentiation	BP	1	CAV1,POSTN,LMX1A,TNN	violet	VSMC_M7
GO:0019752	0.48	0.70	5	659	carboxylic acid metabolic process	BP	1	AVPR1A,FBP1,CAV1,FGF19,GADL1	violet	VSMC_M7
GO:0043436	0.50	0.68	5	677	oxoacid metabolic process	BP	1	AVPR1A,FBP1,CAV1,FGF19,GADL1	violet	VSMC_M7
GO:0043066	0.50	0.68	5	662	negative regulation of apoptotic process	BP	1	CAV1,ACKR3,COMP,CRLF1,NTF3	violet	VSMC_M7
GO:0030162	0.51	0.69	4	538	regulation of proteolysis	BP	1	CCBE1,CAV1,SPINK5,SPOCK1	violet	VSMC_M7
GO:0006082	0.51	0.66	5	689	organic acid metabolic process	BP	1	AVPR1A,FBP1,CAV1,FGF19,GADL1	violet	VSMC_M7
GO:0043069	0.53	0.65	5	681	negative regulation of programmed cell death	BP	1	CAV1,ACKR3,COMP,CRLF1,NTF3	violet	VSMC_M7
GO:0008610	0.53	0.67	4	544	lipid biosynthetic process	BP	1	AVPR1A,DHH,FGF19,PCYT1B	violet	VSMC_M7
GO:0098662	0.54	0.66	4	541	inorganic cation transmembrane transport	BP	1	NETO1,CAV1,STIM1,SLC6A13	violet	VSMC_M7
GO:0008150	0.55	0.62	86	12183	biological_process	BP	1	NETO1,CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,RASSF6,CAV1,GJB4,SVIL,STIM1,VIT,POSTN,SIGIRR,PPP2R2B,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,SV2C,LGR4,DYNLL1,DPPA4,FGF19,PDZK1,LRMP,PTPRU,ACAN,CADM3,EMX2,ACKR3,CMA1,DSCAML1,ADGRG2,LMX1A,STYK1,HOXD11,PCYT1B,PTH2R,SSTR1,MASP1,CYBB,FSCB,TFR2,TNN,COMP,CRLF1,GALK2,FGF7,MYOC,ANO2,NTF3,SLC6A13,JAKMIP1,TNS4,IGF2BP1,CA12,GRAMD2A,COL5A3,OLFM2,ADRB2,TNFRSF13B,GRIA3,EGFLAM,NTNG1,DNM1,SNORD57,CALHM6,ZBP1,CCL8,CD300C,ARSE,SNORD121A,POPDC3,OLFML2A,GADL1,HAPLN1,FGF16,SPAG8,LMX1B,EMP1,SPOCK1	violet	VSMC_M7
GO:0009893	0.55	0.55	20	2815	positive regulation of metabolic process	BP	1	CCBE1,AVPR1A,DMRT2,CAV1,POSTN,FZD10,LGR4,FGF19,LMX1A,PTH2R,CYBB,TFR2,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0006915	0.56	0.57	10	1436	apoptotic process	BP	1	RASSF6,CAV1,PPP2R2B,DYNLL1,ACKR3,COMP,CRLF1,NTF3,TNS4,ZBP1	violet	VSMC_M7
GO:0034330	0.59	0.61	4	541	cell junction organization	BP	1	CAV1,LMX1A,MYOC,NTNG1	violet	VSMC_M7
GO:0010604	0.59	0.51	18	2586	positive regulation of macromolecule metabolic process	BP	1	CCBE1,DMRT2,CAV1,POSTN,FZD10,LGR4,FGF19,LMX1A,CYBB,TFR2,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0051129	0.59	0.61	4	569	negative regulation of cellular component organization	BP	1	CAV1,SVIL,MYOC,SPOCK1	violet	VSMC_M7
GO:0012501	0.60	0.53	10	1474	programmed cell death	BP	1	RASSF6,CAV1,PPP2R2B,DYNLL1,ACKR3,COMP,CRLF1,NTF3,TNS4,ZBP1	violet	VSMC_M7
GO:0045595	0.60	0.54	8	1153	regulation of cell differentiation	BP	1	CAV1,POSTN,SPINK5,LMX1A,TNN,MYOC,NTF3,OLFM2	violet	VSMC_M7
GO:0051128	0.61	0.50	13	1877	regulation of cellular component organization	BP	1	AVPR1A,FBP1,CAV1,SVIL,FZD10,LMX1A,TFR2,MYOC,NTF3,ADRB2,NTNG1,DNM1,SPOCK1	violet	VSMC_M7
GO:0051130	0.61	0.55	6	870	positive regulation of cellular component organization	BP	1	CAV1,TFR2,MYOC,NTF3,ADRB2,DNM1	violet	VSMC_M7
GO:0060548	0.62	0.56	5	754	negative regulation of cell death	BP	1	CAV1,ACKR3,COMP,CRLF1,NTF3	violet	VSMC_M7
GO:0061024	0.62	0.58	4	599	membrane organization	BP	1	CAV1,LRMP,MYOC,DNM1	violet	VSMC_M7
GO:0010941	0.64	0.51	8	1223	regulation of cell death	BP	1	RASSF6,CAV1,ACKR3,COMP,CRLF1,NTF3,SLC6A13,ZBP1	violet	VSMC_M7
GO:0016192	0.64	0.50	8	1192	vesicle-mediated transport	BP	1	CAV1,LRMP,ACKR3,TFR2,NTF3,ADRB2,DNM1,CCL8	violet	VSMC_M7
GO:0010629	0.64	0.53	5	766	negative regulation of gene expression	BP	1	SIGIRR,SPINK5,LGR4,FGF19,IGF2BP1	violet	VSMC_M7
GO:0045944	0.65	0.51	6	904	positive regulation of transcription by RNA polymerase II	BP	1	DMRT2,LMX1A,TFR2,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0042981	0.65	0.50	7	1092	regulation of apoptotic process	BP	1	RASSF6,CAV1,ACKR3,COMP,CRLF1,NTF3,ZBP1	violet	VSMC_M7
GO:0019222	0.67	0.41	33	4858	regulation of metabolic process	BP	1	CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,CAV1,POSTN,SIGIRR,SPINK5,FZD10,SH2B3,DHH,LGR4,DYNLL1,FGF19,EMX2,LMX1A,HOXD11,PTH2R,CYBB,FSCB,TFR2,COMP,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0097435	0.67	0.52	4	622	supramolecular fiber organization	BP	1	SVIL,COMP,MYOC,COL5A3	violet	VSMC_M7
GO:0043067	0.68	0.47	7	1119	regulation of programmed cell death	BP	1	RASSF6,CAV1,ACKR3,COMP,CRLF1,NTF3,ZBP1	violet	VSMC_M7
GO:0010468	0.68	0.41	23	3428	regulation of gene expression	BP	1	CCBE1,FBP1,DMRT2,ERMAP,CAV1,POSTN,SIGIRR,SPINK5,DHH,LGR4,FGF19,EMX2,LMX1A,HOXD11,CYBB,TFR2,COMP,FGF7,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0044281	0.68	0.46	8	1301	small molecule metabolic process	BP	1	AVPR1A,FBP1,CAV1,SAMHD1,FGF19,GALK2,CA12,GADL1	violet	VSMC_M7
GO:0045893	0.69	0.45	8	1244	positive regulation of transcription, DNA-templated	BP	1	DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:1903508	0.69	0.45	8	1244	positive regulation of nucleic acid-templated transcription	BP	1	DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:1902680	0.69	0.45	8	1246	positive regulation of RNA biosynthetic process	BP	1	DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0060255	0.69	0.39	30	4468	regulation of macromolecule metabolic process	BP	1	CCBE1,PTPRB,FBP1,DMRT2,ERMAP,CAV1,POSTN,SIGIRR,SPINK5,FZD10,SH2B3,DHH,LGR4,FGF19,EMX2,LMX1A,HOXD11,CYBB,FSCB,TFR2,COMP,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7

GO:0051173	0.72	0.39	15	2331	positive regulation of nitrogen compound metabolic process	BP	1	CCBE1,DMRT2,CAV1,FZD10,LGR4,FGF19,LMX1A,TFR2,CRLF1,FGF7,NTF3,ADRB2,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0071705	0.72	0.40	10	1609	nitrogen compound transport	BP	1	AVPR1A,CAV1,DYNLL1,PDZK1,TFR2,COMP,SLC6A13,JAKMIP1,IGF2BP1,OLFM2	violet	VSMC_M7
GO:0031325	0.72	0.38	16	2483	positive regulation of cellular metabolic process	BP	1	CCBE1,AVPR1A,DMRT2,CAV1,FZD10,LGR4,FGF19,LMX1A,TFR2,CRLF1,FGF7,NTF3,ADRB2,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0031324	0.72	0.39	12	1896	negative regulation of cellular metabolic process	BP	1	PTPRB,FBP1,CAV1,SPINK5,SH2B3,LGR4,DYNLL1,FGF19,FSCB,NTF3,IGF2BP1,SPOCK1	violet	VSMC_M7
GO:0009987	0.73	0.39	81	11676	cellular process	BP	1	NETO1,CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,RASSF6,CAV1,GJB4,SVIL,STIM1,VIT,POSTN,SIGIRR,PPP2R2B,SPINK5,FZD10,RGS9BP,SH2B3,SAMHD1,DHH,F2RL2,SV2C,LGR4,DYNLL1,FGF19,PDZK1,LRMP,PTPRU,ACAN,CADM3,EMX2,ACKR3,CMA1,DSCAML1,ADGRG2,LMX1A,STYK1,HOXD11,PCYT1B,PTH2R,SSTR1,CYBB,FSCB,TFR2,TNN,COMP,CRLF1,GALK2,FGF7,MYOC,ANO2,NTF3,SLC6A13,TNS4,IGF2BP1,CA12,GRAMD2A,COL5A3,OLFM2,ADRB2,TNFRSF13B,GRIA3,EGFLAM,NTNG1,DNM1,SNORD57,CALHM6,ZBP1,CCL8,SNORD121A,POPDC3,OLFML2A,GADL1,HAPLN1,FGF16,SPAG8,LMX1B,EMP1,SPOCK1	violet	VSMC_M7
GO:0051172	0.74	0.38	11	1770	negative regulation of nitrogen compound metabolic process	BP	1	PTPRB,FBP1,CAV1,SPINK5,SH2B3,LGR4,DYNLL1,FSCB,NTF3,IGF2BP1,SPOCK1	violet	VSMC_M7
GO:0002520	0.74	0.44	4	694	immune system development	BP	1	SPINK5,SH2B3,SAMHD1,TNFRSF13B	violet	VSMC_M7
GO:0031328	0.76	0.35	9	1503	positive regulation of cellular biosynthetic process	BP	1	AVPR1A,DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0051254	0.78	0.35	8	1357	positive regulation of RNA metabolic process	BP	1	DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0080090	0.78	0.29	27	4206	regulation of primary metabolic process	BP	1	CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,CAV1,SIGIRR,SPINK5,FZD10,SH2B3,DHH,LGR4,FGF19,EMX2,LMX1A,HOXD11,FSCB,TFR2,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0019538	0.78	0.29	26	4113	protein metabolic process	BP	1	CCBE1,PTPRB,CAV1,PPP2R2B,SPINK5,FZD10,SH2B3,DHH,FGF19,PTPRU,ACAN,CMA1,STYK1,MASP1,FSCB,TFR2,COMP,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0009891	0.79	0.33	9	1533	positive regulation of biosynthetic process	BP	1	AVPR1A,DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0051171	0.79	0.28	26	4082	regulation of nitrogen compound metabolic process	BP	1	CCBE1,PTPRB,FBP1,DMRT2,CAV1,SIGIRR,SPINK5,FZD10,SH2B3,LGR4,DYNLL1,FGF19,EMX2,LMX1A,HOXD11,FSCB,TFR2,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0016043	0.79	0.27	30	4652	cellular component organization	BP	1	AVPR1A,FBP1,CAV1,SVIL,VIT,POSTN,SPINK5,FZD10,SAMHD1,DYNLL1,LRMP,CMA1,DSCAML1,LMX1A,TFR2,TNN,COMP,FGF7,MYOC,NTF3,IGF2BP1,GRAMD2A,COL5A3,ADRB2,EGFLAM,NTNG1,DNM1,OLFML2A,EMP1,SPOCK1	violet	VSMC_M7
GO:0071702	0.81	0.29	11	1891	organic substance transport	BP	1	AVPR1A,CAV1,DYNLL1,FGF19,PDZK1,TFR2,COMP,SLC6A13,JAKMIP1,IGF2BP1,OLFM2	violet	VSMC_M7
GO:0010557	0.82	0.28	8	1433	positive regulation of macromolecule biosynthetic process	BP	1	DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0033043	0.82	0.31	5	950	regulation of organelle organization	BP	1	SVIL,FZD10,MYOC,NTF3,ADRB2	violet	VSMC_M7
GO:0006629	0.83	0.31	5	982	lipid metabolic process	BP	1	AVPR1A,CAV1,DHH,FGF19,PCYT1B	violet	VSMC_M7
GO:0015031	0.83	0.28	7	1301	protein transport	BP	1	CAV1,DYNLL1,PDZK1,TFR2,COMP,JAKMIP1,OLFM2	violet	VSMC_M7
GO:0010243	0.83	0.32	4	793	response to organonitrogen compound	BP	1	CAV1,CYBB,ADRB2,DNM1	violet	VSMC_M7
GO:0035556	0.83	0.26	12	2063	intracellular signal transduction	BP	1	AVPR1A,FBP1,CAV1,FZD10,SH2B3,F2RL2,FGF19,ACKR3,MYOC,NTF3,ADRB2,CCL8	violet	VSMC_M7
GO:0009894	0.83	0.32	4	806	regulation of catabolic process	BP	1	FBP1,CAV1,IGF2BP1,ADRB2	violet	VSMC_M7
GO:0010605	0.83	0.25	12	2090	negative regulation of macromolecule metabolic process	BP	1	PTPRB,FBP1,CAV1,SIGIRR,SPINK5,SH2B3,LGR4,FGF19,FSCB,NTF3,IGF2BP1,SPOCK1	violet	VSMC_M7
GO:0009892	0.84	0.24	13	2254	negative regulation of metabolic process	BP	1	PTPRB,FBP1,CAV1,SIGIRR,SPINK5,SH2B3,LGR4,DYNLL1,FGF19,FSCB,NTF3,IGF2BP1,SPOCK1	violet	VSMC_M7
GO:0009889	0.84	0.23	18	3010	regulation of biosynthetic process	BP	1	AVPR1A,FBP1,DMRT2,CAV1,SIGIRR,DHH,LGR4,DYNLL1,FGF19,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0006357	0.85	0.24	10	1784	regulation of transcription by RNA polymerase II	BP	1	FBP1,DMRT2,CAV1,EMX2,LMX1A,HOXD11,TFR2,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0010467	0.85	0.21	27	4455	gene expression	BP	1	CCBE1,FBP1,DMRT2,ERMAP,CAV1,POSTN,SIGIRR,SPINK5,SAMHD1,DHH,LGR4,FGF19,EMX2,CMA1,LMX1A,HOXD11,CYBB,TFR2,COMP,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,FGF16,SPAG8,LMX1B	violet	VSMC_M7
GO:0045935	0.85	0.24	8	1489	positive regulation of nucleobase-containing compound metabolic process	BP	1	DMRT2,LGR4,LMX1A,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0031323	0.86	0.20	27	4391	regulation of cellular metabolic process	BP	1	CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,CAV1,SIGIRR,SPINK5,FZD10,SH2B3,LGR4,DYNLL1,FGF19,EMX2,LMX1A,HOXD11,FSCB,TFR2,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0071840	0.86	0.20	30	4827	cellular component organization or biogenesis	BP	1	AVPR1A,FBP1,CAV1,SVIL,VIT,POSTN,SPINK5,FZD10,SAMHD1,DYNLL1,LRMP,CMA1,DSCAML1,LMX1A,TFR2,TNN,COMP,FGF7,MYOC,NTF3,IGF2BP1,GRAMD2A,COL5A3,ADRB2,EGFLAM,NTNG1,DNM1,OLFML2A,EMP1,SPOCK1	violet	VSMC_M7
GO:1901698	0.86	0.27	4	845	response to nitrogen compound	BP	1	CAV1,CYBB,ADRB2,DNM1	violet	VSMC_M7
GO:1901564	0.86	0.19	29	4789	organonitrogen compound metabolic process	BP	1	CCBE1,PTPRB,FBP1,CAV1,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,DHH,FGF19,PTPRU,ACAN,CMA1,STYK1,PCYT1B,MASP1,FSCB,TFR2,COMP,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0009790	0.87	0.26	4	841	embryo development	BP	1	DMRT2,SH2B3,DSCAML1,LMX1B	violet	VSMC_M7
GO:0031327	0.87	0.23	6	1198	negative regulation of cellular biosynthetic process	BP	1	FBP1,CAV1,LGR4,DYNLL1,FGF19,IGF2BP1	violet	VSMC_M7
GO:0045184	0.88	0.22	7	1395	establishment of protein localization	BP	1	CAV1,DYNLL1,PDZK1,TFR2,COMP,JAKMIP1,OLFM2	violet	VSMC_M7
GO:0031326	0.88	0.18	17	2955	regulation of cellular biosynthetic process	BP	1	AVPR1A,FBP1,DMRT2,CAV1,SIGIRR,LGR4,DYNLL1,FGF19,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0006366	0.88	0.19	10	1862	transcription by RNA polymerase II	BP	1	FBP1,DMRT2,CAV1,EMX2,LMX1A,HOXD11,TFR2,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0009890	0.88	0.21	6	1222	negative regulation of biosynthetic process	BP	1	FBP1,CAV1,LGR4,DYNLL1,FGF19,IGF2BP1	violet	VSMC_M7

GO:0006464	0.90	0.16	16	2859	cellular protein modification process	BP	1	PTPRB,CAV1,PPP2R2B,FZD10,SH2B3,FGF19,PTPRU,STYK1,FSCB,CRLF1,FGF7,NTF3,ADRB2,EGFLAM,CCL8,FGF16	violet	VSMC_M7
GO:0036211	0.90	0.16	16	2859	protein modification process	BP	1	PTPRB,CAV1,PPP2R2B,FZD10,SH2B3,FGF19,PTPRU,STYK1,FSCB,CRLF1,FGF7,NTF3,ADRB2,EGFLAM,CCL8,FGF16	violet	VSMC_M7
GO:0006355	0.91	0.15	13	2411	regulation of transcription, DNA-templated	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:1903506	0.91	0.15	13	2412	regulation of nucleic acid-templated transcription	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:2001141	0.91	0.15	13	2416	regulation of RNA biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0051649	0.93	0.14	8	1679	establishment of localization in cell	BP	1	CAV1,DYNLL1,PDZK1,LRMP,TFR2,SLC6A13,ADRB2,DNM1	violet	VSMC_M7
GO:0043170	0.93	0.11	43	7034	macromolecule metabolic process	BP	1	CCBE1,PTPRB,FBP1,DMRT2,ERMAP,CAV1,POSTN,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,LMX1A,STYK1,HOXD11,MASP1,CYBB,FSCB,TFR2,COMP,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,DNM1,SNORD57,CCL8,SNORD121A,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0051252	0.93	0.12	14	2654	regulation of RNA metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0008104	0.93	0.12	10	2028	protein localization	BP	1	CAV1,DYNLL1,PDZK1,PTPRU,TFR2,COMP,FGF7,JAKMIP1,TNS4,OLFM2	violet	VSMC_M7
GO:0006351	0.93	0.11	13	2521	transcription, DNA-templated	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0097659	0.93	0.11	13	2522	nucleic acid-templated transcription	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0033554	0.94	0.12	7	1561	cellular response to stress	BP	1	AVPR1A,CAV1,SAMHD1,FGF19,ACKR3,CYBB,IGF2BP1	violet	VSMC_M7
GO:0032774	0.94	0.11	13	2534	RNA biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0043412	0.94	0.10	16	3029	macromolecule modification	BP	1	PTPRB,CAV1,PPP2R2B,FZD10,SH2B3,FGF19,PTPRU,STYK1,FSCB,CRLF1,FGF7,NTF3,ADRB2,EGFLAM,CCL8,FGF16	violet	VSMC_M7
GO:0007010	0.94	0.13	5	1177	cytoskeleton organization	BP	1	SVIL,FZD10,FGF7,MYOC,NTF3	violet	VSMC_M7
GO:0044267	0.94	0.09	20	3725	cellular protein metabolic process	BP	1	CCBE1,PTPRB,CAV1,PPP2R2B,SPINK5,FZD10,SH2B3,FGF19,PTPRU,STYK1,FSCB,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,CCL8,FGF16,SPOCK1	violet	VSMC_M7
GO:0051253	0.95	0.12	4	1032	negative regulation of RNA metabolic process	BP	1	FBP1,CAV1,LGR4,IGF2BP1	violet	VSMC_M7
GO:0051641	0.95	0.08	11	2295	cellular localization	BP	1	CAV1,DYNLL1,PDZK1,LRMP,PTPRU,TFR2,FGF7,SLC6A13,GRAMD2A,ADRB2,DNM1	violet	VSMC_M7
GO:2000112	0.96	0.07	14	2822	regulation of cellular macromolecule biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:1901362	0.96	0.07	15	3012	organic cyclic compound biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,DHH,LGR4,FGF19,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0033036	0.96	0.07	11	2356	macromolecule localization	BP	1	CAV1,DYNLL1,PDZK1,PTPRU,TFR2,COMP,FGF7,JAKMIP1,TNS4,IGF2BP1,OLFM2	violet	VSMC_M7
GO:0010556	0.96	0.06	14	2846	regulation of macromolecule biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0019219	0.97	0.06	14	2852	regulation of nucleobase-containing compound metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0045934	0.97	0.09	4	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	FBP1,CAV1,LGR4,IGF2BP1	violet	VSMC_M7
GO:2000113	0.97	0.08	4	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	FBP1,CAV1,LGR4,IGF2BP1	violet	VSMC_M7
GO:0010558	0.97	0.07	4	1150	negative regulation of macromolecule biosynthetic process	BP	1	FBP1,CAV1,LGR4,IGF2BP1	violet	VSMC_M7
GO:0016070	0.97	0.05	17	3480	RNA metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,SPAG8,LMX1B	violet	VSMC_M7
GO:0044260	0.98	0.04	33	5916	cellular macromolecule metabolic process	BP	1	CCBE1,PTPRB,FBP1,DMRT2,CAV1,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,LGR4,FGF19,PTPRU,EMX2,ACKR3,LMX1A,STYK1,HOXD11,FSCB,TFR2,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,DNM1,CCL8,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0034654	0.98	0.04	13	2841	nucleobase-containing compound biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0008152	0.98	0.03	50	8467	metabolic process	BP	1	CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,CAV1,POSTN,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,LMX1A,STYK1,HOXD11,PCYT1B,PTH2R,MASP1,CYBB,FSCB,TFR2,COMP,CRLF1,GALK2,FGF7,NTF3,IGF2BP1,CA12,ADRB2,EGFLAM,DNM1,SNORD57,CCL8,SNORD121A,GADL1,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0071704	0.98	0.03	47	8083	organic substance metabolic process	BP	1	CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,ERMAP,CAV1,POSTN,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,FGF19,PTPRU,ACAN,EMX2,ACKR3,CMA1,LMX1A,STYK1,HOXD11,PCYT1B,MASP1,CYBB,FSCB,TFR2,COMP,CRLF1,GALK2,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,DNM1,SNORD57,CCL8,SNORD121A,GADL1,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0018130	0.98	0.03	13	2900	heterocycle biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0019438	0.98	0.03	13	2902	aromatic compound biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0006807	0.99	0.01	40	7284	nitrogen compound metabolic process	BP	1	CCBE1,PTPRB,FBP1,DMRT2,CAV1,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,DYNLL1,FGF19,PTPRU,ACAN,EMX2,CMA1,LMX1A,STYK1,HOXD11,PCYT1B,MASP1,FSCB,TFR2,COMP,CRLF1,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,SNORD57,CCL8,SNORD121A,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0044271	0.99	0.02	15	3436	cellular nitrogen compound biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,LGR4,DYNLL1,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7

GO:0022607	0.99	0.02	8	2230	cellular component assembly	BP	1	CAV1,SVIL,SAMHD1,DYNLL1,MYOC,ADRB2,NTNG1,EMP1	violet	VSMC_M7
GO:0034613	0.99	0.02	4	1451	cellular protein localization	BP	1	CAV1,PDZK1,PTPRU,FGF7	violet	VSMC_M7
GO:0070727	0.99	0.02	4	1462	cellular macromolecule localization	BP	1	CAV1,PDZK1,PTPRU,FGF7	violet	VSMC_M7
GO:0034645	1.00	0.01	15	3533	cellular macromolecule biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0009058	1.00	0.01	20	4393	biosynthetic process	BP	1	AVPR1A,FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,DHH,LGR4,DYNLL1,FGF19,EMX2,LMX1A,HOXD11,PCYT1B,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0090304	1.00	0.01	17	3916	nucleic acid metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,SPAG8,LMX1B	violet	VSMC_M7
GO:0009059	1.00	0.01	15	3569	macromolecule biosynthetic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0044249	1.00	0.01	19	4271	cellular biosynthetic process	BP	1	AVPR1A,FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,DYNLL1,FGF19,EMX2,LMX1A,HOXD11,PCYT1B,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0044237	1.00	0.01	43	7918	cellular metabolic process	BP	1	CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,CAV1,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,LGR4,DYNLL1,FGF19,PTPRU,EMX2,ACKR3,CMA1,LMX1A,STYK1,HOXD11,PCYT1B,CYBB,FSCB,TFR2,CRLF1,GALK2,FGF7,NTF3,IGF2BP1,CA12,ADRB2,EGFLAM,DNM1,SNORD57,CCL8,SNORD121A,GADL1,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:0044238	1.00	0.01	41	7641	primary metabolic process	BP	1	CCBE1,AVPR1A,PTPRB,FBP1,DMRT2,CAV1,SIGIRR,PPP2R2B,SPINK5,FZD10,SH2B3,SAMHD1,DHH,LGR4,FGF19,PTPRU,ACAN,EMX2,CMA1,LMX1A,STYK1,HOXD11,PCYT1B,MASP1,FSCB,TFR2,COMP,CRLF1,GALK2,FGF7,NTF3,IGF2BP1,ADRB2,EGFLAM,SNORD57,CCL8,SNORD121A,FGF16,SPAG8,LMX1B,SPOCK1	violet	VSMC_M7
GO:1901576	1.00	0.01	19	4324	organic substance biosynthetic process	BP	1	AVPR1A,FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,DHH,LGR4,FGF19,EMX2,LMX1A,HOXD11,PCYT1B,TFR2,FGF7,IGF2BP1,ADRB2,SPAG8,LMX1B	violet	VSMC_M7
GO:0006996	1.00	0.01	11	2943	organelle organization	BP	1	CAV1,SVIL,FZD10,DYNLL1,LRMP,FGF7,MYOC,NTF3,GRAMD2A,ADRB2,DNM1	violet	VSMC_M7
GO:1901575	1.00	0.01	4	1628	organic substance catabolic process	BP	1	FBP1,CAV1,SAMHD1,IGF2BP1	violet	VSMC_M7
GO:0044085	1.00	0.01	8	2454	cellular component biogenesis	BP	1	CAV1,SVIL,SAMHD1,DYNLL1,MYOC,ADRB2,NTNG1,EMP1	violet	VSMC_M7
GO:0044248	1.00	0.00	4	1755	cellular catabolic process	BP	1	CAV1,SAMHD1,IGF2BP1,ADRB2	violet	VSMC_M7
GO:1901360	1.00	0.00	19	4575	organic cyclic compound metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,DHH,LGR4,FGF19,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,SPAG8,LMX1B	violet	VSMC_M7
GO:0009056	1.00	0.00	5	2000	catabolic process	BP	1	FBP1,CAV1,SAMHD1,IGF2BP1,ADRB2	violet	VSMC_M7
GO:0006139	1.00	0.00	17	4274	nucleobase-containing compound metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,SPAG8,LMX1B	violet	VSMC_M7
GO:0046483	1.00	0.00	17	4376	heterocycle metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,SPAG8,LMX1B	violet	VSMC_M7
GO:0006725	1.00	0.00	17	4410	cellular aromatic compound metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,EMX2,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,SPAG8,LMX1B	violet	VSMC_M7
GO:0034641	1.00	0.00	19	4878	cellular nitrogen compound metabolic process	BP	1	FBP1,DMRT2,CAV1,SIGIRR,SAMHD1,LGR4,DYNLL1,EMX2,CMA1,LMX1A,HOXD11,TFR2,FGF7,IGF2BP1,ADRB2,SNORD57,SNORD121A,SPAG8,LMX1B	violet	VSMC_M7
GO:0002062	0.00	1.00	20	91	chondrocyte differentiation	BP	0.0166	EXT1,CHADL,WISP1,HOXA11,EIF2AK3,SULF1,SHOX2,SLC39A14,SNX19,CHSY1,CREB3L2,WNT5B,ANXA6,COL11A1,BMPR2,CTGF,NOV,WNT9A,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0019538	0.00	1.00	301	4113	protein metabolic process	BP	0.15479	SOCS6,MALT1,PPM1H,TBK1,CAND1,AZIN1,EXT1,DSE,WDYHV1,CDKL3,PHF20L1,CDC23,ETF1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,TOPORS,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NOA1,FBXO9,EIF5B,MGAT4A,ZNF451,HDAC9,SENP6,PSME4,STAP1,UBA6,CCDC88A,ZMPSTE24,RARS2,UBE2J1,SH3BP5L,GFPT1,ROCK2,INHBA,DDX1,NOCT,FYN,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,NOX4,RB1,RTN2,PICALM,CBLC,CAMK1D,NUB1,ST3GAL3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,TRAK1,NDFIP2,NKTR,BRPF1,DNAJC3,SETD5,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,ADAM32,FAM98A,TMTC2,VPS36,RPL26,KDELC1,UFM1,CAPN7,ABHD13,PIK3R4,ALG5,CCNA1,ACPP,NDFIP1,CUL4A,BRCA2,UBA5,ILK,ITGA5,B3GLCT,TMF1,GALNT7,DHX29,SCYL2,PARG,USP12,CDK8,CNOT7,RNF6,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,IPO7,EIF2AK3,FBXL17,TMED2,EIF2S2,ITCH,NEK1,SULF1,RIOK2,USP47,LNPEP,XRN1,PDE12,PLOD2,LARP4,PI15,AGTR1,TLR2,PFN2,LTN1,BRAP,DCP1A,DHX36,THBS1,NAA25,PPP2R2A,KCTD9,GFM1,ZDHHC16,PDP1,ACVR1,GCNT4,NEDD9,CBLB,DYRK1A,BRD7,EHD4,MAN1A2,ERG,LRRK2,TANK,BRSK2,TMCC2,UBE3A,SLC39A10,CUL3,EIF4E,DNER,UCHL5,CHSY1,DNAJB14,TIMM17A,ADAMTS17,EPRS,IGF1R,IARS2,RAB3GAP2,STK38L,GALNT17,CASP7,CORO1C,ANOS1,NEK7,MRPL47,PSMD12,NTRK3,PTPN1,GRK3,ST8SIA1,CLK1,TAF5L,ABCB10,EIF2B5,TRAK2,G2E3,IQGAP1,LMLN,UBE4A,CCDC47,ADAM12,C10orf90,TLK2,PITHD1,MBTPS2,KLHL18,FASTKD2,EIF3J,TPR,CDC27,PTGS2,FAM20B,CDKL1,MAP4K5,ZC3H15,ITGAV,USP54,FERMT2,RTN3,SMURF1,TNIK,PLD1,CPEB2,BOD1L1,DKK1,FMN2,FAS,AKT3	darkolivegreen	VSMC_M9
GO:0006607	0.00	1.00	6	12	NLS-bearing protein import into nucleus	BP	0.15479	CBLB,KPNA6,KPNA1,RANBP2,KPNA4,NUP35	darkolivegreen	VSMC_M9
GO:0042987	0.00	1.00	12	52	amyloid precursor protein catabolic process	BP	0.15479	ROCK2,GSAP,RTN2,PICALM,LYN,DYRK1A,RTN3,ADAM10,ADAM19,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0035966	0.00	1.00	21	143	response to topologically incorrect protein	BP	0.15861	DNAJB5,UGGT1,DNAJC3,EDEM1,HSPH1,EIF2AK3,TMED2,THBS1,CUL3,DNAJB14,PTPN1,VAPB,ABCB10,ATF3,MBTPS2,CREB3L2,HSPB7,BFAR,DNAJB4,DNAJB9,HSPA13	darkolivegreen	VSMC_M9

GO:0044267	0.00	1.00	274	3725	cellular protein metabolic process	BP	0.18405	SOCS6,MALT1,PPM1H,TBK1,CAND1,EXT1,WDYHV1,CDKL3,PHF20L1,CDC23,ETF1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,TOPORS,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NOA1,FBXO9,EIF5B,MGAT4A,ZNF451,HDAC9,SENP6,PSME4,STAP1,UBA6,CCDC88A,ZMPSTE24,RARS2,UBE2J1,SH3BP5L,GFPT1,ROCK2,INHBA,DDX1,NOCT,FYN,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,NOX4,RB1,PICALM,CBLC,CAMK1D,NUB1,ST3GAL3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,TRAK1,NDFIP2,NKTR,BRPF1,DNAJC3,SETD5,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,FAM98A,TMTC2,VPS36,RPL26,KDELC1,UFM1,ABHD13,PIK3R4,ALG5,CCNA1,ACPP,NDFIP1,CUL4A,BRCA2,UBA5,ILK,ITGA5,B3GLCT,TMF1,GALNT7,DHX29,SCYL2,PARG,USP12,CDK8,CNOT7,RNF6,LYN,PPP2R3A,UBXN2B,MERTK,IPO7,EIF2AK3,FBXL17,TMED2,EIF2S2,ITCH,NEK1,RIOK2,USP47,LNPEP,XRN1,PDE12,PLOD2,LARP4,PI15,AGTR1,TLR2,PFN2,LTN1,BRAP,DCP1A,DHX36,THBS1,NAA25,PPP2R2A,KCTD9,GFM1,ZDHHC16,PDP1,ACVR1,GCNT4,NEDD9,CBLB,DYRK1A,BRD7,EHD4,MAN1A2,ERG,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,CUL3,EIF4E,DNER,UCHL5,DNAJB14,TIMM17A,EPRS,IGF1R,IARS2,RAB3GAP2,STK38L,GALNT17,CORO1C,ANOS1,NEK7,MRPL47,PSMD12,NTRK3,PTPN1,GRK3,ST8SIA1,CLK1,TAF5L,EIF2B5,TRAK2,G2E3,IQGAP1,UBE4A,CCDC47,C10orf90,TLK2,PITHD1,KLHL18,FASTKD2,EIF3J,TPR,CDC27,PTGS2,CDKL1,MAP4K5,ZC3H15,USP54,FERMT2,SMURF1,TNIK,PLD1,CPEB2,BOD1L1,DKK1,FAS,AKT3,CDC42BPA,SRP9,TLR6,ADAM10,MSN,SRCIN1,PHKG2,SPOP,CLK2,DLST,TRIP4,CLPX,RLIM,CYFIP2,RBBP6,SMG8,UACA,C18orf25,PKM,PPM1D,PIGW,MAP2K4,	darkolivegreen	VSMC_M9
GO:0042982	0.00	1.00	13	65	amyloid precursor protein metabolic process	BP	0.20112	ROCK2,GSAP,RTN2,PICALM,LYN,DYRK1A,TMCC2,RTN3,ADAM10,ADAM19,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0051216	0.00	1.00	23	154	cartilage development	BP	0.22226	EXT1,CHADL,WISP1,HOXA11,ZMPSTE24,EIF2AK3,SULF1,SHOX2,SLC39A14,SNX19,CHSY1,CREB3L2,PRRX1,TAPT1,WNT5B,ANXA6,COL11A1,BMPR2,CTGF,NOV,WNT9A,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0006888	0.00	1.00	17	106	endoplasmic reticulum to Golgi vesicle-mediated transport	BP	0.2517	LMAN1,SEC24A,KDELR3,RINT1,YIPF5,TMED2,COPB2,COPB1,USO1,LRRK2,CUL3,VAPB,CREB3L2,SEC23A,TRAPPC8,VAPA,ARF4	darkolivegreen	VSMC_M9
GO:0034205	0.00	1.00	10	44	amyloid-beta formation	BP	0.2517	ROCK2,GSAP,RTN2,PICALM,DYRK1A,RTN3,ADAM10,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0070972	0.00	1.00	12	60	protein localization to endoplasmic reticulum	BP	0.2517	KDELR3,RAB3GAP1,EDEM1,LRRK2,RAB3GAP2,TAPT1,PDIA2,SRP9,VAPA,ANKRD13C,SEC63,SRP19	darkolivegreen	VSMC_M9
GO:0006986	0.00	1.00	18	124	response to unfolded protein	BP	0.2517	DNAJB5,DNAJC3,EDEM1,HSPH1,EIF2AK3,TMED2,THBS1,PTPN1,VAPB,ABCB10,ATF3,MBTPS2,CREB3L2,HSPB7,BFAR,DNAJB4,DNAJB9,HSPA13	darkolivegreen	VSMC_M9
GO:0099175	0.00	1.00	14	73	regulation of postsynapse organization	BP	0.2517	PTPRD,ACTR2,FYN,DHX36,LRRK2,PDLIM5,UBE3A,NTRK3,NRP2,ADAM10,SRCIN1,PAFAH1B1,ARF4,WNT7A	darkolivegreen	VSMC_M9
GO:0033206	0.00	1.00	4	6	meiotic cytokinesis	BP	0.2517	ACTR2,ACTR3,FMN2,SPIRE1	darkolivegreen	VSMC_M9
GO:1901564	0.00	1.00	334	4789	organonitrogen compound metabolic process	BP	0.2517	SOCS6,MALT1,CDO1,PPM1H,TBK1,CAND1,AZIN1,EXT1,DSE,WDYHV1,CDKL3,PHF20L1,CDC23,ETF1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,TOPORS,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NOA1,FBXO9,ELOVL5,EIF5B,GNE,MGAT4A,ZNF451,HDAC9,SENP6,PSME4,STAP1,UBA6,CCDC88A,ZMPSTE24,RARS2,UBE2J1,SH3BP5L,GFPT1,ROCK2,INHBA,PNPLA8,DDX1,NOCT,FYN,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,NOX4,RB1,RTN2,SUCLA2,PICALM,CBLC,CAMK1D,NUB1,ST3GAL3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,TRAK1,NDFIP2,NKTR,BRPF1,DNAJC3,SETD5,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,ADAM32,FAM98A,TMTC2,VPS36,RPL26,KDELC1,UFM1,CAPN7,ABHD13,PIK3R4,ALG5,CCNA1,ACPP,NDFIP1,CUL4A,BRCA2,UBA5,ILK,ITGA5,B3GLCT,TMF1,GALNT7,HSD17B12,DHX29,SCYL2,PARG,USP12,PLPP1,CDK8,CNOT7,RNF6,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,IPO7,PDE7A,EIF2AK3,FBXL17,TDG,TMED2,EIF2S2,ITCH,NEK1,SULF1,RIOK2,USP47,LNPEP,XRN1,PDE12,PLOD2,LARP4,GDAP1,PI15,AGTR1,CERS5,HK2,ALDH18A1,TLR2,PFN2,LTN1,BRAP,DCP1A,DHX36,THBS1,NAA25,PPP2R2A,KCTD9,GFM1,PGAM4,ZDHHC16,PDP1,ACVR1,NUDT9,GCNT4,SLC35B3,NEDD9,CBLB,DYRK1A,BRD7,EHD4,MAN1A2,ERG,LRRK2,TANK,BRSK2,TMCC2,UBE3A,SLC39A10,MBOAT1,CUL3,EIF4E,DNER,UCHL5,CHSY1,DNAJB14,TIMM17A,ADAMTS17,ATP6V1A,EPRS,IGF1R,BPNT1,IARS2,RAB3GAP2,STK38L,GALNT17,CASP7,CORO1C,ANOS1,NEK7,MRPL47,PSMD12,NTRK3,PTPN1,GRK3,ST8SIA1,CLK1,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,G2E3,DERA,IQGAP1,LMLN,UBE4A,CCDC47,ADAM12,C10orf90,TLK2,NPL,PITHD1,MBTPS2	darkolivegreen	VSMC_M9
GO:1902991	0.00	1.00	9	39	regulation of amyloid precursor protein catabolic process	BP	0.27935	ROCK2,GSAP,RTN2,PICALM,LYN,RTN3,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0002063	0.00	1.00	8	27	chondrocyte development	BP	0.27935	EXT1,EIF2AK3,SULF1,SHOX2,CHSY1,COL11A1,BMPR2,CHST11	darkolivegreen	VSMC_M9

GO:0009987	0.00	1.00	733	11676	cellular process	BP	0.29445	SOCS6,LMAN1,MALT1,ELAC1,CDO1,AHI1,PHACTR2,UTRN,MON2,PPM1H,STXBP5,TBK1,CAND1,PLEKHG1,TBC1D15,CEP120,RRM2B,AZIN1,ATP6V1C1,LRP12,EXT1,THBS2,DSE,SLC39A7,WDR46,WDYHV1,CDKL3,SEC24A,DDX46,CHADL,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,SLC35B4,RMI1,KDELR3,PPIL1,UBQLN1,CEP41,PTPRD,HAUS6,DENND4C,PRUNE2,PLAA,BTBD11,SLC30A9,TOPORS,ABCB4,AKAP9,DNAJB5,GCC2,TFPI2,GNG11,TMEM165,JAK2,CLOCK,EXOC1,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,TXNDC9,POLR2B,GNE,ASPN,MGAT4A,BZW2,ZNF451,TRMO,HEMGN,HDAC9,CAVIN4,FAM135A,COL12A1,SENP6,PSME4,MYO6,CENPC,STAP1,UBA6,CDC88A,HOXA9,COX18,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,PDE1C,UGP2,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,IFRD1,CHRM2,TAF1B,TES,CAV2,ROCK2,INHBA,PNPLA8,DDX1,NOCT,GPX7,PCDH18,RAB3B,ITGB1,MPP7,RPF2,COG5,FYN,SYPL1,ZEB1,RINT1,NT5DC1,KIF5B,CEP57,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,SLC36A4,UGGT1,CCDC8,GSAP,PDSS1,NOX4,FNDC3A,GPR4,RB1,RTN2,SUCLA2,PICALM,ZC3H13,CYP27C1,TRDMT1,TOE1,SUSD5,CBLC,CGREF1,ABHD1,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,ESYT2,TRAK1,LRRC32,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,AZI2,CYTH1,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,TNFAIP6,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,ADAM32,FAM98A,TMTC2,VPS36,THSD1,RPL26,KDELC1,GPCPD1,UFM1,CAPN7,LIG4,ABHD13,PIK3R4,MYO16,CEBPZ,SUPT20H,ATP2B1,ALG5,TUBGCP3,SMAD9,EEA1,CCNA1,ATP11A,CEP83,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,YIPF5,SOS1,PDS5B,B	darkolivegreen	VSMC_M9
GO:0034248	0.00	1.00	41	395	regulation of cellular amide metabolic process	BP	0.29445	ETF1,EIF5B,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,GSAP,RTN2,PICALM,DNAJC3,RPL26,DHX29,CNOT7,EIF2AK3,TMED2,XRN1,PDE12,LARP4,LTN1,DCP1A,DHX36,THBS1,EIF4E,EPRS,EIF2B5,FASTKD2,TPR,RTN3,PLD1,CPEB2,SAMD8,SRP9,TRIP4,PKM,PIN1,ROCK1,ITGA2,GSPT1,MIR186	darkolivegreen	VSMC_M9
GO:0009057	0.00	1.00	94	1102	macromolecule catabolic process	BP	0.37538	SOCS6,MALT1,AZIN1,EXT1,CDC23,ETF1,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,ROCK2,NOCT,FYN,PSMB1,EXOSC9,PSMC2,UGGT1,TRDMT1,CBLC,UPF2,NUB1,CLN5,NDFIP2,DNAJC3,EDEM1,VPS36,ABHD13,PIK3R4,NDFIP1,CUL4A,TMF1,USP12,MTREX,CNOT7,RNF6,UBXN2B,FBXL17,ITCH,USP47,XRN1,PDE12,LTN1,DCP1A,DHX36,CBLB,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,PTPN1,UBE4A,CCDC47,TLK2,PITHD1,FASTKD2,CDC27,MYEF2,SMURF1,FMN2,MSN,PHKG2,SPOP,TRIP4,OAZ2,CLPX,RLIM,ZC3H14,RBBP6,SMG8,C18orf25,DICER1,GPRASP1,PIN1,BAG5,ROCK1,BFAR,CIDEA,GSPT1,USP7,LSM5,FASTKD5,GDNF,DNAJB9,ZPR1,VGLL4,FBXL7	darkolivegreen	VSMC_M9
GO:0050435	0.00	1.00	10	50	amyloid-beta metabolic process	BP	0.38926	ROCK2,GSAP,RTN2,PICALM,DYRK1A,RTN3,ADAM10,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0006457	0.00	1.00	20	166	protein folding	BP	0.38926	LMAN1,PPIL1,DNAJB5,TXNDC9,DNAJC1,UGGT1,NKTR,DNAJC3,HSPH1,SACS,DNAJB14,CCDC47,DNAJA4,PDIA2,CLPX,BAG5,DNAJB4,RANBP2,PDCL,HSPA13	darkolivegreen	VSMC_M9
GO:1901566	0.00	1.00	103	1317	organonitrogen compound biosynthetic process	BP	0.38926	CDO1,AZIN1,EXT1,DSE,ETF1,TMEM165,NOA1,ELOVL5,EIF5B,MGAT4A,RARS2,UBE2J1,GFPT1,ROCK2,INHBA,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,UGGT1,SUCLA2,ST3GAL3,MGAT5,GATA3,RAB3GAP1,DARS,TRAK1,DNAJC3,TMTC2,RPL26,KDELC1,ALG5,B3GLCT,GALNT7,HSD17B12,DHX29,PLPP1,CNOT7,CSGALNACT2,EIF2AK3,TMED2,EIF2S2,XRN1,PDE12,PLOD2,LARP4,CERS5,ALDH18A1,LTN1,DCP1A,DHX36,THBS1,GFM1,ZDHHC16,GCNT4,SLC35B3,MAN1A2,EIF4E,CHSY1,ATP6V1A,EPRS,IARS2,RAB3GAP2,GALNT17,MRPL47,ST8SIA1,IDH2,ABCB10,EIF2B5,TRAK2,FASTKD2,EIF3J,TPR,GATM,FAM20B,ZC3H15,PLD1,CPEB2,SAMD8,PAPSS2,ADSS,SRP9,TRIP4,OAZ2,CLTC,PKM,PIGW,ROCK1,ITGA2,C1GALT1C1,SLC1A3,GSPT1,TARS,ACOT7,ENO1,ZDHHC7,DPM2,BMPR2,DPM1,ELOVL4,EIF1AX,CHST11	darkolivegreen	VSMC_M9
GO:0048813	0.00	1.00	19	126	dendrite morphogenesis	BP	0.38926	CDKL3,PTPRD,ACTR2,ITGB1,FYN,PICALM,TRAK1,ILK,DHX36,LRRK2,PDLIM5,UBE3A,TRAK2,TNIK,ADAM10,SRCIN1,PAFAH1B1,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0034976	0.00	1.00	26	222	response to endoplasmic reticulum stress	BP	0.38926	UBQLN1,UBE2J1,UGGT1,DNAJC3,EDEM1,UFM1,UBA5,EIF2AK3,TMED2,ATP2A2,THBS1,LRRK2,BRSK2,DNAJB14,PTPN1,VAPB,EIF2B5,ATF3,UBE4A,CCDC47,MBTPS2,CREB3L2,TMX1,PDIA2,BFAR,DNAJB9	darkolivegreen	VSMC_M9
GO:0060065	0.00	1.00	6	18	uterus development	BP	0.38926	HOXA9,HOXA10,HOXA11,GATA3,MYOCD,WNT7A	darkolivegreen	VSMC_M9
GO:0046907	0.00	1.00	105	1261	intracellular transport	BP	0.38926	LMAN1,MALT1,MON2,TBC1D15,CEP120,SEC24A,KDELR3,GCC2,JAK2,MYO6,CCDC88A,COX18,ZMPSTE24,UBE2J1,ACTR2,FYN,RINT1,KIF5B,RTN2,PICALM,UPF2,CLN5,TRAK1,EDEM1,PPP1R12A,VPS36,UFM1,PIK3R4,EEA1,YIPF5,SCYL2,ARL1,XPO4,IFT88,IPO7,TMED2,COPB2,RIOK2,MAP1B,APPL1,GDAP1,COPB1,ATP2A2,USO1,ARL6,CBLB,EHD4,LRRK2,BRSK2,CUL3,TIMM17A,TRAPPC10,KPNA6,RAB3GAP2,CCDC186,CORO1C,TOMM20,PTPN1,KPNA1,VAPB,TRAK2,ANK3,HEATR5A,CREB3L2,TPR,PTGS2,SEC23A,SORCS2,VAMP4,KIFAP3,SMURF1,ACTR10,AP4E1,FMN2,SRP9,MSN,MYO1E,OAZ2,CLTC,ARMCX3,GPRASP1,TRAPPC8,THOC1,NUP155,RAB31,VAPA,SPIRE1,USP7,MYO1C,PAFAH1B1,PMPCA,KIF1B,ZDHHC7,SSX2IP,RANBP2,MYO1H,KPNA4,TOMM20L,RAB6A,ARF4,SEC63,E2F3,SRP19,ZPR1,NUP35	darkolivegreen	VSMC_M9

GO:0051128	0.00	1.00	151	1877	regulation of cellular component organization	BP	0.38926	LMAN1,AHI1,STXBP5,CAND1,CEP120,THBS2,CDKL3,CHADL,CDC23,ETF1,PTPRD,PLAA,ABCB4,AKAP9,SENP6,STAP1,CCDC88A,ZMPSTE24,ACTR2,CAV2,ROCK2,INHBA,MPP7,FYN,KIF5B,EXOSC9,CEP295,CCDC8,NOX4,RB1,PICALM,CAMK1D,ACTR3,GATA3,RAB3GAP1,TRAK1,SETD5,STK24,FAM98A,LIG4,ILK,SCYL2,RNF6,LYN,SACS,IFT88,ITCH,RIOK2,USP47,XRN1,MAP1B,APPL1,AGTR1,TLR2,PFN2,RASA1,MAP9,DHX36,THBS1,SHOX2,INO80,DYRK1A,SPTBN5,EHD4,LRRK2,BRSK2,PDLIM5,ATP10A,UBE3A,MBOAT1,CUL3,PHLDB2,KIAA1551,IGF1R,CAMSAP2,RAB3GAP2,STK38L,CORO1C,NEK7,NTRK3,PTPN1,SEMA5B,TRAK2,IQGAP1,RBBP7,C10orf90,TLK2,NRP2,HDGFL3,CREB3L2,TPR,CDC27,IQCJ-SCHIP1,DNAJA4,CDKL1,ITGAV,FERMT2,SKIL,VAMP4,PRRX1,SMURF1,TAPT1,TNIK,PLD1,VDAC2,DKK1,ATAD1,TLR6,ADAM10,MSN,SRCIN1,TPM1,TBX6,GPR65,CYFIP2,SRPX2,CLTC,FHOD3,MYOCD,SEMA7A,PIN1,CCP110,BAG5,ROCK1,ITGA2,RICTOR,RAB31,SPIRE1,GSPT1,GPC4,USP7,MYO1C,PAFAH1B1,ENO1,RAPGEF1,WFDC1,PLPPR5,BMPR2,ARF4,SKA2,CDK13,CTGF,LHFPL4,NOV,PMEPA1,RAP2A,VGLL4,COLGALT1,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0033036	0.00	1.00	181	2356	macromolecule localization	BP	0.38926	LMAN1,AHI1,MON2,STXBP5,TBC1D15,CEP120,SEC24A,KDELR3,CEP41,DENND4C,TOPORS,ABCB4,AKAP9,GCC2,JAK2,CLOCK,EXOC1,MYO6,CCDC88A,COX18,UBE2J1,ROCK2,INHBA,PNPLA8,DDX1,RAB3B,ITGB1,MPP7,RPF2,COG5,FYN,RINT1,KIF5B,DNAJC1,CEP295,RB1,RTN2,PICALM,UPF2,RAB3GAP1,ESYT2,TRAK1,NDFIP2,EDEM1,OSBPL8,STAM2,VPS36,UFM1,PIK3R4,ATP11A,CEP83,NDFIP1,YIPF5,BRCA2,DCHS1,TMF1,ARL1,UBXN2B,RAB2A,GRAMD1A,XPO4,IPO7,NUP37,EIF2AK3,TMED2,COPB2,APPL1,GDAP1,AGTR1,HK2,TLR2,COPB1,USO1,DCP1A,DHX36,THBS1,TM9SF3,ARL6,CBLB,EHD4,LRRK2,SNX19,BRSK2,ATP10A,PHLDB2,TIMM17A,KPNA6,EPRS,GPR89A,RAB3GAP2,CCDC186,CORO1C,TOMM20,PTPN1,ATP11B,LARP7,KPNA1,IDH2,TRAK2,PRELID3B,C2CD2L,PIP5K1A,IQGAP1,CEP350,ANK3,OSBPL11,CD3G,CCDC47,HEATR5A,TPR,PTGS2,SEC23A,SORCS2,SEPT5,ITGAV,FERMT2,ATP8B4,KIFAP3,SMURF1,TAPT1,TNIK,KTN1,BLZF1,AP4E1,TNFAIP8L3,KIAA0586,PDIA2,FMN2,ATAD1,SRP9,ADAM10,MSN,SRCIN1,OAZ2,CLTC,ARMCX3,ATG4D,PIGW,PIN1,TRAPPC8,ROCK1,THOC1,ITGA2,MYOM1,NUP155,RAB31,VAPA,C1QTNF3,CIDEA,SPIRE1,GPC4,MYO1C,PAFAH1B1,PMPCA,ZDHHC7,ANKRD13C,RANBP2,KPNA4,XKR9,PLEKHA3,TOMM20L,RAB6A,ARF4,TOR1AIP2,LHFPL4,SEC63,BDKRB2,LAMTOR3,NOV,MZT1,FCN1,E2F3,RAP2A,SRP19,ZPR1,C12orf66,NUP35,CHST11,SCAMP1,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:1902003	0.00	1.00	8	35	regulation of amyloid-beta formation	BP	0.38926	ROCK2,GSAP,RTN2,PICALM,RTN3,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0048666	0.00	1.00	82	877	neuron development	BP	0.39433	AHI1,LRP12,EXT1,CDKL3,PTPRD,PLAA,TOPORS,JAK2,UBA6,CCDC88A,ACTR2,ITGB1,FYN,KIF5B,RB1,PICALM,CAMK1D,GATA3,CLN5,TRAK1,STK24,MYO16,SOS1,NTN4,ILK,SCYL2,RNF6,LYN,IFT88,SLC25A46,PALLD,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,TDP2,CAMSAP2,ANOS1,NTRK3,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,FZD2,SKIL,PRRX1,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,TBX6,CYFIP2,DICER1,SEMA7A,BAG5,ROCK1,ITGA1,SLC1A3,VAPA,AFG3L2,PAFAH1B1,RAPGEF1,PLPPR5,CDH11,BMPR2,FRY,ARF4,GDNF,EFHD1,RAP2A,ZPR1,WNT7A	darkolivegreen	VSMC_M9
GO:0048468	0.00	1.00	133	1587	cell development	BP	0.41338	AHI1,LRP12,EXT1,CDKL3,PTPRD,PLAA,TOPORS,JAK2,CLOCK,HDAC9,PSME4,UBA6,CCDC88A,HOXA11,ZMPSTE24,UBE2J1,ACTR2,CAV2,ROCK2,ITGB1,FYN,KIF5B,CEP57,FNDC3A,GPR4,RB1,PICALM,CAMK1D,GATA3,CLN5,JMJD6,TRAK1,STK24,LIG4,MYO16,SOS1,BRCA2,NTN4,ILK,TMF1,SCYL2,RNF6,LYN,MERTK,IFT88,EIF2AK3,SLC25A46,PALLD,SULF1,MAP1B,RDH10,TLR2,ATP2A2,DHX36,SHOX2,ACVR1,IRX5,NEDD9,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,CUL3,TDP2,DNER,CHSY1,CAMSAP2,CORO1C,ANOS1,NTRK3,SEMA5B,IDH2,ABCB10,EIF2B5,TRAK2,IQGAP1,ANK3,NRP2,HDGFL3,PITHD1,ZFX,CREB3L2,NCAM1,FZD2,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,FMN2,ACTA2,WNT5B,NOTCH3,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,TBX6,CYFIP2,DICER1,FHOD3,MAP2K4,SEMA7A,ANXA6,PIN1,BAG5,ROCK1,ITGA1,SLC1A3,VAPA,AFG3L2,PAFAH1B1,RAPGEF1,COL11A1,PLPPR5,CDH11,BMPR2,FRY,ARF4,GDNF,EFHD1,PAQR8,RAP2A,ZPR1,CHST11,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0035457	0.00	1.00	4	8	cellular response to interferon-alpha	BP	0.45683	GATA3,PDE12,TROVE2,TPR	darkolivegreen	VSMC_M9
GO:0009101	0.00	1.00	28	245	glycoprotein biosynthetic process	BP	0.45683	EXT1,DSE,TMEM165,MGAT4A,UBE2J1,GFPT1,UGGT1,ST3GAL3,MGAT5,TRAK1,TMTC2,KDELC1,ALG5,B3GLCT,GALNT7,CSGALNACT2,GCNT4,MAN1A2,CHSY1,GALNT17,ST8SIA1,TRAK2,FAM20B,C1GALT1C1,DPM2,BMPR2,DPM1,CHST11	darkolivegreen	VSMC_M9

GO:0044265	0.00	1.00	81	947	cellular macromolecule catabolic process	BP	0.45683	SOCS6,MALT1,CDC23,ETF1,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,ROCK2,NOCT,PSMB1,EXOSC9,PSMC2,UGGT1,TRDMT1,CBLC,UPF2,NUB1,NDFIP2,DNAJC3,EDEM1,VPS36,NDFIP1,CUL4A,TMF1,USP12,MTREX,CNOT7,RNF6,UBXN2B,FBXL17,ITCH,USP47,XRN1,PDE12,LTN1,DCP1A,DHX36,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,PITHD1,FASTKD2,CDC27,MYEF2,SMURF1,MSN,SPOP,TRIP4,CLPX,RLIM,ZC3H14,RBBP6,SMG8,C18orf25,DICER1,BAG5,ROCK1,BFAR,CIDEA,GSPT1,USP7,LSM5,FASTKD5,GDNF,DNAJB9,ZPR1,VGLL4,FBXL7	darkolivegreen	VSMC_M9
GO:0031175	0.00	1.00	74	784	neuron projection development	BP	0.45683	LRP12,EXT1,CDKL3,PTPRD,PLAA,JAK2,UBA6,CCDC88A,ACTR2,ITGB1,FYN,KIF5B,RB1,PICALM,CAMK1D,GATA3,TRAK1,STK24,MYO16,SOS1,ILK,RNF6,LYN,IFT88,SLC25A46,PALLD,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,CAMSAP2,ANOS1,NTRK3,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,SKIL,PRRX1,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,TBX6,CYFIP2,DICER1,SEMA7A,BAG5,ROCK1,ITGA1,VAPA,AFG3L2,PAFAH1B1,RAPGEF1,PLPPR5,CDH11,BMPR2,FRY,ARF4,GDNF,EFHD1,RAP2A,ZPR1,WNT7A	darkolivegreen	VSMC_M9
GO:0044238	0.00	1.00	498	7641	primary metabolic process	BP	0.45683	SOCS6,MALT1,ELAC1,CDO1,AHI1,PPM1H,TBK1,CAND1,RRM2B,AZIN1,EXT1,DSE,WDR46,WDYHV1,CDKL3,DDX46,PHF20L1,KHDRBS3,CDC23,ETF1,SLC35B4,RMI1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,SLC30A9,TOPORS,ABCB4,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,POLR2B,GNE,MGAT4A,ZNF451,TRMO,HDAC9,CAVIN4,FAM135A,SENP6,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,RPF2,FYN,ZEB1,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,PDSS1,NOX4,RB1,RTN2,SUCLA2,PICALM,ZC3H13,CYP27C1,TRDMT1,TOE1,CBLC,ABHD1,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,TRAK1,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,PRPF40A,ADAM32,FAM98A,TMTC2,VPS36,RPL26,KDELC1,GPCPD1,UFM1,CAPN7,LIG4,ABHD13,PIK3R4,CEBPZ,SUPT20H,ALG5,SMAD9,CCNA1,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,AC091959.3,ILK,ITGA5,B3GLCT,TMF1,GALNT7,HOXC10,ERI1,HSD17B12,DHX29,SCYL2,PARG,USP12,MTREX,PLPP1,CDK8,CNOT7,RNF6,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,IPO7,PDE7A,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,U2SURP,RDH10,PLOD2,LARP4,PI15,AGTR1,ACTR8,CERS5,HK2,ALDH18A1,TLR2,PFN2,RASA1,MBNL1,LTN1,BRAP,DCP1A,DHX36,THBS1,NAA25,PPP2R2A,SHOX2,KCTD9,GFM1,LIN54	darkolivegreen	VSMC_M9
GO:0061448	0.00	1.00	25	203	connective tissue development	BP	0.45683	EXT1,CHADL,WISP1,HOXA11,ZMPSTE24,GPR4,EIF2AK3,SULF1,SHOX2,SLC39A14,SNX19,CHSY1,CREB3L2,PRRX1,TAPT1,ACTA2,WNT5B,ANXA6,COL11A1,BMPR2,CTGF,NOV,WNT9A,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0033365	0.00	1.00	66	737	protein localization to organelle	BP	0.45683	LMAN1,KDELR3,TOPORS,GCC2,JAK2,CCDC88A,COX18,ROCK2,DDX1,RPF2,FYN,RB1,RAB3GAP1,EDEM1,OSBPL8,VPS36,UFM1,PIK3R4,CEP83,BRCA2,ARL1,UBXN2B,IPO7,EIF2AK3,APPL1,GDAP1,HK2,DCP1A,ARL6,CBLB,LRRK2,TIMM17A,KPNA6,RAB3GAP2,TOMM20,LARP7,KPNA1,CEP350,CCDC47,TPR,PTGS2,FERMT2,SMURF1,TAPT1,PDIA2,SRP9,ADAM10,MSN,PIN1,NUP155,VAPA,GPC4,PMPCA,ANKRD13C,RANBP2,KPNA4,TOM20L,RAB6A,ARF4,TOR1AIP2,SEC63,E2F3,SRP19,ZPR1,C12orf66,NUP35	darkolivegreen	VSMC_M9
GO:0043170	0.00	1.00	464	7034	macromolecule metabolic process	BP	0.46386	SOCS6,MALT1,ELAC1,AHI1,PPM1H,TBK1,CAND1,RRM2B,AZIN1,EXT1,DSE,WDR46,WDYHV1,CDKL3,DDX46,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,RMI1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NPAS2,NOA1,FBXO9,EIF5B,POLR2B,MGAT4A,ZNF451,TRMO,HDAC9,CAVIN4,SENP6,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,ITGB1,RPF2,FYN,ZEB1,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,NOX4,RB1,RTN2,PICALM,ZC3H13,TRDMT1,TOE1,CBLC,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,TRAK1,LRRC32,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,PRPF40A,ADAM32,FAM98A,TMTC2,VPS36,RPL26,KDELC1,UFM1,CAPN7,LIG4,ABHD13,PIK3R4,CEBPZ,SUPT20H,ATP2B1,ALG5,SMAD9,CCNA1,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,AC091959.3,ILK,ITGA5,B3GLCT,HSPH1,TMF1,GALNT7,HOXC10,ERI1,DHX29,SCYL2,PARG,USP12,MTREX,CDK8,CNOT7,RNF6,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,IPO7,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,FFAR4,APPL1,U2SURP,PLOD2,LARP4,PI15,AGTR1,ACTR8,TLR2,PFN2,RASA1,MBNL1,LTN1,BRAP,DCP1A,DHX36,THBS1,NAA25,PPP2R2A,SHOX2,KCTD9,GFM1,LIN54,ZDHHC16,PDP1,ACVR1,WDR75,IRX5,MTERF3,INO80,GCNT4,SNRNP48,NFKBIZ,NEDD9,CBLB,DYRK1A,B	darkolivegreen	VSMC_M9
GO:0006486	0.00	1.00	22	182	protein glycosylation	BP	0.46386	EXT1,TMEM165,MGAT4A,UBE2J1,GFPT1,UGGT1,ST3GAL3,MGAT5,TRAK1,TMTC2,KDELC1,ALG5,B3GLCT,GALNT7,GCNT4,MAN1A2,GALNT17,ST8SIA1,TRAK2,C1GALT1C1,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0043413	0.00	1.00	22	182	macromolecule glycosylation	BP	0.46386	EXT1,TMEM165,MGAT4A,UBE2J1,GFPT1,UGGT1,ST3GAL3,MGAT5,TRAK1,TMTC2,KDELC1,ALG5,B3GLCT,GALNT7,GCNT4,MAN1A2,GALNT17,ST8SIA1,TRAK2,C1GALT1C1,DPM2,DPM1	darkolivegreen	VSMC_M9

GO:0070085	0.00	1.00	23	194	glycosylation	BP	0.46386	EXT1,TMEM165,MGAT4A,UBE2J1,GFPT1,UGGT1,ST3GAL3,MGAT5,CLN5,TRAK1,TMTC2,KDELC1,ALG5,B3GLCT,GALNT7,GCNT4,MAN1A2,GALNT17,ST8SIA1,TRAK2,C1GALT1C1,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0071840	0.00	1.00	340	4827	cellular component organization or biogenesis	BP	0.4796	LMAN1,AHI1,PHACTR2,UTRN,STXBP5,CAND1,CEP120,LRP12,EXT1,THBS2,WDR46,CDKL3,SEC24A,CHADL,CDC23,ETF1,RMI1,UBQLN1,CEP41,PTPRD,HAUS6,PLAA,TOPORS,ABCB4,AKAP9,GCC2,TMEM165,JAK2,TXNDC9,COL12A1,SENP6,PSME4,MYO6,CENPC,STAP1,UBA6,CCDC88A,COX18,ZMPSTE24,ACTR2,TAF1B,CAV2,ROCK2,INHBA,DDX1,NOCT,RAB3B,ITGB1,MPP7,RPF2,FYN,KIF5B,CEP57,EXOSC9,CEP295,CCDC8,NOX4,RB1,PICALM,CAMK1D,ACTR3,GATA3,RAB3GAP1,CLN5,JMJD6,DARS,ESYT2,TRAK1,SETD5,NDUFAF5,STK24,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,FAM98A,VPS36,THSD1,RPL26,UFM1,LIG4,MYO16,TUBGCP3,EEA1,CCNA1,ATP11A,CEP83,ACPP,CUL4A,STARD13,YIPF5,SOS1,PDS5B,BRCA2,NTN4,UBA5,ILK,DCTN6,DCHS1,TMF1,ERI1,HSD17B12,DHX29,SCYL2,MTREX,CNOT7,RNF6,ARL1,LYN,UBXN2B,SACS,RAB2A,GRAMD1A,TMEM41B,IFT88,MYBL1,EIF2AK3,SLC25A46,TDG,TMED2,HCFC2,PALLD,EIF2S2,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,MAT2A,XRN1,BDP1,MICAL2,MAP1B,APPL1,TMEM70,LARP4,GDAP1,AGTR1,ACTR8,HK2,TLR2,PFN2,RASA1,ATP2A2,USO1,MAP9,DHX36,THBS1,SHOX2,KCTD9,LIN54,ARL6,WDR75,MTERF3,INO80,CHD9,NEDD9,DYRK1A,SPTBN5,EHD4,LRRK2,SNX19,BRSK2,PDLIM5,ATP10A,UBE3A,MBOAT1,CUL3,NAP1L4,PHLDB2,DNER,TROVE2,DNAJB14,TIMM17A,KIAA1551,ADAMTS17,RRP15,EPRS,IGF1R,CAMSAP2,RAB3GAP2,HAUS2,STK38L,CORO1C,ANOS1,NEK7,NTRK3,TOMM20,PTPN1,ATP11B,SEMA5B,VAPB,TRAK2,PRELID3B,C2CD2L,SYCP2,PIP5K1A,IQGAP1,CEP350,RBBP7,ANK3,CD3G,CCDC47,SMTN,C10orf90,SH3KBP1,TLK2,NRP2,HDGFL3,BAZ1A,FASTKD2,EHBP1L1,CREB3L2,EIF3J,TPR,CDC27,	darkolivegreen	VSMC_M9
GO:0016043	0.00	1.00	330	4652	cellular component organization	BP	0.48152	LMAN1,AHI1,PHACTR2,UTRN,STXBP5,CAND1,CEP120,LRP12,EXT1,THBS2,CDKL3,SEC24A,CHADL,CDC23,ETF1,RMI1,UBQLN1,CEP41,PTPRD,HAUS6,PLAA,TOPORS,ABCB4,AKAP9,GCC2,TMEM165,JAK2,TXNDC9,COL12A1,SENP6,PSME4,MYO6,CENPC,STAP1,UBA6,CCDC88A,COX18,ZMPSTE24,ACTR2,TAF1B,CAV2,ROCK2,INHBA,DDX1,NOCT,RAB3B,ITGB1,MPP7,RPF2,FYN,KIF5B,CEP57,EXOSC9,CEP295,CCDC8,NOX4,RB1,PICALM,CAMK1D,ACTR3,GATA3,RAB3GAP1,CLN5,JMJD6,DARS,ESYT2,TRAK1,SETD5,NDUFAF5,STK24,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,FAM98A,VPS36,THSD1,UFM1,LIG4,MYO16,TUBGCP3,EEA1,CCNA1,ATP11A,CEP83,ACPP,STARD13,YIPF5,SOS1,PDS5B,BRCA2,NTN4,UBA5,ILK,DCTN6,DCHS1,TMF1,HSD17B12,DHX29,SCYL2,CNOT7,RNF6,ARL1,LYN,UBXN2B,SACS,RAB2A,GRAMD1A,TMEM41B,IFT88,MYBL1,EIF2AK3,SLC25A46,TDG,TMED2,HCFC2,PALLD,EIF2S2,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,MAT2A,XRN1,BDP1,MICAL2,MAP1B,APPL1,TMEM70,LARP4,GDAP1,AGTR1,ACTR8,HK2,TLR2,PFN2,RASA1,ATP2A2,USO1,MAP9,DHX36,THBS1,SHOX2,KCTD9,LIN54,ARL6,MTERF3,INO80,CHD9,NEDD9,DYRK1A,SPTBN5,EHD4,LRRK2,SNX19,BRSK2,PDLIM5,ATP10A,UBE3A,MBOAT1,CUL3,NAP1L4,PHLDB2,DNER,TROVE2,DNAJB14,TIMM17A,KIAA1551,ADAMTS17,EPRS,IGF1R,CAMSAP2,RAB3GAP2,HAUS2,STK38L,CORO1C,ANOS1,NEK7,NTRK3,TOMM20,PTPN1,ATP11B,SEMA5B,VAPB,TRAK2,PRELID3B,C2CD2L,SYCP2,PIP5K1A,IQGAP1,CEP350,RBBP7,ANK3,CD3G,CCDC47,SMTN,C10orf90,SH3KBP1,TLK2,NRP2,HDGFL3,BAZ1A,FASTKD2,EHBP1L1,CREB3L2,EIF3J,TPR,CDC27,SEC23A,NCAM1,IQCJ-	darkolivegreen	VSMC_M9
GO:0045933	0.00	1.00	7	30	positive regulation of muscle contraction	BP	0.50075	ATP1A1,PTGS2,MYOCD,ITGA2,TBXA2R,ENO1,CTGF	darkolivegreen	VSMC_M9
GO:0006807	0.00	1.00	476	7284	nitrogen compound metabolic process	BP	0.50075	SOCS6,MALT1,ELAC1,CDO1,AHI1,PPM1H,TBK1,CAND1,RRM2B,AZIN1,EXT1,DSE,WDR46,WDYHV1,CDKL3,DDX46,PHF20L1,KHDRBS3,CDC23,ETF1,RMI1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,POLR2B,GNE,MGAT4A,ZNF451,TRMO,HDAC9,CAVIN4,SENP6,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,SH3BP5L,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,RPF2,FYN,ZEB1,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,NOX4,RB1,RTN2,SUCLA2,PICALM,ZC3H13,TRDMT1,TOE1,CBLC,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,TRAK1,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,PRPF40A,ADAM32,FAM98A,TMTC2,VPS36,RPL26,KDELC1,UFM1,CAPN7,LIG4,ABHD13,PIK3R4,CEBPZ,SUPT20H,ALG5,SMAD9,CCNA1,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,AC091959.3,ILK,ITGA5,B3GLCT,TMF1,GALNT7,HOXC10,ERI1,HSD17B12,DHX29,SCYL2,PARG,USP12,MTREX,PLPP1,CDK8,CNOT7,RNF6,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,IPO7,PDE7A,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,U2SURP,PLOD2,LARP4,GDAP1,PI15,AGTR1,ACTR8,CERS5,HK2,ALDH18A1,TLR2,PFN2,RASA1,MBNL1,LTN1,BRAP,DCP1A,DHX36,THBS1,NAA25,PPP2R2A,SHOX2,KCTD9,GFM1,LIN54,PGAM4,ZDHHC16,PDP1,ACVR1,WDR75,IRX5,MTERF3,INO80,NUDT9,	darkolivegreen	VSMC_M9
GO:0048193	0.00	1.00	29	259	Golgi vesicle transport	BP	0.51419	LMAN1,MON2,SEC24A,KDELR3,GCC2,EXOC1,COG5,RINT1,YIPF5,ARL1,TMED2,COPB2,COPB1,USO1,LRRK2,CUL3,TRAPPC10,VAPB,ANK3,CREB3L2,SEC23A,BLZF1,TRAPPC8,RAB31,VAPA,SPIRE1,RAB6A,ARF4,SCAMP1	darkolivegreen	VSMC_M9
GO:0000082	0.00	1.00	20	160	G1/S transition of mitotic cell cycle	BP	0.52971	INHBA,ITGB1,RB1,CDK3,RPL26,MYO16,CUL4A,APPL1,ACVR1,INO80,BRD7,CUL3,EIF4E,NPAT,RBBP8,GSPT1,RFWD3,E2F3,ZPR1,ZNF655	darkolivegreen	VSMC_M9

GO:0010975	0.00	1.00	40	376	regulation of neuron projection development	BP	0.55299	CDKL3,PTPRD,CCDC88A,ACTR2,FYN,CAMK1D,GATA3,TRAK1,STK24,ILK,RNF6,LYN,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,CAMSAP2,NTRK3,SEMA5B,TRAK2,IQGAP1,CREB3L2,SKIL,PRRX1,TNIK,ADAM10,SRCIN1,TBX6,SEMA7A,BAG5,PAFAH1B1,RAPGEF1,PLPPR5,BMPR2,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0035967	0.00	1.00	14	103	cellular response to topologically incorrect protein	BP	0.56869	UGGT1,EIF2AK3,TMED2,CUL3,DNAJB14,PTPN1,VAPB,ABCB10,ATF3,MBTPS2,CREB3L2,BFAR,DNAJB9,HSPA13	darkolivegreen	VSMC_M9
GO:0008104	0.00	1.00	156	2028	protein localization	BP	0.56869	LMAN1,AHI1,MON2,STXBP5,TBC1D15,CEP120,SEC24A,KDELR3,CEP41,DENND4C,TOPORS,AKAP9,GCC2,JAK2,CLOCK,EXOC1,MYO6,CCDC88A,COX18,UBE2J1,ROCK2,DDX1,RAB3B,ITGB1,MPP7,RPF2,COG5,FYN,RINT1,KIF5B,DNAJC1,CEP295,RB1,RTN2,PICALM,RAB3GAP1,TRAK1,NDFIP2,EDEM1,OSBPL8,STAM2,VPS36,UFM1,PIK3R4,CEP83,NDFIP1,YIPF5,BRCA2,DCHS1,ARL1,UBXN2B,RAB2A,XPO4,IPO7,NUP37,EIF2AK3,TMED2,COPB2,APPL1,GDAP1,HK2,TLR2,COPB1,USO1,DCP1A,TM9SF3,ARL6,CBLB,EHD4,LRRK2,SNX19,BRSK2,PHLDB2,TIMM17A,KPNA6,GPR89A,RAB3GAP2,CCDC186,CORO1C,TOMM20,PTPN1,LARP7,KPNA1,IDH2,TRAK2,C2CD2L,PIP5K1A,IQGAP1,CEP350,ANK3,CD3G,CCDC47,HEATR5A,TPR,PTGS2,SEC23A,SORCS2,SEPT5,FERMT2,KIFAP3,SMURF1,TAPT1,TNIK,KTN1,BLZF1,AP4E1,KIAA0586,PDIA2,FMN2,ATAD1,SRP9,ADAM10,MSN,SRCIN1,OAZ2,CLTC,ARMCX3,ATG4D,PIGW,PIN1,TRAPPC8,ROCK1,ITGA2,MYOM1,NUP155,RAB31,VAPA,C1QTNF3,SPIRE1,GPC4,MYO1C,PAFAH1B1,PMPCA,ZDHHC7,ANKRD13C,RANBP2,KPNA4,TOMM20L,RAB6A,ARF4,TOR1AIP2,LHFPL4,SEC63,LAMTOR3,NOV,MZT1,FCN1,E2F3,RAP2A,SRP19,ZPR1,C12orf66,NUP35,SCAMP1,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0030182	0.00	1.00	94	1067	neuron differentiation	BP	0.56869	AHI1,LRP12,EXT1,CDKL3,PTPRD,PLAA,TOPORS,JAK2,HDAC9,MYO6,UBA6,CCDC88A,ACTR2,INHBA,ITGB1,FYN,ZEB1,KIF5B,RB1,PICALM,CAMK1D,GATA3,CLN5,TRAK1,STK24,MYO16,SOS1,NTN4,ILK,SCYL2,RNF6,LYN,IFT88,SLC25A46,PALLD,MAP1B,DHX36,SHOX2,IRX5,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,EIF4E,TDP2,CAMSAP2,ANOS1,NTRK3,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,MYEF2,FZD2,SKIL,PRRX1,SMURF1,TNIK,DKK1,WNT5B,NOTCH3,ENAH,ADAM10,SRCIN1,TBX6,CYFIP2,DICER1,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,SLC1A3,VAPA,AFG3L2,PAFAH1B1,RAPGEF1,PLPPR5,CDH11,BMPR2,FRY,ARF4,GDNF,EFHD1,RAP2A,WNT9A,ZPR1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0071704	0.00	1.00	521	8083	organic substance metabolic process	BP	0.57554	SOCS6,MALT1,ELAC1,CDO1,AHI1,PPM1H,TBK1,CAND1,RRM2B,AZIN1,EXT1,DSE,WDR46,WDYHV1,CDKL3,DDX46,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,SLC35B4,RMI1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,SLC30A9,TOPORS,ABCB4,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,POLR2B,GNE,MGAT4A,ZNF451,TRMO,HDAC9,CAVIN4,FAM135A,SENP6,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,ITGB1,RPF2,FYN,ZEB1,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,PDSS1,NOX4,RB1,RTN2,SUCLA2,PICALM,ZC3H13,CYP27C1,TRDMT1,TOE1,CBLC,ABHD1,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,TRAK1,LRRC32,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,PRPF40A,ADAM32,FAM98A,TMTC2,VPS36,RPL26,KDELC1,GPCPD1,UFM1,CAPN7,LIG4,ABHD13,PIK3R4,CEBPZ,SUPT20H,ATP2B1,ALG5,SMAD9,CCNA1,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,AC091959.3,ILK,ITGA5,B3GLCT,HSPH1,TMF1,GALNT7,HOXC10,ERI1,HSD17B12,DHX29,SCYL2,PARG,USP12,MTREX,PLPP1,CDK8,CNOT7,RNF6,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,IPO7,PDE7A,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,MAT2A,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,FFAR4,APPL1,U2SURP,RDH10,PLOD2,LARP4,GDAP1,PI15,AGTR1,ACTR8,CERS5,HK2,ALDH18A1,TLR2,PFN2,RASA1,MBNL1,LTN1,BRA	darkolivegreen	VSMC_M9
GO:0072594	0.00	1.00	35	355	establishment of protein localization to organelle	BP	0.57554	LMAN1,GCC2,JAK2,COX18,RAB3GAP1,EDEM1,VPS36,UFM1,PIK3R4,BRCA2,IPO7,APPL1,GDAP1,HK2,CBLB,LRRK2,TIMM17A,KPNA6,RAB3GAP2,TOMM20,KPNA1,TPR,PTGS2,SMURF1,SRP9,NUP155,PMPCA,RANBP2,KPNA4,TOMM20L,SEC63,E2F3,SRP19,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0007030	0.00	1.00	17	122	Golgi organization	BP	0.57554	LMAN1,AKAP9,GCC2,YIPF5,ARL1,UBXN2B,RAB2A,TMED2,USO1,SPTBN5,LRRK2,CAMSAP2,VAMP4,ATP8B4,BLZF1,TRAPPC8,BAG5	darkolivegreen	VSMC_M9
GO:1902992	0.00	1.00	6	24	negative regulation of amyloid precursor protein catabolic process	BP	0.57554	RTN2,PICALM,RTN3,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0009225	0.00	1.00	7	33	nucleotide-sugar metabolic process	BP	0.57554	GNE,UGP2,GFPT1,UGGT1,PARG,GNPNAT1,DPM1	darkolivegreen	VSMC_M9
GO:0006939	0.00	1.00	13	84	smooth muscle contraction	BP	0.57554	CHRM2,ROCK2,ATP2B1,SULF1,SMTN,PTGS2,ACTA2,MYOCD,ROCK1,ITGA2,TBXA2R,GDNF,BDKRB2	darkolivegreen	VSMC_M9
GO:0043666	0.00	1.00	9	47	regulation of phosphoprotein phosphatase activity	BP	0.57554	JAK2,ROCK2,MGAT5,PPP1R12A,SLC39A10,BOD1L1,ROCK1,ITGA1,PPP1R2	darkolivegreen	VSMC_M9
GO:0070417	0.00	1.00	4	10	cellular response to cold	BP	0.57554	DNAJC3,EIF2AK3,PLIN1,CIDEA	darkolivegreen	VSMC_M9
GO:0006417	0.00	1.00	34	341	regulation of translation	BP	0.57554	ETF1,EIF5B,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,DNAJC3,RPL26,DHX29,CNOT7,EIF2AK3,TMED2,XRN1,PDE12,LARP4,LTN1,DCP1A,DHX36,THBS1,EIF4E,EPRS,EIF2B5,FASTKD2,TPR,PLD1,CPEB2,SRP9,TRIP4,PKM,ROCK1,ITGA2,GSPT1	darkolivegreen	VSMC_M9

GO:0016358	0.00	1.00	25	204	dendrite development	BP	0.57554	CDKL3,PTPRD,UBA6,ACTR2,ITGB1,FYN,PICALM,CAMK1D,TRAK1,ILK,MAP1B,DHX36,LRRK2,PDLIM5,UBE3A,CAMSAP2,TRAK2,IQGAP1,TNIK,ADAM10,SRCIN1,PAFAH1B1,ARF4,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0007029	0.00	1.00	12	80	endoplasmic reticulum organization	BP	0.57554	LMAN1,CAV2,RAB3GAP1,ESYT2,EIF2AK3,TMED2,LRRK2,RAB3GAP2,VAPB,CCDC47,RTN3,TOR1AIP2	darkolivegreen	VSMC_M9
GO:0120035	0.00	1.00	51	524	regulation of plasma membrane bounded cell projection organization	BP	0.57837	CEP120,CDKL3,PTPRD,STAP1,CCDC88A,ACTR2,FYN,CAMK1D,ACTR3,GATA3,TRAK1,STK24,FAM98A,ILK,RNF6,LYN,IFT88,MAP1B,PFN2,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,CAMSAP2,CORO1C,NTRK3,SEMA5B,TRAK2,IQGAP1,CREB3L2,CDKL1,SKIL,PRRX1,TAPT1,TNIK,PLD1,ADAM10,SRCIN1,TBX6,SEMA7A,CCP110,BAG5,PAFAH1B1,RAPGEF1,PLPPR5,BMPR2,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0030030	0.00	1.00	104	1226	cell projection organization	BP	0.57837	AHI1,CEP120,LRP12,EXT1,CDKL3,CEP41,PTPRD,PLAA,JAK2,STAP1,UBA6,CCDC88A,ACTR2,ITGB1,FYN,KIF5B,RB1,PICALM,CAMK1D,ACTR3,GATA3,TRAK1,STK24,FAM98A,MYO16,CEP83,SOS1,ILK,RNF6,LYN,IFT88,SLC25A46,PALLD,NEK1,MAP1B,PFN2,DHX36,SHOX2,ARL6,EHD4,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,CUL3,TROVE2,IGF1R,CAMSAP2,CORO1C,ANOS1,NTRK3,SEMA5B,TRAK2,PIP5K1A,IQGAP1,CEP350,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,CDKL1,SKIL,PRRX1,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,KIAA0586,NOTCH3,ENAH,ADAM10,SRCIN1,TPM1,TBX6,CYFIP2,DICER1,SEMA7A,CCP110,BAG5,ROCK1,ITGA2,ITGA1,VAPA,AFG3L2,PAFAH1B1,VAV2,RAPGEF1,PLPPR5,SSX2IP,CDH11,BMPR2,FXYD5,FRY,ARF4,GDNF,FOPNL,EFHD1,PDCL,RAP2A,ZPR1,WNT7A	darkolivegreen	VSMC_M9
GO:0051246	0.00	1.00	147	1953	regulation of protein metabolic process	BP	0.57837	MALT1,TBK1,AZIN1,ETF1,UBQLN1,PLAA,TOPORS,AKAP9,TFPI2,JAK2,EIF5B,ZNF451,PSME4,STAP1,CCDC88A,ZMPSTE24,SH3BP5L,ROCK2,INHBA,DDX1,NOCT,FYN,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,GSAP,NOX4,RB1,RTN2,PICALM,CBLC,NUB1,MGAT5,GATA3,CCNT2,RAB3GAP1,NDFIP2,DNAJC3,SETD5,RIF1,OSBPL8,PPP1R12A,RPL26,CCNA1,NDFIP1,CUL4A,ILK,ITGA5,TMF1,DHX29,PARG,CNOT7,LYN,IPO7,EIF2AK3,TMED2,ITCH,USP47,XRN1,PDE12,LARP4,PI15,AGTR1,PFN2,LTN1,DCP1A,DHX36,THBS1,ACVR1,NEDD9,CBLB,DYRK1A,BRD7,EHD4,LRRK2,TANK,UBE3A,SLC39A10,CUL3,EIF4E,UCHL5,TIMM17A,EPRS,RAB3GAP2,CORO1C,ANOS1,NTRK3,PTPN1,ABCB10,EIF2B5,IQGAP1,TLK2,PITHD1,FASTKD2,TPR,PTGS2,ITGAV,FERMT2,RTN3,SMURF1,TNIK,PLD1,CPEB2,BOD1L1,DKK1,FMN2,FAS,SRP9,TLR6,MSN,SRCIN1,SPOP,TRIP4,OAZ2,CLPX,CYFIP2,SMG8,UACA,PKM,MAP2K4,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,ITGA2,ITGA1,RICTOR,GSPT1,USP7,GADD45B,ENO1,WFDC1,PRKACB,MIR186,BMPR2,FRY,CTGF,BDKRB2,PMEPA1,RAP2A,VGLL4,TMEM119,WNT7A,PPP1R2	darkolivegreen	VSMC_M9
GO:0051336	0.00	1.00	66	754	regulation of hydrolase activity	BP	0.57837	MALT1,TBC1D15,PLAA,TFPI2,JAK2,HDAC9,PSME4,CAV2,ROCK2,ITGB1,FYN,PICALM,MGAT5,RAB3GAP1,PPP1R12A,ARL1,LYN,EIF2AK3,TDG,TMED2,USP47,CCDC125,PI15,AGTR1,PFN2,RASA1,THBS1,SLC39A14,NEDD9,CBLB,LRRK2,TANK,BRSK2,SLC39A10,UCHL5,RAB3GAP2,CORO1C,ANOS1,NTRK3,PIP5K1A,IQGAP1,PTGS2,ZC3H15,FERMT2,CPEB2,BOD1L1,RGS7,FAS,TPM1,CLPX,GPR65,CYFIP2,UACA,PIN1,ROCK1,ITGA2,ITGA1,RICTOR,PAFAH1B1,VAV2,RAPGEF1,WFDC1,ARF4,TOR1AIP2,CTGF,PPP1R2	darkolivegreen	VSMC_M9
GO:0010608	0.00	1.00	44	480	posttranscriptional regulation of gene expression	BP	0.57837	ETF1,EIF5B,ZMPSTE24,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,TRDMT1,DNAJC3,RPL26,DHX29,CNOT7,EIF2AK3,TMED2,XRN1,PDE12,LARP4,LTN1,DCP1A,DHX36,THBS1,EIF4E,EPRS,EIF2B5,FASTKD2,TPR,MYEF2,PLD1,CPEB2,SRP9,TRIP4,ZC3H14,PKM,DICER1,MYOCD,ROCK1,ITGA2,GSPT1,ZC3H7A,MIR186,FASTKD5,GDNF	darkolivegreen	VSMC_M9
GO:0031344	0.00	1.00	52	538	regulation of cell projection organization	BP	0.57837	CEP120,CDKL3,PTPRD,STAP1,CCDC88A,ACTR2,FYN,CAMK1D,ACTR3,GATA3,TRAK1,STK24,FAM98A,ILK,RNF6,LYN,IFT88,MAP1B,PFN2,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,CAMSAP2,CORO1C,NTRK3,SEMA5B,TRAK2,IQGAP1,CREB3L2,CDKL1,SKIL,PRRX1,TAPT1,TNIK,PLD1,ADAM10,SRCIN1,TBX6,SEMA7A,CCP110,BAG5,ITGA2,PAFAH1B1,RAPGEF1,PLPPR5,BMPR2,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0070727	0.00	1.00	116	1462	cellular macromolecule localization	BP	0.57837	LMAN1,AHI1,TBC1D15,SEC24A,KDELR3,DENND4C,TOPORS,AKAP9,GCC2,JAK2,MYO6,CCDC88A,COX18,UBE2J1,ROCK2,DDX1,RAB3B,ITGB1,RPF2,FYN,KIF5B,RB1,RTN2,PICALM,RAB3GAP1,TRAK1,EDEM1,OSBPL8,VPS36,UFM1,PIK3R4,CEP83,BRCA2,DCHS1,ARL1,UBXN2B,XPO4,IPO7,EIF2AK3,TMED2,COPB2,APPL1,GDAP1,HK2,COPB1,USO1,DCP1A,DHX36,TM9SF3,ARL6,CBLB,EHD4,LRRK2,BRSK2,TIMM17A,KPNA6,RAB3GAP2,TOMM20,PTPN1,LARP7,KPNA1,TRAK2,PIP5K1A,IQGAP1,CEP350,ANK3,CCDC47,TPR,PTGS2,SEC23A,SORCS2,SEPT5,FERMT2,SMURF1,TAPT1,TNIK,BLZF1,AP4E1,PDIA2,ATAD1,SRP9,ADAM10,MSN,OAZ2,CLTC,ARMCX3,PIGW,PIN1,TRAPPC8,ROCK1,NUP155,RAB31,VAPA,GPC4,MYO1C,PMPCA,ZDHHC7,ANKRD13C,RANBP2,KPNA4,TOMM20L,RAB6A,ARF4,TOR1AIP2,LHFPL4,SEC63,LAMTOR3,MZT1,FCN1,E2F3,RAP2A,SRP19,ZPR1,C12orf66,NUP35,SHISA7	darkolivegreen	VSMC_M9

GO:0044260	0.00	1.00	399	5916	cellular macromolecule metabolic process	BP	0.57837	SOCS6,MALT1,AHI1,PPM1H,TBK1,CAND1,RRM2B,EXT1,DSE,WDYHV1,CDKL3,PHF20L1,CDC23,ETF1,RMI1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,NPAS2,NOA1,FBXO9,EIF5B,POLR2B,MGAT4A,ZNF451,TRMO,HDAC9,CAVIN4,SENP6,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,SH3BP5L,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,ITGB1,FYN,ZEB1,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,NOX4,RB1,PICALM,ZC3H13,TRDMT1,CBLC,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,TRAK1,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,FAM98A,TMTC2,VPS36,RPL26,KDELC1,UFM1,LIG4,ABHD13,PIK3R4,CEBPZ,SUPT20H,ALG5,SMAD9,CCNA1,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,ILK,ITGA5,B3GLCT,TMF1,GALNT7,HOXC10,DHX29,SCYL2,PARG,USP12,MTREX,CDK8,CNOT7,RNF6,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,IPO7,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,PLOD2,LARP4,PI15,AGTR1,ACTR8,TLR2,PFN2,LTN1,BRAP,DCP1A,DHX36,THBS1,NAA25,PPP2R2A,SHOX2,KCTD9,GFM1,LIN54,ZDHHC16,PDP1,ACVR1,WDR75,IRX5,MTERF3,INO80,GCNT4,NEDD9,CBLB,DYRK1A,BRD7,EHD4,MAN1A2,ERG,LRRK2,TANK,TBX15,BRSK2,UBE3A,SLC39A10,NFRKB,CUL3,EIF4E,TDP2,DNER,TROVE2,UCHL5,CHSY1,DNAJB14,TIMM17A,KPNA6,EPRS,IGF1R,IARS2,RAB3GAP2,STK38L,GALNT17,CORO1C,AN	darkolivegreen	VSMC_M9
GO:0006464	0.00	1.00	210	2859	cellular protein modification process	BP	0.57837	SOCS6,MALT1,PPM1H,TBK1,CAND1,EXT1,WDYHV1,CDKL3,PHF20L1,CDC23,ETF1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,TOPORS,AKAP9,TMEM165,JAK2,CLOCK,FBXO9,MGAT4A,ZNF451,HDAC9,SENP6,STAP1,UBA6,CCDC88A,ZMPSTE24,UBE2J1,SH3BP5L,GFPT1,ROCK2,INHBA,FYN,CEP295,UGGT1,NOX4,RB1,CBLC,CAMK1D,NUB1,ST3GAL3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,TRAK1,NDFIP2,NKTR,BRPF1,DNAJC3,SETD5,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,FAM98A,TMTC2,KDELC1,UFM1,ABHD13,PIK3R4,ALG5,CCNA1,ACPP,NDFIP1,CUL4A,BRCA2,UBA5,ILK,ITGA5,B3GLCT,GALNT7,SCYL2,PARG,USP12,CDK8,CNOT7,RNF6,LYN,PPP2R3A,MERTK,IPO7,EIF2AK3,FBXL17,TMED2,ITCH,NEK1,RIOK2,USP47,LNPEP,PLOD2,TLR2,PFN2,LTN1,BRAP,THBS1,NAA25,PPP2R2A,KCTD9,ZDHHC16,PDP1,ACVR1,GCNT4,NEDD9,CBLB,DYRK1A,BRD7,EHD4,MAN1A2,ERG,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,CUL3,UCHL5,IGF1R,RAB3GAP2,STK38L,GALNT17,CORO1C,NEK7,NTRK3,PTPN1,GRK3,ST8SIA1,CLK1,TAF5L,TRAK2,G2E3,IQGAP1,UBE4A,C10orf90,TLK2,KLHL18,CDC27,PTGS2,CDKL1,MAP4K5,USP54,FERMT2,SMURF1,TNIK,BOD1L1,DKK1,FAS,AKT3,CDC42BPA,TLR6,ADAM10,SRCIN1,PHKG2,SPOP,CLK2,DLST,RLIM,RBBP6,SMG8,C18orf25,PPM1D,PIGW,MAP2K4,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,C1GALT1C1,RICTOR,PPP4R1,BFAR,GSPT1,MYSM1,USP7,GADD45B,ZDHHC7,DPM2,RFWD3,GTF2B,PRKACB,RABGGTB,RANBP2,BMPR2,PTPN12,FRY,RAB6A,ARF4,CDK13,CTGF,BDKRB2,OTUD6B,DPM1,PDZRN3,PMEPA1,RAP2A,FBXL7,NAA20,TMEM119,UBE2V1,PPTC7,PPP1R2	darkolivegreen	VSMC_M9
GO:0036211	0.00	1.00	210	2859	protein modification process	BP	0.57837	SOCS6,MALT1,PPM1H,TBK1,CAND1,EXT1,WDYHV1,CDKL3,PHF20L1,CDC23,ETF1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,TOPORS,AKAP9,TMEM165,JAK2,CLOCK,FBXO9,MGAT4A,ZNF451,HDAC9,SENP6,STAP1,UBA6,CCDC88A,ZMPSTE24,UBE2J1,SH3BP5L,GFPT1,ROCK2,INHBA,FYN,CEP295,UGGT1,NOX4,RB1,CBLC,CAMK1D,NUB1,ST3GAL3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,TRAK1,NDFIP2,NKTR,BRPF1,DNAJC3,SETD5,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,FAM98A,TMTC2,KDELC1,UFM1,ABHD13,PIK3R4,ALG5,CCNA1,ACPP,NDFIP1,CUL4A,BRCA2,UBA5,ILK,ITGA5,B3GLCT,GALNT7,SCYL2,PARG,USP12,CDK8,CNOT7,RNF6,LYN,PPP2R3A,MERTK,IPO7,EIF2AK3,FBXL17,TMED2,ITCH,NEK1,RIOK2,USP47,LNPEP,PLOD2,TLR2,PFN2,LTN1,BRAP,THBS1,NAA25,PPP2R2A,KCTD9,ZDHHC16,PDP1,ACVR1,GCNT4,NEDD9,CBLB,DYRK1A,BRD7,EHD4,MAN1A2,ERG,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,CUL3,UCHL5,IGF1R,RAB3GAP2,STK38L,GALNT17,CORO1C,NEK7,NTRK3,PTPN1,GRK3,ST8SIA1,CLK1,TAF5L,TRAK2,G2E3,IQGAP1,UBE4A,C10orf90,TLK2,KLHL18,CDC27,PTGS2,CDKL1,MAP4K5,USP54,FERMT2,SMURF1,TNIK,BOD1L1,DKK1,FAS,AKT3,CDC42BPA,TLR6,ADAM10,SRCIN1,PHKG2,SPOP,CLK2,DLST,RLIM,RBBP6,SMG8,C18orf25,PPM1D,PIGW,MAP2K4,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,C1GALT1C1,RICTOR,PPP4R1,BFAR,GSPT1,MYSM1,USP7,GADD45B,ZDHHC7,DPM2,RFWD3,GTF2B,PRKACB,RABGGTB,RANBP2,BMPR2,PTPN12,FRY,RAB6A,ARF4,CDK13,CTGF,BDKRB2,OTUD6B,DPM1,PDZRN3,PMEPA1,RAP2A,FBXL7,NAA20,TMEM119,UBE2V1,PPTC7,PPP1R2	darkolivegreen	VSMC_M9

GO:0034613	0.00	1.00	115	1451	cellular protein localization	BP	0.57837	LMAN1,AHI1,TBC1D15,SEC24A,KDELR3,DENND4C,TOPORS,AKAP9,GCC2,JAK2,MYO6,CCDC88A,COX18,UBE2J1,ROCK2,DDX1,RAB3B,ITGB1,RPF2,FYN,KIF5B,RB1,RTN2,PICALM,RAB3GAP1,TRAK1,EDEM1,OSBPL8,VPS36,UFM1,PIK3R4,CEP83,BRCA2,DCHS1,ARL1,UBXN2B,XPO4,IPO7,EIF2AK3,TMED2,COPB2,APPL1,GDAP1,HK2,COPB1,USO1,DCP1A,TM9SF3,ARL6,CBLB,EHD4,LRRK2,BRSK2,TIMM17A,KPNA6,RAB3GAP2,TOMM20,PTPN1,LARP7,KPNA1,TRAK2,PIP5K1A,IQGAP1,CEP350,ANK3,CCDC47,TPR,PTGS2,SEC23A,SORCS2,SEPT5,FERMT2,SMURF1,TAPT1,TNIK,BLZF1,AP4E1,PDIA2,ATAD1,SRP9,ADAM10,MSN,OAZ2,CLTC,ARMCX3,PIGW,PIN1,TRAPPC8,ROCK1,NUP155,RAB31,VAPA,GPC4,MYO1C,PMPCA,ZDHHC7,ANKRD13C,RANBP2,KPNA4,TOMM20L,RAB6A,ARF4,TOR1AIP2,LHFPL4,SEC63,LAMTOR3,MZT1,FCN1,E2F3,RAP2A,SRP19,ZPR1,C12orf66,NUP35,SHISA7	darkolivegreen	VSMC_M9
GO:0043412	0.00	1.00	220	3029	macromolecule modification	BP	0.57948	SOCS6,MALT1,PPM1H,TBK1,CAND1,EXT1,WDYHV1,CDKL3,PHF20L1,CDC23,ETF1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,TOPORS,AKAP9,TMEM165,JAK2,CLOCK,FBXO9,MGAT4A,ZNF451,TRMO,HDAC9,SENP6,STAP1,UBA6,CCDC88A,ZMPSTE24,UBE2J1,SH3BP5L,GFPT1,ROCK2,INHBA,FYN,PIWIL4,CEP295,UGGT1,NOX4,RB1,ZC3H13,TRDMT1,CBLC,CAMK1D,NUB1,ST3GAL3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,TRAK1,NDFIP2,NKTR,BRPF1,DNAJC3,SETD5,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,FAM98A,TMTC2,KDELC1,UFM1,ABHD13,PIK3R4,ALG5,CCNA1,ACPP,NDFIP1,CUL4A,BRCA2,UBA5,ILK,ITGA5,B3GLCT,GALNT7,SCYL2,PARG,USP12,CDK8,CNOT7,RNF6,LYN,PPP2R3A,MERTK,IPO7,EIF2AK3,FBXL17,TDG,TMED2,ITCH,NEK1,RIOK2,USP47,LNPEP,PLOD2,TLR2,PFN2,LTN1,BRAP,THBS1,NAA25,PPP2R2A,KCTD9,ZDHHC16,PDP1,ACVR1,GCNT4,NEDD9,CBLB,DYRK1A,BRD7,EHD4,MAN1A2,ERG,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,CUL3,PUS3,UCHL5,IGF1R,RAB3GAP2,STK38L,GALNT17,CORO1C,NEK7,NTRK3,PTPN1,GRK3,LARP7,ST8SIA1,CLK1,TAF5L,TRAK2,G2E3,IQGAP1,UBE4A,C10orf90,TLK2,KLHL18,CDC27,PTGS2,CDKL1,MAP4K5,USP54,FERMT2,DTWD1,SMURF1,TNIK,BOD1L1,DKK1,FAS,AKT3,RBM47,CDC42BPA,TLR6,ADAM10,SRCIN1,PHKG2,SPOP,CLK2,DLST,RLIM,RBBP6,SMG8,C18orf25,PPM1D,PIGW,MAP2K4,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,C1GALT1C1,RICTOR,PPP4R1,BFAR,GSPT1,MYSM1,USP7,GADD45B,ZDHHC7,DPM2,RFWD3,GTF2B,PRKACB,RABGGTB,RANBP2,BMPR2,PTPN12,FRY,RAB6A,ARF4,CDK13,CTGF,BDKRB2,OTUD6B,DPM1,PDZRN3,PMEPA1,RAP2A,FBXL7,NAA20,TMEM119,UBE2V1,PPTC7,PPP1R2,TF	darkolivegreen	VSMC_M9
GO:0009100	0.00	1.00	31	299	glycoprotein metabolic process	BP	0.58166	EXT1,DSE,TMEM165,MGAT4A,UBE2J1,GFPT1,UGGT1,ST3GAL3,MGAT5,TRAK1,EDEM1,TMTC2,KDELC1,ALG5,B3GLCT,GALNT7,CSGALNACT2,SULF1,GCNT4,MAN1A2,CHSY1,GALNT17,ST8SIA1,TRAK2,FAM20B,C1GALT1C1,COL11A1,DPM2,BMPR2,DPM1,CHST11	darkolivegreen	VSMC_M9
GO:0043628	0.00	1.00	7	36	ncRNA 3'-end processing	BP	0.62303	ELAC1,EXOSC9,TOE1,ERI1,LARP7,INTS14,INTS6	darkolivegreen	VSMC_M9
GO:0120036	0.00	1.00	101	1193	plasma membrane bounded cell projection organization	BP	0.66594	AHI1,CEP120,LRP12,EXT1,CDKL3,CEP41,PTPRD,PLAA,JAK2,STAP1,UBA6,CCDC88A,ACTR2,ITGB1,FYN,KIF5B,RB1,PICALM,CAMK1D,ACTR3,GATA3,TRAK1,STK24,FAM98A,MYO16,CEP83,SOS1,ILK,RNF6,LYN,IFT88,SLC25A46,PALLD,NEK1,MAP1B,PFN2,DHX36,SHOX2,ARL6,EHD4,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,TROVE2,IGF1R,CAMSAP2,CORO1C,ANOS1,NTRK3,SEMA5B,TRAK2,PIP5K1A,IQGAP1,CEP350,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,CDKL1,SKIL,PRRX1,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,KIAA0586,NOTCH3,ENAH,ADAM10,SRCIN1,TPM1,TBX6,CYFIP2,DICER1,SEMA7A,CCP110,BAG5,ROCK1,ITGA1,VAPA,AFG3L2,PAFAH1B1,VAV2,RAPGEF1,PLPPR5,SSX2IP,CDH11,BMPR2,FXYD5,FRY,ARF4,GDNF,FOPNL,EFHD1,RAP2A,ZPR1,WNT7A	darkolivegreen	VSMC_M9
GO:0006518	0.00	1.00	56	688	peptide metabolic process	BP	0.66844	ETF1,NOA1,EIF5B,RARS2,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,GSAP,RTN2,PICALM,CLN5,DARS,DNAJC3,RPL26,DHX29,CNOT7,EIF2AK3,TMED2,EIF2S2,LNPEP,XRN1,PDE12,LARP4,GDAP1,LTN1,DCP1A,DHX36,THBS1,GFM1,DYRK1A,EIF4E,EPRS,IARS2,MRPL47,EIF2B5,FASTKD2,EIF3J,TPR,ZC3H15,RTN3,PLD1,CPEB2,SRP9,ADAM10,TRIP4,PKM,PIN1,ROCK1,ITGA2,GSPT1,TARS,MIR186,EIF1AX	darkolivegreen	VSMC_M9

GO:0008150	0.00	1.00	752	12183	biological_process	BP	0.73049	SOCS6,LMAN1,MALT1,ELAC1,CDO1,AHI1,LRIG3,PHACTR2,UTRN,MON2,PPM1H,STXBP5,TBK1,CAND1,PLEKHG1,TBC1D15,CEP120,RRM2B,AZIN1,ATP6V1C1,LRP12,EXT1,THBS2,DSE,SLC39A7,WDR46,WDYHV1,CDKL3,SEC24A,DDX46,CHADL,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,SLC35B4,RMI1,KDELR3,PPIL1,UBQLN1,CEP41,PTPRD,HAUS6,DENND4C,CALU,PRUNE2,PLAA,BTBD11,SLC30A9,TOPORS,ABCB4,AKAP9,DNAJB5,GCC2,TFPI2,GNG11,TMEM165,JAK2,CLOCK,EXOC1,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,TXNDC9,POLR2B,GNE,ASPN,MGAT4A,BZW2,ZNF451,TRMO,HEMGN,HDAC9,CAVIN4,FAM135A,COL12A1,SENP6,PSME4,MYO6,CENPC,STAP1,UBA6,CCDC88A,HOXA9,COX18,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,PDE1C,UGP2,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,IFRD1,CHRM2,TAF1B,TES,CAV2,ROCK2,INHBA,GREB1,PNPLA8,DDX1,NOCT,GPX7,PCDH18,RAB3B,ITGB1,MPP7,RPF2,COG5,FYN,SYPL1,ZEB1,RINT1,NT5DC1,KIF5B,CEP57,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,SLC36A4,UGGT1,CCDC8,GSAP,PDSS1,NOX4,FNDC3A,GPR4,RB1,RTN2,SUCLA2,PICALM,ZC3H13,CYP27C1,TRDMT1,TOE1,SUSD5,CBLC,CGREF1,ABHD1,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,ESYT2,TRAK1,LRRC32,NDFIP2,NKTR,BRPF1,SELENOV,SUPT5H,DNAJC3,SETD5,AZI2,CYTH1,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,TNFAIP6,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,ADAM32,FAM98A,TMTC2,VPS36,THSD1,RPL26,KDELC1,GPCPD1,UFM1,CAPN7,LIG4,ABHD13,PIK3R4,MYO16,CEBPZ,SUPT20H,ATP2B1,ALG5,TUBGCP3,SMAD9,EEA1,CCNA1,ATP11A,CEP83,ACPP,NR2C1,NDFIP1,CUL	darkolivegreen	VSMC_M9
GO:0051345	0.00	1.00	42	440	positive regulation of hydrolase activity	BP	0.73049	MALT1,TBC1D15,PLAA,JAK2,PSME4,CAV2,ROCK2,ITGB1,FYN,PICALM,RAB3GAP1,PPP1R12A,ARL1,LYN,EIF2AK3,CCDC125,AGTR1,PFN2,RASA1,NEDD9,LRRK2,TANK,SLC39A10,CORO1C,NTRK3,PIP5K1A,ZC3H15,FERMT2,RGS7,FAS,TPM1,CLPX,GPR65,CYFIP2,UACA,PIN1,ITGA2,ITGA1,RAPGEF1,ARF4,TOR1AIP2,CTGF	darkolivegreen	VSMC_M9
GO:0099173	0.00	1.00	18	137	postsynapse organization	BP	0.73049	PTPRD,ACTR2,FYN,DHX36,LRRK2,PDLIM5,UBE3A,IGF1R,NTRK3,NRP2,ADAM10,SRCIN1,PAFAH1B1,ARF4,GDNF,LHFPL4,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0045842	0.00	1.00	4	12	positive regulation of mitotic metaphase/anaphase transition	BP	0.77742	CDC23,RB1,CUL3,CDC27	darkolivegreen	VSMC_M9
GO:1901970	0.00	1.00	4	12	positive regulation of mitotic sister chromatid separation	BP	0.77742	CDC23,RB1,CUL3,CDC27	darkolivegreen	VSMC_M9
GO:0072498	0.01	1.00	4	13	embryonic skeletal joint development	BP	0.78571	EXT1,HOXA11,SHOX2,WNT9A	darkolivegreen	VSMC_M9
GO:0051234	0.01	1.00	243	3429	establishment of localization	BP	0.78691	LMAN1,MALT1,CDO1,AHI1,UTRN,MON2,STXBP5,TBC1D15,CEP120,AZIN1,ATP6V1C1,LRP12,EXT1,SLC39A7,SEC24A,CDC23,SLC35B4,KDELR3,UBQLN1,CEP41,DENND4C,PLAA,SLC30A9,ABCB4,AKAP9,GCC2,TMEM165,JAK2,CLOCK,EXOC1,MYO6,CENPC,STAP1,CCDC88A,COX18,ZMPSTE24,UBE2J1,ACTR2,CAV2,INHBA,PNPLA8,RAB3B,ITGB1,COG5,FYN,RINT1,KIF5B,DNAJC1,CEP295,SLC36A4,RTN2,PICALM,CAMK1D,UPF2,ACTR3,GATA3,RAB3GAP1,CLN5,JMJD6,ESYT2,TRAK1,NDFIP2,CYTH1,EDEM1,OSBPL8,PPP1R12A,STAM2,VPS36,UFM1,PIK3R4,ATP2B1,EEA1,ATP11A,CEP83,NDFIP1,YIPF5,BRCA2,TMF1,SCYL2,REM1,ARL1,LYN,UBXN2B,MERTK,RAB2A,GRAMD1A,SLC16A12,XPO4,ATP6V0A2,IFT88,IPO7,NUP37,TMED2,COPB2,SLC30A5,RIOK2,FFAR4,MAP1B,APPL1,GDAP1,AGTR1,HK2,TLR2,COPB1,ATP2A2,USO1,THBS1,ARL6,SLC39A14,SLC35B3,CBLB,ATP1A1,SPTBN5,EHD4,LRRK2,SNX19,BRSK2,ATP10A,UBE3A,SLC39A10,CUL3,MRS2,PHLDB2,DNER,TIMM17A,TRAPPC10,ATP6V1A,KPNA6,EPRS,IGF1R,GPR89A,RAB3GAP2,CCDC186,CORO1C,ITPR2,TOMM20,PTPN1,GRK3,ATP11B,KPNA1,IDH2,VAPB,ABCB10,TRAK2,PRELID3B,C2CD2L,PIP5K1A,ANK3,OSBPL11,CD3G,CCDC47,HEATR5A,SH3KBP1,ATP13A3,CREB3L2,TPR,PTGS2,SEC23A,SORCS2,SEPT5,ITGAV,VAMP4,ATP8B4,RTN3,KIFAP3,SMURF1,KTN1,PLD1,BLZF1,ACTR10,AP4E1,TNFAIP8L3,KIAA0586,VDAC2,DKK1,FMN2,ATAD1,PLP2,CLCNKB,SRP9,STIM2,MAGED2,ADAM10,MSN,SRCIN1,MYO1E,KCNMB1,TRIP4,OAZ2,CLINT1,CLTC,ARMCX3,GPRASP1,ATG4D,ANXA6,TRAPPC8,ROCK1,THOC1,ITGA2,MYOM1,NUP155,SLC1A3,RAB31,VAPA,AFG3L2,C1QTNF3,SPIRE1,USP7,MYO1C,PAFAH1B1,PMPCA,KIF1B,VAV2,CL	darkolivegreen	VSMC_M9
GO:0006493	0.01	1.00	11	74	protein O-linked glycosylation	BP	0.78691	ST3GAL3,TRAK1,TMTC2,KDELC1,B3GLCT,GALNT7,GCNT4,TRAK2,C1GALT1C1,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0010256	0.01	1.00	40	422	endomembrane system organization	BP	0.82776	LMAN1,AKAP9,GCC2,ZMPSTE24,CAV2,RAB3GAP1,ESYT2,STAM2,VPS36,EEA1,YIPF5,TMF1,ARL1,UBXN2B,RAB2A,EIF2AK3,TMED2,ATP2A2,USO1,SPTBN5,LRRK2,SNX19,ATP10A,CAMSAP2,RAB3GAP2,CORO1C,VAPB,ANK3,CCDC47,VAMP4,ATP8B4,RTN3,BLZF1,ANXA6,TRAPPC8,BAG5,NUP155,PAFAH1B1,XKR9,TOR1AIP2	darkolivegreen	VSMC_M9
GO:0002042	0.01	1.00	9	55	cell migration involved in sprouting angiogenesis	BP	0.83077	HDAC9,ITGB1,STARD13,THBS1,CLEC14A,PTGS2,AKT3,SRPX2,TBXA2R	darkolivegreen	VSMC_M9
GO:0045184	0.01	1.00	108	1395	establishment of protein localization	BP	0.83796	LMAN1,MON2,STXBP5,TBC1D15,CEP120,SEC24A,KDELR3,CEP41,DENND4C,GCC2,JAK2,CLOCK,EXOC1,MYO6,COX18,UBE2J1,RAB3B,COG5,FYN,RINT1,KIF5B,DNAJC1,CEP295,RTN2,RAB3GAP1,TRAK1,NDFIP2,EDEM1,STAM2,VPS36,UFM1,PIK3R4,NDFIP1,YIPF5,BRCA2,ARL1,RAB2A,XPO4,IPO7,NUP37,TMED2,COPB2,APPL1,GDAP1,HK2,TLR2,COPB1,USO1,ARL6,CBLB,LRRK2,SNX19,BRSK2,PHLDB2,TIMM17A,KPNA6,GPR89A,RAB3GAP2,CCDC186,CORO1C,TOMM20,PTPN1,KPNA1,IDH2,TRAK2,C2CD2L,ANK3,CD3G,CCDC47,TPR,PTGS2,SEC23A,SORCS2,SMURF1,KTN1,BLZF1,AP4E1,KIAA0586,FMN2,ATAD1,SRP9,SRCIN1,OAZ2,CLTC,ATG4D,ITGA2,MYOM1,NUP155,RAB31,C1QTNF3,SPIRE1,MYO1C,PAFAH1B1,PMPCA,ZDHHC7,RANBP2,KPNA4,TOMM20L,RAB6A,ARF4,SEC63,NOV,E2F3,RAP2A,SRP19,ZPR1,NUP35,SCAMP1	darkolivegreen	VSMC_M9

GO:0051603	0.01	1.00	55	639	proteolysis involved in cellular protein catabolic process	BP	0.85668	SOCS6,MALT1,CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,PSMB1,PSMC2,UGGT1,CBLC,NUB1,NDFIP2,DNAJC3,EDEM1,VPS36,NDFIP1,CUL4A,TMF1,USP12,RNF6,UBXN2B,FBXL17,ITCH,USP47,LTN1,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,PITHD1,CDC27,SMURF1,SPOP,TRIP4,CLPX,RLIM,RBBP6,C18orf25,BAG5,BFAR,USP7,DNAJB9,FBXL7	darkolivegreen	VSMC_M9
GO:0015914	0.01	1.00	11	70	phospholipid transport	BP	0.85668	ABCB4,OSBPL8,ATP11A,ATP10A,ATP11B,PRELID3B,C2CD2L,ATP8B4,TNFAIP8L3,XKR9,PLEKHA3	darkolivegreen	VSMC_M9
GO:0035437	0.01	1.00	4	13	maintenance of protein localization in endoplasmic reticulum	BP	0.85668	KDELR3,TAPT1,PDIA2,ANKRD13C	darkolivegreen	VSMC_M9
GO:0051084	0.01	1.00	6	30	'de novo' posttranslational protein folding	BP	0.85668	DNAJB5,UGGT1,HSPH1,DNAJB14,DNAJB4,HSPA13	darkolivegreen	VSMC_M9
GO:0044237	0.01	0.99	506	7918	cellular metabolic process	BP	0.85668	SOCS6,MALT1,ELAC1,CDO1,AHI1,PPM1H,TBK1,CAND1,RRM2B,AZIN1,ATP6V1C1,EXT1,DSE,WDR46,WDYHV1,CDKL3,DDX46,PHF20L1,KHDRBS3,CDC23,ETF1,SLC35B4,RMI1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,EXOC1,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,POLR2B,GNE,MGAT4A,ZNF451,TRMO,HDAC9,CAVIN4,FAM135A,SENP6,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,SH3BP5L,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,ITGB1,RPF2,FYN,ZEB1,NT5DC1,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,PDSS1,NOX4,RB1,RTN2,SUCLA2,PICALM,ZC3H13,CYP27C1,TRDMT1,TOE1,CBLC,ABHD1,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,TRAK1,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,FAM98A,TMTC2,VPS36,RPL26,KDELC1,GPCPD1,UFM1,LIG4,ABHD13,PIK3R4,CEBPZ,SUPT20H,ALG5,SMAD9,CCNA1,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,AC091959.3,ILK,ITGA5,B3GLCT,TMF1,GALNT7,HOXC10,ERI1,HSD17B12,DHX29,SCYL2,PARG,USP12,MTREX,PLPP1,CDK8,CNOT7,RNF6,ARL1,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,GRAMD1A,ATP6V0A2,TMEM41B,IFT88,IPO7,PDE7A,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,MAT2A,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,APPL1,U2SURP,RDH10,PLOD2,LARP4,GDAP1,PI15,AGTR1,ACTR8,CERS5,HK2,ALDH18A1,TLR2,PFN2,RASA1,ATP2A2,	darkolivegreen	VSMC_M9
GO:0006606	0.01	1.00	16	129	protein import into nucleus	BP	0.85668	JAK2,UFM1,IPO7,APPL1,CBLB,LRRK2,KPNA6,KPNA1,TPR,PTGS2,NUP155,RANBP2,KPNA4,E2F3,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:1902101	0.01	1.00	4	13	positive regulation of metaphase/anaphase transition of cell cycle	BP	0.85668	CDC23,RB1,CUL3,CDC27	darkolivegreen	VSMC_M9
GO:0006412	0.01	1.00	45	548	translation	BP	0.85668	ETF1,NOA1,EIF5B,RARS2,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,DARS,DNAJC3,RPL26,DHX29,CNOT7,EIF2AK3,TMED2,EIF2S2,XRN1,PDE12,LARP4,LTN1,DCP1A,DHX36,THBS1,GFM1,EIF4E,EPRS,IARS2,MRPL47,EIF2B5,FASTKD2,EIF3J,TPR,ZC3H15,PLD1,CPEB2,SRP9,TRIP4,PKM,ROCK1,ITGA2,GSPT1,TARS,EIF1AX	darkolivegreen	VSMC_M9
GO:0009266	0.01	1.00	16	137	response to temperature stimulus	BP	0.85668	DNAJC3,ATP2B1,LYN,EIF2AK3,ATP2A2,DHX36,THBS1,ST8SIA1,PLIN1,EIF2B5,RBBP7,TPR,PTGS2,DNAJA4,CIDEA,DNAJB4	darkolivegreen	VSMC_M9
GO:0061001	0.01	1.00	8	42	regulation of dendritic spine morphogenesis	BP	0.85668	ACTR2,DHX36,LRRK2,PDLIM5,UBE3A,ADAM10,SRCIN1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0051641	0.01	0.99	170	2295	cellular localization	BP	0.85668	LMAN1,MALT1,AHI1,MON2,STXBP5,TBC1D15,CEP120,SEC24A,CDC23,KDELR3,DENND4C,PLAA,TOPORS,AKAP9,GCC2,JAK2,EXOC1,MYO6,CENPC,CCDC88A,COX18,ZMPSTE24,UBE2J1,ACTR2,CAV2,ROCK2,DDX1,RAB3B,ITGB1,RPF2,FYN,RINT1,KIF5B,RB1,RTN2,PICALM,UPF2,ACTR3,RAB3GAP1,CLN5,ESYT2,TRAK1,EDEM1,OSBPL8,PPP1R12A,FAM98A,VPS36,UFM1,PIK3R4,EEA1,CEP83,YIPF5,BRCA2,DCHS1,SCYL2,ARL1,LYN,UBXN2B,XPO4,IFT88,IPO7,EIF2AK3,TMED2,COPB2,RIOK2,MAP1B,APPL1,GDAP1,HK2,COPB1,ATP2A2,USO1,DCP1A,DHX36,TM9SF3,ARL6,SLC39A14,CBLB,ATP1A1,EHD4,LRRK2,BRSK2,CUL3,TIMM17A,TRAPPC10,KPNA6,RAB3GAP2,CCDC186,CORO1C,ITPR2,TOMM20,PTPN1,LARP7,KPNA1,VAPB,TRAK2,C2CD2L,PIP5K1A,IQGAP1,CEP350,ANK3,CCDC47,HEATR5A,CREB3L2,TPR,PTGS2,SEC23A,SORCS2,SEPT5,FERMT2,VAMP4,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,BLZF1,ACTR10,AP4E1,PDIA2,FMN2,ATAD1,SRP9,ADAM10,MSN,MYO1E,OAZ2,CLTC,ARMCX3,GPRASP1,PIGW,ANXA6,PIN1,TRAPPC8,ROCK1,THOC1,NUP155,RAB31,VAPA,SPIRE1,GPC4,USP7,MYO1C,PAFAH1B1,PMPCA,KIF1B,ZDHHC7,SSX2IP,ANKRD13C,RANBP2,MYO1H,KPNA4,TOMM20L,RAB6A,ARF4,GDNF,TOR1AIP2,LHFPL4,SEC63,LAMTOR3,MZT1,FCN1,E2F3,RAP2A,SRP19,ZPR1,C12orf66,NUP35,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0048812	0.01	1.00	49	503	neuron projection morphogenesis	BP	0.85668	EXT1,CDKL3,PTPRD,PLAA,ACTR2,ITGB1,FYN,KIF5B,PICALM,GATA3,TRAK1,MYO16,SOS1,ILK,RNF6,PALLD,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,ANOS1,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,NCAM1,SKIL,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,CYFIP2,DICER1,SEMA7A,ROCK1,ITGA1,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0035455	0.01	1.00	4	13	response to interferon-alpha	BP	0.86457	GATA3,PDE12,TROVE2,TPR	darkolivegreen	VSMC_M9

GO:0061024	0.01	1.00	52	599	membrane organization	BP	0.86457	SEC24A,PTPRD,ABCB4,STAP1,CCDC88A,COX18,ZMPSTE24,CAV2,KIF5B,PICALM,OSBPL8,EEA1,ATP11A,YIPF5,UBXN2B,GRAMD1A,SLC25A46,TMED2,HK2,ATP2A2,USO1,THBS1,ATP10A,CUL3,CORO1C,ATP11B,VAPB,PRELID3B,C2CD2L,ANK3,CCDC47,SEC23A,VAMP4,ATP8B4,SMURF1,TNFAIP8L3,VDAC2,ANXA6,ITGA2,NUP155,RAB31,VAPA,AFG3L2,SPIRE1,PAFAH1B1,DNAJC11,XKR9,PLEKHA3,GDNF,TOR1AIP2,LHFPL4,SHISA7	darkolivegreen	VSMC_M9
GO:0051130	0.01	1.00	74	870	positive regulation of cellular component organization	BP	0.86457	LMAN1,AHI1,CAND1,CEP120,THBS2,CDKL3,CDC23,PTPRD,ABCB4,AKAP9,STAP1,CCDC88A,ACTR2,ROCK2,MPP7,FYN,KIF5B,CEP295,NOX4,RB1,CAMK1D,ACTR3,RAB3GAP1,TRAK1,FAM98A,LIG4,ILK,SCYL2,LYN,MAP1B,APPL1,PFN2,DHX36,SHOX2,LRRK2,ATP10A,CUL3,PHLDB2,KIAA1551,IGF1R,RAB3GAP2,CORO1C,NEK7,NTRK3,IQGAP1,CREB3L2,TPR,CDC27,FERMT2,SKIL,TAPT1,ATAD1,TLR6,MSN,TPM1,GPR65,SRPX2,SEMA7A,CCP110,ROCK1,ITGA2,RICTOR,RAB31,SPIRE1,MYO1C,PAFAH1B1,RAPGEF1,PLPPR5,BMPR2,CTGF,COLGALT1,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0097061	0.01	1.00	11	70	dendritic spine organization	BP	0.86457	ACTR2,FYN,DHX36,LRRK2,PDLIM5,UBE3A,IGF1R,ADAM10,SRCIN1,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0044843	0.01	1.00	20	180	cell cycle G1/S phase transition	BP	0.86457	INHBA,ITGB1,RB1,CDK3,RPL26,MYO16,CUL4A,APPL1,ACVR1,INO80,BRD7,CUL3,EIF4E,NPAT,RBBP8,GSPT1,RFWD3,E2F3,ZPR1,ZNF655	darkolivegreen	VSMC_M9
GO:0032268	0.01	0.99	135	1819	regulation of cellular protein metabolic process	BP	0.86457	MALT1,TBK1,ETF1,UBQLN1,PLAA,TOPORS,AKAP9,TFPI2,JAK2,EIF5B,ZNF451,PSME4,STAP1,CCDC88A,ZMPSTE24,SH3BP5L,ROCK2,INHBA,DDX1,NOCT,FYN,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,NOX4,RB1,PICALM,CBLC,NUB1,MGAT5,GATA3,CCNT2,RAB3GAP1,NDFIP2,DNAJC3,SETD5,RIF1,OSBPL8,PPP1R12A,RPL26,CCNA1,NDFIP1,ILK,ITGA5,TMF1,DHX29,PARG,CNOT7,LYN,IPO7,EIF2AK3,TMED2,ITCH,USP47,XRN1,PDE12,LARP4,PI15,AGTR1,PFN2,LTN1,DCP1A,DHX36,THBS1,ACVR1,NEDD9,CBLB,DYRK1A,BRD7,EHD4,LRRK2,TANK,UBE3A,SLC39A10,CUL3,EIF4E,UCHL5,TIMM17A,EPRS,RAB3GAP2,CORO1C,ANOS1,NTRK3,PTPN1,EIF2B5,IQGAP1,TLK2,PITHD1,FASTKD2,TPR,PTGS2,FERMT2,SMURF1,TNIK,PLD1,CPEB2,BOD1L1,DKK1,FAS,SRP9,TLR6,MSN,SRCIN1,TRIP4,CLPX,CYFIP2,SMG8,UACA,PKM,MAP2K4,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,ITGA2,ITGA1,RICTOR,GSPT1,USP7,GADD45B,ENO1,WFDC1,BMPR2,FRY,CTGF,BDKRB2,PMEPA1,RAP2A,VGLL4,TMEM119,WNT7A,PPP1R2	darkolivegreen	VSMC_M9
GO:0090114	0.01	1.00	6	28	COPII-coated vesicle budding	BP	0.86457	SEC24A,TMED2,CUL3,VAPB,SEC23A,VAPA	darkolivegreen	VSMC_M9
GO:0120039	0.01	1.00	50	517	plasma membrane bounded cell projection morphogenesis	BP	0.86457	EXT1,CDKL3,PTPRD,PLAA,ACTR2,ITGB1,FYN,KIF5B,PICALM,GATA3,TRAK1,MYO16,SOS1,ILK,RNF6,PALLD,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,CORO1C,ANOS1,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,NCAM1,SKIL,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,CYFIP2,DICER1,SEMA7A,ROCK1,ITGA1,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0030163	0.01	0.99	67	815	protein catabolic process	BP	0.87852	SOCS6,MALT1,AZIN1,EXT1,CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,FYN,PSMB1,PSMC2,UGGT1,CBLC,NUB1,CLN5,NDFIP2,DNAJC3,EDEM1,VPS36,ABHD13,NDFIP1,CUL4A,TMF1,USP12,RNF6,UBXN2B,FBXL17,ITCH,USP47,LTN1,CBLB,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,PITHD1,CDC27,SMURF1,FMN2,MSN,SPOP,TRIP4,OAZ2,CLPX,RLIM,RBBP6,C18orf25,PIN1,BAG5,ROCK1,BFAR,USP7,DNAJB9,VGLL4,FBXL7	darkolivegreen	VSMC_M9
GO:0051170	0.01	1.00	16	132	import into nucleus	BP	0.87852	JAK2,UFM1,IPO7,APPL1,CBLB,LRRK2,KPNA6,KPNA1,TPR,PTGS2,NUP155,RANBP2,KPNA4,E2F3,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0050807	0.01	1.00	20	165	regulation of synapse organization	BP	0.87852	THBS2,PTPRD,ACTR2,FYN,SETD5,TLR2,DHX36,LRRK2,PDLIM5,UBE3A,NTRK3,NRP2,ADAM10,SRCIN1,SRPX2,GPC4,PAFAH1B1,ARF4,LHFPL4,WNT7A	darkolivegreen	VSMC_M9
GO:0016192	0.01	0.99	96	1192	vesicle-mediated transport	BP	0.87852	LMAN1,AHI1,MON2,STXBP5,LRP12,SEC24A,KDELR3,PLAA,GCC2,EXOC1,MYO6,STAP1,CAV2,RAB3B,ITGB1,COG5,FYN,RINT1,KIF5B,PICALM,CAMK1D,RAB3GAP1,CLN5,JMJD6,ESYT2,TRAK1,CYTH1,VPS36,PIK3R4,EEA1,CEP83,YIPF5,SCYL2,ARL1,LYN,MERTK,TMED2,COPB2,APPL1,TLR2,COPB1,ATP2A2,USO1,THBS1,ARL6,EHD4,LRRK2,SNX19,BRSK2,UBE3A,CUL3,DNER,TRAPPC10,IGF1R,CORO1C,PTPN1,GRK3,VAPB,TRAK2,PIP5K1A,ANK3,HEATR5A,SH3KBP1,CREB3L2,SEC23A,SEPT5,ITGAV,VAMP4,RTN3,PLD1,BLZF1,AP4E1,DKK1,FMN2,ATAD1,MSN,SRCIN1,MYO1E,CLINT1,CLTC,GPRASP1,TRAPPC8,ROCK1,ITGA2,RAB31,VAPA,SPIRE1,USP7,KIF1B,VAV2,XKR9,RAB6A,ARF4,FCN1,SCAMP1,WNT7A	darkolivegreen	VSMC_M9
GO:1902430	0.01	1.00	5	22	negative regulation of amyloid-beta formation	BP	0.87852	RTN2,RTN3,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:1901137	0.01	1.00	43	494	carbohydrate derivative biosynthetic process	BP	0.87852	RRM2B,EXT1,DSE,TMEM165,ELOVL5,GNE,MGAT4A,UBE2J1,GFPT1,UGGT1,ST3GAL3,MGAT5,TRAK1,TMTC2,KDELC1,ALG5,B3GLCT,GALNT7,HSD17B12,CSGALNACT2,GCNT4,SLC35B3,MAN1A2,CHSY1,ATP6V1A,GALNT17,ST8SIA1,TRAK2,FAM20B,TPI1,GNPNAT1,PAPSS2,ADSS,CLTC,PIGW,C1GALT1C1,ACOT7,ENO1,DPM2,BMPR2,DPM1,ELOVL4,CHST11	darkolivegreen	VSMC_M9
GO:0048858	0.01	0.99	50	520	cell projection morphogenesis	BP	0.87852	EXT1,CDKL3,PTPRD,PLAA,ACTR2,ITGB1,FYN,KIF5B,PICALM,GATA3,TRAK1,MYO16,SOS1,ILK,RNF6,PALLD,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,CORO1C,ANOS1,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,NCAM1,SKIL,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,CYFIP2,DICER1,SEMA7A,ROCK1,ITGA1,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9

GO:0006810	0.01	0.99	233	3300	transport	BP	0.87852	LMAN1,MALT1,CDO1,AHI1,UTRN,MON2,STXBP5,TBC1D15,CEP120,AZIN1,ATP6V1C1,LRP12,EXT1,SLC39A7,SEC24A,SLC35B4,KDELR3,UBQLN1,CEP41,DENND4C,PLAA,SLC30A9,ABCB4,AKAP9,GCC2,TMEM165,JAK2,CLOCK,EXOC1,MYO6,STAP1,CCDC88A,COX18,ZMPSTE24,UBE2J1,ACTR2,CAV2,INHBA,PNPLA8,RAB3B,ITGB1,COG5,FYN,RINT1,KIF5B,DNAJC1,SLC36A4,RTN2,PICALM,CAMK1D,UPF2,GATA3,RAB3GAP1,CLN5,JMJD6,ESYT2,TRAK1,NDFIP2,CYTH1,EDEM1,OSBPL8,PPP1R12A,STAM2,VPS36,UFM1,PIK3R4,ATP2B1,EEA1,ATP11A,CEP83,NDFIP1,YIPF5,TMF1,SCYL2,REM1,ARL1,LYN,MERTK,RAB2A,GRAMD1A,SLC16A12,XPO4,ATP6V0A2,IFT88,IPO7,NUP37,TMED2,COPB2,SLC30A5,RIOK2,FFAR4,MAP1B,APPL1,GDAP1,AGTR1,HK2,TLR2,COPB1,ATP2A2,USO1,THBS1,ARL6,SLC39A14,SLC35B3,CBLB,ATP1A1,SPTBN5,EHD4,LRRK2,SNX19,BRSK2,ATP10A,UBE3A,SLC39A10,CUL3,MRS2,DNER,TIMM17A,TRAPPC10,ATP6V1A,KPNA6,EPRS,IGF1R,GPR89A,RAB3GAP2,CCDC186,CORO1C,ITPR2,TOMM20,PTPN1,GRK3,ATP11B,KPNA1,IDH2,VAPB,ABCB10,TRAK2,PRELID3B,C2CD2L,PIP5K1A,ANK3,OSBPL11,CD3G,HEATR5A,SH3KBP1,ATP13A3,CREB3L2,TPR,PTGS2,SEC23A,SORCS2,SEPT5,ITGAV,VAMP4,ATP8B4,RTN3,KIFAP3,SMURF1,KTN1,PLD1,BLZF1,ACTR10,AP4E1,TNFAIP8L3,VDAC2,DKK1,FMN2,ATAD1,PLP2,CLCNKB,SRP9,STIM2,MAGED2,ADAM10,MSN,SRCIN1,MYO1E,KCNMB1,TRIP4,OAZ2,CLINT1,CLTC,ARMCX3,GPRASP1,ATG4D,ANXA6,TRAPPC8,ROCK1,THOC1,ITGA2,MYOM1,NUP155,SLC1A3,RAB31,VAPA,AFG3L2,C1QTNF3,SPIRE1,USP7,MYO1C,PAFAH1B1,PMPCA,KIF1B,VAV2,CLCC1,ZDHHC7,SLC25A24,SSX2IP,MIR186,RANBP2,AQP3,MYO1H,FXYD5,K	darkolivegreen	VSMC_M9
GO:0008152	0.01	0.99	536	8467	metabolic process	BP	0.87852	SOCS6,MALT1,ELAC1,CDO1,AHI1,PPM1H,TBK1,CAND1,RRM2B,AZIN1,ATP6V1C1,EXT1,DSE,WDR46,WDYHV1,CDKL3,DDX46,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,SLC35B4,RMI1,PPIL1,UBQLN1,CEP41,PTPRD,PLAA,SLC30A9,TOPORS,ABCB4,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,EXOC1,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,POLR2B,GNE,MGAT4A,ZNF451,TRMO,HDAC9,CAVIN4,FAM135A,SENP6,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,ITGB1,RPF2,FYN,ZEB1,NT5DC1,PSMB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,UGGT1,GSAP,PDSS1,NOX4,RB1,RTN2,SUCLA2,PICALM,ZC3H13,CYP27C1,TRDMT1,TOE1,CBLC,ABHD1,TSN,CAMK1D,UPF2,NUB1,ST3GAL3,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,DARS,PAX1,TRAK1,LRRC32,NDFIP2,NKTR,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,MBNL2,NDUFAF5,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,ADAM32,FAM98A,TMTC2,VPS36,RPL26,KDELC1,GPCPD1,UFM1,CAPN7,LIG4,ABHD13,PIK3R4,CEBPZ,SUPT20H,ATP2B1,ALG5,SMAD9,CCNA1,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,AC091959.3,ILK,ITGA5,B3GLCT,HSPH1,TMF1,GALNT7,HOXC10,ERI1,HSD17B12,DHX29,SCYL2,PARG,USP12,MTREX,PLPP1,CDK8,CNOT7,RNF6,ARL1,LYN,CSGALNACT2,PPP2R3A,UBXN2B,MERTK,GRAMD1A,ATP6V0A2,TMEM41B,IFT88,IPO7,PDE7A,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,NEK1,CHD1,SULF1,RIOK2,USP47,MAT2A,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,FFAR4,APPL1,U2SURP,RDH10,PLOD2,LARP4,GD	darkolivegreen	VSMC_M9
GO:0010498	0.01	0.99	39	434	proteasomal protein catabolic process	BP	0.87852	SOCS6,CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBE2J1,PSMB1,PSMC2,UGGT1,NUB1,EDEM1,CUL4A,TMF1,UBXN2B,FBXL17,ITCH,LTN1,LRRK2,BRSK2,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,PITHD1,CDC27,SMURF1,SPOP,TRIP4,BAG5,BFAR,USP7,DNAJB9,FBXL7	darkolivegreen	VSMC_M9
GO:0048699	0.01	0.99	98	1177	generation of neurons	BP	0.87852	AHI1,LRP12,EXT1,CDKL3,PTPRD,PLAA,TOPORS,JAK2,HDAC9,MYO6,UBA6,CCDC88A,ACTR2,INHBA,ITGB1,FYN,ZEB1,KIF5B,RB1,PICALM,CAMK1D,GATA3,CLN5,TRAK1,STK24,LIG4,MYO16,SOS1,NTN4,ILK,SCYL2,RNF6,LYN,IFT88,SLC25A46,PALLD,MAP1B,TLR2,DHX36,SHOX2,IRX5,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,EIF4E,TDP2,DNER,CAMSAP2,ANOS1,NTRK3,SEMA5B,IDH2,TRAK2,IQGAP1,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,MYEF2,FZD2,SKIL,PRRX1,SMURF1,TNIK,DKK1,WNT5B,NOTCH3,ENAH,ADAM10,SRCIN1,TBX6,CYFIP2,DICER1,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,SLC1A3,VAPA,AFG3L2,PAFAH1B1,RAPGEF1,PLPPR5,CDH11,BMPR2,FRY,ARF4,GDNF,EFHD1,RAP2A,WNT9A,ZPR1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:1901889	0.01	1.00	6	26	negative regulation of cell junction assembly	BP	0.87852	ROCK2,TLR2,THBS1,PHLDB2,CORO1C,ROCK1	darkolivegreen	VSMC_M9
GO:0017038	0.01	1.00	19	174	protein import	BP	0.87852	JAK2,UFM1,IPO7,APPL1,CBLB,LRRK2,TIMM17A,KPNA6,TOMM20,KPNA1,TPR,PTGS2,NUP155,RANBP2,KPNA4,TOMM20L,E2F3,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0034504	0.01	1.00	25	244	protein localization to nucleus	BP	0.87852	TOPORS,JAK2,RPF2,FYN,OSBPL8,UFM1,IPO7,EIF2AK3,APPL1,CBLB,LRRK2,KPNA6,LARP7,KPNA1,TPR,PTGS2,FERMT2,PIN1,NUP155,RANBP2,KPNA4,TOR1AIP2,E2F3,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0006458	0.01	1.00	6	33	'de novo' protein folding	BP	0.87852	DNAJB5,UGGT1,HSPH1,DNAJB14,DNAJB4,HSPA13	darkolivegreen	VSMC_M9
GO:0007229	0.01	1.00	13	92	integrin-mediated signaling pathway	BP	0.87852	ITGB1,ILK,ITGA5,NEDD9,CUL3,ITGAV,FERMT2,ADAM10,SEMA7A,ITGA2,ITGA1,CD40LG,CTGF	darkolivegreen	VSMC_M9
GO:0009408	0.01	1.00	11	84	response to heat	BP	0.87852	LYN,ATP2A2,DHX36,THBS1,ST8SIA1,EIF2B5,RBBP7,TPR,PTGS2,DNAJA4,DNAJB4	darkolivegreen	VSMC_M9
GO:0090049	0.01	1.00	7	41	regulation of cell migration involved in sprouting angiogenesis	BP	0.87852	HDAC9,STARD13,THBS1,PTGS2,AKT3,SRPX2,TBXA2R	darkolivegreen	VSMC_M9

GO:1901575	0.01	0.99	120	1628	organic substance catabolic process	BP	0.87852	SOCS6,MALT1,CDO1,AZIN1,EXT1,CDC23,ETF1,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,ROCK2,PNPLA8,NOCT,FYN,PSMB1,EXOSC9,PSMC2,UGGT1,TRDMT1,CBLC,ABHD1,UPF2,NUB1,CLN5,NDFIP2,DNAJC3,EDEM1,VPS36,GPCPD1,ABHD13,PIK3R4,NDFIP1,CUL4A,TMF1,USP12,MTREX,CNOT7,RNF6,UBXN2B,PDE7A,FBXL17,TDG,ITCH,USP47,LNPEP,XRN1,PDE12,HK2,LTN1,DCP1A,DHX36,PGAM4,GPD2,NUDT9,CBLB,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,BPNT1,PSMD12,PTPN1,PLIN1,DERA,UBE4A,CCDC47,TLK2,NPL,PITHD1,FASTKD2,CDC27,MYEF2,TPI1,SMURF1,PLD1,FMN2,HK3,MSN,PHKG2,SPOP,DLST,TRIP4,OAZ2,CLPX,RLIM,ZC3H14,RBBP6,SMG8,C18orf25,PKM,DICER1,GPRASP1,PIN1,ETFA,BAG5,ROCK1,BFAR,CIDEA,GSPT1,USP7,LSM5,PAFAH1B1,ACOT7,ENO1,FASTKD5,GDNF,DNAJB9,IMPA1,ZPR1,VGLL4,FBXL7,AKR1D1	darkolivegreen	VSMC_M9
GO:0043603	0.01	0.99	68	897	cellular amide metabolic process	BP	0.87852	ETF1,NOA1,ELOVL5,EIF5B,GNE,RARS2,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,GSAP,RTN2,SUCLA2,PICALM,ST3GAL3,CLN5,DARS,DNAJC3,RPL26,HSD17B12,DHX29,PLPP1,CNOT7,EIF2AK3,TMED2,EIF2S2,LNPEP,XRN1,PDE12,LARP4,GDAP1,CERS5,LTN1,DCP1A,DHX36,THBS1,GFM1,DYRK1A,EIF4E,EPRS,IARS2,MRPL47,EIF2B5,NPL,FASTKD2,EIF3J,TPR,ZC3H15,RTN3,PLD1,CPEB2,SAMD8,SRP9,ADAM10,DLST,TRIP4,PKM,PIN1,ROCK1,ITGA2,GSPT1,TARS,ACOT7,MIR186,ELOVL4,EIF1AX	darkolivegreen	VSMC_M9
GO:1901135	0.01	0.99	63	791	carbohydrate derivative metabolic process	BP	0.87852	RRM2B,EXT1,DSE,TMEM165,ELOVL5,GNE,MGAT4A,UBE2J1,UGP2,GFPT1,UGGT1,SUCLA2,ST3GAL3,MGAT5,TRAK1,EDEM1,TMTC2,KDELC1,ALG5,ACPP,B3GLCT,GALNT7,HSD17B12,PARG,CSGALNACT2,PDE7A,TDG,SULF1,HK2,PGAM4,GPD2,NUDT9,GCNT4,SLC35B3,MAN1A2,LRRK2,CHSY1,ATP6V1A,BPNT1,GALNT17,ST8SIA1,TRAK2,DERA,NPL,FAM20B,TPI1,GNPNAT1,PAPSS2,ADSS,HK3,DLST,CLTC,PKM,PIGW,C1GALT1C1,ACOT7,ENO1,COL11A1,DPM2,BMPR2,DPM1,ELOVL4,CHST11	darkolivegreen	VSMC_M9
GO:0007369	0.01	1.00	17	138	gastrulation	BP	0.87852	EXT1,COL12A1,HOXA11,INHBA,ITGB1,SUPT20H,ITGA5,ACVR1,CUL3,PHLDB2,ITGAV,DKK1,WNT5B,TBX6,ITGA2,COL11A1,BMPR2	darkolivegreen	VSMC_M9
GO:0033554	0.01	0.99	117	1561	cellular response to stress	BP	0.87852	RRM2B,RMI1,UBQLN1,SLC30A9,TOPORS,TFPI2,JAK2,CLOCK,NPAS2,PSME4,MYO6,UBA6,ZMPSTE24,UBE2J1,ACTR2,ROCK2,PNPLA8,DDX1,GPX7,FYN,RINT1,UGGT1,CDK3,DNAJC3,EDEM1,STK24,RIF1,RPL26,UFM1,LIG4,PIK3R4,CUL4A,PDS5B,BRCA2,UBA5,PARG,MTREX,LYN,EIF2AK3,TDG,TMED2,ITCH,NEK1,USP47,MAP1B,ACTR8,HK2,ATP2A2,DHX36,THBS1,ZDHHC16,INO80,DYRK1A,LRRK2,TANK,BRSK2,NFRKB,CUL3,TDP2,UCHL5,DNAJB14,IGF1R,PTPN1,ST8SIA1,PLIN1,VAPB,ABCB10,EIF2B5,ATF3,RBBP7,UBE4A,CCDC47,TLK2,MBTPS2,CREB3L2,TPR,PTGS2,MYEF2,TMX1,SKIL,PRRX1,TNIK,CPEB2,BOD1L1,PDIA2,FMN2,FAS,AKT3,TLR6,KCNMB1,TPM1,RBBP6,PPM1D,MAP2K4,RBBP8,BAG5,THOC1,BFAR,CIDEA,SPIRE1,USP7,PAFAH1B1,GADD45B,ENO1,SLC25A24,RFWD3,BMPR2,AQP3,CTGF,BDKRB2,EFHD1,DNAJB9,HSPA13,RAP2A,C12orf66,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0006886	0.01	0.99	61	739	intracellular protein transport	BP	0.87852	LMAN1,TBC1D15,SEC24A,GCC2,JAK2,MYO6,COX18,UBE2J1,FYN,KIF5B,RTN2,TRAK1,EDEM1,VPS36,UFM1,PIK3R4,ARL1,XPO4,IPO7,TMED2,COPB2,APPL1,GDAP1,COPB1,USO1,ARL6,CBLB,LRRK2,BRSK2,TIMM17A,KPNA6,RAB3GAP2,TOMM20,PTPN1,KPNA1,TRAK2,ANK3,TPR,PTGS2,SEC23A,SORCS2,SMURF1,AP4E1,SRP9,OAZ2,CLTC,NUP155,RAB31,MYO1C,PMPCA,ZDHHC7,RANBP2,KPNA4,TOMM20L,RAB6A,ARF4,SEC63,E2F3,SRP19,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0060997	0.01	1.00	9	54	dendritic spine morphogenesis	BP	0.87852	ACTR2,DHX36,LRRK2,PDLIM5,UBE3A,ADAM10,SRCIN1,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0034620	0.01	1.00	11	86	cellular response to unfolded protein	BP	0.87852	EIF2AK3,TMED2,PTPN1,VAPB,ABCB10,ATF3,MBTPS2,CREB3L2,BFAR,DNAJB9,HSPA13	darkolivegreen	VSMC_M9
GO:0051648	0.01	1.00	18	154	vesicle localization	BP	0.87852	MYO6,KIF5B,PICALM,TRAK1,TMED2,USO1,ARL6,LRRK2,BRSK2,CUL3,CCDC186,TRAK2,SEPT5,KIFAP3,MYO1E,MYO1C,PAFAH1B1,MYO1H	darkolivegreen	VSMC_M9
GO:1901888	0.01	1.00	20	165	regulation of cell junction assembly	BP	0.87852	THBS2,PTPRD,ROCK2,SETD5,TLR2,THBS1,PDLIM5,PHLDB2,CORO1C,NTRK3,IQGAP1,FERMT2,SRPX2,ROCK1,GPC4,MYO1C,RAPGEF1,LHFPL4,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0044087	0.01	0.99	68	801	regulation of cellular component biogenesis	BP	0.87852	STXBP5,CAND1,CEP120,THBS2,PTPRD,AKAP9,SENP6,STAP1,CCDC88A,ACTR2,ROCK2,MPP7,CEP295,NOX4,RB1,ACTR3,RAB3GAP1,SETD5,FAM98A,SACS,IFT88,MAP1B,TLR2,PFN2,RASA1,THBS1,DYRK1A,SPTBN5,LRRK2,PDLIM5,PHLDB2,KIAA1551,CAMSAP2,RAB3GAP2,CORO1C,NTRK3,IQGAP1,C10orf90,TPR,DNAJA4,CDKL1,FERMT2,TAPT1,PLD1,SAMD8,VDAC2,DKK1,TLR6,MSN,TPM1,GPR65,CYFIP2,SRPX2,FHOD3,CCP110,BAG5,ROCK1,RICTOR,SPIRE1,GPC4,MYO1C,RAPGEF1,PLPPR5,CTGF,LHFPL4,PMEPA1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0043434	0.01	0.99	30	308	response to peptide hormone	BP	0.87852	CDO1,DENND4C,JAK2,HDAC9,KBTBD2,CAV2,ROCK2,FYN,OSBPL8,ATP2B1,LYN,MAP1B,APPL1,AGTR1,TLR2,USO1,SLC39A14,EPRS,IGF1R,PTPN1,EIF2B5,IQGAP1,PTGS2,CPEB2,PKM,ROCK1,RAB31,MYO1C,ZDHHC7,CTGF	darkolivegreen	VSMC_M9

GO:0006950	0.01	0.99	192	2715	response to stress	BP	0.87852	SOCS6,LMAN1,MALT1,CDO1,TBK1,RRM2B,EXT1,WISP1,RMI1,UBQLN1,PLAA,SLC30A9,TOPORS,DNAJB5,TFPI2,JAK2,CLOCK,EXOC1,NPAS2,FBXO9,HDAC9,PSME4,MYO6,STAP1,UBA6,ZMPSTE24,UBE2J1,ACTR2,ROCK2,INHBA,PNPLA8,DDX1,GPX7,ITGB1,FYN,RINT1,KIF5B,UGGT1,NOX4,GPR4,RB1,CAMK1D,NUB1,ACTR3,CDK3,GATA3,DNAJC3,EDEM1,STK24,TNFAIP6,RIF1,RPL26,UFM1,LIG4,PIK3R4,ATP2B1,NDFIP1,CUL4A,PDS5B,BRCA2,UBA5,ILK,ITGA5,HSPH1,TMF1,PARG,MTREX,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TDG,TMED2,ITCH,NEK1,USP47,PDE12,FFAR4,MAP1B,APPL1,PLOD2,AGTR1,ACTR8,HK2,TLR2,ATP2A2,DHX36,THBS1,ZDHHC16,ACVR1,INO80,NFKBIZ,DYRK1A,LRRK2,TANK,BRSK2,UBE3A,NFRKB,CUL3,EIF4E,PHLDB2,TDP2,UCHL5,DNAJB14,KPNA6,EPRS,IGF1R,ITPR2,NTRK3,PTPN1,ST8SIA1,PLIN1,VAPB,ABCB10,EIF2B5,LTB4R,GPATCH3,ATF3,RBBP7,UBE4A,CCDC47,TLK2,MBTPS2,CREB3L2,TPR,PTGS2,MYEF2,DNAJA4,TMX1,FERMT2,SKIL,PRRX1,TNIK,F5,CPEB2,BOD1L1,PDIA2,FMN2,FAS,AKT3,WNT5B,HSPB7,TLR6,KCNMB1,TPM1,RBBP6,PPM1D,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,RBBP8,BAG5,THOC1,ITGA2,RICTOR,SLC1A3,BFAR,C1QTNF3,CIDEA,SPIRE1,CD40LG,USP7,MYO1C,TBXA2R,PAFAH1B1,GADD45B,ENO1,VAV2,SLC25A24,WFDC1,RFWD3,DNAJB4,BMPR2,AQP3,CLEC4D,ARF4,GP1BB,CTGF,BDKRB2,EFHD1,DNAJB9,NOV,FCN1,HSPA13,RAP2A,C12orf66,NDUFAF4,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0050803	0.01	0.99	20	170	regulation of synapse structure or activity	BP	0.87852	THBS2,PTPRD,ACTR2,FYN,SETD5,TLR2,DHX36,LRRK2,PDLIM5,UBE3A,NTRK3,NRP2,ADAM10,SRCIN1,SRPX2,GPC4,PAFAH1B1,ARF4,LHFPL4,WNT7A	darkolivegreen	VSMC_M9
GO:0044257	0.01	0.99	57	685	cellular protein catabolic process	BP	0.87852	SOCS6,MALT1,CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,PSMB1,PSMC2,UGGT1,CBLC,NUB1,NDFIP2,DNAJC3,EDEM1,VPS36,NDFIP1,CUL4A,TMF1,USP12,RNF6,UBXN2B,FBXL17,ITCH,USP47,LTN1,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,PITHD1,CDC27,SMURF1,MSN,SPOP,TRIP4,CLPX,RLIM,RBBP6,C18orf25,BAG5,BFAR,USP7,DNAJB9,VGLL4,FBXL7	darkolivegreen	VSMC_M9
GO:0042026	0.01	1.00	4	16	protein refolding	BP	0.87852	DNAJA4,BAG5,PDCL,HSPA13	darkolivegreen	VSMC_M9
GO:0032989	0.01	0.99	56	609	cellular component morphogenesis	BP	0.87852	EXT1,CDKL3,PTPRD,PLAA,ACTR2,ITGB1,FYN,KIF5B,PICALM,GATA3,TRAK1,MYO16,SOS1,ILK,TMF1,RNF6,PALLD,MAP1B,TLR2,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,PHLDB2,CORO1C,ANOS1,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,NCAM1,SKIL,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,TPM1,CYFIP2,DICER1,FHOD3,SEMA7A,ROCK1,ITGA1,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,RAP2A,CFL2,WNT7A	darkolivegreen	VSMC_M9
GO:0099518	0.01	1.00	10	65	vesicle cytoskeletal trafficking	BP	0.87852	MYO6,KIF5B,TRAK1,CCDC186,TRAK2,KIFAP3,MYO1E,MYO1C,PAFAH1B1,MYO1H	darkolivegreen	VSMC_M9
GO:0051770	0.01	1.00	4	14	positive regulation of nitric-oxide synthase biosynthetic process	BP	0.87852	JAK2,TLR2,LRRK2,MAP2K4	darkolivegreen	VSMC_M9
GO:0051640	0.01	0.99	41	447	organelle localization	BP	0.87852	CEP120,CDC23,AKAP9,MYO6,CENPC,ACTR2,CAV2,RAB3B,ITGB1,KIF5B,PICALM,ACTR3,ESYT2,TRAK1,FAM98A,CEP83,LYN,UBXN2B,TMED2,RIOK2,MAP1B,ATP2A2,USO1,ARL6,LRRK2,BRSK2,CUL3,CCDC186,VAPB,TRAK2,SEPT5,KIFAP3,ACTR10,FMN2,MYO1E,ARMCX3,SPIRE1,MYO1C,PAFAH1B1,MYO1H,RAB6A	darkolivegreen	VSMC_M9
GO:0090503	0.01	1.00	7	42	RNA phosphodiester bond hydrolysis, exonucleolytic	BP	0.87852	NOCT,EXOSC9,TOE1,ERI1,CNOT7,XRN1,PDE12	darkolivegreen	VSMC_M9
GO:1905820	0.01	1.00	4	15	positive regulation of chromosome separation	BP	0.87852	CDC23,RB1,CUL3,CDC27	darkolivegreen	VSMC_M9
GO:0022607	0.01	0.99	162	2230	cellular component assembly	BP	0.87852	AHI1,STXBP5,CAND1,CEP120,EXT1,THBS2,UBQLN1,CEP41,PTPRD,HAUS6,AKAP9,JAK2,SENP6,CENPC,STAP1,CCDC88A,COX18,ACTR2,TAF1B,CAV2,ROCK2,DDX1,NOCT,ITGB1,MPP7,RPF2,CEP57,CEP295,NOX4,RB1,PICALM,ACTR3,RAB3GAP1,JMJD6,DARS,SETD5,NDUFAF5,STAM2,FAM98A,VPS36,THSD1,TUBGCP3,CEP83,NTN4,ILK,DCHS1,TMF1,DHX29,CNOT7,UBXN2B,SACS,TMEM41B,IFT88,TMED2,EIF2S2,SMARCA5,NEK1,MAT2A,BDP1,MAP1B,TMEM70,TLR2,PFN2,RASA1,ATP2A2,MAP9,THBS1,KCTD9,LIN54,ARL6,MTERF3,INO80,NEDD9,DYRK1A,SPTBN5,EHD4,LRRK2,PDLIM5,CUL3,NAP1L4,PHLDB2,DNER,TROVE2,DNAJB14,EPRS,CAMSAP2,RAB3GAP2,HAUS2,CORO1C,NEK7,NTRK3,SYCP2,PIP5K1A,IQGAP1,CEP350,ANK3,CD3G,C10orf90,HDGFL3,FASTKD2,EIF3J,TPR,DNAJA4,CDKL1,FERMT2,VAMP4,RTN3,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,KIAA0586,VDAC2,DKK1,FMN2,FAS,TLR6,ADAM10,MSN,TPM1,GPR65,CLINT1,CYFIP2,SRPX2,CLTC,DICER1,FHOD3,TRAPPC8,CCP110,BAG5,ROCK1,ITGA2,RICTOR,AFG3L2,SPIRE1,GPC4,MYO1C,PAFAH1B1,VAV2,RAPGEF1,PLPPR5,GTF2B,SSX2IP,PRKACB,CDH11,FXYD5,ARF4,FOPNL,CTGF,GEMIN6,LHFPL4,OTUD6B,PDCL,MZT1,PMEPA1,RAP2A,SRP19,NDUFAF4,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0010921	0.01	1.00	10	68	regulation of phosphatase activity	BP	0.87852	JAK2,ROCK2,MGAT5,PPP1R12A,SLC39A10,BOD1L1,ROCK1,ITGA2,ITGA1,PPP1R2	darkolivegreen	VSMC_M9

GO:0007049	0.01	0.99	107	1405	cell cycle	BP	0.87852	CEP120,CDKL3,CDC23,RMI1,HAUS6,CLOCK,SENP6,CENPC,ZMPSTE24,ACTR2,THAP5,CAV2,ROCK2,INHBA,ITGB1,RINT1,PIWIL4,CEP295,CCDC8,RB1,CGREF1,ACTR3,CDK3,GATA3,CCNT2,AZI2,RIF1,PPP1R12A,PRPF40A,RPL26,LIG4,PIK3R4,MYO16,TUBGCP3,CCNA1,CUL4A,PDS5B,BRCA2,ILK,DCTN6,CDK8,RASSF4,UBXN2B,IPO7,NUP37,MYBL1,FBXL17,NEK1,RIOK2,USP47,APPL1,ACTR8,RASA1,MAP9,LRRCC1,THBS1,LIN54,ACVR1,INO80,NEDD9,BRD7,BRSK2,CUL3,EIF4E,HAUS2,NEK7,SYCP2,IQGAP1,ANK3,LMLN,C10orf90,TLK2,KLHL18,TPR,CDC27,PTGS2,CDKL1,NPAT,SEPT5,SKIL,TUBA4A,FMN2,ADAM10,CLTC,PPM1D,MYOCD,PIN1,CCP110,RBBP8,ROCK1,THOC1,SPIRE1,GSPT1,PAFAH1B1,GADD45B,RFWD3,SSX2IP,PRKACB,SKA2,CDK13,CTGF,MZT1,E2F3,MPLKIP,ZPR1,FBXL7,ZNF655	darkolivegreen	VSMC_M9
GO:0034605	0.01	1.00	8	53	cellular response to heat	BP	0.87852	LYN,ATP2A2,DHX36,THBS1,ST8SIA1,RBBP7,TPR,PTGS2	darkolivegreen	VSMC_M9
GO:0051301	0.01	0.99	46	525	cell division	BP	0.87852	EXT1,CDC23,HAUS6,CENPC,ACTR2,ROCK2,RB1,ACTR3,CDK3,CCNT2,PRPF40A,LIG4,PIK3R4,CCNA1,PDS5B,BRCA2,NUP37,NEK1,ACTR8,RASA1,MAP9,LRRCC1,INO80,NEDD9,BRSK2,CUL3,HAUS2,SYCP2,ANK3,LMLN,KLHL18,TPR,CDC27,SEPT5,FMN2,CLTC,PIN1,CCP110,RBBP8,ROCK1,SPIRE1,PAFAH1B1,SKA2,MPLKIP,FBXL7,WNT7A	darkolivegreen	VSMC_M9
GO:0051656	0.01	0.99	32	334	establishment of organelle localization	BP	0.87852	CEP120,CDC23,MYO6,CENPC,ACTR2,ITGB1,KIF5B,PICALM,ACTR3,TRAK1,CEP83,LYN,UBXN2B,TMED2,RIOK2,MAP1B,ARL6,LRRK2,CUL3,CCDC186,TRAK2,SEPT5,KIFAP3,ACTR10,FMN2,MYO1E,ARMCX3,SPIRE1,MYO1C,PAFAH1B1,MYO1H,RAB6A	darkolivegreen	VSMC_M9
GO:0051496	0.01	1.00	8	47	positive regulation of stress fiber assembly	BP	0.87852	CCDC88A,ROCK2,NOX4,PFN2,FERMT2,TPM1,GPR65,CTGF	darkolivegreen	VSMC_M9
GO:0071375	0.01	0.99	23	219	cellular response to peptide hormone stimulus	BP	0.87852	DENND4C,JAK2,HDAC9,CAV2,ROCK2,FYN,OSBPL8,ATP2B1,LYN,MAP1B,APPL1,AGTR1,USO1,SLC39A14,EPRS,IGF1R,PTPN1,CPEB2,PKM,ROCK1,RAB31,MYO1C,ZDHHC7	darkolivegreen	VSMC_M9
GO:0006793	0.01	0.99	158	2169	phosphorus metabolic process	BP	0.87852	SOCS6,MALT1,PPM1H,TBK1,RRM2B,CDKL3,PTPRD,PLAA,AKAP9,JAK2,ELOVL5,GNE,STAP1,CCDC88A,ZMPSTE24,UGP2,SH3BP5L,GFPT1,ROCK2,INHBA,PNPLA8,NOCT,FYN,NT5DC1,UGGT1,NOX4,RB1,SUCLA2,CBLC,CAMK1D,CDK3,MGAT5,CCNT2,DNAJC3,STK24,OSBPL8,PPP1R12A,GPCPD1,PIK3R4,CCNA1,ACPP,ILK,ITGA5,HSD17B12,SCYL2,PLPP1,CDK8,CNOT7,LYN,PPP2R3A,MERTK,IPO7,PDE7A,EIF2AK3,TDG,TMED2,NEK1,RIOK2,HK2,ALDH18A1,TLR2,PFN2,THBS1,PPP2R2A,PGAM4,PDP1,GPD2,ACVR1,NUDT9,SLC35B3,ETNK2,NEDD9,CBLB,ATP1A1,DYRK1A,EHD4,ERG,LRRK2,BRSK2,SLC39A10,MBOAT1,ATP6V1A,IGF1R,BPNT1,STK38L,CORO1C,NEK7,NTRK3,PTPN1,GRK3,ETNK1,CLK1,IDH2,PIP5K1A,DERA,IQGAP1,TLK2,PTGS2,CDKL1,MAP4K5,TPI1,GNPNAT1,FERMT2,TNIK,PLD1,TNFAIP8L3,SAMD8,BOD1L1,DKK1,PAPSS2,FAS,AKT3,ADSS,CDC42BPA,TLR6,ADAM10,HK3,SRCIN1,PHKG2,CLK2,DLST,SRPX2,SMG8,PKM,PPM1D,PIGW,MAP2K4,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,ITGA1,RICTOR,PPP4R1,PAFAH1B1,GADD45B,ACOT7,ENO1,VAV2,PLPPR5,DPM2,PRKACB,RANBP2,BMPR2,PTPN12,CDK13,CTGF,BDKRB2,LAMTOR3,IMPA1,DPM1,ELOVL4,PMEPA1,RAP2A,TMEM119,PPTC7,PPP1R2	darkolivegreen	VSMC_M9
GO:0006508	0.01	0.99	97	1295	proteolysis	BP	0.87852	SOCS6,MALT1,CDC23,UBQLN1,PLAA,TOPORS,TFPI2,JAK2,CLOCK,FBXO9,SENP6,PSME4,UBA6,ZMPSTE24,UBE2J1,ROCK2,FYN,PSMB1,DNAJC1,PSMC2,UGGT1,GSAP,PICALM,CBLC,NUB1,CLN5,NDFIP2,DNAJC3,EDEM1,ADAM32,VPS36,CAPN7,NDFIP1,CUL4A,TMF1,USP12,RNF6,LYN,UBXN2B,EIF2AK3,FBXL17,ITCH,USP47,LNPEP,PI15,LTN1,THBS1,LRRK2,TANK,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,TIMM17A,ADAMTS17,CASP7,ANOS1,PSMD12,LMLN,UBE4A,CCDC47,ADAM12,TLK2,PITHD1,MBTPS2,CDC27,PTGS2,USP54,SMURF1,FAS,ADAM10,SPOP,TRIP4,CLPX,RLIM,ADAM19,CYFIP2,RBBP6,UACA,C18orf25,ATG4D,BAG5,ROCK1,BFAR,AFG3L2,MYSM1,USP7,PMPCA,ENO1,WFDC1,PRKACB,CTGF,OTUD6B,DNAJB9,FBXL7,PRSS53	darkolivegreen	VSMC_M9
GO:0006882	0.01	1.00	5	23	cellular zinc ion homeostasis	BP	0.87852	SLC39A7,SLC30A9,SLC30A5,SLC39A14,SLC39A10	darkolivegreen	VSMC_M9

GO:0019222	0.01	0.99	329	4858	regulation of metabolic process	BP	0.87852	SOCS6,MALT1,AHI1,TBK1,CAND1,AZIN1,ATP6V1C1,PHF20L1,WISP1,KHDRBS3,ETF1,SLC35B4,UBQLN1,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,JAK2,CLOCK,EXOC1,NPAS2,NOA1,ELOVL5,EIF5B,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,SH3BP5L,ACTR2,THAP5,GFPT1,ROCK2,INHBA,DDX1,NOCT,ITGB1,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,GSAP,NOX4,RB1,RTN2,PICALM,TRDMT1,CBLC,CAMK1D,UPF2,NUB1,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,MBNL2,RIF1,OSBPL8,PPP1R12A,FAM98A,RPL26,PIK3R4,CEBPZ,SUPT20H,ATP2B1,SMAD9,CCNA1,NR2C1,NDFIP1,CUL4A,BRCA2,ILK,ITGA5,HSPH1,TMF1,HOXC10,ERI1,DHX29,SCYL2,PARG,PLPP1,CNOT7,RNF6,LYN,MERTK,ATP6V0A2,IPO7,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,SULF1,RIOK2,USP47,LNPEP,XRN1,PDE12,STOX2,MICAL2,FFAR4,APPL1,RDH10,LARP4,PI15,AGTR1,ACTR8,HK2,TLR2,PFN2,RASA1,MBNL1,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,NFKBIZ,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,TBX15,UBE3A,SLC39A10,CUL3,EIF4E,TDP2,TROVE2,UCHL5,TIMM17A,KIAA1551,ATP6V1A,KPNA6,EPRS,IGF1R,RAB3GAP2,CORO1C,ANOS1,NEK7,NTRK3,WWC3,PTPN1,LARP7,KPNA1,CLK1,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,IQGAP1,RBBP7,ANK3,EDRF1,BCLAF3,TLK2,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,GATM,PTGS2,MYEF2,FZD2,CWC22,DNAJA4,NPAT,ITGAV,MYNN,FERMT2,SKIL,PRRX1,RTN3,SMURF1,TNIK,PLD1,TNFAIP8L3,CPEB2,SA	darkolivegreen	VSMC_M9
GO:0043043	0.01	0.99	45	566	peptide biosynthetic process	BP	0.87852	ETF1,NOA1,EIF5B,RARS2,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,DARS,DNAJC3,RPL26,DHX29,CNOT7,EIF2AK3,TMED2,EIF2S2,XRN1,PDE12,LARP4,LTN1,DCP1A,DHX36,THBS1,GFM1,EIF4E,EPRS,IARS2,MRPL47,EIF2B5,FASTKD2,EIF3J,TPR,ZC3H15,PLD1,CPEB2,SRP9,TRIP4,PKM,ROCK1,ITGA2,GSPT1,TARS,EIF1AX	darkolivegreen	VSMC_M9
GO:0006413	0.01	1.00	12	99	translational initiation	BP	0.87852	EIF5B,DDX1,DNAJC3,DHX29,EIF2AK3,TMED2,EIF2S2,EIF4E,EIF2B5,EIF3J,TPR,EIF1AX	darkolivegreen	VSMC_M9
GO:0044772	0.01	0.99	32	350	mitotic cell cycle phase transition	BP	0.87852	CDC23,INHBA,ITGB1,RINT1,RB1,CDK3,RPL26,MYO16,CCNA1,CUL4A,FBXL17,RIOK2,USP47,APPL1,ACVR1,INO80,BRD7,BRSK2,CUL3,EIF4E,KLHL18,TPR,CDC27,NPAT,PPM1D,RBBP8,GSPT1,RFWD3,E2F3,ZPR1,FBXL7,ZNF655	darkolivegreen	VSMC_M9
GO:0014033	0.01	1.00	11	77	neural crest cell differentiation	BP	0.87852	EXT1,FBXL17,RDH10,ACVR1,CORO1C,SEMA5B,NRP2,TAPT1,SEMA7A,ANXA6,GDNF	darkolivegreen	VSMC_M9
GO:0044085	0.01	0.99	175	2454	cellular component biogenesis	BP	0.87852	AHI1,STXBP5,CAND1,CEP120,EXT1,THBS2,WDR46,UBQLN1,CEP41,PTPRD,HAUS6,AKAP9,JAK2,SENP6,CENPC,STAP1,CCDC88A,COX18,ACTR2,TAF1B,CAV2,ROCK2,DDX1,NOCT,ITGB1,MPP7,RPF2,CEP57,EXOSC9,CEP295,NOX4,RB1,PICALM,ACTR3,RAB3GAP1,JMJD6,DARS,SETD5,NDUFAF5,STAM2,FAM98A,VPS36,THSD1,RPL26,TUBGCP3,CEP83,CUL4A,NTN4,ILK,DCHS1,TMF1,ERI1,DHX29,MTREX,CNOT7,UBXN2B,SACS,TMEM41B,IFT88,TMED2,EIF2S2,SMARCA5,NEK1,RIOK2,MAT2A,BDP1,MAP1B,TMEM70,TLR2,PFN2,RASA1,ATP2A2,MAP9,THBS1,KCTD9,LIN54,ARL6,WDR75,MTERF3,INO80,NEDD9,DYRK1A,SPTBN5,EHD4,LRRK2,PDLIM5,CUL3,NAP1L4,PHLDB2,DNER,TROVE2,DNAJB14,KIAA1551,RRP15,EPRS,CAMSAP2,RAB3GAP2,HAUS2,CORO1C,NEK7,NTRK3,SYCP2,PIP5K1A,IQGAP1,CEP350,ANK3,CD3G,C10orf90,HDGFL3,FASTKD2,EIF3J,TPR,DNAJA4,CDKL1,FERMT2,VAMP4,RTN3,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,KIAA0586,SAMD8,VDAC2,DKK1,FMN2,FAS,TLR6,ADAM10,MSN,TPM1,GPR65,CLINT1,CYFIP2,SRPX2,CLTC,DICER1,FHOD3,TRAPPC8,CCP110,BAG5,ROCK1,ITGA2,RICTOR,AFG3L2,SPIRE1,GPC4,MYO1C,PAFAH1B1,SURF6,VAV2,RAPGEF1,PLPPR5,GTF2B,SSX2IP,PRKACB,CDH11,FXYD5,ARF4,FOPNL,CTGF,GEMIN6,LHFPL4,OTUD6B,PDCL,MZT1,PMEPA1,RAP2A,SRP19,NDUFAF4,CFL2,IRX3,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0032990	0.01	0.99	50	536	cell part morphogenesis	BP	0.87852	EXT1,CDKL3,PTPRD,PLAA,ACTR2,ITGB1,FYN,KIF5B,PICALM,GATA3,TRAK1,MYO16,SOS1,ILK,RNF6,PALLD,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,CORO1C,ANOS1,SEMA5B,TRAK2,IQGAP1,ANK3,NRP2,NCAM1,SKIL,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,CYFIP2,DICER1,SEMA7A,ROCK1,ITGA1,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0051146	0.01	0.99	23	220	striated muscle cell differentiation	BP	0.87852	HDAC9,ZMPSTE24,CAV2,ITGB1,RB1,ATP11A,SHOX2,ACVR1,PDLIM5,DNER,CASP7,ADAM12,MYEF2,DKK1,TPM1,FHOD3,MAP2K4,MYOCD,PIN1,NOV,TMEM119,CFL2,IRX3	darkolivegreen	VSMC_M9

GO:0060255	0.01	0.99	305	4468	regulation of macromolecule metabolic process	BP	0.87852	MALT1,AHI1,TBK1,CAND1,AZIN1,PHF20L1,WISP1,KHDRBS3,ETF1,UBQLN1,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,JAK2,CLOCK,NPAS2,EIF5B,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,SH3BP5L,ACTR2,THAP5,GFPT1,ROCK2,INHBA,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,GSAP,NOX4,RB1,RTN2,PICALM,TRDMT1,CBLC,CAMK1D,UPF2,NUB1,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,MBNL2,RIF1,OSBPL8,PPP1R12A,FAM98A,RPL26,CEBPZ,SUPT20H,ATP2B1,SMAD9,CCNA1,NR2C1,NDFIP1,CUL4A,BRCA2,ILK,ITGA5,HSPH1,TMF1,HOXC10,ERI1,DHX29,SCYL2,PARG,CNOT7,RNF6,LYN,MERTK,IPO7,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,SULF1,RIOK2,USP47,XRN1,PDE12,STOX2,MICAL2,FFAR4,APPL1,LARP4,PI15,AGTR1,ACTR8,TLR2,PFN2,RASA1,MBNL1,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,NFKBIZ,NEDD9,CBLB,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,TBX15,UBE3A,SLC39A10,CUL3,EIF4E,TDP2,TROVE2,UCHL5,TIMM17A,KIAA1551,KPNA6,EPRS,RAB3GAP2,CORO1C,ANOS1,NEK7,NTRK3,WWC3,PTPN1,LARP7,KPNA1,CLK1,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,IQGAP1,RBBP7,ANK3,EDRF1,BCLAF3,TLK2,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,PTGS2,MYEF2,FZD2,CWC22,DNAJA4,NPAT,ITGAV,MYNN,FERMT2,SKIL,PRRX1,RTN3,SMURF1,TNIK,PLD1,CPEB2,SAMD8,BOD1L1,DKK1,FMN2,ATAD1,ACTA2,FAS,NOTCH3,SRP9,TLR6,MAGED2,ADAM10,MSN,SRCIN1,PHKG2,SPOP,CLK2,TRIP4,TBX6,OAZ2,CLPX,RLI	darkolivegreen	VSMC_M9
GO:0048667	0.01	0.99	43	446	cell morphogenesis involved in neuron differentiation	BP	0.87852	EXT1,CDKL3,PTPRD,ACTR2,ITGB1,FYN,KIF5B,RB1,PICALM,GATA3,TRAK1,SOS1,ILK,RNF6,PALLD,MAP1B,DHX36,SHOX2,LRRK2,BRSK2,PDLIM5,UBE3A,ANOS1,SEMA5B,TRAK2,ANK3,NRP2,NCAM1,SKIL,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,SEMA7A,SLC1A3,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0051649	0.01	0.99	126	1679	establishment of localization in cell	BP	0.87852	LMAN1,MALT1,MON2,STXBP5,TBC1D15,CEP120,SEC24A,CDC23,KDELR3,PLAA,AKAP9,GCC2,JAK2,MYO6,CENPC,CCDC88A,COX18,ZMPSTE24,UBE2J1,ACTR2,RAB3B,ITGB1,FYN,RINT1,KIF5B,RTN2,PICALM,UPF2,ACTR3,RAB3GAP1,CLN5,TRAK1,EDEM1,PPP1R12A,VPS36,UFM1,PIK3R4,EEA1,CEP83,YIPF5,SCYL2,ARL1,LYN,UBXN2B,XPO4,IFT88,IPO7,TMED2,COPB2,RIOK2,MAP1B,APPL1,GDAP1,COPB1,ATP2A2,USO1,ARL6,SLC39A14,CBLB,ATP1A1,EHD4,LRRK2,BRSK2,CUL3,TIMM17A,TRAPPC10,KPNA6,RAB3GAP2,CCDC186,CORO1C,ITPR2,TOMM20,PTPN1,KPNA1,VAPB,TRAK2,C2CD2L,ANK3,HEATR5A,CREB3L2,TPR,PTGS2,SEC23A,SORCS2,SEPT5,VAMP4,KIFAP3,SMURF1,PLD1,ACTR10,AP4E1,FMN2,SRP9,MSN,MYO1E,OAZ2,CLTC,ARMCX3,GPRASP1,TRAPPC8,ROCK1,THOC1,NUP155,RAB31,VAPA,SPIRE1,USP7,MYO1C,PAFAH1B1,PMPCA,KIF1B,ZDHHC7,SSX2IP,RANBP2,MYO1H,KPNA4,TOMM20L,RAB6A,ARF4,GDNF,SEC63,E2F3,SRP19,ZPR1,NUP35,WNT7A	darkolivegreen	VSMC_M9
GO:0015748	0.01	0.99	13	102	organophosphate ester transport	BP	0.88703	ABCB4,OSBPL8,ATP11A,SLC35B3,ATP10A,ATP11B,PRELID3B,C2CD2L,ATP8B4,TNFAIP8L3,SLC25A24,XKR9,PLEKHA3	darkolivegreen	VSMC_M9
GO:0000902	0.01	0.99	70	799	cell morphogenesis	BP	0.89703	EXT1,CDKL3,PTPRD,PLAA,ZMPSTE24,ACTR2,ITGB1,FYN,KIF5B,NOX4,RB1,PICALM,GATA3,TRAK1,PRPF40A,MYO16,SOS1,NTN4,ILK,DCHS1,RNF6,MERTK,PALLD,MAP1B,LARP4,RASA1,DHX36,SHOX2,NEDD9,LRRK2,BRSK2,PDLIM5,ATP10A,UBE3A,CUL3,CORO1C,ANOS1,SEMA5B,TRAK2,IQGAP1,ANK3,SH3KBP1,NRP2,NCAM1,ITGAV,FERMT2,SKIL,SMURF1,TNIK,NOTCH3,ENAH,ADAM10,MSN,SRCIN1,TPM1,CYFIP2,DICER1,SEMA7A,SS18,ROCK1,ITGA1,SLC1A3,AFG3L2,PAFAH1B1,CDH11,BMPR2,FRY,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0032516	0.01	1.00	4	15	positive regulation of phosphoprotein phosphatase activity	BP	0.8993	JAK2,PPP1R12A,SLC39A10,ITGA1	darkolivegreen	VSMC_M9
GO:0048706	0.01	0.99	13	105	embryonic skeletal system development	BP	0.91371	EXT1,HOXA9,HOXA11,SULF1,RDH10,SHOX2,IRX5,TBX15,PRRX1,TAPT1,COL11A1,WNT9A,CHST11	darkolivegreen	VSMC_M9
GO:0051085	0.01	1.00	5	26	chaperone cofactor-dependent protein refolding	BP	0.93573	DNAJB5,HSPH1,DNAJB14,DNAJB4,HSPA13	darkolivegreen	VSMC_M9
GO:0030033	0.01	1.00	4	15	microvillus assembly	BP	0.94909	TNIK,PLD1,FXYD5,RAP2A	darkolivegreen	VSMC_M9
GO:0072599	0.01	1.00	6	34	establishment of protein localization to endoplasmic reticulum	BP	0.95248	RAB3GAP1,EDEM1,RAB3GAP2,SRP9,SEC63,SRP19	darkolivegreen	VSMC_M9

GO:0006796	0.01	0.99	156	2150	phosphate-containing compound metabolic process	BP	0.95973	SOCS6,MALT1,PPM1H,TBK1,RRM2B,CDKL3,PTPRD,PLAA,AKAP9,JAK2,ELOVL5,GNE,STAP1,CCDC88A,ZMPSTE24,UGP2,SH3BP5L,GFPT1,ROCK2,INHBA,PNPLA8,NOCT,FYN,NT5DC1,NOX4,RB1,SUCLA2,CBLC,CAMK1D,CDK3,MGAT5,CCNT2,DNAJC3,STK24,OSBPL8,PPP1R12A,GPCPD1,PIK3R4,CCNA1,ACPP,ILK,ITGA5,HSD17B12,SCYL2,PLPP1,CDK8,CNOT7,LYN,PPP2R3A,MERTK,IPO7,PDE7A,EIF2AK3,TDG,TMED2,NEK1,RIOK2,HK2,ALDH18A1,TLR2,PFN2,THBS1,PPP2R2A,PGAM4,PDP1,GPD2,ACVR1,NUDT9,SLC35B3,ETNK2,NEDD9,CBLB,ATP1A1,DYRK1A,EHD4,ERG,LRRK2,BRSK2,SLC39A10,MBOAT1,ATP6V1A,IGF1R,BPNT1,STK38L,CORO1C,NEK7,NTRK3,PTPN1,GRK3,ETNK1,CLK1,IDH2,PIP5K1A,DERA,IQGAP1,TLK2,PTGS2,CDKL1,MAP4K5,TPI1,FERMT2,TNIK,PLD1,TNFAIP8L3,SAMD8,BOD1L1,DKK1,PAPSS2,FAS,AKT3,ADSS,CDC42BPA,TLR6,ADAM10,HK3,SRCIN1,PHKG2,CLK2,DLST,SRPX2,SMG8,PKM,PPM1D,PIGW,MAP2K4,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,ITGA1,RICTOR,PPP4R1,PAFAH1B1,GADD45B,ACOT7,ENO1,VAV2,PLPPR5,DPM2,PRKACB,RANBP2,BMPR2,PTPN12,CDK13,CTGF,BDKRB2,LAMTOR3,IMPA1,DPM1,ELOVL4,PMEPA1,RAP2A,TMEM119,PPTC7,PPP1R2	darkolivegreen	VSMC_M9
GO:0072657	0.01	0.99	41	466	protein localization to membrane	BP	0.95973	DENND4C,CCDC88A,COX18,ROCK2,RAB3B,ITGB1,FYN,KIF5B,PICALM,RAB3GAP1,DCHS1,TMED2,APPL1,TM9SF3,ARL6,EHD4,RAB3GAP2,PIP5K1A,ANK3,CCDC47,SEC23A,FERMT2,SMURF1,TNIK,BLZF1,ATAD1,SRP9,ADAM10,CLTC,PIGW,ROCK1,NUP155,RAB31,GPC4,MYO1C,ZDHHC7,LHFPL4,SEC63,RAP2A,SRP19,SHISA7	darkolivegreen	VSMC_M9
GO:0071479	0.01	1.00	9	64	cellular response to ionizing radiation	BP	0.95973	CLOCK,ZMPSTE24,NOX4,GATA3,RPL26,LIG4,INO80,TANK,TLK2	darkolivegreen	VSMC_M9
GO:0006909	0.01	0.99	18	163	phagocytosis	BP	0.9662	STAP1,ITGB1,FYN,CAMK1D,JMJD6,LYN,MERTK,APPL1,TLR2,THBS1,CORO1C,PIP5K1A,ITGAV,ITGA2,RAB31,VAV2,XKR9,FCN1	darkolivegreen	VSMC_M9
GO:0034643	0.02	1.00	5	24	establishment of mitochondrion localization, microtubule-mediated	BP	0.9662	TRAK1,MAP1B,TRAK2,ACTR10,ARMCX3	darkolivegreen	VSMC_M9
GO:0047497	0.02	1.00	5	24	mitochondrion transport along microtubule	BP	0.9662	TRAK1,MAP1B,TRAK2,ACTR10,ARMCX3	darkolivegreen	VSMC_M9
GO:0006829	0.02	1.00	5	24	zinc ion transport	BP	0.9662	SLC39A7,SLC30A9,SLC30A5,SLC39A14,SLC39A10	darkolivegreen	VSMC_M9
GO:0009954	0.02	1.00	5	25	proximal/distal pattern formation	BP	0.96916	HOXA9,HOXA10,HOXA11,CHSY1,IRX3	darkolivegreen	VSMC_M9
GO:0048333	0.02	1.00	5	23	mesodermal cell differentiation	BP	0.97503	HOXA11,INHBA,ITGB1,DKK1,ITGA2	darkolivegreen	VSMC_M9
GO:0006996	0.02	0.99	208	2943	organelle organization	BP	0.97503	LMAN1,AHI1,PHACTR2,UTRN,CEP120,EXT1,SEC24A,CDC23,RMI1,UBQLN1,CEP41,PTPRD,HAUS6,AKAP9,GCC2,TMEM165,JAK2,TXNDC9,SENP6,PSME4,MYO6,CENPC,STAP1,CCDC88A,COX18,ZMPSTE24,ACTR2,CAV2,ROCK2,DDX1,NOCT,ITGB1,RPF2,KIF5B,CEP57,CEP295,CCDC8,NOX4,RB1,PICALM,ACTR3,GATA3,RAB3GAP1,CLN5,ESYT2,TRAK1,SETD5,NDUFAF5,RIF1,PPP1R12A,STAM2,PRPF40A,VPS36,UFM1,LIG4,TUBGCP3,EEA1,CCNA1,CEP83,ACPP,STARD13,YIPF5,PDS5B,BRCA2,UBA5,ILK,DCTN6,TMF1,DHX29,CNOT7,ARL1,UBXN2B,RAB2A,TMEM41B,IFT88,MYBL1,EIF2AK3,SLC25A46,TDG,TMED2,HCFC2,PALLD,SMARCA5,NEK1,CHD1,RIOK2,XRN1,MICAL2,MAP1B,TMEM70,LARP4,GDAP1,ACTR8,HK2,PFN2,RASA1,ATP2A2,USO1,MAP9,DHX36,LIN54,ARL6,MTERF3,INO80,CHD9,NEDD9,DYRK1A,SPTBN5,EHD4,LRRK2,SNX19,BRSK2,PDLIM5,CUL3,NAP1L4,PHLDB2,TROVE2,TIMM17A,KIAA1551,CAMSAP2,RAB3GAP2,HAUS2,CORO1C,NEK7,NTRK3,TOMM20,PTPN1,VAPB,TRAK2,SYCP2,PIP5K1A,IQGAP1,CEP350,RBBP7,ANK3,CCDC47,SMTN,C10orf90,SH3KBP1,TLK2,HDGFL3,BAZ1A,FASTKD2,EHBP1L1,TPR,CDC27,SEC23A,IQCJ-SCHIP1,CDKL1,FERMT2,VAMP4,ATP8B4,RTN3,KIFAP3,SMURF1,TAPT1,TNIK,TUBA4A,BLZF1,KIAA0586,VDAC2,FMN2,AKT3,CDC42BPA,ENAH,MSN,MYO1E,TPM1,GPR65,CYFIP2,CLTC,ARMCX3,FHOD3,PIN1,TRAPPC8,CCP110,SS18,BAG5,ROCK1,RICTOR,NUP155,RAB31,VAPA,AFG3L2,SPIRE1,MYSM1,USP7,MYO1C,PAFAH1B1,DNAJC11,PMPCA,RFWD3,SSX2IP,MIGA1,MYO1H,TOMM20L,ARF4,SKA2,CDK13,FOPNL,TOR1AIP2,CTGF,MZT1,RAP2A,ZPR1,NDUFAF4,NUP35,CFL2	darkolivegreen	VSMC_M9
GO:0016073	0.02	1.00	6	35	snRNA metabolic process	BP	0.97503	EXOSC9,TOE1,MTREX,LARP7,INTS14,INTS6	darkolivegreen	VSMC_M9
GO:0000910	0.02	0.99	16	141	cytokinesis	BP	0.9752	ACTR2,ROCK2,ACTR3,PRPF40A,PIK3R4,BRCA2,RASA1,MAP9,CUL3,ANK3,SEPT5,FMN2,PIN1,CCP110,ROCK1,SPIRE1	darkolivegreen	VSMC_M9
GO:0106027	0.02	0.99	11	78	neuron projection organization	BP	0.9752	ACTR2,FYN,DHX36,LRRK2,PDLIM5,UBE3A,IGF1R,ADAM10,SRCIN1,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0036498	0.02	1.00	4	17	IRE1-mediated unfolded protein response	BP	0.9752	PTPN1,VAPB,BFAR,DNAJB9	darkolivegreen	VSMC_M9
GO:0010830	0.02	1.00	6	33	regulation of myotube differentiation	BP	0.9752	HDAC9,ATP11A,SHOX2,MYOCD,NOV,TMEM119	darkolivegreen	VSMC_M9
GO:0019896	0.02	1.00	4	16	axonal transport of mitochondrion	BP	0.99682	TRAK1,TRAK2,ACTR10,ARMCX3	darkolivegreen	VSMC_M9
GO:0034249	0.02	0.99	19	183	negative regulation of cellular amide metabolic process	BP	0.99682	ROCK2,NOCT,EXOSC9,RTN2,CNOT7,EIF2AK3,XRN1,PDE12,DCP1A,DHX36,EIF4E,EPRS,TPR,RTN3,CPEB2,SRP9,PIN1,ROCK1,MIR186	darkolivegreen	VSMC_M9
GO:0030968	0.02	0.99	9	69	endoplasmic reticulum unfolded protein response	BP	0.99682	EIF2AK3,TMED2,PTPN1,VAPB,ATF3,MBTPS2,CREB3L2,BFAR,DNAJB9	darkolivegreen	VSMC_M9
GO:1990776	0.02	1.00	5	24	response to angiotensin	BP	0.99857	ROCK2,AGTR1,IQGAP1,PTGS2,ROCK1	darkolivegreen	VSMC_M9
GO:0050727	0.02	0.99	23	239	regulation of inflammatory response	BP	0.99857	WISP1,JAK2,CLOCK,STAP1,FYN,GPR4,RB1,GATA3,TNFAIP6,NDFIP1,LYN,FFAR4,AGTR1,TLR2,NFKBIZ,LRRK2,PTGS2,SEMA7A,ITGA2,RICTOR,C1QTNF3,WFDC1,NOV	darkolivegreen	VSMC_M9
GO:1902993	0.02	1.00	4	18	positive regulation of amyloid precursor protein catabolic process	BP	0.99857	ROCK2,GSAP,PICALM,LYN	darkolivegreen	VSMC_M9

GO:0032801	0.02	1.00	5	23	receptor catabolic process	BP	0.99857	PIK3R4,ITCH,PTPN1,SMURF1,GPRASP1	darkolivegreen	VSMC_M9
GO:0007017	0.02	0.99	59	715	microtubule-based process	BP	1	CEP120,HAUS6,AKAP9,GCC2,TXNDC9,SENP6,CCDC88A,ACTR2,ROCK2,ITGB1,KIF5B,CEP57,CEP295,CCDC8,ACTR3,TRAK1,PPP1R12A,TUBGCP3,BRCA2,DCTN6,TMF1,UBXN2B,IFT88,DYNLRB1,MAP1B,MAP9,PGAM4,INO80,DYRK1A,BRSK2,PHLDB2,CAMSAP2,HAUS2,NEK7,TRAK2,CEP350,C10orf90,HDGFL3,TPR,VAMP4,KIFAP3,KTN1,TUBA4A,ACTR10,FMN2,CLTC,ARMCX3,CCP110,SS18,ROCK1,SPIRE1,PAFAH1B1,KIF1B,SSX2IP,RAB6A,SKA2,FOPNL,MZT1,ZPR1	darkolivegreen	VSMC_M9
GO:0055069	0.02	1.00	5	25	zinc ion homeostasis	BP	1	SLC39A7,SLC30A9,SLC30A5,SLC39A14,SLC39A10	darkolivegreen	VSMC_M9
GO:0032507	0.02	0.99	8	55	maintenance of protein location in cell	BP	1	KDELR3,TOPORS,CCDC88A,HK2,ANK3,TAPT1,PDIA2,ANKRD13C	darkolivegreen	VSMC_M9
GO:0043032	0.02	1.00	4	18	positive regulation of macrophage activation	BP	1	STAP1,THBS1,LRRK2,TLR6	darkolivegreen	VSMC_M9
GO:0045056	0.02	1.00	4	17	transcytosis	BP	1	PICALM,USO1,IGF1R,CLTC	darkolivegreen	VSMC_M9
GO:0022008	0.02	0.99	102	1272	neurogenesis	BP	1	AHI1,CEP120,LRP12,EXT1,CDKL3,PTPRD,PLAA,TOPORS,JAK2,HDAC9,MYO6,STAP1,UBA6,CCDC88A,ACTR2,INHBA,ITGB1,FYN,ZEB1,KIF5B,RB1,PICALM,CAMK1D,GATA3,CLN5,TRAK1,STK24,LIG4,MYO16,SOS1,NTN4,ILK,DCHS1,SCYL2,RNF6,LYN,IFT88,SLC25A46,PALLD,MAP1B,TLR2,DHX36,SHOX2,IRX5,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,EIF4E,TDP2,DNER,CAMSAP2,ANOS1,NTRK3,SEMA5B,IDH2,EIF2B5,TRAK2,IQGAP1,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,MYEF2,FZD2,SKIL,PRRX1,SMURF1,TNIK,DKK1,WNT5B,NOTCH3,ENAH,ADAM10,SRCIN1,TBX6,CYFIP2,DICER1,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,SLC1A3,VAPA,AFG3L2,PAFAH1B1,RAPGEF1,PLPPR5,CDH11,BMPR2,FRY,ARF4,GDNF,EFHD1,RAP2A,WNT9A,ZPR1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0035850	0.02	0.99	7	41	epithelial cell differentiation involved in kidney development	BP	1	EXT1,GPR4,GATA3,IQGAP1,ACTA2,MYO1E,GDNF	darkolivegreen	VSMC_M9
GO:0032270	0.02	0.99	82	1066	positive regulation of cellular protein metabolic process	BP	1	MALT1,TBK1,UBQLN1,TOPORS,AKAP9,JAK2,PSME4,STAP1,CCDC88A,ROCK2,INHBA,FYN,PSMC2,CEP295,NOX4,PICALM,NUB1,GATA3,CCNT2,RAB3GAP1,NDFIP2,DNAJC3,RIF1,OSBPL8,PPP1R12A,RPL26,NDFIP1,ILK,ITGA5,DHX29,LYN,EIF2AK3,LARP4,AGTR1,PFN2,DHX36,THBS1,ACVR1,NEDD9,CBLB,DYRK1A,BRD7,EHD4,LRRK2,TANK,UBE3A,SLC39A10,CUL3,TIMM17A,RAB3GAP2,NTRK3,PTPN1,EIF2B5,IQGAP1,FASTKD2,PTGS2,FERMT2,SMURF1,TNIK,PLD1,DKK1,FAS,TLR6,MSN,SRCIN1,CLPX,CYFIP2,UACA,PKM,MAP2K4,SEMA7A,PIN1,ITGA2,ITGA1,RICTOR,ENO1,BMPR2,CTGF,RAP2A,VGLL4,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0009628	0.02	0.99	70	891	response to abiotic stimulus	BP	1	EXT1,UBQLN1,AKAP9,CLOCK,ZMPSTE24,ROCK2,ITGB1,FYN,NOX4,GPR4,GATA3,DNAJC3,RPL26,LIG4,ATP2B1,BRCA2,IKBIP,LYN,ATP6V0A2,EIF2AK3,FBXL17,DYNLRB1,USP47,MAP1B,PLOD2,HK2,TLR2,ATP2A2,DHX36,THBS1,INO80,ATP1A1,TANK,TROVE2,ATP6V1A,CASP7,ITPR2,ST8SIA1,PLIN1,SEMA5B,EIF2B5,RBBP7,TLK2,TPR,PTGS2,DNAJA4,CPEB2,FMN2,FAS,ADSS,BNIP2,KCNMB1,CLK2,GPR65,PPM1D,MAP2K4,MYOCD,PIN1,ITGA2,SLC1A3,CIDEA,ENO1,COL11A1,RFWD3,DNAJB4,AQP3,CTGF,BDKRB2,EFHD1,ELOVL4	darkolivegreen	VSMC_M9
GO:0070925	0.02	0.99	58	705	organelle assembly	BP	1	AHI1,CEP120,UBQLN1,CEP41,PTPRD,HAUS6,SENP6,CENPC,CCDC88A,ACTR2,NOCT,ITGB1,RPF2,CEP295,ACTR3,RAB3GAP1,STAM2,VPS36,TUBGCP3,CEP83,TMF1,DHX29,CNOT7,UBXN2B,TMEM41B,IFT88,NEK1,ATP2A2,MAP9,ARL6,MTERF3,INO80,EHD4,LRRK2,TROVE2,RAB3GAP2,HAUS2,NEK7,NTRK3,CEP350,C10orf90,FASTKD2,TPR,CDKL1,SMURF1,TAPT1,KIAA0586,MSN,TPM1,FHOD3,TRAPPC8,CCP110,PAFAH1B1,SSX2IP,ARF4,FOPNL,MZT1,CFL2	darkolivegreen	VSMC_M9
GO:0034250	0.02	0.99	14	130	positive regulation of cellular amide metabolic process	BP	1	ROCK2,GSAP,PICALM,DNAJC3,RPL26,DHX29,LARP4,DHX36,THBS1,EIF2B5,FASTKD2,PLD1,PKM,ITGA2	darkolivegreen	VSMC_M9
GO:0035115	0.02	1.00	5	25	embryonic forelimb morphogenesis	BP	1	HOXA9,HOXA11,RDH10,SHOX2,WNT7A	darkolivegreen	VSMC_M9
GO:0035304	0.02	0.99	10	74	regulation of protein dephosphorylation	BP	1	JAK2,ROCK2,MGAT5,PPP1R12A,SLC39A10,BOD1L1,PIN1,ROCK1,ITGA1,PPP1R2	darkolivegreen	VSMC_M9
GO:0051767	0.02	1.00	4	17	nitric-oxide synthase biosynthetic process	BP	1	JAK2,TLR2,LRRK2,MAP2K4	darkolivegreen	VSMC_M9
GO:0051769	0.02	1.00	4	17	regulation of nitric-oxide synthase biosynthetic process	BP	1	JAK2,TLR2,LRRK2,MAP2K4	darkolivegreen	VSMC_M9
GO:0048864	0.02	0.99	10	72	stem cell development	BP	1	RDH10,ACVR1,CORO1C,SEMA5B,NRP2,TAPT1,SEMA7A,ANXA6,GDNF,WNT7A	darkolivegreen	VSMC_M9
GO:0043604	0.02	0.99	51	672	amide biosynthetic process	BP	1	ETF1,NOA1,ELOVL5,EIF5B,RARS2,ROCK2,DDX1,NOCT,EXOSC9,PIWIL4,DNAJC1,ST3GAL3,DARS,DNAJC3,RPL26,HSD17B12,DHX29,CNOT7,EIF2AK3,TMED2,EIF2S2,XRN1,PDE12,LARP4,CERS5,LTN1,DCP1A,DHX36,THBS1,GFM1,EIF4E,EPRS,IARS2,MRPL47,EIF2B5,FASTKD2,EIF3J,TPR,ZC3H15,PLD1,CPEB2,SAMD8,SRP9,TRIP4,PKM,ROCK1,ITGA2,GSPT1,TARS,ELOVL4,EIF1AX	darkolivegreen	VSMC_M9

GO:0050794	0.02	0.98	498	7581	regulation of cellular process	BP	1	SOCS6,LMAN1,MALT1,AHI1,UTRN,STXBP5,TBK1,CAND1,PLEKHG1,CEP120,RRM2B,AZIN1,ATP6V1C1,LRP12,EXT1,THBS2,CDKL3,CHADL,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,SLC35B4,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,SLC30A9,TOPORS,ABCB4,AKAP9,GCC2,TFPI2,GNG11,JAK2,CLOCK,EXOC1,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,ASPN,ZNF451,HEMGN,HDAC9,CAVIN4,SENP6,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,PDE1C,KBTBD2,SH3BP5L,ACTR2,THAP5,CHRM2,TES,CAV2,ROCK2,INHBA,PNPLA8,DDX1,NOCT,RAB3B,ITGB1,MPP7,RPF2,FYN,ZEB1,RINT1,KIF5B,CEP57,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,CCDC8,GSAP,NOX4,GPR4,RB1,RTN2,PICALM,TRDMT1,SUSD5,CBLC,CGREF1,CAMK1D,NUB1,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,AZI2,CYTH1,MBNL2,EDEM1,STK24,TNFAIP6,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,FAM98A,RPL26,UFM1,CAPN7,LIG4,PIK3R4,MYO16,CEBPZ,SUPT20H,ATP2B1,SMAD9,CCNA1,ATP11A,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,YIPF5,SOS1,PDS5B,BRCA2,UBA5,ILK,ITGA5,GPR84,DCHS1,HSPH1,TMF1,HOXC10,HSD17B12,DHX29,SCYL2,PARG,PLPP1,CDK8,CNOT7,RNF6,REM1,RASSF4,LYN,UBXN2B,MERTK,SACS,XPO4,ATP6V0A2,IFT88,IPO7,PDE7A,TCP11L1,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,SLC30A5,CHD1,SULF1,RIOK2,USP47,CCDC125,LNPEP,XRN1,PDE12,STOX2,MICAL2,FFAR4,MAP1B,APPL1,RDH10,LARP4,PI15,AGTR1,ACTR8,HK2,TLR2,PFN2,RASA1,ATP2A2,USO1,MAP9,MBNL1,LTN1,BRAP,DCP1A,DHX36,THBS1,NUCB2,GPR176,SHOX2,KCTD9,LIN54,PGAM4,ARL	darkolivegreen	VSMC_M9
GO:0035150	0.02	0.99	12	100	regulation of tube size	BP	1	EXT1,ROCK2,ATP2B1,AGTR1,PTGS2,ACTA2,KCNMB1,ROCK1,ITGA1,TBXA2R,BMPR2,BDKRB2	darkolivegreen	VSMC_M9
GO:0035296	0.02	0.99	12	100	regulation of tube diameter	BP	1	EXT1,ROCK2,ATP2B1,AGTR1,PTGS2,ACTA2,KCNMB1,ROCK1,ITGA1,TBXA2R,BMPR2,BDKRB2	darkolivegreen	VSMC_M9
GO:0097746	0.02	0.99	12	100	blood vessel diameter maintenance	BP	1	EXT1,ROCK2,ATP2B1,AGTR1,PTGS2,ACTA2,KCNMB1,ROCK1,ITGA1,TBXA2R,BMPR2,BDKRB2	darkolivegreen	VSMC_M9
GO:1903047	0.02	0.99	50	608	mitotic cell cycle process	BP	1	CDC23,CENPC,ZMPSTE24,CAV2,ROCK2,INHBA,ITGB1,RINT1,CCDC8,RB1,CDK3,RPL26,MYO16,CCNA1,CUL4A,PDS5B,BRCA2,DCTN6,UBXN2B,FBXL17,RIOK2,USP47,APPL1,RASA1,MAP9,ACVR1,INO80,BRD7,BRSK2,CUL3,EIF4E,ANK3,KLHL18,TPR,CDC27,NPAT,CLTC,PPM1D,PIN1,RBBP8,ROCK1,GSPT1,PAFAH1B1,RFWD3,CDK13,MZT1,E2F3,ZPR1,FBXL7,ZNF655	darkolivegreen	VSMC_M9
GO:0051650	0.02	0.99	16	143	establishment of vesicle localization	BP	1	MYO6,KIF5B,PICALM,TRAK1,TMED2,ARL6,LRRK2,CUL3,CCDC186,TRAK2,SEPT5,KIFAP3,MYO1E,MYO1C,PAFAH1B1,MYO1H	darkolivegreen	VSMC_M9
GO:0001707	0.02	0.99	8	53	mesoderm formation	BP	1	HOXA11,INHBA,ITGB1,ACVR1,DKK1,TBX6,ITGA2,BMPR2	darkolivegreen	VSMC_M9
GO:0006094	0.02	0.99	8	58	gluconeogenesis	BP	1	SLC35B4,SLC39A14,ATF3,TPI1,CLK2,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9
GO:0001704	0.02	0.99	12	93	formation of primary germ layer	BP	1	COL12A1,HOXA11,INHBA,ITGB1,ITGA5,ACVR1,ITGAV,DKK1,TBX6,ITGA2,COL11A1,BMPR2	darkolivegreen	VSMC_M9
GO:0030206	0.02	1.00	4	16	chondroitin sulfate biosynthetic process	BP	1	DSE,CSGALNACT2,CHSY1,CHST11	darkolivegreen	VSMC_M9
GO:0050729	0.02	0.99	11	93	positive regulation of inflammatory response	BP	1	WISP1,JAK2,CLOCK,STAP1,GPR4,AGTR1,TLR2,NFKBIZ,LRRK2,PTGS2,ITGA2	darkolivegreen	VSMC_M9
GO:0030512	0.02	0.99	9	64	negative regulation of transforming growth factor beta receptor signaling pathway	BP	1	ASPN,ZNF451,CAV2,SKIL,SMURF1,PIN1,CIDEA,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0061061	0.02	0.99	43	504	muscle structure development	BP	1	UTRN,HDAC9,CAVIN4,ZMPSTE24,IFRD1,CAV2,ITGB1,RB1,CCNT2,GPCPD1,ATP11A,ILK,ATP2A2,MBNL1,SHOX2,ACVR1,PDLIM5,DNER,CASP7,ATF3,SMTN,ADAM12,MYEF2,FZD2,DKK1,WNT5B,TPM1,ITGB1BP2,TRIP4,SGCD,FHOD3,MAP2K4,MYOCD,PIN1,MYOM1,AFG3L2,COL11A1,BMPR2,FOXN2,NOV,TMEM119,CFL2,IRX3	darkolivegreen	VSMC_M9
GO:0006401	0.02	0.99	23	237	RNA catabolic process	BP	1	ETF1,ROCK2,NOCT,EXOSC9,TRDMT1,UPF2,MTREX,CNOT7,XRN1,PDE12,DCP1A,DHX36,FASTKD2,MYEF2,ZC3H14,SMG8,DICER1,ROCK1,GSPT1,LSM5,FASTKD5,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0009056	0.02	0.98	141	2000	catabolic process	BP	1	SOCS6,MALT1,CDO1,TBK1,AZIN1,ATP6V1C1,EXT1,CDC23,ETF1,UBQLN1,PLAA,TOPORS,CLOCK,EXOC1,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,ROCK2,PNPLA8,NOCT,ITGB1,FYN,PSMB1,EXOSC9,PSMC2,UGGT1,TRDMT1,CBLC,ABHD1,UPF2,NUB1,RAB3GAP1,CLN5,NDFIP2,SUPT5H,DNAJC3,EDEM1,STAM2,VPS36,GPCPD1,UFM1,ABHD13,PIK3R4,SUPT20H,NDFIP1,CUL4A,UBA5,TMF1,USP12,MTREX,CNOT7,RNF6,UBXN2B,GRAMD1A,ATP6V0A2,TMEM41B,IFT88,PDE7A,FBXL17,TDG,ITCH,USP47,LNPEP,XRN1,PDE12,HK2,ATP2A2,LTN1,DCP1A,DHX36,PGAM4,GPD2,NUDT9,CBLB,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,ATP6V1A,BPNT1,RAB3GAP2,PSMD12,PTPN1,PLIN1,DERA,UBE4A,CCDC47,TLK2,NPL,PITHD1,FASTKD2,CDC27,MYEF2,TPI1,SMURF1,PLD1,FMN2,HK3,MSN,PHKG2,SPOP,DLST,TRIP4,OAZ2,CLPX,RLIM,ZC3H14,RBBP6,SMG8,C18orf25,CLTC,PKM,DICER1,GPRASP1,ATG4D,PIN1,TRAPPC8,ETFA,BAG5,ROCK1,BFAR,CIDEA,GSPT1,USP7,LSM5,PAFAH1B1,ACOT7,ENO1,ZDHHC7,FASTKD5,GDNF,DNAJB9,IMPA1,ZPR1,VGLL4,FBXL7,AKR1D1	darkolivegreen	VSMC_M9

GO:0051179	0.02	0.98	311	4586	localization	BP	1	LMAN1,MALT1,CDO1,AHI1,UTRN,MON2,STXBP5,TBC1D15,CEP120,AZIN1,ATP6V1C1,LRP12,EXT1,SLC39A7,SEC24A,WISP1,CDC23,SLC35B4,KDELR3,UBQLN1,CEP41,DENND4C,PLAA,SLC30A9,TOPORS,ABCB4,AKAP9,GCC2,TMEM165,JAK2,CLOCK,EXOC1,HDAC9,MYO6,CENPC,STAP1,CCDC88A,COX18,ZMPSTE24,UBE2J1,ACTR2,CAV2,ROCK2,INHBA,PNPLA8,DDX1,RAB3B,ITGB1,MPP7,RPF2,COG5,FYN,RINT1,KIF5B,DNAJC1,CEP295,SLC36A4,NOX4,RB1,RTN2,PICALM,CAMK1D,UPF2,ACTR3,MGAT5,GATA3,RAB3GAP1,CLN5,JMJD6,ESYT2,TRAK1,NDFIP2,CYTH1,EDEM1,STK24,TNFAIP6,OSBPL8,PPP1R12A,STAM2,PRPF40A,FAM98A,VPS36,UFM1,CAPN7,PIK3R4,ATP2B1,EEA1,ATP11A,CEP83,NDFIP1,STARD13,YIPF5,SOS1,BRCA2,NTN4,ILK,ITGA5,DCHS1,TMF1,SCYL2,REM1,ARL1,LYN,UBXN2B,MERTK,RAB2A,GRAMD1A,SLC16A12,XPO4,ATP6V0A2,IFT88,IPO7,NUP37,EIF2AK3,TMED2,PALLD,COPB2,SLC30A5,SULF1,RIOK2,CCDC125,FFAR4,MAP1B,APPL1,GDAP1,AGTR1,HK2,TLR2,PFN2,COPB1,ATP2A2,USO1,DCP1A,DHX36,THBS1,TM9SF3,PGAM4,ARL6,ACVR1,SLC39A14,SLC35B3,NEDD9,CBLB,ATP1A1,SPTBN5,EHD4,LRRK2,SNX19,BRSK2,ATP10A,UBE3A,SLC39A10,CUL3,MRS2,PHLDB2,DNER,TIMM17A,TRAPPC10,ATP6V1A,KPNA6,EPRS,IGF1R,GPR89A,RAB3GAP2,CCDC186,CORO1C,ITPR2,NTRK3,WWC3,TOMM20,PTPN1,GRK3,ATP11B,LARP7,KPNA1,SEMA5B,IDH2,VAPB,ABCB10,TRAK2,PRELID3B,C2CD2L,PIP5K1A,IQGAP1,CEP350,ANK3,OSBPL11,CD3G,CCDC47,HEATR5A,SH3KBP1,NRP2,ATP13A3,CREB3L2,TPR,CLEC14A,PTGS2,SEC23A,DNAJA4,SORCS2,SEPT5,ITGAV,FERMT2,VAMP4,ATP8B4,RTN3,KIFAP3,SMURF1,TAPT1,TNIK,KTN1,PLD1,BLZF1,ACTR10,AP4E1	darkolivegreen	VSMC_M9
GO:0034472	0.02	1.00	4	19	snRNA 3'-end processing	BP	1	EXOSC9,TOE1,INTS14,INTS6	darkolivegreen	VSMC_M9
GO:0061564	0.02	0.98	36	380	axon development	BP	1	EXT1,CDKL3,JAK2,ITGB1,FYN,KIF5B,PICALM,GATA3,TRAK1,STK24,SOS1,ILK,RNF6,SLC25A46,PALLD,MAP1B,SHOX2,BRSK2,CAMSAP2,ANOS1,SEMA5B,TRAK2,ANK3,NRP2,NCAM1,SKIL,NOTCH3,ENAH,SEMA7A,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,ZPR1,WNT7A	darkolivegreen	VSMC_M9
GO:0043277	0.02	0.99	6	37	apoptotic cell clearance	BP	1	JMJD6,MERTK,THBS1,ITGAV,XKR9,FCN1	darkolivegreen	VSMC_M9
GO:0051495	0.02	0.99	20	194	positive regulation of cytoskeleton organization	BP	1	CEP120,AKAP9,STAP1,CCDC88A,ACTR2,ROCK2,CEP295,NOX4,ACTR3,MAP1B,PFN2,NTRK3,FERMT2,TPM1,GPR65,RICTOR,SPIRE1,MYO1C,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:0018279	0.02	1.00	4	20	protein N-linked glycosylation via asparagine	BP	1	UBE2J1,UGGT1,MGAT5,ALG5	darkolivegreen	VSMC_M9
GO:0022402	0.02	0.98	74	951	cell cycle process	BP	1	CEP120,CDC23,RMI1,HAUS6,CLOCK,SENP6,CENPC,ZMPSTE24,ACTR2,CAV2,ROCK2,INHBA,ITGB1,RINT1,CEP295,CCDC8,RB1,ACTR3,CDK3,PPP1R12A,PRPF40A,RPL26,PIK3R4,MYO16,TUBGCP3,CCNA1,CUL4A,PDS5B,BRCA2,DCTN6,UBXN2B,MYBL1,FBXL17,RIOK2,USP47,APPL1,RASA1,MAP9,ACVR1,INO80,BRD7,BRSK2,CUL3,EIF4E,HAUS2,NEK7,SYCP2,ANK3,C10orf90,KLHL18,TPR,CDC27,NPAT,SEPT5,FMN2,CLTC,PPM1D,PIN1,CCP110,RBBP8,ROCK1,THOC1,SPIRE1,GSPT1,PAFAH1B1,RFWD3,SSX2IP,CDK13,CTGF,MZT1,E2F3,ZPR1,FBXL7,ZNF655	darkolivegreen	VSMC_M9
GO:0060351	0.02	0.99	5	25	cartilage development involved in endochondral bone morphogenesis	BP	1	EXT1,HOXA11,ZMPSTE24,SHOX2,ANXA6	darkolivegreen	VSMC_M9
GO:0051247	0.02	0.98	86	1140	positive regulation of protein metabolic process	BP	1	MALT1,TBK1,UBQLN1,TOPORS,AKAP9,JAK2,PSME4,STAP1,CCDC88A,ROCK2,INHBA,FYN,PSMC2,CEP295,GSAP,NOX4,PICALM,NUB1,GATA3,CCNT2,RAB3GAP1,NDFIP2,DNAJC3,RIF1,OSBPL8,PPP1R12A,RPL26,NDFIP1,ILK,ITGA5,DHX29,LYN,EIF2AK3,ITCH,LARP4,AGTR1,PFN2,DHX36,THBS1,ACVR1,NEDD9,CBLB,DYRK1A,BRD7,EHD4,LRRK2,TANK,UBE3A,SLC39A10,CUL3,TIMM17A,RAB3GAP2,NTRK3,PTPN1,ABCB10,EIF2B5,IQGAP1,FASTKD2,PTGS2,FERMT2,SMURF1,TNIK,PLD1,DKK1,FAS,TLR6,MSN,SRCIN1,OAZ2,CLPX,CYFIP2,UACA,PKM,MAP2K4,SEMA7A,PIN1,ITGA2,ITGA1,RICTOR,ENO1,BMPR2,CTGF,RAP2A,VGLL4,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0051654	0.02	0.99	5	27	establishment of mitochondrion localization	BP	1	TRAK1,MAP1B,TRAK2,ACTR10,ARMCX3	darkolivegreen	VSMC_M9
GO:0072595	0.03	0.99	6	38	maintenance of protein localization in organelle	BP	1	KDELR3,TOPORS,HK2,TAPT1,PDIA2,ANKRD13C	darkolivegreen	VSMC_M9
GO:0000278	0.03	0.98	58	729	mitotic cell cycle	BP	1	CDC23,CENPC,ZMPSTE24,CAV2,ROCK2,INHBA,ITGB1,RINT1,CCDC8,RB1,CDK3,AZI2,PPP1R12A,RPL26,MYO16,TUBGCP3,CCNA1,CUL4A,PDS5B,BRCA2,DCTN6,UBXN2B,MYBL1,FBXL17,RIOK2,USP47,APPL1,RASA1,MAP9,ACVR1,INO80,BRD7,BRSK2,CUL3,EIF4E,NEK7,IQGAP1,ANK3,KLHL18,TPR,CDC27,NPAT,TUBA4A,CLTC,PPM1D,PIN1,RBBP8,ROCK1,GSPT1,PAFAH1B1,RFWD3,SKA2,CDK13,MZT1,E2F3,ZPR1,FBXL7,ZNF655	darkolivegreen	VSMC_M9
GO:0010761	0.03	0.99	7	46	fibroblast migration	BP	1	ITGB1,ILK,APPL1,THBS1,CORO1C,PIP5K1A,NOV	darkolivegreen	VSMC_M9
GO:0016051	0.03	0.99	16	155	carbohydrate biosynthetic process	BP	1	EXT1,SLC35B4,UGP2,ST3GAL3,CSGALNACT2,SLC39A14,ATF3,TPI1,PHKG2,CLK2,CLTC,C1QTNF3,USP7,RANBP2,IMPA1,CHST11	darkolivegreen	VSMC_M9
GO:0006954	0.03	0.98	41	497	inflammatory response	BP	1	CDO1,TBK1,EXT1,WISP1,PLAA,JAK2,CLOCK,HDAC9,STAP1,ITGB1,FYN,NOX4,GPR4,RB1,CAMK1D,GATA3,TNFAIP6,NDFIP1,LYN,ITCH,FFAR4,APPL1,AGTR1,TLR2,THBS1,ACVR1,NFKBIZ,LRRK2,KPNA6,LTB4R,PTGS2,TLR6,SEMA7A,ITGA2,RICTOR,C1QTNF3,CD40LG,TBXA2R,WFDC1,BDKRB2,NOV	darkolivegreen	VSMC_M9

GO:0080134	0.03	0.98	74	970	regulation of response to stress	BP	1	TBK1,WISP1,UBQLN1,JAK2,CLOCK,NPAS2,STAP1,ZMPSTE24,ACTR2,ROCK2,PNPLA8,ITGB1,FYN,GPR4,RB1,GATA3,STK24,TNFAIP6,RIF1,RPL26,NDFIP1,CUL4A,PARG,CNOT7,LYN,EIF2AK3,TMED2,ITCH,USP47,FFAR4,APPL1,AGTR1,TLR2,THBS1,NFKBIZ,DYRK1A,LRRK2,PHLDB2,IGF1R,PTPN1,GPATCH3,MBTPS2,PTGS2,FERMT2,SKIL,PRRX1,TNIK,FMN2,FAS,AKT3,TLR6,SEMA7A,BAG5,THOC1,ITGA2,RICTOR,BFAR,C1QTNF3,SPIRE1,TBXA2R,PAFAH1B1,GADD45B,ENO1,WFDC1,RFWD3,CTGF,BDKRB2,EFHD1,DNAJB9,NOV,FCN1,RAP2A,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0010922	0.03	0.99	5	26	positive regulation of phosphatase activity	BP	1	JAK2,PPP1R12A,SLC39A10,ITGA2,ITGA1	darkolivegreen	VSMC_M9
GO:0065007	0.03	0.98	543	8375	biological regulation	BP	1	SOCS6,LMAN1,MALT1,CDO1,AHI1,PHACTR2,UTRN,STXBP5,TBK1,CAND1,PLEKHG1,TBC1D15,CEP120,RRM2B,AZIN1,ATP6V1C1,LRP12,EXT1,THBS2,SLC39A7,CDKL3,CHADL,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,SLC35B4,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,SLC30A9,TOPORS,ABCB4,AKAP9,GCC2,TFPI2,GNG11,TMEM165,JAK2,CLOCK,EXOC1,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,ASPN,ZNF451,HEMGN,HDAC9,CAVIN4,SENP6,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,PDE1C,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,CHRM2,TES,CAV2,ROCK2,INHBA,PNPLA8,DDX1,NOCT,RAB3B,ITGB1,MPP7,RPF2,FYN,ZEB1,RINT1,KIF5B,CEP57,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,CCDC8,GSAP,NOX4,GPR4,RB1,RTN2,PICALM,ZC3H13,CYP27C1,TRDMT1,SUSD5,CBLC,CGREF1,CAMK1D,UPF2,NUB1,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,PAX1,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,AZI2,CYTH1,MBNL2,EDEM1,STK24,TNFAIP6,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,FAM98A,TMTC2,RPL26,UFM1,CAPN7,LIG4,PIK3R4,MYO16,CEBPZ,SUPT20H,ATP2B1,SMAD9,CCNA1,ATP11A,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,YIPF5,SOS1,PDS5B,BRCA2,NTN4,UBA5,ILK,ITGA5,GPR84,DCHS1,HSPH1,TMF1,HOXC10,ERI1,HSD17B12,DHX29,SCYL2,PARG,PLPP1,CDK8,CNOT7,RNF6,REM1,ARL1,RASSF4,LYN,PPP2R3A,UBXN2B,MERTK,SACS,XPO4,ATP6V0A2,IFT88,IPO7,PDE7A,TCP11L1,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,SLC30A5,CHD1,SULF1,RIOK2,USP47,CCDC125,LNPEP,XRN1,PDE12,STOX2,MICAL2,FFAR4,MAP1B,APPL1,RDH10,LARP4,PI15,AGTR1,ACTR8,HK2,TLR2,PFN2,RA	darkolivegreen	VSMC_M9
GO:0043388	0.03	0.99	6	40	positive regulation of DNA binding	BP	1	JAK2,RB1,GATA3,MYOCD,ITGA2,GTF2B	darkolivegreen	VSMC_M9
GO:0035313	0.03	1.00	4	16	wound healing, spreading of epidermal cells	BP	1	ITGA5,PHLDB2,FERMT2,WNT7A	darkolivegreen	VSMC_M9
GO:0002040	0.03	0.99	13	114	sprouting angiogenesis	BP	1	HDAC9,ITGB1,JMJD6,STARD13,ITGA5,AGTR1,THBS1,CLEC14A,PTGS2,AKT3,SRPX2,PKM,TBXA2R	darkolivegreen	VSMC_M9
GO:0048332	0.03	0.99	8	55	mesoderm morphogenesis	BP	1	HOXA11,INHBA,ITGB1,ACVR1,DKK1,TBX6,ITGA2,BMPR2	darkolivegreen	VSMC_M9
GO:0000904	0.03	0.98	50	562	cell morphogenesis involved in differentiation	BP	1	EXT1,CDKL3,PTPRD,ACTR2,ITGB1,FYN,KIF5B,RB1,PICALM,GATA3,TRAK1,SOS1,NTN4,ILK,RNF6,MERTK,PALLD,MAP1B,DHX36,SHOX2,NEDD9,LRRK2,BRSK2,PDLIM5,UBE3A,CUL3,CORO1C,ANOS1,SEMA5B,TRAK2,ANK3,NRP2,NCAM1,ITGAV,FERMT2,SKIL,TNIK,NOTCH3,ENAH,ADAM10,SRCIN1,SEMA7A,SLC1A3,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0051241	0.03	0.98	59	743	negative regulation of multicellular organismal process	BP	1	THBS2,CDKL3,CHADL,WISP1,JAK2,ASPN,HDAC9,ROCK2,INHBA,GPR4,RB1,GATA3,LRRC32,ATP2B1,NDFIP1,CUL4A,STARD13,BRCA2,HOXC10,RNF6,LYN,MERTK,EIF2AK3,ITCH,SULF1,LNPEP,FFAR4,TLR2,PFN2,ATP2A2,THBS1,ATP1A1,CHSY1,CORO1C,NTRK3,WWC3,SEMA5B,IDH2,TRAK2,GPATCH3,PTGS2,DNAJA4,DKK1,TLR6,TLE3,DICER1,MYOCD,SEMA7A,ROCK1,THOC1,C1QTNF3,CIDEA,TBXA2R,BMPR2,NOV,WNT9A,VGLL4,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0090066	0.03	0.98	37	418	regulation of anatomical structure size	BP	1	EXT1,CDKL3,ACTR2,ROCK2,RAB3B,PICALM,ACTR3,ATP2B1,ILK,RNF6,MAP1B,AGTR1,PFN2,RASA1,SPTBN5,LRRK2,SEMA5B,PTGS2,ACTA2,AKT3,MSN,KCNMB1,CYFIP2,FHOD3,SEMA7A,ROCK1,ITGA1,RICTOR,SPIRE1,MYO1C,TBXA2R,PAFAH1B1,VAV2,BMPR2,BDKRB2,CFL2,WNT7A	darkolivegreen	VSMC_M9
GO:0060993	0.03	0.99	10	77	kidney morphogenesis	BP	1	AHI1,HOXA11,ZMPSTE24,GATA3,ILK,DCHS1,GCNT4,LRRK2,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0032784	0.03	0.99	7	49	regulation of DNA-templated transcription, elongation	BP	1	CCNT2,SUPT5H,SETD5,LARP7,THOC1,ZNF326,CDK13	darkolivegreen	VSMC_M9
GO:0000226	0.03	0.98	44	522	microtubule cytoskeleton organization	BP	1	CEP120,HAUS6,AKAP9,GCC2,TXNDC9,SENP6,CCDC88A,ROCK2,ITGB1,CEP57,CEP295,CCDC8,PPP1R12A,TUBGCP3,BRCA2,DCTN6,UBXN2B,MAP1B,MAP9,INO80,DYRK1A,BRSK2,PHLDB2,CAMSAP2,HAUS2,NEK7,CEP350,C10orf90,HDGFL3,TPR,VAMP4,TUBA4A,FMN2,CLTC,CCP110,SS18,ROCK1,SPIRE1,PAFAH1B1,SSX2IP,SKA2,FOPNL,MZT1,ZPR1	darkolivegreen	VSMC_M9
GO:0030204	0.03	0.99	5	26	chondroitin sulfate metabolic process	BP	1	EXT1,DSE,CSGALNACT2,CHSY1,CHST11	darkolivegreen	VSMC_M9
GO:0019319	0.03	0.99	8	61	hexose biosynthetic process	BP	1	SLC35B4,SLC39A14,ATF3,TPI1,CLK2,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9

GO:0080090	0.03	0.98	284	4206	regulation of primary metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,AZIN1,PHF20L1,KHDRBS3,ETF1,SLC35B4,UBQLN1,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,JAK2,CLOCK,NPAS2,ELOVL5,EIF5B,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,SH3BP5L,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,GSAP,NOX4,RB1,RTN2,PICALM,TRDMT1,CBLC,CAMK1D,NUB1,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,MBNL2,RIF1,OSBPL8,PPP1R12A,RPL26,PIK3R4,CEBPZ,SUPT20H,SMAD9,CCNA1,NR2C1,NDFIP1,CUL4A,BRCA2,ILK,ITGA5,TMF1,HOXC10,DHX29,PARG,PLPP1,CNOT7,RNF6,LYN,IPO7,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,MICAL2,RDH10,LARP4,PI15,AGTR1,ACTR8,TLR2,PFN2,RASA1,MBNL1,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,TBX15,UBE3A,SLC39A10,CUL3,EIF4E,TDP2,UCHL5,TIMM17A,KPNA6,EPRS,RAB3GAP2,CORO1C,ANOS1,NEK7,NTRK3,WWC3,PTPN1,LARP7,KPNA1,CLK1,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,IQGAP1,RBBP7,EDRF1,BCLAF3,TLK2,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,PTGS2,MYEF2,FZD2,CWC22,NPAT,ITGAV,MYNN,FERMT2,SKIL,PRRX1,RTN3,SMURF1,TNIK,PLD1,TNFAIP8L3,CPEB2,SAMD8,BOD1L1,DKK1,FMN2,FAS,NOTCH3,SRP9,TLR6,MAGED2,MSN,SRCIN1,PHKG2,SPOP,CLK2,TRIP4,TBX6,OAZ2,CLPX,RLIM,MAGEE2,ZC3H14,CYFIP2,TLE3,SMG8,UACA,CLTC,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MAP2K4,MYOCD,SE	darkolivegreen	VSMC_M9
GO:0007498	0.03	0.99	11	89	mesoderm development	BP	1	EXT1,JAK2,HOXA11,INHBA,ITGB1,ACVR1,DKK1,TBX6,ITGA2,BMPR2,IRX3	darkolivegreen	VSMC_M9
GO:0043161	0.03	0.98	32	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,UBE2J1,PSMC2,NUB1,EDEM1,CUL4A,UBXN2B,FBXL17,ITCH,LTN1,LRRK2,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,CDC27,SMURF1,SPOP,TRIP4,BAG5,BFAR,USP7,DNAJB9,FBXL7	darkolivegreen	VSMC_M9
GO:0080135	0.03	0.98	45	553	regulation of cellular response to stress	BP	1	UBQLN1,NPAS2,ZMPSTE24,ACTR2,ROCK2,PNPLA8,FYN,STK24,RIF1,RPL26,CUL4A,PARG,LYN,EIF2AK3,TMED2,ITCH,USP47,DYRK1A,LRRK2,IGF1R,PTPN1,MBTPS2,PTGS2,SKIL,PRRX1,TNIK,FMN2,FAS,AKT3,TLR6,BAG5,THOC1,BFAR,SPIRE1,PAFAH1B1,GADD45B,ENO1,RFWD3,CTGF,BDKRB2,EFHD1,DNAJB9,RAP2A,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0048598	0.03	0.98	41	469	embryonic morphogenesis	BP	1	AHI1,LRIG3,EXT1,COL12A1,MYO6,HOXA9,HOXA10,HOXA11,ROCK2,INHBA,ITGB1,GATA3,SUPT20H,SOS1,ITGA5,TMED2,SULF1,MICAL2,RDH10,MBNL1,SHOX2,ACVR1,IRX5,TBX15,CUL3,PHLDB2,FZD2,ITGAV,PRRX1,DKK1,WNT5B,TBX6,ROCK1,ITGA2,COL11A1,PRKACB,BMPR2,GDNF,CHST11,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0010629	0.03	0.98	60	766	negative regulation of gene expression	BP	1	TBK1,ETF1,HDAC9,ZMPSTE24,ROCK2,INHBA,NOCT,FYN,EXOSC9,PIWIL4,RB1,PICALM,UPF2,GATA3,LRRC32,NDFIP2,ATP2B1,NDFIP1,TMF1,ERI1,CNOT7,MERTK,EIF2AK3,SMARCA5,ITCH,XRN1,PDE12,FFAR4,DCP1A,DHX36,THBS1,DYRK1A,LRRK2,EIF4E,KIAA1551,EPRS,GPATCH3,FASTKD2,TPR,MYEF2,CPEB2,SRP9,TLR6,ADAM10,ZC3H14,SMG8,DICER1,PPM1D,MYOCD,ROCK1,THOC1,C1QTNF3,CIDEA,GSPT1,ZC3H7A,LSM5,MIR186,FASTKD5,GDNF,CTGF	darkolivegreen	VSMC_M9
GO:0043632	0.03	0.98	46	561	modification-dependent macromolecule catabolic process	BP	1	CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,UBA6,ZMPSTE24,UBE2J1,EXOSC9,PSMC2,CBLC,NUB1,NDFIP2,EDEM1,VPS36,NDFIP1,CUL4A,USP12,RNF6,UBXN2B,FBXL17,ITCH,USP47,LTN1,LRRK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,CDC27,SMURF1,SPOP,TRIP4,RLIM,RBBP6,C18orf25,BAG5,BFAR,USP7,DNAJB9,FBXL7	darkolivegreen	VSMC_M9
GO:0045987	0.03	0.99	4	20	positive regulation of smooth muscle contraction	BP	1	PTGS2,MYOCD,ITGA2,TBXA2R	darkolivegreen	VSMC_M9
GO:0015031	0.03	0.98	96	1301	protein transport	BP	1	LMAN1,MON2,STXBP5,TBC1D15,SEC24A,KDELR3,CEP41,DENND4C,GCC2,JAK2,CLOCK,EXOC1,MYO6,COX18,UBE2J1,RAB3B,COG5,FYN,RINT1,KIF5B,DNAJC1,RTN2,TRAK1,NDFIP2,EDEM1,STAM2,VPS36,UFM1,PIK3R4,NDFIP1,YIPF5,ARL1,RAB2A,XPO4,IPO7,NUP37,TMED2,COPB2,APPL1,GDAP1,TLR2,COPB1,USO1,ARL6,CBLB,LRRK2,SNX19,BRSK2,TIMM17A,KPNA6,GPR89A,RAB3GAP2,CCDC186,TOMM20,PTPN1,KPNA1,IDH2,TRAK2,C2CD2L,ANK3,CD3G,TPR,PTGS2,SEC23A,SORCS2,SMURF1,KTN1,BLZF1,AP4E1,FMN2,SRP9,SRCIN1,OAZ2,CLTC,ATG4D,MYOM1,NUP155,RAB31,C1QTNF3,SPIRE1,MYO1C,PAFAH1B1,PMPCA,ZDHHC7,RANBP2,KPNA4,TOMM20L,RAB6A,ARF4,SEC63,NOV,E2F3,SRP19,ZPR1,NUP35,SCAMP1	darkolivegreen	VSMC_M9
GO:0060986	0.03	0.99	5	27	endocrine hormone secretion	BP	1	INHBA,GATA3,TMF1,AGTR1,C1QTNF3	darkolivegreen	VSMC_M9
GO:0001774	0.03	0.99	5	29	microglial cell activation	BP	1	JAK2,STAP1,TLR2,LRRK2,TLR6	darkolivegreen	VSMC_M9
GO:0018196	0.03	0.99	4	21	peptidyl-asparagine modification	BP	1	UBE2J1,UGGT1,MGAT5,ALG5	darkolivegreen	VSMC_M9
GO:0120009	0.03	0.99	6	38	intermembrane lipid transfer	BP	1	OSBPL8,GRAMD1A,PRELID3B,C2CD2L,TNFAIP8L3,PLEKHA3	darkolivegreen	VSMC_M9
GO:0030050	0.03	0.99	4	17	vesicle transport along actin filament	BP	1	MYO6,MYO1E,MYO1C,MYO1H	darkolivegreen	VSMC_M9
GO:0090101	0.03	0.99	12	101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ASPN,ZNF451,CAV2,ACVR1,SKIL,SMURF1,DKK1,PIN1,CIDEA,NOV,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0034655	0.03	0.98	29	335	nucleobase-containing compound catabolic process	BP	1	ETF1,ROCK2,NOCT,EXOSC9,TRDMT1,UPF2,MTREX,CNOT7,PDE7A,TDG,XRN1,PDE12,DCP1A,DHX36,NUDT9,DERA,FASTKD2,MYEF2,ZC3H14,SMG8,DICER1,ROCK1,CIDEA,GSPT1,LSM5,ACOT7,FASTKD5,GDNF,ZPR1	darkolivegreen	VSMC_M9

GO:0050764	0.03	0.99	8	59	regulation of phagocytosis	BP	1	STAP1,CAMK1D,MERTK,APPL1,TLR2,ITGAV,ITGA2,RAB31	darkolivegreen	VSMC_M9
GO:0071705	0.03	0.98	116	1609	nitrogen compound transport	BP	1	LMAN1,MON2,STXBP5,TBC1D15,AZIN1,SEC24A,SLC35B4,KDELR3,CEP41,DENND4C,GCC2,JAK2,CLOCK,EXOC1,MYO6,COX18,UBE2J1,RAB3B,ITGB1,COG5,FYN,RINT1,KIF5B,DNAJC1,SLC36A4,RTN2,UPF2,RAB3GAP1,TRAK1,NDFIP2,EDEM1,STAM2,VPS36,UFM1,PIK3R4,ATP11A,NDFIP1,YIPF5,ARL1,LYN,RAB2A,SLC16A12,XPO4,IPO7,NUP37,TMED2,COPB2,FFAR4,APPL1,GDAP1,TLR2,COPB1,USO1,ARL6,SLC35B3,CBLB,LRRK2,SNX19,BRSK2,TIMM17A,KPNA6,GPR89A,RAB3GAP2,CCDC186,TOMM20,PTPN1,ATP11B,KPNA1,IDH2,TRAK2,C2CD2L,ANK3,CD3G,ATP13A3,TPR,PTGS2,SEC23A,SORCS2,SMURF1,KTN1,BLZF1,AP4E1,FMN2,SRP9,SRCIN1,OAZ2,CLTC,ATG4D,THOC1,MYOM1,NUP155,SLC1A3,RAB31,C1QTNF3,SPIRE1,MYO1C,PAFAH1B1,PMPCA,ZDHHC7,SLC25A24,RANBP2,AQP3,KPNA4,PLEKHA3,TOMM20L,RAB6A,SLC35D1,ARF4,GDNF,SEC63,NOV,E2F3,SRP19,ZPR1,NUP35,SCAMP1	darkolivegreen	VSMC_M9
GO:0050650	0.03	0.99	4	18	chondroitin sulfate proteoglycan biosynthetic process	BP	1	DSE,CSGALNACT2,CHSY1,CHST11	darkolivegreen	VSMC_M9
GO:0071702	0.03	0.98	135	1891	organic substance transport	BP	1	LMAN1,MON2,STXBP5,TBC1D15,AZIN1,SEC24A,SLC35B4,KDELR3,CEP41,DENND4C,ABCB4,GCC2,JAK2,CLOCK,EXOC1,MYO6,COX18,UBE2J1,INHBA,PNPLA8,RAB3B,ITGB1,COG5,FYN,RINT1,KIF5B,DNAJC1,SLC36A4,RTN2,UPF2,RAB3GAP1,ESYT2,TRAK1,NDFIP2,EDEM1,OSBPL8,STAM2,VPS36,UFM1,PIK3R4,ATP11A,NDFIP1,YIPF5,TMF1,ARL1,LYN,RAB2A,GRAMD1A,SLC16A12,XPO4,IPO7,NUP37,TMED2,COPB2,FFAR4,APPL1,GDAP1,AGTR1,HK2,TLR2,COPB1,USO1,THBS1,ARL6,SLC35B3,CBLB,LRRK2,SNX19,BRSK2,ATP10A,TIMM17A,KPNA6,EPRS,GPR89A,RAB3GAP2,CCDC186,TOMM20,PTPN1,ATP11B,KPNA1,IDH2,TRAK2,PRELID3B,C2CD2L,ANK3,OSBPL11,CD3G,ATP13A3,TPR,PTGS2,SEC23A,SORCS2,ITGAV,ATP8B4,SMURF1,KTN1,BLZF1,AP4E1,TNFAIP8L3,FMN2,SRP9,SRCIN1,OAZ2,CLTC,ATG4D,THOC1,MYOM1,NUP155,SLC1A3,RAB31,C1QTNF3,SPIRE1,MYO1C,PAFAH1B1,PMPCA,ZDHHC7,SLC25A24,RANBP2,AQP3,KPNA4,XKR9,PLEKHA3,TOMM20L,RAB6A,SLC35D1,ARF4,GDNF,SEC63,BDKRB2,NOV,E2F3,SRP19,ZPR1,NUP35,SCAMP1	darkolivegreen	VSMC_M9
GO:0045332	0.03	0.99	6	35	phospholipid translocation	BP	1	ABCB4,ATP11A,ATP10A,ATP11B,ATP8B4,XKR9	darkolivegreen	VSMC_M9
GO:0035987	0.03	0.99	6	34	endodermal cell differentiation	BP	1	COL12A1,INHBA,ITGA5,ITGAV,DKK1,COL11A1	darkolivegreen	VSMC_M9
GO:0050775	0.03	0.99	6	35	positive regulation of dendrite morphogenesis	BP	1	CDKL3,PTPRD,ACTR2,ILK,DHX36,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0032233	0.03	0.99	8	56	positive regulation of actin filament bundle assembly	BP	1	CCDC88A,ROCK2,NOX4,PFN2,FERMT2,TPM1,GPR65,CTGF	darkolivegreen	VSMC_M9
GO:0006936	0.03	0.98	24	256	muscle contraction	BP	1	UTRN,AKAP9,CHRM2,ROCK2,ATP2B1,SULF1,ATP2A2,ATP1A1,LTB4R,SMTN,PTGS2,ACTA2,TPM1,MYOCD,ANXA6,ROCK1,ITGA2,MYOM1,NUP155,TBXA2R,ENO1,GDNF,CTGF,BDKRB2	darkolivegreen	VSMC_M9
GO:0030705	0.03	0.98	18	173	cytoskeleton-dependent intracellular transport	BP	1	MYO6,CCDC88A,KIF5B,TRAK1,IFT88,MAP1B,CCDC186,TRAK2,KIFAP3,ACTR10,MYO1E,ARMCX3,MYO1C,PAFAH1B1,KIF1B,SSX2IP,MYO1H,RAB6A	darkolivegreen	VSMC_M9
GO:0001755	0.03	0.99	7	47	neural crest cell migration	BP	1	ACVR1,CORO1C,SEMA5B,NRP2,SEMA7A,ANXA6,GDNF	darkolivegreen	VSMC_M9
GO:0019941	0.03	0.98	45	550	modification-dependent protein catabolic process	BP	1	CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,UBA6,ZMPSTE24,UBE2J1,PSMC2,CBLC,NUB1,NDFIP2,EDEM1,VPS36,NDFIP1,CUL4A,USP12,RNF6,UBXN2B,FBXL17,ITCH,USP47,LTN1,LRRK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,CDC27,SMURF1,SPOP,TRIP4,RLIM,RBBP6,C18orf25,BAG5,BFAR,USP7,DNAJB9,FBXL7	darkolivegreen	VSMC_M9
GO:0072659	0.03	0.98	23	239	protein localization to plasma membrane	BP	1	DENND4C,CCDC88A,ROCK2,RAB3B,ITGB1,KIF5B,PICALM,DCHS1,TMED2,APPL1,EHD4,PIP5K1A,ANK3,SEC23A,SMURF1,TNIK,BLZF1,CLTC,PIGW,ROCK1,RAB31,ZDHHC7,RAP2A	darkolivegreen	VSMC_M9
GO:0010952	0.03	0.98	14	142	positive regulation of peptidase activity	BP	1	MALT1,JAK2,PSME4,ROCK2,FYN,PICALM,LYN,EIF2AK3,TANK,FAS,CLPX,CYFIP2,UACA,CTGF	darkolivegreen	VSMC_M9
GO:0019674	0.03	0.99	4	21	NAD metabolic process	BP	1	HK2,GPD2,HK3,ENO1	darkolivegreen	VSMC_M9
GO:0071559	0.03	0.98	21	205	response to transforming growth factor beta	BP	1	ASPN,ZNF451,CAV2,ROCK2,FYN,NOX4,LRRC32,SMAD9,APPL1,THBS1,ACVR1,FERMT2,SKIL,SMURF1,MYOCD,PIN1,ROCK1,CIDEA,PMEPA1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0001504	0.03	0.99	4	21	neurotransmitter uptake	BP	1	RAB3B,ITGB1,SLC1A3,GDNF	darkolivegreen	VSMC_M9
GO:0060548	0.03	0.98	58	754	negative regulation of cell death	BP	1	MALT1,AHI1,RRM2B,WISP1,TOPORS,JAK2,NPAS2,ITGB1,FYN,RB1,CAMK1D,GATA3,DNAJC3,UFM1,LIG4,ILK,ITGA5,TMF1,MERTK,ITCH,USP47,PDE12,FFAR4,RASA1,THBS1,ACVR1,LRRK2,SLC39A10,IGF1R,NTRK3,PTPN1,SYCP2,PTGS2,ITGAV,FERMT2,KIFAP3,VDAC2,DKK1,FMN2,FAS,ADAM10,BNIP2,MAP2K4,MYOCD,PIN1,BAG5,BFAR,CIDEA,CD40LG,ENO1,ARF4,GDNF,CTGF,BDKRB2,NOV,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0006470	0.03	0.98	22	228	protein dephosphorylation	BP	1	PPM1H,PTPRD,JAK2,ROCK2,MGAT5,PPP1R12A,ACPP,PPP2R3A,PPP2R2A,PDP1,LRRK2,SLC39A10,PTPN1,BOD1L1,PPM1D,PIN1,ROCK1,ITGA1,PPP4R1,PTPN12,PPTC7,PPP1R2	darkolivegreen	VSMC_M9
GO:0014070	0.03	0.98	56	703	response to organic cyclic compound	BP	1	CDO1,ABCB4,AKAP9,JAK2,CLOCK,ACTR2,CHRM2,CAV2,ROCK2,INHBA,DDX1,NOX4,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,LYN,GRAMD1A,XRN1,PDE12,MAP1B,GDAP1,TLR2,DHX36,THBS1,PPP2R2A,ATP1A1,LRRK2,UBE3A,EIF4E,CASP7,ITPR2,NTRK3,TOMM20,RBBP7,PTGS2,ADSS,MSN,KCNMB1,TRIP4,RBBP8,ITGA2,SLC1A3,CIDEA,TBXA2R,RAPGEF1,WFDC1,PRKACB,AQP3,CTGF,PAQR8,PMEPA1,WNT7A	darkolivegreen	VSMC_M9

GO:0050773	0.03	0.99	11	87	regulation of dendrite development	BP	1	CDKL3,PTPRD,ACTR2,CAMK1D,ILK,DHX36,CAMSAP2,IQGAP1,TNIK,PAFAH1B1,RAP2A	darkolivegreen	VSMC_M9
GO:0060996	0.03	0.99	11	87	dendritic spine development	BP	1	UBA6,ACTR2,DHX36,LRRK2,PDLIM5,UBE3A,ADAM10,SRCIN1,PAFAH1B1,ARF4,WNT7A	darkolivegreen	VSMC_M9
GO:1901576	0.03	0.97	286	4324	organic substance biosynthetic process	BP	1	SOCS6,MALT1,CDO1,AHI1,TBK1,CAND1,RRM2B,AZIN1,EXT1,DSE,PHF20L1,ETF1,SLC35B4,RMI1,SLC30A9,TOPORS,TMEM165,JAK2,CLOCK,NPAS2,NOA1,ELOVL5,EIF5B,POLR2B,GNE,MGAT4A,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,ZEB1,EXOSC9,PIWIL4,DNAJC1,UGGT1,PDSS1,RB1,SUCLA2,PICALM,ABHD1,CAMK1D,ST3GAL3,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,RIF1,PPP1R12A,TMTC2,RPL26,KDELC1,LIG4,CEBPZ,SUPT20H,ALG5,SMAD9,NR2C1,BRCA2,ILK,B3GLCT,HSPH1,TMF1,GALNT7,HOXC10,HSD17B12,DHX29,PLPP1,CNOT7,RNF6,CSGALNACT2,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,USP47,MAT2A,XRN1,PDE12,STOX2,BDP1,MICAL2,APPL1,RDH10,PLOD2,LARP4,ACTR8,CERS5,ALDH18A1,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,GFM1,LIN54,ZDHHC16,ACVR1,WDR75,SLC39A14,IRX5,MTERF3,INO80,GCNT4,SLC35B3,ETNK2,ATP1A1,DYRK1A,BRD7,MAN1A2,ERG,LRRK2,TBX15,UBE3A,MBOAT1,CUL3,EIF4E,TDP2,TROVE2,CHSY1,ATP6V1A,KPNA6,EPRS,BPNT1,IARS2,RAB3GAP2,GALNT17,NEK7,MRPL47,WWC3,ETNK1,LARP7,ST8SIA1,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,PIP5K1A,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,GATM,PTGS2,FAM20B,MYEF2,FZD2,ZC3H15,NPAT,TPI1,MYNN,GNPNAT1,SKIL,PRRX1,PLD1,CPEB2,SAMD8,BOD1L1,DKK1,PAPSS2,ADSS,NOTCH3,ACBD3,SRP9,TLR6,MAGED2,PHKG2,CLK2,TRIP4,TBX6,OAZ2,RLIM,MAGEE2,RBBP6,TLE3,C	darkolivegreen	VSMC_M9
GO:0030154	0.03	0.97	210	2966	cell differentiation	BP	1	MALT1,AHI1,CAND1,CEP120,LRP12,EXT1,CDKL3,CHADL,WISP1,PTPRD,PLAA,TOPORS,JAK2,CLOCK,FBXO9,BZW2,HEMGN,HDAC9,CAVIN4,COL12A1,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA11,ZMPSTE24,UBE2J1,ACTR2,JFRD1,CAV2,ROCK2,INHBA,NOCT,ITGB1,FYN,ZEB1,KIF5B,CEP57,PIWIL4,PSMC2,FNDC3A,GPR4,RB1,PICALM,CAMK1D,GATA3,CLN5,JMJD6,TRAK1,AZI2,STK24,OSBPL8,LIG4,MYO16,SMAD9,ATP11A,NR2C1,NDFIP1,CUL4A,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,DCHS1,TMF1,SCYL2,RNF6,LYN,MERTK,IFT88,MYBL1,EIF2AK3,SLC25A46,FBXL17,PALLD,ITCH,SULF1,MICAL2,FFAR4,MAP1B,RDH10,AGTR1,TLR2,RASA1,ATP2A2,VCAN,MBNL1,DHX36,SHOX2,ACVR1,SLC39A14,IRX5,NFKBIZ,NEDD9,ERG,LRRK2,SNX19,TBX15,BRSK2,PDLIM5,UBE3A,MBOAT1,CUL3,EIF4E,PHLDB2,TDP2,DNER,CHSY1,CAMSAP2,GPR89A,CASP7,CORO1C,ANOS1,NTRK3,LARP7,SEMA5B,IDH2,ABCB10,EIF2B5,TRAK2,ATF3,PIP5K1A,IQGAP1,ANK3,OSBPL11,CD3G,CCDC47,ADAM12,NRP2,HDGFL3,PITHD1,ZFX,CREB3L2,PTGS2,NCAM1,MYEF2,FZD2,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,DKK1,FMN2,ACTA2,RBM47,WNT5B,NOTCH3,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,TRIP4,TBX6,CYFIP2,CLTC,DICER1,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,BAG5,ROCK1,ITGA2,ITGA1,SLC1A3,VAPA,AFG3L2,C1QTNF3,CD40LG,PAFAH1B1,GADD45B,RAPGEF1,ZDHHC7,COL11A1,PLPPR5,CDH11,BMPR2,AQP3,FRY,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,EFHD1,DNAJB9,PAQR8,NOV,RAP2A,WNT9A,ZPR1,SRD5A2,TMEM119,CHST11,UBE2V1,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0006891	0.03	0.99	5	29	intra-Golgi vesicle-mediated transport	BP	1	COG5,COPB2,COPB1,TRAPPC10,RAB6A	darkolivegreen	VSMC_M9
GO:0006029	0.03	0.99	9	67	proteoglycan metabolic process	BP	1	EXT1,DSE,CSGALNACT2,SULF1,CHSY1,FAM20B,COL11A1,BMPR2,CHST11	darkolivegreen	VSMC_M9
GO:0071577	0.03	0.99	4	21	zinc ion transmembrane transport	BP	1	SLC39A7,SLC30A5,SLC39A14,SLC39A10	darkolivegreen	VSMC_M9
GO:0001501	0.03	0.98	36	413	skeletal system development	BP	1	EXT1,CHADL,WISP1,HOXA9,HOXA10,HOXA11,ZMPSTE24,PAX1,DCHS1,EIF2AK3,SULF1,RDH10,VCAN,SHOX2,SLC39A14,IRX5,SNX19,TBX15,CHSY1,MBTPS2,CREB3L2,PRRX1,TAPT1,PAPSS2,WNT5B,ANXA6,PAFAH1B1,COL11A1,CDH11,BMPR2,CTGF,NOV,WNT9A,TMEM119,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0034330	0.04	0.98	48	541	cell junction organization	BP	1	EXT1,THBS2,PTPRD,ACTR2,ROCK2,MPP7,FYN,SETD5,THSD1,DCHS1,MAP1B,TLR2,DHX36,THBS1,LRRK2,PDLIM5,UBE3A,PHLDB2,DNER,IGF1R,CORO1C,NTRK3,PIP5K1A,IQGAP1,ANK3,NRP2,FERMT2,DKK1,ADAM10,SRCIN1,SRPX2,PIN1,ROCK1,ITGA2,AFG3L2,GPC4,MYO1C,PAFAH1B1,AJM1,RAPGEF1,CDH11,ARF4,GDNF,LHFPL4,PDZRN3,SHISA7,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0060350	0.04	0.99	7	46	endochondral bone morphogenesis	BP	1	EXT1,HOXA11,ZMPSTE24,SHOX2,ANXA6,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0006937	0.04	0.98	13	121	regulation of muscle contraction	BP	1	AKAP9,CHRM2,ATP2B1,ATP2A2,ATP1A1,PTGS2,TPM1,MYOCD,ANXA6,ITGA2,TBXA2R,ENO1,CTGF	darkolivegreen	VSMC_M9
GO:0050654	0.04	0.99	5	28	chondroitin sulfate proteoglycan metabolic process	BP	1	EXT1,DSE,CSGALNACT2,CHSY1,CHST11	darkolivegreen	VSMC_M9
GO:0010243	0.04	0.97	62	793	response to organonitrogen compound	BP	1	CDO1,RRM2B,EXT1,UBQLN1,DENND4C,AKAP9,JAK2,HDAC9,UBE2J1,KBTBD2,ACTR2,CHRM2,CAV2,ROCK2,ITGB1,FYN,UGGT1,NOX4,TRDMT1,EDEM1,OSBPL8,ATP2B1,LYN,XRN1,MAP1B,APPL1,AGTR1,TLR2,USO1,PPP2R2A,SLC39A14,LRRK2,BRSK2,UBE3A,DNAJB14,EPRS,IGF1R,CASP7,ITPR2,TOMM20,PTPN1,EIF2B5,IQGAP1,UBE4A,CCDC47,PTGS2,CPEB2,ADSS,TLR6,PKM,ROCK1,ITGA2,SLC1A3,RAB31,MYO1C,RAPGEF1,ZDHHC7,PRKACB,RANBP2,CTGF,LAMTOR3,DNAJB9	darkolivegreen	VSMC_M9
GO:0097242	0.04	0.99	5	29	amyloid-beta clearance	BP	1	PICALM,IGF1R,CLTC,MYOCD,ROCK1	darkolivegreen	VSMC_M9

GO:0035459	0.04	0.99	4	19	vesicle cargo loading	BP	1	SEC24A,PICALM,TMED2,SEC23A	darkolivegreen	VSMC_M9
GO:0014032	0.04	0.99	9	69	neural crest cell development	BP	1	RDH10,ACVR1,CORO1C,SEMA5B,NRP2,TAPT1,SEMA7A,ANXA6,GDNF	darkolivegreen	VSMC_M9
GO:0035988	0.04	0.99	4	20	chondrocyte proliferation	BP	1	EXT1,BMPR2,CTGF,NOV	darkolivegreen	VSMC_M9
GO:0016311	0.04	0.98	30	342	dephosphorylation	BP	1	PPM1H,PTPRD,JAK2,ROCK2,NOCT,NT5DC1,MGAT5,PPP1R12A,ACPP,PLPP1,PPP2R3A,PPP2R2A,PDP1,ATP1A1,LRRK2,SLC39A10,BPNT1,PTPN1,BOD1L1,PPM1D,PIN1,ROCK1,ITGA2,ITGA1,PPP4R1,PLPPR5,PTPN12,IMPA1,PPTC7,PPP1R2	darkolivegreen	VSMC_M9
GO:0090050	0.04	0.99	4	23	positive regulation of cell migration involved in sprouting angiogenesis	BP	1	HDAC9,PTGS2,AKT3,SRPX2	darkolivegreen	VSMC_M9
GO:0046364	0.04	0.99	8	65	monosaccharide biosynthetic process	BP	1	SLC35B4,SLC39A14,ATF3,TPI1,CLK2,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9
GO:0061035	0.04	0.99	8	61	regulation of cartilage development	BP	1	CHADL,WISP1,HOXA11,SHOX2,TAPT1,BMPR2,CTGF,WNT9A	darkolivegreen	VSMC_M9
GO:0043085	0.04	0.97	68	875	positive regulation of catalytic activity	BP	1	MALT1,TBC1D15,PLAA,TOPORS,JAK2,PSME4,STAP1,CCDC88A,CAV2,ROCK2,ITGB1,FYN,NOX4,PICALM,CCNT2,RAB3GAP1,OSBPL8,PPP1R12A,PIK3R4,ILK,ARL1,LYN,MERTK,EIF2AK3,CCDC125,AGTR1,PFN2,RASA1,DCP1A,THBS1,PDP1,NEDD9,LRRK2,TANK,SLC39A10,IGF1R,CORO1C,NEK7,NTRK3,PTPN1,PIP5K1A,IQGAP1,ZC3H15,FERMT2,TNFAIP8L3,DKK1,RGS7,FAS,TLR6,SRCIN1,TPM1,CLPX,GPR65,CYFIP2,UACA,PIN1,ITGA2,ITGA1,RICTOR,VAV2,RAPGEF1,RANBP2,BMPR2,ARF4,GDNF,TOR1AIP2,CTGF,LAMTOR3	darkolivegreen	VSMC_M9
GO:0022603	0.04	0.97	62	761	regulation of anatomical structure morphogenesis	BP	1	AHI1,THBS2,CDKL3,PTPRD,PLAA,HOXA11,ZMPSTE24,ACTR2,ROCK2,ITGB1,FYN,GPR4,GATA3,TRAK1,PRPF40A,NTN4,ILK,ITGA5,RNF6,SULF1,MAP1B,LARP4,HK2,RASA1,DHX36,THBS1,SHOX2,NEDD9,LRRK2,BRSK2,PDLIM5,ATP10A,UBE3A,PHLDB2,CORO1C,SEMA5B,TRAK2,ADAM12,SH3KBP1,FZD2,FERMT2,SKIL,SMURF1,TNIK,DKK1,AKT3,WNT5B,ADAM10,MSN,SRCIN1,TPM1,PKM,SEMA7A,ROCK1,SPIRE1,GPC4,TBXA2R,PAFAH1B1,BMPR2,GDNF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0043112	0.04	0.98	14	131	receptor metabolic process	BP	1	AHI1,ITGB1,PICALM,PIK3R4,SCYL2,ITCH,PTPN1,GRK3,SMURF1,DKK1,ATAD1,CLTC,GPRASP1,RAB31	darkolivegreen	VSMC_M9
GO:1903522	0.04	0.98	18	179	regulation of blood circulation	BP	1	AKAP9,JAK2,ZMPSTE24,CHRM2,ATP2B1,AGTR1,ATP2A2,SHOX2,ATP1A1,PTGS2,HSPB7,TPM1,NUP155,TBXA2R,BMPR2,CTGF,BDKRB2,IRX3	darkolivegreen	VSMC_M9
GO:0051642	0.04	0.99	5	30	centrosome localization	BP	1	AKAP9,KIF5B,CEP83,PAFAH1B1,RANBP2	darkolivegreen	VSMC_M9
GO:0032528	0.04	0.99	4	20	microvillus organization	BP	1	TNIK,PLD1,FXYD5,RAP2A	darkolivegreen	VSMC_M9
GO:0071711	0.04	0.99	5	30	basement membrane organization	BP	1	EXT1,CAV2,ITGB1,NTN4,PHLDB2	darkolivegreen	VSMC_M9
GO:0006511	0.04	0.97	44	542	ubiquitin-dependent protein catabolic process	BP	1	CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,UBA6,UBE2J1,PSMC2,CBLC,NUB1,NDFIP2,EDEM1,VPS36,NDFIP1,CUL4A,USP12,RNF6,UBXN2B,FBXL17,ITCH,USP47,LTN1,LRRK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,UBE4A,CCDC47,TLK2,CDC27,SMURF1,SPOP,TRIP4,RLIM,RBBP6,C18orf25,BAG5,BFAR,USP7,DNAJB9,FBXL7	darkolivegreen	VSMC_M9
GO:0050789	0.04	0.97	513	7907	regulation of biological process	BP	1	SOCS6,LMAN1,MALT1,AHI1,UTRN,STXBP5,TBK1,CAND1,PLEKHG1,CEP120,RRM2B,AZIN1,ATP6V1C1,LRP12,EXT1,THBS2,CDKL3,CHADL,PHF20L1,WISP1,KHDRBS3,CDC23,ETF1,SLC35B4,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,SLC30A9,TOPORS,ABCB4,AKAP9,GCC2,TFPI2,GNG11,JAK2,CLOCK,EXOC1,NPAS2,NOA1,FBXO9,ELOVL5,EIF5B,ASPN,ZNF451,HEMGN,HDAC9,CAVIN4,SENP6,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,PDE1C,KBTBD2,SH3BP5L,ACTR2,THAP5,GFPT1,CHRM2,TES,CAV2,ROCK2,INHBA,PNPLA8,DDX1,NOCT,RAB3B,ITGB1,MPP7,RPF2,FYN,ZEB1,RINT1,KIF5B,CEP57,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,CCDC8,GSAP,NOX4,GPR4,RB1,RTN2,PICALM,ZC3H13,TRDMT1,SUSD5,CBLC,CGREF1,CAMK1D,UPF2,NUB1,ACTR3,CDK3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,AZI2,CYTH1,MBNL2,EDEM1,STK24,TNFAIP6,RIF1,OSBPL8,PPP1R12A,STAM2,PRPF40A,FAM98A,RPL26,UFM1,CAPN7,LIG4,PIK3R4,MYO16,CEBPZ,SUPT20H,ATP2B1,SMAD9,CCNA1,ATP11A,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,YIPF5,SOS1,PDS5B,BRCA2,NTN4,UBA5,ILK,ITGA5,GPR84,DCHS1,HSPH1,TMF1,HOXC10,ERI1,HSD17B12,DHX29,SCYL2,PARG,PLPP1,CDK8,CNOT7,RNF6,REM1,RASSF4,LYN,UBXN2B,MERTK,SACS,XPO4,ATP6V0A2,IFT88,IPO7,PDE7A,TCP11L1,MYBL1,EIF2AK3,FBXL17,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,SLC30A5,CHD1,SULF1,RIOK2,USP47,CCDC125,LNPEP,XRN1,PDE12,STOX2,MICAL2,FFAR4,MAP1B,APPL1,RDH10,LARP4,PI15,AGTR1,ACTR8,HK2,TLR2,PFN2,RASA1,ATP2A2,USO1,MAP9,MBNL1,LTN1,BRAP,DCP1A,DHX36,THBS1,NUCB2,GPR176,	darkolivegreen	VSMC_M9

GO:0031323	0.04	0.97	294	4391	regulation of cellular metabolic process	BP	1	SOCS6,MALT1,AHI1,TBK1,CAND1,ATP6V1C1,PHF20L1,KHDRBS3,ETF1,SLC35B4,UBQLN1,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,JAK2,CLOCK,EXOC1,NPAS2,NOA1,ELOVL5,EIF5B,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,SH3BP5L,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,GSAP,NOX4,RB1,RTN2,PICALM,TRDMT1,CBLC,CAMK1D,NUB1,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,MBNL2,RIF1,OSBPL8,PPP1R12A,RPL26,PIK3R4,CEBPZ,SUPT20H,SMAD9,CCNA1,NR2C1,NDFIP1,CUL4A,BRCA2,ILK,ITGA5,TMF1,HOXC10,DHX29,SCYL2,PARG,CNOT7,RNF6,LYN,MERTK,ATP6V0A2,IPO7,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,MICAL2,APPL1,RDH10,LARP4,PI15,AGTR1,ACTR8,HK2,TLR2,PFN2,RASA1,MBNL1,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,TBX15,UBE3A,SLC39A10,CUL3,EIF4E,TDP2,UCHL5,TIMM17A,ATP6V1A,KPNA6,EPRS,IGF1R,RAB3GAP2,CORO1C,ANOS1,NEK7,NTRK3,WWC3,PTPN1,LARP7,KPNA1,CLK1,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,IQGAP1,RBBP7,EDRF1,BCLAF3,TLK2,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,PTGS2,MYEF2,FZD2,CWC22,NPAT,ITGAV,MYNN,FERMT2,SKIL,PRRX1,RTN3,SMURF1,TNIK,PLD1,TNFAIP8L3,CPEB2,SAMD8,BOD1L1,DKK1,FMN2,ATAD1,FAS,NOTCH3,SRP9,TLR6,MAGED2,MSN,SRCIN1,PHKG2,CLK2,TRIP4,TBX6,CLPX,RLIM,MAGEE2,ZC3H14,CYFIP2,SRPX2,RBB	darkolivegreen	VSMC_M9
GO:1902905	0.04	0.98	18	179	positive regulation of supramolecular fiber organization	BP	1	AKAP9,CCDC88A,ACTR2,ROCK2,NOX4,RB1,ACTR3,MAP1B,PFN2,FERMT2,TPM1,GPR65,RICTOR,SPIRE1,MYO1C,CTGF,COLGALT1,CFL2	darkolivegreen	VSMC_M9
GO:2000300	0.04	0.99	6	39	regulation of synaptic vesicle exocytosis	BP	1	STXBP5,RAB3GAP1,ATP2A2,LRRK2,SEPT5,WNT7A	darkolivegreen	VSMC_M9
GO:0005975	0.04	0.97	37	458	carbohydrate metabolic process	BP	1	EXT1,SLC35B4,GNE,ZMPSTE24,UGP2,KBTBD2,ST3GAL3,EDEM1,B3GLCT,GALNT7,PARG,CSGALNACT2,HK2,PGAM4,GPD2,SLC39A14,GCNT4,MAN1A2,BPNT1,ST8SIA1,IDH2,ATF3,DERA,NPL,TPI1,HK3,PHKG2,CLK2,CLTC,PKM,C1QTNF3,USP7,ENO1,RANBP2,IMPA1,CHST11,PPP1R2	darkolivegreen	VSMC_M9
GO:0033574	0.04	0.99	5	34	response to testosterone	BP	1	ROCK2,XRN1,THBS1,MSN,TBXA2R	darkolivegreen	VSMC_M9
GO:0006913	0.04	0.98	23	257	nucleocytoplasmic transport	BP	1	MALT1,JAK2,UPF2,PPP1R12A,UFM1,XPO4,IPO7,RIOK2,APPL1,CBLB,LRRK2,KPNA6,KPNA1,TPR,PTGS2,SMURF1,THOC1,NUP155,RANBP2,KPNA4,E2F3,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0051169	0.04	0.98	23	257	nuclear transport	BP	1	MALT1,JAK2,UPF2,PPP1R12A,UFM1,XPO4,IPO7,RIOK2,APPL1,CBLB,LRRK2,KPNA6,KPNA1,TPR,PTGS2,SMURF1,THOC1,NUP155,RANBP2,KPNA4,E2F3,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0031023	0.04	0.98	14	127	microtubule organizing center organization	BP	1	CEP120,HAUS6,GCC2,ROCK2,CEP295,PPP1R12A,BRCA2,UBXN2B,MAP9,HAUS2,C10orf90,CCP110,PAFAH1B1,SSX2IP	darkolivegreen	VSMC_M9
GO:0051653	0.04	0.99	7	49	spindle localization	BP	1	ACTR2,ITGB1,ACTR3,UBXN2B,FMN2,SPIRE1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0031532	0.04	0.98	11	94	actin cytoskeleton reorganization	BP	1	STAP1,NEDD9,BRSK2,NTRK3,PTPN1,PIP5K1A,TNIK,CDC42BPA,GPR65,RICTOR,RAP2A	darkolivegreen	VSMC_M9
GO:0035136	0.04	0.99	5	30	forelimb morphogenesis	BP	1	HOXA9,HOXA11,RDH10,SHOX2,WNT7A	darkolivegreen	VSMC_M9
GO:0051588	0.04	0.98	9	73	regulation of neurotransmitter transport	BP	1	STXBP5,RAB3B,ITGB1,RAB3GAP1,ATP2A2,LRRK2,SEPT5,GDNF,WNT7A	darkolivegreen	VSMC_M9
GO:0010033	0.04	0.97	159	2273	response to organic substance	BP	1	MALT1,CDO1,TBK1,RRM2B,EXT1,UBQLN1,DENND4C,PLAA,ABCB4,AKAP9,DNAJB5,JAK2,CLOCK,ASPN,ZNF451,HDAC9,STAP1,UBE2J1,KBTBD2,ACTR2,CHRM2,CAV2,ROCK2,INHBA,DDX1,NOCT,ITGB1,FYN,KIF5B,CEP57,UGGT1,NOX4,TRDMT1,NUB1,ACTR3,GATA3,LRRC32,DNAJC3,EDEM1,RIF1,OSBPL8,UFM1,ATP2B1,SMAD9,NR2C1,SOS1,UBA5,ILK,ITGA5,HSPH1,TMF1,PLPP1,CNOT7,RNF6,LYN,GRAMD1A,EIF2AK3,TMED2,SMARCA5,SULF1,MAT2A,XRN1,PDE12,MAP1B,APPL1,GDAP1,AGTR1,HK2,TLR2,ATP2A2,USO1,DHX36,THBS1,PPP2R2A,ACVR1,SLC39A14,ATP1A1,EHD4,LRRK2,TANK,BRSK2,UBE3A,CUL3,EIF4E,TROVE2,DNAJB14,EPRS,IGF1R,CASP7,CCDC186,ITPR2,NTRK3,TOMM20,PTPN1,VAPB,ABCB10,EIF2B5,C2CD2L,ATF3,IQGAP1,RBBP7,UBE4A,CCDC47,NRP2,MBTPS2,CREB3L2,TPR,PTGS2,ZC3H15,MYNN,FERMT2,SKIL,SMURF1,CPEB2,FAS,PLP2,ADSS,WNT5B,HSPB7,TLR6,ADAM10,MSN,KCNMB1,TRIP4,CYFIP2,PKM,MAP2K4,MYOCD,PIN1,RBBP8,ROCK1,ITGA2,SLC1A3,RAB31,BFAR,CIDEA,MYO1C,TBXA2R,PAFAH1B1,RAPGEF1,ZDHHC7,WFDC1,PRKACB,DNAJB4,RANBP2,BMPR2,AQP3,PTPN12,CTGF,LAMTOR3,DNAJB9,PAQR8,HSPA13,PMEPA1,WNT9A,ZPR1,NUP35,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0006487	0.04	0.99	7	55	protein N-linked glycosylation	BP	1	TMEM165,MGAT4A,UBE2J1,GFPT1,UGGT1,MGAT5,ALG5	darkolivegreen	VSMC_M9
GO:0042692	0.04	0.97	27	303	muscle cell differentiation	BP	1	HDAC9,ZMPSTE24,CAV2,ITGB1,RB1,ATP11A,ATP2A2,SHOX2,ACVR1,PDLIM5,DNER,CASP7,ADAM12,MYEF2,DKK1,WNT5B,TPM1,FHOD3,MAP2K4,MYOCD,PIN1,AFG3L2,BMPR2,NOV,TMEM119,CFL2,IRX3	darkolivegreen	VSMC_M9
GO:0061640	0.04	0.98	10	87	cytoskeleton-dependent cytokinesis	BP	1	ACTR2,ROCK2,ACTR3,RASA1,MAP9,ANK3,SEPT5,FMN2,ROCK1,SPIRE1	darkolivegreen	VSMC_M9
GO:0061005	0.04	0.99	7	49	cell differentiation involved in kidney development	BP	1	EXT1,GPR4,GATA3,IQGAP1,ACTA2,MYO1E,GDNF	darkolivegreen	VSMC_M9
GO:0003170	0.04	0.98	8	58	heart valve development	BP	1	ROCK2,RB1,GATA3,DCHS1,SHOX2,ACVR1,ROCK1,BMPR2	darkolivegreen	VSMC_M9
GO:0010332	0.04	0.99	7	53	response to gamma radiation	BP	1	ZMPSTE24,NOX4,GATA3,RPL26,LIG4,BRCA2,TLK2	darkolivegreen	VSMC_M9

GO:0043066	0.04	0.97	51	662	negative regulation of apoptotic process	BP	1	MALT1,AHI1,RRM2B,TOPORS,JAK2,ITGB1,FYN,RB1,CAMK1D,GATA3,DNAJC3,UFM1,LIG4,ILK,ITGA5,TMF1,MERTK,ITCH,USP47,FFAR4,RASA1,THBS1,ACVR1,LRRK2,SLC39A10,IGF1R,PTPN1,SYCP2,PTGS2,ITGAV,KIFAP3,VDAC2,DKK1,FMN2,FAS,ADAM10,BNIP2,MAP2K4,MYOCD,PIN1,BAG5,BFAR,CIDEA,CD40LG,ENO1,ARF4,GDNF,BDKRB2,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:1901698	0.04	0.97	65	845	response to nitrogen compound	BP	1	CDO1,RRM2B,EXT1,UBQLN1,DENND4C,AKAP9,JAK2,HDAC9,UBE2J1,KBTBD2,ACTR2,CHRM2,CAV2,ROCK2,DDX1,ITGB1,FYN,UGGT1,NOX4,TRDMT1,EDEM1,OSBPL8,ATP2B1,LYN,XRN1,PDE12,MAP1B,APPL1,AGTR1,TLR2,USO1,DHX36,PPP2R2A,SLC39A14,LRRK2,BRSK2,UBE3A,DNAJB14,EPRS,IGF1R,CASP7,ITPR2,TOMM20,PTPN1,EIF2B5,IQGAP1,UBE4A,CCDC47,PTGS2,CPEB2,ADSS,TLR6,PKM,ROCK1,ITGA2,SLC1A3,RAB31,MYO1C,RAPGEF1,ZDHHC7,PRKACB,RANBP2,CTGF,LAMTOR3,DNAJB9	darkolivegreen	VSMC_M9
GO:2001242	0.04	0.98	13	135	regulation of intrinsic apoptotic signaling pathway	BP	1	RRM2B,UBQLN1,RPL26,EIF2AK3,USP47,LRRK2,PTPN1,PTGS2,SKIL,VDAC2,BAG5,ENO1,BDKRB2	darkolivegreen	VSMC_M9
GO:0061842	0.04	0.99	5	31	microtubule organizing center localization	BP	1	AKAP9,KIF5B,CEP83,PAFAH1B1,RANBP2	darkolivegreen	VSMC_M9
GO:0031346	0.04	0.97	28	302	positive regulation of cell projection organization	BP	1	CEP120,CDKL3,PTPRD,CCDC88A,ACTR2,FYN,CAMK1D,ACTR3,TRAK1,FAM98A,ILK,LYN,MAP1B,DHX36,SHOX2,CORO1C,NTRK3,IQGAP1,CREB3L2,SKIL,TAPT1,SEMA7A,CCP110,ITGA2,PAFAH1B1,RAPGEF1,PLPPR5,BMPR2	darkolivegreen	VSMC_M9
GO:0099515	0.04	0.99	4	19	actin filament-based transport	BP	1	MYO6,MYO1E,MYO1C,MYO1H	darkolivegreen	VSMC_M9
GO:0045880	0.04	0.99	5	31	positive regulation of smoothened signaling pathway	BP	1	SHOX2,UCHL5,CHSY1,PRRX1,PDCL	darkolivegreen	VSMC_M9
GO:0018193	0.04	0.97	75	997	peptidyl-amino acid modification	BP	1	TBK1,PHF20L1,PPIL1,CEP41,TOPORS,AKAP9,JAK2,CLOCK,ZNF451,HDAC9,SENP6,STAP1,ZMPSTE24,UBE2J1,SH3BP5L,ROCK2,FYN,UGGT1,NOX4,CBLC,CAMK1D,MGAT5,GATA3,JMJD6,NKTR,BRPF1,SETD5,NDUFAF5,RIF1,KDELC1,ALG5,BRCA2,ILK,ITGA5,CNOT7,LYN,MERTK,EIF2AK3,NEK1,PLOD2,PFN2,NAA25,ACVR1,NEDD9,CBLB,DYRK1A,BRD7,EHD4,LRRK2,BRSK2,IGF1R,STK38L,NTRK3,PTPN1,CLK1,TAF5L,IQGAP1,TLK2,PTGS2,DKK1,AKT3,CDC42BPA,SRCIN1,CLK2,MAP2K4,MYOCD,PIN1,ROCK1,RICTOR,ZDHHC7,GTF2B,RANBP2,RAB6A,BDKRB2,NAA20	darkolivegreen	VSMC_M9
GO:0090102	0.04	0.99	6	40	cochlea development	BP	1	GATA3,DCHS1,NTRK3,FZD2,ADAM10,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0051492	0.04	0.98	10	80	regulation of stress fiber assembly	BP	1	CCDC88A,ROCK2,NOX4,PFN2,PHLDB2,FERMT2,TPM1,GPR65,ROCK1,CTGF	darkolivegreen	VSMC_M9
GO:0030166	0.04	0.98	7	49	proteoglycan biosynthetic process	BP	1	EXT1,DSE,CSGALNACT2,CHSY1,FAM20B,BMPR2,CHST11	darkolivegreen	VSMC_M9
GO:0006446	0.04	0.98	8	66	regulation of translational initiation	BP	1	EIF5B,DDX1,DNAJC3,DHX29,EIF2AK3,TMED2,EIF2B5,TPR	darkolivegreen	VSMC_M9
GO:0032387	0.04	0.99	6	46	negative regulation of intracellular transport	BP	1	LMAN1,UBE2J1,UFM1,MAP1B,LRRK2,TPR	darkolivegreen	VSMC_M9
GO:0010638	0.04	0.97	36	428	positive regulation of organelle organization	BP	1	LMAN1,CEP120,CDC23,AKAP9,STAP1,CCDC88A,ACTR2,ROCK2,KIF5B,CEP295,NOX4,RB1,ACTR3,RAB3GAP1,LIG4,MAP1B,PFN2,DHX36,CUL3,KIAA1551,RAB3GAP2,NEK7,NTRK3,TPR,CDC27,FERMT2,TAPT1,MSN,TPM1,GPR65,CCP110,RICTOR,SPIRE1,MYO1C,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:0001503	0.04	0.97	29	328	ossification	BP	1	EXT1,WISP1,ASPN,HEMGN,ZMPSTE24,NOCT,PSMC2,ATP2B1,ILK,DCHS1,EIF2AK3,FFAR4,VCAN,DHX36,SHOX2,ACVR1,CHSY1,CCDC47,PTGS2,FERMT2,TAPT1,DKK1,CLTC,SEMA7A,COL11A1,CDH11,BMPR2,CTGF,TMEM119	darkolivegreen	VSMC_M9
GO:0048814	0.04	0.98	8	57	regulation of dendrite morphogenesis	BP	1	CDKL3,PTPRD,ACTR2,ILK,DHX36,TNIK,PAFAH1B1,RAP2A	darkolivegreen	VSMC_M9
GO:0038093	0.05	0.99	6	39	Fc receptor signaling pathway	BP	1	FYN,SOS1,LYN,APPL1,MAP2K4,VAV2	darkolivegreen	VSMC_M9
GO:0038095	0.05	0.99	4	20	Fc-epsilon receptor signaling pathway	BP	1	SOS1,LYN,MAP2K4,VAV2	darkolivegreen	VSMC_M9
GO:0030036	0.05	0.97	50	600	actin cytoskeleton organization	BP	1	PHACTR2,UTRN,JAK2,MYO6,STAP1,CCDC88A,ACTR2,ROCK2,ITGB1,NOX4,ACTR3,STARD13,ILK,PALLD,MICAL2,PFN2,RASA1,NEDD9,SPTBN5,BRSK2,PDLIM5,CUL3,PHLDB2,CORO1C,NTRK3,PTPN1,PIP5K1A,IQGAP1,SMTN,SH3KBP1,EHBP1L1,FERMT2,TNIK,FMN2,CDC42BPA,ENAH,MYO1E,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,PAFAH1B1,MYO1H,CTGF,RAP2A,CFL2	darkolivegreen	VSMC_M9
GO:0007010	0.05	0.96	90	1177	cytoskeleton organization	BP	1	PHACTR2,UTRN,CEP120,HAUS6,AKAP9,GCC2,JAK2,TXNDC9,SENP6,MYO6,STAP1,CCDC88A,ACTR2,ROCK2,ITGB1,CEP57,CEP295,CCDC8,NOX4,ACTR3,PPP1R12A,PRPF40A,TUBGCP3,STARD13,BRCA2,ILK,DCTN6,UBXN2B,PALLD,MICAL2,MAP1B,LARP4,PFN2,RASA1,MAP9,INO80,NEDD9,DYRK1A,SPTBN5,BRSK2,PDLIM5,CUL3,PHLDB2,CAMSAP2,HAUS2,CORO1C,NEK7,NTRK3,PTPN1,PIP5K1A,IQGAP1,CEP350,ANK3,SMTN,C10orf90,SH3KBP1,HDGFL3,EHBP1L1,TPR,IQCJ-SCHIP1,FERMT2,VAMP4,TNIK,TUBA4A,FMN2,CDC42BPA,ENAH,MSN,MYO1E,TPM1,GPR65,CYFIP2,CLTC,FHOD3,CCP110,SS18,ROCK1,RICTOR,SPIRE1,MYO1C,PAFAH1B1,SSX2IP,MYO1H,SKA2,FOPNL,CTGF,MZT1,RAP2A,ZPR1,CFL2	darkolivegreen	VSMC_M9
GO:0090092	0.05	0.97	19	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	JAK2,ASPN,ZNF451,CAV2,INHBA,ILK,SULF1,THBS1,ACVR1,SKIL,SMURF1,DKK1,MYOCD,PIN1,CIDEA,BMPR2,NOV,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0050728	0.05	0.98	10	91	negative regulation of inflammatory response	BP	1	FYN,RB1,GATA3,TNFAIP6,NDFIP1,LYN,FFAR4,C1QTNF3,WFDC1,NOV	darkolivegreen	VSMC_M9
GO:0014902	0.05	0.98	10	86	myotube differentiation	BP	1	HDAC9,CAV2,ATP11A,SHOX2,DNER,ADAM12,MYEF2,MYOCD,NOV,TMEM119	darkolivegreen	VSMC_M9

GO:0071310	0.05	0.96	128	1784	cellular response to organic substance	BP	1	MALT1,TBK1,EXT1,DENND4C,PLAA,ABCB4,AKAP9,JAK2,CLOCK,ASPN,ZNF451,HDAC9,STAP1,ACTR2,CHRM2,CAV2,ROCK2,INHBA,FYN,KIF5B,CEP57,UGGT1,NOX4,ACTR3,GATA3,LRRC32,RIF1,OSBPL8,UFM1,ATP2B1,SMAD9,NR2C1,SOS1,UBA5,ILK,ITGA5,TMF1,PLPP1,CNOT7,RNF6,LYN,GRAMD1A,EIF2AK3,TMED2,SMARCA5,SULF1,MAT2A,XRN1,PDE12,MAP1B,APPL1,GDAP1,AGTR1,HK2,TLR2,USO1,THBS1,ACVR1,SLC39A14,ATP1A1,EHD4,LRRK2,TANK,BRSK2,UBE3A,CUL3,EIF4E,TROVE2,DNAJB14,EPRS,IGF1R,CASP7,CCDC186,ITPR2,NTRK3,PTPN1,VAPB,ABCB10,C2CD2L,ATF3,IQGAP1,NRP2,MBTPS2,CREB3L2,TPR,PTGS2,ZC3H15,MYNN,FERMT2,SKIL,SMURF1,CPEB2,FAS,PLP2,WNT5B,TLR6,MSN,KCNMB1,TRIP4,CYFIP2,PKM,MAP2K4,MYOCD,PIN1,ROCK1,ITGA2,SLC1A3,RAB31,BFAR,CIDEA,MYO1C,TBXA2R,PAFAH1B1,RAPGEF1,ZDHHC7,BMPR2,PTPN12,CTGF,LAMTOR3,DNAJB9,PAQR8,HSPA13,PMEPA1,WNT9A,ZPR1,NUP35,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0032515	0.05	0.99	4	23	negative regulation of phosphoprotein phosphatase activity	BP	1	ROCK2,MGAT5,BOD1L1,ROCK1	darkolivegreen	VSMC_M9
GO:0055007	0.05	0.98	11	96	cardiac muscle cell differentiation	BP	1	ZMPSTE24,ITGB1,SHOX2,ACVR1,PDLIM5,DKK1,FHOD3,MAP2K4,MYOCD,PIN1,IRX3	darkolivegreen	VSMC_M9
GO:0051171	0.05	0.96	273	4082	regulation of nitrogen compound metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,AZIN1,PHF20L1,KHDRBS3,ETF1,UBQLN1,PLAA,SLC30A9,TOPORS,AKAP9,TFPI2,JAK2,CLOCK,NPAS2,EIF5B,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,SH3BP5L,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,PSMC2,CEP295,GSAP,NOX4,RB1,RTN2,PICALM,TRDMT1,CBLC,CAMK1D,NUB1,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,MBNL2,RIF1,OSBPL8,PPP1R12A,RPL26,CEBPZ,SUPT20H,SMAD9,CCNA1,NR2C1,NDFIP1,CUL4A,BRCA2,ILK,ITGA5,TMF1,HOXC10,DHX29,PARG,CNOT7,RNF6,LYN,IPO7,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,MICAL2,LARP4,PI15,AGTR1,ACTR8,TLR2,PFN2,RASA1,MBNL1,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,NEDD9,CBLB,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,TBX15,UBE3A,SLC39A10,CUL3,EIF4E,TDP2,UCHL5,TIMM17A,KPNA6,EPRS,RAB3GAP2,CORO1C,ANOS1,NEK7,NTRK3,WWC3,PTPN1,LARP7,KPNA1,CLK1,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,IQGAP1,RBBP7,EDRF1,BCLAF3,TLK2,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,PTGS2,MYEF2,FZD2,CWC22,NPAT,ITGAV,MYNN,FERMT2,SKIL,PRRX1,RTN3,SMURF1,TNIK,PLD1,CPEB2,SAMD8,BOD1L1,DKK1,FMN2,FAS,NOTCH3,SRP9,TLR6,MAGED2,MSN,SRCIN1,SPOP,CLK2,TRIP4,TBX6,OAZ2,CLPX,RLIM,MAGEE2,ZC3H14,CYFIP2,TLE3,SMG8,UACA,CLTC,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MAP2K4,MYOCD,SEMA7A,PIN1,SS18,RBBP8,BAG5,ROCK1,THOC1,ITGA2,ITGA1,RICTOR	darkolivegreen	VSMC_M9
GO:0051954	0.05	0.99	4	22	positive regulation of amine transport	BP	1	RAB3B,ITGB1,RAB3GAP1,GDNF	darkolivegreen	VSMC_M9
GO:0044272	0.05	0.98	13	127	sulfur compound biosynthetic process	BP	1	CDO1,EXT1,DSE,ELOVL5,ST3GAL3,HSD17B12,CSGALNACT2,MAT2A,SLC35B3,CHSY1,PAPSS2,ELOVL4,CHST11	darkolivegreen	VSMC_M9
GO:0000045	0.05	0.98	10	88	autophagosome assembly	BP	1	UBQLN1,RAB3GAP1,UBXN2B,TMEM41B,IFT88,ATP2A2,LRRK2,RAB3GAP2,SMURF1,TRAPPC8	darkolivegreen	VSMC_M9
GO:0030162	0.05	0.97	41	538	regulation of proteolysis	BP	1	MALT1,UBQLN1,TFPI2,JAK2,PSME4,ROCK2,FYN,DNAJC1,PSMC2,GSAP,PICALM,NUB1,TMF1,LYN,EIF2AK3,ITCH,USP47,PI15,THBS1,LRRK2,TANK,UBE3A,UCHL5,TIMM17A,ANOS1,TLK2,PITHD1,PTGS2,SMURF1,FAS,SPOP,CLPX,CYFIP2,UACA,BAG5,ROCK1,USP7,ENO1,WFDC1,PRKACB,CTGF	darkolivegreen	VSMC_M9
GO:0006734	0.05	0.99	4	24	NADH metabolic process	BP	1	HK2,GPD2,HK3,ENO1	darkolivegreen	VSMC_M9
GO:0009059	0.05	0.96	239	3569	macromolecule biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,RRM2B,EXT1,DSE,PHF20L1,ETF1,RMI1,SLC30A9,TOPORS,TMEM165,JAK2,CLOCK,NPAS2,NOA1,EIF5B,POLR2B,MGAT4A,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,ZEB1,EXOSC9,PIWIL4,DNAJC1,UGGT1,RB1,PICALM,CAMK1D,ST3GAL3,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,RIF1,PPP1R12A,TMTC2,RPL26,KDELC1,LIG4,CEBPZ,SUPT20H,ALG5,SMAD9,NR2C1,BRCA2,ILK,B3GLCT,HSPH1,TMF1,GALNT7,HOXC10,DHX29,CNOT7,RNF6,CSGALNACT2,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,LARP4,ACTR8,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,GFM1,LIN54,ZDHHC16,ACVR1,WDR75,IRX5,MTERF3,INO80,GCNT4,DYRK1A,BRD7,MAN1A2,ERG,LRRK2,TBX15,UBE3A,CUL3,EIF4E,TDP2,TROVE2,CHSY1,KPNA6,EPRS,IARS2,RAB3GAP2,GALNT17,NEK7,MRPL47,WWC3,LARP7,ST8SIA1,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,FAM20B,MYEF2,FZD2,ZC3H15,NPAT,MYNN,SKIL,PRRX1,PLD1,CPEB2,SAMD8,BOD1L1,DKK1,NOTCH3,SRP9,TLR6,MAGED2,PHKG2,TRIP4,TBX6,RLIM,MAGEE2,RBBP6,TLE3,CLTC,PKM,DICER1,ARMCX3,PPM1D,PIGW,MAP2K4,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,C1GALT1C1,ZNF280C,GSPT1,TARS,MYSM1,CD40LG,USP7,ENO1,ZDHHC7,DPM2,RFWD3,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,DPM1,R	darkolivegreen	VSMC_M9

GO:0009058	0.05	0.96	288	4393	biosynthetic process	BP	1	SOCS6,MALT1,CDO1,AHI1,TBK1,CAND1,RRM2B,AZIN1,EXT1,DSE,PHF20L1,ETF1,SLC35B4,RMI1,SLC30A9,TOPORS,TMEM165,JAK2,CLOCK,NPAS2,NOA1,ELOVL5,EIF5B,POLR2B,GNE,MGAT4A,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,UGGT1,PDSS1,NOX4,RB1,SUCLA2,PICALM,ABHD1,CAMK1D,ST3GAL3,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,RIF1,PPP1R12A,TMTC2,RPL26,KDELC1,LIG4,CEBPZ,SUPT20H,ALG5,SMAD9,NR2C1,BRCA2,ILK,B3GLCT,HSPH1,TMF1,GALNT7,HOXC10,HSD17B12,DHX29,PLPP1,CNOT7,RNF6,CSGALNACT2,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,USP47,MAT2A,XRN1,PDE12,STOX2,BDP1,MICAL2,APPL1,RDH10,PLOD2,LARP4,ACTR8,CERS5,ALDH18A1,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,GFM1,LIN54,ZDHHC16,ACVR1,WDR75,SLC39A14,IRX5,MTERF3,INO80,GCNT4,SLC35B3,ETNK2,ATP1A1,DYRK1A,BRD7,MAN1A2,ERG,LRRK2,TBX15,UBE3A,MBOAT1,CUL3,EIF4E,TDP2,TROVE2,CHSY1,ATP6V1A,KPNA6,EPRS,BPNT1,IARS2,RAB3GAP2,GALNT17,NEK7,MRPL47,WWC3,ETNK1,LARP7,ST8SIA1,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,PIP5K1A,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,GATM,PTGS2,FAM20B,MYEF2,FZD2,ZC3H15,NPAT,TPI1,MYNN,GNPNAT1,SKIL,PRRX1,PLD1,CPEB2,SAMD8,BOD1L1,DKK1,PAPSS2,ADSS,NOTCH3,ACBD3,SRP9,TLR6,MAGED2,PHKG2,CLK2,TRIP4,TBX6,OAZ2,RLIM,MAGEE2,R	darkolivegreen	VSMC_M9
GO:0006402	0.05	0.97	19	201	mRNA catabolic process	BP	1	ETF1,ROCK2,NOCT,EXOSC9,UPF2,CNOT7,XRN1,PDE12,DCP1A,DHX36,FASTKD2,MYEF2,ZC3H14,SMG8,ROCK1,GSPT1,LSM5,FASTKD5,GDNF	darkolivegreen	VSMC_M9
GO:0002181	0.05	0.98	10	111	cytoplasmic translation	BP	1	ETF1,RPL26,DHX29,EIF2S2,DHX36,EIF3J,ZC3H15,CPEB2,PKM,GSPT1	darkolivegreen	VSMC_M9
GO:0050869	0.05	0.99	4	24	negative regulation of B cell activation	BP	1	INHBA,NDFIP1,LYN,THOC1	darkolivegreen	VSMC_M9
GO:0010604	0.05	0.96	179	2586	positive regulation of macromolecule metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,UBQLN1,SLC30A9,TOPORS,AKAP9,JAK2,CLOCK,NPAS2,ZNF451,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,ROCK2,INHBA,DDX1,NOCT,FYN,EXOSC9,PSMC2,CEP295,GSAP,NOX4,RB1,PICALM,NUB1,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,RIF1,OSBPL8,PPP1R12A,FAM98A,RPL26,CEBPZ,SMAD9,NDFIP1,BRCA2,ILK,ITGA5,HSPH1,TMF1,HOXC10,DHX29,SCYL2,CNOT7,RNF6,LYN,MYBL1,EIF2AK3,TMED2,HCFC2,SMARCA5,ITCH,SULF1,RIOK2,PDE12,STOX2,MICAL2,APPL1,LARP4,AGTR1,TLR2,PFN2,DCP1A,DHX36,THBS1,ACVR1,WDR75,INO80,NEDD9,CBLB,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,UBE3A,SLC39A10,CUL3,TIMM17A,KPNA6,RAB3GAP2,NEK7,NTRK3,PTPN1,LARP7,TAF5L,ABCB10,EIF2B5,GPATCH3,ATF3,IQGAP1,ANK3,EDRF1,BCLAF3,PITHD1,MBTPS2,FASTKD2,CREB3L2,PTGS2,FZD2,DNAJA4,NPAT,FERMT2,PRRX1,SMURF1,TNIK,PLD1,DKK1,FMN2,ATAD1,ACTA2,FAS,TLR6,MSN,SRCIN1,PHKG2,TRIP4,TBX6,OAZ2,CLPX,ADAM19,CYFIP2,UACA,PKM,ARMCX3,MAP2K4,MYOCD,SEMA7A,PIN1,SS18,ROCK1,THOC1,ITGA2,ITGA1,MYOM1,RICTOR,C1QTNF3,SPIRE1,MYSM1,CD40LG,USP7,ENO1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,CTGF,DNAJB9,RFXAP,FCN1,E2F3,RAP2A,GLIS3,ZPR1,VGLL4,TMEM119,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:1902117	0.05	0.98	8	61	positive regulation of organelle assembly	BP	1	CEP120,CCDC88A,CEP295,RAB3GAP1,RAB3GAP2,TAPT1,MSN,CCP110	darkolivegreen	VSMC_M9
GO:0072006	0.05	0.97	13	118	nephron development	BP	1	AHI1,EXT1,HOXA11,GPR4,GATA3,ILK,DCHS1,SULF1,IQGAP1,ACTA2,MYO1E,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0014031	0.05	0.98	9	73	mesenchymal cell development	BP	1	RDH10,ACVR1,CORO1C,SEMA5B,NRP2,TAPT1,SEMA7A,ANXA6,GDNF	darkolivegreen	VSMC_M9
GO:0016310	0.05	0.96	106	1440	phosphorylation	BP	1	SOCS6,MALT1,TBK1,CDKL3,AKAP9,JAK2,GNE,STAP1,CCDC88A,ZMPSTE24,SH3BP5L,ROCK2,INHBA,FYN,NOX4,RB1,CBLC,CAMK1D,CDK3,CCNT2,DNAJC3,STK24,OSBPL8,PIK3R4,CCNA1,ILK,ITGA5,SCYL2,CDK8,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TMED2,NEK1,RIOK2,HK2,ALDH18A1,TLR2,PFN2,THBS1,PGAM4,ACVR1,ETNK2,NEDD9,CBLB,DYRK1A,EHD4,ERG,LRRK2,BRSK2,IGF1R,STK38L,CORO1C,NEK7,NTRK3,PTPN1,GRK3,ETNK1,CLK1,PIP5K1A,IQGAP1,TLK2,PTGS2,CDKL1,MAP4K5,TPI1,FERMT2,TNIK,TNFAIP8L3,DKK1,PAPSS2,FAS,AKT3,CDC42BPA,TLR6,ADAM10,HK3,SRCIN1,PHKG2,CLK2,SRPX2,SMG8,PKM,PPM1D,MAP2K4,MYOCD,SEMA7A,PIN1,ROCK1,RICTOR,PPP4R1,GADD45B,ENO1,VAV2,PRKACB,RANBP2,BMPR2,CDK13,CTGF,BDKRB2,LAMTOR3,PMEPA1,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:0034204	0.05	0.98	6	39	lipid translocation	BP	1	ABCB4,ATP11A,ATP10A,ATP11B,ATP8B4,XKR9	darkolivegreen	VSMC_M9
GO:2000114	0.05	0.99	4	21	regulation of establishment of cell polarity	BP	1	ROCK2,GATA3,ROCK1,RICTOR	darkolivegreen	VSMC_M9
GO:0051963	0.05	0.98	10	79	regulation of synapse assembly	BP	1	THBS2,PTPRD,SETD5,TLR2,PDLIM5,NTRK3,SRPX2,GPC4,LHFPL4,WNT7A	darkolivegreen	VSMC_M9
GO:0022412	0.05	0.97	22	247	cellular process involved in reproduction in multicellular organism	BP	1	PSME4,UBE2J1,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,CCNA1,SOS1,BRCA2,TMF1,MYBL1,EIF2S2,ACVR1,SYCP2,PITHD1,ZFX,FMN2,SPIRE1,PAFAH1B1,PAQR8,TMEM119	darkolivegreen	VSMC_M9

GO:0048869	0.05	0.96	212	3033	cellular developmental process	BP	1	MALT1,AHI1,CAND1,CEP120,LRP12,EXT1,CDKL3,CHADL,WISP1,PTPRD,PLAA,TOPORS,JAK2,CLOCK,FBXO9,BZW2,HEMGN,HDAC9,CAVIN4,COL12A1,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA11,ZMPSTE24,UBE2J1,ACTR2,IFRD1,CAV2,ROCK2,INHBA,NOCT,ITGB1,FYN,ZEB1,KIF5B,CEP57,PIWIL4,PSMC2,NOX4,FNDC3A,GPR4,RB1,PICALM,CAMK1D,GATA3,CLN5,JMJD6,TRAK1,AZI2,STK24,OSBPL8,LIG4,MYO16,SMAD9,ATP11A,NR2C1,NDFIP1,CUL4A,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,DCHS1,TMF1,SCYL2,RNF6,LYN,MERTK,IFT88,MYBL1,EIF2AK3,SLC25A46,FBXL17,PALLD,ITCH,SULF1,MICAL2,FFAR4,MAP1B,RDH10,AGTR1,TLR2,RASA1,ATP2A2,VCAN,MBNL1,DHX36,SHOX2,ACVR1,SLC39A14,IRX5,NFKBIZ,NEDD9,ERG,LRRK2,SNX19,TBX15,BRSK2,PDLIM5,UBE3A,MBOAT1,CUL3,EIF4E,PHLDB2,TDP2,DNER,CHSY1,CAMSAP2,GPR89A,CASP7,CORO1C,ANOS1,NTRK3,LARP7,SEMA5B,IDH2,ABCB10,EIF2B5,TRAK2,ATF3,PIP5K1A,IQGAP1,ANK3,OSBPL11,CD3G,CCDC47,ADAM12,NRP2,HDGFL3,PITHD1,ZFX,CREB3L2,PTGS2,NCAM1,MYEF2,FZD2,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,DKK1,FMN2,ACTA2,AKT3,RBM47,WNT5B,NOTCH3,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,TRIP4,TBX6,CYFIP2,CLTC,DICER1,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,BAG5,ROCK1,ITGA2,ITGA1,SLC1A3,VAPA,AFG3L2,C1QTNF3,CD40LG,PAFAH1B1,GADD45B,RAPGEF1,ZDHHC7,COL11A1,PLPPR5,CDH11,BMPR2,AQP3,FRY,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,EFHD1,DNAJB9,PAQR8,NOV,RAP2A,WNT9A,ZPR1,SRD5A2,TMEM119,CHST11,UBE2V1,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0022406	0.05	0.98	9	76	membrane docking	BP	1	CAV2,RAB3B,ESYT2,CEP83,ATP2A2,USO1,VAPB,MSN,ROCK1	darkolivegreen	VSMC_M9
GO:0070861	0.05	0.99	4	23	regulation of protein exit from endoplasmic reticulum	BP	1	GCC2,UBE2J1,EDEM1,BRSK2	darkolivegreen	VSMC_M9
GO:1901565	0.05	0.96	77	1069	organonitrogen compound catabolic process	BP	1	SOCS6,MALT1,CDO1,AZIN1,EXT1,CDC23,UBQLN1,PLAA,TOPORS,CLOCK,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,PNPLA8,FYN,PSMB1,PSMC2,UGGT1,CBLC,NUB1,CLN5,NDFIP2,DNAJC3,EDEM1,VPS36,ABHD13,NDFIP1,CUL4A,TMF1,USP12,RNF6,UBXN2B,PDE7A,FBXL17,TDG,ITCH,USP47,LNPEP,LTN1,NUDT9,CBLB,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,PSMD12,DERA,UBE4A,CCDC47,TLK2,NPL,PITHD1,CDC27,SMURF1,FMN2,MSN,SPOP,DLST,TRIP4,OAZ2,CLPX,RLIM,RBBP6,C18orf25,PIN1,BAG5,ROCK1,BFAR,USP7,ACOT7,DNAJB9,VGLL4,FBXL7	darkolivegreen	VSMC_M9
GO:1990778	0.05	0.97	25	279	protein localization to cell periphery	BP	1	DENND4C,CCDC88A,ROCK2,RAB3B,ITGB1,KIF5B,PICALM,DCHS1,TMED2,APPL1,EHD4,PIP5K1A,ANK3,SEC23A,SMURF1,TNIK,BLZF1,ADAM10,CLTC,PIGW,ROCK1,RAB31,GPC4,ZDHHC7,RAP2A	darkolivegreen	VSMC_M9
GO:0003179	0.05	0.98	7	50	heart valve morphogenesis	BP	1	ROCK2,RB1,GATA3,DCHS1,ACVR1,ROCK1,BMPR2	darkolivegreen	VSMC_M9
GO:0014075	0.05	0.98	5	36	response to amine	BP	1	RRM2B,HDAC9,TRDMT1,ITGA2,RANBP2	darkolivegreen	VSMC_M9
GO:0007178	0.05	0.97	25	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	EXT1,BTBD11,JAK2,ASPN,ZNF451,CAV2,INHBA,LRRC32,SMAD9,ILK,SULF1,APPL1,THBS1,ACVR1,FERMT2,SKIL,SMURF1,DKK1,MYOCD,PIN1,CIDEA,BMPR2,NOV,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0045727	0.05	0.98	11	109	positive regulation of translation	BP	1	DNAJC3,RPL26,DHX29,LARP4,DHX36,THBS1,EIF2B5,FASTKD2,PLD1,PKM,ITGA2	darkolivegreen	VSMC_M9
GO:0006984	0.05	0.98	6	44	ER-nucleus signaling pathway	BP	1	EIF2AK3,TMED2,ATP2A2,PTPN1,CCDC47,MBTPS2	darkolivegreen	VSMC_M9
GO:0035065	0.05	0.98	6	45	regulation of histone acetylation	BP	1	ZNF451,ZMPSTE24,GATA3,SETD5,BRD7,MYOCD	darkolivegreen	VSMC_M9
GO:1901653	0.05	0.97	24	270	cellular response to peptide	BP	1	DENND4C,JAK2,HDAC9,CAV2,ROCK2,FYN,OSBPL8,ATP2B1,LYN,MAP1B,APPL1,AGTR1,USO1,SLC39A14,EPRS,IGF1R,PTPN1,CPEB2,TLR6,PKM,ROCK1,RAB31,MYO1C,ZDHHC7	darkolivegreen	VSMC_M9
GO:0016180	0.05	0.99	4	24	snRNA processing	BP	1	EXOSC9,TOE1,INTS14,INTS6	darkolivegreen	VSMC_M9
GO:0150076	0.05	0.99	4	24	neuroinflammatory response	BP	1	STAP1,ITGB1,LRRK2,PTGS2	darkolivegreen	VSMC_M9
GO:0048041	0.05	0.98	10	81	focal adhesion assembly	BP	1	ROCK2,THSD1,THBS1,PHLDB2,CORO1C,PIP5K1A,IQGAP1,FERMT2,ROCK1,ITGA2	darkolivegreen	VSMC_M9
GO:2001243	0.05	0.98	9	83	negative regulation of intrinsic apoptotic signaling pathway	BP	1	RRM2B,USP47,LRRK2,PTPN1,PTGS2,VDAC2,BAG5,ENO1,BDKRB2	darkolivegreen	VSMC_M9

GO:0042221	0.05	0.95	199	2921	response to chemical	BP	1	MALT1,CDO1,TBK1,RRM2B,EXT1,UBQLN1,DENND4C,PLAA,ABCB4,AKAP9,DNAJB5,JAK2,CLOCK,NPAS2,ASPN,ZNF451,HDAC9,MYO6,STAP1,UBE2J1,KBTBD2,ACTR2,CHRM2,CAV2,ROCK2,INHBA,PNPLA8,DDX1,NOCT,GPX7,ITGB1,FYN,KIF5B,CEP57,UGGT1,NOX4,RB1,TRDMT1,CAMK1D,NUB1,ACTR3,GATA3,LRRC32,SELENOV,DNAJC3,EDEM1,STK24,RIF1,OSBPL8,PPP1R12A,UFM1,LIG4,ATP2B1,SMAD9,NR2C1,SOS1,UBA5,ILK,ITGA5,HSPH1,TMF1,PLPP1,CNOT7,RNF6,LYN,GRAMD1A,ATP6V0A2,EIF2AK3,TMED2,PALLD,SMARCA5,SLC30A5,SULF1,USP47,MAT2A,XRN1,PDE12,FFAR4,MAP1B,APPL1,GDAP1,AGTR1,HK2,TLR2,ATP2A2,USO1,DHX36,THBS1,NUCB2,PPP2R2A,ACVR1,SLC39A14,ATP1A1,EHD4,LRRK2,TANK,BRSK2,UBE3A,CUL3,EIF4E,TROVE2,DNAJB14,ATP6V1A,EPRS,IGF1R,CASP7,CCDC186,ANOS1,ITPR2,NTRK3,TOMM20,PTPN1,SEMA5B,VAPB,ABCB10,EIF2B5,C2CD2L,ATF3,PIP5K1A,IQGAP1,RBBP7,ANK3,UBE4A,CCDC47,NRP2,MBTPS2,CREB3L2,TPR,PTGS2,NCAM1,ZC3H15,ITGAV,MYNN,FERMT2,SKIL,SMURF1,PLD1,CPEB2,FMN2,FAS,PLP2,ADSS,WNT5B,NOTCH3,HSPB7,TLR6,ENAH,ADAM10,MSN,KCNMB1,TPM1,TRIP4,CYFIP2,PKM,MAP2K4,MYOCD,SEMA7A,PIN1,SS18,RBBP8,BAG5,ROCK1,ITGA2,ITGA1,SLC1A3,RAB31,BFAR,CIDEA,MYO1C,TBXA2R,PAFAH1B1,ENO1,RAPGEF1,ZDHHC7,SLC25A24,WFDC1,PRKACB,DNAJB4,MIR186,RANBP2,BMPR2,AQP3,PTPN12,GDNF,CTGF,BDKRB2,EFHD1,LAMTOR3,DNAJB9,PAQR8,NOV,HSPA13,PMEPA1,RAP2A,WNT9A,ZPR1,NUP35,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0045669	0.05	0.98	7	56	positive regulation of osteoblast differentiation	BP	1	WISP1,ILK,FFAR4,ACVR1,FERMT2,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0003156	0.05	0.99	4	24	regulation of animal organ formation	BP	1	HOXA11,SULF1,DKK1,GDNF	darkolivegreen	VSMC_M9
GO:0045724	0.05	0.99	4	21	positive regulation of cilium assembly	BP	1	CEP120,CCDC88A,TAPT1,CCP110	darkolivegreen	VSMC_M9
GO:0010468	0.05	0.95	232	3428	regulation of gene expression	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,WISP1,KHDRBS3,ETF1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,EIF5B,ZNF451,HDAC9,CAVIN4,MYO6,STAP1,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,ACTR2,THAP5,GFPT1,ROCK2,INHBA,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,PICALM,TRDMT1,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,MBNL2,RIF1,PPP1R12A,FAM98A,RPL26,CEBPZ,SUPT20H,ATP2B1,SMAD9,NR2C1,NDFIP1,BRCA2,ILK,TMF1,HOXC10,ERI1,DHX29,CNOT7,RNF6,LYN,MERTK,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,SULF1,RIOK2,USP47,XRN1,PDE12,STOX2,MICAL2,FFAR4,APPL1,LARP4,ACTR8,TLR2,MBNL1,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,NFKBIZ,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,CUL3,EIF4E,TDP2,TROVE2,TIMM17A,KIAA1551,KPNA6,EPRS,NTRK3,WWC3,LARP7,CLK1,TAF5L,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,ANK3,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,PTGS2,MYEF2,FZD2,CWC22,DNAJA4,NPAT,ITGAV,MYNN,SKIL,PRRX1,PLD1,CPEB2,DKK1,ACTA2,NOTCH3,SRP9,TLR6,MAGED2,ADAM10,MSN,CLK2,TRIP4,TBX6,RLIM,MAGEE2,ADAM19,ZC3H14,TLE3,SMG8,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,SEMA7A,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,MYOM1,RICTOR,ZNF280C,C1QTNF3,CIDEA,GSPT1,ZC3H7A,MYSM1,CD40LG,USP7,LSM5,ENO1,ZNF644,ZNF326,PRKACB,THAP11,MIR186,BMPR2,FASTKD5,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,DNAJB9,RFXAP,NOV,FCN1,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF	darkolivegreen	VSMC_M9
GO:0032869	0.05	0.97	16	161	cellular response to insulin stimulus	BP	1	DENND4C,HDAC9,CAV2,OSBPL8,ATP2B1,APPL1,USO1,SLC39A14,EPRS,IGF1R,PTPN1,CPEB2,PKM,RAB31,MYO1C,ZDHHC7	darkolivegreen	VSMC_M9
GO:0030038	0.05	0.97	11	95	contractile actin filament bundle assembly	BP	1	CCDC88A,ROCK2,NOX4,PFN2,CUL3,PHLDB2,FERMT2,TPM1,GPR65,ROCK1,CTGF	darkolivegreen	VSMC_M9
GO:0043149	0.05	0.97	11	95	stress fiber assembly	BP	1	CCDC88A,ROCK2,NOX4,PFN2,CUL3,PHLDB2,FERMT2,TPM1,GPR65,ROCK1,CTGF	darkolivegreen	VSMC_M9
GO:0099174	0.05	0.99	4	22	regulation of presynapse organization	BP	1	PTPRD,NTRK3,GPC4,WNT7A	darkolivegreen	VSMC_M9
GO:1905606	0.05	0.99	4	22	regulation of presynapse assembly	BP	1	PTPRD,NTRK3,GPC4,WNT7A	darkolivegreen	VSMC_M9
GO:0043401	0.05	0.97	12	111	steroid hormone mediated signaling pathway	BP	1	JAK2,CLOCK,UFM1,NR2C1,UBA5,TMF1,PLPP1,RNF6,UBE3A,TRIP4,PAQR8,PMEPA1	darkolivegreen	VSMC_M9
GO:1902115	0.05	0.97	16	161	regulation of organelle assembly	BP	1	CEP120,PTPRD,SENP6,CCDC88A,CEP295,RAB3GAP1,IFT88,LRRK2,RAB3GAP2,NTRK3,C10orf90,TPR,CDKL1,TAPT1,MSN,CCP110	darkolivegreen	VSMC_M9
GO:0072507	0.06	0.96	28	323	divalent inorganic cation homeostasis	BP	1	SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,TMTC2,ATP2B1,LYN,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,SLC39A10,ITPR2,VAPB,ANK3,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0001738	0.06	0.97	10	84	morphogenesis of a polarized epithelium	BP	1	AHI1,BRSK2,FZD2,SMURF1,DKK1,MSN,GPC4,PAFAH1B1,ZDHHC7,WNT7A	darkolivegreen	VSMC_M9

GO:0051716	0.06	0.95	335	5042	cellular response to stimulus	BP	1	SOCS6,MALT1,AHI1,TBK1,PLEKHG1,RRM2B,LRP12,EXT1,WISP1,RMI1,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,SLC30A9,TOPORS,ABCB4,AKAP9,TFPI2,GNG11,JAK2,CLOCK,EXOC1,NPAS2,FBXO9,ASPN,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,UBA6,CCDC88A,ZMPSTE24,UBE2J1,PDE1C,KBTBD2,SH3BP5L,ACTR2,CHRM2,CAV2,ROCK2,INHBA,PNPLA8,DDX1,GPX7,ITGB1,RPF2,FYN,RINT1,KIF5B,CEP57,UGGT1,NOX4,GPR4,RB1,SUSD5,CBLC,CAMK1D,ACTR3,CDK3,MGAT5,GATA3,RAB3GAP1,JMJD6,LRRC32,NDFIP2,DNAJC3,AZI2,CYTH1,EDEM1,STK24,TNFAIP6,RIF1,OSBPL8,PPP1R12A,STAM2,RPL26,UFM1,LIG4,PIK3R4,MYO16,ATP2B1,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,PDS5B,BRCA2,UBA5,ILK,ITGA5,GPR84,DCHS1,TMF1,SCYL2,PARG,MTREX,PLPP1,CNOT7,RNF6,RASSF4,LYN,MERTK,GRAMD1A,ATP6V0A2,IPO7,PDE7A,TCP11L1,EIF2AK3,FBXL17,TDG,TMED2,SMARCA5,ITCH,NEK1,SULF1,USP47,MAT2A,CCDC125,LNPEP,XRN1,PDE12,FFAR4,MAP1B,APPL1,GDAP1,AGTR1,ACTR8,HK2,TLR2,RASA1,ATP2A2,USO1,BRAP,DHX36,THBS1,NUCB2,GPR176,SHOX2,KCTD9,ZDHHC16,ARL6,ACVR1,SLC39A14,INO80,NFKBIZ,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,NFRKB,CUL3,EIF4E,TDP2,DNER,TROVE2,UCHL5,CHSY1,DNAJB14,ATP6V1A,EPRS,IGF1R,GPR89A,STK38L,CASP7,CCDC186,CORO1C,ITPR2,NTRK3,WWC3,PTPN1,GRK3,ST8SIA1,KPNA1,PLIN1,SEMA5B,VAPB,ABCB10,EIF2B5,LTB4R,GPATCH3,C2CD2L,ATF3,PIP5K1A,IQGAP1,RBBP7,ANK3,UBE4A,CD3G,CCDC47,TLK2,NRP2,HDGFL3,MBTPS2,CREB3L2,TPR,CLEC14A,PTGS2,NCAM1,MYEF2,FZD2,IQCJ-	darkolivegreen	VSMC_M9
GO:0007179	0.06	0.97	16	156	transforming growth factor beta receptor signaling pathway	BP	1	ASPN,ZNF451,CAV2,LRRC32,SMAD9,APPL1,THBS1,ACVR1,FERMT2,SKIL,SMURF1,MYOCD,PIN1,CIDEA,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0030029	0.06	0.96	54	662	actin filament-based process	BP	1	PHACTR2,UTRN,AKAP9,JAK2,MYO6,STAP1,CCDC88A,ACTR2,ROCK2,ITGB1,NOX4,ACTR3,STARD13,ILK,PALLD,MICAL2,PFN2,RASA1,ATP2A2,NEDD9,ATP1A1,SPTBN5,BRSK2,PDLIM5,CUL3,PHLDB2,CORO1C,NTRK3,PTPN1,PIP5K1A,IQGAP1,SMTN,SH3KBP1,EHBP1L1,FERMT2,TNIK,FMN2,CDC42BPA,ENAH,MYO1E,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,NUP155,SPIRE1,MYO1C,PAFAH1B1,MYO1H,CTGF,RAP2A,CFL2	darkolivegreen	VSMC_M9
GO:0060393	0.06	0.98	6	44	regulation of pathway-restricted SMAD protein phosphorylation	BP	1	INHBA,ACVR1,DKK1,PIN1,BMPR2,PMEPA1	darkolivegreen	VSMC_M9
GO:0000956	0.06	0.97	11	102	nuclear-transcribed mRNA catabolic process	BP	1	ETF1,NOCT,EXOSC9,UPF2,CNOT7,XRN1,PDE12,DCP1A,DHX36,SMG8,GSPT1	darkolivegreen	VSMC_M9
GO:0006900	0.06	0.98	7	55	vesicle budding from membrane	BP	1	SEC24A,PICALM,TMED2,CUL3,VAPB,SEC23A,VAPA	darkolivegreen	VSMC_M9
GO:0046700	0.06	0.96	29	357	heterocycle catabolic process	BP	1	ETF1,ROCK2,NOCT,EXOSC9,TRDMT1,UPF2,MTREX,CNOT7,PDE7A,TDG,XRN1,PDE12,DCP1A,DHX36,NUDT9,DERA,FASTKD2,MYEF2,ZC3H14,SMG8,DICER1,ROCK1,CIDEA,GSPT1,LSM5,ACOT7,FASTKD5,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0070887	0.06	0.95	155	2230	cellular response to chemical stimulus	BP	1	MALT1,TBK1,EXT1,UBQLN1,DENND4C,PLAA,ABCB4,AKAP9,JAK2,CLOCK,ASPN,ZNF451,HDAC9,STAP1,ACTR2,CHRM2,CAV2,ROCK2,INHBA,PNPLA8,GPX7,FYN,KIF5B,CEP57,UGGT1,NOX4,RB1,CAMK1D,ACTR3,GATA3,LRRC32,STK24,RIF1,OSBPL8,PPP1R12A,UFM1,LIG4,ATP2B1,SMAD9,NR2C1,SOS1,UBA5,ILK,ITGA5,TMF1,PLPP1,CNOT7,RNF6,LYN,GRAMD1A,ATP6V0A2,EIF2AK3,TMED2,SMARCA5,SULF1,MAT2A,XRN1,PDE12,MAP1B,APPL1,GDAP1,AGTR1,HK2,TLR2,ATP2A2,USO1,DHX36,THBS1,ACVR1,SLC39A14,ATP1A1,EHD4,LRRK2,TANK,BRSK2,UBE3A,CUL3,EIF4E,TROVE2,DNAJB14,ATP6V1A,EPRS,IGF1R,CASP7,CCDC186,ITPR2,NTRK3,PTPN1,VAPB,ABCB10,C2CD2L,ATF3,PIP5K1A,IQGAP1,ANK3,NRP2,MBTPS2,CREB3L2,TPR,PTGS2,ZC3H15,MYNN,FERMT2,SKIL,SMURF1,CPEB2,FMN2,FAS,PLP2,WNT5B,TLR6,ADAM10,MSN,KCNMB1,TPM1,TRIP4,CYFIP2,PKM,MAP2K4,MYOCD,PIN1,BAG5,ROCK1,ITGA2,ITGA1,SLC1A3,RAB31,BFAR,CIDEA,MYO1C,TBXA2R,PAFAH1B1,ENO1,RAPGEF1,ZDHHC7,SLC25A24,BMPR2,AQP3,PTPN12,GDNF,CTGF,BDKRB2,EFHD1,LAMTOR3,DNAJB9,PAQR8,NOV,HSPA13,PMEPA1,RAP2A,WNT9A,ZPR1,NUP35,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0006940	0.06	0.98	6	46	regulation of smooth muscle contraction	BP	1	CHRM2,ATP2B1,PTGS2,MYOCD,ITGA2,TBXA2R	darkolivegreen	VSMC_M9
GO:0033157	0.06	0.97	18	196	regulation of intracellular protein transport	BP	1	LMAN1,GCC2,JAK2,UBE2J1,FYN,KIF5B,EDEM1,UFM1,XPO4,LRRK2,BRSK2,PTPN1,ANK3,TPR,PTGS2,OAZ2,MYO1C,ZPR1	darkolivegreen	VSMC_M9
GO:0032386	0.06	0.96	25	290	regulation of intracellular transport	BP	1	LMAN1,GCC2,JAK2,UBE2J1,FYN,RINT1,KIF5B,EDEM1,PPP1R12A,UFM1,YIPF5,XPO4,RIOK2,MAP1B,LRRK2,BRSK2,PTPN1,ANK3,TPR,PTGS2,MSN,OAZ2,USP7,MYO1C,ZPR1	darkolivegreen	VSMC_M9
GO:0007167	0.06	0.96	60	752	enzyme linked receptor protein signaling pathway	BP	1	AHI1,EXT1,PTPRD,BTBD11,JAK2,ASPN,ZNF451,STAP1,CCDC88A,CAV2,INHBA,FYN,CEP57,CBLC,GATA3,LRRC32,OSBPL8,SMAD9,SOS1,ILK,ITGA5,LYN,MERTK,EIF2AK3,SULF1,APPL1,RASA1,THBS1,ACVR1,SLC39A14,NEDD9,CBLB,IGF1R,NTRK3,PTPN1,IQGAP1,NRP2,CLEC14A,FERMT2,SKIL,SMURF1,DKK1,MYO1E,CYFIP2,MYOCD,PIN1,SS18,ITGA1,CIDEA,MYO1C,VAV2,RAPGEF1,BMPR2,PTPN12,ARF4,CTGF,BDKRB2,NOV,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0007409	0.06	0.96	31	341	axonogenesis	BP	1	EXT1,CDKL3,ITGB1,FYN,KIF5B,PICALM,GATA3,TRAK1,SOS1,ILK,RNF6,PALLD,MAP1B,SHOX2,BRSK2,ANOS1,SEMA5B,TRAK2,ANK3,NRP2,NCAM1,SKIL,NOTCH3,ENAH,SEMA7A,AFG3L2,PAFAH1B1,CDH11,BMPR2,GDNF,WNT7A	darkolivegreen	VSMC_M9

GO:0031347	0.06	0.96	32	397	regulation of defense response	BP	1	TBK1,WISP1,JAK2,CLOCK,NPAS2,STAP1,ZMPSTE24,FYN,GPR4,RB1,GATA3,TNFAIP6,NDFIP1,CNOT7,LYN,ITCH,FFAR4,APPL1,AGTR1,TLR2,NFKBIZ,LRRK2,PTPN1,GPATCH3,PTGS2,SEMA7A,ITGA2,RICTOR,C1QTNF3,WFDC1,NOV,FCN1	darkolivegreen	VSMC_M9
GO:1903421	0.06	0.98	4	24	regulation of synaptic vesicle recycling	BP	1	PLAA,LRRK2,VAMP4,ROCK1	darkolivegreen	VSMC_M9
GO:0009790	0.06	0.95	65	841	embryo development	BP	1	AHI1,LRIG3,EXT1,COL12A1,MYO6,HOXA9,HOXA10,HOXA11,ROCK2,INHBA,NOCT,ITGB1,GATA3,LIG4,SUPT20H,ATP11A,CUL4A,SOS1,BRCA2,ITGA5,DCHS1,PPP2R3A,TDG,TMED2,EIF2S2,SULF1,STOX2,MICAL2,RDH10,MBNL1,DHX36,SHOX2,ACVR1,IRX5,ETNK2,TBX15,CUL3,PHLDB2,NRP2,FZD2,NPAT,ITGAV,SKIL,PRRX1,TAPT1,DKK1,WNT5B,ADAM10,MYO1E,TBX6,RBBP6,RBBP8,ROCK1,ITGA2,RICTOR,PAFAH1B1,COL11A1,PRKACB,BMPR2,GDNF,WNT9A,ZPR1,CHST11,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0051248	0.06	0.95	60	813	negative regulation of protein metabolic process	BP	1	AZIN1,PLAA,TFPI2,ZNF451,SH3BP5L,ROCK2,NOCT,FYN,EXOSC9,DNAJC1,RB1,RTN2,PICALM,CBLC,MGAT5,DNAJC3,ILK,CNOT7,LYN,IPO7,EIF2AK3,TMED2,USP47,XRN1,PDE12,PI15,DCP1A,DHX36,THBS1,CBLB,LRRK2,EIF4E,UCHL5,EPRS,CORO1C,ANOS1,NTRK3,PTPN1,TLK2,TPR,PTGS2,ITGAV,RTN3,CPEB2,BOD1L1,DKK1,FMN2,SRP9,SRCIN1,MYOCD,PIN1,BAG5,ROCK1,USP7,GADD45B,WFDC1,MIR186,FRY,BDKRB2,PMEPA1	darkolivegreen	VSMC_M9
GO:0016339	0.06	0.98	4	22	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	BP	1	DCHS1,KIFAP3,CDH11,FXYD5	darkolivegreen	VSMC_M9
GO:0072384	0.06	0.97	9	78	organelle transport along microtubule	BP	1	KIF5B,TRAK1,MAP1B,TRAK2,KIFAP3,ACTR10,ARMCX3,PAFAH1B1,RAB6A	darkolivegreen	VSMC_M9
GO:0006605	0.06	0.96	22	262	protein targeting	BP	1	LMAN1,GCC2,FYN,TRAK1,EDEM1,PIK3R4,GDAP1,ARL6,LRRK2,TIMM17A,TOMM20,TRAK2,ANK3,SMURF1,AP4E1,SRP9,MYO1C,PMPCA,ZDHHC7,TOMM20L,SEC63,SRP19	darkolivegreen	VSMC_M9
GO:0044249	0.06	0.95	279	4271	cellular biosynthetic process	BP	1	SOCS6,MALT1,CDO1,AHI1,TBK1,CAND1,RRM2B,AZIN1,EXT1,DSE,PHF20L1,ETF1,RMI1,SLC30A9,TOPORS,TMEM165,JAK2,CLOCK,NPAS2,NOA1,ELOVL5,EIF5B,POLR2B,MGAT4A,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,PNPLA8,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,UGGT1,PDSS1,RB1,SUCLA2,PICALM,ABHD1,CAMK1D,ST3GAL3,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,RIF1,PPP1R12A,TMTC2,RPL26,KDELC1,LIG4,CEBPZ,SUPT20H,ALG5,SMAD9,NR2C1,BRCA2,ILK,B3GLCT,TMF1,GALNT7,HOXC10,HSD17B12,DHX29,PLPP1,CNOT7,RNF6,CSGALNACT2,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,USP47,MAT2A,XRN1,PDE12,STOX2,BDP1,MICAL2,APPL1,RDH10,PLOD2,LARP4,ACTR8,CERS5,ALDH18A1,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,GFM1,LIN54,ZDHHC16,ACVR1,WDR75,IRX5,MTERF3,INO80,GCNT4,SLC35B3,ETNK2,ATP1A1,DYRK1A,BRD7,MAN1A2,ERG,TBX15,UBE3A,MBOAT1,CUL3,EIF4E,TDP2,TROVE2,CHSY1,ATP6V1A,KPNA6,EPRS,BPNT1,IARS2,RAB3GAP2,GALNT17,NEK7,MRPL47,WWC3,ETNK1,LARP7,ST8SIA1,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,PIP5K1A,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,GATM,PTGS2,FAM20B,MYEF2,FZD2,ZC3H15,NPAT,TPI1,MYNN,GNPNAT1,SKIL,PRRX1,PLD1,CPEB2,SAMD8,BOD1L1,DKK1,PAPSS2,ADSS,NOTCH3,SRP9,TLR6,MAGED2,PHKG2,CLK2,TRIP4,TBX6,OAZ2,RLIM,MAGEE2,RBBP6,TLE3,PKM,DICER1,ARMCX3,PPM1D,PIGW,	darkolivegreen	VSMC_M9
GO:0010324	0.06	0.98	7	54	membrane invagination	BP	1	STAP1,THBS1,SMURF1,ITGA2,RAB31,SPIRE1,XKR9	darkolivegreen	VSMC_M9
GO:1905037	0.06	0.97	10	92	autophagosome organization	BP	1	UBQLN1,RAB3GAP1,UBXN2B,TMEM41B,IFT88,ATP2A2,LRRK2,RAB3GAP2,SMURF1,TRAPPC8	darkolivegreen	VSMC_M9
GO:0034661	0.06	0.98	5	35	ncRNA catabolic process	BP	1	EXOSC9,TRDMT1,MTREX,XRN1,DICER1	darkolivegreen	VSMC_M9
GO:0050808	0.06	0.96	30	329	synapse organization	BP	1	THBS2,PTPRD,ACTR2,FYN,SETD5,MAP1B,TLR2,DHX36,LRRK2,PDLIM5,UBE3A,DNER,IGF1R,NTRK3,ANK3,NRP2,DKK1,ADAM10,SRCIN1,SRPX2,PIN1,AFG3L2,GPC4,PAFAH1B1,ARF4,GDNF,LHFPL4,PDZRN3,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0032868	0.06	0.96	19	206	response to insulin	BP	1	DENND4C,HDAC9,KBTBD2,CAV2,OSBPL8,ATP2B1,LYN,APPL1,TLR2,USO1,SLC39A14,EPRS,IGF1R,PTPN1,CPEB2,PKM,RAB31,MYO1C,ZDHHC7	darkolivegreen	VSMC_M9
GO:0044089	0.06	0.96	37	441	positive regulation of cellular component biogenesis	BP	1	CAND1,CEP120,THBS2,PTPRD,AKAP9,CCDC88A,ACTR2,ROCK2,MPP7,CEP295,NOX4,ACTR3,RAB3GAP1,FAM98A,MAP1B,PFN2,PHLDB2,KIAA1551,RAB3GAP2,IQGAP1,TPR,FERMT2,TAPT1,TLR6,MSN,TPM1,GPR65,SRPX2,CCP110,ROCK1,RICTOR,SPIRE1,MYO1C,PLPPR5,CTGF,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0031123	0.06	0.97	10	94	RNA 3'-end processing	BP	1	ELAC1,EXOSC9,TOE1,SUPT5H,ERI1,DHX36,LARP7,INTS14,ZC3H14,INTS6	darkolivegreen	VSMC_M9
GO:0006418	0.06	0.98	5	37	tRNA aminoacylation for protein translation	BP	1	RARS2,DARS,EPRS,IARS2,TARS	darkolivegreen	VSMC_M9
GO:0002433	0.06	0.98	4	23	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	BP	1	FYN,LYN,APPL1,VAV2	darkolivegreen	VSMC_M9
GO:0038096	0.06	0.98	4	23	Fc-gamma receptor signaling pathway involved in phagocytosis	BP	1	FYN,LYN,APPL1,VAV2	darkolivegreen	VSMC_M9
GO:0014909	0.06	0.97	8	67	smooth muscle cell migration	BP	1	WISP1,NOX4,ILK,IQGAP1,TPM1,MYOCD,ITGA2,NOV	darkolivegreen	VSMC_M9
GO:0044057	0.06	0.96	33	398	regulation of system process	BP	1	AKAP9,JAK2,ZMPSTE24,CHRM2,ROCK2,INHBA,ATP2B1,ACPP,EIF2AK3,AGTR1,ATP2A2,SHOX2,ATP1A1,LRRK2,PTGS2,HSPB7,TPM1,DICER1,MYOCD,ANXA6,PIN1,ROCK1,ITGA2,NUP155,TBXA2R,ENO1,BMPR2,CTGF,BDKRB2,NOV,SHISA7,IRX3,WNT7A	darkolivegreen	VSMC_M9

GO:1901652	0.06	0.96	31	375	response to peptide	BP	1	CDO1,DENND4C,JAK2,HDAC9,KBTBD2,CAV2,ROCK2,FYN,OSBPL8,ATP2B1,LYN,MAP1B,APPL1,AGTR1,TLR2,USO1,SLC39A14,EPRS,IGF1R,PTPN1,EIF2B5,IQGAP1,PTGS2,CPEB2,TLR6,PKM,ROCK1,RAB31,MYO1C,ZDHHC7,CTGF	darkolivegreen	VSMC_M9
GO:0044270	0.06	0.96	29	361	cellular nitrogen compound catabolic process	BP	1	ETF1,ROCK2,NOCT,EXOSC9,TRDMT1,UPF2,MTREX,CNOT7,PDE7A,TDG,XRN1,PDE12,DCP1A,DHX36,NUDT9,DERA,FASTKD2,MYEF2,ZC3H14,SMG8,DICER1,ROCK1,CIDEA,GSPT1,LSM5,ACOT7,FASTKD5,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0010467	0.06	0.94	286	4455	gene expression	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,EXT1,WDR46,DDX46,PHF20L1,WISP1,KHDRBS3,ETF1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,NOA1,EIF5B,POLR2B,ZNF451,TRMO,HDAC9,CAVIN4,MYO6,STAP1,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,KBTBD2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,NOX4,RB1,RTN2,PICALM,ZC3H13,TRDMT1,TOE1,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,CLN5,JMJD6,DARS,PAX1,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,SETD5,MBNL2,RIF1,PPP1R12A,PRPF40A,FAM98A,RPL26,LIG4,CEBPZ,SUPT20H,ATP2B1,SMAD9,NR2C1,NDFIP1,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,DHX29,MTREX,CNOT7,RNF6,LYN,MERTK,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,SULF1,RIOK2,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,FFAR4,APPL1,U2SURP,LARP4,ACTR8,TLR2,MBNL1,LTN1,DCP1A,DHX36,THBS1,NAA25,SHOX2,GFM1,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SNRNP48,NFKBIZ,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,CUL3,EIF4E,TDP2,PUS3,TROVE2,TIMM17A,KIAA1551,KPNA6,RRP15,EPRS,IARS2,CASP7,MRPL47,NTRK3,WWC3,LARP7,CLK1,TAF5L,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,ANK3,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,PTGS2,MYEF2,FZD2,CWC22,DNAJA4,ZC3H15,NPAT,ITGAV,MYNN,SKIL,DTWD1,PRRX1,PLD1,CPEB2,DKK1,ACTA2,NOTCH3,SRP9,TLR6,MAGED2,ADAM10,MSN,CLK2,TRIP4,TBX6,RLIM,MAGEE2,INTS14,ADAM19,ZC3H14,CYFIP2,RBBP6,TLE3,SMG8,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,SEMA7A,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,MY	darkolivegreen	VSMC_M9
GO:0034645	0.06	0.95	235	3533	cellular macromolecule biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,RRM2B,EXT1,DSE,PHF20L1,ETF1,RMI1,SLC30A9,TOPORS,TMEM165,JAK2,CLOCK,NPAS2,NOA1,EIF5B,POLR2B,MGAT4A,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UBE2J1,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,ZEB1,EXOSC9,PIWIL4,DNAJC1,UGGT1,RB1,PICALM,CAMK1D,ST3GAL3,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,RIF1,PPP1R12A,TMTC2,RPL26,KDELC1,LIG4,CEBPZ,SUPT20H,ALG5,SMAD9,NR2C1,BRCA2,ILK,B3GLCT,TMF1,GALNT7,HOXC10,DHX29,CNOT7,RNF6,CSGALNACT2,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,LARP4,ACTR8,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,GFM1,LIN54,ZDHHC16,ACVR1,WDR75,IRX5,MTERF3,INO80,GCNT4,DYRK1A,BRD7,MAN1A2,ERG,TBX15,UBE3A,CUL3,EIF4E,TDP2,TROVE2,CHSY1,KPNA6,EPRS,IARS2,RAB3GAP2,GALNT17,NEK7,MRPL47,WWC3,LARP7,ST8SIA1,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,FAM20B,MYEF2,FZD2,ZC3H15,NPAT,MYNN,SKIL,PRRX1,PLD1,CPEB2,BOD1L1,DKK1,NOTCH3,SRP9,TLR6,MAGED2,PHKG2,TRIP4,TBX6,RLIM,MAGEE2,RBBP6,TLE3,PKM,DICER1,ARMCX3,PPM1D,PIGW,MAP2K4,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,C1GALT1C1,ZNF280C,GSPT1,TARS,MYSM1,CD40LG,USP7,ENO1,ZDHHC7,DPM2,RFWD3,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,DPM1,RFXAP,ZNF789,E2F3,GLIS3,	darkolivegreen	VSMC_M9
GO:0044248	0.06	0.95	121	1755	cellular catabolic process	BP	1	SOCS6,MALT1,CDO1,TBK1,ATP6V1C1,CDC23,ETF1,UBQLN1,PLAA,TOPORS,CLOCK,EXOC1,FBXO9,PSME4,UBA6,ZMPSTE24,UBE2J1,ROCK2,PNPLA8,NOCT,PSMB1,EXOSC9,PSMC2,UGGT1,TRDMT1,CBLC,ABHD1,UPF2,NUB1,RAB3GAP1,NDFIP2,SUPT5H,DNAJC3,EDEM1,STAM2,VPS36,GPCPD1,UFM1,PIK3R4,SUPT20H,NDFIP1,CUL4A,UBA5,TMF1,USP12,MTREX,CNOT7,RNF6,UBXN2B,GRAMD1A,ATP6V0A2,TMEM41B,IFT88,PDE7A,FBXL17,TDG,ITCH,USP47,LNPEP,XRN1,PDE12,HK2,ATP2A2,LTN1,DCP1A,DHX36,GPD2,NUDT9,LRRK2,BRSK2,UBE3A,CUL3,UCHL5,DNAJB14,ATP6V1A,RAB3GAP2,PSMD12,PTPN1,DERA,UBE4A,CCDC47,TLK2,NPL,PITHD1,FASTKD2,CDC27,MYEF2,TPI1,SMURF1,MSN,PHKG2,SPOP,DLST,TRIP4,CLPX,RLIM,ZC3H14,RBBP6,SMG8,C18orf25,CLTC,DICER1,GPRASP1,ATG4D,TRAPPC8,ETFA,BAG5,ROCK1,BFAR,CIDEA,GSPT1,USP7,LSM5,ACOT7,FASTKD5,GDNF,DNAJB9,ZPR1,VGLL4,FBXL7,AKR1D1	darkolivegreen	VSMC_M9
GO:0017148	0.06	0.96	15	158	negative regulation of translation	BP	1	ROCK2,NOCT,EXOSC9,CNOT7,EIF2AK3,XRN1,PDE12,DCP1A,DHX36,EIF4E,EPRS,TPR,CPEB2,SRP9,ROCK1	darkolivegreen	VSMC_M9
GO:0032786	0.06	0.98	4	25	positive regulation of DNA-templated transcription, elongation	BP	1	CCNT2,SUPT5H,THOC1,CDK13	darkolivegreen	VSMC_M9
GO:0044770	0.06	0.96	34	426	cell cycle phase transition	BP	1	CDC23,CLOCK,INHBA,ITGB1,RINT1,RB1,CDK3,RPL26,MYO16,CCNA1,CUL4A,FBXL17,RIOK2,USP47,APPL1,ACVR1,INO80,BRD7,BRSK2,CUL3,EIF4E,KLHL18,TPR,CDC27,NPAT,PPM1D,RBBP8,THOC1,GSPT1,RFWD3,E2F3,ZPR1,FBXL7,ZNF655	darkolivegreen	VSMC_M9

GO:0043069	0.06	0.95	51	681	negative regulation of programmed cell death	BP	1	MALT1,AHI1,RRM2B,TOPORS,JAK2,ITGB1,FYN,RB1,CAMK1D,GATA3,DNAJC3,UFM1,LIG4,ILK,ITGA5,TMF1,MERTK,ITCH,USP47,FFAR4,RASA1,THBS1,ACVR1,LRRK2,SLC39A10,IGF1R,PTPN1,SYCP2,PTGS2,ITGAV,KIFAP3,VDAC2,DKK1,FMN2,FAS,ADAM10,BNIP2,MAP2K4,MYOCD,PIN1,BAG5,BFAR,CIDEA,CD40LG,ENO1,ARF4,GDNF,BDKRB2,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0003012	0.06	0.96	28	332	muscle system process	BP	1	UTRN,AKAP9,CHRM2,ROCK2,ATP2B1,SULF1,ATP2A2,ATP1A1,PDLIM5,LTB4R,SMTN,GATM,PTGS2,ACTA2,TPM1,MAP2K4,MYOCD,ANXA6,PIN1,ROCK1,ITGA2,MYOM1,NUP155,TBXA2R,ENO1,GDNF,CTGF,BDKRB2	darkolivegreen	VSMC_M9
GO:0110020	0.07	0.97	10	86	regulation of actomyosin structure organization	BP	1	CCDC88A,ROCK2,NOX4,PFN2,PHLDB2,FERMT2,TPM1,GPR65,ROCK1,CTGF	darkolivegreen	VSMC_M9
GO:0048729	0.07	0.95	41	490	tissue morphogenesis	BP	1	AHI1,EXT1,HOXA11,INHBA,ITGB1,GATA3,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,TMED2,SULF1,MICAL2,RDH10,SHOX2,ACVR1,GCNT4,BRSK2,PHLDB2,NRP2,FZD2,FERMT2,SMURF1,DKK1,ACTA2,WNT5B,MSN,TPM1,TBX6,ITGA2,GPC4,PAFAH1B1,ZDHHC7,COL11A1,PRKACB,BMPR2,GDNF,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0010927	0.07	0.97	10	87	cellular component assembly involved in morphogenesis	BP	1	ITGB1,ILK,TMF1,TLR2,PHLDB2,TPM1,DICER1,FHOD3,PAFAH1B1,CFL2	darkolivegreen	VSMC_M9
GO:0031349	0.07	0.96	16	177	positive regulation of defense response	BP	1	TBK1,WISP1,JAK2,CLOCK,NPAS2,STAP1,FYN,GPR4,LYN,AGTR1,TLR2,NFKBIZ,LRRK2,PTGS2,ITGA2,FCN1	darkolivegreen	VSMC_M9
GO:0035336	0.07	0.98	4	25	long-chain fatty-acyl-CoA metabolic process	BP	1	ELOVL5,HSD17B12,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0072009	0.07	0.97	10	89	nephron epithelium development	BP	1	AHI1,EXT1,HOXA11,GATA3,ILK,DCHS1,IQGAP1,MYO1E,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0014812	0.07	0.97	9	79	muscle cell migration	BP	1	WISP1,NOX4,ILK,IQGAP1,TPM1,MYOCD,ROCK1,ITGA2,NOV	darkolivegreen	VSMC_M9
GO:0031325	0.07	0.94	171	2483	positive regulation of cellular metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,UBQLN1,SLC30A9,TOPORS,AKAP9,JAK2,CLOCK,NPAS2,ELOVL5,ZNF451,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ACTR2,ROCK2,INHBA,NOCT,FYN,EXOSC9,PSMC2,CEP295,GSAP,NOX4,RB1,PICALM,NUB1,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,NDFIP2,BRPF1,SUPT5H,DNAJC3,RIF1,OSBPL8,PPP1R12A,RPL26,PIK3R4,CEBPZ,SMAD9,NDFIP1,BRCA2,ILK,ITGA5,TMF1,HOXC10,DHX29,SCYL2,CNOT7,RNF6,LYN,MERTK,MYBL1,EIF2AK3,HCFC2,SMARCA5,ITCH,RIOK2,PDE12,STOX2,MICAL2,APPL1,RDH10,LARP4,AGTR1,TLR2,PFN2,DCP1A,DHX36,THBS1,ACVR1,WDR75,INO80,NEDD9,CBLB,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,UBE3A,SLC39A10,CUL3,TIMM17A,KPNA6,IGF1R,RAB3GAP2,NEK7,NTRK3,PTPN1,LARP7,TAF5L,ABCB10,EIF2B5,GPATCH3,ATF3,IQGAP1,EDRF1,BCLAF3,PITHD1,MBTPS2,FASTKD2,CREB3L2,PTGS2,FZD2,NPAT,FERMT2,PRRX1,SMURF1,TNIK,PLD1,TNFAIP8L3,DKK1,FMN2,ATAD1,FAS,TLR6,MSN,SRCIN1,PHKG2,TRIP4,TBX6,CLPX,CYFIP2,UACA,PKM,ARMCX3,MAP2K4,MYOCD,SEMA7A,PIN1,SS18,ROCK1,THOC1,ITGA2,ITGA1,RICTOR,SPIRE1,MYSM1,USP7,ENO1,VAV2,RANBP2,BMPR2,ANKRD49,ARF4,GDNF,CDK13,CTGF,LAMTOR3,RFXAP,E2F3,RAP2A,GLIS3,ZPR1,VGLL4,TMEM119,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0010770	0.07	0.97	8	65	positive regulation of cell morphogenesis involved in differentiation	BP	1	CDKL3,PTPRD,ACTR2,ILK,DHX36,NEDD9,FERMT2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0050770	0.07	0.96	14	132	regulation of axonogenesis	BP	1	CDKL3,TRAK1,ILK,RNF6,MAP1B,SHOX2,BRSK2,SEMA5B,TRAK2,SKIL,SEMA7A,PAFAH1B1,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0032870	0.07	0.95	37	450	cellular response to hormone stimulus	BP	1	DENND4C,JAK2,CLOCK,HDAC9,CAV2,ROCK2,INHBA,FYN,OSBPL8,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,LYN,MAP1B,APPL1,AGTR1,USO1,SLC39A14,ATP1A1,UBE3A,EIF4E,EPRS,IGF1R,PTPN1,CPEB2,TRIP4,PKM,ROCK1,RAB31,MYO1C,ZDHHC7,PAQR8,PMEPA1	darkolivegreen	VSMC_M9
GO:0038094	0.07	0.98	4	24	Fc-gamma receptor signaling pathway	BP	1	FYN,LYN,APPL1,VAV2	darkolivegreen	VSMC_M9
GO:0048704	0.07	0.97	9	83	embryonic skeletal system morphogenesis	BP	1	HOXA9,HOXA11,RDH10,SHOX2,IRX5,TBX15,PRRX1,COL11A1,CHST11	darkolivegreen	VSMC_M9
GO:0032330	0.07	0.98	6	46	regulation of chondrocyte differentiation	BP	1	CHADL,WISP1,HOXA11,SHOX2,CTGF,WNT9A	darkolivegreen	VSMC_M9
GO:0061099	0.07	0.98	4	26	negative regulation of protein tyrosine kinase activity	BP	1	SH3BP5L,CBLC,CBLB,SRCIN1	darkolivegreen	VSMC_M9
GO:0000184	0.07	0.98	5	34	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	ETF1,UPF2,DCP1A,SMG8,GSPT1	darkolivegreen	VSMC_M9
GO:0045823	0.07	0.98	4	25	positive regulation of heart contraction	BP	1	ATP2A2,ATP1A1,TPM1,CTGF	darkolivegreen	VSMC_M9
GO:0017015	0.07	0.97	11	102	regulation of transforming growth factor beta receptor signaling pathway	BP	1	ASPN,ZNF451,CAV2,THBS1,SKIL,SMURF1,MYOCD,PIN1,CIDEA,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0097035	0.07	0.98	6	43	regulation of membrane lipid distribution	BP	1	ABCB4,ATP11A,ATP10A,ATP11B,ATP8B4,XKR9	darkolivegreen	VSMC_M9
GO:0051493	0.07	0.95	38	457	regulation of cytoskeleton organization	BP	1	CEP120,AKAP9,SENP6,STAP1,CCDC88A,ACTR2,ROCK2,CEP295,NOX4,ACTR3,ILK,MAP1B,PFN2,RASA1,MAP9,DYRK1A,SPTBN5,PHLDB2,CAMSAP2,NTRK3,IQGAP1,HDGFL3,TPR,IQCJ-SCHIP1,FERMT2,TPM1,GPR65,CYFIP2,CLTC,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,PAFAH1B1,SKA2,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:1900027	0.07	0.98	4	26	regulation of ruffle assembly	BP	1	STAP1,FAM98A,PFN2,CORO1C	darkolivegreen	VSMC_M9
GO:0009566	0.07	0.97	11	113	fertilization	BP	1	HOXA9,HOXA10,HOXA11,FNDC3A,ADAM32,TUBGCP3,UBE3A,SYCP2,PITHD1,ZFX,VDAC2	darkolivegreen	VSMC_M9
GO:0071560	0.07	0.96	19	199	cellular response to transforming growth factor beta stimulus	BP	1	ASPN,ZNF451,CAV2,FYN,NOX4,LRRC32,SMAD9,APPL1,THBS1,ACVR1,FERMT2,SKIL,SMURF1,MYOCD,PIN1,CIDEA,PMEPA1,CHST11,WNT7A	darkolivegreen	VSMC_M9

GO:0001706	0.07	0.97	6	43	endoderm formation	BP	1	COL12A1,INHBA,ITGA5,ITGAV,DKK1,COL11A1	darkolivegreen	VSMC_M9
GO:0003015	0.07	0.96	17	180	heart process	BP	1	EXT1,AKAP9,JAK2,ZMPSTE24,CHRM2,FYN,NOX4,ATP2B1,ATP2A2,SHOX2,ATP1A1,HSPB7,TPM1,SGCD,NUP155,CTGF,IRX3	darkolivegreen	VSMC_M9
GO:0046174	0.07	0.98	4	25	polyol catabolic process	BP	1	GPD2,BPNT1,TPI1,IMPA1	darkolivegreen	VSMC_M9
GO:0017145	0.07	0.98	4	27	stem cell division	BP	1	EXT1,CUL3,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0051646	0.07	0.97	6	46	mitochondrion localization	BP	1	TRAK1,MAP1B,LRRK2,TRAK2,ACTR10,ARMCX3	darkolivegreen	VSMC_M9
GO:0072503	0.07	0.95	26	306	cellular divalent inorganic cation homeostasis	BP	1	SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,ATP2B1,LYN,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,SLC39A10,ITPR2,VAPB,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0051726	0.07	0.95	61	827	regulation of cell cycle	BP	1	CEP120,CDKL3,CDC23,CLOCK,SENP6,ZMPSTE24,THAP5,CAV2,ROCK2,INHBA,ITGB1,RINT1,CEP295,CCDC8,RB1,CDK3,GATA3,CCNT2,PRPF40A,RPL26,PIK3R4,MYO16,CCNA1,CUL4A,BRCA2,ILK,CDK8,UBXN2B,IPO7,FBXL17,RIOK2,USP47,APPL1,MAP9,THBS1,INO80,BRD7,CUL3,EIF4E,NEK7,IQGAP1,C10orf90,KLHL18,TPR,CDC27,PTGS2,CDKL1,SKIL,ADAM10,CLTC,MYOCD,PIN1,CCP110,THOC1,PAFAH1B1,GADD45B,RFWD3,PRKACB,CDK13,CTGF,ZNF655	darkolivegreen	VSMC_M9
GO:1902017	0.07	0.97	6	45	regulation of cilium assembly	BP	1	CEP120,CCDC88A,IFT88,CDKL1,TAPT1,CCP110	darkolivegreen	VSMC_M9
GO:0007163	0.07	0.96	18	189	establishment or maintenance of cell polarity	BP	1	ACTR2,ROCK2,ITGB1,MPP7,ACTR3,GATA3,CYTH1,ILK,UBXN2B,MAP1B,BRSK2,CD3G,MSN,ROCK1,RICTOR,PAFAH1B1,ARF4,WNT7A	darkolivegreen	VSMC_M9
GO:0051668	0.07	0.95	42	537	localization within membrane	BP	1	DENND4C,EXOC1,CCDC88A,COX18,ROCK2,RAB3B,ITGB1,FYN,KIF5B,PICALM,RAB3GAP1,DCHS1,TMED2,APPL1,TM9SF3,ARL6,EHD4,RAB3GAP2,PIP5K1A,ANK3,CCDC47,SEC23A,FERMT2,SMURF1,TNIK,BLZF1,ATAD1,SRP9,ADAM10,CLTC,PIGW,ROCK1,NUP155,RAB31,GPC4,MYO1C,ZDHHC7,LHFPL4,SEC63,RAP2A,SRP19,SHISA7	darkolivegreen	VSMC_M9
GO:0018108	0.07	0.95	25	287	peptidyl-tyrosine phosphorylation	BP	1	JAK2,STAP1,SH3BP5L,FYN,NOX4,CBLC,ITGA5,CNOT7,LYN,MERTK,NEK1,ACVR1,NEDD9,CBLB,DYRK1A,EHD4,IGF1R,NTRK3,PTPN1,CLK1,IQGAP1,SRCIN1,CLK2,MAP2K4,RICTOR	darkolivegreen	VSMC_M9
GO:0031401	0.07	0.95	57	747	positive regulation of protein modification process	BP	1	MALT1,TBK1,UBQLN1,TOPORS,AKAP9,JAK2,STAP1,CCDC88A,ROCK2,INHBA,FYN,CEP295,NOX4,GATA3,CCNT2,RAB3GAP1,NDFIP2,RIF1,OSBPL8,PPP1R12A,NDFIP1,ILK,ITGA5,LYN,PFN2,THBS1,ACVR1,NEDD9,CBLB,DYRK1A,BRD7,EHD4,LRRK2,TANK,UBE3A,SLC39A10,CUL3,RAB3GAP2,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,DKK1,FAS,TLR6,SRCIN1,MAP2K4,SEMA7A,PIN1,ITGA1,RICTOR,BMPR2,CTGF,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:0035307	0.07	0.98	5	35	positive regulation of protein dephosphorylation	BP	1	JAK2,PPP1R12A,SLC39A10,PIN1,ITGA1	darkolivegreen	VSMC_M9
GO:0003176	0.07	0.98	5	34	aortic valve development	BP	1	ROCK2,RB1,GATA3,ROCK1,BMPR2	darkolivegreen	VSMC_M9
GO:0043487	0.07	0.96	14	148	regulation of RNA stability	BP	1	ROCK2,NOCT,EXOSC9,TRDMT1,CNOT7,PDE12,DCP1A,DHX36,FASTKD2,MYEF2,ZC3H14,ROCK1,FASTKD5,GDNF	darkolivegreen	VSMC_M9
GO:0009888	0.07	0.94	102	1389	tissue development	BP	1	AHI1,EXT1,CHADL,WISP1,JAK2,CLOCK,ASPN,HDAC9,COL12A1,MYO6,HOXA11,ZMPSTE24,CAV2,ROCK2,INHBA,ITGB1,ZEB1,FNDC3A,GPR4,RB1,GATA3,CCNT2,GPCPD1,ATP2B1,STARD13,SOS1,BRCA2,NTN4,ILK,ITGA5,DCHS1,PPP2R3A,EIF2AK3,FBXL17,TMED2,PALLD,SULF1,MICAL2,RDH10,ATP2A2,SHOX2,ACVR1,SLC39A14,GCNT4,SNX19,BRSK2,PDLIM5,PHLDB2,DNER,CHSY1,CORO1C,SEMA5B,ATF3,PIP5K1A,IQGAP1,NRP2,CREB3L2,PTGS2,FZD2,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,DKK1,ACTA2,WNT5B,MSN,MYO1E,TPM1,TBX6,RBBP6,SGCD,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,ITGA2,MYOM1,GPC4,PAFAH1B1,RAPGEF1,ZDHHC7,COL11A1,PRKACB,BMPR2,AQP3,GDNF,CTGF,FOXN2,NOV,WNT9A,VGLL4,TMEM119,CHST11,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0043087	0.07	0.95	26	285	regulation of GTPase activity	BP	1	TBC1D15,CAV2,ITGB1,PICALM,RAB3GAP1,TMED2,CCDC125,RASA1,NEDD9,CBLB,LRRK2,RAB3GAP2,CORO1C,NTRK3,PIP5K1A,IQGAP1,ZC3H15,FERMT2,CPEB2,RGS7,GPR65,PIN1,RICTOR,PAFAH1B1,VAV2,RAPGEF1	darkolivegreen	VSMC_M9
GO:0019229	0.07	0.97	6	47	regulation of vasoconstriction	BP	1	ATP2B1,AGTR1,PTGS2,TBXA2R,BMPR2,BDKRB2	darkolivegreen	VSMC_M9
GO:0001667	0.07	0.95	30	360	ameboidal-type cell migration	BP	1	HDAC9,ROCK2,ITGB1,GATA3,CAPN7,STARD13,ILK,APPL1,PFN2,THBS1,ACVR1,CORO1C,SEMA5B,PIP5K1A,NRP2,CLEC14A,PTGS2,DNAJA4,AKT3,SRPX2,SEMA7A,ANXA6,ROCK1,ITGA2,TBXA2R,PAFAH1B1,BMPR2,GDNF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0007098	0.07	0.96	12	115	centrosome cycle	BP	1	CEP120,HAUS6,ROCK2,CEP295,PPP1R12A,BRCA2,UBXN2B,MAP9,HAUS2,C10orf90,CCP110,SSX2IP	darkolivegreen	VSMC_M9
GO:0009409	0.07	0.98	5	39	response to cold	BP	1	DNAJC3,ATP2B1,EIF2AK3,PLIN1,CIDEA	darkolivegreen	VSMC_M9
GO:0000413	0.07	0.98	4	32	protein peptidyl-prolyl isomerization	BP	1	PPIL1,NKTR,PIN1,RANBP2	darkolivegreen	VSMC_M9

GO:0048870	0.07	0.94	91	1234	cell motility	BP	1	LRP12,EXT1,WISP1,PLAA,JAK2,HDAC9,STAP1,CCDC88A,ROCK2,ITGB1,FYN,NOX4,CAMK1D,ACTR3,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,PRPF40A,CAPN7,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,TMF1,LYN,MERTK,PALLD,SULF1,CCDC125,MAP1B,APPL1,AGTR1,PFN2,THBS1,PGAM4,ACVR1,NEDD9,LRRK2,CUL3,PHLDB2,DNER,IGF1R,CORO1C,NTRK3,WWC3,SEMA5B,IDH2,PIP5K1A,IQGAP1,SH3KBP1,NRP2,CLEC14A,PTGS2,DNAJA4,ITGAV,FERMT2,PLD1,AKT3,WNT5B,CDC42BPA,ENAH,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,ITGA2,ITGA1,GPC4,MYO1C,TBXA2R,PAFAH1B1,VAV2,SSX2IP,BMPR2,ARF4,GDNF,CTGF,NOV,RAP2A,CFL2,WNT7A	darkolivegreen	VSMC_M9
GO:0051674	0.07	0.94	91	1234	localization of cell	BP	1	LRP12,EXT1,WISP1,PLAA,JAK2,HDAC9,STAP1,CCDC88A,ROCK2,ITGB1,FYN,NOX4,CAMK1D,ACTR3,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,PRPF40A,CAPN7,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,TMF1,LYN,MERTK,PALLD,SULF1,CCDC125,MAP1B,APPL1,AGTR1,PFN2,THBS1,PGAM4,ACVR1,NEDD9,LRRK2,CUL3,PHLDB2,DNER,IGF1R,CORO1C,NTRK3,WWC3,SEMA5B,IDH2,PIP5K1A,IQGAP1,SH3KBP1,NRP2,CLEC14A,PTGS2,DNAJA4,ITGAV,FERMT2,PLD1,AKT3,WNT5B,CDC42BPA,ENAH,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,ITGA2,ITGA1,GPC4,MYO1C,TBXA2R,PAFAH1B1,VAV2,SSX2IP,BMPR2,ARF4,GDNF,CTGF,NOV,RAP2A,CFL2,WNT7A	darkolivegreen	VSMC_M9
GO:1903844	0.07	0.96	11	104	regulation of cellular response to transforming growth factor beta stimulus	BP	1	ASPN,ZNF451,CAV2,THBS1,SKIL,SMURF1,MYOCD,PIN1,CIDEA,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0042147	0.07	0.97	9	80	retrograde transport, endosome to Golgi	BP	1	GCC2,CLN5,ARL1,LRRK2,TRAPPC10,HEATR5A,CLTC,USP7,RAB6A	darkolivegreen	VSMC_M9
GO:0051153	0.08	0.97	8	72	regulation of striated muscle cell differentiation	BP	1	HDAC9,ATP11A,SHOX2,DKK1,MYOCD,PIN1,NOV,TMEM119	darkolivegreen	VSMC_M9
GO:0007519	0.08	0.96	12	122	skeletal muscle tissue development	BP	1	HDAC9,CAV2,RB1,CCNT2,GPCPD1,SHOX2,DNER,ATF3,MYOCD,MYOM1,FOXN2,CFL2	darkolivegreen	VSMC_M9
GO:0007169	0.08	0.95	41	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	AHI1,EXT1,JAK2,STAP1,CCDC88A,CAV2,FYN,CEP57,CBLC,GATA3,OSBPL8,SOS1,ITGA5,LYN,MERTK,EIF2AK3,SULF1,APPL1,RASA1,THBS1,SLC39A14,NEDD9,CBLB,IGF1R,NTRK3,PTPN1,IQGAP1,NRP2,CLEC14A,MYO1E,CYFIP2,MYOCD,SS18,ITGA1,MYO1C,VAV2,RAPGEF1,PTPN12,ARF4,CTGF,BDKRB2	darkolivegreen	VSMC_M9
GO:0030003	0.08	0.95	35	434	cellular cation homeostasis	BP	1	SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,CLN5,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,ATP1A1,LRRK2,UBE3A,SLC39A10,ATP6V1A,GPR89A,ITPR2,VAPB,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,SLC1A3,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0006928	0.08	0.94	114	1565	movement of cell or subcellular component	BP	1	LRP12,EXT1,WISP1,PLAA,AKAP9,JAK2,HDAC9,MYO6,STAP1,CCDC88A,ACTR2,ROCK2,ITGB1,FYN,KIF5B,NOX4,CAMK1D,ACTR3,MGAT5,GATA3,TRAK1,STK24,TNFAIP6,OSBPL8,PRPF40A,CAPN7,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,TMF1,LYN,MERTK,IFT88,PALLD,DYNLRB1,SULF1,CCDC125,MAP1B,APPL1,AGTR1,PFN2,ATP2A2,THBS1,PGAM4,ACVR1,NEDD9,ATP1A1,LRRK2,CUL3,PHLDB2,DNER,IGF1R,CORO1C,ANOS1,NTRK3,WWC3,SEMA5B,IDH2,TRAK2,PIP5K1A,IQGAP1,SH3KBP1,NRP2,CLEC14A,PTGS2,NCAM1,DNAJA4,ITGAV,FERMT2,KIFAP3,KTN1,PLD1,ACTR10,FMN2,AKT3,WNT5B,CDC42BPA,NOTCH3,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,SRPX2,ARMCX3,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,ITGA2,ITGA1,NUP155,GPC4,MYO1C,TBXA2R,PAFAH1B1,KIF1B,VAV2,SSX2IP,BMPR2,MYO1H,RAB6A,ARF4,GDNF,CTGF,NOV,RAP2A,CFL2,WNT7A	darkolivegreen	VSMC_M9
GO:1903524	0.08	0.98	4	26	positive regulation of blood circulation	BP	1	ATP2A2,ATP1A1,TPM1,CTGF	darkolivegreen	VSMC_M9
GO:0055065	0.08	0.95	35	438	metal ion homeostasis	BP	1	EXT1,SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,PICALM,TMTC2,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,ATP1A1,SLC39A10,ATP6V1A,ITPR2,VAPB,ANK3,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,SLC1A3,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0043543	0.08	0.95	18	202	protein acylation	BP	1	PHF20L1,CLOCK,ZNF451,ZMPSTE24,CEP295,GATA3,BRPF1,SETD5,BRCA2,NAA25,ZDHHC16,BRD7,TAF5L,DLST,MYOCD,ZDHHC7,GTF2B,NAA20	darkolivegreen	VSMC_M9
GO:1902903	0.08	0.95	28	327	regulation of supramolecular fiber organization	BP	1	CHADL,AKAP9,CCDC88A,ACTR2,ROCK2,NOX4,RB1,ACTR3,MAP1B,PFN2,RASA1,DYRK1A,SPTBN5,PHLDB2,CAMSAP2,HDGFL3,FERMT2,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,CTGF,COLGALT1,CFL2	darkolivegreen	VSMC_M9
GO:0044093	0.08	0.94	84	1151	positive regulation of molecular function	BP	1	MALT1,TBC1D15,PLAA,TOPORS,AKAP9,JAK2,CLOCK,PSME4,STAP1,CCDC88A,CAV2,ROCK2,ITGB1,FYN,KIF5B,NOX4,RB1,PICALM,CAMK1D,GATA3,CCNT2,RAB3GAP1,CLN5,OSBPL8,PPP1R12A,PIK3R4,ILK,ARL1,LYN,MERTK,EIF2AK3,CCDC125,AGTR1,TLR2,PFN2,RASA1,DCP1A,THBS1,PDP1,NEDD9,LRRK2,TANK,SLC39A10,IGF1R,CORO1C,NEK7,NTRK3,PTPN1,PIP5K1A,IQGAP1,ANK3,MBTPS2,FZD2,ZC3H15,FERMT2,TNFAIP8L3,DKK1,RGS7,FAS,TLR6,STIM2,SRCIN1,TPM1,CLPX,GPR65,CYFIP2,UACA,MYOCD,PIN1,ITGA2,ITGA1,RICTOR,CD40LG,VAV2,RAPGEF1,GTF2B,RANBP2,BMPR2,ARF4,GDNF,TOR1AIP2,CTGF,LAMTOR3,UBE2V1	darkolivegreen	VSMC_M9
GO:0055080	0.08	0.95	39	494	cation homeostasis	BP	1	EXT1,SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,PICALM,CLN5,TMTC2,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,ATP1A1,LRRK2,UBE3A,SLC39A10,ATP6V1A,GPR89A,ITPR2,VAPB,ANK3,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,SLC1A3,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0060260	0.08	0.98	4	27	regulation of transcription initiation from RNA polymerase II promoter	BP	1	CAND1,ZNF451,DHX36,PPM1D	darkolivegreen	VSMC_M9

GO:0052547	0.08	0.95	23	294	regulation of peptidase activity	BP	1	MALT1,TFPI2,JAK2,PSME4,ROCK2,FYN,PICALM,LYN,EIF2AK3,USP47,PI15,THBS1,TANK,UCHL5,ANOS1,PTGS2,FAS,CLPX,CYFIP2,UACA,ROCK1,WFDC1,CTGF	darkolivegreen	VSMC_M9
GO:0030010	0.08	0.96	13	123	establishment of cell polarity	BP	1	ROCK2,ITGB1,MPP7,GATA3,CYTH1,UBXN2B,MAP1B,BRSK2,MSN,ROCK1,RICTOR,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0032880	0.08	0.94	53	693	regulation of protein localization	BP	1	LMAN1,STXBP5,CEP120,GCC2,JAK2,CLOCK,EXOC1,CCDC88A,UBE2J1,ROCK2,ITGB1,FYN,KIF5B,DNAJC1,CEP295,RB1,PICALM,NDFIP2,EDEM1,UFM1,NDFIP1,UBXN2B,XPO4,EIF2AK3,APPL1,TLR2,LRRK2,BRSK2,PTPN1,LARP7,IDH2,C2CD2L,IQGAP1,ANK3,TPR,PTGS2,FERMT2,KIAA0586,ADAM10,MSN,SRCIN1,OAZ2,CLTC,PIN1,MYOM1,C1QTNF3,GPC4,MYO1C,ZDHHC7,NOV,ZPR1,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0051017	0.08	0.96	14	139	actin filament bundle assembly	BP	1	CCDC88A,ROCK2,NOX4,PFN2,NEDD9,CUL3,PHLDB2,FERMT2,FMN2,TPM1,GPR65,ROCK1,SPIRE1,CTGF	darkolivegreen	VSMC_M9
GO:0009893	0.08	0.93	191	2815	positive regulation of metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,UBQLN1,SLC30A9,TOPORS,AKAP9,JAK2,CLOCK,NPAS2,ELOVL5,ZNF451,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,ROCK2,INHBA,DDX1,NOCT,FYN,EXOSC9,PSMC2,CEP295,GSAP,NOX4,RB1,PICALM,CAMK1D,NUB1,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,RIF1,OSBPL8,PPP1R12A,FAM98A,RPL26,PIK3R4,CEBPZ,SMAD9,NDFIP1,BRCA2,ILK,ITGA5,HSPH1,TMF1,HOXC10,DHX29,SCYL2,CNOT7,RNF6,LYN,MERTK,MYBL1,EIF2AK3,TMED2,HCFC2,SMARCA5,ITCH,SULF1,RIOK2,PDE12,STOX2,MICAL2,FFAR4,APPL1,RDH10,LARP4,AGTR1,TLR2,PFN2,DCP1A,DHX36,THBS1,ACVR1,WDR75,INO80,NEDD9,CBLB,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,UBE3A,SLC39A10,CUL3,TIMM17A,KPNA6,IGF1R,RAB3GAP2,NEK7,NTRK3,PTPN1,LARP7,TAF5L,ABCB10,EIF2B5,GPATCH3,ATF3,IQGAP1,ANK3,EDRF1,BCLAF3,PITHD1,MBTPS2,FASTKD2,CREB3L2,GATM,PTGS2,FZD2,DNAJA4,NPAT,FERMT2,PRRX1,SMURF1,TNIK,PLD1,TNFAIP8L3,DKK1,FMN2,ATAD1,ACTA2,FAS,TLR6,MSN,SRCIN1,PHKG2,TRIP4,TBX6,OAZ2,CLPX,ADAM19,CYFIP2,UACA,PKM,ARMCX3,MAP2K4,MYOCD,SEMA7A,PIN1,SS18,ROCK1,THOC1,ITGA2,ITGA1,MYOM1,RICTOR,C1QTNF3,SPIRE1,MYSM1,CD40LG,USP7,ENO1,VAV2,RANBP2,BMPR2,ANKRD49,ARF4,GDNF,CDK13,CTGF,LAMTOR3,DNAJB9,RFXAP,FCN1,E2F3,RAP2A,GLIS3,ZPR1,VGLL4,TMEM119,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0018212	0.08	0.95	25	290	peptidyl-tyrosine modification	BP	1	JAK2,STAP1,SH3BP5L,FYN,NOX4,CBLC,ITGA5,CNOT7,LYN,MERTK,NEK1,ACVR1,NEDD9,CBLB,DYRK1A,EHD4,IGF1R,NTRK3,PTPN1,CLK1,IQGAP1,SRCIN1,CLK2,MAP2K4,RICTOR	darkolivegreen	VSMC_M9
GO:0009725	0.08	0.94	50	652	response to hormone	BP	1	CDO1,DENND4C,JAK2,CLOCK,HDAC9,KBTBD2,CAV2,ROCK2,INHBA,FYN,GATA3,OSBPL8,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,LYN,MAP1B,APPL1,AGTR1,TLR2,USO1,THBS1,SLC39A14,ATP1A1,UBE3A,EIF4EPRS,IGF1R,NTRK3,PTPN1,EIF2B5,IQGAP1,RBBP7,PTGS2,CPEB2,TRIP4,PKM,ROCK1,ITGA2,RAB31,MYO1C,ZDHHC7,CTGF,PAQR8,PMEPA1,WNT7A	darkolivegreen	VSMC_M9
GO:0010628	0.08	0.94	59	803	positive regulation of gene expression	BP	1	MALT1,TBK1,JAK2,STAP1,ZMPSTE24,ROCK2,INHBA,DDX1,NOCT,GATA3,LRRC32,DNAJC3,RIF1,FAM98A,RPL26,TMF1,DHX29,EIF2AK3,TMED2,SULF1,APPL1,LARP4,TLR2,DHX36,THBS1,DYRK1A,LRRK2,TIMM17A,KPNA6,NTRK3,EIF2B5,ATF3,ANK3,FASTKD2,CREB3L2,PTGS2,DNAJA4,PLD1,DKK1,ACTA2,TLR6,MSN,ADAM19,PKM,MYOCD,SEMA7A,ROCK1,ITGA2,MYOM1,C1QTNF3,CD40LG,ENO1,GDNF,CTGF,DNAJB9,FCN1,ZPR1,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0006875	0.08	0.95	31	381	cellular metal ion homeostasis	BP	1	SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,ATP1A1,SLC39A10,ATP6V1A,ITPR2,VAPB,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,SLC1A3,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0060389	0.08	0.97	6	47	pathway-restricted SMAD protein phosphorylation	BP	1	INHBA,ACVR1,DKK1,PIN1,BMPR2,PMEPA1	darkolivegreen	VSMC_M9
GO:0010212	0.08	0.96	13	137	response to ionizing radiation	BP	1	CLOCK,ZMPSTE24,NOX4,GATA3,RPL26,LIG4,BRCA2,IKBIP,INO80,TANK,TLK2,CLK2,RFWD3	darkolivegreen	VSMC_M9
GO:0098930	0.08	0.97	7	58	axonal transport	BP	1	KIF5B,TRAK1,TRAK2,ACTR10,ARMCX3,PAFAH1B1,KIF1B	darkolivegreen	VSMC_M9
GO:0031623	0.08	0.96	9	85	receptor internalization	BP	1	AHI1,ITGB1,PICALM,SCYL2,GRK3,DKK1,ATAD1,CLTC,RAB31	darkolivegreen	VSMC_M9
GO:0048545	0.08	0.95	22	258	response to steroid hormone	BP	1	CDO1,JAK2,CLOCK,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,TLR2,THBS1,ATP1A1,UBE3A,EIF4E,NTRK3,RBBP7,PTGS2,TRIP4,CTGF,PAQR8,PMEPA1	darkolivegreen	VSMC_M9
GO:0097193	0.08	0.95	20	242	intrinsic apoptotic signaling pathway	BP	1	RRM2B,UBQLN1,TOPORS,JAK2,STK24,RPL26,CUL4A,BRCA2,EIF2AK3,USP47,LRRK2,BRSK2,CUL3,PTPN1,PTGS2,SKIL,VDAC2,BAG5,ENO1,BDKRB2	darkolivegreen	VSMC_M9
GO:0048705	0.08	0.95	17	186	skeletal system morphogenesis	BP	1	EXT1,HOXA9,HOXA11,ZMPSTE24,RDH10,SHOX2,IRX5,TBX15,CHSY1,PRRX1,ANXA6,COL11A1,BMPR2,CTGF,TMEM119,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0032878	0.08	0.98	4	24	regulation of establishment or maintenance of cell polarity	BP	1	ROCK2,GATA3,ROCK1,RICTOR	darkolivegreen	VSMC_M9
GO:0043039	0.08	0.97	5	40	tRNA aminoacylation	BP	1	RARS2,DARS,EPRS,IARS2,TARS	darkolivegreen	VSMC_M9
GO:0099024	0.08	0.97	6	47	plasma membrane invagination	BP	1	STAP1,THBS1,ITGA2,RAB31,SPIRE1,XKR9	darkolivegreen	VSMC_M9

GO:0097435	0.08	0.94	49	622	supramolecular fiber organization	BP	1	CEP120,EXT1,CHADL,AKAP9,JAK2,COL12A1,MYO6,CCDC88A,ACTR2,ROCK2,ITGB1,NOX4,RB1,ACTR3,TUBGCP3,ILK,MICAL2,MAP1B,PFN2,RASA1,NEDD9,DYRK1A,SPTBN5,CUL3,PHLDB2,CAMSAP2,HAUS2,CORO1C,SH3KBP1,HDGFL3,FERMT2,FMN2,ENAH,MYO1E,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,PAFAH1B1,COL11A1,MYO1H,CTGF,MZT1,COLGALT1,CFL2	darkolivegreen	VSMC_M9
GO:0007276	0.08	0.94	36	469	gamete generation	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,TNFAIP6,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,EIF2S2,MICAL2,DHX36,ACVR1,LRRK2,LARP7,SYCP2,PITHD1,ZFX,PTGS2,SKIL,FMN2,ADAM10,SPIRE1,PAFAH1B1,ANKRD49,PAQR8,TMEM119	darkolivegreen	VSMC_M9
GO:0043488	0.08	0.95	13	137	regulation of mRNA stability	BP	1	ROCK2,NOCT,EXOSC9,CNOT7,PDE12,DCP1A,DHX36,FASTKD2,MYEF2,ZC3H14,ROCK1,FASTKD5,GDNF	darkolivegreen	VSMC_M9
GO:0035303	0.08	0.96	11	106	regulation of dephosphorylation	BP	1	JAK2,ROCK2,MGAT5,PPP1R12A,SLC39A10,BOD1L1,PIN1,ROCK1,ITGA2,ITGA1,PPP1R2	darkolivegreen	VSMC_M9
GO:1901185	0.09	0.98	4	27	negative regulation of ERBB signaling pathway	BP	1	CBLC,CBLB,ITGA1,PTPN12	darkolivegreen	VSMC_M9
GO:0008219	0.09	0.93	109	1587	cell death	BP	1	MALT1,AHI1,TBK1,RRM2B,WISP1,UBQLN1,PRUNE2,TOPORS,JAK2,NPAS2,NOA1,ZMPSTE24,INHBA,PNPLA8,ITGB1,FYN,NOX4,RB1,PICALM,CAMK1D,GATA3,DNAJC3,STK24,RPL26,UFM1,LIG4,CUL4A,BRCA2,ILK,ITGA5,TMF1,LYN,MERTK,EIF2AK3,ITCH,SULF1,USP47,PDE12,FFAR4,HK2,TLR2,RASA1,THBS1,ZDHHC16,ACVR1,LRRK2,BRSK2,SLC39A10,CUL3,IGF1R,CASP7,NTRK3,PTPN1,KPNA1,EIF2B5,SYCP2,ATF3,G2E3,CD3G,SH3KBP1,FASTKD2,PTGS2,ITGAV,FERMT2,SKIL,RTN3,KIFAP3,TNFAIP8L3,VDAC2,DKK1,FMN2,FAS,TLR6,ADAM10,BNIP2,GPR65,CYFIP2,UACA,PKM,DICER1,ATG4D,MAP2K4,MYOCD,ANXA6,PIN1,BAG5,ROCK1,THOC1,ITGA1,VAPA,BFAR,CIDEA,CD40LG,GADD45B,ENO1,KIF1B,SLC25A24,ANKRD13C,BMPR2,XKR9,ARF4,GDNF,CTGF,BDKRB2,NOV,E2F3,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:1903827	0.09	0.94	36	454	regulation of cellular protein localization	BP	1	LMAN1,GCC2,JAK2,CCDC88A,UBE2J1,ROCK2,ITGB1,FYN,KIF5B,RB1,PICALM,EDEM1,UFM1,UBXN2B,XPO4,EIF2AK3,APPL1,LRRK2,BRSK2,PTPN1,LARP7,IQGAP1,ANK3,TPR,PTGS2,FERMT2,ADAM10,MSN,OAZ2,CLTC,PIN1,GPC4,MYO1C,ZDHHC7,ZPR1,SHISA7	darkolivegreen	VSMC_M9
GO:0034453	0.09	0.98	4	25	microtubule anchoring	BP	1	GCC2,CEP57,CEP350,FOPNL	darkolivegreen	VSMC_M9
GO:0035051	0.09	0.95	12	119	cardiocyte differentiation	BP	1	ZMPSTE24,ITGB1,DHX36,SHOX2,ACVR1,PDLIM5,DKK1,FHOD3,MAP2K4,MYOCD,PIN1,IRX3	darkolivegreen	VSMC_M9
GO:0010769	0.09	0.96	9	80	regulation of cell morphogenesis involved in differentiation	BP	1	CDKL3,PTPRD,ACTR2,ILK,DHX36,NEDD9,CORO1C,FERMT2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0061572	0.09	0.95	14	141	actin filament bundle organization	BP	1	CCDC88A,ROCK2,NOX4,PFN2,NEDD9,CUL3,PHLDB2,FERMT2,FMN2,TPM1,GPR65,ROCK1,SPIRE1,CTGF	darkolivegreen	VSMC_M9
GO:0048799	0.09	0.98	4	25	animal organ maturation	BP	1	EXT1,GATA3,DCHS1,MBTPS2	darkolivegreen	VSMC_M9
GO:0007200	0.09	0.97	6	53	phospholipase C-activating G protein-coupled receptor signaling pathway	BP	1	CHRM2,GPR4,FFAR4,AGTR1,LTB4R,GPR65	darkolivegreen	VSMC_M9
GO:0007292	0.09	0.96	10	101	female gamete generation	BP	1	INHBA,TNFAIP6,SOS1,BRCA2,SYCP2,ZFX,PTGS2,FMN2,SPIRE1,PAQR8	darkolivegreen	VSMC_M9
GO:0048008	0.09	0.97	6	48	platelet-derived growth factor receptor signaling pathway	BP	1	JAK2,CBLB,PTPN1,MYO1E,MYOCD,PTPN12	darkolivegreen	VSMC_M9
GO:0014910	0.09	0.96	7	60	regulation of smooth muscle cell migration	BP	1	WISP1,NOX4,ILK,IQGAP1,TPM1,MYOCD,ITGA2	darkolivegreen	VSMC_M9
GO:0050766	0.09	0.97	5	38	positive regulation of phagocytosis	BP	1	STAP1,CAMK1D,MERTK,ITGA2,RAB31	darkolivegreen	VSMC_M9
GO:0035306	0.09	0.97	6	47	positive regulation of dephosphorylation	BP	1	JAK2,PPP1R12A,SLC39A10,PIN1,ITGA2,ITGA1	darkolivegreen	VSMC_M9
GO:0048863	0.09	0.95	16	171	stem cell differentiation	BP	1	EXT1,FBXL17,ITCH,RDH10,DHX36,ACVR1,CORO1C,SEMA5B,NRP2,TAPT1,MYOCD,SEMA7A,ANXA6,GDNF,CDK13,WNT7A	darkolivegreen	VSMC_M9
GO:0008589	0.09	0.96	8	71	regulation of smoothened signaling pathway	BP	1	RB1,FBXL17,SHOX2,UCHL5,CHSY1,PRRX1,PRKACB,PDCL	darkolivegreen	VSMC_M9
GO:0090257	0.09	0.95	16	179	regulation of muscle system process	BP	1	AKAP9,CHRM2,ROCK2,ATP2B1,ATP2A2,ATP1A1,PTGS2,TPM1,MYOCD,ANXA6,PIN1,ROCK1,ITGA2,TBXA2R,ENO1,CTGF	darkolivegreen	VSMC_M9
GO:0031529	0.09	0.97	6	49	ruffle organization	BP	1	STAP1,FAM98A,PFN2,CORO1C,PIP5K1A,TPM1	darkolivegreen	VSMC_M9
GO:0097178	0.09	0.97	5	38	ruffle assembly	BP	1	STAP1,FAM98A,PFN2,CORO1C,PIP5K1A	darkolivegreen	VSMC_M9
GO:0071480	0.09	0.97	4	29	cellular response to gamma radiation	BP	1	ZMPSTE24,NOX4,RPL26,TLK2	darkolivegreen	VSMC_M9
GO:0071495	0.09	0.93	76	1018	cellular response to endogenous stimulus	BP	1	EXT1,DENND4C,AKAP9,JAK2,CLOCK,ASPN,ZNF451,HDAC9,ZMPSTE24,ACTR2,CHRM2,CAV2,ROCK2,INHBA,FYN,CEP57,NOX4,GATA3,LRRC32,OSBPL8,UFM1,ATP2B1,SMAD9,NR2C1,UBA5,ILK,TMF1,PLPP1,RNF6,LYN,SULF1,XRN1,MAP1B,APPL1,AGTR1,USO1,THBS1,ACVR1,SLC39A14,ATP1A1,LRRK2,UBE3A,EIF4E,EPRS,IGF1R,CASP7,ITPR2,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,SKIL,SMURF1,CPEB2,TLR6,TRIP4,PKM,MYOCD,PIN1,ROCK1,SLC1A3,RAB31,CIDEA,MYO1C,RAPGEF1,ZDHHC7,BMPR2,PTPN12,CTGF,LAMTOR3,PAQR8,PMEPA1,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0061097	0.09	0.96	8	74	regulation of protein tyrosine kinase activity	BP	1	STAP1,SH3BP5L,NOX4,CBLC,NEDD9,CBLB,PTPN1,SRCIN1	darkolivegreen	VSMC_M9
GO:0050731	0.09	0.95	13	136	positive regulation of peptidyl-tyrosine phosphorylation	BP	1	JAK2,STAP1,FYN,NOX4,ITGA5,LYN,ACVR1,NEDD9,EHD4,PTPN1,IQGAP1,SRCIN1,RICTOR	darkolivegreen	VSMC_M9
GO:0021675	0.09	0.96	7	59	nerve development	BP	1	EXT1,ILK,SULF1,NRP2,DICER1,SLC1A3,AFG3L2	darkolivegreen	VSMC_M9
GO:0072078	0.09	0.96	7	60	nephron tubule morphogenesis	BP	1	AHI1,HOXA11,GATA3,ILK,DCHS1,GDNF,IRX3	darkolivegreen	VSMC_M9

GO:1903311	0.09	0.94	21	247	regulation of mRNA metabolic process	BP	1	KHDRBS3,ROCK2,NOCT,EXOSC9,JMJD6,SUPT5H,MBNL2,CNOT7,PDE12,MBNL1,DCP1A,DHX36,DYRK1A,LARP7,FASTKD2,MYEF2,CWC22,ZC3H14,ROCK1,FASTKD5,GDNF	darkolivegreen	VSMC_M9
GO:0019439	0.09	0.94	29	375	aromatic compound catabolic process	BP	1	ETF1,ROCK2,NOCT,EXOSC9,TRDMT1,UPF2,MTREX,CNOT7,PDE7A,TDG,XRN1,PDE12,DCP1A,DHX36,NUDT9,DERA,FASTKD2,MYEF2,ZC3H14,SMG8,DICER1,ROCK1,CIDEA,GSPT1,LSM5,ACOT7,FASTKD5,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0071407	0.09	0.94	36	448	cellular response to organic cyclic compound	BP	1	ABCB4,AKAP9,JAK2,CLOCK,ACTR2,CHRM2,CAV2,ROCK2,INHBA,NOX4,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,GRAMD1A,XRN1,PDE12,GDAP1,ATP1A1,LRRK2,UBE3A,EIF4E,CASP7,ITPR2,PTGS2,MSN,KCNMB1,TRIP4,ITGA2,SLC1A3,RAPGEF1,PAQR8,PMEPA1	darkolivegreen	VSMC_M9
GO:0050772	0.09	0.96	8	68	positive regulation of axonogenesis	BP	1	TRAK1,ILK,MAP1B,SHOX2,SKIL,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:2000027	0.09	0.95	11	108	regulation of animal organ morphogenesis	BP	1	AHI1,HOXA11,GATA3,NTN4,SULF1,FZD2,SMURF1,DKK1,GPC4,GDNF,WNT7A	darkolivegreen	VSMC_M9
GO:0051173	0.09	0.92	159	2331	positive regulation of nitrogen compound metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,UBQLN1,SLC30A9,TOPORS,AKAP9,JAK2,CLOCK,NPAS2,ZNF451,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ACTR2,ROCK2,INHBA,NOCT,FYN,EXOSC9,PSMC2,CEP295,GSAP,NOX4,RB1,PICALM,NUB1,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,NDFIP2,BRPF1,SUPT5H,DNAJC3,RIF1,OSBPL8,PPP1R12A,RPL26,CEBPZ,SMAD9,NDFIP1,BRCA2,ILK,ITGA5,TMF1,HOXC10,DHX29,CNOT7,RNF6,LYN,MYBL1,EIF2AK3,HCFC2,SMARCA5,ITCH,RIOK2,PDE12,STOX2,MICAL2,LARP4,AGTR1,TLR2,PFN2,DCP1A,DHX36,THBS1,ACVR1,WDR75,INO80,NEDD9,CBLB,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,UBE3A,SLC39A10,CUL3,TIMM17A,KPNA6,RAB3GAP2,NEK7,NTRK3,PTPN1,LARP7,TAF5L,ABCB10,EIF2B5,GPATCH3,ATF3,IQGAP1,EDRF1,BCLAF3,PITHD1,MBTPS2,FASTKD2,CREB3L2,PTGS2,FZD2,NPAT,FERMT2,PRRX1,SMURF1,TNIK,PLD1,DKK1,FMN2,FAS,TLR6,MSN,SRCIN1,TRIP4,TBX6,OAZ2,CLPX,CYFIP2,UACA,PKM,ARMCX3,MAP2K4,MYOCD,SEMA7A,PIN1,SS18,ROCK1,THOC1,ITGA2,ITGA1,RICTOR,SPIRE1,MYSM1,USP7,ENO1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,CTGF,RFXAP,E2F3,RAP2A,GLIS3,ZPR1,VGLL4,TMEM119,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0045047	0.09	0.97	4	30	protein targeting to ER	BP	1	EDEM1,SRP9,SEC63,SRP19	darkolivegreen	VSMC_M9
GO:0030521	0.09	0.97	5	37	androgen receptor signaling pathway	BP	1	TMF1,PLPP1,RNF6,UBE3A,PMEPA1	darkolivegreen	VSMC_M9
GO:0032435	0.09	0.97	4	29	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	UCHL5,TLK2,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0060284	0.09	0.94	32	384	regulation of cell development	BP	1	CDKL3,PTPRD,CLOCK,HDAC9,HOXA11,ACTR2,ROCK2,TRAK1,LIG4,ILK,RNF6,LYN,MAP1B,TLR2,DHX36,SHOX2,NEDD9,LRRK2,CORO1C,NTRK3,SEMA5B,IDH2,TRAK2,FERMT2,SKIL,TBX6,DICER1,SEMA7A,ROCK1,PAFAH1B1,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0043038	0.09	0.97	5	41	amino acid activation	BP	1	RARS2,DARS,EPRS,IARS2,TARS	darkolivegreen	VSMC_M9
GO:0002431	0.09	0.97	4	27	Fc receptor mediated stimulatory signaling pathway	BP	1	FYN,LYN,APPL1,VAV2	darkolivegreen	VSMC_M9
GO:0048741	0.09	0.97	4	28	skeletal muscle fiber development	BP	1	HDAC9,CAV2,SHOX2,DNER	darkolivegreen	VSMC_M9
GO:0032879	0.09	0.92	144	2074	regulation of localization	BP	1	LMAN1,AHI1,UTRN,STXBP5,CEP120,AZIN1,WISP1,UBQLN1,PLAA,ABCB4,AKAP9,GCC2,JAK2,CLOCK,EXOC1,HDAC9,MYO6,STAP1,CCDC88A,ZMPSTE24,UBE2J1,ROCK2,INHBA,RAB3B,ITGB1,FYN,RINT1,KIF5B,DNAJC1,CEP295,NOX4,RB1,RTN2,PICALM,CAMK1D,MGAT5,GATA3,RAB3GAP1,NDFIP2,EDEM1,STK24,TNFAIP6,OSBPL8,PPP1R12A,UFM1,CAPN7,ATP2B1,NDFIP1,STARD13,YIPF5,ILK,TMF1,SCYL2,REM1,LYN,UBXN2B,MERTK,XPO4,EIF2AK3,SLC30A5,SULF1,RIOK2,CCDC125,FFAR4,MAP1B,APPL1,AGTR1,HK2,TLR2,PFN2,ATP2A2,DHX36,THBS1,PGAM4,ACVR1,NEDD9,ATP1A1,EHD4,LRRK2,BRSK2,PHLDB2,EPRS,IGF1R,GPR89A,CORO1C,ITPR2,NTRK3,PTPN1,LARP7,SEMA5B,IDH2,C2CD2L,IQGAP1,ANK3,OSBPL11,NRP2,TPR,PTGS2,DNAJA4,SEPT5,ITGAV,FERMT2,VAMP4,PLD1,KIAA0586,DKK1,ATAD1,AKT3,WNT5B,CLCNKB,STIM2,ADAM10,MSN,SRCIN1,KCNMB1,TPM1,OAZ2,SRPX2,CLTC,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,ITGA2,MYOM1,RAB31,C1QTNF3,CIDEA,GPC4,USP7,MYO1C,TBXA2R,ZDHHC7,SSX2IP,MIR186,BMPR2,FXYD5,GDNF,NOV,RAP2A,ZPR1,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0032231	0.09	0.95	10	92	regulation of actin filament bundle assembly	BP	1	CCDC88A,ROCK2,NOX4,PFN2,PHLDB2,FERMT2,TPM1,GPR65,ROCK1,CTGF	darkolivegreen	VSMC_M9
GO:0007015	0.09	0.94	31	373	actin filament organization	BP	1	JAK2,MYO6,CCDC88A,ACTR2,ROCK2,NOX4,ACTR3,MICAL2,PFN2,RASA1,NEDD9,SPTBN5,CUL3,PHLDB2,CORO1C,SH3KBP1,FERMT2,FMN2,ENAH,MYO1E,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,MYO1H,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:0050730	0.09	0.94	17	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	JAK2,STAP1,SH3BP5L,FYN,NOX4,CBLC,ITGA5,CNOT7,LYN,ACVR1,NEDD9,CBLB,EHD4,PTPN1,IQGAP1,SRCIN1,RICTOR	darkolivegreen	VSMC_M9
GO:0030518	0.09	0.95	10	96	intracellular steroid hormone receptor signaling pathway	BP	1	JAK2,CLOCK,UFM1,UBA5,TMF1,PLPP1,RNF6,UBE3A,TRIP4,PMEPA1	darkolivegreen	VSMC_M9
GO:0033627	0.09	0.96	7	60	cell adhesion mediated by integrin	BP	1	EXT1,ITGB1,ITGA5,LYN,ITGAV,ITGA2,NOV	darkolivegreen	VSMC_M9

GO:0098771	0.09	0.93	39	502	inorganic ion homeostasis	BP	1	EXT1,SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,PICALM,CLN5,TMTC2,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,ATP1A1,LRRK2,UBE3A,SLC39A10,ATP6V1A,GPR89A,ITPR2,VAPB,ANK3,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,SLC1A3,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0043484	0.09	0.95	12	126	regulation of RNA splicing	BP	1	KHDRBS3,JMJD6,MBNL2,MBNL1,DYRK1A,LARP7,CLK1,CWC22,CLK2,HNRNPH2,ZNF326,ZPR1	darkolivegreen	VSMC_M9
GO:0048588	0.09	0.94	18	195	developmental cell growth	BP	1	EXT1,CDKL3,PLAA,ITGB1,ILK,RNF6,MAP1B,PDLIM5,SEMA5B,IQGAP1,NRP2,SMURF1,CYFIP2,MAP2K4,SEMA7A,PIN1,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0006006	0.10	0.95	14	155	glucose metabolic process	BP	1	SLC35B4,ZMPSTE24,KBTBD2,HK2,SLC39A14,ATF3,TPI1,HK3,PHKG2,CLK2,C1QTNF3,USP7,ENO1,RANBP2	darkolivegreen	VSMC_M9
GO:0006111	0.10	0.97	5	40	regulation of gluconeogenesis	BP	1	SLC35B4,CLK2,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9
GO:0001893	0.10	0.97	4	29	maternal placenta development	BP	1	TMED2,STOX2,PTGS2,BMPR2	darkolivegreen	VSMC_M9
GO:0006352	0.10	0.95	10	105	DNA-templated transcription, initiation	BP	1	CAND1,ZNF451,TAF1B,SMARCA5,BDP1,DHX36,PPM1D,GTF2B,E2F3,TFB2M	darkolivegreen	VSMC_M9
GO:0007044	0.10	0.95	10	89	cell-substrate junction assembly	BP	1	ROCK2,THSD1,THBS1,PHLDB2,CORO1C,PIP5K1A,IQGAP1,FERMT2,ROCK1,ITGA2	darkolivegreen	VSMC_M9
GO:0002204	0.10	0.97	5	40	somatic recombination of immunoglobulin genes involved in immune response	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0002208	0.10	0.97	5	40	somatic diversification of immunoglobulins involved in immune response	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0045190	0.10	0.97	5	40	isotype switching	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0006873	0.10	0.93	35	444	cellular ion homeostasis	BP	1	SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,CLN5,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,ATP1A1,LRRK2,UBE3A,SLC39A10,ATP6V1A,GPR89A,ITPR2,VAPB,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,SLC1A3,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:1901361	0.10	0.93	30	395	organic cyclic compound catabolic process	BP	1	ETF1,ROCK2,NOCT,EXOSC9,TRDMT1,UPF2,MTREX,CNOT7,PDE7A,TDG,XRN1,PDE12,DCP1A,DHX36,NUDT9,DERA,FASTKD2,MYEF2,ZC3H14,SMG8,DICER1,ROCK1,CIDEA,GSPT1,LSM5,ACOT7,FASTKD5,GDNF,ZPR1,AKR1D1	darkolivegreen	VSMC_M9
GO:0071383	0.10	0.94	15	163	cellular response to steroid hormone stimulus	BP	1	JAK2,CLOCK,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,ATP1A1,UBE3A,EIF4E,TRIP4,PAQR8,PMEPA1	darkolivegreen	VSMC_M9
GO:0070201	0.10	0.93	34	436	regulation of establishment of protein localization	BP	1	LMAN1,STXBP5,CEP120,GCC2,JAK2,CLOCK,EXOC1,UBE2J1,FYN,KIF5B,DNAJC1,CEP295,NDFIP2,EDEM1,UFM1,NDFIP1,XPO4,TLR2,LRRK2,BRSK2,PTPN1,IDH2,C2CD2L,ANK3,TPR,PTGS2,KIAA0586,SRCIN1,OAZ2,MYOM1,C1QTNF3,MYO1C,NOV,ZPR1	darkolivegreen	VSMC_M9
GO:1900182	0.10	0.95	8	76	positive regulation of protein localization to nucleus	BP	1	JAK2,FYN,EIF2AK3,LARP7,TPR,PTGS2,FERMT2,ZPR1	darkolivegreen	VSMC_M9
GO:0045773	0.10	0.97	5	37	positive regulation of axon extension	BP	1	ILK,MAP1B,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0007275	0.10	0.91	259	3815	multicellular organism development	BP	1	MALT1,CDO1,AHI1,LRIG3,UTRN,CEP120,RRM2B,LRP12,EXT1,THBS2,CDKL3,CHADL,WISP1,PTPRD,PLAA,TOPORS,JAK2,CLOCK,NPAS2,ASPN,BZW2,HDAC9,CAVIN4,COL12A1,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UGP2,ACTR2,CHRM2,CAV2,ROCK2,INHBA,GREB1,DDX1,NOCT,PCDH18,ITGB1,FYN,ZEB1,KIF5B,FNDC3A,GPR4,RB1,PICALM,CAMK1D,UPF2,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,PAX1,TRAK1,SETD5,AZI2,STK24,RIF1,GPCPD1,UFM1,LIG4,MYO16,SUPT20H,ATP2B1,ALG5,ATP11A,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,DCHS1,TMF1,SCYL2,RNF6,LYN,PPP2R3A,MERTK,TMEM41B,IFT88,EIF2AK3,SLC25A46,FBXL17,TDG,TMED2,PALLD,EIF2S2,ITCH,SULF1,STOX2,MICAL2,MAP1B,RDH10,AGTR1,HK2,TLR2,RASA1,VCAN,MBNL1,DHX36,THBS1,SHOX2,ZDHHC16,ARL6,ACVR1,SLC39A14,IRX5,GCNT4,ETNK2,NFKBIZ,CBLB,DYRK1A,MAN1A2,ERG,LRRK2,SNX19,TBX15,BRSK2,PDLIM5,UBE3A,MBOAT1,CUL3,EIF4E,PHLDB2,TDP2,DNER,TROVE2,UCHL5,CHSY1,IGF1R,BPNT1,CAMSAP2,GPR89A,CASP7,CORO1C,ANOS1,NTRK3,SEMA5B,IDH2,ABCB10,EIF2B5,TRAK2,SYCP2,ATF3,PIP5K1A,IQGAP1,ANK3,CD3G,CCDC47,SMTN,ADAM12,NRP2,HDGFL3,PITHD1,MBTPS2,ZFX,CREB3L2,GATM,CLEC14A,PTGS2,NCAM1,MYEF2,FZD2,CDKL1,NPAT,ITGAV,GNPNAT1,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,DKK1,PAPSS2,ACTA2,AKT3,RBM47,WNT5B,NOTCH3,HSPB7,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,ITGB1BP2,TBX6,GPR65,ADAM19,CYFIP2,SRPX2,RBBP6,TLE3,SGCD,PKM,DICER1,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,RBBP8,BAG5,ROCK1,THOC1,ITGA2,ITGA1,MYOM1,RICTOR,SLC1A3,VAPA,AFG3L2,	darkolivegreen	VSMC_M9
GO:0042311	0.10	0.97	4	31	vasodilation	BP	1	EXT1,KCNMB1,ITGA1,BDKRB2	darkolivegreen	VSMC_M9
GO:1901983	0.10	0.96	7	63	regulation of protein acetylation	BP	1	ZNF451,ZMPSTE24,CEP295,GATA3,SETD5,BRD7,MYOCD	darkolivegreen	VSMC_M9
GO:0003209	0.10	0.97	4	26	cardiac atrium morphogenesis	BP	1	SOS1,SHOX2,ACVR1,BMPR2	darkolivegreen	VSMC_M9
GO:0046164	0.10	0.96	5	41	alcohol catabolic process	BP	1	GPD2,BPNT1,TPI1,IMPA1,AKR1D1	darkolivegreen	VSMC_M9
GO:0055086	0.10	0.93	32	439	nucleobase-containing small molecule metabolic process	BP	1	RRM2B,ELOVL5,GNE,UGP2,GFPT1,UGGT1,SUCLA2,ACPP,HSD17B12,PARG,PDE7A,TDG,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,IDH2,DERA,TPI1,GNPNAT1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,DPM1,ELOVL4	darkolivegreen	VSMC_M9
GO:0000209	0.10	0.94	18	203	protein polyubiquitination	BP	1	CDC23,PLAA,TOPORS,UBE2J1,RNF6,FBXL17,ITCH,LNPEP,UBE3A,CUL3,UBE4A,C10orf90,CDC27,SMURF1,SPOP,BFAR,FBXL7,UBE2V1	darkolivegreen	VSMC_M9
GO:0055001	0.10	0.94	14	150	muscle cell development	BP	1	HDAC9,ZMPSTE24,CAV2,ITGB1,ATP2A2,SHOX2,PDLIM5,DNER,TPM1,FHOD3,MAP2K4,PIN1,AFG3L2,CFL2	darkolivegreen	VSMC_M9

GO:0072088	0.10	0.96	7	62	nephron epithelium morphogenesis	BP	1	AHI1,HOXA11,GATA3,ILK,DCHS1,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0071709	0.10	0.96	5	39	membrane assembly	BP	1	PTPRD,CAV2,PICALM,UBXN2B,ANK3	darkolivegreen	VSMC_M9
GO:0016049	0.10	0.93	32	399	cell growth	BP	1	EXT1,CDKL3,PLAA,INHBA,ITGB1,EXOSC9,RB1,ILK,RNF6,ITCH,USP47,MAP1B,AGTR1,INO80,PDLIM5,SEMA5B,IQGAP1,RBBP7,NRP2,SMURF1,ADAM10,CYFIP2,MAP2K4,MYOCD,SEMA7A,PIN1,PAFAH1B1,ENO1,WFDC1,BMPR2,NOV,VGLL4	darkolivegreen	VSMC_M9
GO:0010595	0.10	0.95	10	105	positive regulation of endothelial cell migration	BP	1	HDAC9,ROCK2,GATA3,THBS1,NRP2,PTGS2,AKT3,SRPX2,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0031398	0.10	0.95	10	102	positive regulation of protein ubiquitination	BP	1	MALT1,UBQLN1,TOPORS,NDFIP2,NDFIP1,CBLB,LRRK2,UBE3A,CUL3,PIN1	darkolivegreen	VSMC_M9
GO:0007548	0.10	0.94	18	206	sex differentiation	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,BRCA2,TMF1,MERTK,EIF2S2,RDH10,IRX5,UBE3A,EIF2B5,SYCP2,ZFX,SRD5A2,WNT7A	darkolivegreen	VSMC_M9
GO:0042310	0.10	0.96	7	62	vasoconstriction	BP	1	ATP2B1,AGTR1,PTGS2,ACTA2,TBXA2R,BMPR2,BDKRB2	darkolivegreen	VSMC_M9
GO:1905314	0.10	0.96	5	37	semi-lunar valve development	BP	1	ROCK2,RB1,GATA3,ROCK1,BMPR2	darkolivegreen	VSMC_M9
GO:2000146	0.10	0.94	20	234	negative regulation of cell motility	BP	1	STAP1,GATA3,STK24,OSBPL8,STARD13,ILK,SULF1,CCDC125,PFN2,THBS1,PHLDB2,CORO1C,IDH2,DNAJA4,TPM1,MYOCD,PIN1,TBXA2R,NOV,RAP2A	darkolivegreen	VSMC_M9
GO:0140694	0.10	0.93	25	305	non-membrane-bounded organelle assembly	BP	1	CEP120,HAUS6,SENP6,CENPC,NOCT,ITGB1,RPF2,CEP295,TUBGCP3,DHX29,CNOT7,MAP9,MTERF3,INO80,HAUS2,NEK7,C10orf90,FASTKD2,TPR,MSN,TPM1,FHOD3,CCP110,MZT1,CFL2	darkolivegreen	VSMC_M9
GO:0070167	0.10	0.95	8	74	regulation of biomineral tissue development	BP	1	ASPN,ZMPSTE24,ROCK2,ATP2B1,ACVR1,ROCK1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0006952	0.10	0.92	67	949	defense response	BP	1	SOCS6,MALT1,CDO1,TBK1,EXT1,WISP1,PLAA,JAK2,CLOCK,EXOC1,NPAS2,FBXO9,HDAC9,STAP1,ZMPSTE24,ACTR2,INHBA,DDX1,ITGB1,FYN,KIF5B,NOX4,GPR4,RB1,CAMK1D,NUB1,ACTR3,GATA3,DNAJC3,TNFAIP6,NDFIP1,TMF1,CNOT7,LYN,IPO7,ITCH,PDE12,FFAR4,APPL1,AGTR1,TLR2,DHX36,THBS1,ACVR1,NFKBIZ,LRRK2,EIF4E,KPNA6,EPRS,PTPN1,LTB4R,GPATCH3,PTGS2,TLR6,SEMA7A,ITGA2,RICTOR,C1QTNF3,CD40LG,MYO1C,TBXA2R,WFDC1,CLEC4D,BDKRB2,NOV,FCN1,NDUFAF4	darkolivegreen	VSMC_M9
GO:0048856	0.10	0.91	282	4193	anatomical structure development	BP	1	MALT1,CDO1,AHI1,LRIG3,UTRN,CEP120,RRM2B,LRP12,EXT1,THBS2,CDKL3,CHADL,WISP1,PTPRD,PLAA,TOPORS,JAK2,CLOCK,NPAS2,ASPN,BZW2,HDAC9,CAVIN4,COL12A1,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,UGP2,ACTR2,IFRD1,CHRM2,CAV2,ROCK2,INHBA,GREB1,DDX1,NOCT,PCDH18,ITGB1,FYN,ZEB1,KIF5B,CEP57,NOX4,FNDC3A,GPR4,RB1,PICALM,CAMK1D,UPF2,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,PAX1,TRAK1,LRRC32,SETD5,AZI2,STK24,RIF1,PRPF40A,GPCPD1,UFM1,LIG4,MYO16,SUPT20H,ATP2B1,ALG5,SMAD9,ATP11A,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,DCHS1,TMF1,SCYL2,RNF6,LYN,PPP2R3A,MERTK,TMEM41B,IFT88,EIF2AK3,SLC25A46,FBXL17,TDG,TMED2,PALLD,EIF2S2,ITCH,SULF1,STOX2,MICAL2,MAP1B,RDH10,LARP4,AGTR1,HK2,TLR2,RASA1,ATP2A2,VCAN,MBNL1,DHX36,THBS1,SHOX2,ZDHHC16,ARL6,ACVR1,SLC39A14,IRX5,GCNT4,ETNK2,NFKBIZ,NEDD9,CBLB,DYRK1A,MAN1A2,ERG,LRRK2,SNX19,TBX15,BRSK2,PDLIM5,ATP10A,UBE3A,MBOAT1,CUL3,EIF4E,PHLDB2,TDP2,DNER,TROVE2,UCHL5,CHSY1,IGF1R,BPNT1,CAMSAP2,GPR89A,CASP7,CORO1C,ANOS1,NTRK3,KPNA1,SEMA5B,IDH2,ABCB10,EIF2B5,TRAK2,SYCP2,ATF3,PIP5K1A,IQGAP1,ANK3,CD3G,CCDC47,SMTN,ADAM12,SH3KBP1,NRP2,HDGFL3,PITHD1,MBTPS2,ZFX,CREB3L2,GATM,CLEC14A,PTGS2,NCAM1,MYEF2,FZD2,CDKL1,NPAT,ITGAV,GNPNAT1,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,DKK1,FMN2,PAPSS2,ACTA2,AKT3,RBM47,WNT5B,NOTCH3,HSPB7,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,ITGB1BP2,TRIP4,TBX6,GPR65,ADAM19,CYFIP2,SRPX2,RBBP6,TLE3,SGCD,PKM,DICER1,FHOD3,MAP2K4,MYOCD,SEMA7A,ANK3,PIN1,SS1	darkolivegreen	VSMC_M9
GO:0071526	0.10	0.96	5	38	semaphorin-plexin signaling pathway	BP	1	SEMA5B,NRP2,NCAM1,SEMA7A,GDNF	darkolivegreen	VSMC_M9
GO:0048010	0.10	0.96	6	48	vascular endothelial growth factor receptor signaling pathway	BP	1	FYN,ITGA5,SULF1,PTPN1,CLEC14A,VAV2	darkolivegreen	VSMC_M9
GO:0006473	0.10	0.94	15	168	protein acetylation	BP	1	PHF20L1,CLOCK,ZNF451,ZMPSTE24,CEP295,GATA3,BRPF1,SETD5,BRCA2,NAA25,BRD7,TAF5L,MYOCD,GTF2B,NAA20	darkolivegreen	VSMC_M9
GO:0031399	0.10	0.92	84	1182	regulation of protein modification process	BP	1	MALT1,TBK1,UBQLN1,PLAA,TOPORS,AKAP9,JAK2,ZNF451,STAP1,CCDC88A,ZMPSTE24,SH3BP5L,ROCK2,INHBA,FYN,CEP295,NOX4,RB1,CBLC,MGAT5,GATA3,CCNT2,RAB3GAP1,NDFIP2,DNAJC3,SETD5,RIF1,OSBPL8,PPP1R12A,CCNA1,NDFIP1,ILK,ITGA5,PARG,CNOT7,LYN,IPO7,EIF2AK3,TMED2,ITCH,PFN2,THBS1,ACVR1,NEDD9,CBLB,DYRK1A,BRD7,EHD4,LRRK2,TANK,UBE3A,SLC39A10,CUL3,RAB3GAP2,CORO1C,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,BOD1L1,DKK1,FAS,TLR6,SRCIN1,SMG8,MAP2K4,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,RICTOR,GADD45B,BMPR2,FRY,CTGF,BDKRB2,PMEPA1,RAP2A,TMEM119,PPP1R2	darkolivegreen	VSMC_M9
GO:0051258	0.10	0.93	21	250	protein polymerization	BP	1	AKAP9,JAK2,ACTR2,ACTR3,TUBGCP3,MAP1B,PFN2,RASA1,ARL6,DYRK1A,SPTBN5,CAMSAP2,HAUS2,HDGFL3,VDAC2,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C,MZT1	darkolivegreen	VSMC_M9
GO:0070897	0.10	0.97	4	31	transcription preinitiation complex assembly	BP	1	CAND1,TAF1B,BDP1,GTF2B	darkolivegreen	VSMC_M9
GO:0016236	0.10	0.93	22	265	macroautophagy	BP	1	TBK1,ATP6V1C1,UBQLN1,PLAA,EXOC1,RAB3GAP1,SUPT5H,STAM2,VPS36,UFM1,PIK3R4,UBA5,UBXN2B,ATP6V0A2,TMEM41B,IFT88,ATP2A2,LRRK2,ATP6V1A,RAB3GAP2,SMURF1,TRAPPC8	darkolivegreen	VSMC_M9
GO:0042551	0.10	0.96	5	38	neuron maturation	BP	1	RB1,CLN5,NTN4,LRRK2,TBX6	darkolivegreen	VSMC_M9

GO:0071346	0.10	0.95	8	80	cellular response to interferon-gamma	BP	1	JAK2,ACTR2,KIF5B,ACTR3,PDE12,TLR2,EPRS,MYO1C	darkolivegreen	VSMC_M9
GO:0003007	0.10	0.94	18	197	heart morphogenesis	BP	1	AHI1,EXT1,ZMPSTE24,GATA3,SOS1,ILK,DCHS1,TMED2,MICAL2,SHOX2,ACVR1,NRP2,FZD2,DKK1,TPM1,TBX6,COL11A1,BMPR2	darkolivegreen	VSMC_M9
GO:0007033	0.11	0.94	14	157	vacuole organization	BP	1	EXT1,UBQLN1,TMEM165,RAB3GAP1,CLN5,ACPP,UBXN2B,TMEM41B,IFT88,ATP2A2,LRRK2,RAB3GAP2,SMURF1,TRAPPC8	darkolivegreen	VSMC_M9
GO:0046785	0.11	0.95	8	74	microtubule polymerization	BP	1	AKAP9,TUBGCP3,MAP1B,DYRK1A,CAMSAP2,HAUS2,HDGFL3,MZT1	darkolivegreen	VSMC_M9
GO:0032886	0.11	0.93	18	202	regulation of microtubule-based process	BP	1	CEP120,AKAP9,SENP6,ROCK2,CEP295,MAP1B,MAP9,PGAM4,DYRK1A,PHLDB2,CAMSAP2,C10orf90,HDGFL3,TPR,CLTC,ROCK1,PAFAH1B1,SKA2	darkolivegreen	VSMC_M9
GO:0090303	0.11	0.96	5	42	positive regulation of wound healing	BP	1	WISP1,ITGB1,THBS1,FERMT2,TBXA2R	darkolivegreen	VSMC_M9
GO:0007492	0.11	0.95	7	59	endoderm development	BP	1	EXT1,COL12A1,INHBA,ITGA5,ITGAV,DKK1,COL11A1	darkolivegreen	VSMC_M9
GO:0110110	0.11	0.97	4	30	positive regulation of animal organ morphogenesis	BP	1	HOXA11,GATA3,DKK1,GDNF	darkolivegreen	VSMC_M9
GO:1901976	0.11	0.97	4	31	regulation of cell cycle checkpoint	BP	1	CUL4A,TPR,THOC1,RFWD3	darkolivegreen	VSMC_M9
GO:0010562	0.11	0.92	51	669	positive regulation of phosphorus metabolic process	BP	1	MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,ROCK2,INHBA,FYN,NOX4,CCNT2,OSBPL8,PPP1R12A,PIK3R4,ILK,ITGA5,LYN,MERTK,PFN2,THBS1,ACVR1,NEDD9,EHD4,LRRK2,SLC39A10,IGF1R,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,TNFAIP8L3,DKK1,FAS,TLR6,SRCIN1,MAP2K4,SEMA7A,PIN1,ITGA2,ITGA1,RICTOR,ENO1,VAV2,RANBP2,BMPR2,CTGF,LAMTOR3,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:0045937	0.11	0.92	51	669	positive regulation of phosphate metabolic process	BP	1	MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,ROCK2,INHBA,FYN,NOX4,CCNT2,OSBPL8,PPP1R12A,PIK3R4,ILK,ITGA5,LYN,MERTK,PFN2,THBS1,ACVR1,NEDD9,EHD4,LRRK2,SLC39A10,IGF1R,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,TNFAIP8L3,DKK1,FAS,TLR6,SRCIN1,MAP2K4,SEMA7A,PIN1,ITGA2,ITGA1,RICTOR,ENO1,VAV2,RANBP2,BMPR2,CTGF,LAMTOR3,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:0051897	0.11	0.95	9	88	positive regulation of protein kinase B signaling	BP	1	ITGB1,GATA3,OSBPL8,ILK,THBS1,IGF1R,FERMT2,TNFAIP8L3,RICTOR	darkolivegreen	VSMC_M9
GO:0034329	0.11	0.93	28	318	cell junction assembly	BP	1	THBS2,PTPRD,ROCK2,MPP7,SETD5,THSD1,DCHS1,MAP1B,TLR2,THBS1,PDLIM5,PHLDB2,DNER,CORO1C,NTRK3,PIP5K1A,IQGAP1,FERMT2,SRPX2,ROCK1,ITGA2,GPC4,MYO1C,RAPGEF1,CDH11,LHFPL4,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0046031	0.11	0.95	7	66	ADP metabolic process	BP	1	HK2,PGAM4,NUDT9,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0008406	0.11	0.94	15	166	gonad development	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,BRCA2,TMF1,EIF2S2,RDH10,IRX5,UBE3A,EIF2B5,ZFX,SRD5A2	darkolivegreen	VSMC_M9
GO:0002768	0.11	0.94	14	158	immune response-regulating cell surface receptor signaling pathway	BP	1	MALT1,STAP1,FYN,GATA3,SOS1,LYN,APPL1,NFKBIZ,CBLB,SLC39A10,EIF2B5,MAP2K4,VAV2,FCN1	darkolivegreen	VSMC_M9
GO:0040013	0.11	0.93	22	261	negative regulation of locomotion	BP	1	STAP1,GATA3,STK24,OSBPL8,STARD13,ILK,SULF1,CCDC125,PFN2,THBS1,PHLDB2,CORO1C,SEMA5B,IDH2,DNAJA4,TPM1,MYOCD,SEMA7A,PIN1,TBXA2R,NOV,RAP2A	darkolivegreen	VSMC_M9
GO:0110149	0.11	0.95	8	75	regulation of biomineralization	BP	1	ASPN,ZMPSTE24,ROCK2,ATP2B1,ACVR1,ROCK1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0061157	0.11	0.95	8	79	mRNA destabilization	BP	1	ROCK2,NOCT,EXOSC9,CNOT7,PDE12,DCP1A,DHX36,ROCK1	darkolivegreen	VSMC_M9
GO:0070507	0.11	0.94	13	135	regulation of microtubule cytoskeleton organization	BP	1	AKAP9,SENP6,MAP1B,MAP9,DYRK1A,PHLDB2,CAMSAP2,HDGFL3,TPR,CLTC,ROCK1,PAFAH1B1,SKA2	darkolivegreen	VSMC_M9
GO:0030071	0.11	0.96	6	55	regulation of mitotic metaphase/anaphase transition	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:2000756	0.11	0.96	6	53	regulation of peptidyl-lysine acetylation	BP	1	ZNF451,ZMPSTE24,GATA3,SETD5,BRD7,MYOCD	darkolivegreen	VSMC_M9
GO:0016032	0.11	0.93	26	325	viral process	BP	1	MGAT4A,CAV2,ROCK2,ITGB1,ST3GAL3,MGAT5,CCNT2,LIG4,EEA1,ITGA5,CNOT7,HCFC2,ITCH,CHD1,PDE12,AGTR1,KIAA1551,KPNA6,LARP7,VAPB,NCAM1,ITGAV,ITGA2,VAPA,GTF2B,FCN1	darkolivegreen	VSMC_M9
GO:0051049	0.11	0.91	90	1276	regulation of transport	BP	1	LMAN1,AHI1,UTRN,STXBP5,AZIN1,UBQLN1,PLAA,ABCB4,AKAP9,GCC2,JAK2,CLOCK,EXOC1,MYO6,STAP1,ZMPSTE24,UBE2J1,INHBA,RAB3B,ITGB1,FYN,RINT1,KIF5B,DNAJC1,RTN2,PICALM,CAMK1D,RAB3GAP1,NDFIP2,EDEM1,OSBPL8,PPP1R12A,UFM1,ATP2B1,NDFIP1,YIPF5,TMF1,SCYL2,REM1,LYN,MERTK,XPO4,SLC30A5,RIOK2,FFAR4,MAP1B,APPL1,AGTR1,HK2,TLR2,ATP2A2,THBS1,ATP1A1,EHD4,LRRK2,BRSK2,EPRS,GPR89A,PTPN1,IDH2,C2CD2L,ANK3,TPR,PTGS2,SEPT5,ITGAV,VAMP4,PLD1,DKK1,ATAD1,CLCNKB,STIM2,MSN,SRCIN1,KCNMB1,OAZ2,ROCK1,ITGA2,MYOM1,RAB31,C1QTNF3,USP7,MYO1C,MIR186,FXYD5,GDNF,NOV,ZPR1,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0000288	0.11	0.96	6	53	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	BP	1	NOCT,EXOSC9,CNOT7,PDE12,DCP1A,DHX36	darkolivegreen	VSMC_M9
GO:0006911	0.11	0.96	5	39	phagocytosis, engulfment	BP	1	STAP1,THBS1,ITGA2,RAB31,XKR9	darkolivegreen	VSMC_M9
GO:0050854	0.11	0.96	5	43	regulation of antigen receptor-mediated signaling pathway	BP	1	MALT1,STAP1,LYN,CBLB,SLC39A10	darkolivegreen	VSMC_M9
GO:0034341	0.11	0.95	9	95	response to interferon-gamma	BP	1	JAK2,ACTR2,KIF5B,NUB1,ACTR3,PDE12,TLR2,EPRS,MYO1C	darkolivegreen	VSMC_M9
GO:0009593	0.11	0.96	4	32	detection of chemical stimulus	BP	1	FFAR4,TLR2,TLR6,KCNMB1	darkolivegreen	VSMC_M9
GO:0044262	0.11	0.93	19	229	cellular carbohydrate metabolic process	BP	1	EXT1,SLC35B4,GNE,ZMPSTE24,UGP2,CSGALNACT2,HK2,GPD2,BPNT1,IDH2,TPI1,HK3,PHKG2,CLK2,C1QTNF3,USP7,RANBP2,IMPA1,PPP1R2	darkolivegreen	VSMC_M9
GO:0046824	0.11	0.95	6	54	positive regulation of nucleocytoplasmic transport	BP	1	JAK2,XPO4,RIOK2,TPR,PTGS2,ZPR1	darkolivegreen	VSMC_M9

GO:0031345	0.11	0.94	14	150	negative regulation of cell projection organization	BP	1	CDKL3,STAP1,FYN,RNF6,PFN2,LRRK2,UBE3A,SEMA5B,TRAK2,TBX6,SEMA7A,CCP110,BAG5,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0050790	0.11	0.91	125	1823	regulation of catalytic activity	BP	1	SOCS6,MALT1,PHACTR2,STXBP5,CAND1,PLEKHG1,TBC1D15,AZIN1,DENND4C,PLAA,TOPORS,AKAP9,TFPI2,JAK2,HDAC9,PSME4,STAP1,CCDC88A,SH3BP5L,CAV2,ROCK2,ITGB1,FYN,DNAJC1,NOX4,RB1,PICALM,CBLC,MGAT5,CCNT2,RAB3GAP1,BRPF1,DNAJC3,CYTH1,OSBPL8,PPP1R12A,PIK3R4,CCNA1,STARD13,SOS1,ILK,HSPH1,ARL1,LYN,PPP2R3A,MERTK,IPO7,EIF2AK3,TDG,TMED2,USP47,CCDC125,PI15,AGTR1,PFN2,RASA1,DCP1A,THBS1,NUCB2,PPP2R2A,PDP1,SLC39A14,NEDD9,CBLB,LRRK2,TANK,BRSK2,SLC39A10,UCHL5,IGF1R,RAB3GAP2,CORO1C,ANOS1,NEK7,NTRK3,PTPN1,EIF2B5,PIP5K1A,IQGAP1,PTGS2,SEC23A,ZC3H15,FERMT2,TNFAIP8L3,CPEB2,BOD1L1,DKK1,RGS7,FAS,TLR6,SRCIN1,BNIP2,TPM1,OAZ2,CLPX,GPR65,CYFIP2,SMG8,UACA,MYOCD,PIN1,BAG5,ROCK1,ITGA2,ITGA1,RICTOR,PPP4R1,TBXA2R,CALML6,PAFAH1B1,GADD45B,VAV2,RAPGEF1,WFDC1,DPM2,DNAJB4,RANBP2,BMPR2,FRY,ARF4,GDNF,TOR1AIP2,CTGF,LAMTOR3,PPP1R2	darkolivegreen	VSMC_M9
GO:0016477	0.11	0.91	82	1120	cell migration	BP	1	LRP12,EXT1,WISP1,PLAA,JAK2,HDAC9,STAP1,CCDC88A,ROCK2,ITGB1,FYN,NOX4,CAMK1D,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,PRPF40A,CAPN7,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,LYN,MERTK,PALLD,SULF1,MAP1B,APPL1,AGTR1,PFN2,THBS1,ACVR1,NEDD9,LRRK2,CUL3,PHLDB2,DNER,IGF1R,CORO1C,NTRK3,WWC3,SEMA5B,IDH2,PIP5K1A,IQGAP1,SH3KBP1,NRP2,CLEC14A,PTGS2,DNAJA4,ITGAV,FERMT2,AKT3,WNT5B,CDC42BPA,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,ANXA6,ROCK1,ITGA2,ITGA1,GPC4,MYO1C,TBXA2R,PAFAH1B1,VAV2,BMPR2,ARF4,GDNF,CTGF,NOV,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0006399	0.11	0.94	13	162	tRNA metabolic process	BP	1	ELAC1,TRMO,RARS2,DDX1,EXOSC9,TRDMT1,DARS,PUS3,EPRS,IARS2,DTWD1,DICER1,TARS	darkolivegreen	VSMC_M9
GO:0010165	0.11	0.96	4	29	response to X-ray	BP	1	GATA3,LIG4,BRCA2,IKBIP	darkolivegreen	VSMC_M9
GO:0060538	0.11	0.94	12	132	skeletal muscle organ development	BP	1	HDAC9,CAV2,RB1,CCNT2,GPCPD1,SHOX2,DNER,ATF3,MYOCD,MYOM1,FOXN2,CFL2	darkolivegreen	VSMC_M9
GO:0016573	0.11	0.94	12	131	histone acetylation	BP	1	PHF20L1,CLOCK,ZNF451,ZMPSTE24,GATA3,BRPF1,SETD5,BRCA2,BRD7,TAF5L,MYOCD,GTF2B	darkolivegreen	VSMC_M9
GO:0006790	0.11	0.93	21	270	sulfur compound metabolic process	BP	1	CDO1,EXT1,DSE,ELOVL5,NOX4,SUCLA2,ST3GAL3,ACPP,HSD17B12,CSGALNACT2,MAT2A,MICAL2,GDAP1,SLC35B3,CHSY1,BPNT1,PAPSS2,DLST,ACOT7,ELOVL4,CHST11	darkolivegreen	VSMC_M9
GO:0010950	0.11	0.94	11	127	positive regulation of endopeptidase activity	BP	1	MALT1,JAK2,ROCK2,FYN,PICALM,LYN,EIF2AK3,FAS,CYFIP2,UACA,CTGF	darkolivegreen	VSMC_M9
GO:0002700	0.11	0.94	10	106	regulation of production of molecular mediator of immune response	BP	1	MALT1,DDX1,GATA3,RIF1,NDFIP1,DHX36,SEMA7A,THOC1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0007507	0.11	0.92	38	474	heart development	BP	1	AHI1,EXT1,HDAC9,ZMPSTE24,ROCK2,ITGB1,RB1,GATA3,JMJD6,SOS1,ILK,DCHS1,TMED2,MICAL2,DHX36,SHOX2,ZDHHC16,ACVR1,PDLIM5,CASP7,NTRK3,NRP2,FZD2,CDKL1,DKK1,HSPB7,TPM1,TBX6,SGCD,FHOD3,MAP2K4,MYOCD,PIN1,ROCK1,COL11A1,BMPR2,VGLL4,IRX3	darkolivegreen	VSMC_M9
GO:0055082	0.11	0.91	43	564	cellular chemical homeostasis	BP	1	SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,KIF5B,GPR4,CLN5,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FAR4,AGTR1,HK2,ATP2A2,SLC39A14,ATP1A1,LRRK2,BRSK2,UBE3A,SLC39A10,ATP6V1A,IGF1R,GPR89A,CCDC186,ITPR2,VAPB,C2CD2L,CCDC47,ATP13A3,ITGAV,STIM2,HK3,GPR65,ANXA6,SLC1A3,AFG3L2,C1QTNF3,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0009611	0.12	0.92	33	422	response to wounding	BP	1	LMAN1,EXT1,WISP1,TFPI2,JAK2,ITGB1,GPR4,STK24,ILK,ITGA5,LYN,MERTK,MAP1B,THBS1,PHLDB2,NTRK3,CREB3L2,FERMT2,F5,WNT5B,TPM1,MAP2K4,ANXA6,ITGA2,SLC1A3,CD40LG,TBXA2R,VAV2,WFDC1,ARF4,GP1BB,CTGF,WNT7A	darkolivegreen	VSMC_M9
GO:0035308	0.12	0.96	4	30	negative regulation of protein dephosphorylation	BP	1	ROCK2,MGAT5,BOD1L1,ROCK1	darkolivegreen	VSMC_M9
GO:0033280	0.12	0.96	4	30	response to vitamin D	BP	1	ATP2B1,GDAP1,PTGS2,AQP3	darkolivegreen	VSMC_M9
GO:0090130	0.12	0.92	22	266	tissue migration	BP	1	HDAC9,ROCK2,ITGB1,GATA3,CAPN7,STARD13,PFN2,THBS1,CORO1C,NRP2,CLEC14A,PTGS2,DNAJA4,ACTA2,AKT3,SRPX2,ROCK1,ITGA2,TBXA2R,BMPR2,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0051239	0.12	0.90	134	1937	regulation of multicellular organismal process	BP	1	MALT1,AHI1,TBK1,THBS2,CDKL3,CHADL,WISP1,PTPRD,AKAP9,JAK2,CLOCK,NPAS2,ASPN,HDAC9,HOXA9,HOXA11,ZMPSTE24,UBE2J1,ACTR2,CHRM2,ROCK2,INHBA,DDX1,NOCT,ITGB1,ZEB1,GPR4,RB1,ZC3H13,GATA3,TRAK1,LRRC32,RIF1,CAPN7,LIG4,ATP2B1,ACPP,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,ILK,ITGA5,TMF1,HOXC10,RNF6,LYN,MERTK,EIF2AK3,TDG,ITCH,SULF1,LNPEP,FFAR4,MAP1B,APPL1,AGTR1,HK2,TLR2,PFN2,ATP2A2,DHX36,THBS1,SHOX2,ACVR1,NFKBIZ,CBLB,ATP1A1,LRRK2,PHLDB2,CHSY1,KPNA6,IGF1R,CORO1C,NTRK3,WWC3,SEMA5B,IDH2,TAF5L,ABCB10,TRAK2,GPATCH3,ADAM12,NRP2,PITHD1,GATM,PTGS2,DNAJA4,ITGAV,FERMT2,SKIL,TAPT1,DKK1,AKT3,HSPB7,TLR6,ADAM10,TPM1,SRPX2,TLE3,PKM,DICER1,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,THOC1,ITGA2,NUP155,AFG3L2,C1QTNF3,CIDEA,MYSM1,CD40LG,TBXA2R,PAFAH1B1,ENO1,BMPR2,AQP3,GDNF,CTGF,BDKRB2,NOV,FCN1,WNT9A,ZPR1,VGLL4,TMEM119,SHISA7,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0061333	0.12	0.95	7	63	renal tubule morphogenesis	BP	1	AHI1,HOXA11,GATA3,ILK,DCHS1,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:1990823	0.12	0.94	8	78	response to leukemia inhibitory factor	BP	1	EXT1,RIF1,SMARCA5,MAT2A,HK2,NRP2,MYNN,NUP35	darkolivegreen	VSMC_M9

GO:0061013	0.12	0.93	13	144	regulation of mRNA catabolic process	BP	1	ROCK2,NOCT,EXOSC9,CNOT7,PDE12,DCP1A,DHX36,FASTKD2,MYEF2,ZC3H14,ROCK1,FASTKD5,GDNF	darkolivegreen	VSMC_M9
GO:0065002	0.12	0.96	5	47	intracellular protein transmembrane transport	BP	1	RTN2,TIMM17A,TOMM20,TOMM20L,SEC63	darkolivegreen	VSMC_M9
GO:0051893	0.12	0.95	7	60	regulation of focal adhesion assembly	BP	1	ROCK2,THBS1,PHLDB2,CORO1C,IQGAP1,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:0090109	0.12	0.95	7	60	regulation of cell-substrate junction assembly	BP	1	ROCK2,THBS1,PHLDB2,CORO1C,IQGAP1,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:1905897	0.12	0.95	7	70	regulation of response to endoplasmic reticulum stress	BP	1	UBQLN1,EIF2AK3,LRRK2,PTPN1,MBTPS2,BFAR,DNAJB9	darkolivegreen	VSMC_M9
GO:0048854	0.12	0.96	4	27	brain morphogenesis	BP	1	SOS1,UCHL5,AKT3,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0043086	0.12	0.91	40	555	negative regulation of catalytic activity	BP	1	PHACTR2,CAND1,AKAP9,TFPI2,HDAC9,SH3BP5L,ROCK2,RB1,PICALM,CBLC,MGAT5,DNAJC3,PPP1R12A,ILK,LYN,IPO7,TMED2,USP47,PI15,THBS1,SLC39A14,CBLB,LRRK2,UCHL5,CORO1C,ANOS1,PTPN1,IQGAP1,PTGS2,CPEB2,BOD1L1,SRCIN1,OAZ2,MYOCD,BAG5,ROCK1,GADD45B,WFDC1,FRY,PPP1R2	darkolivegreen	VSMC_M9
GO:0003008	0.12	0.90	89	1240	system process	BP	1	UTRN,RRM2B,EXT1,AKAP9,JAK2,MYO6,UBA6,ZMPSTE24,ACTR2,CHRM2,ROCK2,INHBA,ITGB1,FYN,NOX4,GPR4,PICALM,GATA3,RAB3GAP1,SETD5,ATP2B1,ACPP,UBA5,TMF1,SLC16A12,EIF2AK3,SULF1,LNPEP,FFAR4,RDH10,AGTR1,TLR2,ATP2A2,SHOX2,ARL6,IRX5,ATP1A1,LRRK2,PDLIM5,UBE3A,SEMA5B,LTB4R,ANK3,SMTN,GATM,PTGS2,FZD2,FERMT2,F5,DKK1,ATAD1,ACTA2,CLCNKB,HSPB7,MAGED2,MYO1E,KCNMB1,TPM1,SGCD,DICER1,MAP2K4,MYOCD,ANXA6,PIN1,ROCK1,ITGA2,ITGA1,MYOM1,NUP155,SLC1A3,C1QTNF3,TBXA2R,PAFAH1B1,ENO1,COL11A1,PRKACB,RABGGTB,BMPR2,AQP3,ARF4,GDNF,CTGF,LHFPL4,BDKRB2,NOV,PDCL,SHISA7,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0072655	0.12	0.94	9	103	establishment of protein localization to mitochondrion	BP	1	LMAN1,COX18,GDAP1,HK2,LRRK2,TIMM17A,TOMM20,PMPCA,TOMM20L	darkolivegreen	VSMC_M9
GO:0014904	0.12	0.96	4	31	myotube cell development	BP	1	HDAC9,CAV2,SHOX2,DNER	darkolivegreen	VSMC_M9
GO:0006468	0.12	0.90	88	1223	protein phosphorylation	BP	1	MALT1,TBK1,CDKL3,AKAP9,JAK2,STAP1,CCDC88A,ZMPSTE24,SH3BP5L,ROCK2,INHBA,FYN,NOX4,RB1,CBLC,CAMK1D,CDK3,CCNT2,DNAJC3,STK24,OSBPL8,PIK3R4,CCNA1,ILK,ITGA5,SCYL2,CDK8,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TMED2,NEK1,RIOK2,TLR2,PFN2,THBS1,ACVR1,NEDD9,CBLB,DYRK1A,EHD4,ERG,LRRK2,BRSK2,IGF1R,STK38L,CORO1C,NEK7,NTRK3,PTPN1,GRK3,CLK1,IQGAP1,TLK2,PTGS2,CDKL1,MAP4K5,FERMT2,TNIK,DKK1,FAS,AKT3,CDC42BPA,TLR6,ADAM10,SRCIN1,PHKG2,CLK2,SMG8,PPM1D,MAP2K4,MYOCD,SEMA7A,PIN1,ROCK1,RICTOR,PPP4R1,GADD45B,PRKACB,BMPR2,CDK13,CTGF,BDKRB2,PMEPA1,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:1903322	0.12	0.94	11	121	positive regulation of protein modification by small protein conjugation or removal	BP	1	MALT1,UBQLN1,TOPORS,NDFIP2,NDFIP1,CBLB,LRRK2,TANK,UBE3A,CUL3,PIN1	darkolivegreen	VSMC_M9
GO:0072001	0.12	0.92	22	256	renal system development	BP	1	AHI1,RRM2B,EXT1,HOXA11,ZMPSTE24,GPR4,GATA3,JMJD6,ILK,DCHS1,IFT88,SULF1,RDH10,AGTR1,GCNT4,LRRK2,IQGAP1,ACTA2,MYO1E,MYOCD,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0031348	0.12	0.93	13	149	negative regulation of defense response	BP	1	FYN,RB1,GATA3,TNFAIP6,NDFIP1,CNOT7,LYN,ITCH,FFAR4,GPATCH3,C1QTNF3,WFDC1,NOV	darkolivegreen	VSMC_M9
GO:0045185	0.12	0.94	8	80	maintenance of protein location	BP	1	KDELR3,TOPORS,CCDC88A,HK2,ANK3,TAPT1,PDIA2,ANKRD13C	darkolivegreen	VSMC_M9
GO:0051224	0.12	0.94	9	96	negative regulation of protein transport	BP	1	LMAN1,UBE2J1,NDFIP2,UFM1,NDFIP1,LRRK2,IDH2,SRCIN1,NOV	darkolivegreen	VSMC_M9
GO:0060688	0.12	0.95	5	42	regulation of morphogenesis of a branching structure	BP	1	NTN4,SULF1,SHOX2,LRRK2,GDNF	darkolivegreen	VSMC_M9
GO:0007088	0.12	0.94	9	96	regulation of mitotic nuclear division	BP	1	CDC23,CAV2,CCDC8,RB1,CUL3,TPR,CDC27,PIN1,CDK13	darkolivegreen	VSMC_M9
GO:2001233	0.12	0.92	22	292	regulation of apoptotic signaling pathway	BP	1	RRM2B,UBQLN1,INHBA,FYN,RB1,RPL26,EIF2AK3,USP47,THBS1,ACVR1,LRRK2,PTPN1,ATF3,PTGS2,ITGAV,SKIL,VDAC2,FAS,BAG5,ENO1,GDNF,BDKRB2	darkolivegreen	VSMC_M9
GO:0031644	0.12	0.94	10	100	regulation of nervous system process	BP	1	AKAP9,ROCK2,ACPP,EIF2AK3,LRRK2,DICER1,ITGA2,NOV,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0051962	0.12	0.92	19	216	positive regulation of nervous system development	BP	1	THBS2,CDKL3,PTPRD,ACTR2,TRAK1,LIG4,ILK,LYN,MAP1B,TLR2,DHX36,SHOX2,SKIL,SRPX2,DICER1,SEMA7A,PAFAH1B1,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0051154	0.12	0.96	4	32	negative regulation of striated muscle cell differentiation	BP	1	DKK1,MYOCD,NOV,TMEM119	darkolivegreen	VSMC_M9
GO:0045137	0.12	0.93	15	170	development of primary sexual characteristics	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,BRCA2,TMF1,EIF2S2,RDH10,IRX5,UBE3A,EIF2B5,ZFX,SRD5A2	darkolivegreen	VSMC_M9
GO:0072028	0.12	0.94	7	65	nephron morphogenesis	BP	1	AHI1,HOXA11,GATA3,ILK,DCHS1,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0018393	0.12	0.93	12	134	internal peptidyl-lysine acetylation	BP	1	PHF20L1,CLOCK,ZNF451,ZMPSTE24,GATA3,BRPF1,SETD5,BRCA2,BRD7,TAF5L,MYOCD,GTF2B	darkolivegreen	VSMC_M9
GO:0007091	0.12	0.95	6	57	metaphase/anaphase transition of mitotic cell cycle	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0033866	0.12	0.95	6	57	nucleoside bisphosphate biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,PAPSS2,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0034030	0.12	0.95	6	57	ribonucleoside bisphosphate biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,PAPSS2,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0034033	0.12	0.95	6	57	purine nucleoside bisphosphate biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,PAPSS2,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0000460	0.12	0.96	4	34	maturation of 5.8S rRNA	BP	1	EXOSC9,ERI1,MTREX,RRP15	darkolivegreen	VSMC_M9
GO:0002720	0.12	0.95	5	42	positive regulation of cytokine production involved in immune response	BP	1	MALT1,DDX1,GATA3,DHX36,SEMA7A	darkolivegreen	VSMC_M9
GO:0003180	0.13	0.96	4	29	aortic valve morphogenesis	BP	1	ROCK2,RB1,GATA3,ROCK1	darkolivegreen	VSMC_M9

GO:2000147	0.13	0.91	35	455	positive regulation of cell motility	BP	1	WISP1,PLAA,JAK2,HDAC9,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,TNFAIP6,CAPN7,ILK,LYN,THBS1,PGAM4,ACVR1,NEDD9,IGF1R,NTRK3,SEMA5B,IQGAP1,NRP2,PTGS2,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,SRPX2,SEMA7A,ITGA2,MYO1C,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0045931	0.13	0.94	9	97	positive regulation of mitotic cell cycle	BP	1	CDC23,RB1,CUL4A,BRCA2,CUL3,EIF4E,KLHL18,CDC27,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0051271	0.13	0.92	20	241	negative regulation of cellular component movement	BP	1	STAP1,GATA3,STK24,OSBPL8,STARD13,ILK,SULF1,CCDC125,PFN2,THBS1,PHLDB2,CORO1C,IDH2,DNAJA4,TPM1,MYOCD,PIN1,TBXA2R,NOV,RAP2A	darkolivegreen	VSMC_M9
GO:0048736	0.13	0.93	13	140	appendage development	BP	1	EXT1,HOXA9,HOXA10,HOXA11,RDH10,MBNL1,SHOX2,FERMT2,PRRX1,DKK1,BMPR2,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0060173	0.13	0.93	13	140	limb development	BP	1	EXT1,HOXA9,HOXA10,HOXA11,RDH10,MBNL1,SHOX2,FERMT2,PRRX1,DKK1,BMPR2,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0048731	0.13	0.89	241	3556	system development	BP	1	MALT1,CDO1,AHI1,LRIG3,UTRN,CEP120,RRM2B,LRP12,EXT1,THBS2,CDKL3,CHADL,WISP1,PTPRD,PLAA,TOPORS,JAK2,CLOCK,NPAS2,ASPN,BZW2,HDAC9,CAVIN4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UGP2,ACTR2,CHRM2,CAV2,ROCK2,INHBA,PCDH18,ITGB1,FYN,ZEB1,KIF5B,FNDC3A,GPR4,RB1,PICALM,CAMK1D,UPF2,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,PAX1,TRAK1,SETD5,AZI2,STK24,RIF1,GPCPD1,UFM1,LIG4,MYO16,ATP2B1,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,DCHS1,TMF1,SCYL2,RNF6,LYN,MERTK,TMEM41B,IFT88,EIF2AK3,SLC25A46,FBXL17,TMED2,PALLD,EIF2S2,ITCH,SULF1,STOX2,MICAL2,MAP1B,RDH10,AGTR1,HK2,TLR2,RASA1,VCAN,MBNL1,DHX36,THBS1,SHOX2,ZDHHC16,ACVR1,SLC39A14,IRX5,GCNT4,ETNK2,NFKBIZ,CBLB,DYRK1A,MAN1A2,LRRK2,SNX19,TBX15,BRSK2,PDLIM5,UBE3A,MBOAT1,CUL3,EIF4E,PHLDB2,TDP2,DNER,TROVE2,UCHL5,CHSY1,BPNT1,CAMSAP2,GPR89A,CASP7,CORO1C,ANOS1,NTRK3,SEMA5B,IDH2,ABCB10,EIF2B5,TRAK2,SYCP2,ATF3,PIP5K1A,IQGAP1,ANK3,CD3G,SMTN,ADAM12,NRP2,HDGFL3,PITHD1,MBTPS2,ZFX,CREB3L2,CLEC14A,PTGS2,NCAM1,MYEF2,FZD2,CDKL1,ITGAV,GNPNAT1,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,DKK1,PAPSS2,ACTA2,AKT3,RBM47,WNT5B,NOTCH3,HSPB7,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,ITGB1BP2,TBX6,ADAM19,CYFIP2,SRPX2,RBBP6,TLE3,SGCD,PKM,DICER1,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,BAG5,ROCK1,THOC1,ITGA2,ITGA1,MYOM1,SLC1A3,VAPA,AFG3L2,GPC4,MYSM1,CD40LG,TBXA2R,PAFAH1B1,VAV2,RAPGEF1,COL11A1,PLPPR5,PRKACB,CDH11,BMPR2,AQP3,TMX2,FRY,ARF4,GDNF,CRNN,CTCF,LMTK1,FOXN2,FSCN2,FHL1,RNASE1,PFN2,BRSK2,TPM1,TOR1AIP2	darkolivegreen	VSMC_M9
GO:0043462	0.13	0.96	4	37	regulation of ATPase activity	BP	1	JAK2,CLOCK,UFM1,NR2C1,UBA5,TMF1,PLPP1,RNF6,APPL1,UBE3A,TRIP4,PAQR8,PMEPA1	darkolivegreen	VSMC_M9
GO:0009755	0.13	0.93	13	142	hormone-mediated signaling pathway	BP	1	CAV2,CNOT7,PDE12,KPNA6,VAPB,VAPA	darkolivegreen	VSMC_M9
GO:0048524	0.13	0.95	6	55	positive regulation of viral process	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,INHBA,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,BRPF1,SUPT5H,DNAJC3,PPP1R12A,RPL26,CEBPZ,SMAD9,BRCA2,ILK,HSPH1,TMF1,HOXC10,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,STOX2,MICAL2,APPL1,RDH10,LARP4,TLR2,DHX36,THBS1,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,LRRK2,UBE3A,KPNA6,RAB3GAP2,NEK7,LARP7,TAF5L,ABCB10,EIF2B5,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,FASTKD2,CREB3L2,PTGS2,FZD2,NPAT,PRRX1,PLD1,TLR6,TRIP4,TBX6,PKM,ARMCX3,MAP2K4,MYOCD,PIN1,SS18,THOC1,ITGA2,MYSM1,ENO1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,CTGF,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0009891	0.13	0.89	106	1533	positive regulation of biosynthetic process	BP	1	RDH10,IRX5,TBX15,PRRX1,CHST11	darkolivegreen	VSMC_M9
GO:0048701	0.13	0.95	5	40	embryonic cranial skeleton morphogenesis	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:1902099	0.13	0.95	6	58	regulation of metaphase/anaphase transition of cell cycle	BP	1	HDAC9,ZMPSTE24,CAV2,ITGB1,RB1,CCNT2,GPCPD1,SHOX2,ACVR1,PDLIM5,DNER,ATF3,DKK1,TPM1,SGCD,FHOD3,MAP2K4,MYOCD,PIN1,MYOM1,COL11A1,FOXN2,VGLL4,CFL2,IRX3	darkolivegreen	VSMC_M9
GO:0014706	0.13	0.91	25	307	striated muscle tissue development	BP	1	CDC23,RB1,CUL3,CDC27	darkolivegreen	VSMC_M9
GO:0045840	0.13	0.96	4	32	positive regulation of mitotic nuclear division	BP	1	ROCK2,NOCT,EXOSC9,CNOT7,PDE12,DCP1A,DHX36,ROCK1	darkolivegreen	VSMC_M9
GO:0050779	0.13	0.94	8	82	RNA destabilization	BP	1	SOCS6,INHBA,LRRC32,NDFIP1,LYN,MERTK,ITCH,CBLB,THOC1	darkolivegreen	VSMC_M9
GO:0051250	0.13	0.93	9	99	negative regulation of lymphocyte activation	BP	1	CEP120,STAP1,CCDC88A,ACTR2,ACTR3,FAM98A,IFT88,PFN2,CORO1C,CDKL1,TAPT1,PLD1,CCP110,PLPPR5	darkolivegreen	VSMC_M9
GO:0120032	0.13	0.92	14	158	regulation of plasma membrane bounded cell projection assembly	BP	1	UBQLN1,NDFIP2,NDFIP1,REM1,ANK3,MIR186	darkolivegreen	VSMC_M9
GO:0032410	0.13	0.95	6	57	negative regulation of transporter activity	BP	1	CDKL3,PLAA,ITGB1,ILK,RNF6,MAP1B,SEMA5B,IQGAP1,NRP2,SMURF1,CYFIP2,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:1990138	0.13	0.92	14	147	neuron projection extension	BP	1	ZMPSTE24,GATA3,RDH10,ATP1A1	darkolivegreen	VSMC_M9
GO:0032350	0.13	0.96	4	30	regulation of hormone metabolic process	BP	1	ROCK2,NOCT,EXOSC9,CNOT7,PDE12,DCP1A,DHX36,ROCK1	darkolivegreen	VSMC_M9
GO:0061014	0.13	0.94	8	82	positive regulation of mRNA catabolic process	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0010965	0.13	0.94	6	58	regulation of mitotic sister chromatid separation	BP	1	IFRD1,GATA3,PRRX1,WNT7A	darkolivegreen	VSMC_M9
GO:0001709	0.13	0.96	4	30	cell fate determination	BP	1	BRSK2,FZD2,SMURF1,DKK1,GPC4,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0001736	0.13	0.94	7	64	establishment of planar polarity	BP	1		darkolivegreen	VSMC_M9

GO:0007164	0.13	0.94	7	64	establishment of tissue polarity	BP	1	BRSK2,FZD2,SMURF1,DKK1,GPC4,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0048589	0.13	0.90	39	501	developmental growth	BP	1	EXT1,CDKL3,PLAA,HOXA11,ZMPSTE24,ITGB1,GATA3,SOS1,BRCA2,ILK,RNF6,TMED2,MAP1B,RDH10,ETNK2,PDLIM5,UBE3A,WWC3,KPNA1,SEMA5B,IQGAP1,NRP2,ZFX,SMURF1,CYFIP2,RBBP6,MAP2K4,SEMA7A,ANXA6,PIN1,AFG3L2,PAFAH1B1,BMPR2,PTPN12,NOV,ZPR1,VGLL4,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0090317	0.13	0.96	4	34	negative regulation of intracellular protein transport	BP	1	LMAN1,UBE2J1,UFM1,LRRK2	darkolivegreen	VSMC_M9
GO:0006040	0.13	0.96	4	32	amino sugar metabolic process	BP	1	GNE,GFPT1,NPL,GNPNAT1	darkolivegreen	VSMC_M9
GO:0016482	0.13	0.92	14	153	cytosolic transport	BP	1	MON2,GCC2,ACTR2,KIF5B,CLN5,EEA1,ARL1,LRRK2,TRAPPC10,HEATR5A,MSN,CLTC,USP7,RAB6A	darkolivegreen	VSMC_M9
GO:0010923	0.13	0.96	4	32	negative regulation of phosphatase activity	BP	1	ROCK2,MGAT5,BOD1L1,ROCK1	darkolivegreen	VSMC_M9
GO:0150115	0.13	0.93	10	95	cell-substrate junction organization	BP	1	ROCK2,THSD1,THBS1,PHLDB2,CORO1C,PIP5K1A,IQGAP1,FERMT2,ROCK1,ITGA2	darkolivegreen	VSMC_M9
GO:2000145	0.13	0.90	57	772	regulation of cell motility	BP	1	WISP1,PLAA,JAK2,HDAC9,STAP1,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,CAPN7,STARD13,ILK,LYN,SULF1,CCDC125,APPL1,PFN2,THBS1,PGAM4,ACVR1,NEDD9,PHLDB2,IGF1R,CORO1C,NTRK3,SEMA5B,IDH2,IQGAP1,NRP2,PTGS2,DNAJA4,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,MYO1C,TBXA2R,SSX2IP,BMPR2,NOV,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0060349	0.13	0.94	8	76	bone morphogenesis	BP	1	EXT1,HOXA11,ZMPSTE24,SHOX2,CHSY1,ANXA6,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:2000142	0.13	0.96	4	32	regulation of DNA-templated transcription, initiation	BP	1	CAND1,ZNF451,DHX36,PPM1D	darkolivegreen	VSMC_M9
GO:0140056	0.13	0.94	7	67	organelle localization by membrane tethering	BP	1	CAV2,RAB3B,ESYT2,CEP83,ATP2A2,USO1,VAPB	darkolivegreen	VSMC_M9
GO:0030335	0.13	0.90	34	443	positive regulation of cell migration	BP	1	WISP1,PLAA,JAK2,HDAC9,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,TNFAIP6,CAPN7,ILK,LYN,THBS1,ACVR1,NEDD9,IGF1R,NTRK3,SEMA5B,IQGAP1,NRP2,PTGS2,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,SRPX2,SEMA7A,ITGA2,MYO1C,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0007338	0.13	0.93	8	86	single fertilization	BP	1	HOXA9,HOXA10,HOXA11,ADAM32,TUBGCP3,UBE3A,PITHD1,VDAC2	darkolivegreen	VSMC_M9
GO:2001234	0.13	0.92	15	187	negative regulation of apoptotic signaling pathway	BP	1	RRM2B,FYN,RB1,USP47,THBS1,ACVR1,LRRK2,PTPN1,PTGS2,ITGAV,VDAC2,BAG5,ENO1,GDNF,BDKRB2	darkolivegreen	VSMC_M9
GO:0006475	0.13	0.92	12	136	internal protein amino acid acetylation	BP	1	PHF20L1,CLOCK,ZNF451,ZMPSTE24,GATA3,BRPF1,SETD5,BRCA2,BRD7,TAF5L,MYOCD,GTF2B	darkolivegreen	VSMC_M9
GO:0099504	0.13	0.92	13	138	synaptic vesicle cycle	BP	1	STXBP5,PLAA,RAB3B,PICALM,RAB3GAP1,ATP2A2,LRRK2,BRSK2,SEPT5,VAMP4,PLD1,ROCK1,WNT7A	darkolivegreen	VSMC_M9
GO:0006869	0.13	0.91	22	273	lipid transport	BP	1	ABCB4,INHBA,PNPLA8,ESYT2,OSBPL8,ATP11A,TMF1,GRAMD1A,AGTR1,THBS1,ATP10A,EPRS,ATP11B,PRELID3B,C2CD2L,OSBPL11,ITGAV,ATP8B4,TNFAIP8L3,XKR9,PLEKHA3,BDKRB2	darkolivegreen	VSMC_M9
GO:0040011	0.13	0.89	96	1349	locomotion	BP	1	LRP12,EXT1,WISP1,PLAA,JAK2,HDAC9,STAP1,CCDC88A,ROCK2,ITGB1,FYN,KIF5B,NOX4,CAMK1D,ACTR3,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,PRPF40A,CAPN7,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,TMF1,LYN,MERTK,PALLD,SULF1,CCDC125,MAP1B,APPL1,AGTR1,PFN2,THBS1,PGAM4,ACVR1,NEDD9,LRRK2,CUL3,PHLDB2,DNER,IGF1R,CORO1C,ANOS1,NTRK3,WWC3,SEMA5B,IDH2,PIP5K1A,IQGAP1,SH3KBP1,NRP2,CLEC14A,PTGS2,NCAM1,DNAJA4,ITGAV,FERMT2,PLD1,PLP2,AKT3,WNT5B,CDC42BPA,NOTCH3,ENAH,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,ITGA2,ITGA1,GPC4,MYO1C,TBXA2R,PAFAH1B1,VAV2,SSX2IP,BMPR2,ARF4,GDNF,CTGF,NOV,RAP2A,CFL2,WNT7A	darkolivegreen	VSMC_M9
GO:0060491	0.13	0.92	14	159	regulation of cell projection assembly	BP	1	CEP120,STAP1,CCDC88A,ACTR2,ACTR3,FAM98A,IFT88,PFN2,CORO1C,CDKL1,TAPT1,PLD1,CCP110,PLPPR5	darkolivegreen	VSMC_M9
GO:0030100	0.13	0.92	15	174	regulation of endocytosis	BP	1	AHI1,STAP1,PICALM,SCYL2,APPL1,EHD4,LRRK2,PTPN1,ITGAV,VAMP4,DKK1,ATAD1,ROCK1,ITGA2,RAB31	darkolivegreen	VSMC_M9
GO:2000134	0.13	0.94	6	56	negative regulation of G1/S transition of mitotic cell cycle	BP	1	RB1,RPL26,MYO16,BRD7,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0008015	0.13	0.90	29	369	blood circulation	BP	1	EXT1,AKAP9,JAK2,ZMPSTE24,CHRM2,ROCK2,GPR4,ATP2B1,LNPEP,AGTR1,ATP2A2,SHOX2,ATP1A1,PTGS2,FERMT2,F5,ACTA2,HSPB7,KCNMB1,TPM1,SGCD,ROCK1,ITGA1,NUP155,TBXA2R,BMPR2,CTGF,BDKRB2,IRX3	darkolivegreen	VSMC_M9
GO:0050769	0.14	0.92	16	181	positive regulation of neurogenesis	BP	1	CDKL3,PTPRD,ACTR2,TRAK1,LIG4,ILK,LYN,MAP1B,TLR2,DHX36,SHOX2,SKIL,DICER1,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0042116	0.14	0.94	7	69	macrophage activation	BP	1	JAK2,STAP1,JMJD6,TLR2,THBS1,LRRK2,TLR6	darkolivegreen	VSMC_M9
GO:1902532	0.14	0.90	31	407	negative regulation of intracellular signal transduction	BP	1	RRM2B,ITGB1,CBLC,LYN,ITCH,USP47,CCDC125,RASA1,THBS1,DYRK1A,LRRK2,TANK,CUL3,IGF1R,WWC3,PTPN1,GPATCH3,ATF3,PTGS2,VDAC2,UACA,PIN1,BAG5,THOC1,C1QTNF3,PAFAH1B1,ENO1,BDKRB2,NOV,VGLL4,C12orf66	darkolivegreen	VSMC_M9
GO:0006890	0.14	0.95	5	45	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	BP	1	KDELR3,RINT1,COPB2,RAB6A,ARF4	darkolivegreen	VSMC_M9
GO:0060627	0.14	0.90	31	403	regulation of vesicle-mediated transport	BP	1	AHI1,STXBP5,STAP1,RAB3B,RINT1,KIF5B,PICALM,CAMK1D,RAB3GAP1,YIPF5,SCYL2,LYN,MERTK,APPL1,TLR2,ATP2A2,EHD4,LRRK2,PTPN1,SEPT5,ITGAV,VAMP4,PLD1,DKK1,ATAD1,MSN,ROCK1,ITGA2,RAB31,USP7,WNT7A	darkolivegreen	VSMC_M9
GO:0008016	0.14	0.92	13	144	regulation of heart contraction	BP	1	AKAP9,JAK2,ZMPSTE24,CHRM2,ATP2B1,ATP2A2,SHOX2,ATP1A1,HSPB7,TPM1,NUP155,CTGF,IRX3	darkolivegreen	VSMC_M9

GO:0003230	0.14	0.95	4	30	cardiac atrium development	BP	1	SOS1,SHOX2,ACVR1,BMPR2	darkolivegreen	VSMC_M9
GO:0110053	0.14	0.91	20	237	regulation of actin filament organization	BP	1	CCDC88A,ACTR2,ROCK2,NOX4,ACTR3,PFN2,RASA1,SPTBN5,PHLDB2,FERMT2,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:0097484	0.14	0.95	4	30	dendrite extension	BP	1	CDKL3,PLAA,SMURF1,CYFIP2	darkolivegreen	VSMC_M9
GO:0010092	0.14	0.95	4	32	specification of animal organ identity	BP	1	EXT1,HOXA11,DKK1,GDNF	darkolivegreen	VSMC_M9
GO:0060047	0.14	0.92	15	172	heart contraction	BP	1	EXT1,AKAP9,JAK2,ZMPSTE24,CHRM2,ATP2B1,ATP2A2,SHOX2,ATP1A1,HSPB7,TPM1,SGCD,NUP155,CTGF,IRX3	darkolivegreen	VSMC_M9
GO:0002637	0.14	0.95	5	48	regulation of immunoglobulin production	BP	1	RIF1,NDFIP1,THOC1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0071417	0.14	0.90	36	466	cellular response to organonitrogen compound	BP	1	DENND4C,AKAP9,JAK2,HDAC9,ACTR2,CHRM2,CAV2,ROCK2,FYN,NOX4,OSBPL8,ATP2B1,LYN,XRN1,MAP1B,APPL1,AGTR1,USO1,SLC39A14,LRRK2,EPRS,IGF1R,CASP7,ITPR2,PTPN1,PTGS2,CPEB2,TLR6,PKM,ROCK1,SLC1A3,RAB31,MYO1C,RAPGEF1,ZDHHC7,LAMTOR3	darkolivegreen	VSMC_M9
GO:1902275	0.14	0.95	4	29	regulation of chromatin organization	BP	1	SETD5,KIAA1551,TLK2,TPR	darkolivegreen	VSMC_M9
GO:0051051	0.14	0.90	24	314	negative regulation of transport	BP	1	LMAN1,UBQLN1,UBE2J1,INHBA,PICALM,NDFIP2,UFM1,NDFIP1,REM1,FFAR4,MAP1B,APPL1,TLR2,THBS1,LRRK2,IDH2,ANK3,TPR,PTGS2,ITGAV,SRCIN1,OAZ2,MIR186,NOV	darkolivegreen	VSMC_M9
GO:0048645	0.14	0.94	6	56	animal organ formation	BP	1	EXT1,HOXA11,SULF1,RDH10,DKK1,GDNF	darkolivegreen	VSMC_M9
GO:0034660	0.14	0.90	29	412	ncRNA metabolic process	BP	1	ELAC1,WDR46,TRMO,RARS2,DDX1,RPF2,EXOSC9,PIWIL4,TRDMT1,TOE1,DARS,RPL26,ERI1,MTREX,MYBL1,RIOK2,XRN1,WDR75,PUS3,RRP15,EPRS,IARS2,LARP7,DTWD1,INTS14,DICER1,TARS,INTS6,TFB2M	darkolivegreen	VSMC_M9
GO:0001822	0.14	0.91	21	248	kidney development	BP	1	AHI1,RRM2B,EXT1,HOXA11,ZMPSTE24,GPR4,GATA3,JMJD6,ILK,DCHS1,IFT88,SULF1,RDH10,AGTR1,GCNT4,LRRK2,IQGAP1,ACTA2,MYO1E,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0036503	0.14	0.93	9	99	ERAD pathway	BP	1	UBQLN1,UBE2J1,UGGT1,EDEM1,BRSK2,DNAJB14,UBE4A,CCDC47,DNAJB9	darkolivegreen	VSMC_M9
GO:0033865	0.14	0.93	9	102	nucleoside bisphosphate metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,SLC35B3,BPNT1,PAPSS2,DLST,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0033875	0.14	0.93	9	102	ribonucleoside bisphosphate metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,SLC35B3,BPNT1,PAPSS2,DLST,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0034032	0.14	0.93	9	102	purine nucleoside bisphosphate metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,SLC35B3,BPNT1,PAPSS2,DLST,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0043552	0.14	0.95	4	28	positive regulation of phosphatidylinositol 3-kinase activity	BP	1	PIK3R4,LYN,TNFAIP8L3,VAV2	darkolivegreen	VSMC_M9
GO:0042327	0.14	0.89	46	612	positive regulation of phosphorylation	BP	1	MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,ROCK2,INHBA,FYN,NOX4,CCNT2,OSBPL8,PIK3R4,ILK,ITGA5,LYN,MERTK,PFN2,THBS1,ACVR1,NEDD9,EHD4,LRRK2,IGF1R,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,TNFAIP8L3,DKK1,FAS,TLR6,SRCIN1,MAP2K4,SEMA7A,PIN1,RICTOR,VAV2,RANBP2,BMPR2,CTGF,LAMTOR3,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:2000045	0.14	0.93	9	97	regulation of G1/S transition of mitotic cell cycle	BP	1	RB1,RPL26,MYO16,CUL4A,APPL1,INO80,BRD7,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0061098	0.14	0.94	5	44	positive regulation of protein tyrosine kinase activity	BP	1	STAP1,NOX4,NEDD9,PTPN1,SRCIN1	darkolivegreen	VSMC_M9
GO:0030307	0.14	0.92	12	134	positive regulation of cell growth	BP	1	PLAA,EXOSC9,ILK,USP47,MAP1B,INO80,SMURF1,ADAM10,SEMA7A,PIN1,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0048608	0.14	0.90	26	330	reproductive structure development	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,BRCA2,TMF1,MERTK,TMED2,EIF2S2,SULF1,STOX2,RDH10,IRX5,ETNK2,UBE3A,EIF2B5,SYCP2,ZFX,PTGS2,ADAM19,MYOCD,BMPR2,SRD5A2,WNT7A	darkolivegreen	VSMC_M9
GO:0009966	0.14	0.88	152	2237	regulation of signal transduction	BP	1	SOCS6,MALT1,TBK1,PLEKHG1,RRM2B,WISP1,UBQLN1,PTPRD,DENND4C,AKAP9,JAK2,CLOCK,FBXO9,ASPN,ZNF451,CAVIN4,STAP1,CCDC88A,ZMPSTE24,CAV2,ROCK2,INHBA,DDX1,ITGB1,RPF2,FYN,GPR4,RB1,CBLC,MGAT5,GATA3,NDFIP2,CYTH1,OSBPL8,RPL26,UFM1,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,UBA5,ILK,ITGA5,SCYL2,CNOT7,RNF6,LYN,EIF2AK3,FBXL17,TMED2,ITCH,SULF1,USP47,CCDC125,FFAR4,APPL1,TLR2,RASA1,BRAP,DHX36,THBS1,SHOX2,ACVR1,SLC39A14,CBLB,DYRK1A,LRRK2,TANK,UBE3A,SLC39A10,CUL3,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,WWC3,PTPN1,GRK3,KPNA1,GPATCH3,ATF3,PIP5K1A,IQGAP1,TPR,PTGS2,NCAM1,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TNIK,TNFAIP8L3,VDAC2,DKK1,RGS7,FAS,AKT3,WNT5B,TLR6,ADAM10,GPR65,CYFIP2,TLE3,UACA,GPRASP1,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,THOC1,ITGA1,RICTOR,VAPA,BFAR,C1QTNF3,CIDEA,GPC4,USP7,MYO1C,PAFAH1B1,GADD45B,ENO1,VAV2,ZDHHC7,RFWD3,SSX2IP,PRKACB,ANKRD13C,BMPR2,PTPN12,GDNF,CTGF,BDKRB2,LAMTOR3,DNAJB9,NOV,PDCL,PMEPA1,RAP2A,VGLL4,C12orf66,CHST11,UBE2V1,SHISA7,WNT7A,PPP1R2	darkolivegreen	VSMC_M9
GO:0016071	0.14	0.89	42	586	mRNA metabolic process	BP	1	DDX46,KHDRBS3,ETF1,PPIL1,ROCK2,DDX1,NOCT,EXOSC9,ZC3H13,UPF2,JMJD6,SUPT5H,MBNL2,PRPF40A,AC091959.3,MTREX,CNOT7,XRN1,PDE12,MBNL1,DCP1A,DHX36,SNRNP48,DYRK1A,PUS3,LARP7,FASTKD2,MYEF2,CWC22,ZC3H14,RBBP6,SMG8,ROCK1,THOC1,GSPT1,LSM5,ZNF326,FASTKD5,GDNF,CDK13,GEMIN6,ZPR1	darkolivegreen	VSMC_M9
GO:0051306	0.14	0.94	6	60	mitotic sister chromatid separation	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0120163	0.14	0.94	5	44	negative regulation of cold-induced thermogenesis	BP	1	RB1,HOXC10,LNPEP,TLE3,CIDEA	darkolivegreen	VSMC_M9
GO:0044091	0.14	0.94	5	44	membrane biogenesis	BP	1	PTPRD,CAV2,PICALM,UBXN2B,ANK3	darkolivegreen	VSMC_M9

GO:0070585	0.14	0.92	9	107	protein localization to mitochondrion	BP	1	LMAN1,COX18,GDAP1,HK2,LRRK2,TIMM17A,TOMM20,PMPCA,TOMM20L	darkolivegreen	VSMC_M9
GO:0006024	0.14	0.93	7	66	glycosaminoglycan biosynthetic process	BP	1	EXT1,DSE,ST3GAL3,CSGALNACT2,CHSY1,CLTC,CHST11	darkolivegreen	VSMC_M9
GO:0042181	0.14	0.95	4	36	ketone biosynthetic process	BP	1	PDSS1,TPI1,SRD5A2,PPTC7	darkolivegreen	VSMC_M9
GO:0016266	0.15	0.95	4	33	O-glycan processing	BP	1	ST3GAL3,GALNT7,GCNT4,C1GALT1C1	darkolivegreen	VSMC_M9
GO:0044784	0.15	0.94	6	60	metaphase/anaphase transition of cell cycle	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0007224	0.15	0.92	11	119	smoothened signaling pathway	BP	1	EXT1,RB1,FBXL17,SHOX2,TROVE2,UCHL5,CHSY1,PRRX1,KIAA0586,PRKACB,PDCL	darkolivegreen	VSMC_M9
GO:1904950	0.15	0.92	9	100	negative regulation of establishment of protein localization	BP	1	LMAN1,UBE2J1,NDFIP2,UFM1,NDFIP1,LRRK2,IDH2,SRCIN1,NOV	darkolivegreen	VSMC_M9
GO:0032835	0.15	0.93	6	52	glomerulus development	BP	1	EXT1,GPR4,SULF1,IQGAP1,ACTA2,MYO1E	darkolivegreen	VSMC_M9
GO:0040017	0.15	0.89	35	462	positive regulation of locomotion	BP	1	WISP1,PLAA,JAK2,HDAC9,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,TNFAIP6,CAPN7,ILK,LYN,THBS1,PGAM4,ACVR1,NEDD9,IGF1R,NTRK3,SEMA5B,IQGAP1,NRP2,PTGS2,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,SRPX2,SEMA7A,ITGA2,MYO1C,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0046916	0.15	0.93	8	86	cellular transition metal ion homeostasis	BP	1	SLC39A7,SLC30A9,NDFIP1,ATP6V0A2,SLC30A5,SLC39A14,SLC39A10,ATP6V1A	darkolivegreen	VSMC_M9
GO:1904888	0.15	0.93	6	54	cranial skeletal system development	BP	1	EXT1,RDH10,IRX5,TBX15,PRRX1,CHST11	darkolivegreen	VSMC_M9
GO:0010631	0.15	0.90	21	261	epithelial cell migration	BP	1	HDAC9,ROCK2,ITGB1,GATA3,CAPN7,STARD13,PFN2,THBS1,CORO1C,NRP2,CLEC14A,PTGS2,DNAJA4,AKT3,SRPX2,ROCK1,ITGA2,TBXA2R,BMPR2,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0032970	0.15	0.89	27	337	regulation of actin filament-based process	BP	1	AKAP9,STAP1,CCDC88A,ACTR2,ROCK2,NOX4,ACTR3,ILK,PFN2,RASA1,ATP2A2,ATP1A1,SPTBN5,PHLDB2,NTRK3,IQGAP1,FERMT2,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:0042177	0.15	0.92	9	101	negative regulation of protein catabolic process	BP	1	AZIN1,FYN,UCHL5,TLK2,FMN2,PIN1,BAG5,ROCK1,USP7	darkolivegreen	VSMC_M9
GO:0044319	0.15	0.95	4	30	wound healing, spreading of cells	BP	1	ITGA5,PHLDB2,FERMT2,WNT7A	darkolivegreen	VSMC_M9
GO:0090505	0.15	0.95	4	30	epiboly involved in wound healing	BP	1	ITGA5,PHLDB2,FERMT2,WNT7A	darkolivegreen	VSMC_M9
GO:0070482	0.15	0.90	22	280	response to oxygen levels	BP	1	UBQLN1,ROCK2,NOX4,ATP6V0A2,PLOD2,HK2,TLR2,THBS1,ATP6V1A,ITPR2,PTGS2,CPEB2,FMN2,FAS,BNIP2,KCNMB1,MYOCD,PIN1,ITGA2,ENO1,AQP3,CTGF	darkolivegreen	VSMC_M9
GO:0007034	0.15	0.91	12	137	vacuolar transport	BP	1	GCC2,TRAK1,NDFIP2,VPS36,PIK3R4,NDFIP1,SCYL2,SPTBN5,LRRK2,TRAK2,SMURF1,GPRASP1	darkolivegreen	VSMC_M9
GO:0007160	0.15	0.90	17	192	cell-matrix adhesion	BP	1	UTRN,ROCK2,ITGB1,THSD1,ILK,RASA1,THBS1,PHLDB2,CORO1C,PIP5K1A,IQGAP1,ITGAV,FERMT2,ROCK1,ITGA2,ITGA1,CTGF	darkolivegreen	VSMC_M9
GO:0035337	0.15	0.95	4	35	fatty-acyl-CoA metabolic process	BP	1	ELOVL5,HSD17B12,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0051223	0.15	0.89	31	412	regulation of protein transport	BP	1	LMAN1,STXBP5,GCC2,JAK2,CLOCK,EXOC1,UBE2J1,FYN,KIF5B,DNAJC1,NDFIP2,EDEM1,UFM1,NDFIP1,XPO4,TLR2,LRRK2,BRSK2,PTPN1,IDH2,C2CD2L,ANK3,TPR,PTGS2,SRCIN1,OAZ2,MYOM1,C1QTNF3,MYO1C,NOV,ZPR1	darkolivegreen	VSMC_M9
GO:0007346	0.15	0.89	27	360	regulation of mitotic cell cycle	BP	1	CDC23,ZMPSTE24,CAV2,RINT1,CCDC8,RB1,RPL26,MYO16,CUL4A,BRCA2,RIOK2,USP47,APPL1,INO80,BRD7,CUL3,EIF4E,NEK7,IQGAP1,KLHL18,TPR,CDC27,PIN1,PAFAH1B1,RFWD3,CDK13,ZNF655	darkolivegreen	VSMC_M9
GO:1902531	0.15	0.87	91	1309	regulation of intracellular signal transduction	BP	1	MALT1,TBK1,PLEKHG1,RRM2B,UBQLN1,DENND4C,JAK2,FBXO9,CAVIN4,ZMPSTE24,CAV2,ROCK2,DDX1,ITGB1,RPF2,FYN,GPR4,CBLC,GATA3,NDFIP2,CYTH1,OSBPL8,RPL26,NDFIP1,CUL4A,STARD13,SOS1,ILK,LYN,EIF2AK3,ITCH,USP47,CCDC125,FFAR4,TLR2,RASA1,DHX36,THBS1,DYRK1A,LRRK2,TANK,UBE3A,CUL3,IGF1R,GPR89A,NTRK3,WWC3,PTPN1,GPATCH3,ATF3,PIP5K1A,IQGAP1,TPR,PTGS2,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,TNIK,TNFAIP8L3,VDAC2,DKK1,FAS,AKT3,TLR6,GPR65,UACA,SEMA7A,PIN1,BAG5,ROCK1,THOC1,RICTOR,VAPA,C1QTNF3,USP7,PAFAH1B1,GADD45B,ENO1,VAV2,RFWD3,SSX2IP,CTGF,BDKRB2,LAMTOR3,NOV,RAP2A,VGLL4,C12orf66,UBE2V1,WNT7A	darkolivegreen	VSMC_M9

GO:0048519	0.15	0.86	259	3961	negative regulation of biological process	BP	1	SOCS6,LMAN1,MALT1,AHI1,TBK1,RRM2B,AZIN1,THBS2,CDKL3,CHADL,WISP1,ETF1,UBQLN1,PTPRD,PLAA,TOPORS,TFPI2,JAK2,CLOCK,NPAS2,ASPN,ZNF451,HDAC9,STAP1,HOXA9,ZMPSTE24,UBE2J1,SH3BP5L,THAP5,TES,CAV2,ROCK2,INHBA,NOCT,ITGB1,FYN,ZEB1,RINT1,EXOSC9,PIWIL4,DNAJC1,NOX4,GPR4,RB1,RTN2,PICALM,TRDMT1,CBLC,CGREF1,CAMK1D,UPF2,MGAT5,GATA3,LRRC32,NDFIP2,SUPT5H,DNAJC3,STK24,TNFAIP6,RIF1,OSBPL8,RPL26,UFM1,LIG4,MYO16,ATP2B1,NR2C1,NDFIP1,CUL4A,STARD13,PDS5B,BRCA2,ILK,ITGA5,TMF1,HOXC10,ERI1,SCYL2,PLPP1,CNOT7,RNF6,REM1,LYN,UBXN2B,MERTK,SACS,IPO7,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SMARCA5,ITCH,SULF1,USP47,CCDC125,LNPEP,XRN1,PDE12,FFAR4,MAP1B,APPL1,PI15,HK2,TLR2,PFN2,RASA1,ATP2A2,BRAP,DCP1A,DHX36,THBS1,NUCB2,SHOX2,ACVR1,MTERF3,CBLB,ATP1A1,DYRK1A,SPTBN5,BRD7,LRRK2,TANK,TBX15,UBE3A,SLC39A10,CUL3,EIF4E,PHLDB2,TDP2,UCHL5,CHSY1,KIAA1551,EPRS,IGF1R,CAMSAP2,CORO1C,ANOS1,ITPR2,NTRK3,WWC3,PTPN1,GRK3,LARP7,SEMA5B,IDH2,TRAK2,GPATCH3,SYCP2,LRRFIP1,ATF3,RBBP7,ANK3,TLK2,HDGFL3,FASTKD2,TPR,PTGS2,MYEF2,IQCJ-SCHIP1,DNAJA4,SORCS2,NPAT,ITGAV,FERMT2,SKIL,PRRX1,RTN3,KIFAP3,SMURF1,CPEB2,VDAC2,BOD1L1,DKK1,FMN2,ATAD1,RGS7,FAS,AKT3,SRP9,TLR6,MAGED2,ADAM10,SRCIN1,BNIP2,TPM1,CLK2,TBX6,OAZ2,RLIM,MAGEE2,ZC3H14,TLE3,SMG8,UACA,CLTC,DICER1,PPM1D,GPRASP1,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,CCP110,RBBP8,BAG5,ROCK1,THOC1,ITGA1,BFAR,C1QTNF3,CIDEA,GSPT1,ZC3H7A,CD40LG,USP7,TBXA2R,LSM5,PAFAH1B1,GADD45B,ENO1,ZDHHC	darkolivegreen	VSMC_M9
GO:0031328	0.15	0.87	103	1503	positive regulation of cellular biosynthetic process	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,INHBA,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,BRPF1,SUPT5H,DNAJC3,PPP1R12A,RPL26,CEBPZ,SMAD9,BRCA2,ILK,TMF1,HOXC10,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,STOX2,MICAL2,APPL1,RDH10,LARP4,TLR2,DHX36,THBS1,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,UBE3A,KPNA6,RAB3GAP2,NEK7,LARP7,TAF5L,ABCB10,EIF2B5,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,FASTKD2,CREB3L2,PTGS2,FZD2,NPAT,PRRX1,PLD1,TLR6,TRIP4,TBX6,PKM,ARMCX3,MAP2K4,MYOCD,PIN1,SS18,THOC1,ITGA2,MYSM1,ENO1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0090132	0.15	0.90	21	262	epithelium migration	BP	1	HDAC9,ROCK2,ITGB1,GATA3,CAPN7,STARD13,PFN2,THBS1,CORO1C,NRP2,CLEC14A,PTGS2,DNAJA4,AKT3,SRPX2,ROCK1,ITGA2,TBXA2R,BMPR2,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0090224	0.15	0.95	4	34	regulation of spindle organization	BP	1	SENP6,MAP9,TPR,CLTC	darkolivegreen	VSMC_M9
GO:0043542	0.15	0.90	16	195	endothelial cell migration	BP	1	HDAC9,ROCK2,ITGB1,GATA3,STARD13,THBS1,NRP2,CLEC14A,PTGS2,DNAJA4,AKT3,SRPX2,TBXA2R,BMPR2,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0051272	0.15	0.89	35	466	positive regulation of cellular component movement	BP	1	WISP1,PLAA,JAK2,HDAC9,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,TNFAIP6,CAPN7,ILK,LYN,THBS1,PGAM4,ACVR1,NEDD9,IGF1R,NTRK3,SEMA5B,IQGAP1,NRP2,PTGS2,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,SRPX2,SEMA7A,ITGA2,MYO1C,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0002218	0.15	0.95	4	33	activation of innate immune response	BP	1	TBK1,FYN,LYN,FCN1	darkolivegreen	VSMC_M9
GO:0001952	0.15	0.91	10	105	regulation of cell-matrix adhesion	BP	1	UTRN,ROCK2,ILK,RASA1,THBS1,PHLDB2,CORO1C,IQGAP1,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:0061458	0.15	0.89	26	333	reproductive system development	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,BRCA2,TMF1,MERTK,TMED2,EIF2S2,SULF1,STOX2,RDH10,IRX5,ETNK2,UBE3A,EIF2B5,SYCP2,ZFX,PTGS2,ADAM19,MYOCD,BMPR2,SRD5A2,WNT7A	darkolivegreen	VSMC_M9
GO:0040012	0.15	0.88	58	796	regulation of locomotion	BP	1	WISP1,PLAA,JAK2,HDAC9,STAP1,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,CAPN7,STARD13,ILK,LYN,SULF1,CCDC125,APPL1,PFN2,THBS1,PGAM4,ACVR1,NEDD9,LRRK2,PHLDB2,IGF1R,CORO1C,NTRK3,SEMA5B,IDH2,IQGAP1,NRP2,PTGS2,DNAJA4,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,MYO1C,TBXA2R,SSX2IP,BMPR2,NOV,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0002381	0.15	0.94	5	48	immunoglobulin production involved in immunoglobulin-mediated immune response	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0055067	0.16	0.91	10	108	monovalent inorganic cation homeostasis	BP	1	EXT1,TMEM165,CLN5,ATP6V0A2,AGTR1,ATP1A1,LRRK2,UBE3A,GPR89A,SLC1A3	darkolivegreen	VSMC_M9
GO:0008088	0.16	0.92	7	68	axo-dendritic transport	BP	1	KIF5B,TRAK1,TRAK2,ACTR10,ARMCX3,PAFAH1B1,KIF1B	darkolivegreen	VSMC_M9

GO:0010646	0.16	0.86	170	2513	regulation of cell communication	BP	1	SOCS6,MALT1,STXBP5,TBK1,PLEKHG1,RRM2B,WISP1,UBQLN1,PTPRD,DENND4C,AKAP9,JAK2,CLOCK,FBXO9,ASPN,ZNF451,CAVIN4,STAP1,CCDC88A,ZMPSTE24,CAV2,ROCK2,INHBA,DDX1,ITGB1,RPF2,FYN,KIF5B,GPR4,RB1,CBLC,MGAT5,GATA3,RAB3GAP1,NDFIP2,CYTH1,OSBPL8,RPL26,UFM1,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,UBA5,ILK,ITGA5,TMF1,SCYL2,CNOT7,RNF6,LYN,EIF2AK3,FBXL17,TMED2,ITCH,SULF1,USP47,CCDC125,FFAR4,MAP1B,APPL1,AGTR1,TLR2,RASA1,ATP2A2,BRAP,DHX36,THBS1,SHOX2,ACVR1,SLC39A14,CBLB,DYRK1A,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,CUL3,EIF4E,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,WWC3,PTPN1,GRK3,KPNA1,GPATCH3,C2CD2L,ATF3,PIP5K1A,IQGAP1,ANK3,TPR,PTGS2,NCAM1,IQCJ-SCHIP1,SORCS2,SEPT5,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TNIK,TNFAIP8L3,VDAC2,DKK1,ATAD1,RGS7,FAS,AKT3,WNT5B,TLR6,ADAM10,GPR65,CYFIP2,TLE3,UACA,GPRASP1,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,THOC1,ITGA2,ITGA1,RICTOR,SLC1A3,VAPA,BFAR,C1QTNF3,CIDEA,GPC4,USP7,MYO1C,PAFAH1B1,GADD45B,ENO1,VAV2,ZDHHC7,RFWD3,SSX2IP,PRKACB,ANKRD13C,CDH11,BMPR2,PTPN12,GDNF,CTGF,BDKRB2,LAMTOR3,DNAJB9,NOV,PDCL,PMEPA1,RAP2A,VGLL4,C12orf66,CHST11,UBE2V1,SHISA7,IRX3,WNT7A,PPP1R2	darkolivegreen	VSMC_M9
GO:0040007	0.16	0.88	54	742	growth	BP	1	SOCS6,LRP12,EXT1,CDKL3,PLAA,HOXA11,ZMPSTE24,INHBA,ITGB1,EXOSC9,RB1,GATA3,SOS1,BRCA2,ILK,RNF6,TMED2,ITCH,USP47,MAP1B,RDH10,AGTR1,INO80,ETNK2,NEDD9,PDLIM5,UBE3A,WWC3,KPNA1,SEMA5B,IQGAP1,RBBP7,NRP2,ZFX,SMURF1,ADAM10,CYFIP2,RBBP6,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,AFG3L2,PAFAH1B1,ENO1,WFDC1,BMPR2,PTPN12,NOV,ZPR1,VGLL4,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0019318	0.16	0.90	15	185	hexose metabolic process	BP	1	SLC35B4,ZMPSTE24,KBTBD2,B3GLCT,HK2,SLC39A14,ATF3,TPI1,HK3,PHKG2,CLK2,C1QTNF3,USP7,ENO1,RANBP2	darkolivegreen	VSMC_M9
GO:0071396	0.16	0.89	32	422	cellular response to lipid	BP	1	MALT1,PLAA,ABCB4,JAK2,CLOCK,STAP1,ROCK2,INHBA,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,LYN,GRAMD1A,GDAP1,TLR2,ATP1A1,UBE3A,EIF4E,NTRK3,WNT5B,MSN,KCNMB1,TRIP4,ITGA2,TBXA2R,PAQR8,PMEPA1,WNT9A	darkolivegreen	VSMC_M9
GO:0045214	0.16	0.94	4	33	sarcomere organization	BP	1	ITGB1,TPM1,FHOD3,CFL2	darkolivegreen	VSMC_M9
GO:0001817	0.16	0.88	36	492	regulation of cytokine production	BP	1	MALT1,TBK1,WISP1,JAK2,HDAC9,UBE2J1,ROCK2,INHBA,DDX1,GATA3,LRRC32,ATP2B1,NDFIP1,TMF1,LYN,MERTK,EIF2AK3,ITCH,SULF1,FFAR4,APPL1,TLR2,DHX36,THBS1,LRRK2,KPNA6,GPATCH3,PTGS2,ITGAV,TLR6,DICER1,SEMA7A,C1QTNF3,CIDEA,CD40LG,FCN1	darkolivegreen	VSMC_M9
GO:0006414	0.16	0.94	5	50	translational elongation	BP	1	LTN1,GFM1,CPEB2,SRP9,TRIP4	darkolivegreen	VSMC_M9
GO:0006396	0.16	0.87	59	950	RNA processing	BP	1	ELAC1,WDR46,DDX46,KHDRBS3,PPIL1,TRMO,ZMPSTE24,DDX1,RPF2,EXOSC9,ZC3H13,TRDMT1,TOE1,JMJD6,SUPT5H,MBNL2,PRPF40A,RPL26,AC091959.3,ERI1,MTREX,RIOK2,PDE12,U2SURP,MBNL1,DHX36,WDR75,SNRNP48,DYRK1A,PUS3,RRP15,LARP7,CLK1,FASTKD2,CWC22,DTWD1,CLK2,INTS14,ZC3H14,RBBP6,HNRNPH2,DICER1,MYOCD,THOC1,ZC3H7A,LSM5,DNTTIP2,ZNF326,SNORA21,SNORA3A,FASTKD5,INTS6,SNORA51,SNORD27,SNORD71,CDK13,GEMIN6,ZPR1,TFB2M	darkolivegreen	VSMC_M9
GO:0032269	0.16	0.88	53	760	negative regulation of cellular protein metabolic process	BP	1	PLAA,TFPI2,ZNF451,SH3BP5L,ROCK2,NOCT,FYN,EXOSC9,DNAJC1,RB1,PICALM,CBLC,MGAT5,DNAJC3,ILK,CNOT7,LYN,IPO7,EIF2AK3,TMED2,USP47,XRN1,PDE12,PI15,DCP1A,DHX36,THBS1,CBLB,LRRK2,EIF4E,UCHL5,EPRS,CORO1C,ANOS1,NTRK3,PTPN1,TLK2,TPR,PTGS2,CPEB2,BOD1L1,DKK1,SRP9,SRCIN1,MYOCD,BAG5,ROCK1,USP7,GADD45B,WFDC1,FRY,BDKRB2,PMEPA1	darkolivegreen	VSMC_M9
GO:2001238	0.16	0.94	4	37	positive regulation of extrinsic apoptotic signaling pathway	BP	1	INHBA,THBS1,ATF3,SKIL	darkolivegreen	VSMC_M9
GO:0046467	0.16	0.91	10	120	membrane lipid biosynthetic process	BP	1	ELOVL5,ST3GAL3,PLPP1,CERS5,ST8SIA1,SAMD8,PIGW,DPM2,DPM1,ELOVL4	darkolivegreen	VSMC_M9
GO:0038034	0.16	0.93	5	49	signal transduction in absence of ligand	BP	1	INHBA,FYN,ITGAV,FAS,GDNF	darkolivegreen	VSMC_M9
GO:0097192	0.16	0.93	5	49	extrinsic apoptotic signaling pathway in absence of ligand	BP	1	INHBA,FYN,ITGAV,FAS,GDNF	darkolivegreen	VSMC_M9
GO:0070647	0.16	0.87	57	806	protein modification by small protein conjugation or removal	BP	1	SOCS6,MALT1,CAND1,CDC23,UBQLN1,PLAA,TOPORS,FBXO9,ZNF451,SENP6,UBA6,UBE2J1,FYN,CBLC,NUB1,NDFIP2,UFM1,NDFIP1,CUL4A,UBA5,USP12,RNF6,FBXL17,ITCH,USP47,LNPEP,LTN1,BRAP,KCTD9,CBLB,LRRK2,TANK,UBE3A,CUL3,UCHL5,G2E3,UBE4A,C10orf90,KLHL18,CDC27,USP54,SMURF1,SPOP,RLIM,RBBP6,C18orf25,PIN1,BAG5,BFAR,MYSM1,USP7,RFWD3,RANBP2,OTUD6B,PDZRN3,FBXL7,UBE2V1	darkolivegreen	VSMC_M9
GO:0030004	0.16	0.92	8	81	cellular monovalent inorganic cation homeostasis	BP	1	TMEM165,CLN5,ATP6V0A2,ATP1A1,LRRK2,UBE3A,GPR89A,SLC1A3	darkolivegreen	VSMC_M9
GO:0010632	0.16	0.90	17	208	regulation of epithelial cell migration	BP	1	HDAC9,ROCK2,GATA3,CAPN7,STARD13,PFN2,THBS1,CORO1C,NRP2,PTGS2,DNAJA4,AKT3,SRPX2,ITGA2,TBXA2R,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0010633	0.16	0.93	6	59	negative regulation of epithelial cell migration	BP	1	STARD13,PFN2,THBS1,CORO1C,DNAJA4,TBXA2R	darkolivegreen	VSMC_M9
GO:0070848	0.16	0.88	43	570	response to growth factor	BP	1	EXT1,ASPN,ZNF451,CAV2,ROCK2,FYN,CEP57,NOX4,GATA3,LRRC32,SMAD9,SOS1,ILK,ITGA5,SULF1,MAP1B,APPL1,THBS1,ACVR1,EHD4,UBE3A,NTRK3,PTPN1,IQGAP1,NRP2,TPR,FERMT2,SKIL,SMURF1,CYFIP2,MYOCD,PIN1,ROCK1,CIDEA,MYO1C,RAPGEF1,BMPR2,PTPN12,CTGF,PMEPA1,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9

GO:0150116	0.16	0.92	7	65	regulation of cell-substrate junction organization	BP	1	ROCK2,THBS1,PHLDB2,CORO1C,IQGAP1,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:0001953	0.16	0.94	4	32	negative regulation of cell-matrix adhesion	BP	1	RASA1,THBS1,PHLDB2,CORO1C	darkolivegreen	VSMC_M9
GO:0051293	0.16	0.93	5	44	establishment of spindle localization	BP	1	ITGB1,UBXN2B,FMN2,SPIRE1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0032446	0.16	0.87	50	703	protein modification by small protein conjugation	BP	1	SOCS6,MALT1,CAND1,CDC23,UBQLN1,PLAA,TOPORS,FBXO9,ZNF451,SENP6,UBA6,UBE2J1,FYN,CBLC,NUB1,NDFIP2,UFM1,NDFIP1,CUL4A,UBA5,RNF6,FBXL17,ITCH,LNPEP,LTN1,BRAP,KCTD9,CBLB,LRRK2,UBE3A,CUL3,G2E3,UBE4A,C10orf90,KLHL18,CDC27,SMURF1,SPOP,RLIM,RBBP6,C18orf25,PIN1,BAG5,BFAR,USP7,RFWD3,RANBP2,PDZRN3,FBXL7,UBE2V1	darkolivegreen	VSMC_M9
GO:0035019	0.16	0.94	4	32	somatic stem cell population maintenance	BP	1	LIG4,CUL4A,TAF5L,WNT7A	darkolivegreen	VSMC_M9
GO:0006636	0.16	0.94	4	36	unsaturated fatty acid biosynthetic process	BP	1	ELOVL5,PNPLA8,PTGS2,ELOVL4	darkolivegreen	VSMC_M9
GO:0032502	0.16	0.86	302	4589	developmental process	BP	1	MALT1,CDO1,AHI1,LRIG3,UTRN,CAND1,CEP120,RRM2B,LRP12,EXT1,THBS2,CDKL3,CHADL,WISP1,PTPRD,PLAA,TOPORS,JAK2,CLOCK,NPAS2,FBXO9,ASPN,BZW2,HEMGN,HDAC9,CAVIN4,COL12A1,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,UGP2,ACTR2,IFRD1,CHRM2,CAV2,ROCK2,INHBA,GREB1,DDX1,NOCT,PCDH18,ITGB1,FYN,ZEB1,KIF5B,CEP57,PIWIL4,PSMC2,NOX4,FNDC3A,GPR4,RB1,PICALM,ZC3H13,CAMK1D,UPF2,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,PAX1,TRAK1,LRRC32,SETD5,AZI2,STK24,RIF1,OSBPL8,PRPF40A,GPCPD1,UFM1,LIG4,MYO16,SUPT20H,ATP2B1,ALG5,SMAD9,CCNA1,ATP11A,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,DCHS1,TMF1,SCYL2,RNF6,LYN,PPP2R3A,MERTK,TMEM41B,IFT88,MYBL1,EIF2AK3,SLC25A46,FBXL17,TDG,TMED2,PALLD,EIF2S2,ITCH,SULF1,STOX2,MICAL2,FFAR4,MAP1B,RDH10,LARP4,AGTR1,HK2,TLR2,RASA1,ATP2A2,VCAN,MBNL1,DHX36,THBS1,SHOX2,ZDHHC16,ARL6,ACVR1,SLC39A14,IRX5,GCNT4,ETNK2,NFKBIZ,NEDD9,CBLB,DYRK1A,MAN1A2,ERG,LRRK2,SNX19,TBX15,BRSK2,PDLIM5,ATP10A,UBE3A,MBOAT1,CUL3,EIF4E,PHLDB2,TDP2,DNER,TROVE2,UCHL5,CHSY1,IGF1R,BPNT1,CAMSAP2,GPR89A,CASP7,CORO1C,ANOS1,NTRK3,WWC3,LARP7,KPNA1,SEMA5B,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,SYCP2,ATF3,PIP5K1A,IQGAP1,ANK3,OSBPL11,CD3G,CCDC47,SMTN,ADAM12,SH3KBP1,NRP2,HDGFL3,PITHD1,MBTPS2,ZFX,CREB3L2,GATM,CLEC14A,PTGS2,NCAM1,MYEF2,FZD2,CDKL1,NPAT,ITGAV,GNPNAT1,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,DKK1,FMN2,PAPSS2,ACTA2,AKT3,RBM47,WNT5B,NOTCH3,HSPB7,ENAH,ADAM10,M	darkolivegreen	VSMC_M9
GO:0070613	0.16	0.93	5	52	regulation of protein processing	BP	1	THBS1,LRRK2,TIMM17A,ENO1,PRKACB	darkolivegreen	VSMC_M9
GO:0045807	0.16	0.92	8	82	positive regulation of endocytosis	BP	1	AHI1,STAP1,SCYL2,APPL1,LRRK2,ATAD1,ITGA2,RAB31	darkolivegreen	VSMC_M9
GO:0007218	0.16	0.94	4	36	neuropeptide signaling pathway	BP	1	GPR84,LTB4R,SORCS2,NXPH3	darkolivegreen	VSMC_M9
GO:0007140	0.16	0.94	4	35	male meiotic nuclear division	BP	1	CCNA1,BRCA2,MYBL1,SYCP2	darkolivegreen	VSMC_M9
GO:0009889	0.16	0.86	198	3010	regulation of biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,ETF1,SLC35B4,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,EIF5B,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,RIF1,PPP1R12A,RPL26,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,HSPH1,TMF1,HOXC10,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,PDE12,STOX2,MICAL2,APPL1,RDH10,LARP4,ACTR8,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,ATP1A1,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,CUL3,EIF4E,TDP2,KPNA6,EPRS,RAB3GAP2,NEK7,WWC3,LARP7,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,PTGS2,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,PLD1,CPEB2,SAMD8,DKK1,NOTCH3,SRP9,TLR6,MAGED2,CLK2,TRIP4,TBX6,RLIM,MAGEE2,RBBP6,TLE3,CLTC,PKM,DICER1,ARMCX3,PPM1D,MAP2K4,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,ZNF280C,C1QTNF3,GSPT1,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,RANBP2,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,PPTC7,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0030199	0.16	0.93	6	56	collagen fibril organization	BP	1	EXT1,CHADL,COL12A1,RB1,COL11A1,COLGALT1	darkolivegreen	VSMC_M9

GO:0007154	0.16	0.86	283	4300	cell communication	BP	1	SOCS6,MALT1,AHI1,STXBP5,TBK1,PLEKHG1,RRM2B,LRP12,EXT1,WISP1,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,TOPORS,AKAP9,GNG11,JAK2,CLOCK,EXOC1,FBXO9,ASPN,ZNF451,CAVIN4,MYO6,STAP1,CCDC88A,ZMPSTE24,PDE1C,KBTBD2,SH3BP5L,CHRM2,CAV2,ROCK2,INHBA,DDX1,RAB3B,ITGB1,RPF2,FYN,SYPL1,RINT1,KIF5B,CEP57,GPR4,RB1,SUSD5,CBLC,MGAT5,GATA3,RAB3GAP1,JMJD6,LRRC32,NDFIP2,AZI2,CYTH1,STK24,TNFAIP6,OSBPL8,PPP1R12A,STAM2,RPL26,UFM1,PIK3R4,MYO16,ATP2B1,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,GPR84,DCHS1,TMF1,SCYL2,PLPP1,CNOT7,RNF6,RASSF4,LYN,MERTK,IPO7,PDE7A,TCP11L1,EIF2AK3,FBXL17,TMED2,ITCH,SULF1,USP47,CCDC125,LNPEP,FFAR4,MAP1B,APPL1,GDAP1,AGTR1,TLR2,RASA1,ATP2A2,USO1,BRAP,DHX36,THBS1,NUCB2,GPR176,SHOX2,KCTD9,ARL6,ACVR1,SLC39A14,NFKBIZ,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,ERG,LRRK2,TANK,SNX19,BRSK2,UBE3A,SLC39A10,CUL3,EIF4E,TDP2,DNER,TROVE2,UCHL5,CHSY1,IGF1R,GPR89A,STK38L,CCDC186,CORO1C,ITPR2,NTRK3,WWC3,PTPN1,GRK3,KPNA1,SEMA5B,VAPB,EIF2B5,LTB4R,GPATCH3,C2CD2L,ATF3,PIP5K1A,IQGAP1,ANK3,CD3G,CCDC47,SH3KBP1,TLK2,NRP2,HDGFL3,MBTPS2,CREB3L2,TPR,CLEC14A,PTGS2,NCAM1,FZD2,IQCJ-SCHIP1,MAP4K5,SORCS2,GPR34,GPR82,ZC3H15,SEPT5,ITGAV,FERMT2,SKIL,PRRX1,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,TNFAIP8L3,KIAA0586,VDAC2,DKK1,FMN2,ATAD1,RGS7,FAS,PLP2,AKT3,WNT5B,CDC42BPA,NOTCH3,TLR6,ADAM10,MYO1E,KCNMB1,ITGB1BP2,TRIP4,TBX6,GPR65,CYFIP2,TLE3,UACA,DICER1,PPM1D,GP	darkolivegreen	VSMC_M9
GO:0006023	0.16	0.92	7	68	aminoglycan biosynthetic process	BP	1	EXT1,DSE,ST3GAL3,CSGALNACT2,CHSY1,CLTC,CHST11	darkolivegreen	VSMC_M9
GO:0070936	0.16	0.93	6	58	protein K48-linked ubiquitination	BP	1	TOPORS,RNF6,ITCH,UBE3A,CUL3,BFAR	darkolivegreen	VSMC_M9
GO:0051453	0.16	0.93	6	58	regulation of intracellular pH	BP	1	TMEM165,CLN5,ATP6V0A2,LRRK2,UBE3A,GPR89A	darkolivegreen	VSMC_M9
GO:0065009	0.16	0.86	154	2307	regulation of molecular function	BP	1	SOCS6,MALT1,PHACTR2,UTRN,STXBP5,CAND1,PLEKHG1,TBC1D15,AZIN1,UBQLN1,DENND4C,PLAA,TOPORS,AKAP9,TFPI2,JAK2,CLOCK,HDAC9,PSME4,STAP1,CCDC88A,ZMPSTE24,SH3BP5L,CAV2,ROCK2,ITGB1,FYN,KIF5B,DNAJC1,NOX4,RB1,PICALM,CBLC,CAMK1D,MGAT5,GATA3,CCNT2,RAB3GAP1,CLN5,NDFIP2,BRPF1,DNAJC3,CYTH1,OSBPL8,PPP1R12A,PIK3R4,CCNA1,NDFIP1,STARD13,SOS1,ILK,HSPH1,REM1,ARL1,LYN,PPP2R3A,MERTK,IPO7,EIF2AK3,TDG,TMED2,ITCH,USP47,CCDC125,PI15,AGTR1,TLR2,PFN2,RASA1,ATP2A2,DCP1A,THBS1,NUCB2,PPP2R2A,PDP1,SLC39A14,NEDD9,CBLB,LRRK2,TANK,BRSK2,SLC39A10,UCHL5,IGF1R,RAB3GAP2,CORO1C,ANOS1,NEK7,NTRK3,PTPN1,EIF2B5,PIP5K1A,IQGAP1,ANK3,MBTPS2,PTGS2,SEC23A,FZD2,ZC3H15,ITGAV,FERMT2,TNFAIP8L3,CPEB2,BOD1L1,DKK1,RGS7,FAS,TLR6,STIM2,SRCIN1,BNIP2,TPM1,TBX6,OAZ2,CLPX,RLIM,GPR65,CYFIP2,SMG8,UACA,MYOCD,PIN1,BAG5,ROCK1,ITGA2,ITGA1,RICTOR,PPP4R1,CD40LG,USP7,TBXA2R,CALML6,PAFAH1B1,GADD45B,VAV2,RAPGEF1,WFDC1,DPM2,GTF2B,DNAJB4,ANKRD13C,MIR186,RANBP2,BMPR2,FXYD5,FRY,ARF4,GDNF,TOR1AIP2,CTGF,LAMTOR3,UBE2V1,SHISA7,PPP1R2	darkolivegreen	VSMC_M9
GO:0001655	0.16	0.89	23	283	urogenital system development	BP	1	AHI1,RRM2B,EXT1,HOXA11,ZMPSTE24,GPR4,GATA3,JMJD6,ILK,DCHS1,IFT88,SULF1,RDH10,AGTR1,GCNT4,LRRK2,UBE3A,IQGAP1,ACTA2,MYO1E,MYOCD,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0032945	0.17	0.93	5	48	negative regulation of mononuclear cell proliferation	BP	1	LRRC32,NDFIP1,LYN,ITCH,CBLB	darkolivegreen	VSMC_M9
GO:0050672	0.17	0.93	5	48	negative regulation of lymphocyte proliferation	BP	1	LRRC32,NDFIP1,LYN,ITCH,CBLB	darkolivegreen	VSMC_M9
GO:0090504	0.17	0.94	4	31	epiboly	BP	1	ITGA5,PHLDB2,FERMT2,WNT7A	darkolivegreen	VSMC_M9
GO:0007020	0.17	0.94	4	32	microtubule nucleation	BP	1	AKAP9,TUBGCP3,HAUS2,MZT1	darkolivegreen	VSMC_M9
GO:0051270	0.17	0.87	60	830	regulation of cellular component movement	BP	1	WISP1,PLAA,AKAP9,JAK2,HDAC9,STAP1,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,CAPN7,STARD13,ILK,LYN,SULF1,CCDC125,APPL1,PFN2,ATP2A2,THBS1,PGAM4,ACVR1,NEDD9,ATP1A1,PHLDB2,IGF1R,CORO1C,NTRK3,SEMA5B,IDH2,IQGAP1,NRP2,PTGS2,DNAJA4,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,MYO1C,TBXA2R,SSX2IP,BMPR2,NOV,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0036473	0.17	0.92	7	76	cell death in response to oxidative stress	BP	1	UBQLN1,JAK2,FYN,STK24,LRRK2,TLR6,BAG5	darkolivegreen	VSMC_M9
GO:0045471	0.17	0.91	8	87	response to ethanol	BP	1	CDO1,ACTR2,FYN,GATA3,ITPR2,NTRK3,KCNMB1,TBXA2R	darkolivegreen	VSMC_M9
GO:0002702	0.17	0.92	7	75	positive regulation of production of molecular mediator of immune response	BP	1	MALT1,DDX1,GATA3,RIF1,DHX36,SEMA7A,DNAJB9	darkolivegreen	VSMC_M9

GO:0007165	0.17	0.85	258	3919	signal transduction	BP	1	SOCS6,MALT1,AHI1,TBK1,PLEKHG1,RRM2B,LRP12,EXT1,WISP1,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,TOPORS,AKAP9,GNG11,JAK2,CLOCK,EXOC1,FBXO9,ASPN,ZNF451,CAVIN4,MYO6,STAP1,CCDC88A,ZMPSTE24,PDE1C,KBTBD2,SH3BP5L,CHRM2,CAV2,ROCK2,INHBA,DDX1,ITGB1,RPF2,FYN,RINT1,CEP57,GPR4,RB1,SUSD5,CBLC,MGAT5,GATA3,RAB3GAP1,JMJD6,LRRC32,NDFIP2,AZI2,CYTH1,STK24,TNFAIP6,OSBPL8,PPP1R12A,STAM2,RPL26,UFM1,MYO16,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,UBA5,ILK,ITGA5,GPR84,DCHS1,TMF1,SCYL2,PLPP1,CNOT7,RNF6,RASSF4,LYN,MERTK,IPO7,PDE7A,TCP11L1,EIF2AK3,FBXL17,TMED2,ITCH,SULF1,USP47,CCDC125,LNPEP,FFAR4,APPL1,AGTR1,TLR2,RASA1,ATP2A2,USO1,BRAP,DHX36,THBS1,NUCB2,GPR176,SHOX2,KCTD9,ARL6,ACVR1,SLC39A14,NFKBIZ,NEDD9,CBLB,DYRK1A,BRD7,ERG,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,CUL3,TDP2,DNER,TROVE2,UCHL5,CHSY1,IGF1R,GPR89A,STK38L,CORO1C,ITPR2,NTRK3,WWC3,PTPN1,GRK3,KPNA1,SEMA5B,VAPB,EIF2B5,LTB4R,GPATCH3,ATF3,PIP5K1A,IQGAP1,ANK3,CD3G,CCDC47,TLK2,NRP2,HDGFL3,MBTPS2,CREB3L2,TPR,CLEC14A,PTGS2,NCAM1,FZD2,IQCJ-SCHIP1,MAP4K5,SORCS2,GPR34,GPR82,ZC3H15,ITGAV,FERMT2,SKIL,PRRX1,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,TNFAIP8L3,KIAA0586,VDAC2,DKK1,FMN2,RGS7,FAS,PLP2,AKT3,WNT5B,CDC42BPA,NOTCH3,TLR6,ADAM10,MYO1E,ITGB1BP2,TRIP4,TBX6,GPR65,CYFIP2,TLE3,UACA,DICER1,PPM1D,GPRASP1,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,SS18,BAG5,ROCK1,THOC1,ITGA2,ITGA1,MYOM1,RICTOR,PPP4R1,VAPA,BFAR,C1QTNF3,CIDEA,GPC4,CD40LG,USP7,MYO1C,TBXA2R,PAF	darkolivegreen	VSMC_M9
GO:0042307	0.17	0.94	4	35	positive regulation of protein import into nucleus	BP	1	JAK2,TPR,PTGS2,ZPR1	darkolivegreen	VSMC_M9
GO:0016447	0.17	0.93	5	48	somatic recombination of immunoglobulin gene segments	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0055078	0.17	0.94	4	34	sodium ion homeostasis	BP	1	EXT1,AGTR1,ATP1A1,SLC1A3	darkolivegreen	VSMC_M9
GO:0006096	0.17	0.92	6	60	glycolytic process	BP	1	HK2,PGAM4,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0006757	0.17	0.92	6	60	ATP generation from ADP	BP	1	HK2,PGAM4,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0019953	0.17	0.87	40	565	sexual reproduction	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,TNFAIP6,ADAM32,TUBGCP3,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,EIF2S2,MICAL2,DHX36,ACVR1,LRRK2,UBE3A,LARP7,SYCP2,PITHD1,ZFX,PTGS2,SKIL,VDAC2,FMN2,ADAM10,SPIRE1,PAFAH1B1,ANKRD49,PAQR8,TMEM119	darkolivegreen	VSMC_M9
GO:0010720	0.17	0.89	19	231	positive regulation of cell development	BP	1	CDKL3,PTPRD,HOXA11,ACTR2,TRAK1,LIG4,ILK,LYN,MAP1B,TLR2,DHX36,SHOX2,NEDD9,FERMT2,SKIL,DICER1,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:1902807	0.17	0.92	6	60	negative regulation of cell cycle G1/S phase transition	BP	1	RB1,RPL26,MYO16,BRD7,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0072665	0.17	0.92	6	60	protein localization to vacuole	BP	1	GCC2,ROCK2,VPS36,PIK3R4,SMURF1,C12orf66	darkolivegreen	VSMC_M9
GO:0032543	0.17	0.92	6	72	mitochondrial translation	BP	1	NOA1,RARS2,GFM1,IARS2,MRPL47,FASTKD2	darkolivegreen	VSMC_M9
GO:0047496	0.17	0.93	5	45	vesicle transport along microtubule	BP	1	KIF5B,TRAK1,TRAK2,KIFAP3,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0051961	0.17	0.90	10	106	negative regulation of nervous system development	BP	1	CDKL3,RNF6,TLR2,NTRK3,SEMA5B,IDH2,TRAK2,DICER1,SEMA7A,WNT7A	darkolivegreen	VSMC_M9
GO:0007155	0.17	0.86	76	1044	cell adhesion	BP	1	SOCS6,MALT1,UTRN,EXT1,THBS2,WISP1,PTPRD,JAK2,GNE,COL12A1,ROCK2,PCDH18,ITGB1,FYN,FNDC3A,GPR4,SUSD5,CGREF1,GATA3,LRRC32,CYTH1,TNFAIP6,PPP1R12A,ADAM32,THSD1,NDFIP1,NTN4,ILK,ITGA5,DCHS1,HSPH1,HSD17B12,LYN,MERTK,PALLD,ITCH,RASA1,ATP2A2,VCAN,THBS1,ACVR1,NFKBIZ,NEDD9,CBLB,PDLIM5,PHLDB2,CORO1C,ANOS1,PIP5K1A,IQGAP1,ANK3,LMLN,ADAM12,NRP2,NCAM1,ITGAV,FERMT2,KIFAP3,ADAM10,MSN,SRCIN1,TPM1,ADAM19,CYFIP2,SRPX2,ROCK1,ITGA2,ITGA1,GPC4,CD40LG,SSX2IP,CDH11,FXYD5,GP1BB,CTGF,NOV	darkolivegreen	VSMC_M9
GO:0010594	0.17	0.89	13	157	regulation of endothelial cell migration	BP	1	HDAC9,ROCK2,GATA3,STARD13,THBS1,NRP2,PTGS2,DNAJA4,AKT3,SRPX2,TBXA2R,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:1902414	0.17	0.91	8	82	protein localization to cell junction	BP	1	MPP7,KIF5B,FERMT2,ADAM10,GPC4,ZDHHC7,LAMTOR3,WNT7A	darkolivegreen	VSMC_M9
GO:0010647	0.17	0.86	86	1251	positive regulation of cell communication	BP	1	MALT1,TBK1,WISP1,JAK2,STAP1,CCDC88A,CAV2,ROCK2,INHBA,DDX1,ITGB1,FYN,KIF5B,GPR4,MGAT5,GATA3,RAB3GAP1,NDFIP2,OSBPL8,RPL26,ACPP,NR2C1,NDFIP1,SOS1,ILK,ITGA5,TMF1,LYN,SULF1,USP47,FFAR4,TLR2,DHX36,THBS1,SHOX2,ACVR1,SLC39A14,LRRK2,UBE3A,SLC39A10,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,PTPN1,C2CD2L,ATF3,IQGAP1,ANK3,TPR,PTGS2,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,PRRX1,TNIK,TNFAIP8L3,DKK1,FAS,AKT3,WNT5B,TLR6,GPR65,CYFIP2,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,RICTOR,SLC1A3,VAPA,C1QTNF3,MYO1C,PAFAH1B1,GADD45B,BMPR2,CTGF,LAMTOR3,NOV,PDCL,UBE2V1,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0044092	0.17	0.86	55	806	negative regulation of molecular function	BP	1	PHACTR2,CAND1,UBQLN1,AKAP9,TFPI2,JAK2,HDAC9,SH3BP5L,ROCK2,RB1,PICALM,CBLC,MGAT5,NDFIP2,DNAJC3,PPP1R12A,NDFIP1,ILK,REM1,LYN,IPO7,TMED2,ITCH,USP47,PI15,ATP2A2,THBS1,SLC39A14,CBLB,LRRK2,UCHL5,CORO1C,ANOS1,PTPN1,IQGAP1,ANK3,PTGS2,ITGAV,CPEB2,BOD1L1,DKK1,SRCIN1,TBX6,OAZ2,RLIM,MYOCD,PIN1,BAG5,ROCK1,USP7,GADD45B,WFDC1,MIR186,FRY,PPP1R2	darkolivegreen	VSMC_M9
GO:0071634	0.17	0.94	4	33	regulation of transforming growth factor beta production	BP	1	LRRC32,THBS1,PTGS2,ITGAV	darkolivegreen	VSMC_M9

GO:0030326	0.17	0.91	9	96	embryonic limb morphogenesis	BP	1	HOXA9,HOXA10,HOXA11,RDH10,MBNL1,SHOX2,PRRX1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0035113	0.17	0.91	9	96	embryonic appendage morphogenesis	BP	1	HOXA9,HOXA10,HOXA11,RDH10,MBNL1,SHOX2,PRRX1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0051452	0.17	0.93	4	36	intracellular pH reduction	BP	1	CLN5,ATP6V0A2,UBE3A,GPR89A	darkolivegreen	VSMC_M9
GO:0048609	0.17	0.87	40	563	multicellular organismal reproductive process	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,TNFAIP6,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,TMED2,EIF2S2,STOX2,MICAL2,DHX36,ACVR1,LRRK2,KPNA6,LARP7,SYCP2,PITHD1,ZFX,PTGS2,SKIL,FMN2,ADAM10,SPIRE1,PAFAH1B1,BMPR2,ANKRD49,PAQR8,TMEM119	darkolivegreen	VSMC_M9
GO:0090287	0.17	0.88	19	230	regulation of cellular response to growth factor stimulus	BP	1	ASPN,ZNF451,CAV2,GATA3,ILK,ITGA5,SULF1,THBS1,PTPN1,SKIL,SMURF1,CYFIP2,MYOCD,PIN1,CIDEA,MYO1C,BMPR2,PMEPA1,CHST11	darkolivegreen	VSMC_M9
GO:0051225	0.17	0.90	9	101	spindle assembly	BP	1	HAUS6,SENP6,TUBGCP3,MAP9,INO80,HAUS2,NEK7,TPR,MZT1	darkolivegreen	VSMC_M9
GO:0090218	0.17	0.94	4	31	positive regulation of lipid kinase activity	BP	1	PIK3R4,LYN,TNFAIP8L3,VAV2	darkolivegreen	VSMC_M9
GO:2000677	0.17	0.93	4	37	regulation of transcription regulatory region DNA binding	BP	1	ZMPSTE24,RB1,GATA3,GTF2B	darkolivegreen	VSMC_M9
GO:0006997	0.17	0.90	10	112	nucleus organization	BP	1	PSME4,ZMPSTE24,TMF1,UBXN2B,SMARCA5,TPR,NUP155,PAFAH1B1,ZPR1,NUP35	darkolivegreen	VSMC_M9
GO:0006367	0.17	0.92	6	65	transcription initiation from RNA polymerase II promoter	BP	1	CAND1,ZNF451,DHX36,PPM1D,GTF2B,E2F3	darkolivegreen	VSMC_M9
GO:0008543	0.17	0.92	6	59	fibroblast growth factor receptor signaling pathway	BP	1	EXT1,CEP57,GATA3,SULF1,THBS1,CTGF	darkolivegreen	VSMC_M9
GO:0007399	0.17	0.85	131	1867	nervous system development	BP	1	AHI1,CEP120,LRP12,EXT1,THBS2,CDKL3,PTPRD,PLAA,TOPORS,JAK2,NPAS2,BZW2,HDAC9,MYO6,STAP1,UBA6,CCDC88A,UGP2,ACTR2,CHRM2,INHBA,PCDH18,ITGB1,FYN,ZEB1,KIF5B,RB1,PICALM,CAMK1D,GATA3,RAB3GAP1,CLN5,TRAK1,SETD5,STK24,UFM1,LIG4,MYO16,ATP2B1,SOS1,BRCA2,NTN4,ILK,DCHS1,SCYL2,RNF6,LYN,MERTK,TMEM41B,IFT88,EIF2AK3,SLC25A46,FBXL17,TMED2,PALLD,SULF1,MAP1B,TLR2,VCAN,MBNL1,DHX36,SHOX2,ZDHHC16,IRX5,DYRK1A,LRRK2,BRSK2,PDLIM5,UBE3A,MBOAT1,EIF4E,TDP2,DNER,UCHL5,BPNT1,CAMSAP2,ANOS1,NTRK3,SEMA5B,IDH2,EIF2B5,TRAK2,IQGAP1,ANK3,NRP2,HDGFL3,CREB3L2,NCAM1,MYEF2,FZD2,SKIL,PRRX1,SMURF1,TNIK,DKK1,AKT3,WNT5B,NOTCH3,ENAH,ADAM10,SRCIN1,TBX6,CYFIP2,SRPX2,DICER1,SEMA7A,PIN1,BAG5,ROCK1,ITGA1,SLC1A3,VAPA,AFG3L2,GPC4,PAFAH1B1,RAPGEF1,PLPPR5,PRKACB,CDH11,BMPR2,TMX2,FRY,ARF4,GDNF,LHFPL4,EFHD1,RAP2A,WNT9A,ZPR1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0051346	0.17	0.88	18	242	negative regulation of hydrolase activity	BP	1	TFPI2,HDAC9,ROCK2,PICALM,MGAT5,TMED2,USP47,PI15,THBS1,SLC39A14,LRRK2,UCHL5,ANOS1,PTGS2,CPEB2,BOD1L1,ROCK1,WFDC1	darkolivegreen	VSMC_M9
GO:0140053	0.18	0.91	8	101	mitochondrial gene expression	BP	1	NOA1,RARS2,GFM1,IARS2,MRPL47,FASTKD2,FASTKD5,TFB2M	darkolivegreen	VSMC_M9
GO:0006897	0.18	0.87	34	444	endocytosis	BP	1	AHI1,LRP12,MYO6,STAP1,CAV2,ITGB1,PICALM,JMJD6,ESYT2,EEA1,SCYL2,APPL1,THBS1,EHD4,LRRK2,UBE3A,DNER,PTPN1,GRK3,HEATR5A,SH3KBP1,ITGAV,VAMP4,AP4E1,DKK1,ATAD1,MYO1E,CLINT1,CLTC,ROCK1,ITGA2,RAB31,XKR9,FCN1	darkolivegreen	VSMC_M9
GO:0046718	0.18	0.90	9	100	viral entry into host cell	BP	1	CAV2,ITGB1,ITGA5,ITCH,AGTR1,NCAM1,ITGAV,ITGA2,FCN1	darkolivegreen	VSMC_M9
GO:0035023	0.18	0.91	7	69	regulation of Rho protein signal transduction	BP	1	CAVIN4,ITGB1,GPR4,STARD13,CCDC125,CUL3,GPR65	darkolivegreen	VSMC_M9
GO:0038179	0.18	0.93	4	34	neurotrophin signaling pathway	BP	1	SOS1,NTRK3,CYFIP2,RAPGEF1	darkolivegreen	VSMC_M9
GO:0023052	0.18	0.84	280	4258	signaling	BP	1	SOCS6,MALT1,AHI1,STXBP5,TBK1,PLEKHG1,RRM2B,LRP12,EXT1,WISP1,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,TOPORS,AKAP9,GNG11,JAK2,CLOCK,EXOC1,FBXO9,ASPN,ZNF451,CAVIN4,MYO6,STAP1,CCDC88A,ZMPSTE24,PDE1C,KBTBD2,SH3BP5L,CHRM2,CAV2,ROCK2,INHBA,DDX1,RAB3B,ITGB1,RPF2,FYN,SYPL1,RINT1,KIF5B,CEP57,GPR4,RB1,SUSD5,CBLC,MGAT5,GATA3,RAB3GAP1,JMJD6,LRRC32,NDFIP2,AZI2,CYTH1,STK24,TNFAIP6,OSBPL8,PPP1R12A,STAM2,RPL26,UFM1,MYO16,ATP2B1,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,GPR84,DCHS1,TMF1,SCYL2,PLPP1,CNOT7,RNF6,RASSF4,LYN,MERTK,IPO7,PDE7A,TCP11L1,EIF2AK3,FBXL17,TMED2,ITCH,SULF1,USP47,CCDC125,LNPEP,FFAR4,MAP1B,APPL1,AGTR1,TLR2,RASA1,ATP2A2,USO1,BRAP,DHX36,THBS1,NUCB2,GPR176,SHOX2,KCTD9,ARL6,ACVR1,SLC39A14,NFKBIZ,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,ERG,LRRK2,TANK,SNX19,BRSK2,UBE3A,SLC39A10,CUL3,EIF4E,TDP2,DNER,TROVE2,UCHL5,CHSY1,IGF1R,GPR89A,STK38L,CCDC186,CORO1C,ITPR2,NTRK3,WWC3,PTPN1,GRK3,KPNA1,SEMA5B,VAPB,EIF2B5,LTB4R,GPATCH3,C2CD2L,ATF3,PIP5K1A,IQGAP1,ANK3,CD3G,CCDC47,SH3KBP1,TLK2,NRP2,HDGFL3,MBTPS2,CREB3L2,TPR,CLEC14A,PTGS2,NCAM1,FZD2,IQCJ-SCHIP1,MAP4K5,SORCS2,GPR34,GPR82,ZC3H15,SEPT5,ITGAV,FERMT2,SKIL,PRRX1,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,TNFAIP8L3,KIAA0586,VDAC2,DKK1,FMN2,ATAD1,RGS7,FAS,PLP2,AKT3,WNT5B,CDC42BPA,NOTCH3,TLR6,ADAM10,MYO1E,KCNMB1,ITGB1BP2,TRIP4,TBX6,GPR65,CYFIP2,TLE3,UACA,DICER1,PPM1D,GPRASP1,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,SS18,	darkolivegreen	VSMC_M9
GO:1900180	0.18	0.90	10	116	regulation of protein localization to nucleus	BP	1	JAK2,FYN,UFM1,EIF2AK3,LARP7,TPR,PTGS2,FERMT2,PIN1,ZPR1	darkolivegreen	VSMC_M9
GO:0010634	0.18	0.89	12	143	positive regulation of epithelial cell migration	BP	1	HDAC9,ROCK2,GATA3,CAPN7,THBS1,NRP2,PTGS2,AKT3,SRPX2,ITGA2,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0042058	0.18	0.92	6	62	regulation of epidermal growth factor receptor signaling pathway	BP	1	CCDC88A,CBLC,SOS1,CBLB,ITGA1,PTPN12	darkolivegreen	VSMC_M9

GO:0032956	0.18	0.87	24	304	regulation of actin cytoskeleton organization	BP	1	STAP1,CCDC88A,ACTR2,ROCK2,NOX4,ACTR3,ILK,PFN2,RASA1,SPTBN5,PHLDB2,NTRK3,IQGAP1,FERMT2,TPM1,GPR65,CYFIP2,FHOD3,ROCK1,RICTOR,SPIRE1,MYO1C,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:1903510	0.18	0.91	7	71	mucopolysaccharide metabolic process	BP	1	EXT1,DSE,ST3GAL3,CSGALNACT2,CHSY1,CLTC,CHST11	darkolivegreen	VSMC_M9
GO:0046634	0.18	0.92	6	63	regulation of alpha-beta T cell activation	BP	1	MALT1,GATA3,HSPH1,ITCH,NFKBIZ,CBLB	darkolivegreen	VSMC_M9
GO:0018394	0.18	0.89	12	143	peptidyl-lysine acetylation	BP	1	PHF20L1,CLOCK,ZNF451,ZMPSTE24,GATA3,BRPF1,SETD5,BRCA2,BRD7,TAF5L,MYOCD,GTF2B	darkolivegreen	VSMC_M9
GO:0071806	0.18	0.92	5	54	protein transmembrane transport	BP	1	RTN2,TIMM17A,TOMM20,TOMM20L,SEC63	darkolivegreen	VSMC_M9
GO:0009719	0.18	0.85	84	1202	response to endogenous stimulus	BP	1	CDO1,EXT1,DENND4C,AKAP9,JAK2,CLOCK,ASPN,ZNF451,HDAC9,ZMPSTE24,KBTBD2,ACTR2,CHRM2,CAV2,ROCK2,INHBA,ITGB1,FYN,CEP57,NOX4,GATA3,LRRC32,OSBPL8,UFM1,ATP2B1,SMAD9,NR2C1,UBA5,ILK,TMF1,PLPP1,RNF6,LYN,SULF1,XRN1,MAP1B,APPL1,AGTR1,TLR2,USO1,THBS1,ACVR1,SLC39A14,ATP1A1,LRRK2,UBE3A,EIF4E,EPRS,IGF1R,CASP7,ITPR2,NTRK3,PTPN1,EIF2B5,IQGAP1,RBBP7,TPR,PTGS2,FERMT2,SKIL,SMURF1,CPEB2,TLR6,TRIP4,PKM,MYOCD,PIN1,ROCK1,ITGA2,SLC1A3,RAB31,CIDEA,MYO1C,RAPGEF1,ZDHHC7,BMPR2,PTPN12,CTGF,LAMTOR3,PAQR8,PMEPA1,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0003014	0.18	0.91	7	74	renal system process	BP	1	RRM2B,SULF1,AGTR1,MAGED2,MYO1E,PRKACB,AQP3	darkolivegreen	VSMC_M9
GO:0042273	0.18	0.92	5	56	ribosomal large subunit biogenesis	BP	1	RPF2,RPL26,RRP15,FASTKD2,SURF6	darkolivegreen	VSMC_M9
GO:0032465	0.18	0.91	7	72	regulation of cytokinesis	BP	1	PRPF40A,PIK3R4,BRCA2,MAP9,CUL3,PIN1,CCP110	darkolivegreen	VSMC_M9
GO:0001818	0.18	0.88	15	195	negative regulation of cytokine production	BP	1	HDAC9,INHBA,GATA3,LRRC32,ATP2B1,NDFIP1,MERTK,ITCH,FFAR4,THBS1,GPATCH3,TLR6,DICER1,C1QTNF3,CIDEA	darkolivegreen	VSMC_M9
GO:0033045	0.18	0.91	6	64	regulation of sister chromatid segregation	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0031032	0.18	0.88	15	172	actomyosin structure organization	BP	1	CCDC88A,ROCK2,ITGB1,NOX4,PFN2,CUL3,PHLDB2,FERMT2,CDC42BPA,TPM1,GPR65,FHOD3,ROCK1,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:2000781	0.18	0.93	4	36	positive regulation of double-strand break repair	BP	1	ACTR2,RIF1,FMN2,SPIRE1	darkolivegreen	VSMC_M9
GO:0060135	0.18	0.92	5	49	maternal process involved in female pregnancy	BP	1	TMED2,STOX2,KPNA6,PTGS2,BMPR2	darkolivegreen	VSMC_M9
GO:0048675	0.18	0.90	10	106	axon extension	BP	1	CDKL3,ITGB1,ILK,RNF6,MAP1B,SEMA5B,NRP2,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0061077	0.18	0.92	5	55	chaperone-mediated protein folding	BP	1	DNAJB5,HSPH1,DNAJB14,DNAJB4,HSPA13	darkolivegreen	VSMC_M9
GO:0006915	0.18	0.85	95	1436	apoptotic process	BP	1	MALT1,AHI1,RRM2B,UBQLN1,PRUNE2,TOPORS,JAK2,NOA1,ZMPSTE24,INHBA,ITGB1,FYN,NOX4,RB1,CAMK1D,GATA3,DNAJC3,STK24,RPL26,UFM1,LIG4,CUL4A,BRCA2,ILK,ITGA5,TMF1,LYN,MERTK,EIF2AK3,ITCH,SULF1,USP47,FFAR4,HK2,TLR2,RASA1,THBS1,ZDHHC16,ACVR1,LRRK2,BRSK2,SLC39A10,CUL3,IGF1R,CASP7,PTPN1,KPNA1,EIF2B5,SYCP2,ATF3,G2E3,CD3G,SH3KBP1,FASTKD2,PTGS2,ITGAV,SKIL,RTN3,KIFAP3,TNFAIP8L3,VDAC2,DKK1,FMN2,FAS,ADAM10,BNIP2,GPR65,CYFIP2,UACA,DICER1,ATG4D,MAP2K4,MYOCD,ANXA6,PIN1,BAG5,ROCK1,THOC1,ITGA1,BFAR,CIDEA,CD40LG,GADD45B,ENO1,KIF1B,ANKRD13C,BMPR2,XKR9,ARF4,GDNF,BDKRB2,E2F3,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0055076	0.18	0.90	9	107	transition metal ion homeostasis	BP	1	SLC39A7,SLC30A9,PICALM,NDFIP1,ATP6V0A2,SLC30A5,SLC39A14,SLC39A10,ATP6V1A	darkolivegreen	VSMC_M9
GO:0031589	0.18	0.87	24	294	cell-substrate adhesion	BP	1	UTRN,JAK2,ROCK2,ITGB1,THSD1,NTN4,ILK,ITGA5,HSD17B12,MERTK,RASA1,THBS1,NEDD9,PHLDB2,CORO1C,PIP5K1A,IQGAP1,ITGAV,FERMT2,SRCIN1,ROCK1,ITGA2,ITGA1,CTGF	darkolivegreen	VSMC_M9
GO:0003013	0.18	0.86	33	437	circulatory system process	BP	1	EXT1,AKAP9,JAK2,ZMPSTE24,CHRM2,ROCK2,FYN,NOX4,GPR4,ATP2B1,SLC16A12,LNPEP,AGTR1,ATP2A2,SHOX2,ATP1A1,PTGS2,FERMT2,F5,ACTA2,HSPB7,KCNMB1,TPM1,SGCD,ROCK1,ITGA1,NUP155,SLC1A3,TBXA2R,BMPR2,CTGF,BDKRB2,IRX3	darkolivegreen	VSMC_M9
GO:0033619	0.18	0.92	5	48	membrane protein proteolysis	BP	1	MBTPS2,ADAM10,ADAM19,ROCK1,AFG3L2	darkolivegreen	VSMC_M9
GO:0048513	0.18	0.84	170	2529	animal organ development	BP	1	MALT1,CDO1,AHI1,LRIG3,UTRN,CEP120,RRM2B,EXT1,CHADL,WISP1,TOPORS,JAK2,CLOCK,ASPN,HDAC9,CAVIN4,MYO6,UBA6,HOXA9,HOXA10,HOXA11,ZMPSTE24,UGP2,CAV2,ROCK2,INHBA,PCDH18,ITGB1,FYN,KIF5B,FNDC3A,GPR4,RB1,PICALM,UPF2,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,AZI2,GPCPD1,UFM1,LIG4,MYO16,ATP2B1,NDFIP1,CUL4A,SOS1,BRCA2,NTN4,UBA5,ILK,DCHS1,TMF1,SCYL2,LYN,MERTK,IFT88,EIF2AK3,FBXL17,TMED2,PALLD,EIF2S2,ITCH,SULF1,STOX2,MICAL2,RDH10,AGTR1,HK2,TLR2,DHX36,SHOX2,ZDHHC16,ACVR1,SLC39A14,IRX5,GCNT4,ETNK2,NFKBIZ,MAN1A2,LRRK2,SNX19,TBX15,PDLIM5,UBE3A,CUL3,EIF4E,PHLDB2,DNER,UCHL5,CHSY1,GPR89A,CASP7,CORO1C,NTRK3,SEMA5B,ABCB10,EIF2B5,SYCP2,ATF3,PIP5K1A,IQGAP1,CD3G,SMTN,NRP2,PITHD1,MBTPS2,ZFX,CREB3L2,PTGS2,FZD2,CDKL1,GNPNAT1,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,DKK1,ACTA2,AKT3,RBM47,WNT5B,HSPB7,ADAM10,MSN,MYO1E,TPM1,ITGB1BP2,TBX6,ADAM19,RBBP6,TLE3,SGCD,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,ROCK1,ITGA2,MYOM1,GPC4,MYSM1,CD40LG,PAFAH1B1,COL11A1,BMPR2,AQP3,TMX2,ARF4,GDNF,CDK13,CTGF,FOXN2,SEC63,DNAJB9,NOV,WNT9A,ZPR1,VGLL4,SRD5A2,TMEM119,CHST11,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9

GO:0030330	0.18	0.91	6	63	DNA damage response, signal transduction by p53 class mediator	BP	1	MYO6,ZMPSTE24,RPL26,BRCA2,DYRK1A,PPM1D	darkolivegreen	VSMC_M9
GO:0006497	0.18	0.91	7	81	protein lipidation	BP	1	RAB3GAP1,ZDHHC16,RAB3GAP2,PIGW,ZDHHC7,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0022610	0.18	0.85	76	1050	biological adhesion	BP	1	SOCS6,MALT1,UTRN,EXT1,THBS2,WISP1,PTPRD,JAK2,GNE,COL12A1,ROCK2,PCDH18,ITGB1,FYN,FNDC3A,GPR4,SUSD5,CGREF1,GATA3,LRRC32,CYTH1,TNFAIP6,PPP1R12A,ADAM32,THSD1,NDFIP1,NTN4,ILK,ITGA5,DCHS1,HSPH1,HSD17B12,LYN,MERTK,PALLD,ITCH,RASA1,ATP2A2,VCAN,THBS1,ACVR1,NFKBIZ,NEDD9,CBLB,PDLIM5,PHLDB2,CORO1C,ANOS1,PIP5K1A,IQGAP1,ANK3,LMLN,ADAM12,NRP2,NCAM1,ITGAV,FERMT2,KIFAP3,ADAM10,MSN,SRCIN1,TPM1,ADAM19,CYFIP2,SRPX2,ROCK1,ITGA2,ITGA1,GPC4,CD40LG,SSX2IP,CDH11,FXYD5,GP1BB,CTGF,NOV	darkolivegreen	VSMC_M9
GO:1903317	0.18	0.92	5	54	regulation of protein maturation	BP	1	THBS1,LRRK2,TIMM17A,ENO1,PRKACB	darkolivegreen	VSMC_M9
GO:0010762	0.19	0.93	4	35	regulation of fibroblast migration	BP	1	ITGB1,APPL1,THBS1,CORO1C	darkolivegreen	VSMC_M9
GO:0050922	0.19	0.92	5	46	negative regulation of chemotaxis	BP	1	STAP1,THBS1,SEMA5B,SEMA7A,NOV	darkolivegreen	VSMC_M9
GO:1905818	0.19	0.91	6	65	regulation of chromosome separation	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0042157	0.19	0.90	9	111	lipoprotein metabolic process	BP	1	RAB3GAP1,ABHD13,ZDHHC16,RAB3GAP2,ITGAV,PIGW,ZDHHC7,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0001954	0.19	0.92	5	49	positive regulation of cell-matrix adhesion	BP	1	UTRN,ILK,IQGAP1,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:0010970	0.19	0.89	12	139	transport along microtubule	BP	1	KIF5B,TRAK1,IFT88,MAP1B,TRAK2,KIFAP3,ACTR10,ARMCX3,PAFAH1B1,KIF1B,SSX2IP,RAB6A	darkolivegreen	VSMC_M9
GO:0048562	0.19	0.87	18	225	embryonic organ morphogenesis	BP	1	AHI1,LRIG3,MYO6,HOXA9,HOXA11,GATA3,TMED2,MICAL2,RDH10,SHOX2,ACVR1,IRX5,TBX15,FZD2,PRRX1,TBX6,COL11A1,CHST11	darkolivegreen	VSMC_M9
GO:0006289	0.19	0.92	5	50	nucleotide-excision repair	BP	1	SLC30A9,LIG4,CUL4A,BRCA2,USP7	darkolivegreen	VSMC_M9
GO:1901799	0.19	0.93	4	38	negative regulation of proteasomal protein catabolic process	BP	1	UCHL5,TLK2,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0043030	0.19	0.93	4	38	regulation of macrophage activation	BP	1	STAP1,THBS1,LRRK2,TLR6	darkolivegreen	VSMC_M9
GO:0030516	0.19	0.90	8	83	regulation of axon extension	BP	1	CDKL3,ILK,RNF6,MAP1B,SEMA5B,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0060485	0.19	0.87	19	235	mesenchyme development	BP	1	EXT1,ROCK2,GATA3,DCHS1,FBXL17,RDH10,ACVR1,PHLDB2,CORO1C,SEMA5B,NRP2,FERMT2,TAPT1,ACTA2,SEMA7A,ANXA6,ROCK1,BMPR2,GDNF	darkolivegreen	VSMC_M9
GO:1904591	0.19	0.93	4	37	positive regulation of protein import	BP	1	JAK2,TPR,PTGS2,ZPR1	darkolivegreen	VSMC_M9
GO:0009968	0.19	0.84	67	973	negative regulation of signal transduction	BP	1	SOCS6,RRM2B,PTPRD,CLOCK,ASPN,ZNF451,STAP1,CAV2,ITGB1,FYN,RB1,CBLC,GATA3,SCYL2,CNOT7,LYN,ITCH,SULF1,USP47,CCDC125,APPL1,RASA1,BRAP,THBS1,ACVR1,CBLB,DYRK1A,LRRK2,TANK,CUL3,IGF1R,WWC3,PTPN1,GRK3,GPATCH3,ATF3,PTGS2,ITGAV,SKIL,SMURF1,VDAC2,DKK1,RGS7,TLR6,TLE3,UACA,GPRASP1,MYOCD,PIN1,BAG5,THOC1,ITGA1,BFAR,C1QTNF3,CIDEA,PAFAH1B1,ENO1,PRKACB,PTPN12,GDNF,BDKRB2,DNAJB9,NOV,PMEPA1,VGLL4,C12orf66,CHST11	darkolivegreen	VSMC_M9
GO:0090100	0.19	0.90	8	85	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	JAK2,INHBA,ILK,SULF1,THBS1,ACVR1,MYOCD,BMPR2	darkolivegreen	VSMC_M9
GO:0002429	0.19	0.88	12	148	immune response-activating cell surface receptor signaling pathway	BP	1	MALT1,STAP1,FYN,GATA3,LYN,APPL1,NFKBIZ,CBLB,SLC39A10,EIF2B5,VAV2,FCN1	darkolivegreen	VSMC_M9
GO:0002757	0.19	0.88	12	148	immune response-activating signal transduction	BP	1	MALT1,STAP1,FYN,GATA3,LYN,APPL1,NFKBIZ,CBLB,SLC39A10,EIF2B5,VAV2,FCN1	darkolivegreen	VSMC_M9
GO:0060537	0.19	0.86	25	323	muscle tissue development	BP	1	HDAC9,ZMPSTE24,CAV2,ITGB1,RB1,CCNT2,GPCPD1,SHOX2,ACVR1,PDLIM5,DNER,ATF3,DKK1,TPM1,SGCD,FHOD3,MAP2K4,MYOCD,PIN1,MYOM1,COL11A1,FOXN2,VGLL4,CFL2,IRX3	darkolivegreen	VSMC_M9
GO:0008631	0.19	0.93	4	39	intrinsic apoptotic signaling pathway in response to oxidative stress	BP	1	UBQLN1,JAK2,STK24,BAG5	darkolivegreen	VSMC_M9
GO:0018105	0.19	0.87	20	249	peptidyl-serine phosphorylation	BP	1	TBK1,AKAP9,ROCK2,CAMK1D,ILK,EIF2AK3,PFN2,DYRK1A,LRRK2,BRSK2,STK38L,NTRK3,CLK1,TLK2,PTGS2,DKK1,AKT3,ROCK1,RICTOR,BDKRB2	darkolivegreen	VSMC_M9
GO:0030334	0.19	0.85	53	735	regulation of cell migration	BP	1	WISP1,PLAA,JAK2,HDAC9,STAP1,ROCK2,ITGB1,NOX4,CAMK1D,MGAT5,GATA3,STK24,TNFAIP6,OSBPL8,CAPN7,STARD13,ILK,LYN,SULF1,APPL1,PFN2,THBS1,ACVR1,NEDD9,PHLDB2,IGF1R,CORO1C,NTRK3,SEMA5B,IDH2,IQGAP1,NRP2,PTGS2,DNAJA4,ITGAV,FERMT2,AKT3,WNT5B,ADAM10,MSN,SRCIN1,TPM1,SRPX2,MYOCD,SEMA7A,ROCK1,ITGA2,MYO1C,TBXA2R,BMPR2,NOV,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0014911	0.19	0.93	4	35	positive regulation of smooth muscle cell migration	BP	1	WISP1,NOX4,IQGAP1,ITGA2	darkolivegreen	VSMC_M9
GO:0045851	0.19	0.92	4	38	pH reduction	BP	1	CLN5,ATP6V0A2,UBE3A,GPR89A	darkolivegreen	VSMC_M9
GO:0015931	0.19	0.88	14	181	nucleobase-containing compound transport	BP	1	SLC35B4,UPF2,NUP37,SLC35B3,TOMM20,TPR,THOC1,NUP155,MYO1C,SLC25A24,RANBP2,TOMM20L,SLC35D1,NUP35	darkolivegreen	VSMC_M9
GO:0007517	0.19	0.87	20	259	muscle organ development	BP	1	UTRN,HDAC9,CAVIN4,CAV2,RB1,CCNT2,GPCPD1,SHOX2,DNER,ATF3,SMTN,FZD2,TPM1,ITGB1BP2,SGCD,MYOCD,MYOM1,COL11A1,FOXN2,CFL2	darkolivegreen	VSMC_M9
GO:1901216	0.19	0.90	7	78	positive regulation of neuron death	BP	1	FYN,PICALM,DKK1,TLR6,MAP2K4,PIN1,ITGA1	darkolivegreen	VSMC_M9
GO:0010564	0.19	0.85	37	515	regulation of cell cycle process	BP	1	CEP120,CDC23,CLOCK,SENP6,ZMPSTE24,CAV2,ROCK2,RINT1,CEP295,CCDC8,RB1,PRPF40A,RPL26,PIK3R4,MYO16,CUL4A,BRCA2,UBXN2B,RIOK2,USP47,APPL1,MAP9,INO80,BRD7,CUL3,C10orf90,KLHL18,TPR,CDC27,CLTC,PIN1,CCP110,THOC1,RFWD3,CDK13,CTGF,ZNF655	darkolivegreen	VSMC_M9

GO:0050886	0.19	0.91	5	49	endocrine process	BP	1	INHBA,GATA3,TMF1,AGTR1,C1QTNF3	darkolivegreen	VSMC_M9
GO:0032504	0.19	0.85	40	571	multicellular organism reproduction	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,TNFAIP6,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,TMED2,EIF2S2,STOX2,MICAL2,DHX36,ACVR1,LRRK2,KPNA6,LARP7,SYCP2,PITHD1,ZFX,PTGS2,SKIL,FMN2,ADAM10,SPIRE1,PAFAH1B1,BMPR2,ANKRD49,PAQR8,TMEM119	darkolivegreen	VSMC_M9
GO:2000785	0.19	0.92	4	37	regulation of autophagosome assembly	BP	1	RAB3GAP1,IFT88,LRRK2,RAB3GAP2	darkolivegreen	VSMC_M9
GO:0046822	0.19	0.89	8	94	regulation of nucleocytoplasmic transport	BP	1	JAK2,PPP1R12A,UFM1,XPO4,RIOK2,TPR,PTGS2,ZPR1	darkolivegreen	VSMC_M9
GO:0006626	0.20	0.90	7	86	protein targeting to mitochondrion	BP	1	LMAN1,GDAP1,LRRK2,TIMM17A,TOMM20,PMPCA,TOMM20L	darkolivegreen	VSMC_M9
GO:0048839	0.20	0.88	12	139	inner ear development	BP	1	AHI1,LRIG3,MYO6,GATA3,DCHS1,IFT88,NTRK3,FZD2,PRRX1,ADAM10,PAFAH1B1,COL11A1	darkolivegreen	VSMC_M9
GO:0009135	0.20	0.90	7	78	purine nucleoside diphosphate metabolic process	BP	1	HK2,PGAM4,NUDT9,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0009179	0.20	0.90	7	78	purine ribonucleoside diphosphate metabolic process	BP	1	HK2,PGAM4,NUDT9,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0051865	0.20	0.91	6	62	protein autoubiquitination	BP	1	ITCH,LTN1,LRRK2,UBE3A,CUL3,BFAR	darkolivegreen	VSMC_M9
GO:0031297	0.20	0.92	4	35	replication fork processing	BP	1	BRCA2,BOD1L1,THOC1,RFWD3	darkolivegreen	VSMC_M9
GO:1903573	0.20	0.92	4	39	negative regulation of response to endoplasmic reticulum stress	BP	1	LRRK2,PTPN1,BFAR,DNAJB9	darkolivegreen	VSMC_M9
GO:0030433	0.20	0.90	7	78	ubiquitin-dependent ERAD pathway	BP	1	UBQLN1,UBE2J1,EDEM1,DNAJB14,UBE4A,CCDC47,DNAJB9	darkolivegreen	VSMC_M9
GO:0016485	0.20	0.88	13	170	protein processing	BP	1	ZMPSTE24,CLN5,THBS1,LRRK2,TIMM17A,CASP7,ADAM10,ADAM19,CYFIP2,AFG3L2,PMPCA,ENO1,PRKACB	darkolivegreen	VSMC_M9
GO:0071478	0.20	0.88	12	150	cellular response to radiation	BP	1	CLOCK,ZMPSTE24,NOX4,GATA3,RPL26,LIG4,USP47,DHX36,INO80,TANK,TLK2,PTGS2	darkolivegreen	VSMC_M9
GO:0042306	0.20	0.91	5	52	regulation of protein import into nucleus	BP	1	JAK2,UFM1,TPR,PTGS2,ZPR1	darkolivegreen	VSMC_M9
GO:0048678	0.20	0.90	6	65	response to axon injury	BP	1	JAK2,STK24,LYN,MAP1B,NTRK3,ARF4	darkolivegreen	VSMC_M9
GO:0030501	0.20	0.92	4	37	positive regulation of bone mineralization	BP	1	ATP2B1,ACVR1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:2000059	0.20	0.92	4	39	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	UCHL5,TLK2,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0050867	0.20	0.87	17	226	positive regulation of cell activation	BP	1	MALT1,JAK2,STAP1,FYN,GATA3,RIF1,HSPH1,LYN,THBS1,NFKBIZ,LRRK2,SLC39A10,SH3KBP1,TLR6,CD40LG,CLEC4D,CTGF	darkolivegreen	VSMC_M9
GO:0048285	0.20	0.85	29	401	organelle fission	BP	1	CDC23,RMI1,CENPC,ACTR2,CAV2,CCDC8,RB1,ACTR3,CCNA1,PDS5B,BRCA2,UBXN2B,MYBL1,SLC25A46,RIOK2,GDAP1,MAP9,INO80,LRRK2,CUL3,CORO1C,SYCP2,TPR,CDC27,FMN2,PIN1,SPIRE1,CDK13,MZT1	darkolivegreen	VSMC_M9
GO:1900407	0.20	0.90	6	66	regulation of cellular response to oxidative stress	BP	1	UBQLN1,PNPLA8,FYN,LRRK2,TLR6,BAG5	darkolivegreen	VSMC_M9
GO:0003205	0.20	0.88	12	135	cardiac chamber development	BP	1	ZMPSTE24,GATA3,SOS1,SHOX2,ACVR1,NRP2,FZD2,TPM1,TBX6,MYOCD,COL11A1,BMPR2	darkolivegreen	VSMC_M9
GO:0001708	0.20	0.90	6	62	cell fate specification	BP	1	HOXA11,ITGB1,TBX15,NTRK3,DKK1,TBX6	darkolivegreen	VSMC_M9
GO:0001816	0.20	0.85	36	504	cytokine production	BP	1	MALT1,TBK1,WISP1,JAK2,HDAC9,UBE2J1,ROCK2,INHBA,DDX1,GATA3,LRRC32,ATP2B1,NDFIP1,TMF1,LYN,MERTK,EIF2AK3,ITCH,SULF1,FFAR4,APPL1,TLR2,DHX36,THBS1,LRRK2,KPNA6,GPATCH3,PTGS2,ITGAV,TLR6,DICER1,SEMA7A,C1QTNF3,CIDEA,CD40LG,FCN1	darkolivegreen	VSMC_M9
GO:0023051	0.20	0.82	169	2524	regulation of signaling	BP	1	SOCS6,MALT1,STXBP5,TBK1,PLEKHG1,RRM2B,WISP1,UBQLN1,PTPRD,DENND4C,AKAP9,JAK2,CLOCK,FBXO9,ASPN,ZNF451,CAVIN4,STAP1,CCDC88A,ZMPSTE24,CAV2,ROCK2,INHBA,DDX1,ITGB1,RPF2,FYN,KIF5B,GPR4,RB1,CBLC,MGAT5,GATA3,RAB3GAP1,NDFIP2,CYTH1,OSBPL8,RPL26,UFM1,ATP2B1,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,UBA5,ILK,ITGA5,TMF1,SCYL2,CNOT7,RNF6,LYN,EIF2AK3,FBXL17,TMED2,ITCH,SULF1,USP47,CCDC125,FFAR4,MAP1B,APPL1,AGTR1,TLR2,RASA1,ATP2A2,BRAP,DHX36,THBS1,SHOX2,ACVR1,SLC39A14,CBLB,DYRK1A,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,CUL3,EIF4E,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,WWC3,PTPN1,GRK3,KPNA1,GPATCH3,C2CD2L,ATF3,PIP5K1A,IQGAP1,TPR,PTGS2,NCAM1,IQCJ-SCHIP1,SORCS2,SEPT5,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TNIK,TNFAIP8L3,VDAC2,DKK1,ATAD1,RGS7,FAS,AKT3,WNT5B,TLR6,ADAM10,GPR65,CYFIP2,TLE3,UACA,GPRASP1,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,THOC1,ITGA2,ITGA1,RICTOR,SLC1A3,VAPA,BFAR,C1QTNF3,CIDEA,GPC4,USP7,MYO1C,PAFAH1B1,GADD45B,ENO1,VAV2,ZDHHC7,RFWD3,SSX2IP,PRKACB,ANKRD13C,CDH11,BMPR2,PTPN12,GDNF,CTGF,BDKRB2,LAMTOR3,DNAJB9,NOV,PDCL,PMEPA1,RAP2A,VGLL4,C12orf66,CHST11,UBE2V1,SHISA7,WNT7A,PPP1R2	darkolivegreen	VSMC_M9
GO:0043547	0.20	0.87	17	202	positive regulation of GTPase activity	BP	1	TBC1D15,CAV2,ITGB1,PICALM,RAB3GAP1,CCDC125,RASA1,NEDD9,CORO1C,NTRK3,PIP5K1A,ZC3H15,FERMT2,RGS7,GPR65,PIN1,RAPGEF1	darkolivegreen	VSMC_M9
GO:0050801	0.20	0.84	39	542	ion homeostasis	BP	1	EXT1,SLC39A7,SLC30A9,TMEM165,JAK2,CAV2,FYN,GPR4,PICALM,CLN5,TMTC2,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,ATP2A2,SLC39A14,ATP1A1,LRRK2,UBE3A,SLC39A10,ATP6V1A,GPR89A,ITPR2,VAPB,ANK3,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,SLC1A3,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0071604	0.20	0.92	4	35	transforming growth factor beta production	BP	1	LRRC32,THBS1,PTGS2,ITGAV	darkolivegreen	VSMC_M9

GO:0018209	0.20	0.86	21	267	peptidyl-serine modification	BP	1	TBK1,AKAP9,ROCK2,CAMK1D,KDELC1,ILK,EIF2AK3,PFN2,DYRK1A,LRRK2,BRSK2,STK38L,NTRK3,CLK1,TLK2,PTGS2,DKK1,AKT3,ROCK1,RICTOR,BDKRB2	darkolivegreen	VSMC_M9
GO:0032535	0.20	0.85	25	325	regulation of cellular component size	BP	1	CDKL3,ACTR2,RAB3B,PICALM,ACTR3,ILK,RNF6,MAP1B,PFN2,RASA1,SPTBN5,SEMA5B,AKT3,MSN,CYFIP2,FHOD3,SEMA7A,RICTOR,SPIRE1,MYO1C,PAFAH1B1,VAV2,BMPR2,CFL2,WNT7A	darkolivegreen	VSMC_M9
GO:0051155	0.20	0.92	4	37	positive regulation of striated muscle cell differentiation	BP	1	ATP11A,SHOX2,MYOCD,PIN1	darkolivegreen	VSMC_M9
GO:1901890	0.20	0.89	8	82	positive regulation of cell junction assembly	BP	1	THBS2,PTPRD,IQGAP1,FERMT2,SRPX2,ROCK1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0042060	0.20	0.85	25	329	wound healing	BP	1	LMAN1,EXT1,WISP1,TFPI2,JAK2,ITGB1,GPR4,ILK,ITGA5,LYN,MERTK,THBS1,PHLDB2,FERMT2,F5,WNT5B,TPM1,ANXA6,ITGA2,CD40LG,TBXA2R,VAV2,WFDC1,GP1BB,WNT7A	darkolivegreen	VSMC_M9
GO:0050684	0.20	0.88	10	118	regulation of mRNA processing	BP	1	KHDRBS3,JMJD6,SUPT5H,MBNL2,MBNL1,DHX36,DYRK1A,LARP7,CWC22,ZC3H14	darkolivegreen	VSMC_M9
GO:0008217	0.20	0.88	10	122	regulation of blood pressure	BP	1	EXT1,ATP2B1,LNPEP,AGTR1,ATP1A1,PTGS2,ACTA2,TPM1,TBXA2R,BMPR2	darkolivegreen	VSMC_M9
GO:0048013	0.21	0.91	5	45	ephrin receptor signaling pathway	BP	1	FYN,LYN,RASA1,NTRK3,SS18	darkolivegreen	VSMC_M9
GO:1903036	0.21	0.91	5	53	positive regulation of response to wounding	BP	1	WISP1,ITGB1,THBS1,FERMT2,TBXA2R	darkolivegreen	VSMC_M9
GO:0010557	0.21	0.82	97	1433	positive regulation of macromolecule biosynthetic process	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,INHBA,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,JMJD6,BRPF1,SUPT5H,DNAJC3,PPP1R12A,RPL26,CEBPZ,SMAD9,BRCA2,ILK,HSPH1,TMF1,HOXC10,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,STOX2,MICAL2,LARP4,TLR2,DHX36,THBS1,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,LRRK2,UBE3A,KPNA6,NEK7,LARP7,TAF5L,ABCB10,EIF2B5,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,FASTKD2,CREB3L2,FZD2,NPAT,PRRX1,PLD1,TRIP4,TBX6,PKM,ARMCX3,MAP2K4,MYOCD,PIN1,SS18,THOC1,ITGA2,MYSM1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:1901796	0.21	0.89	7	83	regulation of signal transduction by p53 class mediator	BP	1	RRM2B,ZMPSTE24,RPF2,RPL26,DYRK1A,USP7,BDKRB2	darkolivegreen	VSMC_M9
GO:0043550	0.21	0.90	6	58	regulation of lipid kinase activity	BP	1	SOCS6,RB1,PIK3R4,LYN,TNFAIP8L3,VAV2	darkolivegreen	VSMC_M9
GO:0001649	0.21	0.86	15	190	osteoblast differentiation	BP	1	WISP1,HEMGN,NOCT,PSMC2,ILK,FFAR4,VCAN,SHOX2,ACVR1,CCDC47,FERMT2,CLTC,SEMA7A,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0042158	0.21	0.89	7	84	lipoprotein biosynthetic process	BP	1	RAB3GAP1,ZDHHC16,RAB3GAP2,PIGW,ZDHHC7,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0050906	0.21	0.91	5	52	detection of stimulus involved in sensory perception	BP	1	FYN,FFAR4,SEMA5B,ITGA2,COL11A1	darkolivegreen	VSMC_M9
GO:0090068	0.21	0.87	14	180	positive regulation of cell cycle process	BP	1	CEP120,CDC23,ROCK2,CEP295,RB1,CUL4A,UBXN2B,INO80,CUL3,KLHL18,TPR,CDC27,THOC1,CTGF	darkolivegreen	VSMC_M9
GO:0007596	0.21	0.87	13	164	blood coagulation	BP	1	LMAN1,TFPI2,JAK2,ILK,LYN,MERTK,THBS1,F5,ITGA2,CD40LG,TBXA2R,VAV2,GP1BB	darkolivegreen	VSMC_M9
GO:0006354	0.21	0.89	7	80	DNA-templated transcription, elongation	BP	1	CCNT2,SUPT5H,SETD5,LARP7,THOC1,ZNF326,CDK13	darkolivegreen	VSMC_M9
GO:0052548	0.21	0.86	19	270	regulation of endopeptidase activity	BP	1	MALT1,TFPI2,JAK2,ROCK2,FYN,PICALM,LYN,EIF2AK3,USP47,THBS1,UCHL5,ANOS1,PTGS2,FAS,CYFIP2,UACA,ROCK1,WFDC1,CTGF	darkolivegreen	VSMC_M9
GO:0038061	0.21	0.88	8	99	NIK/NF-kappaB signaling	BP	1	MALT1,ILK,TLR2,TLR6,UACA,DICER1,C1QTNF3,NOV	darkolivegreen	VSMC_M9
GO:0055074	0.21	0.85	22	291	calcium ion homeostasis	BP	1	TMEM165,JAK2,CAV2,FYN,GPR4,TMTC2,ATP2B1,LYN,FFAR4,AGTR1,ATP2A2,ITPR2,VAPB,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0009653	0.21	0.82	142	2050	anatomical structure morphogenesis	BP	1	AHI1,LRIG3,EXT1,THBS2,CDKL3,PTPRD,PLAA,TOPORS,ASPN,HDAC9,COL12A1,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,ROCK2,INHBA,ITGB1,FYN,KIF5B,NOX4,GPR4,RB1,PICALM,GATA3,RAB3GAP1,JMJD6,TRAK1,PRPF40A,MYO16,SUPT20H,SMAD9,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,TMF1,RNF6,MERTK,EIF2AK3,TMED2,PALLD,SULF1,MICAL2,MAP1B,RDH10,LARP4,AGTR1,HK2,TLR2,RASA1,MBNL1,DHX36,THBS1,SHOX2,ACVR1,IRX5,GCNT4,NEDD9,LRRK2,TBX15,BRSK2,PDLIM5,ATP10A,UBE3A,CUL3,PHLDB2,UCHL5,CHSY1,CORO1C,ANOS1,SEMA5B,TRAK2,SYCP2,IQGAP1,ANK3,ADAM12,SH3KBP1,NRP2,CLEC14A,PTGS2,NCAM1,FZD2,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TNIK,DKK1,ACTA2,AKT3,WNT5B,NOTCH3,ENAH,ADAM10,MSN,SRCIN1,MYO1E,TPM1,TBX6,CYFIP2,SRPX2,TLE3,PKM,DICER1,FHOD3,MYOCD,SEMA7A,ANXA6,SS18,ROCK1,ITGA2,ITGA1,SLC1A3,AFG3L2,SPIRE1,GPC4,TBXA2R,PAFAH1B1,VAV2,ZDHHC7,COL11A1,PRKACB,CDH11,BMPR2,AQP3,FRY,GDNF,CTGF,NOV,RAP2A,WNT9A,TMEM119,CHST11,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0044703	0.21	0.83	47	688	multi-organism reproductive process	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,TNFAIP6,ADAM32,TUBGCP3,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,TMED2,EIF2S2,LNPEP,STOX2,MICAL2,DHX36,ACVR1,LRRK2,UBE3A,KPNA6,LARP7,SYCP2,PITHD1,ZFX,PTGS2,SKIL,VDAC2,FMN2,MAGED2,ADAM10,ITGA2,SPIRE1,PAFAH1B1,BMPR2,ANKRD49,PAQR8,TMEM119	darkolivegreen	VSMC_M9
GO:1990830	0.21	0.89	7	77	cellular response to leukemia inhibitory factor	BP	1	RIF1,SMARCA5,MAT2A,HK2,NRP2,MYNN,NUP35	darkolivegreen	VSMC_M9
GO:0060395	0.21	0.90	6	62	SMAD protein signal transduction	BP	1	BTBD11,JAK2,INHBA,SMAD9,BMPR2,NOV	darkolivegreen	VSMC_M9
GO:0070664	0.21	0.90	5	53	negative regulation of leukocyte proliferation	BP	1	LRRC32,NDFIP1,LYN,ITCH,CBLB	darkolivegreen	VSMC_M9

GO:2000026	0.21	0.82	71	1014	regulation of multicellular organismal development	BP	1	MALT1,AHI1,THBS2,CDKL3,CHADL,WISP1,PTPRD,ASPN,HOXA9,HOXA11,ZMPSTE24,ACTR2,ROCK2,INHBA,NOCT,ITGB1,ZEB1,GPR4,RB1,GATA3,TRAK1,LIG4,ATP2B1,NDFIP1,CUL4A,SOS1,ILK,ITGA5,RNF6,LYN,EIF2AK3,TDG,SULF1,MAP1B,HK2,TLR2,DHX36,THBS1,SHOX2,ACVR1,NFKBIZ,PHLDB2,NTRK3,SEMA5B,IDH2,ABCB10,TRAK2,ADAM12,PITHD1,SKIL,TAPT1,AKT3,ADAM10,SRPX2,PKM,DICER1,SEMA7A,PIN1,ROCK1,MYSM1,TBXA2R,PAFAH1B1,BMPR2,AQP3,GDNF,CTGF,WNT9A,ZPR1,VGLL4,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0009792	0.21	0.83	39	537	embryo development ending in birth or egg hatching	BP	1	EXT1,HOXA9,HOXA11,ITGB1,GATA3,LIG4,ATP11A,CUL4A,BRCA2,DCHS1,TMED2,EIF2S2,SULF1,STOX2,RDH10,MBNL1,SHOX2,ACVR1,IRX5,ETNK2,TBX15,CUL3,FZD2,NPAT,SKIL,PRRX1,TAPT1,ADAM10,MYO1E,TBX6,RBBP6,RBBP8,RICTOR,COL11A1,PRKACB,BMPR2,WNT9A,ZPR1,CHST11	darkolivegreen	VSMC_M9
GO:0060071	0.21	0.90	5	48	Wnt signaling pathway, planar cell polarity pathway	BP	1	FZD2,SMURF1,DKK1,GPC4,WNT7A	darkolivegreen	VSMC_M9
GO:0002440	0.21	0.87	11	138	production of molecular mediator of immune response	BP	1	MALT1,DDX1,GATA3,RIF1,LIG4,NDFIP1,DHX36,SEMA7A,THOC1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0051303	0.21	0.89	6	68	establishment of chromosome localization	BP	1	CDC23,CENPC,ACTR2,ACTR3,CUL3,FMN2	darkolivegreen	VSMC_M9
GO:0043536	0.21	0.90	5	53	positive regulation of blood vessel endothelial cell migration	BP	1	HDAC9,THBS1,PTGS2,AKT3,SRPX2	darkolivegreen	VSMC_M9
GO:0030148	0.21	0.89	7	83	sphingolipid biosynthetic process	BP	1	ELOVL5,ST3GAL3,PLPP1,CERS5,ST8SIA1,SAMD8,ELOVL4	darkolivegreen	VSMC_M9
GO:0010556	0.21	0.81	186	2846	regulation of macromolecule biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,ETF1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,EIF5B,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,RIF1,PPP1R12A,RPL26,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,HSPH1,TMF1,HOXC10,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,PDE12,STOX2,MICAL2,LARP4,ACTR8,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,CUL3,EIF4E,TDP2,KPNA6,EPRS,RAB3GAP2,NEK7,WWC3,LARP7,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,PLD1,CPEB2,SAMD8,DKK1,NOTCH3,SRP9,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,RBBP6,TLE3,CLTC,PKM,DICER1,ARMCX3,PPM1D,MAP2K4,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,ZNF280C,GSPT1,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0048017	0.21	0.87	12	137	inositol lipid-mediated signaling	BP	1	JAK2,EXOC1,KBTBD2,FYN,GATA3,MYO16,UBE3A,IGF1R,NTRK3,PIP5K1A,PLD1,TNFAIP8L3	darkolivegreen	VSMC_M9
GO:0009314	0.21	0.84	26	359	response to radiation	BP	1	EXT1,CLOCK,ZMPSTE24,ITGB1,NOX4,GATA3,RPL26,LIG4,BRCA2,IKBIP,FBXL17,DYNLRB1,USP47,DHX36,INO80,TANK,TROVE2,CASP7,SEMA5B,TLK2,PTGS2,CLK2,PPM1D,SLC1A3,RFWD3,ELOVL4	darkolivegreen	VSMC_M9
GO:0042255	0.21	0.91	4	45	ribosome assembly	BP	1	RPF2,DHX29,MTERF3,FASTKD2	darkolivegreen	VSMC_M9
GO:0034198	0.21	0.91	4	39	cellular response to amino acid starvation	BP	1	EIF2AK3,ATF3,FAS,C12orf66	darkolivegreen	VSMC_M9
GO:0051093	0.21	0.83	48	676	negative regulation of developmental process	BP	1	THBS2,CDKL3,CHADL,WISP1,ASPN,HOXA9,ROCK2,INHBA,NOCT,ITGB1,ZEB1,GPR4,RB1,GATA3,NDFIP1,CUL4A,RNF6,LYN,SULF1,TLR2,THBS1,UBE3A,EIF4E,CORO1C,NTRK3,WWC3,SEMA5B,IDH2,TRAK2,ITGAV,FERMT2,SKIL,DKK1,AKT3,TBX6,DICER1,MYOCD,SEMA7A,ROCK1,THOC1,BMPR2,CDK13,NOV,WNT9A,VGLL4,TMEM119,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0048762	0.22	0.86	16	198	mesenchymal cell differentiation	BP	1	EXT1,ROCK2,GATA3,FBXL17,RDH10,ACVR1,PHLDB2,CORO1C,SEMA5B,NRP2,FERMT2,TAPT1,SEMA7A,ANXA6,ROCK1,GDNF	darkolivegreen	VSMC_M9
GO:0048846	0.22	0.91	4	34	axon extension involved in axon guidance	BP	1	SEMA5B,NRP2,SEMA7A,BMPR2	darkolivegreen	VSMC_M9
GO:1902284	0.22	0.91	4	34	neuron projection extension involved in neuron projection guidance	BP	1	SEMA5B,NRP2,SEMA7A,BMPR2	darkolivegreen	VSMC_M9
GO:0099003	0.22	0.86	13	151	vesicle-mediated transport in synapse	BP	1	STXBP5,PLAA,RAB3B,PICALM,RAB3GAP1,ATP2A2,LRRK2,BRSK2,SEPT5,VAMP4,PLD1,ROCK1,WNT7A	darkolivegreen	VSMC_M9
GO:1905475	0.22	0.86	12	147	regulation of protein localization to membrane	BP	1	ITGB1,FYN,KIF5B,PICALM,APPL1,ANK3,ADAM10,CLTC,GPC4,MYO1C,ZDHHC7,SHISA7	darkolivegreen	VSMC_M9
GO:0035107	0.22	0.87	10	115	appendage morphogenesis	BP	1	EXT1,HOXA9,HOXA10,HOXA11,RDH10,MBNL1,SHOX2,PRRX1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0035108	0.22	0.87	10	115	limb morphogenesis	BP	1	EXT1,HOXA9,HOXA10,HOXA11,RDH10,MBNL1,SHOX2,PRRX1,CHST11,WNT7A	darkolivegreen	VSMC_M9

GO:0050793	0.22	0.81	126	1852	regulation of developmental process	BP	1	MALT1,AHI1,THBS2,CDKL3,CHADL,WISP1,PTPRD,PLAA,JAK2,CLOCK,ASPN,HEMGN,HDAC9,HOXA9,HOXA11,ZMPSTE24,ACTR2,ROCK2,INHBA,NOCT,ITGB1,FYN,ZEB1,GPR4,RB1,ZC3H13,CAMK1D,GATA3,TRAK1,STK24,RIF1,PRPF40A,LIG4,ATP2B1,ATP11A,NDFIP1,CUL4A,SOS1,NTN4,ILK,ITGA5,RNF6,LYN,EIF2AK3,TDG,ITCH,SULF1,FFAR4,MAP1B,LARP4,AGTR1,HK2,TLR2,RASA1,DHX36,THBS1,SHOX2,ACVR1,NFKBIZ,NEDD9,LRRK2,BRSK2,PDLIM5,ATP10A,UBE3A,EIF4E,PHLDB2,CAMSAP2,CORO1C,NTRK3,WWC3,SEMA5B,IDH2,TAF5L,ABCB10,TRAK2,IQGAP1,ADAM12,SH3KBP1,PITHD1,PTGS2,FZD2,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,DKK1,AKT3,WNT5B,NOTCH3,ADAM10,MSN,SRCIN1,TPM1,TRIP4,TBX6,SRPX2,PKM,DICER1,MYOCD,SEMA7A,PIN1,ROCK1,THOC1,AFG3L2,SPIRE1,GPC4,MYSM1,TBXA2R,PAFAH1B1,BMPR2,AQP3,GDNF,CDK13,CTGF,NOV,RAP2A,WNT9A,ZPR1,VGLL4,TMEM119,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0010605	0.22	0.81	137	2090	negative regulation of macromolecule metabolic process	BP	1	TBK1,AZIN1,ETF1,PLAA,TFPI2,CLOCK,ZNF451,HDAC9,ZMPSTE24,SH3BP5L,THAP5,ROCK2,INHBA,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,RTN2,PICALM,TRDMT1,CBLC,UPF2,MGAT5,GATA3,LRRC32,NDFIP2,SUPT5H,DNAJC3,RIF1,ATP2B1,NR2C1,NDFIP1,BRCA2,ILK,TMF1,ERI1,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TDG,TMED2,HCFC2,SMARCA5,ITCH,USP47,XRN1,PDE12,FFAR4,PI15,DCP1A,DHX36,THBS1,SHOX2,MTERF3,CBLB,DYRK1A,BRD7,LRRK2,TBX15,CUL3,EIF4E,TDP2,UCHL5,KIAA1551,EPRS,CORO1C,ANOS1,NTRK3,WWC3,PTPN1,LARP7,GPATCH3,LRRFIP1,ATF3,RBBP7,TLK2,FASTKD2,TPR,PTGS2,MYEF2,NPAT,ITGAV,SKIL,PRRX1,RTN3,CPEB2,BOD1L1,DKK1,FMN2,SRP9,TLR6,MAGED2,ADAM10,SRCIN1,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,SMG8,CLTC,DICER1,PPM1D,MYOCD,PIN1,RBBP8,BAG5,ROCK1,THOC1,C1QTNF3,CIDEA,GSPT1,ZC3H7A,USP7,LSM5,GADD45B,ENO1,WFDC1,THAP11,MIR186,BMPR2,FASTKD5,FRY,GDNF,CTGF,BDKRB2,PMEPA1,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0072331	0.22	0.87	11	139	signal transduction by p53 class mediator	BP	1	RRM2B,TOPORS,MYO6,ZMPSTE24,RPF2,RPL26,BRCA2,DYRK1A,PPM1D,USP7,BDKRB2	darkolivegreen	VSMC_M9
GO:0072080	0.22	0.88	7	75	nephron tubule development	BP	1	AHI1,HOXA11,GATA3,ILK,DCHS1,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0048659	0.22	0.87	10	128	smooth muscle cell proliferation	BP	1	WISP1,JAK2,ILK,THBS1,PTGS2,TPM1,MYOCD,ITGA2,BMPR2,NOV	darkolivegreen	VSMC_M9
GO:0051785	0.22	0.91	4	41	positive regulation of nuclear division	BP	1	CDC23,RB1,CUL3,CDC27	darkolivegreen	VSMC_M9
GO:0016925	0.22	0.91	4	42	protein sumoylation	BP	1	TOPORS,ZNF451,SENP6,RANBP2	darkolivegreen	VSMC_M9
GO:0007266	0.22	0.87	10	116	Rho protein signal transduction	BP	1	CAVIN4,ROCK2,ITGB1,GPR4,STARD13,CCDC125,AGTR1,CUL3,GPR65,ROCK1	darkolivegreen	VSMC_M9
GO:0072073	0.22	0.87	10	115	kidney epithelium development	BP	1	AHI1,EXT1,HOXA11,GATA3,ILK,DCHS1,IQGAP1,MYO1E,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0001934	0.22	0.83	39	543	positive regulation of protein phosphorylation	BP	1	MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,ROCK2,INHBA,FYN,NOX4,CCNT2,OSBPL8,ILK,ITGA5,LYN,PFN2,THBS1,ACVR1,NEDD9,EHD4,LRRK2,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,DKK1,FAS,TLR6,SRCIN1,MAP2K4,SEMA7A,PIN1,RICTOR,BMPR2,CTGF,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:0045995	0.22	0.90	5	50	regulation of embryonic development	BP	1	NOCT,TDG,DHX36,PHLDB2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:1901699	0.22	0.83	37	508	cellular response to nitrogen compound	BP	1	DENND4C,AKAP9,JAK2,HDAC9,ACTR2,CHRM2,CAV2,ROCK2,FYN,NOX4,OSBPL8,ATP2B1,LYN,XRN1,PDE12,MAP1B,APPL1,AGTR1,USO1,SLC39A14,LRRK2,EPRS,IGF1R,CASP7,ITPR2,PTPN1,PTGS2,CPEB2,TLR6,PKM,ROCK1,SLC1A3,RAB31,MYO1C,RAPGEF1,ZDHHC7,LAMTOR3	darkolivegreen	VSMC_M9
GO:0007416	0.22	0.86	12	132	synapse assembly	BP	1	THBS2,PTPRD,SETD5,MAP1B,TLR2,PDLIM5,DNER,NTRK3,SRPX2,GPC4,LHFPL4,WNT7A	darkolivegreen	VSMC_M9
GO:0050817	0.22	0.86	13	166	coagulation	BP	1	LMAN1,TFPI2,JAK2,ILK,LYN,MERTK,THBS1,F5,ITGA2,CD40LG,TBXA2R,VAV2,GP1BB	darkolivegreen	VSMC_M9
GO:0007173	0.22	0.88	8	90	epidermal growth factor receptor signaling pathway	BP	1	CCDC88A,CBLC,SOS1,CBLB,IQGAP1,ITGA1,PTPN12,ARF4	darkolivegreen	VSMC_M9
GO:0001541	0.22	0.91	4	39	ovarian follicle development	BP	1	INHBA,UBE3A,EIF2B5,ZFX	darkolivegreen	VSMC_M9
GO:0007599	0.22	0.86	13	166	hemostasis	BP	1	LMAN1,TFPI2,JAK2,ILK,LYN,MERTK,THBS1,F5,ITGA2,CD40LG,TBXA2R,VAV2,GP1BB	darkolivegreen	VSMC_M9
GO:0051701	0.22	0.86	12	150	biological process involved in interaction with host	BP	1	CAV2,ITGB1,ITGA5,ITCH,AGTR1,VAPB,NCAM1,ITGAV,THOC1,ITGA2,VAPA,FCN1	darkolivegreen	VSMC_M9
GO:0005996	0.22	0.85	15	199	monosaccharide metabolic process	BP	1	SLC35B4,ZMPSTE24,KBTBD2,B3GLCT,HK2,SLC39A14,ATF3,TPI1,HK3,PHKG2,CLK2,C1QTNF3,USP7,ENO1,RANBP2	darkolivegreen	VSMC_M9
GO:0071363	0.22	0.83	40	545	cellular response to growth factor stimulus	BP	1	EXT1,ASPN,ZNF451,CAV2,FYN,CEP57,NOX4,GATA3,LRRC32,SMAD9,SOS1,ILK,ITGA5,SULF1,MAP1B,APPL1,THBS1,ACVR1,EHD4,UBE3A,NTRK3,PTPN1,IQGAP1,NRP2,FERMT2,SKIL,SMURF1,CYFIP2,MYOCD,PIN1,CIDEA,MYO1C,RAPGEF1,BMPR2,PTPN12,CTGF,PMEPA1,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0044409	0.22	0.87	9	106	entry into host	BP	1	CAV2,ITGB1,ITGA5,ITCH,AGTR1,NCAM1,ITGAV,ITGA2,FCN1	darkolivegreen	VSMC_M9
GO:0009185	0.22	0.88	7	81	ribonucleoside diphosphate metabolic process	BP	1	HK2,PGAM4,NUDT9,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0002437	0.22	0.91	4	40	inflammatory response to antigenic stimulus	BP	1	EXT1,FYN,GATA3,LYN	darkolivegreen	VSMC_M9
GO:0045165	0.22	0.85	14	172	cell fate commitment	BP	1	EXT1,HOXA11,IFRD1,ITGB1,GATA3,ACVR1,TBX15,NTRK3,PRRX1,DKK1,WNT5B,TBX6,WNT9A,WNT7A	darkolivegreen	VSMC_M9

GO:0031326	0.22	0.80	192	2955	regulation of cellular biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,ETF1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,EIF5B,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,RIF1,PPP1R12A,RPL26,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,PDE12,STOX2,MICAL2,APPL1,RDH10,LARP4,ACTR8,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,ATP1A1,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,EIF4E,TDP2,KPNA6,EPRS,RAB3GAP2,NEK7,WWC3,LARP7,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,PTGS2,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,PLD1,CPEB2,SAMD8,DKK1,NOTCH3,SRP9,TLR6,MAGED2,CLK2,TRIP4,TBX6,RLIM,MAGEE2,RBBP6,TLE3,PKM,DICER1,ARMCX3,PPM1D,MAP2K4,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,ZNF280C,C1QTNF3,GSPT1,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,PPTC7,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0023056	0.22	0.81	85	1258	positive regulation of signaling	BP	1	MALT1,TBK1,WISP1,JAK2,STAP1,CCDC88A,CAV2,ROCK2,INHBA,DDX1,ITGB1,FYN,KIF5B,GPR4,MGAT5,GATA3,RAB3GAP1,NDFIP2,OSBPL8,RPL26,ACPP,NR2C1,NDFIP1,SOS1,ILK,ITGA5,TMF1,LYN,SULF1,USP47,FFAR4,TLR2,DHX36,THBS1,SHOX2,ACVR1,SLC39A14,LRRK2,UBE3A,SLC39A10,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,PTPN1,C2CD2L,ATF3,IQGAP1,TPR,PTGS2,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,PRRX1,TNIK,TNFAIP8L3,DKK1,FAS,AKT3,WNT5B,TLR6,GPR65,CYFIP2,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,RICTOR,SLC1A3,VAPA,C1QTNF3,MYO1C,PAFAH1B1,GADD45B,BMPR2,CTGF,LAMTOR3,NOV,PDCL,UBE2V1,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0010648	0.22	0.81	71	1047	negative regulation of cell communication	BP	1	SOCS6,RRM2B,PTPRD,CLOCK,ASPN,ZNF451,STAP1,CAV2,INHBA,ITGB1,FYN,RB1,CBLC,GATA3,SCYL2,CNOT7,LYN,ITCH,SULF1,USP47,CCDC125,FFAR4,APPL1,RASA1,BRAP,THBS1,ACVR1,CBLB,DYRK1A,LRRK2,TANK,CUL3,IGF1R,WWC3,PTPN1,GRK3,GPATCH3,ATF3,PTGS2,SORCS2,ITGAV,SKIL,SMURF1,VDAC2,DKK1,ATAD1,RGS7,TLR6,TLE3,UACA,GPRASP1,MYOCD,PIN1,BAG5,THOC1,ITGA1,BFAR,C1QTNF3,CIDEA,PAFAH1B1,ENO1,PRKACB,PTPN12,GDNF,BDKRB2,DNAJB9,NOV,PMEPA1,VGLL4,C12orf66,CHST11	darkolivegreen	VSMC_M9
GO:0048232	0.22	0.83	26	371	male gamete generation	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,CEP57,PIWIL4,FNDC3A,CCNA1,BRCA2,TMF1,MERTK,MYBL1,MICAL2,DHX36,LRRK2,LARP7,SYCP2,PITHD1,ZFX,SKIL,ADAM10,PAFAH1B1,ANKRD49,TMEM119	darkolivegreen	VSMC_M9
GO:0120031	0.22	0.83	32	435	plasma membrane bounded cell projection assembly	BP	1	AHI1,CEP120,CEP41,STAP1,CCDC88A,ACTR2,ITGB1,ACTR3,FAM98A,CEP83,IFT88,NEK1,PFN2,ARL6,EHD4,TROVE2,CORO1C,PIP5K1A,CEP350,CDKL1,TAPT1,TNIK,PLD1,KIAA0586,CCP110,VAV2,PLPPR5,SSX2IP,FXYD5,ARF4,FOPNL,RAP2A	darkolivegreen	VSMC_M9
GO:0003206	0.22	0.87	9	101	cardiac chamber morphogenesis	BP	1	GATA3,SOS1,SHOX2,ACVR1,NRP2,FZD2,TPM1,COL11A1,BMPR2	darkolivegreen	VSMC_M9
GO:0031111	0.22	0.91	4	36	negative regulation of microtubule polymerization or depolymerization	BP	1	MAP1B,DYRK1A,CAMSAP2,HDGFL3	darkolivegreen	VSMC_M9
GO:0030641	0.22	0.89	6	64	regulation of cellular pH	BP	1	TMEM165,CLN5,ATP6V0A2,LRRK2,UBE3A,GPR89A	darkolivegreen	VSMC_M9
GO:0007283	0.22	0.83	25	357	spermatogenesis	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,CEP57,PIWIL4,FNDC3A,CCNA1,BRCA2,TMF1,MERTK,MYBL1,MICAL2,DHX36,LRRK2,LARP7,PITHD1,ZFX,SKIL,ADAM10,PAFAH1B1,ANKRD49,TMEM119	darkolivegreen	VSMC_M9
GO:0043933	0.23	0.81	89	1370	protein-containing complex subunit organization	BP	1	STXBP5,CAND1,EXT1,ETF1,UBQLN1,AKAP9,JAK2,SENP6,PSME4,CENPC,COX18,ZMPSTE24,ACTR2,TAF1B,DDX1,MPP7,RPF2,KIF5B,CEP57,RB1,PICALM,ACTR3,JMJD6,DARS,NDUFAF5,TUBGCP3,DHX29,TMED2,EIF2S2,SMARCA5,MAT2A,BDP1,MICAL2,MAP1B,TMEM70,AGTR1,PFN2,RASA1,ATP2A2,KCTD9,LIN54,ARL6,INO80,DYRK1A,SPTBN5,EHD4,LRRK2,CUL3,NAP1L4,DNAJB14,EPRS,IGF1R,CAMSAP2,HAUS2,CD3G,HDGFL3,FASTKD2,EIF3J,TPR,FERMT2,VAMP4,KIFAP3,VDAC2,DKK1,FAS,TLR6,ADAM10,MSN,CLINT1,CYFIP2,CLTC,DICER1,FHOD3,RICTOR,AFG3L2,SPIRE1,GSPT1,MYO1C,GTF2B,PRKACB,GEMIN6,OTUD6B,PDCL,MZT1,PMEPA1,SRP19,NDUFAF4,NUP35,CFL2	darkolivegreen	VSMC_M9
GO:2001020	0.23	0.85	15	200	regulation of response to DNA damage stimulus	BP	1	NPAS2,ZMPSTE24,ACTR2,RIF1,RPL26,CUL4A,PARG,USP47,DYRK1A,SKIL,FMN2,THOC1,SPIRE1,RFWD3,UBE2V1	darkolivegreen	VSMC_M9
GO:0042130	0.23	0.91	4	40	negative regulation of T cell proliferation	BP	1	LRRC32,NDFIP1,ITCH,CBLB	darkolivegreen	VSMC_M9

GO:0023057	0.23	0.81	71	1048	negative regulation of signaling	BP	1	SOCS6,RRM2B,PTPRD,CLOCK,ASPN,ZNF451,STAP1,CAV2,INHBA,ITGB1,FYN,RB1,CBLC,GATA3,SCYL2,CNOT7,LYN,ITCH,SULF1,USP47,CCDC125,FFAR4,APPL1,RASA1,BRAP,THBS1,ACVR1,CBLB,DYRK1A,LRRK2,TANK,CUL3,IGF1R,WWC3,PTPN1,GRK3,GPATCH3,ATF3,PTGS2,SORCS2,ITGAV,SKIL,SMURF1,VDAC2,DKK1,ATAD1,RGS7,TLR6,TLE3,UACA,GPRASP1,MYOCD,PIN1,BAG5,THOC1,ITGA1,BFAR,C1QTNF3,CIDEA,PAFAH1B1,ENO1,PRKACB,PTPN12,GDNF,BDKRB2,DNAJB9,NOV,PMEPA1,VGLL4,C12orf66,CHST11	darkolivegreen	VSMC_M9
GO:1901184	0.23	0.89	6	67	regulation of ERBB signaling pathway	BP	1	CCDC88A,CBLC,SOS1,CBLB,ITGA1,PTPN12	darkolivegreen	VSMC_M9
GO:0043534	0.23	0.87	9	108	blood vessel endothelial cell migration	BP	1	HDAC9,ITGB1,STARD13,THBS1,CLEC14A,PTGS2,AKT3,SRPX2,TBXA2R	darkolivegreen	VSMC_M9
GO:0016445	0.23	0.89	5	54	somatic diversification of immunoglobulins	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0010876	0.23	0.84	23	311	lipid localization	BP	1	ABCB4,INHBA,PNPLA8,ESYT2,OSBPL8,ATP11A,TMF1,GRAMD1A,AGTR1,THBS1,ATP10A,EPRS,ATP11B,PRELID3B,C2CD2L,OSBPL11,ITGAV,ATP8B4,TNFAIP8L3,CIDEA,XKR9,PLEKHA3,BDKRB2	darkolivegreen	VSMC_M9
GO:1904589	0.23	0.89	5	55	regulation of protein import	BP	1	JAK2,UFM1,TPR,PTGS2,ZPR1	darkolivegreen	VSMC_M9
GO:0051704	0.23	0.82	48	709	multi-organism process	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,CAV2,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,TNFAIP6,ADAM32,TUBGCP3,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,TMED2,EIF2S2,LNPEP,STOX2,MICAL2,DHX36,ACVR1,LRRK2,UBE3A,KPNA6,LARP7,SYCP2,PITHD1,ZFX,PTGS2,SKIL,VDAC2,FMN2,MAGED2,ADAM10,ITGA2,SPIRE1,PAFAH1B1,BMPR2,ANKRD49,PAQR8,TMEM119	darkolivegreen	VSMC_M9
GO:0099054	0.23	0.91	4	35	presynapse assembly	BP	1	PTPRD,NTRK3,GPC4,WNT7A	darkolivegreen	VSMC_M9
GO:0035329	0.23	0.91	4	35	hippo signaling	BP	1	DCHS1,WWC3,IQCJ-SCHIP1,VGLL4	darkolivegreen	VSMC_M9
GO:0044283	0.23	0.83	28	414	small molecule biosynthetic process	BP	1	CDO1,SLC35B4,ELOVL5,PNPLA8,PDSS1,SUCLA2,ABHD1,HSD17B12,RDH10,PLOD2,ALDH18A1,SLC39A14,ATF3,MBTPS2,GATM,PTGS2,TPI1,CLK2,SLC1A3,C1QTNF3,USP7,ACOT7,RANBP2,IMPA1,ELOVL4,SRD5A2,AKR1D1,PPTC7	darkolivegreen	VSMC_M9
GO:0030048	0.23	0.87	9	97	actin filament-based movement	BP	1	AKAP9,MYO6,ATP2A2,ATP1A1,MYO1E,TPM1,NUP155,MYO1C,MYO1H	darkolivegreen	VSMC_M9
GO:0006612	0.23	0.87	8	97	protein targeting to membrane	BP	1	FYN,ARL6,ANK3,SRP9,MYO1C,ZDHHC7,SEC63,SRP19	darkolivegreen	VSMC_M9
GO:0033674	0.23	0.83	28	373	positive regulation of kinase activity	BP	1	MALT1,JAK2,STAP1,CCDC88A,NOX4,CCNT2,OSBPL8,PIK3R4,ILK,LYN,MERTK,THBS1,NEDD9,LRRK2,IGF1R,NTRK3,PTPN1,IQGAP1,FERMT2,TNFAIP8L3,DKK1,TLR6,SRCIN1,RICTOR,VAV2,RANBP2,BMPR2,LAMTOR3	darkolivegreen	VSMC_M9
GO:0043551	0.23	0.89	5	47	regulation of phosphatidylinositol 3-kinase activity	BP	1	SOCS6,PIK3R4,LYN,TNFAIP8L3,VAV2	darkolivegreen	VSMC_M9
GO:0003018	0.23	0.84	16	200	vascular process in circulatory system	BP	1	EXT1,ROCK2,GPR4,ATP2B1,SLC16A12,AGTR1,PTGS2,FERMT2,ACTA2,KCNMB1,ROCK1,ITGA1,SLC1A3,TBXA2R,BMPR2,BDKRB2	darkolivegreen	VSMC_M9
GO:0019725	0.23	0.82	45	638	cellular homeostasis	BP	1	SLC39A7,PLAA,SLC30A9,TMEM165,JAK2,CAV2,FYN,KIF5B,GPR4,CLN5,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,HK2,ATP2A2,SLC39A14,ATP1A1,LRRK2,BRSK2,UBE3A,SLC39A10,ATP6V1A,IGF1R,GPR89A,CCDC186,ITPR2,VAPB,C2CD2L,CCDC47,ATP13A3,ITGAV,STIM2,HK3,GPR65,ANXA6,SLC1A3,AFG3L2,C1QTNF3,TBXA2R,BDKRB2,CFL2	darkolivegreen	VSMC_M9
GO:0012501	0.23	0.80	96	1474	programmed cell death	BP	1	MALT1,AHI1,RRM2B,UBQLN1,PRUNE2,TOPORS,JAK2,NOA1,ZMPSTE24,INHBA,ITGB1,FYN,NOX4,RB1,CAMK1D,GATA3,DNAJC3,STK24,RPL26,UFM1,LIG4,CUL4A,BRCA2,ILK,ITGA5,TMF1,LYN,MERTK,EIF2AK3,ITCH,SULF1,USP47,FFAR4,HK2,TLR2,RASA1,THBS1,ZDHHC16,ACVR1,LRRK2,BRSK2,SLC39A10,CUL3,IGF1R,CASP7,PTPN1,KPNA1,EIF2B5,SYCP2,ATF3,G2E3,CD3G,SH3KBP1,FASTKD2,PTGS2,ITGAV,SKIL,RTN3,KIFAP3,TNFAIP8L3,VDAC2,DKK1,FMN2,FAS,ADAM10,BNIP2,GPR65,CYFIP2,UACA,PKM,DICER1,ATG4D,MAP2K4,MYOCD,ANXA6,PIN1,BAG5,ROCK1,THOC1,ITGA1,BFAR,CIDEA,CD40LG,GADD45B,ENO1,KIF1B,ANKRD13C,BMPR2,XKR9,ARF4,GDNF,BDKRB2,E2F3,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0051651	0.23	0.85	13	163	maintenance of location in cell	BP	1	KDELR3,TOPORS,AKAP9,CCDC88A,LYN,HK2,ITPR2,ANK3,TAPT1,PDIA2,ANXA6,PAFAH1B1,ANKRD13C	darkolivegreen	VSMC_M9
GO:1900076	0.23	0.89	5	51	regulation of cellular response to insulin stimulus	BP	1	OSBPL8,ATP2B1,USO1,PTPN1,MYO1C	darkolivegreen	VSMC_M9
GO:0001558	0.23	0.83	25	339	regulation of cell growth	BP	1	CDKL3,PLAA,INHBA,EXOSC9,RB1,ILK,RNF6,ITCH,USP47,MAP1B,AGTR1,INO80,SEMA5B,RBBP7,SMURF1,ADAM10,MYOCD,SEMA7A,PIN1,PAFAH1B1,ENO1,WFDC1,BMPR2,NOV,VGLL4	darkolivegreen	VSMC_M9
GO:0050000	0.23	0.88	6	70	chromosome localization	BP	1	CDC23,CENPC,ACTR2,ACTR3,CUL3,FMN2	darkolivegreen	VSMC_M9
GO:0009967	0.23	0.81	76	1127	positive regulation of signal transduction	BP	1	MALT1,TBK1,WISP1,JAK2,STAP1,CCDC88A,CAV2,ROCK2,INHBA,DDX1,ITGB1,FYN,GPR4,MGAT5,GATA3,NDFIP2,OSBPL8,RPL26,ACPP,NR2C1,NDFIP1,SOS1,ILK,ITGA5,LYN,SULF1,USP47,FFAR4,TLR2,DHX36,THBS1,SHOX2,ACVR1,SLC39A14,LRRK2,UBE3A,SLC39A10,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,PTPN1,ATF3,IQGAP1,TPR,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,PRRX1,TNIK,TNFAIP8L3,DKK1,FAS,AKT3,WNT5B,TLR6,GPR65,CYFIP2,MYOCD,SEMA7A,PIN1,ROCK1,RICTOR,VAPA,MYO1C,PAFAH1B1,GADD45B,BMPR2,CTGF,LAMTOR3,NOV,PDCL,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0051783	0.23	0.86	9	114	regulation of nuclear division	BP	1	CDC23,CAV2,CCDC8,RB1,CUL3,TPR,CDC27,PIN1,CDK13	darkolivegreen	VSMC_M9

GO:0048662	0.23	0.90	4	44	negative regulation of smooth muscle cell proliferation	BP	1	ILK,TPM1,MYOCD,BMPR2	darkolivegreen	VSMC_M9
GO:0003143	0.23	0.89	5	50	embryonic heart tube morphogenesis	BP	1	AHI1,TMED2,MICAL2,ACVR1,TBX6	darkolivegreen	VSMC_M9
GO:0010977	0.23	0.86	10	116	negative regulation of neuron projection development	BP	1	CDKL3,RNF6,LRRK2,UBE3A,SEMA5B,TRAK2,TBX6,SEMA7A,BAG5,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0120034	0.23	0.87	8	92	positive regulation of plasma membrane bounded cell projection assembly	BP	1	CEP120,CCDC88A,ACTR2,ACTR3,FAM98A,TAPT1,CCP110,PLPPR5	darkolivegreen	VSMC_M9
GO:0045862	0.23	0.83	21	297	positive regulation of proteolysis	BP	1	MALT1,UBQLN1,JAK2,PSME4,ROCK2,FYN,PSMC2,PICALM,NUB1,LYN,EIF2AK3,LRRK2,TANK,TIMM17A,SMURF1,FAS,CLPX,CYFIP2,UACA,ENO1,CTGF	darkolivegreen	VSMC_M9
GO:1901616	0.23	0.89	5	56	organic hydroxy compound catabolic process	BP	1	GPD2,BPNT1,TPI1,IMPA1,AKR1D1	darkolivegreen	VSMC_M9
GO:0010817	0.24	0.83	24	331	regulation of hormone levels	BP	1	JAK2,CLOCK,ZMPSTE24,INHBA,KIF5B,CYP27C1,GATA3,TMF1,HSD17B12,LYN,FFAR4,RDH10,AGTR1,SLC39A14,GCNT4,ATP1A1,SNX19,BRSK2,CCDC186,C2CD2L,C1QTNF3,NOV,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0002009	0.24	0.82	31	412	morphogenesis of an epithelium	BP	1	AHI1,EXT1,HOXA11,GATA3,STARD13,SOS1,NTN4,ILK,ITGA5,DCHS1,TMED2,SULF1,MICAL2,RDH10,ACVR1,BRSK2,PHLDB2,FZD2,FERMT2,SMURF1,DKK1,WNT5B,MSN,TBX6,GPC4,PAFAH1B1,ZDHHC7,PRKACB,GDNF,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0018208	0.24	0.90	4	48	peptidyl-proline modification	BP	1	PPIL1,NKTR,PIN1,RANBP2	darkolivegreen	VSMC_M9
GO:0010883	0.24	0.90	4	41	regulation of lipid storage	BP	1	OSBPL8,OSBPL11,ITGAV,CIDEA	darkolivegreen	VSMC_M9
GO:0002562	0.24	0.89	5	54	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0016444	0.24	0.89	5	54	somatic cell DNA recombination	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0090316	0.24	0.85	11	136	positive regulation of intracellular protein transport	BP	1	JAK2,FYN,KIF5B,EDEM1,XPO4,ANK3,TPR,PTGS2,OAZ2,MYO1C,ZPR1	darkolivegreen	VSMC_M9
GO:0061326	0.24	0.87	7	77	renal tubule development	BP	1	AHI1,HOXA11,GATA3,ILK,DCHS1,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0050768	0.24	0.86	9	102	negative regulation of neurogenesis	BP	1	CDKL3,RNF6,NTRK3,SEMA5B,IDH2,TRAK2,DICER1,SEMA7A,WNT7A	darkolivegreen	VSMC_M9
GO:0045445	0.24	0.88	6	67	myoblast differentiation	BP	1	IFRD1,RB1,ILK,MBNL1,TRIP4,MYOCD	darkolivegreen	VSMC_M9
GO:0060271	0.24	0.83	20	266	cilium assembly	BP	1	AHI1,CEP120,CEP41,CCDC88A,ACTR2,ACTR3,CEP83,IFT88,NEK1,ARL6,EHD4,TROVE2,CEP350,CDKL1,TAPT1,KIAA0586,CCP110,SSX2IP,ARF4,FOPNL	darkolivegreen	VSMC_M9
GO:1903201	0.24	0.89	5	56	regulation of oxidative stress-induced cell death	BP	1	UBQLN1,FYN,LRRK2,TLR6,BAG5	darkolivegreen	VSMC_M9
GO:0072359	0.24	0.80	64	902	circulatory system development	BP	1	AHI1,EXT1,THBS2,HDAC9,ZMPSTE24,ROCK2,ITGB1,GPR4,RB1,GATA3,JMJD6,STARD13,SOS1,ILK,ITGA5,DCHS1,EIF2AK3,TMED2,SULF1,MICAL2,AGTR1,HK2,RASA1,DHX36,THBS1,SHOX2,ZDHHC16,ACVR1,PDLIM5,CASP7,NTRK3,ADAM12,NRP2,CLEC14A,PTGS2,FZD2,CDKL1,ITGAV,PRRX1,DKK1,ACTA2,AKT3,HSPB7,ADAM10,MYO1E,TPM1,TBX6,SRPX2,SGCD,PKM,FHOD3,MAP2K4,MYOCD,PIN1,ROCK1,TBXA2R,VAV2,COL11A1,BMPR2,CTGF,NOV,VGLL4,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0060675	0.24	0.89	5	52	ureteric bud morphogenesis	BP	1	HOXA11,GATA3,ILK,DCHS1,GDNF	darkolivegreen	VSMC_M9
GO:0045787	0.24	0.83	18	243	positive regulation of cell cycle	BP	1	CEP120,CDC23,ROCK2,CEP295,RB1,CCNT2,CUL4A,BRCA2,UBXN2B,INO80,CUL3,EIF4E,KLHL18,TPR,CDC27,THOC1,PAFAH1B1,CTGF	darkolivegreen	VSMC_M9
GO:0010660	0.24	0.89	5	57	regulation of muscle cell apoptotic process	BP	1	JAK2,ILK,MAP2K4,MYOCD,E2F3	darkolivegreen	VSMC_M9
GO:0048738	0.24	0.84	15	186	cardiac muscle tissue development	BP	1	ZMPSTE24,ITGB1,SHOX2,ACVR1,PDLIM5,DKK1,TPM1,SGCD,FHOD3,MAP2K4,MYOCD,PIN1,COL11A1,VGLL4,IRX3	darkolivegreen	VSMC_M9
GO:0030517	0.24	0.90	4	36	negative regulation of axon extension	BP	1	CDKL3,RNF6,SEMA5B,SEMA7A	darkolivegreen	VSMC_M9
GO:0048872	0.24	0.83	17	229	homeostasis of number of cells	BP	1	EXT1,JAK2,INHBA,RB1,GATA3,JMJD6,SOS1,UBA5,LYN,MERTK,GCNT4,ABCB10,ZFX,SKIL,FAS,AKT3,NOV	darkolivegreen	VSMC_M9
GO:0045861	0.24	0.84	15	213	negative regulation of proteolysis	BP	1	TFPI2,DNAJC1,PICALM,USP47,PI15,THBS1,LRRK2,UCHL5,ANOS1,TLK2,PTGS2,BAG5,ROCK1,USP7,WFDC1	darkolivegreen	VSMC_M9
GO:0016052	0.24	0.86	9	113	carbohydrate catabolic process	BP	1	HK2,PGAM4,GPD2,DERA,TPI1,HK3,PHKG2,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0045667	0.24	0.86	9	109	regulation of osteoblast differentiation	BP	1	WISP1,HEMGN,NOCT,ILK,FFAR4,ACVR1,FERMT2,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0016050	0.24	0.83	19	255	vesicle organization	BP	1	SEC24A,CAV2,KIF5B,PICALM,STAM2,VPS36,EEA1,YIPF5,TMF1,TMED2,USO1,SNX19,CUL3,CORO1C,VAPB,SEC23A,VAMP4,VAPA,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0000266	0.24	0.90	4	40	mitochondrial fission	BP	1	SLC25A46,GDAP1,LRRK2,SPIRE1	darkolivegreen	VSMC_M9
GO:0043966	0.24	0.88	5	54	histone H3 acetylation	BP	1	ZNF451,GATA3,BRPF1,BRCA2,TAF5L	darkolivegreen	VSMC_M9
GO:0060348	0.24	0.84	14	172	bone development	BP	1	EXT1,WISP1,HOXA11,ZMPSTE24,DCHS1,SULF1,SHOX2,CHSY1,MBTPS2,TAPT1,ANXA6,PAFAH1B1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0006874	0.24	0.82	21	283	cellular calcium ion homeostasis	BP	1	TMEM165,JAK2,CAV2,FYN,GPR4,ATP2B1,LYN,FFAR4,AGTR1,ATP2A2,ITPR2,VAPB,CCDC47,ATP13A3,ITGAV,STIM2,GPR65,ANXA6,AFG3L2,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9

GO:0050896	0.24	0.78	373	5876	response to stimulus	BP	1	SOCS6,LMAN1,MALT1,CDO1,AHI1,TBK1,PLEKHG1,RRM2B,LRP12,EXT1,WISP1,RMI1,UBQLN1,PTPRD,DENND4C,PLAA,BTBD11,SLC30A9,TOPORS,ABCB4,AKAP9,DNAJB5,TFPI2,GNG11,JAK2,CLOCK,EXOC1,NPAS2,FBXO9,ASPN,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,UBA6,CCDC88A,ZMPSTE24,UBE2J1,PDE1C,KBTBD2,SH3BP5L,ACTR2,CHRM2,CAV2,ROCK2,INHBA,PNPLA8,DDX1,NOCT,GPX7,ITGB1,RPF2,FYN,RINT1,KIF5B,CEP57,EXOSC9,UGGT1,NOX4,GPR4,RB1,TRDMT1,SUSD5,CBLC,CAMK1D,NUB1,ACTR3,CDK3,MGAT5,GATA3,RAB3GAP1,JMJD6,LRRC32,NDFIP2,SELENOV,DNAJC3,AZI2,CYTH1,EDEM1,STK24,TNFAIP6,RIF1,OSBPL8,PPP1R12A,STAM2,RPL26,UFM1,LIG4,PIK3R4,MYO16,ATP2B1,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,PDS5B,BRCA2,UBA5,ILK,ITGA5,GPR84,DCHS1,HSPH1,TMF1,IKBIP,SCYL2,PARG,MTREX,PLPP1,CNOT7,RNF6,RASSF4,LYN,MERTK,GRAMD1A,ATP6V0A2,IPO7,PDE7A,TCP11L1,EIF2AK3,FBXL17,TDG,TMED2,PALLD,SMARCA5,ITCH,DYNLRB1,NEK1,SLC30A5,SULF1,USP47,MAT2A,CCDC125,LNPEP,XRN1,PDE12,FFAR4,MAP1B,APPL1,PLOD2,GDAP1,AGTR1,ACTR8,HK2,TLR2,RASA1,ATP2A2,USO1,BRAP,DHX36,THBS1,NUCB2,GPR176,PPP2R2A,SHOX2,KCTD9,ZDHHC16,ARL6,ACVR1,SLC39A14,IRX5,INO80,NFKBIZ,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,BRSK2,UBE3A,SLC39A10,NFRKB,CUL3,EIF4E,PHLDB2,TDP2,DNER,TROVE2,UCHL5,CHSY1,DNAJB14,ATP6V1A,KPNA6,EPRS,IGF1R,GPR89A,STK38L,CASP7,CCDC186,CORO1C,ANOS1,ITPR2,NTRK3,WWC3,TOMM20,PTPN1,GRK3,ST8SIA1,KPNA1,PLIN1,SEMA5B,VAPB,ABCB10,EIF2B5,LTB4R,GPATCH3,C2CD2L,ATF3,PIP5K1A,IQGAP1,RBBP7,ANK3,	darkolivegreen	VSMC_M9
GO:0035305	0.24	0.90	4	40	negative regulation of dephosphorylation	BP	1	ROCK2,MGAT5,BOD1L1,ROCK1	darkolivegreen	VSMC_M9
GO:0050767	0.24	0.82	22	285	regulation of neurogenesis	BP	1	CDKL3,PTPRD,ACTR2,TRAK1,LIG4,ILK,RNF6,LYN,MAP1B,TLR2,DHX36,SHOX2,NTRK3,SEMA5B,IDH2,TRAK2,SKIL,DICER1,SEMA7A,PAFAH1B1,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0051148	0.24	0.88	5	55	negative regulation of muscle cell differentiation	BP	1	DKK1,MYOCD,BMPR2,NOV,TMEM119	darkolivegreen	VSMC_M9
GO:0034446	0.24	0.86	8	89	substrate adhesion-dependent cell spreading	BP	1	NTN4,ILK,MERTK,NEDD9,CORO1C,ITGAV,FERMT2,SRCIN1	darkolivegreen	VSMC_M9
GO:0010721	0.24	0.85	11	130	negative regulation of cell development	BP	1	CDKL3,RNF6,CORO1C,NTRK3,SEMA5B,IDH2,TRAK2,TBX6,DICER1,SEMA7A,WNT7A	darkolivegreen	VSMC_M9
GO:0010824	0.24	0.89	4	39	regulation of centrosome duplication	BP	1	CEP120,ROCK2,CEP295,C10orf90	darkolivegreen	VSMC_M9
GO:0034641	0.25	0.78	299	4878	cellular nitrogen compound metabolic process	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,RRM2B,AZIN1,WDR46,DDX46,PHF20L1,KHDRBS3,ETF1,RMI1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,NOA1,ELOVL5,EIF5B,POLR2B,GNE,ZNF451,TRMO,HDAC9,CAVIN4,PSME4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,ZEB1,EXOSC9,PIWIL4,DNAJC1,UGGT1,GSAP,RB1,RTN2,SUCLA2,PICALM,ZC3H13,TRDMT1,TOE1,TSN,CAMK1D,UPF2,ST3GAL3,ACTR3,GATA3,CCNT2,CLN5,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,ORC4,MBNL2,RIF1,PPP1R12A,PRPF40A,RPL26,LIG4,CEBPZ,SUPT20H,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,HSD17B12,DHX29,PARG,MTREX,PLPP1,CNOT7,RNF6,PDE7A,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,LNPEP,XRN1,PDE12,STOX2,BDP1,MICAL2,U2SURP,LARP4,GDAP1,ACTR8,CERS5,HK2,TLR2,RASA1,MBNL1,LTN1,DCP1A,DHX36,THBS1,SHOX2,GFM1,LIN54,PGAM4,ACVR1,WDR75,IRX5,MTERF3,INO80,NUDT9,SNRNP48,SLC35B3,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,NFRKB,CUL3,EIF4E,TDP2,PUS3,TROVE2,UCHL5,ATP6V1A,KPNA6,RRP15,EPRS,BPNT1,IARS2,NEK7,MRPL47,WWC3,LARP7,KPNA1,CLK1,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,DERA,RBBP7,EDRF1,BCLAF3,NPL,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,PTGS2,MYEF2,FZD2,CWC22,ZC3H15,NPAT,TPI1,MYNN,GNPNAT1,SKIL,DTWD1,PRRX1,RTN3,PLD1,CPEB2,SAMD8,BOD1L1,DKK1,FMN2,PAPSS2,ADSS,RBM47,NOTCH3,SRP9,TLR6,MAGED2,ADAM10,HK3,CLK2,DLST,TRIP4,TBX6,OAZ2,RLIM,MAG	darkolivegreen	VSMC_M9
GO:0070169	0.25	0.89	4	41	positive regulation of biomineral tissue development	BP	1	ATP2B1,ACVR1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0009150	0.25	0.82	20	286	purine ribonucleotide metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,PDE7A,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0072171	0.25	0.88	5	53	mesonephric tubule morphogenesis	BP	1	HOXA11,GATA3,ILK,DCHS1,GDNF	darkolivegreen	VSMC_M9
GO:0002695	0.25	0.85	9	118	negative regulation of leukocyte activation	BP	1	SOCS6,INHBA,LRRC32,NDFIP1,LYN,MERTK,ITCH,CBLB,THOC1	darkolivegreen	VSMC_M9
GO:0030336	0.25	0.83	17	223	negative regulation of cell migration	BP	1	STAP1,STK24,OSBPL8,STARD13,ILK,SULF1,PFN2,THBS1,PHLDB2,CORO1C,IDH2,DNAJA4,TPM1,MYOCD,TBXA2R,NOV,RAP2A	darkolivegreen	VSMC_M9
GO:0033044	0.25	0.84	13	168	regulation of chromosome organization	BP	1	CDC23,SENP6,RB1,LIG4,RIOK2,XRN1,DHX36,CUL3,KIAA1551,NEK7,TPR,CDC27,USP7	darkolivegreen	VSMC_M9
GO:0099172	0.25	0.89	4	37	presynapse organization	BP	1	PTPRD,NTRK3,GPC4,WNT7A	darkolivegreen	VSMC_M9
GO:0002886	0.25	0.89	4	41	regulation of myeloid leukocyte mediated immunity	BP	1	STAP1,DDX1,LYN,DHX36	darkolivegreen	VSMC_M9
GO:0046928	0.25	0.87	6	66	regulation of neurotransmitter secretion	BP	1	STXBP5,RAB3GAP1,ATP2A2,LRRK2,SEPT5,WNT7A	darkolivegreen	VSMC_M9
GO:0061647	0.25	0.89	4	38	histone H3-K9 modification	BP	1	ZNF451,GATA3,SETD5,RIF1	darkolivegreen	VSMC_M9
GO:0008277	0.25	0.86	8	96	regulation of G protein-coupled receptor signaling pathway	BP	1	ROCK2,ACPP,SLC39A14,GRK3,GPRASP1,ROCK1,ZDHHC7,PDCL	darkolivegreen	VSMC_M9
GO:0019079	0.25	0.85	8	99	viral genome replication	BP	1	ROCK2,EEA1,CNOT7,PDE12,KIAA1551,KPNA6,VAPB,VAPA	darkolivegreen	VSMC_M9

GO:0019220	0.25	0.79	73	1074	regulation of phosphate metabolic process	BP	1	SOCS6,MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,SH3BP5L,ROCK2,INHBA,FYN,NOX4,RB1,CBLC,MGAT5,CCNT2,DNAJC3,OSBPL8,PPP1R12A,PIK3R4,CCNA1,ILK,ITGA5,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TMED2,PFN2,THBS1,ACVR1,NEDD9,CBLB,EHD4,LRRK2,SLC39A10,IGF1R,CORO1C,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,TNFAIP8L3,BOD1L1,DKK1,FAS,TLR6,SRCIN1,SRPX2,SMG8,MAP2K4,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,ITGA1,RICTOR,GADD45B,ENO1,VAV2,RANBP2,BMPR2,CTGF,BDKRB2,LAMTOR3,PMEPA1,RAP2A,TMEM119,PPP1R2	darkolivegreen	VSMC_M9
GO:0051174	0.25	0.79	73	1074	regulation of phosphorus metabolic process	BP	1	SOCS6,MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,SH3BP5L,ROCK2,INHBA,FYN,NOX4,RB1,CBLC,MGAT5,CCNT2,DNAJC3,OSBPL8,PPP1R12A,PIK3R4,CCNA1,ILK,ITGA5,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TMED2,PFN2,THBS1,ACVR1,NEDD9,CBLB,EHD4,LRRK2,SLC39A10,IGF1R,CORO1C,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,TNFAIP8L3,BOD1L1,DKK1,FAS,TLR6,SRCIN1,SRPX2,SMG8,MAP2K4,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,ITGA1,RICTOR,GADD45B,ENO1,VAV2,RANBP2,BMPR2,CTGF,BDKRB2,LAMTOR3,PMEPA1,RAP2A,TMEM119,PPP1R2	darkolivegreen	VSMC_M9
GO:1901992	0.25	0.87	6	73	positive regulation of mitotic cell cycle phase transition	BP	1	CDC23,RB1,CUL4A,CUL3,KLHL18,CDC27	darkolivegreen	VSMC_M9
GO:0043583	0.25	0.83	13	162	ear development	BP	1	AHI1,LRIG3,MYO6,GATA3,DCHS1,IFT88,RDH10,NTRK3,FZD2,PRRX1,ADAM10,PAFAH1B1,COL11A1	darkolivegreen	VSMC_M9
GO:0032527	0.25	0.89	4	43	protein exit from endoplasmic reticulum	BP	1	GCC2,UBE2J1,EDEM1,BRSK2	darkolivegreen	VSMC_M9
GO:0044088	0.25	0.89	4	42	regulation of vacuole organization	BP	1	RAB3GAP1,IFT88,LRRK2,RAB3GAP2	darkolivegreen	VSMC_M9
GO:1990928	0.25	0.89	4	42	response to amino acid starvation	BP	1	EIF2AK3,ATF3,FAS,C12orf66	darkolivegreen	VSMC_M9
GO:0090175	0.25	0.88	5	51	regulation of establishment of planar polarity	BP	1	FZD2,SMURF1,DKK1,GPC4,WNT7A	darkolivegreen	VSMC_M9
GO:0030031	0.25	0.80	32	443	cell projection assembly	BP	1	AHI1,CEP120,CEP41,STAP1,CCDC88A,ACTR2,ITGB1,ACTR3,FAM98A,CEP83,IFT88,NEK1,PFN2,ARL6,EHD4,TROVE2,CORO1C,PIP5K1A,CEP350,CDKL1,TAPT1,TNIK,PLD1,KIAA0586,CCP110,VAV2,PLPPR5,SSX2IP,FXYD5,ARF4,FOPNL,RAP2A	darkolivegreen	VSMC_M9
GO:0051304	0.25	0.86	7	85	chromosome separation	BP	1	CDC23,RMI1,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0051896	0.25	0.84	10	125	regulation of protein kinase B signaling	BP	1	ITGB1,GATA3,OSBPL8,ILK,THBS1,IGF1R,NTRK3,FERMT2,TNFAIP8L3,RICTOR	darkolivegreen	VSMC_M9
GO:0036293	0.25	0.82	19	258	response to decreased oxygen levels	BP	1	UBQLN1,ROCK2,NOX4,PLOD2,HK2,TLR2,THBS1,ITPR2,PTGS2,CPEB2,FMN2,BNIP2,KCNMB1,MYOCD,PIN1,ITGA2,ENO1,AQP3,CTGF	darkolivegreen	VSMC_M9
GO:0046651	0.25	0.83	13	177	lymphocyte proliferation	BP	1	MALT1,TBK1,FYN,LRRC32,AZI2,NDFIP1,SOS1,LYN,ITCH,CBLB,SLC39A10,MSN,CD40LG	darkolivegreen	VSMC_M9
GO:1901990	0.26	0.82	17	237	regulation of mitotic cell cycle phase transition	BP	1	CDC23,RINT1,RB1,RPL26,MYO16,CUL4A,RIOK2,USP47,APPL1,INO80,BRD7,CUL3,KLHL18,TPR,CDC27,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0090150	0.26	0.83	15	210	establishment of protein localization to membrane	BP	1	COX18,FYN,RAB3GAP1,ARL6,RAB3GAP2,ANK3,CCDC47,BLZF1,ATAD1,SRP9,RAB31,MYO1C,ZDHHC7,SEC63,SRP19	darkolivegreen	VSMC_M9
GO:0055013	0.26	0.87	6	65	cardiac muscle cell development	BP	1	ZMPSTE24,SHOX2,PDLIM5,FHOD3,MAP2K4,PIN1	darkolivegreen	VSMC_M9
GO:0044786	0.26	0.89	4	40	cell cycle DNA replication	BP	1	ZMPSTE24,BRCA2,INO80,ZPR1	darkolivegreen	VSMC_M9
GO:0110151	0.26	0.89	4	42	positive regulation of biomineralization	BP	1	ATP2B1,ACVR1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0030308	0.26	0.83	12	153	negative regulation of cell growth	BP	1	CDKL3,INHBA,RB1,RNF6,SEMA5B,RBBP7,SEMA7A,ENO1,WFDC1,BMPR2,NOV,VGLL4	darkolivegreen	VSMC_M9
GO:0007099	0.26	0.89	4	37	centriole replication	BP	1	CEP120,CEP295,C10orf90,CCP110	darkolivegreen	VSMC_M9
GO:0000280	0.26	0.81	25	355	nuclear division	BP	1	CDC23,RMI1,CENPC,ACTR2,CAV2,CCDC8,RB1,ACTR3,CCNA1,PDS5B,BRCA2,UBXN2B,MYBL1,RIOK2,MAP9,INO80,CUL3,SYCP2,TPR,CDC27,FMN2,PIN1,SPIRE1,CDK13,MZT1	darkolivegreen	VSMC_M9
GO:0033043	0.26	0.78	65	950	regulation of organelle organization	BP	1	LMAN1,CEP120,CDC23,PTPRD,AKAP9,SENP6,STAP1,CCDC88A,ACTR2,CAV2,ROCK2,KIF5B,CEP295,CCDC8,NOX4,RB1,ACTR3,RAB3GAP1,LIG4,ILK,IFT88,RIOK2,XRN1,MAP1B,PFN2,RASA1,MAP9,DHX36,DYRK1A,SPTBN5,LRRK2,CUL3,PHLDB2,KIAA1551,CAMSAP2,RAB3GAP2,NEK7,NTRK3,IQGAP1,C10orf90,HDGFL3,TPR,CDC27,IQCJ-SCHIP1,CDKL1,FERMT2,TAPT1,MSN,TPM1,GPR65,CYFIP2,CLTC,FHOD3,PIN1,CCP110,ROCK1,RICTOR,SPIRE1,USP7,MYO1C,PAFAH1B1,SKA2,CDK13,CTGF,CFL2	darkolivegreen	VSMC_M9
GO:0006974	0.26	0.79	47	699	cellular response to DNA damage stimulus	BP	1	RRM2B,RMI1,SLC30A9,TOPORS,CLOCK,NPAS2,PSME4,MYO6,UBA6,ZMPSTE24,ACTR2,DDX1,RINT1,CDK3,RIF1,RPL26,LIG4,CUL4A,PDS5B,BRCA2,PARG,MTREX,LYN,TDG,NEK1,USP47,ACTR8,ZDHHC16,INO80,DYRK1A,TANK,NFRKB,TDP2,UCHL5,TLK2,SKIL,PRRX1,BOD1L1,FMN2,RBBP6,PPM1D,RBBP8,THOC1,SPIRE1,USP7,RFWD3,UBE2V1	darkolivegreen	VSMC_M9
GO:0007411	0.26	0.82	15	181	axon guidance	BP	1	EXT1,FYN,KIF5B,GATA3,SOS1,PALLD,ANOS1,SEMA5B,NRP2,NCAM1,NOTCH3,ENAH,SEMA7A,BMPR2,GDNF	darkolivegreen	VSMC_M9
GO:0016579	0.26	0.84	9	108	protein deubiquitination	BP	1	USP12,ITCH,USP47,TANK,UCHL5,USP54,MYSM1,USP7,OTUD6B	darkolivegreen	VSMC_M9
GO:0036465	0.26	0.86	6	64	synaptic vesicle recycling	BP	1	PLAA,PICALM,LRRK2,VAMP4,ROCK1,WNT7A	darkolivegreen	VSMC_M9
GO:0051960	0.26	0.80	26	344	regulation of nervous system development	BP	1	THBS2,CDKL3,PTPRD,ACTR2,TRAK1,LIG4,ILK,RNF6,LYN,EIF2AK3,MAP1B,TLR2,DHX36,SHOX2,NTRK3,SEMA5B,IDH2,TRAK2,SKIL,SRPX2,DICER1,SEMA7A,PAFAH1B1,BMPR2,ZPR1,WNT7A	darkolivegreen	VSMC_M9
GO:1905330	0.26	0.87	5	56	regulation of morphogenesis of an epithelium	BP	1	GATA3,NTN4,SULF1,WNT5B,GDNF	darkolivegreen	VSMC_M9

GO:1903053	0.26	0.88	4	43	regulation of extracellular matrix organization	BP	1	CHADL,RB1,PHLDB2,COLGALT1	darkolivegreen	VSMC_M9
GO:0006998	0.26	0.88	4	43	nuclear envelope organization	BP	1	ZMPSTE24,UBXN2B,NUP155,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0008037	0.26	0.85	8	97	cell recognition	BP	1	EXT1,JMJD6,ADAM32,PALLD,VCAN,VDAC2,MSN,FCN1	darkolivegreen	VSMC_M9
GO:0071453	0.26	0.83	11	142	cellular response to oxygen levels	BP	1	UBQLN1,ROCK2,ATP6V0A2,ATP6V1A,PTGS2,CPEB2,FMN2,FAS,KCNMB1,ENO1,AQP3	darkolivegreen	VSMC_M9
GO:0097194	0.26	0.87	5	60	execution phase of apoptosis	BP	1	STK24,CASP7,DICER1,CIDEA,XKR9	darkolivegreen	VSMC_M9
GO:0051298	0.26	0.86	6	64	centrosome duplication	BP	1	CEP120,ROCK2,CEP295,BRCA2,C10orf90,CCP110	darkolivegreen	VSMC_M9
GO:0007612	0.26	0.84	9	104	learning	BP	1	UBA6,ACTR2,ITGB1,FYN,TLR2,UBE3A,PTGS2,ATAD1,ARF4	darkolivegreen	VSMC_M9
GO:0009743	0.26	0.82	14	186	response to carbohydrate	BP	1	KIF5B,LYN,MAP1B,THBS1,SLC39A14,BRSK2,IGF1R,CCDC186,EIF2B5,C2CD2L,PTGS2,MAP2K4,ITGA2,CTGF	darkolivegreen	VSMC_M9
GO:0016567	0.26	0.79	45	656	protein ubiquitination	BP	1	SOCS6,MALT1,CAND1,CDC23,UBQLN1,PLAA,TOPORS,FBXO9,UBA6,UBE2J1,FYN,CBLC,NUB1,NDFIP2,NDFIP1,CUL4A,RNF6,FBXL17,ITCH,LNPEP,LTN1,BRAP,KCTD9,CBLB,LRRK2,UBE3A,CUL3,G2E3,UBE4A,C10orf90,KLHL18,CDC27,SMURF1,SPOP,RLIM,RBBP6,C18orf25,PIN1,BAG5,BFAR,USP7,RFWD3,PDZRN3,FBXL7,UBE2V1	darkolivegreen	VSMC_M9
GO:0032103	0.26	0.81	20	286	positive regulation of response to external stimulus	BP	1	TBK1,WISP1,JAK2,CLOCK,STAP1,FYN,GPR4,CAMK1D,LYN,AGTR1,TLR2,THBS1,NFKBIZ,LRRK2,NTRK3,PTGS2,ADAM10,ITGA2,BMPR2,FCN1	darkolivegreen	VSMC_M9
GO:0009166	0.26	0.87	5	61	nucleotide catabolic process	BP	1	PDE7A,TDG,NUDT9,DERA,ACOT7	darkolivegreen	VSMC_M9
GO:0002011	0.26	0.87	5	50	morphogenesis of an epithelial sheet	BP	1	SOS1,ITGA5,PHLDB2,FERMT2,WNT7A	darkolivegreen	VSMC_M9
GO:0097485	0.26	0.82	15	182	neuron projection guidance	BP	1	EXT1,FYN,KIF5B,GATA3,SOS1,PALLD,ANOS1,SEMA5B,NRP2,NCAM1,NOTCH3,ENAH,SEMA7A,BMPR2,GDNF	darkolivegreen	VSMC_M9
GO:0043009	0.26	0.79	37	522	chordate embryonic development	BP	1	EXT1,HOXA9,HOXA11,ITGB1,GATA3,LIG4,ATP11A,CUL4A,BRCA2,DCHS1,TMED2,EIF2S2,SULF1,RDH10,MBNL1,SHOX2,ACVR1,IRX5,ETNK2,TBX15,CUL3,FZD2,NPAT,SKIL,PRRX1,TAPT1,ADAM10,MYO1E,TBX6,RBBP6,RBBP8,COL11A1,PRKACB,BMPR2,WNT9A,ZPR1,CHST11	darkolivegreen	VSMC_M9
GO:0002064	0.26	0.82	14	173	epithelial cell development	BP	1	CLOCK,ROCK2,FNDC3A,GPR4,PALLD,IQGAP1,ACTA2,WNT5B,MSN,MYO1E,ROCK1,PAFAH1B1,RAPGEF1,WNT7A	darkolivegreen	VSMC_M9
GO:0008285	0.26	0.79	37	548	negative regulation of cell population proliferation	BP	1	JAK2,TES,CAV2,INHBA,NOX4,RB1,CGREF1,GATA3,LRRC32,MYO16,NDFIP1,PDS5B,BRCA2,ILK,PLPP1,CNOT7,LYN,ITCH,SULF1,TLR2,THBS1,CBLB,BRD7,IDH2,PTGS2,KIFAP3,TPM1,DICER1,PPM1D,MYOCD,ITGA1,WFDC1,BMPR2,NOV,E2F3,WNT9A,VGLL4	darkolivegreen	VSMC_M9
GO:2001056	0.27	0.84	8	105	positive regulation of cysteine-type endopeptidase activity	BP	1	MALT1,JAK2,FYN,EIF2AK3,FAS,CYFIP2,UACA,CTGF	darkolivegreen	VSMC_M9
GO:0035637	0.27	0.83	10	114	multicellular organismal signaling	BP	1	AKAP9,ZMPSTE24,ATP2B1,ATP2A2,ATP1A1,ANK3,ITGA2,NUP155,PAFAH1B1,IRX3	darkolivegreen	VSMC_M9
GO:0070646	0.27	0.83	10	125	protein modification by small protein removal	BP	1	SENP6,USP12,ITCH,USP47,TANK,UCHL5,USP54,MYSM1,USP7,OTUD6B	darkolivegreen	VSMC_M9
GO:0019827	0.27	0.84	9	106	stem cell population maintenance	BP	1	ZC3H13,RIF1,LIG4,CUL4A,EIF4E,TAF5L,PRRX1,SS18,WNT7A	darkolivegreen	VSMC_M9
GO:0008154	0.27	0.82	14	183	actin polymerization or depolymerization	BP	1	JAK2,ACTR2,ACTR3,MICAL2,PFN2,RASA1,SPTBN5,ENAH,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C,CFL2	darkolivegreen	VSMC_M9
GO:0071824	0.27	0.82	12	163	protein-DNA complex subunit organization	BP	1	CAND1,SENP6,PSME4,CENPC,TAF1B,RB1,SMARCA5,BDP1,LIN54,INO80,NAP1L4,GTF2B	darkolivegreen	VSMC_M9
GO:0033993	0.27	0.78	45	657	response to lipid	BP	1	MALT1,CDO1,PLAA,ABCB4,JAK2,CLOCK,STAP1,ROCK2,INHBA,NOCT,UFM1,ATP2B1,NR2C1,UBA5,TMF1,PLPP1,RNF6,LYN,GRAMD1A,XRN1,MAP1B,GDAP1,TLR2,ATP2A2,THBS1,ATP1A1,UBE3A,EIF4E,NTRK3,RBBP7,PTGS2,WNT5B,MSN,KCNMB1,TRIP4,RBBP8,ITGA2,TBXA2R,WFDC1,AQP3,CTGF,PAQR8,PMEPA1,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:0048024	0.27	0.85	7	85	regulation of mRNA splicing, via spliceosome	BP	1	KHDRBS3,JMJD6,MBNL2,MBNL1,DYRK1A,LARP7,CWC22	darkolivegreen	VSMC_M9
GO:0006165	0.27	0.86	6	72	nucleoside diphosphate phosphorylation	BP	1	HK2,PGAM4,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0044728	0.27	0.86	6	67	DNA methylation or demethylation	BP	1	ZMPSTE24,PIWIL4,GATA3,TDG,PPM1D,USP7	darkolivegreen	VSMC_M9
GO:0071320	0.27	0.88	4	37	cellular response to cAMP	BP	1	AKAP9,NOX4,ITPR2,RAPGEF1	darkolivegreen	VSMC_M9
GO:0016053	0.27	0.81	15	215	organic acid biosynthetic process	BP	1	CDO1,ELOVL5,PNPLA8,SUCLA2,ABHD1,HSD17B12,RDH10,PLOD2,ALDH18A1,GATM,PTGS2,SLC1A3,ACOT7,ELOVL4,AKR1D1	darkolivegreen	VSMC_M9
GO:0045132	0.27	0.86	6	73	meiotic chromosome segregation	BP	1	RMI1,CENPC,ACTR2,ACTR3,SYCP2,FMN2	darkolivegreen	VSMC_M9
GO:0120193	0.27	0.87	5	54	tight junction organization	BP	1	EXT1,ROCK2,MPP7,ROCK1,MYO1C	darkolivegreen	VSMC_M9
GO:0000959	0.27	0.88	4	44	mitochondrial RNA metabolic process	BP	1	PDE12,FASTKD2,FASTKD5,TFB2M	darkolivegreen	VSMC_M9
GO:0032943	0.27	0.82	13	179	mononuclear cell proliferation	BP	1	MALT1,TBK1,FYN,LRRC32,AZI2,NDFIP1,SOS1,LYN,ITCH,CBLB,SLC39A10,MSN,CD40LG	darkolivegreen	VSMC_M9
GO:0045428	0.27	0.88	4	43	regulation of nitric oxide biosynthetic process	BP	1	JAK2,ROCK2,PTGS2,TLR6	darkolivegreen	VSMC_M9
GO:0009247	0.27	0.87	5	61	glycolipid biosynthetic process	BP	1	ST3GAL3,ST8SIA1,PIGW,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0051966	0.27	0.88	4	40	regulation of synaptic transmission, glutamatergic	BP	1	RAB3GAP1,LRRK2,PTGS2,ATAD1	darkolivegreen	VSMC_M9
GO:0051147	0.27	0.84	9	115	regulation of muscle cell differentiation	BP	1	HDAC9,ATP11A,SHOX2,DKK1,MYOCD,PIN1,BMPR2,NOV,TMEM119	darkolivegreen	VSMC_M9
GO:0000041	0.27	0.85	7	86	transition metal ion transport	BP	1	SLC39A7,SLC30A9,TMEM165,SLC30A5,SLC39A14,SLC39A10,CLTC	darkolivegreen	VSMC_M9

GO:0032271	0.27	0.81	15	199	regulation of protein polymerization	BP	1	AKAP9,ACTR2,ACTR3,MAP1B,PFN2,RASA1,DYRK1A,SPTBN5,CAMSAP2,VDAC2,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C	darkolivegreen	VSMC_M9
GO:0006839	0.27	0.82	14	210	mitochondrial transport	BP	1	LMAN1,COX18,GDAP1,HK2,LRRK2,MRS2,TIMM17A,TOMM20,ABCB10,VDAC2,AFG3L2,PMPCA,SLC25A24,TOMM20L	darkolivegreen	VSMC_M9
GO:1902882	0.27	0.85	6	74	regulation of response to oxidative stress	BP	1	UBQLN1,PNPLA8,FYN,LRRK2,TLR6,BAG5	darkolivegreen	VSMC_M9
GO:0043406	0.27	0.84	8	93	positive regulation of MAP kinase activity	BP	1	ILK,THBS1,LRRK2,NTRK3,PTPN1,IQGAP1,DKK1,TLR6	darkolivegreen	VSMC_M9
GO:0009791	0.27	0.85	6	68	post-embryonic development	BP	1	GATA3,ETNK2,CCDC47,ZFX,MYO1E,CHST11	darkolivegreen	VSMC_M9
GO:1903320	0.27	0.81	15	211	regulation of protein modification by small protein conjugation or removal	BP	1	MALT1,UBQLN1,PLAA,TOPORS,FYN,NDFIP2,NDFIP1,ITCH,CBLB,LRRK2,TANK,UBE3A,CUL3,PIN1,BAG5	darkolivegreen	VSMC_M9
GO:0051240	0.27	0.77	71	1050	positive regulation of multicellular organismal process	BP	1	MALT1,TBK1,THBS2,CDKL3,PTPRD,JAK2,NPAS2,HOXA11,ACTR2,ROCK2,INHBA,DDX1,ITGB1,RB1,GATA3,TRAK1,RIF1,LIG4,ATP2B1,ILK,ITGA5,TMF1,LYN,EIF2AK3,ITCH,SULF1,FFAR4,MAP1B,APPL1,HK2,TLR2,ATP2A2,DHX36,THBS1,SHOX2,ACVR1,NFKBIZ,CBLB,ATP1A1,LRRK2,KPNA6,IGF1R,ADAM12,GATM,PTGS2,FERMT2,SKIL,TAPT1,DKK1,AKT3,TLR6,TPM1,SRPX2,PKM,DICER1,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,C1QTNF3,CD40LG,TBXA2R,PAFAH1B1,ENO1,BMPR2,GDNF,CTGF,FCN1,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0072577	0.27	0.88	4	43	endothelial cell apoptotic process	BP	1	GATA3,THBS1,CD40LG,BMPR2	darkolivegreen	VSMC_M9
GO:1903828	0.27	0.84	8	99	negative regulation of cellular protein localization	BP	1	LMAN1,UBE2J1,ROCK2,PICALM,UFM1,UBXN2B,LRRK2,CLTC	darkolivegreen	VSMC_M9
GO:0046887	0.27	0.85	7	86	positive regulation of hormone secretion	BP	1	JAK2,INHBA,KIF5B,TMF1,FFAR4,C2CD2L,C1QTNF3	darkolivegreen	VSMC_M9
GO:0010657	0.27	0.86	5	60	muscle cell apoptotic process	BP	1	JAK2,ILK,MAP2K4,MYOCD,E2F3	darkolivegreen	VSMC_M9
GO:0010941	0.27	0.77	79	1223	regulation of cell death	BP	1	MALT1,AHI1,TBK1,RRM2B,WISP1,UBQLN1,TOPORS,JAK2,NPAS2,NOA1,INHBA,ITGB1,FYN,NOX4,RB1,PICALM,CAMK1D,GATA3,DNAJC3,RPL26,UFM1,LIG4,ILK,ITGA5,TMF1,LYN,MERTK,EIF2AK3,ITCH,USP47,PDE12,FFAR4,RASA1,THBS1,ACVR1,LRRK2,SLC39A10,IGF1R,NTRK3,PTPN1,KPNA1,EIF2B5,SYCP2,ATF3,CD3G,PTGS2,ITGAV,FERMT2,SKIL,KIFAP3,TNFAIP8L3,VDAC2,DKK1,FMN2,FAS,TLR6,ADAM10,BNIP2,MAP2K4,MYOCD,PIN1,BAG5,ITGA1,BFAR,CIDEA,CD40LG,GADD45B,ENO1,SLC25A24,ANKRD13C,ARF4,GDNF,CTGF,BDKRB2,NOV,E2F3,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0070849	0.27	0.88	4	41	response to epidermal growth factor	BP	1	IQGAP1,TPR,PTPN12,ZPR1	darkolivegreen	VSMC_M9
GO:0031396	0.27	0.82	13	180	regulation of protein ubiquitination	BP	1	MALT1,UBQLN1,PLAA,TOPORS,FYN,NDFIP2,NDFIP1,CBLB,LRRK2,UBE3A,CUL3,PIN1,BAG5	darkolivegreen	VSMC_M9
GO:0045005	0.27	0.88	4	41	DNA-dependent DNA replication maintenance of fidelity	BP	1	BRCA2,BOD1L1,THOC1,RFWD3	darkolivegreen	VSMC_M9
GO:0044782	0.27	0.80	21	288	cilium organization	BP	1	AHI1,CEP120,CEP41,CCDC88A,ACTR2,ACTR3,CEP83,IFT88,NEK1,ARL6,EHD4,TROVE2,CEP350,CDKL1,KIFAP3,TAPT1,KIAA0586,CCP110,SSX2IP,ARF4,FOPNL	darkolivegreen	VSMC_M9
GO:0061337	0.27	0.85	7	76	cardiac conduction	BP	1	AKAP9,ZMPSTE24,ATP2B1,ATP2A2,ATP1A1,NUP155,IRX3	darkolivegreen	VSMC_M9
GO:0031122	0.27	0.86	5	52	cytoplasmic microtubule organization	BP	1	CEP120,CCDC88A,TUBGCP3,CAMSAP2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0010563	0.27	0.79	25	356	negative regulation of phosphorus metabolic process	BP	1	STAP1,SH3BP5L,ROCK2,INHBA,RB1,CBLC,MGAT5,DNAJC3,ILK,LYN,IPO7,TMED2,CBLB,LRRK2,CORO1C,NTRK3,PTPN1,BOD1L1,DKK1,SRCIN1,MYOCD,ROCK1,GADD45B,BDKRB2,PMEPA1	darkolivegreen	VSMC_M9
GO:0045936	0.27	0.79	25	356	negative regulation of phosphate metabolic process	BP	1	STAP1,SH3BP5L,ROCK2,INHBA,RB1,CBLC,MGAT5,DNAJC3,ILK,LYN,IPO7,TMED2,CBLB,LRRK2,CORO1C,NTRK3,PTPN1,BOD1L1,DKK1,SRCIN1,MYOCD,ROCK1,GADD45B,BDKRB2,PMEPA1	darkolivegreen	VSMC_M9
GO:0045778	0.28	0.88	4	42	positive regulation of ossification	BP	1	ATP2B1,ACVR1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0015909	0.28	0.87	4	46	long-chain fatty acid transport	BP	1	PNPLA8,THBS1,EPRS,BDKRB2	darkolivegreen	VSMC_M9
GO:0010518	0.28	0.87	4	41	positive regulation of phospholipase activity	BP	1	PLAA,ARL1,AGTR1,ARF4	darkolivegreen	VSMC_M9
GO:1902806	0.28	0.83	9	115	regulation of cell cycle G1/S phase transition	BP	1	RB1,RPL26,MYO16,CUL4A,APPL1,INO80,BRD7,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0007249	0.28	0.81	16	222	I-kappaB kinase/NF-kappaB signaling	BP	1	MALT1,TBK1,ROCK2,DDX1,FYN,NDFIP2,AZI2,NDFIP1,TLR2,DHX36,TANK,GPR89A,TLR6,ROCK1,VAPA,UBE2V1	darkolivegreen	VSMC_M9
GO:0033555	0.28	0.87	4	42	multicellular organismal response to stress	BP	1	EXT1,NPAS2,THBS1,EIF4E	darkolivegreen	VSMC_M9
GO:0030282	0.28	0.84	8	97	bone mineralization	BP	1	ASPN,ZMPSTE24,ATP2B1,EIF2AK3,ACVR1,PTGS2,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0050851	0.28	0.83	9	117	antigen receptor-mediated signaling pathway	BP	1	MALT1,STAP1,FYN,GATA3,LYN,NFKBIZ,CBLB,SLC39A10,EIF2B5	darkolivegreen	VSMC_M9
GO:0008584	0.28	0.83	9	111	male gonad development	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,TMF1,EIF2S2,SRD5A2	darkolivegreen	VSMC_M9
GO:0052126	0.28	0.82	10	127	movement in host environment	BP	1	CAV2,ITGB1,ITGA5,ITCH,AGTR1,NCAM1,ITGAV,ITGA2,VAPA,FCN1	darkolivegreen	VSMC_M9
GO:0043535	0.28	0.84	7	87	regulation of blood vessel endothelial cell migration	BP	1	HDAC9,STARD13,THBS1,PTGS2,AKT3,SRPX2,TBXA2R	darkolivegreen	VSMC_M9
GO:0008643	0.28	0.83	9	112	carbohydrate transport	BP	1	SLC35B4,RTN2,OSBPL8,FFAR4,APPL1,HK2,ZDHHC7,AQP3,SLC35D1	darkolivegreen	VSMC_M9
GO:0072666	0.28	0.87	4	42	establishment of protein localization to vacuole	BP	1	GCC2,VPS36,PIK3R4,SMURF1	darkolivegreen	VSMC_M9
GO:0060560	0.28	0.80	16	200	developmental growth involved in morphogenesis	BP	1	EXT1,CDKL3,PLAA,ITGB1,ILK,RNF6,MAP1B,RDH10,SEMA5B,IQGAP1,NRP2,SMURF1,CYFIP2,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9

GO:0050805	0.28	0.87	4	42	negative regulation of synaptic transmission	BP	1	LRRK2,PTGS2,SORCS2,ATAD1	darkolivegreen	VSMC_M9
GO:0031214	0.28	0.82	10	126	biomineral tissue development	BP	1	ASPN,ZMPSTE24,ROCK2,ATP2B1,EIF2AK3,ACVR1,PTGS2,ROCK1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0007528	0.28	0.87	4	39	neuromuscular junction development	BP	1	LRRK2,ANK3,AFG3L2,PDZRN3	darkolivegreen	VSMC_M9
GO:0006081	0.28	0.87	4	46	cellular aldehyde metabolic process	BP	1	CYP27C1,RDH10,IDH2,TPI1	darkolivegreen	VSMC_M9
GO:0003006	0.28	0.77	46	685	developmental process involved in reproduction	BP	1	CLOCK,PSME4,HOXA9,HOXA10,HOXA11,UBE2J1,INHBA,CEP57,PIWIL4,FNDC3A,GATA3,CCNA1,BRCA2,TMF1,MERTK,MYBL1,TMED2,EIF2S2,SULF1,STOX2,MICAL2,RDH10,DHX36,ACVR1,IRX5,ETNK2,LRRK2,UBE3A,LARP7,EIF2B5,SYCP2,PITHD1,ZFX,PTGS2,SKIL,FMN2,ADAM10,ADAM19,MYOCD,PAFAH1B1,BMPR2,ANKRD49,PAQR8,SRD5A2,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0061028	0.28	0.87	4	38	establishment of endothelial barrier	BP	1	ROCK2,MSN,ROCK1,RAPGEF1	darkolivegreen	VSMC_M9
GO:0098727	0.28	0.83	9	108	maintenance of cell number	BP	1	ZC3H13,RIF1,LIG4,CUL4A,EIF4E,TAF5L,PRRX1,SS18,WNT7A	darkolivegreen	VSMC_M9
GO:0031109	0.28	0.83	9	109	microtubule polymerization or depolymerization	BP	1	AKAP9,TUBGCP3,MAP1B,DYRK1A,CAMSAP2,HAUS2,HDGFL3,SKA2,MZT1	darkolivegreen	VSMC_M9
GO:0002694	0.28	0.79	24	352	regulation of leukocyte activation	BP	1	SOCS6,MALT1,STAP1,INHBA,FYN,GATA3,LRRC32,RIF1,NDFIP1,SOS1,HSPH1,LYN,MERTK,ITCH,THBS1,NFKBIZ,CBLB,LRRK2,SLC39A10,SH3KBP1,TLR6,THOC1,CD40LG,CLEC4D	darkolivegreen	VSMC_M9
GO:0019882	0.28	0.86	5	61	antigen processing and presentation	BP	1	EXT1,RAB3B,LNPEP,THBS1,RAB6A	darkolivegreen	VSMC_M9
GO:0046939	0.28	0.85	6	74	nucleotide phosphorylation	BP	1	HK2,PGAM4,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:2000112	0.28	0.75	182	2822	regulation of cellular macromolecule biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,ETF1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,EIF5B,ZNF451,HDAC9,CAVIN4,MYO6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,RAB3GAP1,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,RIF1,PPP1R12A,RPL26,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,PDE12,STOX2,MICAL2,LARP4,ACTR8,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,EIF4E,TDP2,KPNA6,EPRS,RAB3GAP2,NEK7,WWC3,LARP7,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,PLD1,CPEB2,DKK1,NOTCH3,SRP9,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,RBBP6,TLE3,PKM,DICER1,ARMCX3,PPM1D,MAP2K4,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,ZNF280C,GSPT1,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:1901989	0.28	0.84	7	91	positive regulation of cell cycle phase transition	BP	1	CDC23,RB1,CUL4A,CUL3,KLHL18,CDC27,THOC1	darkolivegreen	VSMC_M9
GO:0022604	0.28	0.79	20	261	regulation of cell morphogenesis	BP	1	CDKL3,PTPRD,PLAA,ZMPSTE24,ACTR2,FYN,PRPF40A,ILK,LARP4,RASA1,DHX36,NEDD9,ATP10A,CORO1C,SH3KBP1,FERMT2,SMURF1,MSN,TPM1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0002244	0.28	0.83	8	96	hematopoietic progenitor cell differentiation	BP	1	EXT1,INHBA,GATA3,LIG4,SOS1,ITCH,DHX36,RBM47	darkolivegreen	VSMC_M9
GO:0009117	0.28	0.78	25	381	nucleotide metabolic process	BP	1	RRM2B,ELOVL5,SUCLA2,ACPP,HSD17B12,PDE7A,TDG,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,IDH2,DERA,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0051321	0.29	0.80	14	192	meiotic cell cycle	BP	1	RMI1,CENPC,ACTR2,PIWIL4,ACTR3,TUBGCP3,CCNA1,BRCA2,MYBL1,SYCP2,FMN2,RBBP8,SPIRE1,PRKACB	darkolivegreen	VSMC_M9
GO:0110148	0.29	0.82	10	127	biomineralization	BP	1	ASPN,ZMPSTE24,ROCK2,ATP2B1,EIF2AK3,ACVR1,PTGS2,ROCK1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0042326	0.29	0.79	22	311	negative regulation of phosphorylation	BP	1	STAP1,SH3BP5L,INHBA,RB1,CBLC,DNAJC3,ILK,LYN,IPO7,TMED2,CBLB,LRRK2,CORO1C,NTRK3,PTPN1,DKK1,SRCIN1,MYOCD,ROCK1,GADD45B,BDKRB2,PMEPA1	darkolivegreen	VSMC_M9
GO:0046323	0.29	0.85	5	54	glucose import	BP	1	RTN2,OSBPL8,APPL1,HK2,ZDHHC7	darkolivegreen	VSMC_M9
GO:2000649	0.29	0.87	4	43	regulation of sodium ion transmembrane transporter activity	BP	1	UTRN,KIF5B,ANK3,FXYD5	darkolivegreen	VSMC_M9
GO:0019080	0.29	0.83	7	86	viral gene expression	BP	1	MGAT4A,ST3GAL3,MGAT5,CCNT2,CHD1,LARP7,GTF2B	darkolivegreen	VSMC_M9
GO:0006885	0.29	0.84	6	70	regulation of pH	BP	1	TMEM165,CLN5,ATP6V0A2,LRRK2,UBE3A,GPR89A	darkolivegreen	VSMC_M9
GO:0046546	0.29	0.82	9	112	development of primary male sexual characteristics	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,TMF1,EIF2S2,SRD5A2	darkolivegreen	VSMC_M9
GO:0097190	0.29	0.77	31	471	apoptotic signaling pathway	BP	1	RRM2B,UBQLN1,TOPORS,JAK2,INHBA,FYN,RB1,STK24,RPL26,CUL4A,BRCA2,EIF2AK3,USP47,THBS1,ACVR1,LRRK2,BRSK2,CUL3,PTPN1,ATF3,PTGS2,ITGAV,SKIL,VDAC2,FAS,UACA,ANXA6,BAG5,ENO1,GDNF,BDKRB2	darkolivegreen	VSMC_M9
GO:1905952	0.29	0.82	9	118	regulation of lipid localization	BP	1	ABCB4,OSBPL8,TMF1,AGTR1,THBS1,EPRS,OSBPL11,ITGAV,CIDEA	darkolivegreen	VSMC_M9
GO:0035567	0.29	0.84	6	68	non-canonical Wnt signaling pathway	BP	1	FZD2,SMURF1,DKK1,WNT5B,GPC4,WNT7A	darkolivegreen	VSMC_M9

GO:0032102	0.29	0.79	19	266	negative regulation of response to external stimulus	BP	1	STAP1,FYN,RB1,GATA3,TNFAIP6,NDFIP1,CNOT7,LYN,ITCH,FFAR4,THBS1,NUCB2,PHLDB2,SEMA5B,GPATCH3,SEMA7A,C1QTNF3,WFDC1,NOV	darkolivegreen	VSMC_M9
GO:0090305	0.29	0.80	15	213	nucleic acid phosphodiester bond hydrolysis	BP	1	ELAC1,DDX1,NOCT,EXOSC9,TOE1,TSN,ERI1,CNOT7,XRN1,PDE12,DCP1A,TDP2,DICER1,RBBP8,CIDEA	darkolivegreen	VSMC_M9
GO:0071214	0.29	0.79	19	267	cellular response to abiotic stimulus	BP	1	CLOCK,ZMPSTE24,NOX4,GATA3,RPL26,LIG4,USP47,DHX36,INO80,ATP1A1,TANK,TLK2,PTGS2,FAS,ADSS,MAP2K4,ITGA2,BDKRB2,EFHD1	darkolivegreen	VSMC_M9
GO:0104004	0.29	0.79	19	267	cellular response to environmental stimulus	BP	1	CLOCK,ZMPSTE24,NOX4,GATA3,RPL26,LIG4,USP47,DHX36,INO80,ATP1A1,TANK,TLK2,PTGS2,FAS,ADSS,MAP2K4,ITGA2,BDKRB2,EFHD1	darkolivegreen	VSMC_M9
GO:0098534	0.29	0.86	4	40	centriole assembly	BP	1	CEP120,CEP295,C10orf90,CCP110	darkolivegreen	VSMC_M9
GO:0080164	0.29	0.86	4	45	regulation of nitric oxide metabolic process	BP	1	JAK2,ROCK2,PTGS2,TLR6	darkolivegreen	VSMC_M9
GO:0046605	0.29	0.86	4	42	regulation of centrosome cycle	BP	1	CEP120,ROCK2,CEP295,C10orf90	darkolivegreen	VSMC_M9
GO:0046879	0.29	0.79	15	206	hormone secretion	BP	1	JAK2,CLOCK,INHBA,KIF5B,GATA3,TMF1,LYN,FFAR4,AGTR1,SNX19,BRSK2,CCDC186,C2CD2L,C1QTNF3,NOV	darkolivegreen	VSMC_M9
GO:1903313	0.29	0.82	8	105	positive regulation of mRNA metabolic process	BP	1	ROCK2,NOCT,EXOSC9,CNOT7,PDE12,DCP1A,DHX36,ROCK1	darkolivegreen	VSMC_M9
GO:0035050	0.30	0.85	5	55	embryonic heart tube development	BP	1	AHI1,TMED2,MICAL2,ACVR1,TBX6	darkolivegreen	VSMC_M9
GO:0046209	0.30	0.85	5	60	nitric oxide metabolic process	BP	1	JAK2,ROCK2,TLR2,PTGS2,TLR6	darkolivegreen	VSMC_M9
GO:0050657	0.30	0.81	10	135	nucleic acid transport	BP	1	UPF2,NUP37,TOMM20,TPR,THOC1,NUP155,MYO1C,RANBP2,TOMM20L,NUP35	darkolivegreen	VSMC_M9
GO:0050658	0.30	0.81	10	135	RNA transport	BP	1	UPF2,NUP37,TOMM20,TPR,THOC1,NUP155,MYO1C,RANBP2,TOMM20L,NUP35	darkolivegreen	VSMC_M9
GO:0006637	0.30	0.84	6	78	acyl-CoA metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,DLST,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0035383	0.30	0.84	6	78	thioester metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,DLST,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0050865	0.30	0.77	26	385	regulation of cell activation	BP	1	SOCS6,MALT1,JAK2,STAP1,INHBA,FYN,GATA3,LRRC32,RIF1,NDFIP1,SOS1,HSPH1,LYN,MERTK,ITCH,THBS1,NFKBIZ,CBLB,LRRK2,SLC39A10,SH3KBP1,TLR6,THOC1,CD40LG,CLEC4D,CTGF	darkolivegreen	VSMC_M9
GO:0051347	0.30	0.77	31	441	positive regulation of transferase activity	BP	1	MALT1,TOPORS,JAK2,STAP1,CCDC88A,NOX4,CCNT2,OSBPL8,PIK3R4,ILK,LYN,MERTK,THBS1,NEDD9,LRRK2,IGF1R,NEK7,NTRK3,PTPN1,IQGAP1,FERMT2,TNFAIP8L3,DKK1,TLR6,SRCIN1,PIN1,RICTOR,VAV2,RANBP2,BMPR2,LAMTOR3	darkolivegreen	VSMC_M9
GO:0048515	0.30	0.82	8	106	spermatid differentiation	BP	1	PSME4,UBE2J1,CEP57,FNDC3A,TMF1,PITHD1,PAFAH1B1,TMEM119	darkolivegreen	VSMC_M9
GO:0046661	0.30	0.81	10	128	male sex differentiation	BP	1	HOXA9,HOXA10,HOXA11,INHBA,FNDC3A,GATA3,TMF1,EIF2S2,SYCP2,SRD5A2	darkolivegreen	VSMC_M9
GO:0070830	0.30	0.86	4	44	bicellular tight junction assembly	BP	1	ROCK2,MPP7,ROCK1,MYO1C	darkolivegreen	VSMC_M9
GO:0048284	0.30	0.81	9	120	organelle fusion	BP	1	CAV2,KIF5B,EEA1,YIPF5,GDAP1,USO1,VAMP4,AFG3L2,MIGA1	darkolivegreen	VSMC_M9
GO:0043524	0.30	0.81	9	115	negative regulation of neuron apoptotic process	BP	1	JAK2,FYN,LIG4,ILK,RASA1,MAP2K4,PIN1,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0051101	0.30	0.82	7	91	regulation of DNA binding	BP	1	JAK2,ZMPSTE24,RB1,GATA3,MYOCD,ITGA2,GTF2B	darkolivegreen	VSMC_M9
GO:0051606	0.30	0.81	10	135	detection of stimulus	BP	1	FYN,NEK1,FFAR4,TLR2,SEMA5B,TLR6,KCNMB1,ITGA2,COL11A1,ELOVL4	darkolivegreen	VSMC_M9
GO:0035239	0.30	0.75	49	699	tube morphogenesis	BP	1	AHI1,EXT1,THBS2,HDAC9,HOXA11,ROCK2,ITGB1,GPR4,GATA3,JMJD6,STARD13,SOS1,ILK,ITGA5,DCHS1,EIF2AK3,TMED2,SULF1,MICAL2,RDH10,AGTR1,HK2,RASA1,THBS1,SHOX2,ACVR1,ADAM12,NRP2,CLEC14A,PTGS2,FZD2,ITGAV,PRRX1,AKT3,MYO1E,TBX6,SRPX2,PKM,MYOCD,ROCK1,TBXA2R,VAV2,PRKACB,BMPR2,GDNF,CTGF,NOV,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0045814	0.30	0.86	4	43	negative regulation of gene expression, epigenetic	BP	1	SMARCA5,KIAA1551,TPR,PPM1D	darkolivegreen	VSMC_M9
GO:0050732	0.30	0.86	4	46	negative regulation of peptidyl-tyrosine phosphorylation	BP	1	SH3BP5L,CBLC,CBLB,SRCIN1	darkolivegreen	VSMC_M9
GO:0006397	0.30	0.77	27	407	mRNA processing	BP	1	DDX46,KHDRBS3,PPIL1,DDX1,ZC3H13,JMJD6,SUPT5H,MBNL2,PRPF40A,AC091959.3,MTREX,PDE12,MBNL1,DHX36,SNRNP48,DYRK1A,LARP7,CWC22,ZC3H14,RBBP6,THOC1,LSM5,ZNF326,FASTKD5,CDK13,GEMIN6,ZPR1	darkolivegreen	VSMC_M9
GO:0019083	0.30	0.86	4	45	viral transcription	BP	1	CCNT2,CHD1,LARP7,GTF2B	darkolivegreen	VSMC_M9
GO:0050919	0.30	0.86	4	40	negative chemotaxis	BP	1	SEMA5B,NRP2,ITGAV,SEMA7A	darkolivegreen	VSMC_M9
GO:0000271	0.30	0.84	5	58	polysaccharide biosynthetic process	BP	1	EXT1,UGP2,CSGALNACT2,PHKG2,CLTC	darkolivegreen	VSMC_M9
GO:0002090	0.30	0.86	4	43	regulation of receptor internalization	BP	1	AHI1,SCYL2,DKK1,ATAD1	darkolivegreen	VSMC_M9
GO:0009267	0.30	0.80	10	130	cellular response to starvation	BP	1	STK24,PIK3R4,EIF2AK3,LRRK2,BRSK2,ATF3,FAS,PPM1D,BMPR2,C12orf66	darkolivegreen	VSMC_M9
GO:0050792	0.30	0.81	9	119	regulation of viral process	BP	1	CAV2,CNOT7,PDE12,KIAA1551,KPNA6,LARP7,VAPB,VAPA,FCN1	darkolivegreen	VSMC_M9
GO:0016241	0.30	0.80	10	128	regulation of macroautophagy	BP	1	TBK1,ATP6V1C1,UBQLN1,EXOC1,RAB3GAP1,SUPT5H,ATP6V0A2,LRRK2,ATP6V1A,RAB3GAP2	darkolivegreen	VSMC_M9
GO:0048660	0.30	0.81	9	124	regulation of smooth muscle cell proliferation	BP	1	WISP1,JAK2,ILK,THBS1,PTGS2,TPM1,MYOCD,ITGA2,BMPR2	darkolivegreen	VSMC_M9
GO:0008089	0.30	0.86	4	44	anterograde axonal transport	BP	1	KIF5B,TRAK1,TRAK2,KIF1B	darkolivegreen	VSMC_M9

GO:0042325	0.31	0.74	65	967	regulation of phosphorylation	BP	1	SOCS6,MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,SH3BP5L,ROCK2,INHBA,FYN,NOX4,RB1,CBLC,CCNT2,DNAJC3,OSBPL8,PIK3R4,CCNA1,ILK,ITGA5,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TMED2,PFN2,THBS1,ACVR1,NEDD9,CBLB,EHD4,LRRK2,IGF1R,CORO1C,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,TNFAIP8L3,DKK1,FAS,TLR6,SRCIN1,SRPX2,SMG8,MAP2K4,MYOCD,SEMA7A,PIN1,ROCK1,RICTOR,GADD45B,VAV2,RANBP2,BMPR2,CTGF,BDKRB2,LAMTOR3,PMEPA1,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:0034622	0.31	0.75	52	830	cellular protein-containing complex assembly	BP	1	STXBP5,CAND1,AKAP9,JAK2,SENP6,CENPC,COX18,ACTR2,TAF1B,DDX1,RPF2,RB1,PICALM,ACTR3,NDUFAF5,TUBGCP3,DHX29,EIF2S2,SMARCA5,BDP1,MAP1B,TMEM70,PFN2,RASA1,ARL6,DYRK1A,SPTBN5,NAP1L4,DNAJB14,CAMSAP2,HAUS2,HDGFL3,FASTKD2,EIF3J,VAMP4,VDAC2,TLR6,CLINT1,CYFIP2,CLTC,DICER1,FHOD3,RICTOR,SPIRE1,MYO1C,GTF2B,GEMIN6,OTUD6B,MZT1,PMEPA1,SRP19,NDUFAF4	darkolivegreen	VSMC_M9
GO:2001057	0.31	0.84	5	61	reactive nitrogen species metabolic process	BP	1	JAK2,ROCK2,TLR2,PTGS2,TLR6	darkolivegreen	VSMC_M9
GO:0050771	0.31	0.84	5	52	negative regulation of axonogenesis	BP	1	CDKL3,RNF6,SEMA5B,TRAK2,SEMA7A	darkolivegreen	VSMC_M9
GO:0010811	0.31	0.81	8	100	positive regulation of cell-substrate adhesion	BP	1	UTRN,JAK2,ILK,HSD17B12,NEDD9,IQGAP1,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:0061387	0.31	0.81	8	95	regulation of extent of cell growth	BP	1	CDKL3,ILK,RNF6,MAP1B,SEMA5B,SEMA7A,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0032388	0.31	0.79	13	173	positive regulation of intracellular transport	BP	1	JAK2,FYN,KIF5B,EDEM1,XPO4,RIOK2,ANK3,TPR,PTGS2,MSN,OAZ2,MYO1C,ZPR1	darkolivegreen	VSMC_M9
GO:0019058	0.31	0.78	17	239	viral life cycle	BP	1	CAV2,ROCK2,ITGB1,EEA1,ITGA5,CNOT7,ITCH,PDE12,AGTR1,KIAA1551,KPNA6,VAPB,NCAM1,ITGAV,ITGA2,VAPA,FCN1	darkolivegreen	VSMC_M9
GO:0048523	0.31	0.72	233	3647	negative regulation of cellular process	BP	1	SOCS6,LMAN1,MALT1,AHI1,RRM2B,CDKL3,CHADL,WISP1,UBQLN1,PTPRD,PLAA,TOPORS,TFPI2,JAK2,CLOCK,NPAS2,ASPN,ZNF451,HDAC9,STAP1,HOXA9,ZMPSTE24,UBE2J1,SH3BP5L,THAP5,TES,CAV2,ROCK2,INHBA,NOCT,ITGB1,FYN,ZEB1,RINT1,EXOSC9,PIWIL4,DNAJC1,NOX4,RB1,RTN2,PICALM,TRDMT1,CBLC,CGREF1,CAMK1D,MGAT5,GATA3,LRRC32,SUPT5H,DNAJC3,STK24,RIF1,OSBPL8,RPL26,UFM1,LIG4,MYO16,NR2C1,NDFIP1,CUL4A,STARD13,PDS5B,BRCA2,ILK,ITGA5,TMF1,SCYL2,PLPP1,CNOT7,RNF6,REM1,LYN,UBXN2B,MERTK,SACS,IPO7,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,ITCH,SULF1,USP47,CCDC125,XRN1,PDE12,FFAR4,MAP1B,APPL1,PI15,HK2,TLR2,PFN2,RASA1,BRAP,DCP1A,DHX36,THBS1,SHOX2,ACVR1,MTERF3,CBLB,ATP1A1,DYRK1A,SPTBN5,BRD7,LRRK2,TANK,TBX15,UBE3A,SLC39A10,CUL3,EIF4E,PHLDB2,TDP2,UCHL5,EPRS,IGF1R,CAMSAP2,CORO1C,ANOS1,ITPR2,NTRK3,WWC3,PTPN1,GRK3,LARP7,SEMA5B,IDH2,TRAK2,GPATCH3,SYCP2,LRRFIP1,ATF3,RBBP7,ANK3,TLK2,HDGFL3,TPR,PTGS2,IQCJ-SCHIP1,DNAJA4,SORCS2,NPAT,ITGAV,FERMT2,SKIL,PRRX1,RTN3,KIFAP3,SMURF1,CPEB2,VDAC2,BOD1L1,DKK1,FMN2,ATAD1,RGS7,FAS,AKT3,SRP9,TLR6,MAGED2,ADAM10,SRCIN1,BNIP2,TPM1,CLK2,TBX6,OAZ2,RLIM,MAGEE2,ZC3H14,TLE3,UACA,CLTC,DICER1,PPM1D,GPRASP1,FHOD3,MAP2K4,MYOCD,SEMA7A,ANXA6,PIN1,CCP110,RBBP8,BAG5,ROCK1,THOC1,ITGA1,BFAR,C1QTNF3,CIDEA,CD40LG,USP7,TBXA2R,PAFAH1B1,GADD45B,ENO1,WFDC1,RFWD3,PRKACB,THAP11,MIR186,BMPR2,FXYD5,PTPN12,FRY,ARF4,GDNF,CDK13,CTGF,BDKRB2,DNAJB9,NOV,PDCL,E2F3,PMEPA1,RAP	darkolivegreen	VSMC_M9
GO:0031146	0.31	0.85	4	44	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	BP	1	FBXO9,CUL4A,FBXL17,FBXL7	darkolivegreen	VSMC_M9
GO:0045596	0.31	0.75	34	489	negative regulation of cell differentiation	BP	1	CDKL3,CHADL,WISP1,HOXA9,INHBA,NOCT,ITGB1,ZEB1,RB1,GATA3,CUL4A,RNF6,LYN,EIF4E,CORO1C,NTRK3,SEMA5B,IDH2,TRAK2,ITGAV,FERMT2,SKIL,DKK1,TBX6,DICER1,MYOCD,SEMA7A,BMPR2,CDK13,NOV,WNT9A,TMEM119,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0043491	0.31	0.79	11	147	protein kinase B signaling	BP	1	ITGB1,GATA3,OSBPL8,ILK,MERTK,THBS1,IGF1R,NTRK3,FERMT2,TNFAIP8L3,RICTOR	darkolivegreen	VSMC_M9
GO:0010466	0.31	0.80	10	145	negative regulation of peptidase activity	BP	1	TFPI2,PICALM,USP47,PI15,THBS1,UCHL5,ANOS1,PTGS2,ROCK1,WFDC1	darkolivegreen	VSMC_M9
GO:0006753	0.31	0.76	25	387	nucleoside phosphate metabolic process	BP	1	RRM2B,ELOVL5,SUCLA2,ACPP,HSD17B12,PDE7A,TDG,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,IDH2,DERA,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0007610	0.31	0.76	29	406	behavior	BP	1	AHI1,EXT1,NPAS2,UBA6,ZMPSTE24,ACTR2,ITGB1,FYN,PICALM,DYNLRB1,TLR2,THBS1,GPR176,GCNT4,LRRK2,UBE3A,EIF4E,ZFX,GATM,PTGS2,SEPT5,DKK1,ATAD1,SRPX2,SLC1A3,PAFAH1B1,ARF4,GDNF,SHISA7	darkolivegreen	VSMC_M9
GO:0034332	0.31	0.85	4	39	adherens junction organization	BP	1	DCHS1,FERMT2,ADAM10,CDH11	darkolivegreen	VSMC_M9
GO:0033135	0.31	0.81	8	104	regulation of peptidyl-serine phosphorylation	BP	1	TBK1,AKAP9,PFN2,NTRK3,PTGS2,DKK1,RICTOR,BDKRB2	darkolivegreen	VSMC_M9
GO:0071496	0.31	0.77	19	267	cellular response to external stimulus	BP	1	STK24,PIK3R4,ATP2B1,LYN,EIF2AK3,GDAP1,ATP1A1,LRRK2,BRSK2,ATF3,PTGS2,FAS,PPM1D,MAP2K4,MYOCD,ITGA2,BMPR2,AQP3,C12orf66	darkolivegreen	VSMC_M9
GO:1903900	0.31	0.81	8	104	regulation of viral life cycle	BP	1	CAV2,CNOT7,PDE12,KIAA1551,KPNA6,VAPB,VAPA,FCN1	darkolivegreen	VSMC_M9

GO:0009892	0.31	0.72	144	2254	negative regulation of metabolic process	BP	1	TBK1,AZIN1,ETF1,PLAA,TFPI2,CLOCK,ZNF451,HDAC9,STAP1,ZMPSTE24,SH3BP5L,THAP5,ROCK2,INHBA,NOCT,FYN,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,RTN2,PICALM,TRDMT1,CBLC,UPF2,MGAT5,GATA3,LRRC32,NDFIP2,SUPT5H,DNAJC3,RIF1,ATP2B1,NR2C1,NDFIP1,BRCA2,ILK,TMF1,HOXC10,ERI1,CNOT7,LYN,MERTK,IPO7,EIF2AK3,TDG,TMED2,HCFC2,SMARCA5,ITCH,USP47,LNPEP,XRN1,PDE12,FFAR4,PI15,HK2,DCP1A,DHX36,THBS1,SHOX2,MTERF3,CBLB,ATP1A1,DYRK1A,BRD7,LRRK2,TBX15,CUL3,EIF4E,TDP2,UCHL5,KIAA1551,EPRS,CORO1C,ANOS1,NTRK3,WWC3,PTPN1,LARP7,GPATCH3,LRRFIP1,ATF3,RBBP7,TLK2,FASTKD2,TPR,PTGS2,MYEF2,NPAT,ITGAV,SKIL,PRRX1,RTN3,CPEB2,BOD1L1,DKK1,FMN2,SRP9,TLR6,MAGED2,ADAM10,SRCIN1,CLK2,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,SMG8,CLTC,DICER1,PPM1D,MYOCD,PIN1,RBBP8,BAG5,ROCK1,THOC1,C1QTNF3,CIDEA,GSPT1,ZC3H7A,USP7,LSM5,GADD45B,ENO1,ZDHHC7,WFDC1,THAP11,MIR186,BMPR2,FASTKD5,FRY,GDNF,CTGF,BDKRB2,PMEPA1,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0010976	0.32	0.79	11	140	positive regulation of neuron projection development	BP	1	ACTR2,FYN,CAMK1D,LYN,DHX36,NTRK3,IQGAP1,CREB3L2,PAFAH1B1,RAPGEF1,PLPPR5	darkolivegreen	VSMC_M9
GO:0007159	0.32	0.77	16	234	leukocyte cell-cell adhesion	BP	1	SOCS6,MALT1,EXT1,ITGB1,FYN,GATA3,LRRC32,NDFIP1,HSPH1,LYN,ITCH,NFKBIZ,CBLB,MSN,ROCK1,CD40LG	darkolivegreen	VSMC_M9
GO:0001819	0.32	0.76	21	304	positive regulation of cytokine production	BP	1	MALT1,TBK1,JAK2,ROCK2,DDX1,GATA3,TMF1,EIF2AK3,SULF1,APPL1,TLR2,DHX36,THBS1,LRRK2,KPNA6,PTGS2,TLR6,SEMA7A,C1QTNF3,CD40LG,FCN1	darkolivegreen	VSMC_M9
GO:0043254	0.32	0.76	25	361	regulation of protein-containing complex assembly	BP	1	STXBP5,CAND1,AKAP9,SENP6,ACTR2,MPP7,RB1,ACTR3,MAP1B,PFN2,RASA1,DYRK1A,SPTBN5,CAMSAP2,FERMT2,VDAC2,DKK1,TLR6,MSN,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C,PMEPA1	darkolivegreen	VSMC_M9
GO:0007051	0.32	0.78	12	165	spindle organization	BP	1	CEP120,HAUS6,SENP6,TUBGCP3,DCTN6,MAP9,INO80,HAUS2,NEK7,TPR,CLTC,MZT1	darkolivegreen	VSMC_M9
GO:0043244	0.32	0.80	9	107	regulation of protein-containing complex disassembly	BP	1	ETF1,ZMPSTE24,MAP1B,SPTBN5,IGF1R,CAMSAP2,HDGFL3,GSPT1,CFL2	darkolivegreen	VSMC_M9
GO:0030218	0.32	0.80	8	102	erythrocyte differentiation	BP	1	JAK2,INHBA,RB1,GATA3,JMJD6,UBA5,LYN,ABCB10	darkolivegreen	VSMC_M9
GO:1900024	0.32	0.85	4	44	regulation of substrate adhesion-dependent cell spreading	BP	1	ILK,NEDD9,CORO1C,FERMT2	darkolivegreen	VSMC_M9
GO:0008380	0.32	0.76	23	356	RNA splicing	BP	1	DDX46,KHDRBS3,PPIL1,DDX1,ZC3H13,JMJD6,MBNL2,PRPF40A,MTREX,MBNL1,SNRNP48,DYRK1A,LARP7,CLK1,CWC22,CLK2,HNRNPH2,THOC1,LSM5,ZNF326,CDK13,GEMIN6,ZPR1	darkolivegreen	VSMC_M9
GO:0031668	0.32	0.77	15	205	cellular response to extracellular stimulus	BP	1	STK24,PIK3R4,ATP2B1,LYN,EIF2AK3,GDAP1,LRRK2,BRSK2,ATF3,FAS,PPM1D,MYOCD,BMPR2,AQP3,C12orf66	darkolivegreen	VSMC_M9
GO:0002200	0.32	0.83	5	61	somatic diversification of immune receptors	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0033273	0.32	0.82	6	75	response to vitamin	BP	1	ATP2B1,MAP1B,GDAP1,PTGS2,ITGA2,AQP3	darkolivegreen	VSMC_M9
GO:0007127	0.32	0.81	7	94	meiosis I	BP	1	RMI1,CENPC,CCNA1,BRCA2,MYBL1,SYCP2,FMN2	darkolivegreen	VSMC_M9
GO:0033559	0.32	0.83	5	64	unsaturated fatty acid metabolic process	BP	1	PLAA,ELOVL5,PNPLA8,PTGS2,ELOVL4	darkolivegreen	VSMC_M9
GO:0060021	0.32	0.82	6	71	roof of mouth development	BP	1	INHBA,LRRC32,SOS1,FZD2,PRRX1,WNT7A	darkolivegreen	VSMC_M9
GO:0072521	0.32	0.76	21	319	purine-containing compound metabolic process	BP	1	ELOVL5,SUCLA2,ACPP,HSD17B12,PDE7A,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0006090	0.32	0.82	6	76	pyruvate metabolic process	BP	1	HK2,PGAM4,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0002377	0.32	0.82	6	81	immunoglobulin production	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0035249	0.32	0.83	5	57	synaptic transmission, glutamatergic	BP	1	EXT1,RAB3GAP1,LRRK2,PTGS2,ATAD1	darkolivegreen	VSMC_M9
GO:0009259	0.32	0.76	20	302	ribonucleotide metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,PDE7A,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0070997	0.32	0.76	20	288	neuron death	BP	1	TBK1,JAK2,FYN,RB1,PICALM,GATA3,LIG4,ILK,RASA1,LRRK2,CASP7,DKK1,FAS,TLR6,MAP2K4,PIN1,BAG5,ITGA1,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0002705	0.32	0.82	6	76	positive regulation of leukocyte mediated immunity	BP	1	MALT1,STAP1,DDX1,GATA3,RIF1,DHX36	darkolivegreen	VSMC_M9
GO:0003300	0.32	0.82	6	75	cardiac muscle hypertrophy	BP	1	ROCK2,ATP2A2,PDLIM5,MAP2K4,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:0002696	0.32	0.77	15	218	positive regulation of leukocyte activation	BP	1	MALT1,STAP1,FYN,GATA3,RIF1,HSPH1,LYN,THBS1,NFKBIZ,LRRK2,SLC39A10,SH3KBP1,TLR6,CD40LG,CLEC4D	darkolivegreen	VSMC_M9
GO:0050864	0.32	0.81	7	93	regulation of B cell activation	BP	1	INHBA,RIF1,NDFIP1,LYN,SLC39A10,SH3KBP1,THOC1	darkolivegreen	VSMC_M9
GO:0007611	0.32	0.77	14	183	learning or memory	BP	1	UBA6,ACTR2,ITGB1,FYN,PICALM,TLR2,UBE3A,GATM,PTGS2,DKK1,ATAD1,PAFAH1B1,ARF4,SHISA7	darkolivegreen	VSMC_M9
GO:0032890	0.32	0.84	4	47	regulation of organic acid transport	BP	1	ITGB1,RAB3GAP1,THBS1,EPRS	darkolivegreen	VSMC_M9
GO:0014065	0.32	0.79	9	111	phosphatidylinositol 3-kinase signaling	BP	1	JAK2,KBTBD2,FYN,GATA3,MYO16,UBE3A,IGF1R,NTRK3,PIP5K1A	darkolivegreen	VSMC_M9
GO:0033077	0.32	0.83	5	61	T cell differentiation in thymus	BP	1	GATA3,JMJD6,LIG4,SOS1,CD3G	darkolivegreen	VSMC_M9
GO:0043123	0.32	0.78	11	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	MALT1,TBK1,DDX1,FYN,NDFIP2,NDFIP1,DHX36,GPR89A,TLR6,VAPA,UBE2V1	darkolivegreen	VSMC_M9
GO:0060193	0.33	0.84	4	46	positive regulation of lipase activity	BP	1	PLAA,ARL1,AGTR1,ARF4	darkolivegreen	VSMC_M9
GO:0009132	0.33	0.80	7	94	nucleoside diphosphate metabolic process	BP	1	HK2,PGAM4,NUDT9,TPI1,HK3,PKM,ENO1	darkolivegreen	VSMC_M9

GO:1902533	0.33	0.73	48	731	positive regulation of intracellular signal transduction	BP	1	MALT1,TBK1,JAK2,CAV2,ROCK2,DDX1,ITGB1,FYN,GPR4,GATA3,NDFIP2,OSBPL8,RPL26,NDFIP1,SOS1,ILK,LYN,FFAR4,TLR2,DHX36,THBS1,LRRK2,UBE3A,IGF1R,GPR89A,NTRK3,PTPN1,IQGAP1,TPR,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,TNIK,TNFAIP8L3,DKK1,AKT3,TLR6,GPR65,SEMA7A,ROCK1,RICTOR,VAPA,GADD45B,CTGF,LAMTOR3,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0051236	0.33	0.78	10	138	establishment of RNA localization	BP	1	UPF2,NUP37,TOMM20,TPR,THOC1,NUP155,MYO1C,RANBP2,TOMM20L,NUP35	darkolivegreen	VSMC_M9
GO:0006163	0.33	0.75	20	302	purine nucleotide metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,PDE7A,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0072332	0.33	0.82	5	63	intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	RRM2B,TOPORS,RPL26,BRCA2,BDKRB2	darkolivegreen	VSMC_M9
GO:0048522	0.33	0.70	268	4212	positive regulation of cellular process	BP	1	LMAN1,MALT1,AHI1,UTRN,STXBP5,TBK1,CAND1,CEP120,AZIN1,THBS2,CDKL3,WISP1,CDC23,UBQLN1,PTPRD,PLAA,SLC30A9,TOPORS,ABCB4,AKAP9,JAK2,CLOCK,EXOC1,NPAS2,ELOVL5,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ACTR2,CAV2,ROCK2,INHBA,DDX1,NOCT,ITGB1,MPP7,FYN,ZEB1,KIF5B,EXOSC9,PSMC2,CEP295,GSAP,NOX4,GPR4,RB1,PICALM,CAMK1D,NUB1,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,TRAK1,NDFIP2,BRPF1,SUPT5H,DNAJC3,EDEM1,TNFAIP6,RIF1,OSBPL8,PPP1R12A,FAM98A,RPL26,CAPN7,LIG4,PIK3R4,CEBPZ,SMAD9,ATP11A,ACPP,NR2C1,NDFIP1,CUL4A,SOS1,BRCA2,ILK,ITGA5,HSPH1,TMF1,HOXC10,HSD17B12,DHX29,SCYL2,CNOT7,RNF6,LYN,UBXN2B,MERTK,XPO4,MYBL1,EIF2AK3,HCFC2,SMARCA5,ITCH,SULF1,RIOK2,USP47,PDE12,STOX2,MICAL2,FFAR4,MAP1B,APPL1,RDH10,LARP4,AGTR1,TLR2,PFN2,DCP1A,DHX36,THBS1,SHOX2,PGAM4,ACVR1,WDR75,SLC39A14,INO80,NFKBIZ,NEDD9,CBLB,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,ATP10A,UBE3A,SLC39A10,CUL3,EIF4E,PHLDB2,UCHL5,CHSY1,TIMM17A,KIAA1551,KPNA6,IGF1R,GPR89A,RAB3GAP2,CORO1C,NEK7,NTRK3,PTPN1,LARP7,ST8SIA1,SEMA5B,TAF5L,ABCB10,EIF2B5,GPATCH3,C2CD2L,ATF3,IQGAP1,ANK3,EDRF1,SH3KBP1,BCLAF3,NRP2,PITHD1,MBTPS2,KLHL18,FASTKD2,CREB3L2,TPR,CDC27,PTGS2,FZD2,IQCJ-SCHIP1,NPAT,ITGAV,FERMT2,SKIL,PRRX1,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,TNFAIP8L3,DKK1,FMN2,ATAD1,FAS,AKT3,WNT5B,TLR6,STIM2,ADAM10,MSN,SRCIN1,PHKG2,KCNMB1,TPM1,TRIP4,TBX6,OAZ2,CLPX,GPR65,ADAM19,CYFIP2,SRPX2,UACA,PKM,DICER1,ARMCX3,MAP2K4,MYOCD,SEMA7A,PIN1,SGK110,SGK	darkolivegreen	VSMC_M9
GO:0090501	0.33	0.79	9	124	RNA phosphodiester bond hydrolysis	BP	1	ELAC1,NOCT,EXOSC9,TOE1,ERI1,CNOT7,XRN1,PDE12,DICER1	darkolivegreen	VSMC_M9
GO:0071887	0.33	0.81	6	79	leukocyte apoptotic process	BP	1	LYN,MERTK,SLC39A10,CASP7,CD3G,FAS	darkolivegreen	VSMC_M9
GO:0042149	0.33	0.84	4	44	cellular response to glucose starvation	BP	1	PIK3R4,EIF2AK3,BRSK2,C12orf66	darkolivegreen	VSMC_M9
GO:0031929	0.33	0.80	8	105	TOR signaling	BP	1	FBXO9,CCDC88A,ZMPSTE24,GATA3,AKT3,RICTOR,LAMTOR3,C12orf66	darkolivegreen	VSMC_M9
GO:0055006	0.33	0.81	6	71	cardiac cell development	BP	1	ZMPSTE24,SHOX2,PDLIM5,FHOD3,MAP2K4,PIN1	darkolivegreen	VSMC_M9
GO:0046434	0.33	0.79	9	126	organophosphate catabolic process	BP	1	PNPLA8,GPCPD1,PDE7A,TDG,NUDT9,BPNT1,DERA,ACOT7,IMPA1	darkolivegreen	VSMC_M9
GO:0046324	0.33	0.84	4	44	regulation of glucose import	BP	1	RTN2,OSBPL8,APPL1,HK2	darkolivegreen	VSMC_M9
GO:0043436	0.33	0.73	42	677	oxoacid metabolic process	BP	1	CDO1,AZIN1,PLAA,ELOVL5,GNE,RARS2,GFPT1,PNPLA8,NOX4,SUCLA2,CYP27C1,ABHD1,DARS,HSD17B12,RDH10,PLOD2,HK2,ALDH18A1,TLR2,PGAM4,SLC35B3,MRS2,EPRS,BPNT1,IARS2,IDH2,NPL,GATM,PTGS2,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ETFA,SLC1A3,TARS,ACOT7,ENO1,ELOVL4,AKR1D1	darkolivegreen	VSMC_M9
GO:0001763	0.33	0.77	12	157	morphogenesis of a branching structure	BP	1	EXT1,HOXA11,NTN4,ILK,DCHS1,TMED2,SULF1,RDH10,SHOX2,ACVR1,LRRK2,GDNF	darkolivegreen	VSMC_M9
GO:0019637	0.33	0.72	47	743	organophosphate metabolic process	BP	1	SOCS6,RRM2B,PLAA,ELOVL5,UGP2,GFPT1,PNPLA8,SUCLA2,OSBPL8,GPCPD1,ACPP,HSD17B12,PLPP1,PDE7A,TDG,HK2,PGAM4,GPD2,NUDT9,SLC35B3,ETNK2,LRRK2,MBOAT1,ATP6V1A,BPNT1,ETNK1,IDH2,PIP5K1A,DERA,TPI1,PLD1,TNFAIP8L3,SAMD8,PAPSS2,ADSS,HK3,DLST,PKM,PIGW,PAFAH1B1,ACOT7,ENO1,PLPPR5,DPM2,IMPA1,DPM1,ELOVL4	darkolivegreen	VSMC_M9
GO:0140013	0.33	0.78	10	139	meiotic nuclear division	BP	1	RMI1,CENPC,ACTR2,ACTR3,CCNA1,BRCA2,MYBL1,SYCP2,FMN2,SPIRE1	darkolivegreen	VSMC_M9
GO:0051983	0.33	0.81	6	78	regulation of chromosome segregation	BP	1	CDC23,RB1,RIOK2,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0009887	0.33	0.72	54	784	animal organ morphogenesis	BP	1	AHI1,LRIG3,EXT1,TOPORS,ASPN,MYO6,HOXA9,HOXA11,ZMPSTE24,INHBA,GATA3,SOS1,NTN4,ILK,DCHS1,TMED2,SULF1,MICAL2,RDH10,SHOX2,ACVR1,IRX5,GCNT4,LRRK2,TBX15,CUL3,UCHL5,CHSY1,SYCP2,NRP2,FZD2,PRRX1,SMURF1,DKK1,ACTA2,AKT3,MSN,TPM1,TBX6,TLE3,ANXA6,ITGA2,GPC4,PAFAH1B1,COL11A1,BMPR2,AQP3,GDNF,CTGF,WNT9A,TMEM119,CHST11,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0019233	0.33	0.82	5	63	sensory perception of pain	BP	1	FYN,ACPP,PTGS2,ITGA2,NOV	darkolivegreen	VSMC_M9
GO:0038127	0.33	0.79	8	102	ERBB signaling pathway	BP	1	CCDC88A,CBLC,SOS1,CBLB,IQGAP1,ITGA1,PTPN12,ARF4	darkolivegreen	VSMC_M9
GO:0010827	0.33	0.82	5	58	regulation of glucose transmembrane transport	BP	1	RTN2,OSBPL8,FFAR4,APPL1,HK2	darkolivegreen	VSMC_M9
GO:0042176	0.33	0.74	23	342	regulation of protein catabolic process	BP	1	AZIN1,UBQLN1,FYN,PSMC2,NUB1,NDFIP1,TMF1,ITCH,CBLB,LRRK2,UBE3A,UCHL5,TLK2,PITHD1,SMURF1,FMN2,MSN,OAZ2,PIN1,BAG5,ROCK1,USP7,VGLL4	darkolivegreen	VSMC_M9
GO:1903051	0.34	0.83	4	50	negative regulation of proteolysis involved in cellular protein catabolic process	BP	1	UCHL5,TLK2,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0018107	0.34	0.79	8	98	peptidyl-threonine phosphorylation	BP	1	TBK1,ROCK2,ACVR1,DYRK1A,LRRK2,CLK1,CDC42BPA,ROCK1	darkolivegreen	VSMC_M9

GO:0043903	0.34	0.83	4	49	regulation of biological process involved in symbiotic interaction	BP	1	CAV2,ITGAV,VAPA,FCN1	darkolivegreen	VSMC_M9
GO:0051028	0.34	0.79	8	109	mRNA transport	BP	1	UPF2,NUP37,TPR,THOC1,NUP155,MYO1C,RANBP2,NUP35	darkolivegreen	VSMC_M9
GO:0002260	0.34	0.83	4	50	lymphocyte homeostasis	BP	1	SOS1,LYN,SKIL,FAS	darkolivegreen	VSMC_M9
GO:0042098	0.34	0.78	9	127	T cell proliferation	BP	1	MALT1,FYN,LRRC32,NDFIP1,SOS1,ITCH,CBLB,MSN,CD40LG	darkolivegreen	VSMC_M9
GO:0051402	0.34	0.76	14	198	neuron apoptotic process	BP	1	JAK2,FYN,RB1,GATA3,LIG4,ILK,RASA1,CASP7,FAS,MAP2K4,PIN1,ITGA1,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0044271	0.34	0.69	214	3436	cellular nitrogen compound biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,RRM2B,AZIN1,PHF20L1,ETF1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,NOA1,ELOVL5,EIF5B,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,ZEB1,EXOSC9,PIWIL4,DNAJC1,RB1,SUCLA2,PICALM,CAMK1D,ST3GAL3,ACTR3,GATA3,CCNT2,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,DNAJC3,SETD5,RIF1,PPP1R12A,RPL26,LIG4,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,HSD17B12,DHX29,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,TMED2,HCFC2,EIF2S2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,LARP4,ACTR8,CERS5,TLR2,LTN1,DCP1A,DHX36,THBS1,SHOX2,GFM1,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SLC35B3,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,EIF4E,TDP2,TROVE2,ATP6V1A,KPNA6,EPRS,IARS2,NEK7,MRPL47,WWC3,LARP7,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,EIF3J,TPR,PTGS2,MYEF2,FZD2,ZC3H15,NPAT,MYNN,GNPNAT1,SKIL,PRRX1,PLD1,CPEB2,SAMD8,DKK1,PAPSS2,ADSS,NOTCH3,SRP9,TLR6,MAGED2,TRIP4,TBX6,OAZ2,RLIM,MAGEE2,TLE3,PKM,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ITGA2,ZNF280C,GSPT1,TARS,MYSM1,CD40LG,USP7,ACOT7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,RFXAP,ELOVL4,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,EIF1AX,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0009914	0.34	0.75	15	212	hormone transport	BP	1	JAK2,CLOCK,INHBA,KIF5B,GATA3,TMF1,LYN,FFAR4,AGTR1,SNX19,BRSK2,CCDC186,C2CD2L,C1QTNF3,NOV	darkolivegreen	VSMC_M9
GO:1901654	0.34	0.77	11	151	response to ketone	BP	1	ABCB4,ROCK2,ATP2B1,XRN1,TLR2,THBS1,UBE3A,EIF4E,NTRK3,MSN,TBXA2R	darkolivegreen	VSMC_M9
GO:0046580	0.34	0.83	4	43	negative regulation of Ras protein signal transduction	BP	1	ITGB1,CCDC125,RASA1,CUL3	darkolivegreen	VSMC_M9
GO:0051604	0.34	0.75	15	230	protein maturation	BP	1	ZMPSTE24,CLN5,THBS1,NAA25,LRRK2,TIMM17A,CASP7,ADAM10,ADAM19,CYFIP2,AFG3L2,PMPCA,ENO1,PRKACB,NAA20	darkolivegreen	VSMC_M9
GO:0001947	0.34	0.83	4	45	heart looping	BP	1	AHI1,TMED2,MICAL2,TBX6	darkolivegreen	VSMC_M9
GO:0097479	0.34	0.83	4	46	synaptic vesicle localization	BP	1	KIF5B,PICALM,LRRK2,BRSK2	darkolivegreen	VSMC_M9
GO:0001933	0.34	0.74	19	276	negative regulation of protein phosphorylation	BP	1	SH3BP5L,RB1,CBLC,DNAJC3,ILK,LYN,IPO7,TMED2,CBLB,LRRK2,CORO1C,NTRK3,PTPN1,DKK1,SRCIN1,MYOCD,GADD45B,BDKRB2,PMEPA1	darkolivegreen	VSMC_M9
GO:0060191	0.34	0.81	5	63	regulation of lipase activity	BP	1	PLAA,HDAC9,ARL1,AGTR1,ARF4	darkolivegreen	VSMC_M9
GO:0048518	0.34	0.68	287	4533	positive regulation of biological process	BP	1	LMAN1,MALT1,AHI1,UTRN,STXBP5,TBK1,CAND1,CEP120,AZIN1,THBS2,CDKL3,WISP1,CDC23,UBQLN1,PTPRD,PLAA,SLC30A9,TOPORS,ABCB4,AKAP9,JAK2,CLOCK,EXOC1,NPAS2,ELOVL5,ZNF451,HDAC9,CAVIN4,PSME4,MYO6,STAP1,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,CAV2,ROCK2,INHBA,DDX1,NOCT,RAB3B,ITGB1,MPP7,FYN,ZEB1,KIF5B,EXOSC9,PSMC2,CEP295,GSAP,NOX4,GPR4,RB1,PICALM,CAMK1D,NUB1,ACTR3,MGAT5,GATA3,CCNT2,RAB3GAP1,JMJD6,TRAK1,LRRC32,NDFIP2,BRPF1,SUPT5H,DNAJC3,EDEM1,TNFAIP6,RIF1,OSBPL8,PPP1R12A,FAM98A,RPL26,CAPN7,LIG4,PIK3R4,CEBPZ,ATP2B1,SMAD9,ATP11A,ACPP,NR2C1,NDFIP1,CUL4A,SOS1,BRCA2,ILK,ITGA5,HSPH1,TMF1,HOXC10,HSD17B12,DHX29,SCYL2,CNOT7,RNF6,LYN,UBXN2B,MERTK,XPO4,MYBL1,EIF2AK3,TMED2,HCFC2,SMARCA5,ITCH,SULF1,RIOK2,USP47,PDE12,STOX2,MICAL2,FFAR4,MAP1B,APPL1,RDH10,LARP4,AGTR1,HK2,TLR2,PFN2,ATP2A2,DCP1A,DHX36,THBS1,SHOX2,PGAM4,ACVR1,WDR75,SLC39A14,INO80,NFKBIZ,NEDD9,CBLB,ATP1A1,DYRK1A,BRD7,EHD4,ERG,LRRK2,TANK,ATP10A,UBE3A,SLC39A10,CUL3,EIF4E,PHLDB2,UCHL5,CHSY1,TIMM17A,KIAA1551,KPNA6,IGF1R,GPR89A,RAB3GAP2,CORO1C,NEK7,NTRK3,PTPN1,LARP7,ST8SIA1,SEMA5B,VAPB,TAF5L,ABCB10,EIF2B5,GPATCH3,C2CD2L,ATF3,IQGAP1,ANK3,OSBPL11,EDRF1,ADAM12,SH3KBP1,BCLAF3,NRP2,PITHD1,MBTPS2,KLHL18,FASTKD2,CREB3L2,TPR,CDC27,GATM,PTGS2,FZD2,IQCJ-SCHIP1,DNAJA4,NPAT,ITGAV,FERMT2,SKIL,PRRX1,KIFAP3,SMURF1,TAPT1,TNIK,PLD1,TNFAIP8L3,DKK1,FMN2,ATAD1,ACTA2,FAS,AKT3,WNT5B,TLR6,STIM2,ADAM9,MSN,CORO1A,RHOC,KCNMA1,TRIM4,TRIM47,TBX6	darkolivegreen	VSMC_M9
GO:0014897	0.35	0.80	6	77	striated muscle hypertrophy	BP	1	ROCK2,ATP2A2,PDLIM5,MAP2K4,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:0070059	0.35	0.83	4	50	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP	1	EIF2AK3,LRRK2,BRSK2,PTPN1	darkolivegreen	VSMC_M9
GO:0009615	0.35	0.74	17	253	response to virus	BP	1	TBK1,EXT1,EXOC1,ZMPSTE24,CHRM2,DDX1,GATA3,DNAJC3,CNOT7,ITCH,PDE12,TLR2,DHX36,GPATCH3,ACTA2,ENO1,NDUFAF4	darkolivegreen	VSMC_M9
GO:0007368	0.35	0.79	7	90	determination of left/right symmetry	BP	1	AHI1,ALG5,TMED2,MICAL2,ARL6,ACVR1,TBX6	darkolivegreen	VSMC_M9
GO:0034637	0.35	0.81	5	63	cellular carbohydrate biosynthetic process	BP	1	EXT1,UGP2,CSGALNACT2,PHKG2,IMPA1	darkolivegreen	VSMC_M9
GO:0042770	0.35	0.76	11	155	signal transduction in response to DNA damage	BP	1	CLOCK,MYO6,ZMPSTE24,RINT1,RPL26,CUL4A,BRCA2,DYRK1A,PPM1D,THOC1,RFWD3	darkolivegreen	VSMC_M9

GO:0031050	0.35	0.82	4	46	dsRNA processing	BP	1	ZMPSTE24,DICER1,MYOCD,ZC3H7A	darkolivegreen	VSMC_M9
GO:0035196	0.35	0.82	4	46	production of miRNAs involved in gene silencing by miRNA	BP	1	ZMPSTE24,DICER1,MYOCD,ZC3H7A	darkolivegreen	VSMC_M9
GO:0070918	0.35	0.82	4	46	production of small RNA involved in gene silencing by RNA	BP	1	ZMPSTE24,DICER1,MYOCD,ZC3H7A	darkolivegreen	VSMC_M9
GO:0097306	0.35	0.80	6	71	cellular response to alcohol	BP	1	INHBA,ATP2B1,GRAMD1A,XRN1,ITPR2,KCNMB1	darkolivegreen	VSMC_M9
GO:0072330	0.35	0.76	10	144	monocarboxylic acid biosynthetic process	BP	1	ELOVL5,PNPLA8,ABHD1,HSD17B12,RDH10,GATM,PTGS2,ACOT7,ELOVL4,AKR1D1	darkolivegreen	VSMC_M9
GO:0010596	0.35	0.82	4	48	negative regulation of endothelial cell migration	BP	1	STARD13,THBS1,DNAJA4,TBXA2R	darkolivegreen	VSMC_M9
GO:0001666	0.35	0.74	17	244	response to hypoxia	BP	1	UBQLN1,ROCK2,NOX4,PLOD2,HK2,TLR2,THBS1,ITPR2,PTGS2,CPEB2,FMN2,KCNMB1,MYOCD,PIN1,ITGA2,ENO1,AQP3	darkolivegreen	VSMC_M9
GO:1904375	0.35	0.78	8	107	regulation of protein localization to cell periphery	BP	1	ITGB1,KIF5B,PICALM,APPL1,ADAM10,CLTC,GPC4,ZDHHC7	darkolivegreen	VSMC_M9
GO:0060341	0.35	0.71	45	675	regulation of cellular localization	BP	1	LMAN1,GCC2,JAK2,CCDC88A,UBE2J1,ROCK2,ITGB1,FYN,RINT1,KIF5B,RB1,PICALM,EDEM1,PPP1R12A,UFM1,YIPF5,LYN,UBXN2B,XPO4,EIF2AK3,RIOK2,MAP1B,APPL1,DHX36,LRRK2,BRSK2,PTPN1,LARP7,C2CD2L,IQGAP1,ANK3,TPR,PTGS2,FERMT2,ADAM10,MSN,OAZ2,CLTC,PIN1,GPC4,USP7,MYO1C,ZDHHC7,ZPR1,SHISA7	darkolivegreen	VSMC_M9
GO:0042303	0.35	0.79	6	75	molting cycle	BP	1	EXT1,CLOCK,ZMPSTE24,INHBA,SOS1,PTGS2	darkolivegreen	VSMC_M9
GO:0042633	0.35	0.79	6	75	hair cycle	BP	1	EXT1,CLOCK,ZMPSTE24,INHBA,SOS1,PTGS2	darkolivegreen	VSMC_M9
GO:0048584	0.35	0.69	95	1488	positive regulation of response to stimulus	BP	1	MALT1,TBK1,WISP1,UBQLN1,JAK2,CLOCK,NPAS2,STAP1,CCDC88A,ACTR2,CAV2,ROCK2,INHBA,DDX1,ITGB1,FYN,GPR4,CAMK1D,MGAT5,GATA3,NDFIP2,RIF1,OSBPL8,RPL26,ACPP,NR2C1,NDFIP1,SOS1,ILK,ITGA5,LYN,SULF1,USP47,FFAR4,APPL1,AGTR1,TLR2,DHX36,THBS1,SHOX2,ACVR1,SLC39A14,NFKBIZ,CBLB,LRRK2,UBE3A,SLC39A10,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,PTPN1,EIF2B5,ATF3,IQGAP1,TPR,PTGS2,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,PRRX1,TNIK,TNFAIP8L3,DKK1,FMN2,FAS,AKT3,WNT5B,TLR6,ADAM10,GPR65,CYFIP2,MYOCD,SEMA7A,PIN1,ROCK1,ITGA2,RICTOR,VAPA,SPIRE1,MYO1C,TBXA2R,PAFAH1B1,GADD45B,VAV2,BMPR2,CTGF,LAMTOR3,NOV,PDCL,FCN1,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0014896	0.35	0.79	6	78	muscle hypertrophy	BP	1	ROCK2,ATP2A2,PDLIM5,MAP2K4,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:1901292	0.35	0.80	5	69	nucleoside phosphate catabolic process	BP	1	PDE7A,TDG,NUDT9,DERA,ACOT7	darkolivegreen	VSMC_M9
GO:0061041	0.35	0.78	7	96	regulation of wound healing	BP	1	WISP1,ITGB1,THBS1,PHLDB2,FERMT2,TBXA2R,WFDC1	darkolivegreen	VSMC_M9
GO:0046328	0.35	0.77	8	104	regulation of JNK cascade	BP	1	ITCH,IGF1R,TNIK,PAFAH1B1,GADD45B,CTGF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0042246	0.35	0.82	4	53	tissue regeneration	BP	1	KPNA1,PTPN12,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0106106	0.35	0.77	9	123	cold-induced thermogenesis	BP	1	JAK2,RB1,HOXC10,LNPEP,FFAR4,IGF1R,GATM,TLE3,CIDEA	darkolivegreen	VSMC_M9
GO:0120161	0.35	0.77	9	123	regulation of cold-induced thermogenesis	BP	1	JAK2,RB1,HOXC10,LNPEP,FFAR4,IGF1R,GATM,TLE3,CIDEA	darkolivegreen	VSMC_M9
GO:0043266	0.35	0.80	5	59	regulation of potassium ion transport	BP	1	AKAP9,ITGB1,KIF5B,ANK3,KCNMB1	darkolivegreen	VSMC_M9
GO:0016070	0.36	0.67	214	3480	RNA metabolic process	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,WDR46,DDX46,PHF20L1,KHDRBS3,ETF1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,POLR2B,ZNF451,TRMO,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,ACTR2,THAP5,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,ZEB1,EXOSC9,PIWIL4,RB1,PICALM,ZC3H13,TRDMT1,TOE1,TSN,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,MBNL2,RIF1,PPP1R12A,PRPF40A,RPL26,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,MTREX,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,U2SURP,ACTR8,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SNRNP48,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,PUS3,TROVE2,KPNA6,RRP15,EPRS,IARS2,WWC3,LARP7,CLK1,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,MYNN,SKIL,DTWD1,PRRX1,DKK1,RBM47,NOTCH3,TLR6,MAGED2,CLK2,TRIP4,TBX6,RLIM,MAGEE2,INTS14,ZC3H14,RBBP6,TLE3,SMG8,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,GSPT1,TARS,ZC3H7A,MYSM1,CD40LG,USP7,LSM5,ENO1,DNTTIP2,ZNF644,ZNF326,GTF2B,THAP11,SNORA21,SNORA3A,BMPR2,FASTKD5,ZNF654,INTS6,SNORA51,SNORD27,SNORD71,ANKRD49,ARF4,GDNF,CDK13,GEMIN6,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0070534	0.36	0.82	4	50	protein K63-linked ubiquitination	BP	1	PLAA,ITCH,BFAR,UBE2V1	darkolivegreen	VSMC_M9
GO:0071426	0.36	0.80	5	66	ribonucleoprotein complex export from nucleus	BP	1	UPF2,RIOK2,TPR,THOC1,NUP155	darkolivegreen	VSMC_M9
GO:0070302	0.36	0.75	11	151	regulation of stress-activated protein kinase signaling cascade	BP	1	ZMPSTE24,LYN,ITCH,IGF1R,TNIK,FAS,PAFAH1B1,GADD45B,CTGF,RAP2A,WNT7A	darkolivegreen	VSMC_M9

GO:0006139	0.36	0.67	261	4274	nucleobase-containing compound metabolic process	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,RRM2B,WDR46,DDX46,PHF20L1,KHDRBS3,ETF1,RMI1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,GNE,ZNF451,TRMO,HDAC9,CAVIN4,PSME4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,ZEB1,EXOSC9,PIWIL4,UGGT1,RB1,SUCLA2,PICALM,ZC3H13,TRDMT1,TOE1,TSN,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,ORC4,MBNL2,RIF1,PPP1R12A,PRPF40A,RPL26,LIG4,CEBPZ,SUPT20H,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,HSD17B12,PARG,MTREX,CNOT7,RNF6,PDE7A,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,U2SURP,ACTR8,HK2,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,PGAM4,ACVR1,WDR75,IRX5,MTERF3,INO80,NUDT9,SNRNP48,SLC35B3,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,NFRKB,CUL3,TDP2,PUS3,TROVE2,UCHL5,ATP6V1A,KPNA6,RRP15,EPRS,BPNT1,IARS2,NEK7,WWC3,LARP7,KPNA1,CLK1,IDH2,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,DERA,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,TPI1,MYNN,GNPNAT1,SKIL,DTWD1,PRRX1,BOD1L1,DKK1,FMN2,PAPSS2,ADSS,RBM47,NOTCH3,TLR6,MAGED2,HK3,CLK2,DLST,TRIP4,TBX6,RLIM,MAGEE2,INTS14,ZC3H14,RBBP6,TLE3,SMG8,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,CIDEA,SPIRE1,GSPT1,TARS,ZC3H7A,MYSM1,CD40LG,USP7,LSM5,ACOT7,ENO1,RFWD3,DNTTIP2,ZNF644,ZNF326,	darkolivegreen	VSMC_M9
GO:0046394	0.36	0.74	14	213	carboxylic acid biosynthetic process	BP	1	ELOVL5,PNPLA8,SUCLA2,ABHD1,HSD17B12,RDH10,PLOD2,ALDH18A1,GATM,PTGS2,SLC1A3,ACOT7,ELOVL4,AKR1D1	darkolivegreen	VSMC_M9
GO:0051249	0.36	0.73	19	287	regulation of lymphocyte activation	BP	1	SOCS6,MALT1,INHBA,FYN,GATA3,LRRC32,RIF1,NDFIP1,SOS1,HSPH1,LYN,MERTK,ITCH,NFKBIZ,CBLB,SLC39A10,SH3KBP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0061982	0.36	0.78	7	99	meiosis I cell cycle process	BP	1	RMI1,CENPC,CCNA1,BRCA2,MYBL1,SYCP2,FMN2	darkolivegreen	VSMC_M9
GO:0042472	0.36	0.79	6	73	inner ear morphogenesis	BP	1	LRIG3,MYO6,GATA3,FZD2,PRRX1,COL11A1	darkolivegreen	VSMC_M9
GO:2001022	0.36	0.78	7	95	positive regulation of response to DNA damage stimulus	BP	1	NPAS2,ACTR2,RIF1,RPL26,SKIL,FMN2,SPIRE1	darkolivegreen	VSMC_M9
GO:1904951	0.36	0.73	18	257	positive regulation of establishment of protein localization	BP	1	CEP120,JAK2,EXOC1,FYN,KIF5B,CEP295,EDEM1,XPO4,TLR2,C2CD2L,ANK3,TPR,PTGS2,OAZ2,MYOM1,C1QTNF3,MYO1C,ZPR1	darkolivegreen	VSMC_M9
GO:0002312	0.36	0.80	5	64	B cell activation involved in immune response	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0001658	0.36	0.82	4	47	branching involved in ureteric bud morphogenesis	BP	1	HOXA11,ILK,DCHS1,GDNF	darkolivegreen	VSMC_M9
GO:0045739	0.36	0.80	5	66	positive regulation of DNA repair	BP	1	NPAS2,ACTR2,RIF1,FMN2,SPIRE1	darkolivegreen	VSMC_M9
GO:0051050	0.36	0.70	44	660	positive regulation of transport	BP	1	AHI1,STXBP5,AZIN1,PLAA,ABCB4,AKAP9,JAK2,EXOC1,STAP1,INHBA,RAB3B,ITGB1,FYN,KIF5B,CAMK1D,RAB3GAP1,EDEM1,OSBPL8,ATP2B1,TMF1,SCYL2,MERTK,XPO4,RIOK2,FFAR4,APPL1,TLR2,LRRK2,C2CD2L,ANK3,TPR,PTGS2,ATAD1,STIM2,MSN,KCNMB1,OAZ2,ITGA2,MYOM1,RAB31,C1QTNF3,MYO1C,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0030032	0.36	0.80	5	61	lamellipodium assembly	BP	1	CCDC88A,ACTR2,ITGB1,ACTR3,VAV2	darkolivegreen	VSMC_M9
GO:0099111	0.36	0.75	12	165	microtubule-based transport	BP	1	KIF5B,TRAK1,IFT88,MAP1B,TRAK2,KIFAP3,ACTR10,ARMCX3,PAFAH1B1,KIF1B,SSX2IP,RAB6A	darkolivegreen	VSMC_M9
GO:0120192	0.36	0.81	4	48	tight junction assembly	BP	1	ROCK2,MPP7,ROCK1,MYO1C	darkolivegreen	VSMC_M9
GO:0031102	0.36	0.81	4	49	neuron projection regeneration	BP	1	JAK2,STK24,MAP1B,PRRX1	darkolivegreen	VSMC_M9
GO:0043255	0.36	0.79	6	78	regulation of carbohydrate biosynthetic process	BP	1	SLC35B4,CLK2,CLTC,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9
GO:0035914	0.36	0.81	4	48	skeletal muscle cell differentiation	BP	1	RB1,ATF3,MYOCD,FOXN2	darkolivegreen	VSMC_M9
GO:0070227	0.36	0.81	4	52	lymphocyte apoptotic process	BP	1	LYN,SLC39A10,CD3G,FAS	darkolivegreen	VSMC_M9
GO:0001764	0.36	0.76	9	113	neuron migration	BP	1	LRP12,PLAA,FYN,GATA3,MAP1B,DNER,NTRK3,NRP2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0009880	0.36	0.81	4	47	embryonic pattern specification	BP	1	TMED2,NRP2,TBX6,WNT7A	darkolivegreen	VSMC_M9
GO:0007254	0.36	0.75	10	134	JNK cascade	BP	1	ITCH,LRRK2,IGF1R,TNIK,MAP2K4,PAFAH1B1,GADD45B,CTGF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0002253	0.36	0.74	13	191	activation of immune response	BP	1	MALT1,TBK1,STAP1,FYN,GATA3,LYN,APPL1,NFKBIZ,CBLB,SLC39A10,EIF2B5,VAV2,FCN1	darkolivegreen	VSMC_M9
GO:0045834	0.36	0.77	8	109	positive regulation of lipid metabolic process	BP	1	ELOVL5,PIK3R4,LYN,RDH10,AGTR1,PTGS2,TNFAIP8L3,VAV2	darkolivegreen	VSMC_M9
GO:0000281	0.36	0.80	5	63	mitotic cytokinesis	BP	1	ROCK2,RASA1,MAP9,ANK3,ROCK1	darkolivegreen	VSMC_M9
GO:0051607	0.37	0.74	12	174	defense response to virus	BP	1	TBK1,EXOC1,ZMPSTE24,DDX1,DNAJC3,CNOT7,ITCH,PDE12,TLR2,DHX36,GPATCH3,NDUFAF4	darkolivegreen	VSMC_M9
GO:0140546	0.37	0.74	12	174	defense response to symbiont	BP	1	TBK1,EXOC1,ZMPSTE24,DDX1,DNAJC3,CNOT7,ITCH,PDE12,TLR2,DHX36,GPATCH3,NDUFAF4	darkolivegreen	VSMC_M9
GO:0071166	0.37	0.79	5	67	ribonucleoprotein complex localization	BP	1	UPF2,RIOK2,TPR,THOC1,NUP155	darkolivegreen	VSMC_M9
GO:0045785	0.37	0.72	21	306	positive regulation of cell adhesion	BP	1	MALT1,UTRN,JAK2,FYN,GATA3,ILK,HSPH1,HSD17B12,LYN,NFKBIZ,NEDD9,IQGAP1,ANK3,ITGAV,FERMT2,KIFAP3,TPM1,ADAM19,ROCK1,ITGA2,CD40LG	darkolivegreen	VSMC_M9
GO:0019693	0.37	0.72	20	312	ribose phosphate metabolic process	BP	1	ELOVL5,SUCLA2,HSD17B12,PDE7A,HK2,PGAM4,NUDT9,SLC35B3,LRRK2,ATP6V1A,BPNT1,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0060113	0.37	0.81	4	48	inner ear receptor cell differentiation	BP	1	MYO6,IFT88,FZD2,PAFAH1B1	darkolivegreen	VSMC_M9

GO:0065004	0.37	0.75	9	132	protein-DNA complex assembly	BP	1	CAND1,SENP6,CENPC,TAF1B,RB1,SMARCA5,BDP1,NAP1L4,GTF2B	darkolivegreen	VSMC_M9
GO:0006469	0.37	0.74	12	172	negative regulation of protein kinase activity	BP	1	SH3BP5L,RB1,CBLC,ILK,LYN,IPO7,CBLB,CORO1C,PTPN1,SRCIN1,MYOCD,GADD45B	darkolivegreen	VSMC_M9
GO:0031669	0.37	0.74	13	182	cellular response to nutrient levels	BP	1	STK24,PIK3R4,ATP2B1,EIF2AK3,GDAP1,LRRK2,BRSK2,ATF3,FAS,PPM1D,BMPR2,AQP3,C12orf66	darkolivegreen	VSMC_M9
GO:0030500	0.37	0.79	5	62	regulation of bone mineralization	BP	1	ZMPSTE24,ATP2B1,ACVR1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0010810	0.37	0.74	13	175	regulation of cell-substrate adhesion	BP	1	UTRN,JAK2,ROCK2,ILK,HSD17B12,RASA1,THBS1,NEDD9,PHLDB2,CORO1C,IQGAP1,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:0033002	0.37	0.74	12	174	muscle cell proliferation	BP	1	WISP1,JAK2,ILK,THBS1,KPNA1,PTGS2,TPM1,MYOCD,ITGA2,BMPR2,NOV,VGLL4	darkolivegreen	VSMC_M9
GO:0006914	0.37	0.70	30	450	autophagy	BP	1	TBK1,ATP6V1C1,UBQLN1,PLAA,EXOC1,ZMPSTE24,RAB3GAP1,SUPT5H,STAM2,VPS36,UFM1,PIK3R4,SUPT20H,UBA5,UBXN2B,GRAMD1A,ATP6V0A2,TMEM41B,IFT88,HK2,ATP2A2,LRRK2,ATP6V1A,RAB3GAP2,TLK2,SMURF1,CLTC,ATG4D,TRAPPC8,ROCK1	darkolivegreen	VSMC_M9
GO:0061919	0.37	0.70	30	450	process utilizing autophagic mechanism	BP	1	TBK1,ATP6V1C1,UBQLN1,PLAA,EXOC1,ZMPSTE24,RAB3GAP1,SUPT5H,STAM2,VPS36,UFM1,PIK3R4,SUPT20H,UBA5,UBXN2B,GRAMD1A,ATP6V0A2,TMEM41B,IFT88,HK2,ATP2A2,LRRK2,ATP6V1A,RAB3GAP2,TLK2,SMURF1,CLTC,ATG4D,TRAPPC8,ROCK1	darkolivegreen	VSMC_M9
GO:0002718	0.37	0.79	5	63	regulation of cytokine production involved in immune response	BP	1	MALT1,DDX1,GATA3,DHX36,SEMA7A	darkolivegreen	VSMC_M9
GO:0002699	0.37	0.75	10	142	positive regulation of immune effector process	BP	1	MALT1,STAP1,DDX1,GATA3,RIF1,LYN,DHX36,NFKBIZ,SEMA7A,DNAJB9	darkolivegreen	VSMC_M9
GO:0006261	0.37	0.75	10	137	DNA-dependent DNA replication	BP	1	RRM2B,ZMPSTE24,ORC4,BRCA2,INO80,BAZ1A,BOD1L1,THOC1,RFWD3,ZPR1	darkolivegreen	VSMC_M9
GO:0061371	0.37	0.81	4	47	determination of heart left/right asymmetry	BP	1	AHI1,TMED2,MICAL2,TBX6	darkolivegreen	VSMC_M9
GO:2000116	0.37	0.74	11	167	regulation of cysteine-type endopeptidase activity	BP	1	MALT1,JAK2,FYN,EIF2AK3,USP47,THBS1,PTGS2,FAS,CYFIP2,UACA,CTGF	darkolivegreen	VSMC_M9
GO:0021761	0.37	0.78	6	75	limbic system development	BP	1	UBA6,KIF5B,RAB3GAP1,EIF2B5,NRP2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0045123	0.37	0.80	4	50	cellular extravasation	BP	1	EXT1,ITGB1,ROCK1,ITGA1	darkolivegreen	VSMC_M9
GO:0006520	0.37	0.73	14	224	cellular amino acid metabolic process	BP	1	CDO1,AZIN1,RARS2,GFPT1,NOX4,DARS,PLOD2,ALDH18A1,EPRS,IARS2,ADSS,DLST,SLC1A3,TARS	darkolivegreen	VSMC_M9
GO:0086001	0.37	0.79	5	58	cardiac muscle cell action potential	BP	1	AKAP9,ATP2A2,ATP1A1,ANK3,NUP155	darkolivegreen	VSMC_M9
GO:0016197	0.38	0.72	15	209	endosomal transport	BP	1	GCC2,PICALM,CLN5,VPS36,EEA1,ARL1,EHD4,LRRK2,TRAPPC10,CORO1C,HEATR5A,VAMP4,CLTC,USP7,RAB6A	darkolivegreen	VSMC_M9
GO:0042509	0.38	0.80	4	52	regulation of tyrosine phosphorylation of STAT protein	BP	1	JAK2,FYN,CNOT7,LYN	darkolivegreen	VSMC_M9
GO:0001938	0.38	0.77	6	78	positive regulation of endothelial cell proliferation	BP	1	CAV2,AGTR1,NRP2,AKT3,RICTOR,BMPR2	darkolivegreen	VSMC_M9
GO:0050708	0.38	0.73	14	200	regulation of protein secretion	BP	1	STXBP5,JAK2,CLOCK,EXOC1,KIF5B,DNAJC1,TLR2,BRSK2,IDH2,C2CD2L,SRCIN1,MYOM1,C1QTNF3,NOV	darkolivegreen	VSMC_M9
GO:0006935	0.38	0.70	29	426	chemotaxis	BP	1	EXT1,STAP1,FYN,KIF5B,CAMK1D,GATA3,SOS1,LYN,PALLD,AGTR1,THBS1,ANOS1,NTRK3,SEMA5B,PIP5K1A,NRP2,NCAM1,ITGAV,PLD1,PLP2,NOTCH3,ENAH,ADAM10,SEMA7A,ITGA2,ITGA1,BMPR2,GDNF,NOV	darkolivegreen	VSMC_M9
GO:0010906	0.38	0.76	7	96	regulation of glucose metabolic process	BP	1	SLC35B4,ZMPSTE24,PHKG2,CLK2,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9
GO:0006082	0.38	0.68	42	689	organic acid metabolic process	BP	1	CDO1,AZIN1,PLAA,ELOVL5,GNE,RARS2,GFPT1,PNPLA8,NOX4,SUCLA2,CYP27C1,ABHD1,DARS,HSD17B12,RDH10,PLOD2,HK2,ALDH18A1,TLR2,PGAM4,SLC35B3,MRS2,EPRS,BPNT1,IARS2,IDH2,NPL,GATM,PTGS2,TPI1,PAPSS2,ADSS,HK3,DLST,PKM,ETFA,SLC1A3,TARS,ACOT7,ENO1,ELOVL4,AKR1D1	darkolivegreen	VSMC_M9
GO:0002367	0.38	0.78	5	64	cytokine production involved in immune response	BP	1	MALT1,DDX1,GATA3,DHX36,SEMA7A	darkolivegreen	VSMC_M9
GO:0048278	0.38	0.80	4	50	vesicle docking	BP	1	CAV2,RAB3B,CEP83,USO1	darkolivegreen	VSMC_M9
GO:0031400	0.38	0.69	28	426	negative regulation of protein modification process	BP	1	PLAA,ZNF451,SH3BP5L,ROCK2,FYN,RB1,CBLC,MGAT5,DNAJC3,ILK,LYN,IPO7,TMED2,CBLB,LRRK2,CORO1C,NTRK3,PTPN1,BOD1L1,DKK1,SRCIN1,MYOCD,BAG5,ROCK1,GADD45B,FRY,BDKRB2,PMEPA1	darkolivegreen	VSMC_M9
GO:0009306	0.38	0.71	18	266	protein secretion	BP	1	STXBP5,JAK2,CLOCK,EXOC1,RAB3B,KIF5B,DNAJC1,TLR2,SNX19,BRSK2,CCDC186,IDH2,C2CD2L,SRCIN1,MYOM1,C1QTNF3,PAFAH1B1,NOV	darkolivegreen	VSMC_M9
GO:0035592	0.38	0.71	18	266	establishment of protein localization to extracellular region	BP	1	STXBP5,JAK2,CLOCK,EXOC1,RAB3B,KIF5B,DNAJC1,TLR2,SNX19,BRSK2,CCDC186,IDH2,C2CD2L,SRCIN1,MYOM1,C1QTNF3,PAFAH1B1,NOV	darkolivegreen	VSMC_M9
GO:0030278	0.38	0.76	7	91	regulation of ossification	BP	1	ZMPSTE24,ATP2B1,ACVR1,CHSY1,DKK1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0010951	0.38	0.74	9	137	negative regulation of endopeptidase activity	BP	1	TFPI2,PICALM,USP47,THBS1,UCHL5,ANOS1,PTGS2,ROCK1,WFDC1	darkolivegreen	VSMC_M9
GO:0003231	0.38	0.75	8	101	cardiac ventricle development	BP	1	ZMPSTE24,GATA3,ACVR1,FZD2,TPM1,MYOCD,COL11A1,BMPR2	darkolivegreen	VSMC_M9
GO:0045216	0.38	0.73	11	146	cell-cell junction organization	BP	1	EXT1,ROCK2,MPP7,DCHS1,FERMT2,ADAM10,ROCK1,MYO1C,AJM1,CDH11,IRX3	darkolivegreen	VSMC_M9
GO:0034470	0.38	0.70	21	345	ncRNA processing	BP	1	ELAC1,WDR46,TRMO,DDX1,RPF2,EXOSC9,TRDMT1,TOE1,RPL26,ERI1,MTREX,RIOK2,WDR75,PUS3,RRP15,LARP7,DTWD1,INTS14,DICER1,INTS6,TFB2M	darkolivegreen	VSMC_M9
GO:0006406	0.38	0.80	4	53	mRNA export from nucleus	BP	1	UPF2,TPR,THOC1,NUP155	darkolivegreen	VSMC_M9
GO:0071427	0.38	0.80	4	53	mRNA-containing ribonucleoprotein complex export from nucleus	BP	1	UPF2,TPR,THOC1,NUP155	darkolivegreen	VSMC_M9
GO:0030838	0.38	0.77	6	82	positive regulation of actin filament polymerization	BP	1	ACTR2,ACTR3,PFN2,RICTOR,SPIRE1,MYO1C	darkolivegreen	VSMC_M9

GO:0042330	0.38	0.69	29	427	taxis	BP	1	EXT1,STAP1,FYN,KIF5B,CAMK1D,GATA3,SOS1,LYN,PALLD,AGTR1,THBS1,ANOS1,NTRK3,SEMA5B,PIP5K1A,NRP2,NCAM1,ITGAV,PLD1,PLP2,NOTCH3,ENAH,ADAM10,SEMA7A,ITGA2,ITGA1,BMPR2,GDNF,NOV	darkolivegreen	VSMC_M9
GO:1901568	0.38	0.80	4	54	fatty acid derivative metabolic process	BP	1	ELOVL5,HSD17B12,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0065008	0.39	0.65	177	2770	regulation of biological quality	BP	1	LMAN1,CDO1,STXBP5,EXT1,THBS2,SLC39A7,CDKL3,WISP1,PTPRD,PLAA,SLC30A9,ABCB4,AKAP9,TFPI2,TMEM165,JAK2,CLOCK,HDAC9,ZMPSTE24,ACTR2,CAV2,ROCK2,INHBA,PNPLA8,NOCT,RAB3B,ITGB1,FYN,KIF5B,EXOSC9,PIWIL4,GPR4,RB1,PICALM,CYP27C1,TRDMT1,ACTR3,GATA3,RAB3GAP1,CLN5,JMJD6,SETD5,PRPF40A,TMTC2,ATP2B1,ATP11A,NDFIP1,SOS1,UBA5,ILK,TMF1,HOXC10,HSD17B12,CNOT7,RNF6,LYN,MERTK,ATP6V0A2,SLC30A5,USP47,LNPEP,PDE12,FFAR4,MAP1B,RDH10,AGTR1,HK2,TLR2,PFN2,RASA1,ATP2A2,DCP1A,DHX36,THBS1,NUCB2,SHOX2,SLC39A14,GCNT4,ATP1A1,SPTBN5,LRRK2,SNX19,BRSK2,PDLIM5,ATP10A,UBE3A,SLC39A10,CUL3,ATP6V1A,IGF1R,IARS2,GPR89A,CCDC186,ITPR2,NTRK3,ATP11B,SEMA5B,VAPB,ABCB10,C2CD2L,ANK3,CCDC47,C10orf90,SH3KBP1,NRP2,ZFX,FASTKD2,ATP13A3,GATM,PTGS2,MYEF2,SORCS2,SEPT5,ITGAV,FERMT2,SKIL,ATP8B4,F5,VDAC2,DKK1,ACTA2,FAS,AKT3,STIM2,ADAM10,HK3,MSN,SRCIN1,KCNMB1,TPM1,GPR65,ZC3H14,CYFIP2,SRPX2,TLE3,FHOD3,SEMA7A,ANXA6,PIN1,BAG5,ROCK1,ITGA2,ITGA1,RICTOR,NUP155,SLC1A3,AFG3L2,C1QTNF3,CIDEA,SPIRE1,GPC4,CD40LG,USP7,MYO1C,TBXA2R,PAFAH1B1,VAV2,DPM2,PRKACB,BMPR2,AQP3,FASTKD5,XKR9,ARF4,GDNF,GP1BB,CTGF,LHFPL4,BDKRB2,NOV,SRD5A2,TMEM119,AKR1D1,SHISA7,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0001659	0.39	0.73	10	141	temperature homeostasis	BP	1	JAK2,RB1,HOXC10,LNPEP,FFAR4,IGF1R,GATM,PTGS2,TLE3,CIDEA	darkolivegreen	VSMC_M9
GO:0032611	0.39	0.80	4	52	interleukin-1 beta production	BP	1	MALT1,JAK2,FFAR4,TLR6	darkolivegreen	VSMC_M9
GO:0032651	0.39	0.80	4	52	regulation of interleukin-1 beta production	BP	1	MALT1,JAK2,FFAR4,TLR6	darkolivegreen	VSMC_M9
GO:0023061	0.39	0.70	22	325	signal release	BP	1	STXBP5,JAK2,CLOCK,INHBA,KIF5B,GATA3,RAB3GAP1,TMF1,LYN,FFAR4,AGTR1,ATP2A2,LRRK2,SNX19,BRSK2,CCDC186,C2CD2L,SEPT5,C1QTNF3,GDNF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0030203	0.39	0.75	7	93	glycosaminoglycan metabolic process	BP	1	EXT1,DSE,ST3GAL3,CSGALNACT2,CHSY1,CLTC,CHST11	darkolivegreen	VSMC_M9
GO:0008333	0.39	0.79	4	50	endosome to lysosome transport	BP	1	TRAK1,SCYL2,TRAK2,GPRASP1	darkolivegreen	VSMC_M9
GO:0006360	0.39	0.79	4	50	transcription by RNA polymerase I	BP	1	ZMPSTE24,TAF1B,EIF2AK3,WDR75	darkolivegreen	VSMC_M9
GO:0018210	0.39	0.74	8	104	peptidyl-threonine modification	BP	1	TBK1,ROCK2,ACVR1,DYRK1A,LRRK2,CLK1,CDC42BPA,ROCK1	darkolivegreen	VSMC_M9
GO:0034101	0.39	0.74	8	111	erythrocyte homeostasis	BP	1	JAK2,INHBA,RB1,GATA3,JMJD6,UBA5,LYN,ABCB10	darkolivegreen	VSMC_M9
GO:1901701	0.39	0.66	58	887	cellular response to oxygen-containing compound	BP	1	MALT1,DENND4C,PLAA,ABCB4,AKAP9,JAK2,HDAC9,STAP1,ACTR2,CHRM2,CAV2,ROCK2,INHBA,FYN,KIF5B,NOX4,OSBPL8,ATP2B1,LYN,GRAMD1A,XRN1,MAP1B,APPL1,GDAP1,AGTR1,TLR2,USO1,DHX36,SLC39A14,LRRK2,BRSK2,EIF4E,EPRS,IGF1R,CCDC186,ITPR2,NTRK3,PTPN1,C2CD2L,PTGS2,CPEB2,WNT5B,TLR6,MSN,KCNMB1,TPM1,PKM,MAP2K4,ROCK1,ITGA2,SLC1A3,RAB31,MYO1C,TBXA2R,RAPGEF1,ZDHHC7,LAMTOR3,WNT9A	darkolivegreen	VSMC_M9
GO:1902305	0.39	0.79	4	50	regulation of sodium ion transmembrane transport	BP	1	UTRN,KIF5B,ANK3,FXYD5	darkolivegreen	VSMC_M9
GO:0051149	0.39	0.79	4	53	positive regulation of muscle cell differentiation	BP	1	ATP11A,SHOX2,MYOCD,PIN1	darkolivegreen	VSMC_M9
GO:0007260	0.39	0.79	4	53	tyrosine phosphorylation of STAT protein	BP	1	JAK2,FYN,CNOT7,LYN	darkolivegreen	VSMC_M9
GO:0070373	0.39	0.79	4	53	negative regulation of ERK1 and ERK2 cascade	BP	1	LYN,PTPN1,ATF3,PIN1	darkolivegreen	VSMC_M9
GO:0001932	0.39	0.66	55	845	regulation of protein phosphorylation	BP	1	MALT1,TBK1,AKAP9,JAK2,STAP1,CCDC88A,SH3BP5L,ROCK2,INHBA,FYN,NOX4,RB1,CBLC,CCNT2,DNAJC3,OSBPL8,CCNA1,ILK,ITGA5,CNOT7,LYN,IPO7,EIF2AK3,TMED2,PFN2,THBS1,ACVR1,NEDD9,CBLB,EHD4,LRRK2,CORO1C,NTRK3,PTPN1,IQGAP1,PTGS2,FERMT2,TNIK,DKK1,FAS,TLR6,SRCIN1,SMG8,MAP2K4,MYOCD,SEMA7A,PIN1,RICTOR,GADD45B,BMPR2,CTGF,BDKRB2,PMEPA1,RAP2A,TMEM119	darkolivegreen	VSMC_M9
GO:0007286	0.39	0.75	7	100	spermatid development	BP	1	PSME4,UBE2J1,CEP57,FNDC3A,TMF1,PITHD1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0007281	0.39	0.72	12	177	germ cell development	BP	1	PSME4,UBE2J1,CEP57,FNDC3A,BRCA2,TMF1,ACVR1,PITHD1,ZFX,FMN2,PAFAH1B1,PAQR8	darkolivegreen	VSMC_M9
GO:0045893	0.39	0.65	81	1244	positive regulation of transcription, DNA-templated	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,CLOCK,NPAS2,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,INHBA,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,JMJD6,BRPF1,SUPT5H,PPP1R12A,CEBPZ,SMAD9,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,STOX2,MICAL2,TLR2,DHX36,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,UBE3A,KPNA6,LARP7,TAF5L,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,CREB3L2,FZD2,NPAT,PRRX1,TRIP4,TBX6,ARMCX3,MYOCD,PIN1,SS18,THOC1,MYSM1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9

GO:1903508	0.39	0.65	81	1244	positive regulation of nucleic acid-templated transcription	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,CLOCK,NPAS2,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,INHBA,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,JMJD6,BRPF1,SUPT5H,PPP1R12A,CEBPZ,SMAD9,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,STOX2,MICAL2,TLR2,DHX36,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,UBE3A,KPNA6,LARP7,TAF5L,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,CREB3L2,FZD2,NPAT,PRRX1,TRIP4,TBX6,ARMCX3,MYOCD,PIN1,SS18,THOC1,MYSM1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0051235	0.39	0.70	17	248	maintenance of location	BP	1	KDELR3,TOPORS,AKAP9,CCDC88A,OSBPL8,LYN,HK2,ITPR2,ANK3,OSBPL11,ITGAV,TAPT1,PDIA2,ANXA6,CIDEA,PAFAH1B1,ANKRD13C	darkolivegreen	VSMC_M9
GO:0009152	0.39	0.73	9	137	purine ribonucleotide biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,ATP6V1A,PAPSS2,ADSS,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0002697	0.39	0.71	14	206	regulation of immune effector process	BP	1	MALT1,STAP1,DDX1,GATA3,RIF1,NDFIP1,LYN,APPL1,DHX36,NFKBIZ,SEMA7A,THOC1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0043648	0.39	0.77	5	73	dicarboxylic acid metabolic process	BP	1	SUCLA2,ALDH18A1,IDH2,ADSS,DLST	darkolivegreen	VSMC_M9
GO:0010517	0.39	0.79	4	50	regulation of phospholipase activity	BP	1	PLAA,ARL1,AGTR1,ARF4	darkolivegreen	VSMC_M9
GO:0001510	0.39	0.77	5	73	RNA methylation	BP	1	TRMO,ZC3H13,TRDMT1,LARP7,TFB2M	darkolivegreen	VSMC_M9
GO:0001936	0.39	0.74	8	111	regulation of endothelial cell proliferation	BP	1	CAV2,SULF1,AGTR1,THBS1,NRP2,AKT3,RICTOR,BMPR2	darkolivegreen	VSMC_M9
GO:0009451	0.39	0.73	9	141	RNA modification	BP	1	TRMO,ZC3H13,TRDMT1,JMJD6,PUS3,LARP7,DTWD1,RBM47,TFB2M	darkolivegreen	VSMC_M9
GO:0035264	0.40	0.74	8	108	multicellular organism growth	BP	1	EXT1,ZMPSTE24,SOS1,TMED2,ETNK2,ZFX,RBBP6,AFG3L2	darkolivegreen	VSMC_M9
GO:0098657	0.40	0.72	11	155	import into cell	BP	1	RAB3B,ITGB1,FYN,SLC36A4,THBS1,SLC39A14,ATP1A1,SLC39A10,EPRS,SLC1A3,GDNF	darkolivegreen	VSMC_M9
GO:0071902	0.40	0.72	12	170	positive regulation of protein serine/threonine kinase activity	BP	1	CCNT2,ILK,THBS1,LRRK2,NTRK3,PTPN1,IQGAP1,FERMT2,DKK1,TLR6,RICTOR,BMPR2	darkolivegreen	VSMC_M9
GO:0009416	0.40	0.70	16	239	response to light stimulus	BP	1	EXT1,CLOCK,ITGB1,RPL26,BRCA2,FBXL17,DYNLRB1,USP47,DHX36,INO80,TROVE2,CASP7,SEMA5B,PTGS2,SLC1A3,ELOVL4	darkolivegreen	VSMC_M9
GO:0031056	0.40	0.73	9	124	regulation of histone modification	BP	1	ZNF451,ZMPSTE24,GATA3,SETD5,RIF1,PARG,BRD7,LRRK2,MYOCD	darkolivegreen	VSMC_M9
GO:1902680	0.40	0.65	81	1246	positive regulation of RNA biosynthetic process	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,CLOCK,NPAS2,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,INHBA,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,JMJD6,BRPF1,SUPT5H,PPP1R12A,CEBPZ,SMAD9,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,STOX2,MICAL2,TLR2,DHX36,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,UBE3A,KPNA6,LARP7,TAF5L,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,CREB3L2,FZD2,NPAT,PRRX1,TRIP4,TBX6,ARMCX3,MYOCD,PIN1,SS18,THOC1,MYSM1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0003229	0.40	0.79	4	47	ventricular cardiac muscle tissue development	BP	1	ZMPSTE24,TPM1,COL11A1,IRX3	darkolivegreen	VSMC_M9
GO:0032501	0.40	0.63	318	5003	multicellular organismal process	BP	1	LMAN1,MALT1,CDO1,AHI1,LRIG3,UTRN,TBK1,CEP120,RRM2B,LRP12,EXT1,THBS2,CDKL3,CHADL,WISP1,PTPRD,PLAA,TOPORS,AKAP9,TFPI2,JAK2,CLOCK,NPAS2,ASPN,BZW2,HEMGN,HDAC9,CAVIN4,COL12A1,PSME4,MYO6,STAP1,UBA6,CCDC88A,HOXA9,HOXA10,HOXA11,ZMPSTE24,UBE2J1,UGP2,ACTR2,GFPT1,CHRM2,CAV2,ROCK2,INHBA,GREB1,DDX1,NOCT,PCDH18,ITGB1,FYN,ZEB1,KIF5B,CEP57,PIWIL4,PSMC2,NOX4,FNDC3A,GPR4,RB1,PICALM,ZC3H13,CAMK1D,UPF2,GATA3,CCNT2,RAB3GAP1,CLN5,JMJD6,PAX1,TRAK1,LRRC32,SETD5,AZI2,STK24,TNFAIP6,RIF1,GPCPD1,UFM1,CAPN7,LIG4,MYO16,SUPT20H,ATP2B1,ALG5,CCNA1,ATP11A,ACPP,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,NTN4,UBA5,ILK,ITGA5,DCHS1,TMF1,HOXC10,SCYL2,RNF6,LYN,PPP2R3A,MERTK,SLC16A12,TMEM41B,IFT88,MYBL1,EIF2AK3,SLC25A46,FBXL17,TDG,TMED2,PALLD,EIF2S2,ITCH,DYNLRB1,SULF1,LNPEP,STOX2,MICAL2,FFAR4,MAP1B,APPL1,RDH10,AGTR1,HK2,TLR2,PFN2,RASA1,ATP2A2,VCAN,MBNL1,DHX36,THBS1,SHOX2,ZDHHC16,ARL6,ACVR1,SLC39A14,IRX5,GCNT4,ETNK2,NFKBIZ,CBLB,ATP1A1,DYRK1A,MAN1A2,ERG,LRRK2,SNX19,TBX15,BRSK2,PDLIM5,UBE3A,MBOAT1,CUL3,EIF4E,PHLDB2,TDP2,DNER,TROVE2,UCHL5,CHSY1,KPNA6,IGF1R,BPNT1,CAMSAP2,GPR89A,CASP7,CORO1C,ANOS1,NTRK3,WWC3,LARP7,SEMA5B,IDH2,TAF5L,ABCB10,EIF2B5,TRAK2,LTB4R,GPATCH3,SYCP2,ATF3,PIP5K1A,IQGAP1,ANK3,CD3G,CCDC47,SMTN,ADAM12,NRP2,HDGFL3,PITHD1,MBTPS2,ZFX,CREB3L2,GATM,CLEC14A,PTGS2,NCAM1,MYEF2,FZD2,DNAJA4,CDKL1,NPAT,SEPT5,ITGAV,GNPNAT1,FERMT2,SKIL,PRRX1,SMURF1,TAPT1,TNIK,F5,DKK1,FMN2,PAPSS2,ATAD1,ACTA2,AKT3,RPA43,WNT5B,GLCAK8,NOTCH3,USP37,TLR6	darkolivegreen	VSMC_M9
GO:0016525	0.40	0.75	6	82	negative regulation of angiogenesis	BP	1	THBS2,ROCK2,GPR4,SULF1,THBS1,ROCK1	darkolivegreen	VSMC_M9
GO:0043954	0.40	0.78	4	47	cellular component maintenance	BP	1	FYN,IGF1R,FERMT2,MYOCD	darkolivegreen	VSMC_M9
GO:0060429	0.40	0.65	54	810	epithelium development	BP	1	AHI1,EXT1,JAK2,CLOCK,MYO6,HOXA11,ZMPSTE24,ROCK2,INHBA,ZEB1,FNDC3A,GPR4,GATA3,STARD13,SOS1,BRCA2,NTN4,ILK,ITGA5,DCHS1,PPP2R3A,TMED2,PALLD,SULF1,MICAL2,RDH10,ACVR1,BRSK2,PHLDB2,PIP5K1A,IQGAP1,FZD2,FERMT2,SKIL,SMURF1,DKK1,ACTA2,WNT5B,MSN,MYO1E,TBX6,RBBP6,ROCK1,ITGA2,GPC4,PAFAH1B1,RAPGEF1,ZDHHC7,PRKACB,BMPR2,AQP3,GDNF,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0090288	0.40	0.75	6	78	negative regulation of cellular response to growth factor stimulus	BP	1	GATA3,SULF1,THBS1,PTPN1,SKIL,SMURF1	darkolivegreen	VSMC_M9

GO:0042113	0.40	0.71	13	193	B cell activation	BP	1	MALT1,HDAC9,INHBA,ITGB1,RIF1,LIG4,NDFIP1,LYN,SLC39A10,SH3KBP1,THOC1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0097581	0.40	0.75	6	78	lamellipodium organization	BP	1	CCDC88A,ACTR2,ITGB1,ACTR3,CORO1C,VAV2	darkolivegreen	VSMC_M9
GO:0050852	0.40	0.75	6	85	T cell receptor signaling pathway	BP	1	MALT1,FYN,GATA3,NFKBIZ,CBLB,EIF2B5	darkolivegreen	VSMC_M9
GO:0006260	0.40	0.69	16	230	DNA replication	BP	1	RRM2B,RMI1,CCDC88A,ZMPSTE24,ORC4,LIG4,BRCA2,INO80,RBBP7,BAZ1A,BOD1L1,RBBP6,MAP2K4,THOC1,RFWD3,ZPR1	darkolivegreen	VSMC_M9
GO:0031113	0.40	0.78	4	49	regulation of microtubule polymerization	BP	1	AKAP9,MAP1B,DYRK1A,CAMSAP2	darkolivegreen	VSMC_M9
GO:0006836	0.40	0.72	10	139	neurotransmitter transport	BP	1	STXBP5,RAB3B,ITGB1,RAB3GAP1,ATP2A2,LRRK2,SEPT5,SLC1A3,GDNF,WNT7A	darkolivegreen	VSMC_M9
GO:0007018	0.40	0.69	19	283	microtubule-based movement	BP	1	ACTR2,KIF5B,ACTR3,TRAK1,TMF1,IFT88,DYNLRB1,MAP1B,PGAM4,TRAK2,KIFAP3,KTN1,ACTR10,FMN2,ARMCX3,PAFAH1B1,KIF1B,SSX2IP,RAB6A	darkolivegreen	VSMC_M9
GO:0010469	0.41	0.73	8	112	regulation of signaling receptor activity	BP	1	AKAP9,JAK2,ITGB1,CBLC,CBLB,DKK1,ANKRD13C,SHISA7	darkolivegreen	VSMC_M9
GO:0120254	0.41	0.75	6	86	olefinic compound metabolic process	BP	1	ELOVL5,PNPLA8,CYP27C1,RDH10,PTGS2,SRD5A2	darkolivegreen	VSMC_M9
GO:0002028	0.41	0.76	5	66	regulation of sodium ion transport	BP	1	UTRN,KIF5B,ATP1A1,ANK3,FXYD5	darkolivegreen	VSMC_M9
GO:2000181	0.41	0.75	6	83	negative regulation of blood vessel morphogenesis	BP	1	THBS2,ROCK2,GPR4,SULF1,THBS1,ROCK1	darkolivegreen	VSMC_M9
GO:0065003	0.41	0.64	74	1210	protein-containing complex assembly	BP	1	STXBP5,CAND1,EXT1,AKAP9,JAK2,SENP6,CENPC,COX18,ACTR2,TAF1B,DDX1,MPP7,RPF2,CEP57,RB1,PICALM,ACTR3,JMJD6,DARS,NDUFAF5,TUBGCP3,DHX29,TMED2,EIF2S2,SMARCA5,MAT2A,BDP1,MAP1B,TMEM70,PFN2,RASA1,KCTD9,ARL6,DYRK1A,SPTBN5,EHD4,LRRK2,CUL3,NAP1L4,DNAJB14,EPRS,CAMSAP2,HAUS2,CD3G,HDGFL3,FASTKD2,EIF3J,FERMT2,VAMP4,KIFAP3,VDAC2,DKK1,FAS,TLR6,ADAM10,MSN,CLINT1,CYFIP2,CLTC,DICER1,FHOD3,RICTOR,AFG3L2,SPIRE1,MYO1C,GTF2B,PRKACB,GEMIN6,OTUD6B,PDCL,MZT1,PMEPA1,SRP19,NDUFAF4	darkolivegreen	VSMC_M9
GO:0050866	0.41	0.72	9	136	negative regulation of cell activation	BP	1	SOCS6,INHBA,LRRC32,NDFIP1,LYN,MERTK,ITCH,CBLB,THOC1	darkolivegreen	VSMC_M9
GO:0016458	0.41	0.71	11	169	gene silencing	BP	1	ZMPSTE24,PIWIL4,ERI1,CNOT7,SMARCA5,KIAA1551,TPR,DICER1,MYOCD,ZC3H7A,MIR186	darkolivegreen	VSMC_M9
GO:0030177	0.41	0.72	9	124	positive regulation of Wnt signaling pathway	BP	1	WISP1,ILK,SULF1,USP47,TLR2,LRRK2,DKK1,WNT5B,PIN1	darkolivegreen	VSMC_M9
GO:2000736	0.41	0.78	4	50	regulation of stem cell differentiation	BP	1	ITCH,DHX36,GDNF,CDK13	darkolivegreen	VSMC_M9
GO:0071260	0.41	0.76	5	69	cellular response to mechanical stimulus	BP	1	ATP1A1,PTGS2,FAS,MAP2K4,ITGA2	darkolivegreen	VSMC_M9
GO:0033692	0.41	0.78	4	52	cellular polysaccharide biosynthetic process	BP	1	EXT1,UGP2,CSGALNACT2,PHKG2	darkolivegreen	VSMC_M9
GO:1903305	0.41	0.74	7	95	regulation of regulated secretory pathway	BP	1	STXBP5,RAB3GAP1,LYN,ATP2A2,LRRK2,SEPT5,WNT7A	darkolivegreen	VSMC_M9
GO:0045597	0.41	0.65	42	639	positive regulation of cell differentiation	BP	1	MALT1,AHI1,CDKL3,WISP1,PTPRD,JAK2,HOXA11,ACTR2,INHBA,NOCT,ZEB1,RB1,GATA3,TRAK1,LIG4,ATP11A,ILK,LYN,FFAR4,MAP1B,AGTR1,TLR2,DHX36,SHOX2,ACVR1,NFKBIZ,NEDD9,ABCB10,PITHD1,PTGS2,FERMT2,SKIL,DICER1,MYOCD,SEMA7A,PIN1,PAFAH1B1,BMPR2,GDNF,CTGF,TMEM119,IRX3	darkolivegreen	VSMC_M9
GO:0048015	0.41	0.71	10	133	phosphatidylinositol-mediated signaling	BP	1	JAK2,EXOC1,KBTBD2,FYN,GATA3,MYO16,UBE3A,IGF1R,NTRK3,PIP5K1A	darkolivegreen	VSMC_M9
GO:0016055	0.41	0.67	25	373	Wnt signaling pathway	BP	1	EXT1,WISP1,GATA3,ILK,SCYL2,SULF1,USP47,TLR2,ARL6,BRD7,LRRK2,CUL3,KPNA1,FZD2,FERMT2,SMURF1,TNIK,DKK1,WNT5B,TLE3,PIN1,GPC4,WNT9A,VGLL4,WNT7A	darkolivegreen	VSMC_M9
GO:0097305	0.41	0.70	12	174	response to alcohol	BP	1	CDO1,ACTR2,INHBA,FYN,GATA3,ATP2B1,GRAMD1A,XRN1,ITPR2,NTRK3,KCNMB1,TBXA2R	darkolivegreen	VSMC_M9
GO:0009855	0.41	0.73	7	97	determination of bilateral symmetry	BP	1	AHI1,ALG5,TMED2,MICAL2,ARL6,ACVR1,TBX6	darkolivegreen	VSMC_M9
GO:0071692	0.41	0.68	18	271	protein localization to extracellular region	BP	1	STXBP5,JAK2,CLOCK,EXOC1,RAB3B,KIF5B,DNAJC1,TLR2,SNX19,BRSK2,CCDC186,IDH2,C2CD2L,SRCIN1,MYOM1,C1QTNF3,PAFAH1B1,NOV	darkolivegreen	VSMC_M9
GO:0043489	0.41	0.77	4	52	RNA stabilization	BP	1	NOCT,TRDMT1,DHX36,GDNF	darkolivegreen	VSMC_M9
GO:0003158	0.41	0.72	8	107	endothelium development	BP	1	ROCK2,ZEB1,STARD13,ACVR1,MSN,ROCK1,RAPGEF1,BMPR2	darkolivegreen	VSMC_M9
GO:0043297	0.42	0.77	4	52	apical junction assembly	BP	1	ROCK2,MPP7,ROCK1,MYO1C	darkolivegreen	VSMC_M9
GO:1901343	0.42	0.74	6	84	negative regulation of vasculature development	BP	1	THBS2,ROCK2,GPR4,SULF1,THBS1,ROCK1	darkolivegreen	VSMC_M9
GO:0030155	0.42	0.65	36	541	regulation of cell adhesion	BP	1	SOCS6,MALT1,UTRN,JAK2,ROCK2,FYN,GPR4,GATA3,LRRC32,CYTH1,PPP1R12A,NDFIP1,ILK,HSPH1,HSD17B12,LYN,ITCH,RASA1,THBS1,NFKBIZ,NEDD9,CBLB,PHLDB2,CORO1C,IQGAP1,ANK3,ITGAV,FERMT2,KIFAP3,ADAM10,TPM1,ADAM19,ROCK1,ITGA2,CD40LG,FXYD5	darkolivegreen	VSMC_M9
GO:0051952	0.42	0.77	4	55	regulation of amine transport	BP	1	RAB3B,ITGB1,RAB3GAP1,GDNF	darkolivegreen	VSMC_M9
GO:0001775	0.42	0.64	44	692	cell activation	BP	1	SOCS6,MALT1,TBK1,JAK2,HDAC9,STAP1,HOXA9,INHBA,ITGB1,FYN,GATA3,JMJD6,LRRC32,AZI2,RIF1,LIG4,NDFIP1,SOS1,ILK,HSPH1,LYN,MERTK,ITCH,TLR2,THBS1,NFKBIZ,CBLB,LRRK2,SLC39A10,GPR89A,KPNA1,CD3G,SH3KBP1,TLR6,ADAM10,MSN,THOC1,CD40LG,VAV2,CLEC4D,GP1BB,CTGF,DNAJB9,WNT7A	darkolivegreen	VSMC_M9
GO:0051965	0.42	0.77	4	46	positive regulation of synapse assembly	BP	1	THBS2,PTPRD,SRPX2,WNT7A	darkolivegreen	VSMC_M9
GO:0000380	0.42	0.75	5	66	alternative mRNA splicing, via spliceosome	BP	1	KHDRBS3,MBNL2,MBNL1,DYRK1A,CDK13	darkolivegreen	VSMC_M9

GO:0030833	0.42	0.71	10	145	regulation of actin filament polymerization	BP	1	ACTR2,ACTR3,PFN2,RASA1,SPTBN5,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C	darkolivegreen	VSMC_M9
GO:0008064	0.42	0.70	11	159	regulation of actin polymerization or depolymerization	BP	1	ACTR2,ACTR3,PFN2,RASA1,SPTBN5,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C,CFL2	darkolivegreen	VSMC_M9
GO:0048585	0.42	0.63	78	1229	negative regulation of response to stimulus	BP	1	SOCS6,RRM2B,PTPRD,CLOCK,ASPN,ZNF451,STAP1,CAV2,ITGB1,FYN,RB1,CBLC,GATA3,TNFAIP6,RIF1,NDFIP1,SCYL2,CNOT7,LYN,ITCH,SULF1,USP47,CCDC125,FFAR4,APPL1,RASA1,BRAP,THBS1,NUCB2,ACVR1,CBLB,DYRK1A,LRRK2,TANK,CUL3,PHLDB2,IGF1R,WWC3,PTPN1,GRK3,SEMA5B,GPATCH3,ATF3,PTGS2,ITGAV,SKIL,SMURF1,VDAC2,DKK1,RGS7,AKT3,TLR6,TLE3,UACA,GPRASP1,MYOCD,SEMA7A,PIN1,BAG5,THOC1,ITGA1,BFAR,C1QTNF3,CIDEA,PAFAH1B1,ENO1,WFDC1,PRKACB,MIR186,PTPN12,GDNF,BDKRB2,DNAJB9,NOV,PMEPA1,VGLL4,C12orf66,CHST11	darkolivegreen	VSMC_M9
GO:0016079	0.42	0.74	6	79	synaptic vesicle exocytosis	BP	1	STXBP5,RAB3GAP1,ATP2A2,LRRK2,SEPT5,WNT7A	darkolivegreen	VSMC_M9
GO:0006310	0.42	0.68	16	245	DNA recombination	BP	1	RMI1,ACTR2,TSN,RIF1,LIG4,NDFIP1,BRCA2,ACTR8,INO80,NFRKB,UCHL5,KPNA1,RBBP8,THOC1,CD40LG,RFWD3	darkolivegreen	VSMC_M9
GO:0042445	0.42	0.71	9	133	hormone metabolic process	BP	1	ZMPSTE24,CYP27C1,GATA3,HSD17B12,RDH10,GCNT4,ATP1A1,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0045944	0.42	0.63	59	904	positive regulation of transcription by RNA polymerase II	BP	1	AHI1,TBK1,CAND1,SLC30A9,CLOCK,NPAS2,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,ACTR2,INHBA,EXOSC9,RB1,ACTR3,GATA3,CCNT2,JMJD6,SUPT5H,PPP1R12A,CEBPZ,SMAD9,TMF1,HOXC10,CNOT7,MYBL1,SMARCA5,STOX2,MICAL2,TLR2,DHX36,ACVR1,INO80,ERG,UBE3A,KPNA6,LARP7,ATF3,BCLAF3,MBTPS2,CREB3L2,NPAT,PRRX1,TBX6,ARMCX3,MYOCD,PIN1,SS18,MYSM1,BMPR2,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0050878	0.42	0.67	18	273	regulation of body fluid levels	BP	1	LMAN1,CDO1,EXT1,TFPI2,JAK2,ILK,LYN,MERTK,HK2,THBS1,F5,ITGA2,CD40LG,TBXA2R,VAV2,PRKACB,AQP3,GP1BB	darkolivegreen	VSMC_M9
GO:0031110	0.42	0.74	6	79	regulation of microtubule polymerization or depolymerization	BP	1	AKAP9,MAP1B,DYRK1A,CAMSAP2,HDGFL3,SKA2	darkolivegreen	VSMC_M9
GO:0198738	0.42	0.66	25	374	cell-cell signaling by wnt	BP	1	EXT1,WISP1,GATA3,ILK,SCYL2,SULF1,USP47,TLR2,ARL6,BRD7,LRRK2,CUL3,KPNA1,FZD2,FERMT2,SMURF1,TNIK,DKK1,WNT5B,TLE3,PIN1,GPC4,WNT9A,VGLL4,WNT7A	darkolivegreen	VSMC_M9
GO:0048583	0.42	0.61	179	2834	regulation of response to stimulus	BP	1	SOCS6,MALT1,TBK1,PLEKHG1,RRM2B,WISP1,UBQLN1,PTPRD,DENND4C,AKAP9,JAK2,CLOCK,NPAS2,FBXO9,ASPN,ZNF451,CAVIN4,STAP1,CCDC88A,ZMPSTE24,ACTR2,CAV2,ROCK2,INHBA,PNPLA8,DDX1,ITGB1,RPF2,FYN,GPR4,RB1,CBLC,CAMK1D,MGAT5,GATA3,NDFIP2,CYTH1,STK24,TNFAIP6,RIF1,OSBPL8,RPL26,UFM1,ATP2B1,ACPP,NR2C1,NDFIP1,CUL4A,STARD13,SOS1,UBA5,ILK,ITGA5,SCYL2,PARG,CNOT7,RNF6,LYN,EIF2AK3,FBXL17,TMED2,ITCH,SULF1,USP47,CCDC125,FFAR4,APPL1,AGTR1,TLR2,RASA1,ATP2A2,USO1,BRAP,DHX36,THBS1,NUCB2,SHOX2,ACVR1,SLC39A14,NFKBIZ,CBLB,DYRK1A,LRRK2,TANK,UBE3A,SLC39A10,CUL3,PHLDB2,UCHL5,CHSY1,IGF1R,GPR89A,NTRK3,WWC3,PTPN1,GRK3,KPNA1,SEMA5B,EIF2B5,GPATCH3,ATF3,PIP5K1A,IQGAP1,MBTPS2,TPR,PTGS2,NCAM1,IQCJ-SCHIP1,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TNIK,TNFAIP8L3,VDAC2,DKK1,FMN2,RGS7,FAS,AKT3,WNT5B,TLR6,ADAM10,GPR65,CYFIP2,TLE3,UACA,GPRASP1,MAP2K4,MYOCD,SEMA7A,PIN1,BAG5,ROCK1,THOC1,ITGA2,ITGA1,RICTOR,VAPA,BFAR,C1QTNF3,CIDEA,SPIRE1,GPC4,USP7,MYO1C,TBXA2R,PAFAH1B1,GADD45B,ENO1,VAV2,ZDHHC7,WFDC1,RFWD3,SSX2IP,PRKACB,ANKRD13C,MIR186,BMPR2,PTPN12,GDNF,CTGF,BDKRB2,EFHD1,LAMTOR3,DNAJB9,NOV,PDCL,FCN1,PMEPA1,RAP2A,VGLL4,C12orf66,CHST11,UBE2V1,SHISA7,WNT7A,PPP1R2	darkolivegreen	VSMC_M9
GO:0050890	0.42	0.68	15	214	cognition	BP	1	UBA6,ACTR2,ITGB1,FYN,PICALM,SETD5,TLR2,UBE3A,GATM,PTGS2,DKK1,ATAD1,PAFAH1B1,ARF4,SHISA7	darkolivegreen	VSMC_M9
GO:0045786	0.42	0.67	20	306	negative regulation of cell cycle	BP	1	CLOCK,THAP5,INHBA,RINT1,RB1,GATA3,RPL26,MYO16,CUL4A,IPO7,USP47,BRD7,TPR,PTGS2,MYOCD,CCP110,THOC1,RFWD3,PRKACB,ZNF655	darkolivegreen	VSMC_M9
GO:0055072	0.42	0.75	5	72	iron ion homeostasis	BP	1	PICALM,NDFIP1,ATP6V0A2,SLC39A14,ATP6V1A	darkolivegreen	VSMC_M9
GO:0006720	0.42	0.75	5	73	isoprenoid metabolic process	BP	1	PDSS1,CYP27C1,RDH10,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0030041	0.42	0.70	11	160	actin filament polymerization	BP	1	JAK2,ACTR2,ACTR3,PFN2,RASA1,SPTBN5,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C	darkolivegreen	VSMC_M9
GO:0045446	0.42	0.73	7	91	endothelial cell differentiation	BP	1	ROCK2,ZEB1,ACVR1,MSN,ROCK1,RAPGEF1,BMPR2	darkolivegreen	VSMC_M9
GO:0032006	0.42	0.74	6	84	regulation of TOR signaling	BP	1	FBXO9,ZMPSTE24,AKT3,RICTOR,LAMTOR3,C12orf66	darkolivegreen	VSMC_M9
GO:0007186	0.42	0.65	30	458	G protein-coupled receptor signaling pathway	BP	1	GNG11,JAK2,CHRM2,ROCK2,GPR4,ACPP,GPR84,PLPP1,FFAR4,AGTR1,GPR176,SLC39A14,GRK3,LTB4R,FZD2,SORCS2,GPR34,GPR82,TAPT1,RGS7,GPR65,GPRASP1,ROCK1,TBXA2R,ZDHHC7,PRKACB,BDKRB2,PDCL,NXPH3,FCN1	darkolivegreen	VSMC_M9
GO:0006304	0.42	0.74	6	84	DNA modification	BP	1	ZMPSTE24,PIWIL4,GATA3,TDG,PPM1D,USP7	darkolivegreen	VSMC_M9
GO:0009799	0.42	0.72	7	98	specification of symmetry	BP	1	AHI1,ALG5,TMED2,MICAL2,ARL6,ACVR1,TBX6	darkolivegreen	VSMC_M9
GO:0032101	0.42	0.64	41	646	regulation of response to external stimulus	BP	1	TBK1,WISP1,JAK2,CLOCK,STAP1,ZMPSTE24,FYN,GPR4,RB1,CAMK1D,GATA3,STK24,TNFAIP6,NDFIP1,CNOT7,LYN,ITCH,FFAR4,APPL1,AGTR1,TLR2,THBS1,NUCB2,NFKBIZ,LRRK2,PHLDB2,NTRK3,PTPN1,SEMA5B,GPATCH3,PTGS2,ADAM10,SEMA7A,ITGA2,RICTOR,C1QTNF3,TBXA2R,WFDC1,BMPR2,NOV,FCN1	darkolivegreen	VSMC_M9

GO:0070661	0.42	0.69	13	201	leukocyte proliferation	BP	1	MALT1,TBK1,FYN,LRRC32,AZI2,NDFIP1,SOS1,LYN,ITCH,CBLB,SLC39A10,MSN,CD40LG	darkolivegreen	VSMC_M9
GO:0001776	0.42	0.75	5	70	leukocyte homeostasis	BP	1	SOS1,LYN,MERTK,SKIL,FAS	darkolivegreen	VSMC_M9
GO:0030168	0.42	0.72	7	96	platelet activation	BP	1	JAK2,ILK,LYN,MERTK,CD40LG,VAV2,GP1BB	darkolivegreen	VSMC_M9
GO:0051094	0.42	0.63	64	982	positive regulation of developmental process	BP	1	MALT1,AHI1,THBS2,CDKL3,WISP1,PTPRD,PLAA,JAK2,HOXA11,ACTR2,INHBA,NOCT,ITGB1,ZEB1,RB1,GATA3,TRAK1,RIF1,LIG4,ATP2B1,ATP11A,ILK,ITGA5,LYN,FFAR4,MAP1B,AGTR1,HK2,TLR2,DHX36,THBS1,SHOX2,ACVR1,NFKBIZ,NEDD9,PHLDB2,CORO1C,ABCB10,IQGAP1,ADAM12,PITHD1,PTGS2,FERMT2,SKIL,SMURF1,TAPT1,DKK1,AKT3,WNT5B,SRPX2,PKM,DICER1,MYOCD,SEMA7A,PIN1,SPIRE1,TBXA2R,PAFAH1B1,BMPR2,GDNF,CTGF,TMEM119,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0006282	0.42	0.71	8	118	regulation of DNA repair	BP	1	NPAS2,ACTR2,RIF1,CUL4A,PARG,FMN2,SPIRE1,UBE2V1	darkolivegreen	VSMC_M9
GO:0032272	0.43	0.75	5	66	negative regulation of protein polymerization	BP	1	PFN2,DYRK1A,SPTBN5,VDAC2,FHOD3	darkolivegreen	VSMC_M9
GO:0045321	0.43	0.64	37	586	leukocyte activation	BP	1	SOCS6,MALT1,TBK1,JAK2,HDAC9,STAP1,INHBA,ITGB1,FYN,GATA3,JMJD6,LRRC32,AZI2,RIF1,LIG4,NDFIP1,SOS1,HSPH1,LYN,MERTK,ITCH,TLR2,THBS1,NFKBIZ,CBLB,LRRK2,SLC39A10,GPR89A,CD3G,SH3KBP1,TLR6,ADAM10,MSN,THOC1,CD40LG,CLEC4D,DNAJB9	darkolivegreen	VSMC_M9
GO:0006281	0.43	0.65	29	455	DNA repair	BP	1	RRM2B,RMI1,SLC30A9,NPAS2,PSME4,ZMPSTE24,ACTR2,DDX1,RIF1,LIG4,CUL4A,PDS5B,BRCA2,PARG,TDG,USP47,ACTR8,INO80,NFRKB,TDP2,UCHL5,PRRX1,BOD1L1,FMN2,RBBP8,SPIRE1,USP7,RFWD3,UBE2V1	darkolivegreen	VSMC_M9
GO:0042490	0.43	0.76	4	52	mechanoreceptor differentiation	BP	1	MYO6,IFT88,FZD2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0001701	0.43	0.66	21	314	in utero embryonic development	BP	1	ITGB1,GATA3,LIG4,ATP11A,CUL4A,BRCA2,TMED2,EIF2S2,RDH10,MBNL1,ACVR1,ETNK2,CUL3,NPAT,SKIL,ADAM10,MYO1E,RBBP6,RBBP8,ZPR1,CHST11	darkolivegreen	VSMC_M9
GO:0030832	0.43	0.69	11	160	regulation of actin filament length	BP	1	ACTR2,ACTR3,PFN2,RASA1,SPTBN5,CYFIP2,FHOD3,RICTOR,SPIRE1,MYO1C,CFL2	darkolivegreen	VSMC_M9
GO:1903530	0.43	0.65	26	399	regulation of secretion by cell	BP	1	STXBP5,JAK2,CLOCK,EXOC1,INHBA,RAB3B,KIF5B,DNAJC1,RAB3GAP1,TMF1,LYN,FFAR4,AGTR1,TLR2,ATP2A2,LRRK2,BRSK2,IDH2,C2CD2L,SEPT5,SRCIN1,MYOM1,C1QTNF3,GDNF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0051254	0.43	0.62	87	1357	positive regulation of RNA metabolic process	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,CLOCK,NPAS2,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,ROCK2,INHBA,NOCT,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,JMJD6,BRPF1,SUPT5H,PPP1R12A,CEBPZ,SMAD9,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,RIOK2,PDE12,STOX2,MICAL2,TLR2,DCP1A,DHX36,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,UBE3A,KPNA6,LARP7,TAF5L,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,CREB3L2,FZD2,NPAT,PRRX1,TRIP4,TBX6,ARMCX3,MYOCD,PIN1,SS18,ROCK1,THOC1,MYSM1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0034121	0.43	0.76	4	54	regulation of toll-like receptor signaling pathway	BP	1	LYN,APPL1,TLR2,TLR6	darkolivegreen	VSMC_M9
GO:0035556	0.43	0.61	132	2063	intracellular signal transduction	BP	1	SOCS6,MALT1,TBK1,PLEKHG1,RRM2B,UBQLN1,DENND4C,TOPORS,JAK2,CLOCK,EXOC1,FBXO9,CAVIN4,MYO6,CCDC88A,ZMPSTE24,KBTBD2,SH3BP5L,CAV2,ROCK2,DDX1,ITGB1,RPF2,FYN,RINT1,GPR4,RB1,CBLC,GATA3,NDFIP2,AZI2,CYTH1,STK24,OSBPL8,RPL26,MYO16,NDFIP1,CUL4A,STARD13,SOS1,BRCA2,ILK,DCHS1,LYN,MERTK,PDE7A,EIF2AK3,ITCH,USP47,CCDC125,FFAR4,AGTR1,TLR2,RASA1,ATP2A2,USO1,BRAP,DHX36,THBS1,NUCB2,KCTD9,CBLB,DYRK1A,LRRK2,TANK,BRSK2,UBE3A,CUL3,IGF1R,GPR89A,STK38L,ITPR2,NTRK3,WWC3,PTPN1,GPATCH3,ATF3,PIP5K1A,IQGAP1,TLK2,TPR,PTGS2,IQCJ-SCHIP1,MAP4K5,ITGAV,FERMT2,SKIL,TNIK,PLD1,TNFAIP8L3,VDAC2,DKK1,FMN2,RGS7,FAS,AKT3,CDC42BPA,TLR6,GPR65,UACA,DICER1,PPM1D,MAP2K4,SEMA7A,PIN1,SS18,BAG5,ROCK1,THOC1,MYOM1,RICTOR,VAPA,C1QTNF3,USP7,TBXA2R,PAFAH1B1,GADD45B,ENO1,VAV2,RAPGEF1,RFWD3,SSX2IP,PRKACB,CTGF,BDKRB2,LAMTOR3,NOV,RAP2A,VGLL4,C12orf66,UBE2V1,WNT7A	darkolivegreen	VSMC_M9
GO:0006809	0.43	0.76	4	55	nitric oxide biosynthetic process	BP	1	JAK2,ROCK2,PTGS2,TLR6	darkolivegreen	VSMC_M9
GO:1904659	0.43	0.73	6	80	glucose transmembrane transport	BP	1	RTN2,OSBPL8,FFAR4,APPL1,HK2,ZDHHC7	darkolivegreen	VSMC_M9
GO:0140014	0.43	0.67	16	244	mitotic nuclear division	BP	1	CDC23,CENPC,CAV2,CCDC8,RB1,PDS5B,UBXN2B,RIOK2,MAP9,INO80,CUL3,TPR,CDC27,PIN1,CDK13,MZT1	darkolivegreen	VSMC_M9
GO:0014074	0.44	0.70	8	109	response to purine-containing compound	BP	1	CDO1,AKAP9,NOX4,XRN1,ITPR2,PTGS2,ADSS,RAPGEF1	darkolivegreen	VSMC_M9
GO:0048514	0.44	0.63	34	508	blood vessel morphogenesis	BP	1	THBS2,HDAC9,ROCK2,ITGB1,GPR4,JMJD6,STARD13,SOS1,ITGA5,EIF2AK3,SULF1,AGTR1,HK2,RASA1,THBS1,ACVR1,ADAM12,NRP2,CLEC14A,PTGS2,ITGAV,PRRX1,AKT3,MYO1E,SRPX2,PKM,MYOCD,ROCK1,TBXA2R,VAV2,BMPR2,CTGF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0034284	0.44	0.68	11	164	response to monosaccharide	BP	1	KIF5B,THBS1,SLC39A14,BRSK2,IGF1R,CCDC186,EIF2B5,C2CD2L,PTGS2,ITGA2,CTGF	darkolivegreen	VSMC_M9
GO:0034763	0.44	0.72	6	88	negative regulation of transmembrane transport	BP	1	UBQLN1,REM1,THBS1,ANK3,OAZ2,MIR186	darkolivegreen	VSMC_M9
GO:1901222	0.44	0.74	5	75	regulation of NIK/NF-kappaB signaling	BP	1	ILK,TLR2,UACA,C1QTNF3,NOV	darkolivegreen	VSMC_M9
GO:0032273	0.44	0.70	8	116	positive regulation of protein polymerization	BP	1	AKAP9,ACTR2,ACTR3,MAP1B,PFN2,RICTOR,SPIRE1,MYO1C	darkolivegreen	VSMC_M9

GO:0000381	0.44	0.75	4	52	regulation of alternative mRNA splicing, via spliceosome	BP	1	KHDRBS3,MBNL2,MBNL1,DYRK1A	darkolivegreen	VSMC_M9
GO:0044281	0.44	0.61	77	1301	small molecule metabolic process	BP	1	CDO1,RRM2B,AZIN1,SLC35B4,PLAA,ELOVL5,GNE,ZMPSTE24,RARS2,UGP2,KBTBD2,GFPT1,PNPLA8,UGGT1,PDSS1,NOX4,SUCLA2,CYP27C1,ABHD1,DARS,ACPP,B3GLCT,HSD17B12,PARG,PLPP1,PDE7A,TDG,MAT2A,RDH10,PLOD2,HK2,ALDH18A1,TLR2,PGAM4,GPD2,SLC39A14,NUDT9,SLC35B3,LRRK2,MRS2,ATP6V1A,EPRS,BPNT1,IARS2,IDH2,ATF3,DERA,NPL,MBTPS2,GATM,PTGS2,TPI1,GNPNAT1,PAPSS2,ADSS,HK3,PHKG2,CLK2,DLST,PKM,ETFA,DHRS7B,SLC1A3,C1QTNF3,TARS,USP7,PAFAH1B1,ACOT7,ENO1,DPM2,RANBP2,IMPA1,DPM1,ELOVL4,SRD5A2,AKR1D1,PPTC7	darkolivegreen	VSMC_M9
GO:0006879	0.44	0.75	4	56	cellular iron ion homeostasis	BP	1	NDFIP1,ATP6V0A2,SLC39A14,ATP6V1A	darkolivegreen	VSMC_M9
GO:0005976	0.44	0.72	6	83	polysaccharide metabolic process	BP	1	EXT1,UGP2,CSGALNACT2,PHKG2,CLTC,PPP1R2	darkolivegreen	VSMC_M9
GO:2001236	0.44	0.70	8	121	regulation of extrinsic apoptotic signaling pathway	BP	1	INHBA,FYN,THBS1,ACVR1,ATF3,ITGAV,SKIL,GDNF	darkolivegreen	VSMC_M9
GO:0006403	0.44	0.68	11	171	RNA localization	BP	1	UPF2,NUP37,DHX36,TOMM20,TPR,THOC1,NUP155,MYO1C,RANBP2,TOMM20L,NUP35	darkolivegreen	VSMC_M9
GO:0002688	0.44	0.72	6	92	regulation of leukocyte chemotaxis	BP	1	STAP1,CAMK1D,LYN,THBS1,ADAM10,NOV	darkolivegreen	VSMC_M9
GO:0034762	0.44	0.64	26	396	regulation of transmembrane transport	BP	1	UTRN,AZIN1,UBQLN1,AKAP9,ZMPSTE24,ITGB1,FYN,KIF5B,RTN2,OSBPL8,REM1,LYN,SLC30A5,FFAR4,APPL1,HK2,THBS1,GPR89A,ANK3,CLCNKB,STIM2,KCNMB1,OAZ2,MIR186,FXYD5,SHISA7	darkolivegreen	VSMC_M9
GO:0006022	0.44	0.71	7	98	aminoglycan metabolic process	BP	1	EXT1,DSE,ST3GAL3,CSGALNACT2,CHSY1,CLTC,CHST11	darkolivegreen	VSMC_M9
GO:0006644	0.44	0.65	20	314	phospholipid metabolic process	BP	1	SOCS6,PLAA,PNPLA8,OSBPL8,GPCPD1,PLPP1,ETNK2,MBOAT1,BPNT1,ETNK1,PIP5K1A,PLD1,TNFAIP8L3,SAMD8,PIGW,PAFAH1B1,PLPPR5,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0051058	0.44	0.75	4	49	negative regulation of small GTPase mediated signal transduction	BP	1	ITGB1,CCDC125,RASA1,CUL3	darkolivegreen	VSMC_M9
GO:0030239	0.44	0.75	4	51	myofibril assembly	BP	1	ITGB1,TPM1,FHOD3,CFL2	darkolivegreen	VSMC_M9
GO:0002526	0.44	0.75	4	58	acute inflammatory response	BP	1	EXT1,GATA3,ACVR1,PTGS2	darkolivegreen	VSMC_M9
GO:0050920	0.44	0.68	11	167	regulation of chemotaxis	BP	1	STAP1,CAMK1D,LYN,THBS1,NTRK3,SEMA5B,ADAM10,SEMA7A,ITGA2,BMPR2,NOV	darkolivegreen	VSMC_M9
GO:1990845	0.45	0.69	9	132	adaptive thermogenesis	BP	1	JAK2,RB1,HOXC10,LNPEP,FFAR4,IGF1R,GATM,TLE3,CIDEA	darkolivegreen	VSMC_M9
GO:0071300	0.45	0.75	4	52	cellular response to retinoic acid	BP	1	LYN,NTRK3,WNT5B,WNT9A	darkolivegreen	VSMC_M9
GO:1903533	0.45	0.73	5	69	regulation of protein targeting	BP	1	LMAN1,FYN,LRRK2,ANK3,MYO1C	darkolivegreen	VSMC_M9
GO:1903046	0.45	0.68	10	153	meiotic cell cycle process	BP	1	RMI1,CENPC,ACTR2,ACTR3,CCNA1,BRCA2,MYBL1,SYCP2,FMN2,SPIRE1	darkolivegreen	VSMC_M9
GO:0031047	0.45	0.69	8	129	gene silencing by RNA	BP	1	ZMPSTE24,PIWIL4,ERI1,CNOT7,DICER1,MYOCD,ZC3H7A,MIR186	darkolivegreen	VSMC_M9
GO:0014068	0.45	0.73	5	66	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	JAK2,FYN,UBE3A,IGF1R,NTRK3	darkolivegreen	VSMC_M9
GO:0015837	0.45	0.74	4	58	amine transport	BP	1	RAB3B,ITGB1,RAB3GAP1,GDNF	darkolivegreen	VSMC_M9
GO:0042254	0.45	0.65	15	256	ribosome biogenesis	BP	1	WDR46,RPF2,EXOSC9,RPL26,CUL4A,ERI1,DHX29,MTREX,RIOK2,WDR75,MTERF3,RRP15,FASTKD2,SURF6,TFB2M	darkolivegreen	VSMC_M9
GO:0042981	0.45	0.60	67	1092	regulation of apoptotic process	BP	1	MALT1,AHI1,RRM2B,UBQLN1,TOPORS,JAK2,INHBA,ITGB1,FYN,NOX4,RB1,CAMK1D,GATA3,DNAJC3,RPL26,UFM1,LIG4,ILK,ITGA5,TMF1,LYN,MERTK,EIF2AK3,ITCH,USP47,FFAR4,RASA1,THBS1,ACVR1,LRRK2,SLC39A10,IGF1R,PTPN1,KPNA1,EIF2B5,SYCP2,ATF3,CD3G,PTGS2,ITGAV,SKIL,KIFAP3,TNFAIP8L3,VDAC2,DKK1,FMN2,FAS,ADAM10,BNIP2,MAP2K4,MYOCD,PIN1,BAG5,ITGA1,BFAR,CIDEA,CD40LG,GADD45B,ENO1,ANKRD13C,ARF4,GDNF,BDKRB2,E2F3,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0002764	0.45	0.64	18	278	immune response-regulating signaling pathway	BP	1	MALT1,STAP1,FYN,GATA3,SOS1,LYN,ITCH,APPL1,TLR2,NFKBIZ,CBLB,SLC39A10,EIF2B5,GPATCH3,TLR6,MAP2K4,VAV2,FCN1	darkolivegreen	VSMC_M9
GO:0002262	0.45	0.68	9	134	myeloid cell homeostasis	BP	1	JAK2,INHBA,RB1,GATA3,JMJD6,UBA5,LYN,MERTK,ABCB10	darkolivegreen	VSMC_M9
GO:0062197	0.45	0.64	18	282	cellular response to chemical stress	BP	1	UBQLN1,JAK2,PNPLA8,GPX7,FYN,STK24,EIF2AK3,ATP2A2,LRRK2,PTGS2,CPEB2,FAS,TLR6,TPM1,BAG5,SLC25A24,BDKRB2,EFHD1	darkolivegreen	VSMC_M9
GO:0015908	0.45	0.74	4	60	fatty acid transport	BP	1	PNPLA8,THBS1,EPRS,BDKRB2	darkolivegreen	VSMC_M9
GO:0006633	0.45	0.70	7	107	fatty acid biosynthetic process	BP	1	ELOVL5,PNPLA8,ABHD1,HSD17B12,PTGS2,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0002532	0.45	0.74	4	59	production of molecular mediator involved in inflammatory response	BP	1	LYN,APPL1,KPNA6,TLR6	darkolivegreen	VSMC_M9
GO:1901264	0.45	0.74	4	61	carbohydrate derivative transport	BP	1	SLC35B4,SLC35B3,SLC25A24,SLC35D1	darkolivegreen	VSMC_M9
GO:0051052	0.45	0.64	19	297	regulation of DNA metabolic process	BP	1	NPAS2,ZMPSTE24,ACTR2,GATA3,RIF1,NDFIP1,CUL4A,PARG,XRN1,DHX36,NEK7,KPNA1,FMN2,THOC1,CIDEA,SPIRE1,USP7,BMPR2,UBE2V1	darkolivegreen	VSMC_M9
GO:0048646	0.45	0.60	58	877	anatomical structure formation involved in morphogenesis	BP	1	AHI1,EXT1,THBS2,TOPORS,HDAC9,COL12A1,HOXA11,ROCK2,INHBA,ITGB1,GPR4,GATA3,JMJD6,STARD13,ILK,ITGA5,DCHS1,TMF1,EIF2AK3,TMED2,SULF1,RDH10,AGTR1,HK2,TLR2,THBS1,ACVR1,CUL3,PHLDB2,ADAM12,NRP2,CLEC14A,PTGS2,FZD2,ITGAV,SKIL,DKK1,AKT3,TPM1,TBX6,SRPX2,PKM,DICER1,FHOD3,ROCK1,ITGA2,TBXA2R,PAFAH1B1,VAV2,COL11A1,PRKACB,BMPR2,GDNF,CTGF,NOV,CFL2,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0071772	0.45	0.68	9	126	response to BMP	BP	1	EXT1,GATA3,SMAD9,ILK,SULF1,ACVR1,SKIL,SMURF1,BMPR2	darkolivegreen	VSMC_M9

GO:0071773	0.45	0.68	9	126	cellular response to BMP stimulus	BP	1	EXT1,GATA3,SMAD9,ILK,SULF1,ACVR1,SKIL,SMURF1,BMPR2	darkolivegreen	VSMC_M9
GO:0007032	0.45	0.72	5	71	endosome organization	BP	1	STAM2,VPS36,EEA1,CORO1C,VAMP4	darkolivegreen	VSMC_M9
GO:0045926	0.45	0.66	13	195	negative regulation of growth	BP	1	CDKL3,INHBA,RB1,RNF6,WWC3,SEMA5B,RBBP7,SEMA7A,ENO1,WFDC1,BMPR2,NOV,VGLL4	darkolivegreen	VSMC_M9
GO:0055002	0.46	0.74	4	52	striated muscle cell development	BP	1	ITGB1,TPM1,FHOD3,CFL2	darkolivegreen	VSMC_M9
GO:0071456	0.46	0.69	8	119	cellular response to hypoxia	BP	1	UBQLN1,ROCK2,PTGS2,CPEB2,FMN2,KCNMB1,ENO1,AQP3	darkolivegreen	VSMC_M9
GO:0019752	0.46	0.61	39	659	carboxylic acid metabolic process	BP	1	CDO1,AZIN1,PLAA,ELOVL5,GNE,RARS2,GFPT1,PNPLA8,NOX4,SUCLA2,CYP27C1,ABHD1,DARS,HSD17B12,RDH10,PLOD2,HK2,ALDH18A1,TLR2,PGAM4,MRS2,EPRS,IARS2,IDH2,NPL,GATM,PTGS2,TPI1,ADSS,HK3,DLST,PKM,ETFA,SLC1A3,TARS,ACOT7,ENO1,ELOVL4,AKR1D1	darkolivegreen	VSMC_M9
GO:0006906	0.46	0.70	6	90	vesicle fusion	BP	1	CAV2,KIF5B,EEA1,YIPF5,USO1,VAMP4	darkolivegreen	VSMC_M9
GO:1903362	0.46	0.65	14	222	regulation of cellular protein catabolic process	BP	1	UBQLN1,PSMC2,NUB1,TMF1,LRRK2,UBE3A,UCHL5,TLK2,PITHD1,SMURF1,MSN,BAG5,USP7,VGLL4	darkolivegreen	VSMC_M9
GO:0032409	0.46	0.65	13	198	regulation of transporter activity	BP	1	UTRN,UBQLN1,AKAP9,ITGB1,KIF5B,NDFIP2,NDFIP1,REM1,ANK3,STIM2,MIR186,FXYD5,SHISA7	darkolivegreen	VSMC_M9
GO:0051099	0.46	0.68	9	141	positive regulation of binding	BP	1	JAK2,RB1,GATA3,CLN5,LRRK2,MYOCD,PIN1,ITGA2,GTF2B	darkolivegreen	VSMC_M9
GO:0050863	0.46	0.65	13	206	regulation of T cell activation	BP	1	SOCS6,MALT1,FYN,GATA3,LRRC32,NDFIP1,SOS1,HSPH1,LYN,ITCH,NFKBIZ,CBLB,CD40LG	darkolivegreen	VSMC_M9
GO:1903532	0.46	0.65	13	196	positive regulation of secretion by cell	BP	1	STXBP5,JAK2,EXOC1,INHBA,KIF5B,RAB3GAP1,TMF1,FAR4,TLR2,C2CD2L,MYOM1,C1QTNF3,GDNF	darkolivegreen	VSMC_M9
GO:0045860	0.46	0.63	20	305	positive regulation of protein kinase activity	BP	1	MALT1,JAK2,STAP1,CCDC88A,NOX4,CCNT2,OSBPL8,ILK,THBS1,NEDD9,LRRK2,NTRK3,PTPN1,IQGAP1,FERMT2,DKK1,TLR6,SRCIN1,RICTOR,BMPR2	darkolivegreen	VSMC_M9
GO:0032355	0.46	0.69	7	105	response to estradiol	BP	1	MAP1B,PTGS2,RBBP8,ITGA2,WFDC1,CTGF,WNT7A	darkolivegreen	VSMC_M9
GO:1990542	0.46	0.72	5	84	mitochondrial transmembrane transport	BP	1	MRS2,TIMM17A,TOMM20,AFG3L2,TOMM20L	darkolivegreen	VSMC_M9
GO:0022414	0.46	0.59	64	1029	reproductive process	BP	1	RMI1,CLOCK,PSME4,CENPC,HOXA9,HOXA10,HOXA11,UBE2J1,ACTR2,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,ACTR3,GATA3,TNFAIP6,ADAM32,TUBGCP3,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,TMED2,EIF2S2,SULF1,LNPEP,STOX2,MICAL2,RDH10,DHX36,PGAM4,ACVR1,IRX5,ETNK2,LRRK2,UBE3A,KPNA6,LARP7,EIF2B5,SYCP2,PITHD1,ZFX,PTGS2,SKIL,VDAC2,FMN2,MAGED2,ADAM10,ADAM19,MYOCD,RBBP8,ITGA2,SPIRE1,PAFAH1B1,PRKACB,BMPR2,ANKRD49,PAQR8,SRD5A2,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0002274	0.46	0.67	10	156	myeloid leukocyte activation	BP	1	JAK2,STAP1,JMJD6,LYN,TLR2,THBS1,LRRK2,TLR6,ADAM10,CLEC4D	darkolivegreen	VSMC_M9
GO:0007041	0.46	0.69	7	100	lysosomal transport	BP	1	GCC2,TRAK1,SCYL2,SPTBN5,LRRK2,TRAK2,GPRASP1	darkolivegreen	VSMC_M9
GO:0097696	0.46	0.69	7	105	receptor signaling pathway via STAT	BP	1	SOCS6,PTPRD,JAK2,FYN,MGAT5,CNOT7,LYN	darkolivegreen	VSMC_M9
GO:1903050	0.46	0.66	12	192	regulation of proteolysis involved in cellular protein catabolic process	BP	1	UBQLN1,PSMC2,NUB1,TMF1,LRRK2,UBE3A,UCHL5,TLK2,PITHD1,SMURF1,BAG5,USP7	darkolivegreen	VSMC_M9
GO:2000379	0.46	0.73	4	57	positive regulation of reactive oxygen species metabolic process	BP	1	NOX4,AGTR1,THBS1,TLR6	darkolivegreen	VSMC_M9
GO:1904019	0.46	0.70	6	86	epithelial cell apoptotic process	BP	1	JAK2,RB1,GATA3,THBS1,CD40LG,BMPR2	darkolivegreen	VSMC_M9
GO:0051222	0.46	0.64	16	241	positive regulation of protein transport	BP	1	JAK2,EXOC1,FYN,KIF5B,EDEM1,XPO4,TLR2,C2CD2L,ANK3,TPR,PTGS2,OAZ2,MYOM1,C1QTNF3,MYO1C,ZPR1	darkolivegreen	VSMC_M9
GO:0090630	0.46	0.69	7	93	activation of GTPase activity	BP	1	TBC1D15,CCDC125,NEDD9,CORO1C,NTRK3,PIP5K1A,GPR65	darkolivegreen	VSMC_M9
GO:0014013	0.46	0.71	5	73	regulation of gliogenesis	BP	1	LYN,TLR2,NTRK3,IDH2,DICER1	darkolivegreen	VSMC_M9
GO:1903034	0.46	0.68	8	123	regulation of response to wounding	BP	1	WISP1,ITGB1,STK24,THBS1,PHLDB2,FERMT2,TBXA2R,WFDC1	darkolivegreen	VSMC_M9
GO:0043405	0.46	0.66	10	146	regulation of MAP kinase activity	BP	1	CBLC,ILK,LYN,THBS1,LRRK2,NTRK3,PTPN1,IQGAP1,DKK1,TLR6	darkolivegreen	VSMC_M9
GO:0071216	0.46	0.66	10	157	cellular response to biotic stimulus	BP	1	MALT1,PLAA,STAP1,ZMPSTE24,LYN,EIF2AK3,TLR2,CCDC47,TLR6,TBXA2R	darkolivegreen	VSMC_M9
GO:0051129	0.46	0.60	37	569	negative regulation of cellular component organization	BP	1	CDKL3,CHADL,STAP1,ROCK2,FYN,PICALM,RNF6,SACS,XRN1,MAP1B,TLR2,PFN2,THBS1,DYRK1A,SPTBN5,LRRK2,UBE3A,PHLDB2,CAMSAP2,CORO1C,SEMA5B,TRAK2,HDGFL3,TPR,IQCJ-SCHIP1,DNAJA4,ITGAV,VDAC2,DKK1,TBX6,FHOD3,SEMA7A,CCP110,BAG5,ROCK1,PAFAH1B1,PMEPA1	darkolivegreen	VSMC_M9
GO:2001235	0.46	0.70	6	98	positive regulation of apoptotic signaling pathway	BP	1	INHBA,RPL26,THBS1,ATF3,SKIL,FAS	darkolivegreen	VSMC_M9
GO:0008645	0.46	0.70	6	83	hexose transmembrane transport	BP	1	RTN2,OSBPL8,FFAR4,APPL1,HK2,ZDHHC7	darkolivegreen	VSMC_M9
GO:0008361	0.47	0.66	11	157	regulation of cell size	BP	1	CDKL3,ILK,RNF6,MAP1B,SEMA5B,AKT3,MSN,SEMA7A,PAFAH1B1,VAV2,BMPR2	darkolivegreen	VSMC_M9
GO:0048878	0.47	0.59	53	832	chemical homeostasis	BP	1	EXT1,SLC39A7,WISP1,SLC30A9,ABCB4,TMEM165,JAK2,HDAC9,CAV2,PNPLA8,FYN,KIF5B,GPR4,PICALM,CLN5,TMTC2,ATP2B1,NDFIP1,LYN,ATP6V0A2,SLC30A5,FFAR4,AGTR1,HK2,ATP2A2,SLC39A14,ATP1A1,LRRK2,BRSK2,UBE3A,SLC39A10,ATP6V1A,IGF1R,GPR89A,CCDC186,ITPR2,VAPB,C2CD2L,ANK3,CCDC47,ATP13A3,ITGAV,STIM2,HK3,GPR65,ANXA6,SLC1A3,AFG3L2,C1QTNF3,TBXA2R,PRKACB,AQP3,BDKRB2	darkolivegreen	VSMC_M9
GO:2001252	0.47	0.71	5	72	positive regulation of chromosome organization	BP	1	LIG4,DHX36,KIAA1551,NEK7,TPR	darkolivegreen	VSMC_M9
GO:0001505	0.47	0.66	10	147	regulation of neurotransmitter levels	BP	1	STXBP5,RAB3B,ITGB1,RAB3GAP1,ATP2A2,LRRK2,SEPT5,SLC1A3,GDNF,WNT7A	darkolivegreen	VSMC_M9

GO:0000003	0.47	0.59	64	1031	reproduction	BP	1	RMI1,CLOCK,PSME4,CENPC,HOXA9,HOXA10,HOXA11,UBE2J1,ACTR2,INHBA,ITGB1,CEP57,PIWIL4,FNDC3A,ACTR3,GATA3,TNFAIP6,ADAM32,TUBGCP3,CCNA1,SOS1,BRCA2,TMF1,MERTK,MYBL1,TMED2,EIF2S2,SULF1,LNPEP,STOX2,MICAL2,RDH10,DHX36,PGAM4,ACVR1,IRX5,ETNK2,LRRK2,UBE3A,KPNA6,LARP7,EIF2B5,SYCP2,PITHD1,ZFX,PTGS2,SKIL,VDAC2,FMN2,MAGED2,ADAM10,ADAM19,MYOCD,RBBP8,ITGA2,SPIRE1,PAFAH1B1,PRKACB,BMPR2,ANKRD49,PAQR8,SRD5A2,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0002703	0.47	0.67	9	136	regulation of leukocyte mediated immunity	BP	1	MALT1,STAP1,DDX1,GATA3,RIF1,NDFIP1,LYN,DHX36,THOC1	darkolivegreen	VSMC_M9
GO:0007043	0.47	0.68	7	99	cell-cell junction assembly	BP	1	ROCK2,MPP7,DCHS1,ROCK1,MYO1C,CDH11,IRX3	darkolivegreen	VSMC_M9
GO:0032526	0.47	0.70	6	84	response to retinoic acid	BP	1	LYN,GDAP1,NTRK3,WNT5B,AQP3,WNT9A	darkolivegreen	VSMC_M9
GO:0050868	0.47	0.71	5	76	negative regulation of T cell activation	BP	1	SOCS6,LRRC32,NDFIP1,ITCH,CBLB	darkolivegreen	VSMC_M9
GO:0044344	0.47	0.69	6	86	cellular response to fibroblast growth factor stimulus	BP	1	EXT1,CEP57,GATA3,SULF1,THBS1,CTGF	darkolivegreen	VSMC_M9
GO:0031334	0.47	0.64	13	199	positive regulation of protein-containing complex assembly	BP	1	CAND1,AKAP9,ACTR2,MPP7,ACTR3,MAP1B,PFN2,FERMT2,TLR6,MSN,RICTOR,SPIRE1,MYO1C	darkolivegreen	VSMC_M9
GO:0048259	0.47	0.69	6	85	regulation of receptor-mediated endocytosis	BP	1	AHI1,PICALM,SCYL2,ITGAV,DKK1,ATAD1	darkolivegreen	VSMC_M9
GO:0050714	0.47	0.68	7	100	positive regulation of protein secretion	BP	1	JAK2,EXOC1,KIF5B,TLR2,C2CD2L,MYOM1,C1QTNF3	darkolivegreen	VSMC_M9
GO:0046483	0.47	0.56	263	4376	heterocycle metabolic process	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,RRM2B,WDR46,DDX46,PHF20L1,KHDRBS3,ETF1,RMI1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,GNE,ZNF451,TRMO,HDAC9,CAVIN4,PSME4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,ZEB1,EXOSC9,PIWIL4,UGGT1,RB1,SUCLA2,PICALM,ZC3H13,TRDMT1,TOE1,TSN,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,ORC4,MBNL2,RIF1,PPP1R12A,PRPF40A,RPL26,LIG4,CEBPZ,SUPT20H,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,HSD17B12,PARG,MTREX,CNOT7,RNF6,PDE7A,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,U2SURP,ACTR8,HK2,ALDH18A1,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,PGAM4,ACVR1,WDR75,IRX5,MTERF3,INO80,NUDT9,SNRNP48,SLC35B3,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,NFRKB,CUL3,TDP2,PUS3,TROVE2,UCHL5,ATP6V1A,KPNA6,RRP15,EPRS,BPNT1,IARS2,NEK7,WWC3,LARP7,KPNA1,CLK1,IDH2,TAF5L,ABCB10,TRAK2,GPATCH3,LRRFIP1,ATF3,DERA,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,TPI1,MYNN,GNPNAT1,SKIL,DTWD1,PRRX1,BOD1L1,DKK1,FMN2,PAPSS2,ADSS,RBM47,NOTCH3,TLR6,MAGED2,HK3,CLK2,DLST,TRIP4,TBX6,RLIM,MAGEE2,INTS14,ZC3H14,RBBP6,TLE3,SMG8,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,CIDEA,SPIRE1,GSPT1,TARS,ZC3H7A,MYSM1,CD40LG,USP7,LSM5,ACOT7,ENO1,RFWD3,DNTTIP2	darkolivegreen	VSMC_M9
GO:0035265	0.47	0.66	9	134	organ growth	BP	1	EXT1,ZMPSTE24,PDLIM5,UBE3A,WWC3,MAP2K4,ANXA6,PIN1,VGLL4	darkolivegreen	VSMC_M9
GO:0007265	0.47	0.62	20	296	Ras protein signal transduction	BP	1	DENND4C,CAVIN4,ROCK2,ITGB1,GPR4,RB1,CYTH1,STARD13,SOS1,CCDC125,AGTR1,RASA1,BRAP,CUL3,PLD1,GPR65,ROCK1,RAPGEF1,SSX2IP,RAP2A	darkolivegreen	VSMC_M9
GO:0030855	0.47	0.61	28	430	epithelial cell differentiation	BP	1	AHI1,EXT1,CLOCK,MYO6,ROCK2,ZEB1,FNDC3A,GPR4,GATA3,PALLD,ACVR1,PIP5K1A,IQGAP1,FZD2,SKIL,ACTA2,WNT5B,MSN,MYO1E,ROCK1,ITGA2,PAFAH1B1,RAPGEF1,ZDHHC7,BMPR2,AQP3,GDNF,WNT7A	darkolivegreen	VSMC_M9
GO:0031098	0.47	0.64	13	197	stress-activated protein kinase signaling cascade	BP	1	ZMPSTE24,LYN,ITCH,LRRK2,IGF1R,TNIK,FAS,MAP2K4,PAFAH1B1,GADD45B,CTGF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0035418	0.47	0.72	4	54	protein localization to synapse	BP	1	KIF5B,ADAM10,GPC4,WNT7A	darkolivegreen	VSMC_M9
GO:0048488	0.48	0.72	4	52	synaptic vesicle endocytosis	BP	1	PICALM,LRRK2,VAMP4,ROCK1	darkolivegreen	VSMC_M9
GO:0140238	0.48	0.72	4	52	presynaptic endocytosis	BP	1	PICALM,LRRK2,VAMP4,ROCK1	darkolivegreen	VSMC_M9
GO:0001525	0.48	0.60	28	428	angiogenesis	BP	1	THBS2,HDAC9,ROCK2,ITGB1,GPR4,JMJD6,STARD13,ITGA5,EIF2AK3,SULF1,AGTR1,HK2,THBS1,ACVR1,ADAM12,NRP2,CLEC14A,PTGS2,ITGAV,AKT3,SRPX2,PKM,ROCK1,TBXA2R,VAV2,CTGF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:1903829	0.48	0.62	16	241	positive regulation of cellular protein localization	BP	1	JAK2,CCDC88A,ROCK2,ITGB1,FYN,KIF5B,EIF2AK3,LARP7,IQGAP1,ANK3,TPR,PTGS2,FERMT2,MSN,MYO1C,ZPR1	darkolivegreen	VSMC_M9
GO:0015749	0.48	0.68	6	84	monosaccharide transmembrane transport	BP	1	RTN2,OSBPL8,FFAR4,APPL1,HK2,ZDHHC7	darkolivegreen	VSMC_M9
GO:0033138	0.48	0.70	5	74	positive regulation of peptidyl-serine phosphorylation	BP	1	TBK1,AKAP9,PFN2,NTRK3,PTGS2	darkolivegreen	VSMC_M9
GO:0032091	0.48	0.70	5	76	negative regulation of protein binding	BP	1	ATP2A2,LRRK2,DKK1,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:0008585	0.48	0.70	5	72	female gonad development	BP	1	INHBA,BRCA2,UBE3A,EIF2B5,ZFX	darkolivegreen	VSMC_M9
GO:0010812	0.48	0.72	4	53	negative regulation of cell-substrate adhesion	BP	1	RASA1,THBS1,PHLDB2,CORO1C	darkolivegreen	VSMC_M9
GO:0007568	0.48	0.62	16	252	aging	BP	1	ZMPSTE24,NOX4,PICALM,ATP2B1,BRCA2,ILK,LRRK2,CASP7,EIF2B5,PTGS2,DKK1,AKT3,KCNMB1,MAP2K4,CTGF,SEC63	darkolivegreen	VSMC_M9
GO:0043523	0.48	0.64	11	169	regulation of neuron apoptotic process	BP	1	JAK2,FYN,GATA3,LIG4,ILK,RASA1,MAP2K4,PIN1,ITGA1,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0051591	0.48	0.70	5	68	response to cAMP	BP	1	CDO1,AKAP9,NOX4,ITPR2,RAPGEF1	darkolivegreen	VSMC_M9

GO:0006690	0.48	0.71	4	62	icosanoid metabolic process	BP	1	PLAA,PNPLA8,TLR2,PTGS2	darkolivegreen	VSMC_M9
GO:0030865	0.48	0.72	4	55	cortical cytoskeleton organization	BP	1	ROCK2,FHOD3,ROCK1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0040029	0.48	0.68	6	86	regulation of gene expression, epigenetic	BP	1	TDG,SMARCA5,KIAA1551,TPR,RLIM,PPM1D	darkolivegreen	VSMC_M9
GO:0032922	0.48	0.71	4	55	circadian regulation of gene expression	BP	1	CLOCK,NPAS2,GFPT1,NOCT	darkolivegreen	VSMC_M9
GO:2000106	0.48	0.71	4	59	regulation of leukocyte apoptotic process	BP	1	LYN,MERTK,SLC39A10,CD3G	darkolivegreen	VSMC_M9
GO:0070988	0.48	0.71	4	52	demethylation	BP	1	GATA3,JMJD6,TDG,USP7	darkolivegreen	VSMC_M9
GO:1903363	0.48	0.71	4	60	negative regulation of cellular protein catabolic process	BP	1	UCHL5,TLK2,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0003002	0.49	0.62	16	251	regionalization	BP	1	AHI1,EXT1,HOXA9,HOXA10,HOXA11,TMED2,ACVR1,CHSY1,NRP2,DKK1,TBX6,PRKACB,BMPR2,GDNF,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0009260	0.49	0.65	9	149	ribonucleotide biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,ATP6V1A,PAPSS2,ADSS,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0046660	0.49	0.68	6	88	female sex differentiation	BP	1	INHBA,BRCA2,MERTK,UBE3A,EIF2B5,ZFX	darkolivegreen	VSMC_M9
GO:0016239	0.49	0.71	4	56	positive regulation of macroautophagy	BP	1	TBK1,RAB3GAP1,SUPT5H,RAB3GAP2	darkolivegreen	VSMC_M9
GO:0046854	0.49	0.71	4	54	phosphatidylinositol phosphate biosynthetic process	BP	1	SOCS6,BPNT1,PIP5K1A,IMPA1	darkolivegreen	VSMC_M9
GO:0035773	0.49	0.71	4	58	insulin secretion involved in cellular response to glucose stimulus	BP	1	KIF5B,BRSK2,CCDC186,C2CD2L	darkolivegreen	VSMC_M9
GO:0043280	0.49	0.68	6	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MALT1,JAK2,EIF2AK3,FAS,UACA,CTGF	darkolivegreen	VSMC_M9
GO:1901700	0.49	0.56	77	1234	response to oxygen-containing compound	BP	1	MALT1,CDO1,EXT1,DENND4C,PLAA,ABCB4,AKAP9,JAK2,HDAC9,STAP1,KBTBD2,ACTR2,CHRM2,CAV2,ROCK2,INHBA,NOCT,FYN,KIF5B,NOX4,GATA3,EDEM1,STK24,OSBPL8,ATP2B1,LYN,GRAMD1A,XRN1,MAP1B,APPL1,GDAP1,AGTR1,TLR2,ATP2A2,USO1,DHX36,THBS1,SLC39A14,ATP1A1,LRRK2,BRSK2,UBE3A,EIF4E,EPRS,IGF1R,CCDC186,ITPR2,NTRK3,TOMM20,PTPN1,EIF2B5,C2CD2L,IQGAP1,PTGS2,CPEB2,WNT5B,TLR6,MSN,KCNMB1,TPM1,PKM,MAP2K4,RBBP8,ROCK1,ITGA2,SLC1A3,RAB31,MYO1C,TBXA2R,RAPGEF1,ZDHHC7,WFDC1,AQP3,CTGF,LAMTOR3,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:0006643	0.49	0.64	10	164	membrane lipid metabolic process	BP	1	ELOVL5,ST3GAL3,PLPP1,CERS5,ST8SIA1,SAMD8,PIGW,DPM2,DPM1,ELOVL4	darkolivegreen	VSMC_M9
GO:0061138	0.49	0.64	10	147	morphogenesis of a branching epithelium	BP	1	EXT1,HOXA11,NTN4,ILK,DCHS1,TMED2,SULF1,RDH10,ACVR1,GDNF	darkolivegreen	VSMC_M9
GO:0051252	0.49	0.54	166	2654	regulation of RNA metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,KHDRBS3,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,PICALM,TRDMT1,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,MBNL2,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,PDE12,STOX2,MICAL2,ACTR8,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,KPNA6,WWC3,LARP7,CLK1,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,MYNN,SKIL,PRRX1,DKK1,NOTCH3,TLR6,MAGED2,CLK2,TRIP4,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,FASTKD5,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0061025	0.49	0.65	8	125	membrane fusion	BP	1	CAV2,KIF5B,EEA1,YIPF5,UBXN2B,USO1,VAMP4,VAPA	darkolivegreen	VSMC_M9
GO:0042752	0.49	0.67	6	89	regulation of circadian rhythm	BP	1	CLOCK,ROCK2,NOCT,FBXL17,UBE3A,USP7	darkolivegreen	VSMC_M9
GO:0006164	0.49	0.64	9	149	purine nucleotide biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,ATP6V1A,PAPSS2,ADSS,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0034644	0.49	0.69	5	77	cellular response to UV	BP	1	RPL26,USP47,DHX36,INO80,PTGS2	darkolivegreen	VSMC_M9
GO:2000058	0.49	0.64	9	143	regulation of ubiquitin-dependent protein catabolic process	BP	1	UBQLN1,NUB1,LRRK2,UBE3A,UCHL5,TLK2,SMURF1,BAG5,USP7	darkolivegreen	VSMC_M9
GO:1901214	0.49	0.61	16	251	regulation of neuron death	BP	1	TBK1,JAK2,FYN,PICALM,GATA3,LIG4,ILK,RASA1,LRRK2,DKK1,TLR6,MAP2K4,PIN1,ITGA1,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0034754	0.50	0.68	5	79	cellular hormone metabolic process	BP	1	CYP27C1,HSD17B12,RDH10,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0009953	0.50	0.70	4	60	dorsal/ventral pattern formation	BP	1	HOXA11,ACVR1,PRKACB,WNT7A	darkolivegreen	VSMC_M9
GO:0009894	0.50	0.56	50	806	regulation of catabolic process	BP	1	TBK1,AZIN1,ATP6V1C1,UBQLN1,EXOC1,ZMPSTE24,ROCK2,NOCT,ITGB1,FYN,EXOSC9,PSMC2,TRDMT1,NUB1,RAB3GAP1,SUPT5H,NDFIP1,TMF1,CNOT7,ATP6V0A2,ITCH,PDE12,DCP1A,DHX36,CBLB,LRRK2,UBE3A,UCHL5,ATP6V1A,RAB3GAP2,PTPN1,TLK2,PITHD1,FASTKD2,MYEF2,SMURF1,FMN2,MSN,PHKG2,OAZ2,ZC3H14,PIN1,BAG5,ROCK1,CIDEA,USP7,ZDHHC7,FASTKD5,GDNF,VGLL4	darkolivegreen	VSMC_M9
GO:0000377	0.50	0.61	15	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1	DDX46,KHDRBS3,PPIL1,DDX1,JMJD6,MBNL2,PRPF40A,MTREX,MBNL1,DYRK1A,LARP7,CWC22,LSM5,CDK13,GEMIN6	darkolivegreen	VSMC_M9

GO:0000398	0.50	0.61	15	255	mRNA splicing, via spliceosome	BP	1	DDX46,KHDRBS3,PPIL1,DDX1,JMJD6,MBNL2,PRPF40A,MTREX,MBNL1,DYRK1A,LARP7,CWC22,LSM5,CDK13,GEMIN6	darkolivegreen	VSMC_M9
GO:0008360	0.50	0.64	9	134	regulation of cell shape	BP	1	ZMPSTE24,FYN,PRPF40A,RASA1,ATP10A,SH3KBP1,FERMT2,MSN,TPM1	darkolivegreen	VSMC_M9
GO:1903312	0.50	0.68	5	74	negative regulation of mRNA metabolic process	BP	1	NOCT,SUPT5H,DYRK1A,ZC3H14,GDNF	darkolivegreen	VSMC_M9
GO:0030509	0.50	0.64	8	116	BMP signaling pathway	BP	1	EXT1,SMAD9,ILK,SULF1,ACVR1,SKIL,SMURF1,BMPR2	darkolivegreen	VSMC_M9
GO:0055117	0.50	0.70	4	58	regulation of cardiac muscle contraction	BP	1	AKAP9,ATP2A2,ATP1A1,CTGF	darkolivegreen	VSMC_M9
GO:0034219	0.50	0.66	6	86	carbohydrate transmembrane transport	BP	1	RTN2,OSBPL8,FFAR4,APPL1,HK2,ZDHHC7	darkolivegreen	VSMC_M9
GO:0007166	0.50	0.54	122	1935	cell surface receptor signaling pathway	BP	1	SOCS6,MALT1,AHI1,TBK1,EXT1,WISP1,PTPRD,BTBD11,JAK2,ASPN,ZNF451,STAP1,CCDC88A,CAV2,INHBA,ITGB1,FYN,CEP57,RB1,SUSD5,CBLC,MGAT5,GATA3,RAB3GAP1,JMJD6,LRRC32,OSBPL8,SMAD9,ACPP,SOS1,ILK,ITGA5,SCYL2,CNOT7,LYN,MERTK,EIF2AK3,FBXL17,SULF1,USP47,APPL1,TLR2,RASA1,THBS1,SHOX2,ARL6,ACVR1,SLC39A14,NFKBIZ,NEDD9,CBLB,BRD7,LRRK2,SLC39A10,CUL3,TDP2,DNER,TROVE2,UCHL5,CHSY1,IGF1R,NTRK3,PTPN1,KPNA1,SEMA5B,EIF2B5,ATF3,IQGAP1,CD3G,NRP2,CLEC14A,NCAM1,FZD2,GPR34,ZC3H15,ITGAV,FERMT2,SKIL,PRRX1,SMURF1,TNIK,KIAA0586,DKK1,FAS,PLP2,WNT5B,NOTCH3,ADAM10,MYO1E,CYFIP2,TLE3,MAP2K4,MYOCD,SEMA7A,PIN1,SS18,ITGA2,ITGA1,CIDEA,GPC4,CD40LG,MYO1C,PAFAH1B1,VAV2,RAPGEF1,ZDHHC7,PRKACB,BMPR2,PTPN12,ARF4,GDNF,GP1BB,CTGF,BDKRB2,NOV,PDCL,FCN1,PMEPA1,WNT9A,VGLL4,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:1901991	0.50	0.63	9	142	negative regulation of mitotic cell cycle phase transition	BP	1	RINT1,RB1,RPL26,MYO16,USP47,BRD7,TPR,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0001656	0.50	0.68	5	74	metanephros development	BP	1	HOXA11,GATA3,RDH10,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0006893	0.50	0.70	4	56	Golgi to plasma membrane transport	BP	1	EXOC1,ANK3,BLZF1,RAB31	darkolivegreen	VSMC_M9
GO:0090174	0.50	0.66	6	94	organelle membrane fusion	BP	1	CAV2,KIF5B,EEA1,YIPF5,USO1,VAMP4	darkolivegreen	VSMC_M9
GO:0044403	0.50	0.61	13	206	biological process involved in symbiotic interaction	BP	1	CAV2,ITGB1,ITGA5,ITCH,CHD1,AGTR1,VAPB,NCAM1,ITGAV,THOC1,ITGA2,VAPA,FCN1	darkolivegreen	VSMC_M9
GO:0043549	0.50	0.56	39	612	regulation of kinase activity	BP	1	SOCS6,MALT1,JAK2,STAP1,CCDC88A,SH3BP5L,NOX4,RB1,CBLC,CCNT2,OSBPL8,PIK3R4,CCNA1,ILK,LYN,MERTK,IPO7,THBS1,NEDD9,CBLB,LRRK2,IGF1R,CORO1C,NTRK3,PTPN1,IQGAP1,FERMT2,TNFAIP8L3,DKK1,TLR6,SRCIN1,SMG8,MYOCD,RICTOR,GADD45B,VAV2,RANBP2,BMPR2,LAMTOR3	darkolivegreen	VSMC_M9
GO:0050680	0.50	0.65	7	108	negative regulation of epithelial cell proliferation	BP	1	CAV2,RB1,GATA3,BRCA2,SULF1,THBS1,WFDC1	darkolivegreen	VSMC_M9
GO:0014066	0.50	0.66	6	86	regulation of phosphatidylinositol 3-kinase signaling	BP	1	JAK2,FYN,UBE3A,IGF1R,NTRK3,PIP5K1A	darkolivegreen	VSMC_M9
GO:0051057	0.51	0.69	4	55	positive regulation of small GTPase mediated signal transduction	BP	1	GPR4,SOS1,ITGAV,GPR65	darkolivegreen	VSMC_M9
GO:1903076	0.51	0.66	6	90	regulation of protein localization to plasma membrane	BP	1	ITGB1,KIF5B,PICALM,APPL1,CLTC,ZDHHC7	darkolivegreen	VSMC_M9
GO:1901379	0.51	0.69	4	56	regulation of potassium ion transmembrane transport	BP	1	AKAP9,ITGB1,ANK3,KCNMB1	darkolivegreen	VSMC_M9
GO:0060415	0.51	0.69	4	56	muscle tissue morphogenesis	BP	1	SHOX2,FZD2,TPM1,COL11A1	darkolivegreen	VSMC_M9
GO:0034308	0.51	0.69	4	61	primary alcohol metabolic process	BP	1	CYP27C1,ACPP,RDH10,GPD2	darkolivegreen	VSMC_M9
GO:0006725	0.51	0.52	264	4410	cellular aromatic compound metabolic process	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,RRM2B,WDR46,DDX46,PHF20L1,KHDRBS3,ETF1,RMI1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,GNE,ZNF451,TRMO,HDAC9,CAVIN4,PSME4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,ZEB1,EXOSC9,PIWIL4,UGGT1,RB1,SUCLA2,PICALM,ZC3H13,TRDMT1,TOE1,TSN,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,ORC4,MBNL2,RIF1,PPP1R12A,PRPF40A,RPL26,LIG4,CEBPZ,SUPT20H,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,HSD17B12,PARG,MTREX,CNOT7,RNF6,PDE7A,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,APPL1,U2SURP,ACTR8,HK2,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,PGAM4,ACVR1,WDR75,IRX5,MTERF3,INO80,NUDT9,GCNT4,SNRNP48,SLC35B3,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,NFRKB,CUL3,TDP2,PUS3,TROVE2,UCHL5,ATP6V1A,KPNA6,RRP15,EPRS,BPNT1,IARS2,NEK7,WWC3,LARP7,KPNA1,CLK1,IDH2,TAF5L,ABCB10,TRAK2,GPATCH3,LRRFIP1,ATF3,DERA,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,TPI1,MYNN,GNPNAT1,SKIL,DTWD1,PRRX1,BOD1L1,DKK1,FMN2,PAPSS2,ADSS,RBM47,NOTCH3,TLR6,MAGED2,HK3,CLK2,DLST,TRIP4,TBX6,RLIM,MAGEE2,INTS14,ZC3H14,RBBP6,TLE3,SMG8,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,CIDEA,SPIRE1,GSPT1,TARS,ZC3H7A,MYSM1,CD40LG,USP7,LSM5,ACOT7,ENO1,RFWD3,DNTTIP2,ZNF644,ZNF326,CTF2P,THAP11,ENOPA31,SNORA	darkolivegreen	VSMC_M9
GO:0009411	0.51	0.64	8	127	response to UV	BP	1	RPL26,BRCA2,USP47,DHX36,INO80,TROVE2,CASP7,PTGS2	darkolivegreen	VSMC_M9
GO:0001885	0.51	0.69	4	53	endothelial cell development	BP	1	ROCK2,MSN,ROCK1,RAPGEF1	darkolivegreen	VSMC_M9
GO:0001935	0.51	0.63	8	123	endothelial cell proliferation	BP	1	CAV2,SULF1,AGTR1,THBS1,NRP2,AKT3,RICTOR,BMPR2	darkolivegreen	VSMC_M9
GO:0071901	0.51	0.65	6	93	negative regulation of protein serine/threonine kinase activity	BP	1	RB1,CBLC,LYN,IPO7,PTPN1,MYOCD	darkolivegreen	VSMC_M9

GO:0046883	0.51	0.61	11	174	regulation of hormone secretion	BP	1	JAK2,CLOCK,INHBA,KIF5B,TMF1,FFAR4,AGTR1,BRSK2,C2CD2L,C1QTNF3,NOV	darkolivegreen	VSMC_M9
GO:0045927	0.51	0.60	13	199	positive regulation of growth	BP	1	PLAA,EXOSC9,ILK,USP47,MAP1B,INO80,SMURF1,ADAM10,SEMA7A,PIN1,PAFAH1B1,BMPR2,ZPR1	darkolivegreen	VSMC_M9
GO:0046777	0.51	0.60	14	204	protein autophosphorylation	BP	1	JAK2,FYN,STK24,LYN,EIF2AK3,RIOK2,DYRK1A,LRRK2,IGF1R,CLK1,IQGAP1,TNIK,CLK2,RAP2A	darkolivegreen	VSMC_M9
GO:0045935	0.51	0.53	93	1489	positive regulation of nucleobase-containing compound metabolic process	BP	1	AHI1,TBK1,CAND1,SLC30A9,TOPORS,CLOCK,NPAS2,ZNF451,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,ROCK2,INHBA,NOCT,EXOSC9,RB1,PICALM,ACTR3,GATA3,CCNT2,JMJD6,BRPF1,SUPT5H,RIF1,PPP1R12A,CEBPZ,SMAD9,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,HCFC2,SMARCA5,RIOK2,PDE12,STOX2,MICAL2,TLR2,DCP1A,DHX36,ACVR1,WDR75,INO80,DYRK1A,BRD7,ERG,UBE3A,KPNA6,NEK7,LARP7,TAF5L,GPATCH3,ATF3,EDRF1,BCLAF3,PITHD1,MBTPS2,CREB3L2,FZD2,NPAT,PRRX1,FMN2,TRIP4,TBX6,ARMCX3,MYOCD,PIN1,SS18,ROCK1,THOC1,SPIRE1,MYSM1,USP7,ENO1,BMPR2,ANKRD49,ARF4,GDNF,CDK13,RFXAP,E2F3,GLIS3,ZPR1,UBE2V1,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0046649	0.51	0.56	29	470	lymphocyte activation	BP	1	SOCS6,MALT1,TBK1,HDAC9,INHBA,ITGB1,FYN,GATA3,JMJD6,LRRC32,AZI2,RIF1,LIG4,NDFIP1,SOS1,HSPH1,LYN,MERTK,ITCH,NFKBIZ,CBLB,SLC39A10,GPR89A,CD3G,SH3KBP1,MSN,THOC1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0001570	0.51	0.67	5	71	vasculogenesis	BP	1	RASA1,ITGAV,MYO1E,MYOCD,WNT7A	darkolivegreen	VSMC_M9
GO:0009895	0.52	0.59	16	254	negative regulation of catabolic process	BP	1	AZIN1,NOCT,FYN,TRDMT1,DHX36,LRRK2,UCHL5,TLK2,FMN2,PIN1,BAG5,ROCK1,CIDEA,USP7,ZDHHC7,GDNF	darkolivegreen	VSMC_M9
GO:0071774	0.52	0.65	6	91	response to fibroblast growth factor	BP	1	EXT1,CEP57,GATA3,SULF1,THBS1,CTGF	darkolivegreen	VSMC_M9
GO:0046545	0.52	0.66	5	75	development of primary female sexual characteristics	BP	1	INHBA,BRCA2,UBE3A,EIF2B5,ZFX	darkolivegreen	VSMC_M9
GO:0008544	0.52	0.60	13	201	epidermis development	BP	1	EXT1,MYO6,ZMPSTE24,ROCK2,INHBA,SOS1,PALLD,ATP2A2,PIP5K1A,ROCK1,PAFAH1B1,AQP3,CTGF	darkolivegreen	VSMC_M9
GO:0030856	0.52	0.64	7	106	regulation of epithelial cell differentiation	BP	1	AHI1,ROCK2,ZEB1,GATA3,ROCK1,AQP3,GDNF	darkolivegreen	VSMC_M9
GO:0033673	0.52	0.60	12	191	negative regulation of kinase activity	BP	1	SH3BP5L,RB1,CBLC,ILK,LYN,IPO7,CBLB,CORO1C,PTPN1,SRCIN1,MYOCD,GADD45B	darkolivegreen	VSMC_M9
GO:0032612	0.52	0.68	4	62	interleukin-1 production	BP	1	MALT1,JAK2,FFAR4,TLR6	darkolivegreen	VSMC_M9
GO:0032652	0.52	0.68	4	62	regulation of interleukin-1 production	BP	1	MALT1,JAK2,FFAR4,TLR6	darkolivegreen	VSMC_M9
GO:0061136	0.52	0.61	10	166	regulation of proteasomal protein catabolic process	BP	1	UBQLN1,PSMC2,NUB1,TMF1,LRRK2,UCHL5,TLK2,PITHD1,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0006259	0.52	0.54	45	741	DNA metabolic process	BP	1	RRM2B,RMI1,SLC30A9,NPAS2,PSME4,ZMPSTE24,ACTR2,DDX1,PIWIL4,TSN,GATA3,ORC4,RIF1,LIG4,NDFIP1,CUL4A,PDS5B,BRCA2,PARG,TDG,USP47,XRN1,ACTR8,DHX36,INO80,NFRKB,TDP2,UCHL5,NEK7,KPNA1,PRRX1,BOD1L1,FMN2,DICER1,PPM1D,RBBP8,THOC1,CIDEA,SPIRE1,CD40LG,USP7,RFWD3,BMPR2,CTGF,UBE2V1	darkolivegreen	VSMC_M9
GO:0000375	0.52	0.59	15	259	RNA splicing, via transesterification reactions	BP	1	DDX46,KHDRBS3,PPIL1,DDX1,JMJD6,MBNL2,PRPF40A,MTREX,MBNL1,DYRK1A,LARP7,CWC22,LSM5,CDK13,GEMIN6	darkolivegreen	VSMC_M9
GO:0060968	0.52	0.68	4	59	regulation of gene silencing	BP	1	ZMPSTE24,KIAA1551,TPR,MYOCD	darkolivegreen	VSMC_M9
GO:0048661	0.52	0.66	5	78	positive regulation of smooth muscle cell proliferation	BP	1	WISP1,JAK2,THBS1,PTGS2,ITGA2	darkolivegreen	VSMC_M9
GO:0007040	0.52	0.68	4	61	lysosome organization	BP	1	TMEM165,CLN5,ACPP,LRRK2	darkolivegreen	VSMC_M9
GO:0080171	0.52	0.68	4	61	lytic vacuole organization	BP	1	TMEM165,CLN5,ACPP,LRRK2	darkolivegreen	VSMC_M9
GO:0050900	0.52	0.59	15	245	leukocyte migration	BP	1	EXT1,STAP1,ITGB1,FYN,CAMK1D,GATA3,SOS1,LYN,THBS1,ADAM10,MSN,ROCK1,ITGA2,ITGA1,NOV	darkolivegreen	VSMC_M9
GO:0031503	0.52	0.60	12	186	protein-containing complex localization	BP	1	AKAP9,KIF5B,UPF2,IFT88,RIOK2,TPR,ADAM10,THOC1,NUP155,GPC4,SSX2IP,MZT1	darkolivegreen	VSMC_M9
GO:0042594	0.52	0.61	10	158	response to starvation	BP	1	STK24,PIK3R4,EIF2AK3,LRRK2,BRSK2,ATF3,FAS,PPM1D,BMPR2,C12orf66	darkolivegreen	VSMC_M9
GO:0062207	0.52	0.66	5	77	regulation of pattern recognition receptor signaling pathway	BP	1	LYN,APPL1,TLR2,GPATCH3,TLR6	darkolivegreen	VSMC_M9
GO:0043010	0.52	0.58	16	242	camera-type eye development	BP	1	AHI1,TOPORS,INHBA,GATA3,RAB3GAP1,JMJD6,ATP2B1,SOS1,MERTK,RDH10,SKIL,WNT5B,MYOM1,BMPR2,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:0032368	0.52	0.64	6	95	regulation of lipid transport	BP	1	ABCB4,TMF1,AGTR1,THBS1,EPRS,ITGAV	darkolivegreen	VSMC_M9
GO:0048477	0.52	0.68	4	62	oogenesis	BP	1	BRCA2,ZFX,FMN2,PAQR8	darkolivegreen	VSMC_M9
GO:1901987	0.52	0.57	19	311	regulation of cell cycle phase transition	BP	1	CDC23,CLOCK,RINT1,RB1,RPL26,MYO16,CUL4A,RIOK2,USP47,APPL1,INO80,BRD7,CUL3,KLHL18,TPR,CDC27,THOC1,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0009746	0.52	0.61	10	159	response to hexose	BP	1	KIF5B,THBS1,SLC39A14,BRSK2,IGF1R,CCDC186,EIF2B5,C2CD2L,PTGS2,CTGF	darkolivegreen	VSMC_M9
GO:0070252	0.52	0.66	5	70	actin-mediated cell contraction	BP	1	AKAP9,ATP2A2,ATP1A1,TPM1,NUP155	darkolivegreen	VSMC_M9
GO:0032479	0.52	0.66	5	75	regulation of type I interferon production	BP	1	TBK1,ITCH,TLR2,DHX36,GPATCH3	darkolivegreen	VSMC_M9
GO:0032606	0.52	0.66	5	75	type I interferon production	BP	1	TBK1,ITCH,TLR2,DHX36,GPATCH3	darkolivegreen	VSMC_M9
GO:0022409	0.53	0.60	11	176	positive regulation of cell-cell adhesion	BP	1	MALT1,JAK2,FYN,GATA3,HSPH1,LYN,NFKBIZ,ANK3,KIFAP3,ADAM19,CD40LG	darkolivegreen	VSMC_M9
GO:1902369	0.53	0.68	4	60	negative regulation of RNA catabolic process	BP	1	NOCT,TRDMT1,DHX36,GDNF	darkolivegreen	VSMC_M9
GO:0044264	0.53	0.66	5	75	cellular polysaccharide metabolic process	BP	1	EXT1,UGP2,CSGALNACT2,PHKG2,PPP1R2	darkolivegreen	VSMC_M9

GO:0051046	0.53	0.55	27	434	regulation of secretion	BP	1	STXBP5,JAK2,CLOCK,EXOC1,MYO6,INHBA,RAB3B,KIF5B,DNAJC1,RAB3GAP1,TMF1,LYN,FFAR4,AGTR1,TLR2,ATP2A2,LRRK2,BRSK2,IDH2,C2CD2L,SEPT5,SRCIN1,MYOM1,C1QTNF3,GDNF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0032984	0.53	0.59	13	195	protein-containing complex disassembly	BP	1	ETF1,UBQLN1,ZMPSTE24,KIF5B,MICAL2,MAP1B,ATP2A2,SPTBN5,IGF1R,CAMSAP2,HDGFL3,GSPT1,CFL2	darkolivegreen	VSMC_M9
GO:0000070	0.53	0.61	9	143	mitotic sister chromatid segregation	BP	1	CDC23,CENPC,RB1,PDS5B,RIOK2,INO80,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0042471	0.53	0.64	6	89	ear morphogenesis	BP	1	LRIG3,MYO6,GATA3,FZD2,PRRX1,COL11A1	darkolivegreen	VSMC_M9
GO:0060998	0.53	0.67	4	54	regulation of dendritic spine development	BP	1	ACTR2,DHX36,UBE3A,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0007423	0.53	0.55	27	415	sensory organ development	BP	1	AHI1,LRIG3,TOPORS,MYO6,INHBA,GATA3,RAB3GAP1,JMJD6,ATP2B1,SOS1,DCHS1,MERTK,IFT88,RDH10,ZDHHC16,NTRK3,FZD2,SKIL,PRRX1,WNT5B,ADAM10,MYOM1,PAFAH1B1,COL11A1,BMPR2,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:0009798	0.53	0.67	4	59	axis specification	BP	1	AHI1,TMED2,TBX6,WNT7A	darkolivegreen	VSMC_M9
GO:0002824	0.53	0.67	4	64	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	MALT1,GATA3,RIF1,NFKBIZ	darkolivegreen	VSMC_M9
GO:0043281	0.53	0.61	9	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	MALT1,JAK2,EIF2AK3,USP47,THBS1,PTGS2,FAS,UACA,CTGF	darkolivegreen	VSMC_M9
GO:2001237	0.53	0.65	5	79	negative regulation of extrinsic apoptotic signaling pathway	BP	1	FYN,THBS1,ACVR1,ITGAV,GDNF	darkolivegreen	VSMC_M9
GO:0071675	0.53	0.65	5	81	regulation of mononuclear cell migration	BP	1	LYN,THBS1,ADAM10,MSN,NOV	darkolivegreen	VSMC_M9
GO:0043200	0.53	0.63	6	93	response to amino acid	BP	1	CDO1,FYN,LYN,TOMM20,CTGF,LAMTOR3	darkolivegreen	VSMC_M9
GO:0009410	0.53	0.56	19	314	response to xenobiotic stimulus	BP	1	NPAS2,MYO6,INHBA,FYN,RB1,GATA3,PPP1R12A,LYN,USP47,MAP1B,ATP1A1,PTGS2,SS18,ITGA2,SLC1A3,TBXA2R,WFDC1,MIR186,RAP2A	darkolivegreen	VSMC_M9
GO:0030216	0.54	0.65	5	74	keratinocyte differentiation	BP	1	ROCK2,PALLD,PIP5K1A,ROCK1,AQP3	darkolivegreen	VSMC_M9
GO:0070509	0.54	0.66	4	58	calcium ion import	BP	1	ZMPSTE24,FYN,ATP2A2,AFG3L2	darkolivegreen	VSMC_M9
GO:0046390	0.54	0.60	9	156	ribose phosphate biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,ATP6V1A,PAPSS2,ADSS,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0042110	0.54	0.56	19	310	T cell activation	BP	1	SOCS6,MALT1,FYN,GATA3,JMJD6,LRRC32,AZI2,LIG4,NDFIP1,SOS1,HSPH1,LYN,ITCH,NFKBIZ,CBLB,GPR89A,CD3G,MSN,CD40LG	darkolivegreen	VSMC_M9
GO:0051053	0.54	0.63	6	94	negative regulation of DNA metabolic process	BP	1	GATA3,RIF1,NDFIP1,XRN1,THOC1,BMPR2	darkolivegreen	VSMC_M9
GO:0048640	0.54	0.63	6	90	negative regulation of developmental growth	BP	1	CDKL3,RNF6,WWC3,SEMA5B,SEMA7A,VGLL4	darkolivegreen	VSMC_M9
GO:0031099	0.54	0.60	9	150	regeneration	BP	1	JAK2,UPF2,STK24,MAP1B,KPNA1,PRRX1,PTPN12,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0045069	0.54	0.66	4	62	regulation of viral genome replication	BP	1	CNOT7,PDE12,KIAA1551,VAPB	darkolivegreen	VSMC_M9
GO:0018205	0.54	0.55	19	313	peptidyl-lysine modification	BP	1	PHF20L1,TOPORS,CLOCK,ZNF451,HDAC9,SENP6,ZMPSTE24,GATA3,JMJD6,BRPF1,SETD5,RIF1,BRCA2,PLOD2,BRD7,TAF5L,MYOCD,GTF2B,RANBP2	darkolivegreen	VSMC_M9
GO:0061515	0.54	0.66	4	59	myeloid cell development	BP	1	JMJD6,TLR2,ABCB10,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0046578	0.54	0.58	11	161	regulation of Ras protein signal transduction	BP	1	DENND4C,CAVIN4,ITGB1,GPR4,CYTH1,STARD13,CCDC125,RASA1,CUL3,GPR65,SSX2IP	darkolivegreen	VSMC_M9
GO:0001676	0.54	0.66	4	66	long-chain fatty acid metabolic process	BP	1	ELOVL5,PNPLA8,PTGS2,ACOT7	darkolivegreen	VSMC_M9
GO:0035195	0.54	0.62	6	107	gene silencing by miRNA	BP	1	ZMPSTE24,CNOT7,DICER1,MYOCD,ZC3H7A,MIR186	darkolivegreen	VSMC_M9
GO:0048844	0.54	0.66	4	57	artery morphogenesis	BP	1	PRRX1,AKT3,MYOCD,BMPR2	darkolivegreen	VSMC_M9
GO:0043067	0.54	0.51	67	1119	regulation of programmed cell death	BP	1	MALT1,AHI1,RRM2B,UBQLN1,TOPORS,JAK2,INHBA,ITGB1,FYN,NOX4,RB1,CAMK1D,GATA3,DNAJC3,RPL26,UFM1,LIG4,ILK,ITGA5,TMF1,LYN,MERTK,EIF2AK3,ITCH,USP47,FFAR4,RASA1,THBS1,ACVR1,LRRK2,SLC39A10,IGF1R,PTPN1,KPNA1,EIF2B5,SYCP2,ATF3,CD3G,PTGS2,ITGAV,SKIL,KIFAP3,TNFAIP8L3,VDAC2,DKK1,FMN2,FAS,ADAM10,BNIP2,MAP2K4,MYOCD,PIN1,BAG5,ITGA1,BFAR,CIDEA,CD40LG,GADD45B,ENO1,ANKRD13C,ARF4,GDNF,BDKRB2,E2F3,ZPR1,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0042592	0.55	0.50	80	1295	homeostatic process	BP	1	EXT1,SLC39A7,WISP1,PLAA,SLC30A9,ABCB4,TMEM165,JAK2,HDAC9,CAV2,INHBA,PNPLA8,ITGB1,FYN,KIF5B,PIWIL4,GPR4,RB1,PICALM,GATA3,CLN5,JMJD6,TMTC2,ATP2B1,NDFIP1,SOS1,UBA5,HOXC10,LYN,MERTK,ATP6V0A2,SLC30A5,LNPEP,FFAR4,AGTR1,HK2,ATP2A2,SLC39A14,GCNT4,ATP1A1,LRRK2,BRSK2,UBE3A,SLC39A10,ATP6V1A,IGF1R,GPR89A,CCDC186,ITPR2,VAPB,ABCB10,C2CD2L,ANK3,CCDC47,ZFX,ATP13A3,GATM,PTGS2,ITGAV,SKIL,FAS,AKT3,STIM2,HK3,GPR65,TLE3,ANXA6,SLC1A3,AFG3L2,C1QTNF3,CIDEA,TBXA2R,PRKACB,AQP3,CTGF,BDKRB2,NOV,TMEM119,CFL2,IRX3	darkolivegreen	VSMC_M9
GO:0001678	0.55	0.60	8	124	cellular glucose homeostasis	BP	1	KIF5B,HK2,SLC39A14,BRSK2,IGF1R,CCDC186,C2CD2L,HK3	darkolivegreen	VSMC_M9
GO:0006338	0.55	0.58	11	175	chromatin remodeling	BP	1	PSME4,RB1,GATA3,HCFC2,SMARCA5,ACTR8,LIN54,INO80,NAP1L4,BAZ1A,MYSM1	darkolivegreen	VSMC_M9
GO:0051168	0.55	0.60	8	131	nuclear export	BP	1	MALT1,UPF2,XPO4,RIOK2,TPR,SMURF1,THOC1,NUP155	darkolivegreen	VSMC_M9
GO:0032640	0.55	0.61	7	111	tumor necrosis factor production	BP	1	JAK2,UBE2J1,TLR2,THBS1,LRRK2,DICER1,CIDEA	darkolivegreen	VSMC_M9
GO:0032680	0.55	0.61	7	111	regulation of tumor necrosis factor production	BP	1	JAK2,UBE2J1,TLR2,THBS1,LRRK2,DICER1,CIDEA	darkolivegreen	VSMC_M9

GO:0072522	0.55	0.59	9	157	purine-containing compound biosynthetic process	BP	1	ELOVL5,HSD17B12,SLC35B3,ATP6V1A,PAPSS2,ADSS,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0002285	0.55	0.60	8	127	lymphocyte activation involved in immune response	BP	1	MALT1,GATA3,RIF1,LIG4,NDFIP1,NFKBIZ,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0016064	0.55	0.63	5	85	immunoglobulin mediated immune response	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0098739	0.55	0.59	8	123	import across plasma membrane	BP	1	ITGB1,FYN,SLC36A4,THBS1,SLC39A14,ATP1A1,SLC39A10,SLC1A3	darkolivegreen	VSMC_M9
GO:0036294	0.55	0.59	8	129	cellular response to decreased oxygen levels	BP	1	UBQLN1,ROCK2,PTGS2,CPEB2,FMN2,KCNMB1,ENO1,AQP3	darkolivegreen	VSMC_M9
GO:0043122	0.55	0.57	12	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	MALT1,TBK1,DDX1,FYN,NDFIP2,NDFIP1,DHX36,TANK,GPR89A,TLR6,VAPA,UBE2V1	darkolivegreen	VSMC_M9
GO:0030510	0.55	0.63	5	74	regulation of BMP signaling pathway	BP	1	ILK,SULF1,SKIL,SMURF1,BMPR2	darkolivegreen	VSMC_M9
GO:1902904	0.55	0.58	9	139	negative regulation of supramolecular fiber organization	BP	1	CHADL,MAP1B,PFN2,DYRK1A,SPTBN5,PHLDB2,CAMSAP2,HDGFL3,FHOD3	darkolivegreen	VSMC_M9
GO:0098813	0.55	0.56	14	230	nuclear chromosome segregation	BP	1	CDC23,RMI1,CENPC,ACTR2,RB1,ACTR3,PDS5B,RIOK2,INO80,CUL3,SYCP2,TPR,CDC27,FMN2	darkolivegreen	VSMC_M9
GO:0010675	0.56	0.60	7	114	regulation of cellular carbohydrate metabolic process	BP	1	SLC35B4,ZMPSTE24,PHKG2,CLK2,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9
GO:0006275	0.56	0.61	6	92	regulation of DNA replication	BP	1	CCDC88A,ZMPSTE24,BRCA2,INO80,RBBP6,MAP2K4	darkolivegreen	VSMC_M9
GO:0042552	0.56	0.60	7	109	myelination	BP	1	ILK,EIF2AK3,TLR2,EIF2B5,DICER1,AFG3L2,ZPR1	darkolivegreen	VSMC_M9
GO:0021700	0.56	0.56	13	204	developmental maturation	BP	1	EXT1,RB1,PICALM,GATA3,CLN5,BRCA2,NTN4,DCHS1,MAP1B,LRRK2,SNX19,MBTPS2,TBX6	darkolivegreen	VSMC_M9
GO:1901215	0.56	0.57	10	161	negative regulation of neuron death	BP	1	JAK2,FYN,LIG4,ILK,RASA1,LRRK2,MAP2K4,PIN1,GDNF,ZPR1	darkolivegreen	VSMC_M9
GO:0086003	0.56	0.64	4	57	cardiac muscle cell contraction	BP	1	AKAP9,ATP2A2,ATP1A1,NUP155	darkolivegreen	VSMC_M9
GO:0021766	0.56	0.64	4	59	hippocampus development	BP	1	UBA6,KIF5B,EIF2B5,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0002088	0.56	0.64	4	63	lens development in camera-type eye	BP	1	GATA3,SKIL,WNT5B,WNT7A	darkolivegreen	VSMC_M9
GO:0043624	0.56	0.59	8	119	cellular protein complex disassembly	BP	1	ETF1,MICAL2,MAP1B,SPTBN5,CAMSAP2,HDGFL3,GSPT1,CFL2	darkolivegreen	VSMC_M9
GO:0001942	0.56	0.64	4	61	hair follicle development	BP	1	EXT1,ZMPSTE24,INHBA,SOS1	darkolivegreen	VSMC_M9
GO:0042129	0.56	0.61	6	102	regulation of T cell proliferation	BP	1	LRRC32,NDFIP1,SOS1,ITCH,CBLB,CD40LG	darkolivegreen	VSMC_M9
GO:0001657	0.56	0.62	5	78	ureteric bud development	BP	1	HOXA11,GATA3,ILK,DCHS1,GDNF	darkolivegreen	VSMC_M9
GO:0003151	0.56	0.64	4	59	outflow tract morphogenesis	BP	1	ILK,NRP2,FZD2,BMPR2	darkolivegreen	VSMC_M9
GO:1904035	0.56	0.64	4	65	regulation of epithelial cell apoptotic process	BP	1	JAK2,GATA3,THBS1,CD40LG	darkolivegreen	VSMC_M9
GO:0051047	0.56	0.55	13	211	positive regulation of secretion	BP	1	STXBP5,JAK2,EXOC1,INHBA,KIF5B,RAB3GAP1,TMF1,FFAR4,TLR2,C2CD2L,MYOM1,C1QTNF3,GDNF	darkolivegreen	VSMC_M9
GO:0030183	0.56	0.61	6	96	B cell differentiation	BP	1	MALT1,HDAC9,INHBA,ITGB1,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0030198	0.56	0.54	16	250	extracellular matrix organization	BP	1	EXT1,CHADL,COL12A1,CAV2,ITGB1,RB1,NTN4,HSD17B12,SULF1,PHLDB2,ADAMTS17,ADAM10,MYO1E,COL11A1,CTGF,COLGALT1	darkolivegreen	VSMC_M9
GO:0045638	0.56	0.64	4	64	negative regulation of myeloid cell differentiation	BP	1	HOXA9,INHBA,CUL4A,LYN	darkolivegreen	VSMC_M9
GO:1901605	0.56	0.58	8	146	alpha-amino acid metabolic process	BP	1	CDO1,AZIN1,GFPT1,NOX4,PLOD2,ALDH18A1,ADSS,DLST	darkolivegreen	VSMC_M9
GO:0040008	0.56	0.51	32	518	regulation of growth	BP	1	SOCS6,LRP12,CDKL3,PLAA,ZMPSTE24,INHBA,EXOSC9,RB1,ILK,RNF6,ITCH,USP47,MAP1B,AGTR1,INO80,NEDD9,WWC3,SEMA5B,RBBP7,SMURF1,ADAM10,MYOCD,SEMA7A,PIN1,AFG3L2,PAFAH1B1,ENO1,WFDC1,BMPR2,NOV,ZPR1,VGLL4	darkolivegreen	VSMC_M9
GO:0007623	0.56	0.57	10	160	circadian rhythm	BP	1	CLOCK,NPAS2,GFPT1,ROCK2,NOCT,FBXL17,GPR176,DYRK1A,UBE3A,USP7	darkolivegreen	VSMC_M9
GO:0002821	0.56	0.64	4	66	positive regulation of adaptive immune response	BP	1	MALT1,GATA3,RIF1,NFKBIZ	darkolivegreen	VSMC_M9
GO:0048644	0.56	0.64	4	61	muscle organ morphogenesis	BP	1	SHOX2,FZD2,TPM1,COL11A1	darkolivegreen	VSMC_M9
GO:0043409	0.57	0.58	8	131	negative regulation of MAPK cascade	BP	1	CBLC,LYN,ITCH,IGF1R,PTPN1,ATF3,PIN1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0007272	0.57	0.59	7	110	ensheathment of neurons	BP	1	ILK,EIF2AK3,TLR2,EIF2B5,DICER1,AFG3L2,ZPR1	darkolivegreen	VSMC_M9
GO:0008366	0.57	0.59	7	110	axon ensheathment	BP	1	ILK,EIF2AK3,TLR2,EIF2B5,DICER1,AFG3L2,ZPR1	darkolivegreen	VSMC_M9
GO:0045229	0.57	0.54	16	251	external encapsulating structure organization	BP	1	EXT1,CHADL,COL12A1,CAV2,ITGB1,RB1,NTN4,HSD17B12,SULF1,PHLDB2,ADAMTS17,ADAM10,MYO1E,COL11A1,CTGF,COLGALT1	darkolivegreen	VSMC_M9
GO:0019724	0.57	0.61	5	87	B cell mediated immunity	BP	1	RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:2000377	0.57	0.59	7	120	regulation of reactive oxygen species metabolic process	BP	1	FYN,NOX4,AGTR1,HK2,THBS1,TLR6,ARF4	darkolivegreen	VSMC_M9
GO:0050670	0.57	0.58	8	137	regulation of lymphocyte proliferation	BP	1	LRRC32,NDFIP1,SOS1,LYN,ITCH,CBLB,SLC39A10,CD40LG	darkolivegreen	VSMC_M9
GO:0008630	0.57	0.61	5	84	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	TOPORS,RPL26,BRCA2,USP47,SKIL	darkolivegreen	VSMC_M9
GO:0043062	0.57	0.53	16	251	extracellular structure organization	BP	1	EXT1,CHADL,COL12A1,CAV2,ITGB1,RB1,NTN4,HSD17B12,SULF1,PHLDB2,ADAMTS17,ADAM10,MYO1E,COL11A1,CTGF,COLGALT1	darkolivegreen	VSMC_M9
GO:1901655	0.57	0.61	5	77	cellular response to ketone	BP	1	ROCK2,ATP2B1,XRN1,EIF4E,MSN	darkolivegreen	VSMC_M9
GO:1903037	0.57	0.55	12	206	regulation of leukocyte cell-cell adhesion	BP	1	SOCS6,MALT1,FYN,GATA3,LRRC32,NDFIP1,HSPH1,LYN,ITCH,NFKBIZ,CBLB,CD40LG	darkolivegreen	VSMC_M9
GO:0006664	0.57	0.61	5	87	glycolipid metabolic process	BP	1	ST3GAL3,ST8SIA1,PIGW,DPM2,DPM1	darkolivegreen	VSMC_M9

GO:1903509	0.57	0.61	5	87	liposaccharide metabolic process	BP	1	ST3GAL3,ST8SIA1,PIGW,DPM2,DPM1	darkolivegreen	VSMC_M9
GO:0019915	0.57	0.63	4	65	lipid storage	BP	1	OSBPL8,OSBPL11,ITGAV,CIDEA	darkolivegreen	VSMC_M9
GO:0007259	0.57	0.60	6	98	receptor signaling pathway via JAK-STAT	BP	1	SOCS6,PTPRD,JAK2,FYN,CNOT7,LYN	darkolivegreen	VSMC_M9
GO:0001824	0.57	0.61	5	86	blastocyst development	BP	1	BRCA2,CUL3,SKIL,RBBP8,ZPR1	darkolivegreen	VSMC_M9
GO:1903038	0.57	0.61	5	87	negative regulation of leukocyte cell-cell adhesion	BP	1	SOCS6,LRRC32,NDFIP1,ITCH,CBLB	darkolivegreen	VSMC_M9
GO:0045595	0.57	0.48	72	1153	regulation of cell differentiation	BP	1	MALT1,AHI1,CDKL3,CHADL,WISP1,PTPRD,JAK2,CLOCK,HEMGN,HDAC9,HOXA9,HOXA11,ACTR2,ROCK2,INHBA,NOCT,ITGB1,ZEB1,RB1,GATA3,TRAK1,LIG4,ATP11A,NDFIP1,CUL4A,SOS1,ILK,RNF6,LYN,ITCH,FFAR4,MAP1B,AGTR1,TLR2,DHX36,SHOX2,ACVR1,NFKBIZ,NEDD9,LRRK2,EIF4E,PHLDB2,CORO1C,NTRK3,SEMA5B,IDH2,ABCB10,TRAK2,PITHD1,PTGS2,ITGAV,FERMT2,SKIL,DKK1,TRIP4,TBX6,DICER1,MYOCD,SEMA7A,PIN1,ROCK1,PAFAH1B1,BMPR2,AQP3,GDNF,CDK13,CTGF,NOV,WNT9A,TMEM119,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0006665	0.57	0.58	7	120	sphingolipid metabolic process	BP	1	ELOVL5,ST3GAL3,PLPP1,CERS5,ST8SIA1,SAMD8,ELOVL4	darkolivegreen	VSMC_M9
GO:0031331	0.57	0.52	22	366	positive regulation of cellular catabolic process	BP	1	TBK1,UBQLN1,ROCK2,NOCT,EXOSC9,PSMC2,NUB1,RAB3GAP1,SUPT5H,CNOT7,ITCH,PDE12,DCP1A,DHX36,LRRK2,RAB3GAP2,PTPN1,SMURF1,MSN,PHKG2,ROCK1,VGLL4	darkolivegreen	VSMC_M9
GO:0008286	0.57	0.59	6	93	insulin receptor signaling pathway	BP	1	CAV2,OSBPL8,APPL1,SLC39A14,IGF1R,PTPN1	darkolivegreen	VSMC_M9
GO:0046631	0.57	0.59	6	97	alpha-beta T cell activation	BP	1	MALT1,GATA3,HSPH1,ITCH,NFKBIZ,CBLB	darkolivegreen	VSMC_M9
GO:0051348	0.57	0.54	13	219	negative regulation of transferase activity	BP	1	SH3BP5L,RB1,CBLC,ILK,LYN,IPO7,CBLB,CORO1C,PTPN1,SRCIN1,MYOCD,BAG5,GADD45B	darkolivegreen	VSMC_M9
GO:0051494	0.57	0.56	9	138	negative regulation of cytoskeleton organization	BP	1	MAP1B,PFN2,DYRK1A,SPTBN5,PHLDB2,CAMSAP2,HDGFL3,IQCJ-SCHIP1,FHOD3	darkolivegreen	VSMC_M9
GO:0072163	0.57	0.61	5	79	mesonephric epithelium development	BP	1	HOXA11,GATA3,ILK,DCHS1,GDNF	darkolivegreen	VSMC_M9
GO:0072164	0.57	0.61	5	79	mesonephric tubule development	BP	1	HOXA11,GATA3,ILK,DCHS1,GDNF	darkolivegreen	VSMC_M9
GO:0048565	0.58	0.59	6	92	digestive tract development	BP	1	AHI1,EXT1,RB1,DCHS1,SHOX2,MYOCD	darkolivegreen	VSMC_M9
GO:0006898	0.58	0.54	12	192	receptor-mediated endocytosis	BP	1	AHI1,CAV2,ITGB1,PICALM,SCYL2,GRK3,ITGAV,AP4E1,DKK1,ATAD1,CLTC,RAB31	darkolivegreen	VSMC_M9
GO:1901136	0.58	0.58	7	126	carbohydrate derivative catabolic process	BP	1	EDEM1,PDE7A,TDG,NUDT9,DERA,NPL,ACOT7	darkolivegreen	VSMC_M9
GO:0032944	0.58	0.57	8	138	regulation of mononuclear cell proliferation	BP	1	LRRC32,NDFIP1,SOS1,LYN,ITCH,CBLB,SLC39A10,CD40LG	darkolivegreen	VSMC_M9
GO:0033143	0.58	0.63	4	63	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	CLOCK,UFM1,UBA5,RNF6	darkolivegreen	VSMC_M9
GO:0090277	0.58	0.63	4	65	positive regulation of peptide hormone secretion	BP	1	JAK2,KIF5B,FFAR4,C2CD2L	darkolivegreen	VSMC_M9
GO:0002822	0.58	0.59	6	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	MALT1,GATA3,RIF1,NDFIP1,NFKBIZ,THOC1	darkolivegreen	VSMC_M9
GO:0060411	0.58	0.63	4	59	cardiac septum morphogenesis	BP	1	ACVR1,NRP2,FZD2,BMPR2	darkolivegreen	VSMC_M9
GO:0007009	0.58	0.59	6	94	plasma membrane organization	BP	1	CAV2,ATP2A2,ATP10A,ANK3,ANXA6,XKR9	darkolivegreen	VSMC_M9
GO:0000018	0.58	0.60	5	83	regulation of DNA recombination	BP	1	ACTR2,RIF1,NDFIP1,KPNA1,THOC1	darkolivegreen	VSMC_M9
GO:0061912	0.58	0.62	4	63	selective autophagy	BP	1	TBK1,UBQLN1,UFM1,UBA5	darkolivegreen	VSMC_M9
GO:0022404	0.58	0.62	4	63	molting cycle process	BP	1	EXT1,ZMPSTE24,INHBA,SOS1	darkolivegreen	VSMC_M9
GO:0022405	0.58	0.62	4	63	hair cycle process	BP	1	EXT1,ZMPSTE24,INHBA,SOS1	darkolivegreen	VSMC_M9
GO:1901988	0.58	0.54	12	201	negative regulation of cell cycle phase transition	BP	1	CLOCK,RINT1,RB1,RPL26,MYO16,CUL4A,USP47,BRD7,TPR,THOC1,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0051338	0.58	0.48	43	706	regulation of transferase activity	BP	1	SOCS6,MALT1,TOPORS,JAK2,STAP1,CCDC88A,SH3BP5L,NOX4,RB1,CBLC,CCNT2,OSBPL8,PIK3R4,CCNA1,ILK,LYN,MERTK,IPO7,THBS1,NEDD9,CBLB,LRRK2,IGF1R,CORO1C,NEK7,NTRK3,PTPN1,IQGAP1,FERMT2,TNFAIP8L3,DKK1,TLR6,SRCIN1,SMG8,MYOCD,PIN1,BAG5,RICTOR,GADD45B,VAV2,RANBP2,BMPR2,LAMTOR3	darkolivegreen	VSMC_M9
GO:0002793	0.58	0.62	4	66	positive regulation of peptide secretion	BP	1	JAK2,KIF5B,FFAR4,C2CD2L	darkolivegreen	VSMC_M9
GO:0002683	0.58	0.52	17	290	negative regulation of immune system process	BP	1	SOCS6,STAP1,INHBA,FYN,LRRC32,NDFIP1,CUL4A,CNOT7,LYN,MERTK,ITCH,APPL1,THBS1,CBLB,GPATCH3,THOC1,NOV	darkolivegreen	VSMC_M9
GO:0016072	0.58	0.54	11	206	rRNA metabolic process	BP	1	WDR46,RPF2,EXOSC9,RPL26,ERI1,MTREX,RIOK2,XRN1,WDR75,RRP15,TFB2M	darkolivegreen	VSMC_M9
GO:0043414	0.58	0.52	15	254	macromolecule methylation	BP	1	ETF1,TRMO,ZMPSTE24,PIWIL4,ZC3H13,TRDMT1,GATA3,SETD5,RIF1,FAM98A,LARP7,PPM1D,GSPT1,RAB6A,TFB2M	darkolivegreen	VSMC_M9
GO:0009165	0.59	0.54	11	198	nucleotide biosynthetic process	BP	1	RRM2B,ELOVL5,HSD17B12,SLC35B3,ATP6V1A,IDH2,PAPSS2,ADSS,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0032434	0.59	0.57	7	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	UBQLN1,NUB1,LRRK2,UCHL5,TLK2,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0007569	0.59	0.58	6	98	cell aging	BP	1	ZMPSTE24,NOX4,BRCA2,ILK,AKT3,MAP2K4	darkolivegreen	VSMC_M9
GO:0071706	0.59	0.57	7	115	tumor necrosis factor superfamily cytokine production	BP	1	JAK2,UBE2J1,TLR2,THBS1,LRRK2,DICER1,CIDEA	darkolivegreen	VSMC_M9
GO:1903555	0.59	0.57	7	115	regulation of tumor necrosis factor superfamily cytokine production	BP	1	JAK2,UBE2J1,TLR2,THBS1,LRRK2,DICER1,CIDEA	darkolivegreen	VSMC_M9

GO:0009991	0.59	0.50	23	385	response to extracellular stimulus	BP	1	NOCT,STK24,PIK3R4,ATP2B1,LYN,EIF2AK3,MAP1B,GDAP1,NUCB2,LRRK2,BRSK2,CHSY1,ATF3,PTGS2,FAS,BNIP2,PPM1D,MYOCD,ITGA2,TBXA2R,BMPR2,AQP3,C12orf66	darkolivegreen	VSMC_M9
GO:0051480	0.59	0.53	13	212	regulation of cytosolic calcium ion concentration	BP	1	JAK2,CAV2,FYN,GPR4,ATP2B1,LYN,FFAR4,AGTR1,ITPR2,ITGAV,GPR65,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0051817	0.59	0.61	4	67	modulation of process of other organism involved in symbiotic interaction	BP	1	CAV2,CHD1,VAPB,VAPA	darkolivegreen	VSMC_M9
GO:0015718	0.59	0.61	4	66	monocarboxylic acid transport	BP	1	ABCB4,PNPLA8,SLC16A12,BDKRB2	darkolivegreen	VSMC_M9
GO:0140029	0.59	0.61	4	66	exocytic process	BP	1	STXBP5,RAB3B,LYN,SEPT5	darkolivegreen	VSMC_M9
GO:1902850	0.59	0.56	8	133	microtubule cytoskeleton organization involved in mitosis	BP	1	ITGB1,DCTN6,UBXN2B,MAP9,TPR,CLTC,PAFAH1B1,MZT1	darkolivegreen	VSMC_M9
GO:0007389	0.59	0.50	20	329	pattern specification process	BP	1	AHI1,EXT1,HOXA9,HOXA10,HOXA11,ALG5,DCHS1,TMED2,MICAL2,ARL6,ACVR1,CHSY1,NRP2,DKK1,TBX6,PRKACB,BMPR2,GDNF,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0019219	0.59	0.45	175	2852	regulation of nucleobase-containing compound metabolic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,KHDRBS3,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,ROCK2,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,PICALM,TRDMT1,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,MBNL2,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,NDFIP1,CUL4A,BRCA2,ILK,TMF1,HOXC10,PARG,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,MICAL2,ACTR8,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,KPNA6,NEK7,WWC3,LARP7,KPNA1,CLK1,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,MYNN,SKIL,PRRX1,DKK1,FMN2,NOTCH3,TLR6,MAGED2,CLK2,TRIP4,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,CIDEA,SPIRE1,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,FASTKD5,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0090304	0.59	0.44	233	3916	nucleic acid metabolic process	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,RRM2B,WDR46,DDX46,PHF20L1,KHDRBS3,ETF1,RMI1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,POLR2B,ZNF451,TRMO,HDAC9,CAVIN4,PSME4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,ACTR2,THAP5,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,ZEB1,EXOSC9,PIWIL4,RB1,PICALM,ZC3H13,TRDMT1,TOE1,TSN,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,ORC4,MBNL2,RIF1,PPP1R12A,PRPF40A,RPL26,LIG4,CEBPZ,SUPT20H,SMAD9,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,PARG,MTREX,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,U2SURP,ACTR8,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SNRNP48,DYRK1A,BRD7,ERG,TBX15,UBE3A,NFRKB,CUL3,TDP2,PUS3,TROVE2,UCHL5,KPNA6,RRP15,EPRS,IARS2,NEK7,WWC3,LARP7,KPNA1,CLK1,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,MYNN,SKIL,DTWD1,PRRX1,BOD1L1,DKK1,FMN2,RBM47,NOTCH3,TLR6,MAGED2,CLK2,TRIP4,TBX6,RLIM,MAGEE2,INTS14,ZC3H14,RBBP6,TLE3,SMG8,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,CIDEA,SPIRE1,GSPT1,TARS,ZC3H7A,MYSM1,CD40LG,USP7,LSM5,ENO1,RFWD3,DNTTIP2,ZNF644,ZNF326,GTF2B,THAP11,SNORA21,SNORA3A,BMPR2,FASTKD5,ZNF654,INTS6,SNORA51,SNORD27,SNORD71,ANKRD49,ARF4,GDNF,CDK13,CTGF,GEMIN6,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0001823	0.59	0.59	5	81	mesonephros development	BP	1	HOXA11,GATA3,ILK,DCHS1,GDNF	darkolivegreen	VSMC_M9
GO:1901293	0.59	0.53	11	199	nucleoside phosphate biosynthetic process	BP	1	RRM2B,ELOVL5,HSD17B12,SLC35B3,ATP6V1A,IDH2,PAPSS2,ADSS,ACOT7,ENO1,ELOVL4	darkolivegreen	VSMC_M9
GO:0045859	0.59	0.48	31	513	regulation of protein kinase activity	BP	1	MALT1,JAK2,STAP1,CCDC88A,SH3BP5L,NOX4,RB1,CBLC,CCNT2,OSBPL8,CCNA1,ILK,LYN,IPO7,THBS1,NEDD9,CBLB,LRRK2,CORO1C,NTRK3,PTPN1,IQGAP1,FERMT2,DKK1,TLR6,SRCIN1,SMG8,MYOCD,RICTOR,GADD45B,BMPR2	darkolivegreen	VSMC_M9
GO:0071900	0.59	0.50	18	300	regulation of protein serine/threonine kinase activity	BP	1	RB1,CBLC,CCNT2,CCNA1,ILK,LYN,IPO7,THBS1,LRRK2,NTRK3,PTPN1,IQGAP1,FERMT2,DKK1,TLR6,MYOCD,RICTOR,BMPR2	darkolivegreen	VSMC_M9
GO:0097191	0.59	0.53	10	173	extrinsic apoptotic signaling pathway	BP	1	JAK2,INHBA,FYN,THBS1,ACVR1,ATF3,ITGAV,SKIL,FAS,GDNF	darkolivegreen	VSMC_M9
GO:0035194	0.59	0.57	6	112	post-transcriptional gene silencing by RNA	BP	1	ZMPSTE24,CNOT7,DICER1,MYOCD,ZC3H7A,MIR186	darkolivegreen	VSMC_M9
GO:2001257	0.59	0.56	7	116	regulation of cation channel activity	BP	1	UBQLN1,ITGB1,KIF5B,REM1,ANK3,STIM2,SHISA7	darkolivegreen	VSMC_M9
GO:0032872	0.60	0.54	9	148	regulation of stress-activated MAPK cascade	BP	1	ITCH,IGF1R,TNIK,FAS,PAFAH1B1,GADD45B,CTGF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0016331	0.60	0.55	8	127	morphogenesis of embryonic epithelium	BP	1	GATA3,TMED2,SULF1,RDH10,FZD2,PRKACB,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0046683	0.60	0.57	6	94	response to organophosphorus	BP	1	CDO1,AKAP9,NOX4,ITPR2,PTGS2,RAPGEF1	darkolivegreen	VSMC_M9
GO:1901879	0.60	0.58	5	75	regulation of protein depolymerization	BP	1	MAP1B,SPTBN5,CAMSAP2,HDGFL3,CFL2	darkolivegreen	VSMC_M9

GO:0006661	0.60	0.56	7	115	phosphatidylinositol biosynthetic process	BP	1	SOCS6,BPNT1,PIP5K1A,PIGW,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0009582	0.60	0.58	5	83	detection of abiotic stimulus	BP	1	FYN,SEMA5B,ITGA2,COL11A1,ELOVL4	darkolivegreen	VSMC_M9
GO:0045766	0.60	0.54	8	133	positive regulation of angiogenesis	BP	1	ITGB1,ITGA5,HK2,THBS1,ADAM12,AKT3,PKM,TBXA2R	darkolivegreen	VSMC_M9
GO:1904018	0.60	0.54	8	133	positive regulation of vasculature development	BP	1	ITGB1,ITGA5,HK2,THBS1,ADAM12,AKT3,PKM,TBXA2R	darkolivegreen	VSMC_M9
GO:1901342	0.60	0.51	14	232	regulation of vasculature development	BP	1	THBS2,ROCK2,ITGB1,GPR4,ITGA5,SULF1,HK2,THBS1,ADAM12,AKT3,ADAM10,PKM,ROCK1,TBXA2R	darkolivegreen	VSMC_M9
GO:0006355	0.60	0.44	148	2411	regulation of transcription, DNA-templated	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,INHBA,DDX1,ZEB1,EXOSC9,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,STOX2,MICAL2,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,KPNA6,WWC3,LARP7,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,DKK1,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0009896	0.60	0.48	25	420	positive regulation of catabolic process	BP	1	TBK1,UBQLN1,ROCK2,NOCT,EXOSC9,PSMC2,NUB1,RAB3GAP1,SUPT5H,NDFIP1,CNOT7,ITCH,PDE12,DCP1A,DHX36,CBLB,LRRK2,RAB3GAP2,PTPN1,SMURF1,MSN,PHKG2,OAZ2,ROCK1,VGLL4	darkolivegreen	VSMC_M9
GO:0051172	0.60	0.44	107	1770	negative regulation of nitrogen compound metabolic process	BP	1	AZIN1,PLAA,TFPI2,CLOCK,ZNF451,HDAC9,ZMPSTE24,SH3BP5L,THAP5,ROCK2,NOCT,FYN,ZEB1,EXOSC9,DNAJC1,RB1,RTN2,PICALM,TRDMT1,CBLC,MGAT5,GATA3,SUPT5H,DNAJC3,RIF1,NR2C1,NDFIP1,ILK,CNOT7,LYN,IPO7,EIF2AK3,TDG,TMED2,HCFC2,USP47,XRN1,PDE12,PI15,DCP1A,DHX36,THBS1,SHOX2,MTERF3,CBLB,DYRK1A,BRD7,LRRK2,TBX15,CUL3,EIF4E,TDP2,UCHL5,EPRS,CORO1C,ANOS1,NTRK3,WWC3,PTPN1,LARP7,LRRFIP1,ATF3,RBBP7,TLK2,TPR,PTGS2,NPAT,ITGAV,SKIL,PRRX1,RTN3,CPEB2,BOD1L1,DKK1,FMN2,SRP9,MAGED2,SRCIN1,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,CLTC,DICER1,MYOCD,PIN1,RBBP8,BAG5,ROCK1,THOC1,USP7,GADD45B,ENO1,WFDC1,THAP11,MIR186,BMPR2,FRY,GDNF,BDKRB2,PMEPA1,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0021954	0.60	0.60	4	61	central nervous system neuron development	BP	1	SCYL2,NRP2,PAFAH1B1,CDH11	darkolivegreen	VSMC_M9
GO:0048469	0.60	0.55	7	116	cell maturation	BP	1	RB1,GATA3,CLN5,BRCA2,NTN4,LRRK2,TBX6	darkolivegreen	VSMC_M9
GO:0007059	0.60	0.50	17	288	chromosome segregation	BP	1	CDC23,RMI1,CENPC,ACTR2,RB1,ACTR3,PDS5B,NUP37,RIOK2,INO80,CUL3,SYCP2,TLK2,TPR,CDC27,FMN2,SKA2	darkolivegreen	VSMC_M9
GO:1903506	0.60	0.43	148	2412	regulation of nucleic acid-templated transcription	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,INHBA,DDX1,ZEB1,EXOSC9,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,STOX2,MICAL2,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,KPNA6,WWC3,LARP7,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,DKK1,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0071695	0.60	0.52	10	163	anatomical structure maturation	BP	1	EXT1,RB1,GATA3,CLN5,BRCA2,NTN4,DCHS1,LRRK2,MBTPS2,TBX6	darkolivegreen	VSMC_M9
GO:0061053	0.60	0.60	4	63	somite development	BP	1	PPP2R3A,TMED2,TBX6,RBBP6	darkolivegreen	VSMC_M9
GO:0006112	0.61	0.60	4	65	energy reserve metabolic process	BP	1	UGP2,GFPT1,PHKG2,PPP1R2	darkolivegreen	VSMC_M9
GO:0007565	0.61	0.54	8	139	female pregnancy	BP	1	TMED2,LNPEP,STOX2,KPNA6,PTGS2,MAGED2,ITGA2,BMPR2	darkolivegreen	VSMC_M9
GO:0001568	0.61	0.46	36	576	blood vessel development	BP	1	THBS2,HDAC9,ROCK2,ITGB1,GPR4,JMJD6,STARD13,SOS1,ITGA5,EIF2AK3,TMED2,SULF1,AGTR1,HK2,RASA1,THBS1,ACVR1,ADAM12,NRP2,CLEC14A,PTGS2,ITGAV,PRRX1,ACTA2,AKT3,MYO1E,SRPX2,PKM,MYOCD,ROCK1,TBXA2R,VAV2,BMPR2,CTGF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0009581	0.61	0.57	5	84	detection of external stimulus	BP	1	FYN,SEMA5B,ITGA2,COL11A1,ELOVL4	darkolivegreen	VSMC_M9
GO:0098773	0.61	0.59	4	65	skin epidermis development	BP	1	EXT1,ZMPSTE24,INHBA,SOS1	darkolivegreen	VSMC_M9

GO:0071826	0.61	0.52	9	170	ribonucleoprotein complex subunit organization	BP	1	DDX1,RPF2,KIF5B,DHX29,EIF2S2,FASTKD2,EIF3J,DICER1,GEMIN6	darkolivegreen	VSMC_M9
GO:2001141	0.61	0.42	148	2416	regulation of RNA biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,INHBA,DDX1,ZEB1,EXOSC9,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,STOX2,MICAL2,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,KPNA6,WWC3,LARP7,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,DKK1,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0002761	0.61	0.57	5	86	regulation of myeloid leukocyte differentiation	BP	1	INHBA,RB1,NDFIP1,CUL4A,LYN	darkolivegreen	VSMC_M9
GO:0050804	0.61	0.48	20	317	modulation of chemical synaptic transmission	BP	1	STXBP5,PTPRD,AKAP9,JAK2,ITGB1,FYN,KIF5B,RAB3GAP1,MAP1B,ATP2A2,LRRK2,EIF4E,PTGS2,SORCS2,SEPT5,ATAD1,SLC1A3,CDH11,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0008033	0.61	0.55	6	117	tRNA processing	BP	1	ELAC1,TRMO,DDX1,TRDMT1,PUS3,DTWD1	darkolivegreen	VSMC_M9
GO:0006650	0.61	0.49	15	257	glycerophospholipid metabolic process	BP	1	SOCS6,PNPLA8,OSBPL8,GPCPD1,ETNK2,MBOAT1,BPNT1,ETNK1,PIP5K1A,PLD1,PIGW,PAFAH1B1,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0006351	0.61	0.42	154	2521	transcription, DNA-templated	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,TAF1B,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,STOX2,BDP1,MICAL2,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,TROVE2,KPNA6,WWC3,LARP7,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,DKK1,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0009749	0.61	0.52	9	153	response to glucose	BP	1	KIF5B,THBS1,SLC39A14,BRSK2,IGF1R,CCDC186,EIF2B5,C2CD2L,CTGF	darkolivegreen	VSMC_M9
GO:0003281	0.61	0.59	4	60	ventricular septum development	BP	1	GATA3,ACVR1,FZD2,BMPR2	darkolivegreen	VSMC_M9
GO:1901360	0.62	0.41	270	4575	organic cyclic compound metabolic process	BP	1	MALT1,ELAC1,AHI1,TBK1,CAND1,RRM2B,WDR46,DDX46,PHF20L1,KHDRBS3,ETF1,RMI1,PPIL1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,GNE,ZNF451,TRMO,HDAC9,CAVIN4,PSME4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,RARS2,UGP2,ACTR2,THAP5,GFPT1,TAF1B,ROCK2,INHBA,DDX1,NOCT,RPF2,ZEB1,EXOSC9,PIWIL4,UGGT1,RB1,SUCLA2,PICALM,ZC3H13,TRDMT1,TOE1,TSN,CAMK1D,UPF2,ACTR3,GATA3,CCNT2,JMJD6,DARS,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,ORC4,MBNL2,RIF1,PPP1R12A,PRPF40A,RPL26,LIG4,CEBPZ,SUPT20H,SMAD9,ACPP,NR2C1,NDFIP1,CUL4A,PDS5B,BRCA2,AC091959.3,ILK,TMF1,HOXC10,ERI1,HSD17B12,PARG,MTREX,CNOT7,RNF6,PDE7A,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,RIOK2,USP47,XRN1,PDE12,STOX2,BDP1,MICAL2,APPL1,U2SURP,AGTR1,ACTR8,HK2,ALDH18A1,TLR2,RASA1,MBNL1,DCP1A,DHX36,SHOX2,LIN54,PGAM4,ACVR1,WDR75,IRX5,MTERF3,INO80,NUDT9,GCNT4,SNRNP48,SLC35B3,ATP1A1,DYRK1A,BRD7,ERG,LRRK2,TBX15,UBE3A,NFRKB,CUL3,TDP2,PUS3,TROVE2,UCHL5,ATP6V1A,KPNA6,RRP15,EPRS,BPNT1,IARS2,NEK7,WWC3,LARP7,KPNA1,CLK1,IDH2,TAF5L,ABCB10,TRAK2,GPATCH3,LRRFIP1,ATF3,DERA,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,FASTKD2,CREB3L2,TPR,MYEF2,FZD2,CWC22,NPAT,TPI1,MYNN,GNPNAT1,SKIL,DTWD1,PRRX1,BOD1L1,DKK1,FMN2,PAPSS2,ADSS,RBM47,NOTCH3,ACBD3,TLR6,MAGED2,HK3,CLK2,DLST,TRIP4,TBX6,RLIM,MAGEE2,INTS14,ZC3H14,RBBP6,TLE3,SMG8,PKM,HNRNPH2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ROCK1,THOC1,ZNF280C,CIDEA,SPIRE1,GSPT1,TARS,ZC3H7A,MYSM1,CD40LG,US	darkolivegreen	VSMC_M9
GO:0030879	0.62	0.54	7	114	mammary gland development	BP	1	CDO1,JAK2,HOXA9,GATA3,BRCA2,HK2,ITGA2	darkolivegreen	VSMC_M9
GO:0099177	0.62	0.47	20	318	regulation of trans-synaptic signaling	BP	1	STXBP5,PTPRD,AKAP9,JAK2,ITGB1,FYN,KIF5B,RAB3GAP1,MAP1B,ATP2A2,LRRK2,EIF4E,PTGS2,SORCS2,SEPT5,ATAD1,SLC1A3,CDH11,SHISA7,WNT7A	darkolivegreen	VSMC_M9

GO:0097659	0.62	0.42	154	2522	nucleic acid-templated transcription	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,TAF1B,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,STOX2,BDP1,MICAL2,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,TROVE2,KPNA6,WWC3,LARP7,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,DKK1,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0019751	0.62	0.56	5	88	polyol metabolic process	BP	1	PLPP1,GPD2,BPNT1,TPI1,IMPA1	darkolivegreen	VSMC_M9
GO:0006405	0.62	0.58	4	69	RNA export from nucleus	BP	1	UPF2,TPR,THOC1,NUP155	darkolivegreen	VSMC_M9
GO:2001021	0.62	0.58	4	72	negative regulation of response to DNA damage stimulus	BP	1	RIF1,USP47,DYRK1A,THOC1	darkolivegreen	VSMC_M9
GO:0031329	0.62	0.44	41	689	regulation of cellular catabolic process	BP	1	TBK1,ATP6V1C1,UBQLN1,EXOC1,ZMPSTE24,ROCK2,NOCT,EXOSC9,PSMC2,TRDMT1,NUB1,RAB3GAP1,SUPT5H,TMF1,CNOT7,ATP6V0A2,ITCH,PDE12,DCP1A,DHX36,LRRK2,UBE3A,UCHL5,ATP6V1A,RAB3GAP2,PTPN1,TLK2,PITHD1,FASTKD2,MYEF2,SMURF1,MSN,PHKG2,ZC3H14,BAG5,ROCK1,CIDEA,USP7,FASTKD5,GDNF,VGLL4	darkolivegreen	VSMC_M9
GO:0016441	0.62	0.54	6	115	posttranscriptional gene silencing	BP	1	ZMPSTE24,CNOT7,DICER1,MYOCD,ZC3H7A,MIR186	darkolivegreen	VSMC_M9
GO:0043410	0.62	0.47	21	356	positive regulation of MAPK cascade	BP	1	CAV2,ROCK2,ILK,FFAR4,THBS1,LRRK2,IGF1R,NTRK3,PTPN1,IQGAP1,FERMT2,TNIK,TNFAIP8L3,DKK1,TLR6,SEMA7A,ROCK1,GADD45B,CTGF,LAMTOR3,WNT7A	darkolivegreen	VSMC_M9
GO:0098742	0.62	0.50	10	152	cell-cell adhesion via plasma-membrane adhesion molecules	BP	1	PTPRD,PCDH18,ITGB1,DCHS1,PALLD,ACVR1,KIFAP3,GPC4,CDH11,FXYD5	darkolivegreen	VSMC_M9
GO:0050921	0.62	0.54	6	109	positive regulation of chemotaxis	BP	1	CAMK1D,THBS1,NTRK3,ADAM10,ITGA2,BMPR2	darkolivegreen	VSMC_M9
GO:0031333	0.62	0.53	7	115	negative regulation of protein-containing complex assembly	BP	1	PFN2,DYRK1A,SPTBN5,VDAC2,DKK1,FHOD3,PMEPA1	darkolivegreen	VSMC_M9
GO:0002573	0.62	0.51	9	154	myeloid leukocyte differentiation	BP	1	WISP1,INHBA,RB1,GATA3,NDFIP1,CUL4A,LYN,TLR2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0071674	0.62	0.53	7	126	mononuclear cell migration	BP	1	EXT1,GATA3,LYN,THBS1,ADAM10,MSN,NOV	darkolivegreen	VSMC_M9
GO:0022613	0.63	0.46	20	376	ribonucleoprotein complex biogenesis	BP	1	WDR46,DDX1,RPF2,EXOSC9,RPL26,CUL4A,ERI1,DHX29,MTREX,EIF2S2,RIOK2,WDR75,MTERF3,RRP15,FASTKD2,EIF3J,DICER1,SURF6,GEMIN6,TFB2M	darkolivegreen	VSMC_M9
GO:0008283	0.63	0.42	86	1442	cell population proliferation	BP	1	MALT1,TBK1,CEP120,EXT1,WISP1,TOPORS,JAK2,CCDC88A,ZMPSTE24,TES,CAV2,INHBA,ITGB1,FYN,NOX4,RB1,CGREF1,CDK3,GATA3,LRRC32,AZI2,FAM98A,LIG4,MYO16,NDFIP1,CUL4A,SOS1,PDS5B,BRCA2,ILK,DCHS1,HOXC10,PLPP1,CNOT7,LYN,EIF2S2,ITCH,SULF1,AGTR1,TLR2,THBS1,SHOX2,CBLB,BRD7,LRRK2,SLC39A10,CUL3,IGF1R,NTRK3,ST8SIA1,KPNA1,IDH2,ATF3,NRP2,PTGS2,ITGAV,FERMT2,PRRX1,KIFAP3,AKT3,ADAM10,MSN,TPM1,TBX6,DICER1,PPM1D,MYOCD,ITGA2,ITGA1,RICTOR,CD40LG,PAFAH1B1,WFDC1,BMPR2,GDNF,CDK13,CTGF,OTUD6B,NOV,E2F3,WNT9A,ZPR1,VGLL4,TMEM119,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0044706	0.63	0.51	9	159	multi-multicellular organism process	BP	1	TMED2,LNPEP,STOX2,KPNA6,PITHD1,PTGS2,MAGED2,ITGA2,BMPR2	darkolivegreen	VSMC_M9
GO:1904062	0.63	0.48	14	241	regulation of cation transmembrane transport	BP	1	UTRN,UBQLN1,AKAP9,ITGB1,FYN,KIF5B,REM1,LYN,SLC30A5,ANK3,STIM2,KCNMB1,FXYD5,SHISA7	darkolivegreen	VSMC_M9
GO:0007005	0.63	0.46	23	436	mitochondrion organization	BP	1	LMAN1,COX18,CAV2,TRAK1,NDUFAF5,SLC25A46,TMEM70,GDAP1,HK2,LRRK2,TIMM17A,TOMM20,TRAK2,VDAC2,AKT3,ARMCX3,AFG3L2,SPIRE1,DNAJC11,PMPCA,MIGA1,TOMM20L,NDUFAF4	darkolivegreen	VSMC_M9
GO:0030522	0.63	0.48	13	217	intracellular receptor signaling pathway	BP	1	JAK2,CLOCK,UFM1,NR2C1,UBA5,TMF1,PLPP1,RNF6,ITCH,UBE3A,GPATCH3,TRIP4,PMEPA1	darkolivegreen	VSMC_M9
GO:0043500	0.63	0.55	5	88	muscle adaptation	BP	1	ROCK2,ATP2A2,GATM,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:0007006	0.63	0.55	5	99	mitochondrial membrane organization	BP	1	COX18,HK2,VDAC2,AFG3L2,DNAJC11	darkolivegreen	VSMC_M9
GO:0140352	0.63	0.44	37	618	export from cell	BP	1	STXBP5,JAK2,CLOCK,EXOC1,INHBA,RAB3B,KIF5B,DNAJC1,GATA3,RAB3GAP1,ATP2B1,TMF1,LYN,MERTK,FFAR4,AGTR1,TLR2,ATP2A2,ATP1A1,LRRK2,SNX19,BRSK2,CCDC186,IDH2,C2CD2L,SEPT5,SRCIN1,MYOM1,RAB31,C1QTNF3,PAFAH1B1,MIR186,GDNF,CTGF,NOV,SCAMP1,WNT7A	darkolivegreen	VSMC_M9
GO:1901880	0.63	0.57	4	62	negative regulation of protein depolymerization	BP	1	MAP1B,SPTBN5,CAMSAP2,HDGFL3	darkolivegreen	VSMC_M9
GO:0072676	0.63	0.57	4	72	lymphocyte migration	BP	1	EXT1,GATA3,ADAM10,MSN	darkolivegreen	VSMC_M9
GO:0000077	0.63	0.53	6	105	DNA damage checkpoint signaling	BP	1	CLOCK,RINT1,RPL26,CUL4A,THOC1,RFWD3	darkolivegreen	VSMC_M9
GO:0006892	0.63	0.53	6	99	post-Golgi vesicle-mediated transport	BP	1	MON2,EXOC1,ANK3,BLZF1,RAB31,SCAMP1	darkolivegreen	VSMC_M9
GO:0006302	0.63	0.48	13	225	double-strand break repair	BP	1	RMI1,ACTR2,DDX1,RIF1,LIG4,BRCA2,ACTR8,INO80,TDP2,FMN2,RBBP8,SPIRE1,RFWD3	darkolivegreen	VSMC_M9
GO:0002444	0.63	0.56	4	70	myeloid leukocyte mediated immunity	BP	1	STAP1,DDX1,LYN,DHX36	darkolivegreen	VSMC_M9

GO:0006942	0.64	0.56	4	68	regulation of striated muscle contraction	BP	1	AKAP9,ATP2A2,ATP1A1,CTGF	darkolivegreen	VSMC_M9
GO:0055123	0.64	0.53	6	99	digestive system development	BP	1	AHI1,EXT1,RB1,DCHS1,SHOX2,MYOCD	darkolivegreen	VSMC_M9
GO:0002684	0.64	0.43	31	542	positive regulation of immune system process	BP	1	MALT1,TBK1,STAP1,DDX1,FYN,RB1,CAMK1D,GATA3,RIF1,HSPH1,LYN,ITCH,APPL1,DHX36,THBS1,NFKBIZ,CBLB,LRRK2,SLC39A10,EIF2B5,SH3KBP1,TLR6,ADAM10,SEMA7A,ITGA2,CD40LG,VAV2,AQP3,CLEC4D,DNAJB9,FCN1	darkolivegreen	VSMC_M9
GO:0046330	0.64	0.56	4	68	positive regulation of JNK cascade	BP	1	TNIK,GADD45B,CTGF,WNT7A	darkolivegreen	VSMC_M9
GO:0008610	0.64	0.43	31	544	lipid biosynthetic process	BP	1	SOCS6,ELOVL5,PNPLA8,PDSS1,ABHD1,ST3GAL3,HSD17B12,PLPP1,RDH10,CERS5,ETNK2,ATP1A1,MBOAT1,BPNT1,ETNK1,ST8SIA1,PIP5K1A,MBTPS2,PTGS2,PLD1,SAMD8,ACBD3,PIGW,DHRS7B,ACOT7,DPM2,IMPA1,DPM1,ELOVL4,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0045444	0.64	0.48	11	188	fat cell differentiation	BP	1	WISP1,FBXO9,NOCT,GATA3,OSBPL8,FFAR4,OSBPL11,PTGS2,FERMT2,WNT5B,C1QTNF3	darkolivegreen	VSMC_M9
GO:0032774	0.64	0.39	154	2534	RNA biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,TAF1B,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,STOX2,BDP1,MICAL2,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,TROVE2,KPNA6,WWC3,LARP7,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,SKIL,PRRX1,DKK1,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0010508	0.64	0.52	6	105	positive regulation of autophagy	BP	1	TBK1,RAB3GAP1,SUPT5H,LRRK2,RAB3GAP2,ROCK1	darkolivegreen	VSMC_M9
GO:0006575	0.64	0.51	7	136	cellular modified amino acid metabolic process	BP	1	GATA3,OSBPL8,PLOD2,GDAP1,GCNT4,MBOAT1,GATM	darkolivegreen	VSMC_M9
GO:0006364	0.64	0.48	10	198	rRNA processing	BP	1	WDR46,RPF2,EXOSC9,RPL26,ERI1,MTREX,RIOK2,WDR75,RRP15,TFB2M	darkolivegreen	VSMC_M9
GO:0033209	0.64	0.55	4	75	tumor necrosis factor-mediated signaling pathway	BP	1	EXT1,JAK2,ILK,FAS	darkolivegreen	VSMC_M9
GO:0046903	0.64	0.42	40	673	secretion	BP	1	CDO1,STXBP5,ABCB4,JAK2,CLOCK,EXOC1,MYO6,INHBA,PNPLA8,RAB3B,KIF5B,DNAJC1,GATA3,RAB3GAP1,TMF1,LYN,MERTK,FFAR4,AGTR1,HK2,TLR2,ATP2A2,LRRK2,SNX19,BRSK2,CCDC186,IDH2,C2CD2L,SEPT5,SRCIN1,MYOM1,RAB31,C1QTNF3,PAFAH1B1,GDNF,CTGF,BDKRB2,NOV,SCAMP1,WNT7A	darkolivegreen	VSMC_M9
GO:0060048	0.64	0.52	6	103	cardiac muscle contraction	BP	1	AKAP9,ATP2A2,ATP1A1,TPM1,NUP155,CTGF	darkolivegreen	VSMC_M9
GO:0022407	0.64	0.45	17	293	regulation of cell-cell adhesion	BP	1	SOCS6,MALT1,JAK2,FYN,GATA3,LRRC32,NDFIP1,HSPH1,LYN,ITCH,NFKBIZ,CBLB,ANK3,KIFAP3,ADAM19,CD40LG,FXYD5	darkolivegreen	VSMC_M9
GO:0006109	0.64	0.50	8	139	regulation of carbohydrate metabolic process	BP	1	SLC35B4,ZMPSTE24,PHKG2,CLK2,CLTC,C1QTNF3,USP7,RANBP2	darkolivegreen	VSMC_M9
GO:0021782	0.65	0.53	5	86	glial cell development	BP	1	ILK,LYN,TLR2,EIF2B5,DICER1	darkolivegreen	VSMC_M9
GO:0007267	0.65	0.40	70	1146	cell-cell signaling	BP	1	STXBP5,EXT1,WISP1,PTPRD,AKAP9,JAK2,CLOCK,CHRM2,INHBA,RAB3B,ITGB1,FYN,SYPL1,KIF5B,GATA3,RAB3GAP1,TNFAIP6,ILK,TMF1,SCYL2,LYN,MERTK,SULF1,USP47,LNPEP,FFAR4,MAP1B,AGTR1,TLR2,ATP2A2,GPR176,ARL6,BRD7,LRRK2,SNX19,BRSK2,CUL3,EIF4E,CCDC186,KPNA1,C2CD2L,SH3KBP1,PTGS2,FZD2,SORCS2,SEPT5,FERMT2,SMURF1,TNIK,DKK1,ATAD1,WNT5B,ADAM10,KCNMB1,TLE3,PIN1,NUP155,SLC1A3,C1QTNF3,GPC4,PAFAH1B1,KIF1B,CDH11,GDNF,NOV,WNT9A,VGLL4,SRD5A2,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0032940	0.65	0.42	34	574	secretion by cell	BP	1	STXBP5,JAK2,CLOCK,EXOC1,INHBA,RAB3B,KIF5B,DNAJC1,GATA3,RAB3GAP1,TMF1,LYN,MERTK,FFAR4,AGTR1,TLR2,ATP2A2,LRRK2,SNX19,BRSK2,CCDC186,IDH2,C2CD2L,SEPT5,SRCIN1,MYOM1,RAB31,C1QTNF3,PAFAH1B1,GDNF,CTGF,NOV,SCAMP1,WNT7A	darkolivegreen	VSMC_M9
GO:0044419	0.65	0.41	55	948	biological process involved in interspecies interaction between organisms	BP	1	MALT1,TBK1,EXT1,PLAA,JAK2,EXOC1,FBXO9,STAP1,ZMPSTE24,ACTR2,CHRM2,CAV2,DDX1,NOCT,ITGB1,FYN,KIF5B,NUB1,ACTR3,GATA3,DNAJC3,ITGA5,TMF1,CNOT7,LYN,IPO7,ITCH,CHD1,PDE12,APPL1,AGTR1,TLR2,ATP2A2,DHX36,EPRS,CCDC186,PTPN1,VAPB,GPATCH3,PTGS2,NCAM1,ITGAV,ACTA2,TLR6,PPM1D,THOC1,ITGA2,VAPA,MYO1C,TBXA2R,LSM5,ENO1,CLEC4D,FCN1,NDUFAF4	darkolivegreen	VSMC_M9
GO:0006325	0.65	0.44	18	301	chromatin organization	BP	1	PSME4,RB1,GATA3,SETD5,TDG,HCFC2,SMARCA5,ACTR8,LIN54,INO80,CHD9,NAP1L4,KIAA1551,RBBP7,TLK2,BAZ1A,TPR,MYSM1	darkolivegreen	VSMC_M9
GO:0043502	0.65	0.55	4	71	regulation of muscle adaptation	BP	1	ROCK2,ATP2A2,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:0034612	0.65	0.47	10	181	response to tumor necrosis factor	BP	1	EXT1,JAK2,NUB1,GATA3,ILK,THBS1,TANK,PTGS2,FAS,ADAM10	darkolivegreen	VSMC_M9

GO:0055085	0.65	0.40	62	1047	transmembrane transport	BP	1	UTRN,AZIN1,ATP6V1C1,SLC39A7,SLC35B4,UBQLN1,SLC30A9,ABCB4,AKAP9,TMEM165,ZMPSTE24,ITGB1,FYN,KIF5B,SLC36A4,RTN2,OSBPL8,ATP2B1,REM1,LYN,SLC16A12,ATP6V0A2,SLC30A5,FFAR4,APPL1,HK2,ATP2A2,THBS1,SLC39A14,SLC35B3,ATP1A1,ATP10A,SLC39A10,MRS2,TIMM17A,ATP6V1A,GPR89A,ITPR2,TOMM20,ATP11B,ABCB10,ANK3,ATP13A3,ITGAV,VDAC2,PLP2,CLCNKB,STIM2,KCNMB1,OAZ2,ANXA6,SLC1A3,AFG3L2,ZDHHC7,SLC25A24,MIR186,AQP3,FXYD5,TOMM20L,SLC35D1,SEC63,SHISA7	darkolivegreen	VSMC_M9
GO:0042180	0.65	0.48	8	150	cellular ketone metabolic process	BP	1	ELOVL5,PDSS1,RDH10,GPD2,PTGS2,TPI1,SRD5A2,PPTC7	darkolivegreen	VSMC_M9
GO:0071322	0.65	0.49	7	121	cellular response to carbohydrate stimulus	BP	1	KIF5B,SLC39A14,BRSK2,IGF1R,CCDC186,C2CD2L,MAP2K4	darkolivegreen	VSMC_M9
GO:0009612	0.65	0.47	10	176	response to mechanical stimulus	BP	1	FYN,MAP1B,THBS1,ATP1A1,PTGS2,FAS,MAP2K4,ITGA2,SLC1A3,COL11A1	darkolivegreen	VSMC_M9
GO:0050870	0.65	0.49	7	130	positive regulation of T cell activation	BP	1	MALT1,FYN,GATA3,HSPH1,LYN,NFKBIZ,CD40LG	darkolivegreen	VSMC_M9
GO:0007268	0.66	0.42	29	471	chemical synaptic transmission	BP	1	STXBP5,EXT1,PTPRD,AKAP9,JAK2,CHRM2,RAB3B,ITGB1,FYN,SYPL1,KIF5B,RAB3GAP1,MAP1B,ATP2A2,GPR176,LRRK2,EIF4E,PTGS2,SORCS2,SEPT5,ATAD1,KCNMB1,SLC1A3,PAFAH1B1,KIF1B,CDH11,GDNF,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0098916	0.66	0.42	29	471	anterograde trans-synaptic signaling	BP	1	STXBP5,EXT1,PTPRD,AKAP9,JAK2,CHRM2,RAB3B,ITGB1,FYN,SYPL1,KIF5B,RAB3GAP1,MAP1B,ATP2A2,GPR176,LRRK2,EIF4E,PTGS2,SORCS2,SEPT5,ATAD1,KCNMB1,SLC1A3,PAFAH1B1,KIF1B,CDH11,GDNF,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0032147	0.66	0.50	6	105	activation of protein kinase activity	BP	1	MALT1,JAK2,CCDC88A,OSBPL8,NTRK3,TLR6	darkolivegreen	VSMC_M9
GO:0010959	0.66	0.44	15	263	regulation of metal ion transport	BP	1	UTRN,UBQLN1,AKAP9,ITGB1,FYN,KIF5B,ATP2B1,REM1,LYN,ATP1A1,ANK3,PTGS2,STIM2,KCNMB1,FXYD5	darkolivegreen	VSMC_M9
GO:0015711	0.66	0.45	13	228	organic anion transport	BP	1	SLC35B4,ABCB4,PNPLA8,ITGB1,SLC36A4,RAB3GAP1,SLC16A12,SLC35B3,SLC1A3,SLC25A24,PLEKHA3,SLC35D1,BDKRB2	darkolivegreen	VSMC_M9
GO:0034599	0.66	0.45	13	234	cellular response to oxidative stress	BP	1	UBQLN1,JAK2,PNPLA8,GPX7,FYN,STK24,ATP2A2,LRRK2,CPEB2,TLR6,TPM1,BAG5,SLC25A24	darkolivegreen	VSMC_M9
GO:0000724	0.66	0.49	7	124	double-strand break repair via homologous recombination	BP	1	RMI1,ACTR2,RIF1,BRCA2,INO80,RBBP8,RFWD3	darkolivegreen	VSMC_M9
GO:0002819	0.66	0.50	6	111	regulation of adaptive immune response	BP	1	MALT1,GATA3,RIF1,NDFIP1,NFKBIZ,THOC1	darkolivegreen	VSMC_M9
GO:0051403	0.66	0.46	11	190	stress-activated MAPK cascade	BP	1	ITCH,LRRK2,IGF1R,TNIK,FAS,MAP2K4,PAFAH1B1,GADD45B,CTGF,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0032760	0.66	0.53	4	69	positive regulation of tumor necrosis factor production	BP	1	JAK2,TLR2,THBS1,LRRK2	darkolivegreen	VSMC_M9
GO:0050877	0.66	0.40	41	678	nervous system process	BP	1	AKAP9,MYO6,UBA6,ZMPSTE24,ACTR2,ROCK2,ITGB1,FYN,PICALM,RAB3GAP1,SETD5,ACPP,UBA5,EIF2AK3,FAR4,RDH10,TLR2,ATP2A2,ARL6,IRX5,LRRK2,UBE3A,SEMA5B,ANK3,GATM,PTGS2,FZD2,DKK1,ATAD1,DICER1,ITGA2,SLC1A3,PAFAH1B1,COL11A1,RABGGTB,ARF4,LHFPL4,NOV,PDCL,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0042127	0.66	0.39	72	1230	regulation of cell population proliferation	BP	1	WISP1,TOPORS,JAK2,CCDC88A,ZMPSTE24,TES,CAV2,INHBA,ITGB1,NOX4,RB1,CGREF1,GATA3,LRRC32,FAM98A,LIG4,MYO16,NDFIP1,CUL4A,SOS1,PDS5B,BRCA2,ILK,HOXC10,PLPP1,CNOT7,LYN,ITCH,SULF1,AGTR1,TLR2,THBS1,SHOX2,CBLB,BRD7,LRRK2,SLC39A10,CUL3,IGF1R,NTRK3,ST8SIA1,IDH2,ATF3,NRP2,PTGS2,ITGAV,FERMT2,PRRX1,KIFAP3,AKT3,ADAM10,TPM1,TBX6,DICER1,PPM1D,MYOCD,ITGA2,ITGA1,RICTOR,CD40LG,WFDC1,BMPR2,GDNF,CDK13,CTGF,NOV,E2F3,WNT9A,VGLL4,TMEM119,CHST11,WNT7A	darkolivegreen	VSMC_M9
GO:0048639	0.66	0.48	8	134	positive regulation of developmental growth	BP	1	PLAA,ILK,MAP1B,SMURF1,SEMA7A,PIN1,PAFAH1B1,BMPR2	darkolivegreen	VSMC_M9
GO:0035295	0.66	0.39	52	849	tube development	BP	1	AHI1,EXT1,THBS2,HDAC9,HOXA11,ROCK2,ITGB1,GPR4,RB1,GATA3,JMJD6,STARD13,SOS1,ILK,ITGA5,DCHS1,EIF2AK3,TMED2,SULF1,MICAL2,RDH10,AGTR1,HK2,RASA1,THBS1,SHOX2,ACVR1,MAN1A2,EIF4E,ADAM12,NRP2,CLEC14A,PTGS2,FZD2,ITGAV,PRRX1,AKT3,MYO1E,TBX6,SRPX2,PKM,MYOCD,ROCK1,TBXA2R,VAV2,PRKACB,BMPR2,GDNF,CTGF,NOV,IRX3,WNT7A	darkolivegreen	VSMC_M9
GO:0030098	0.67	0.43	15	259	lymphocyte differentiation	BP	1	MALT1,HDAC9,INHBA,ITGB1,GATA3,JMJD6,LIG4,NDFIP1,SOS1,MERTK,NFKBIZ,GPR89A,CD3G,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0002520	0.67	0.39	41	694	immune system development	BP	1	MALT1,EXT1,WISP1,JAK2,HDAC9,HOXA9,ZMPSTE24,INHBA,ITGB1,RB1,PICALM,GATA3,JMJD6,AZI2,RIF1,LIG4,NDFIP1,CUL4A,SOS1,BRCA2,UBA5,LYN,MERTK,ITCH,TLR2,DHX36,NFKBIZ,CBLB,TROVE2,GPR89A,ABCB10,CD3G,PITHD1,RBM47,MYO1E,THOC1,MYSM1,CD40LG,PAFAH1B1,CDK13,DNAJB9	darkolivegreen	VSMC_M9
GO:0009913	0.67	0.48	7	120	epidermal cell differentiation	BP	1	MYO6,ROCK2,PALLD,PIP5K1A,ROCK1,PAFAH1B1,AQP3	darkolivegreen	VSMC_M9
GO:0021537	0.67	0.45	11	184	telencephalon development	BP	1	CEP120,EXT1,UBA6,INHBA,KIF5B,ZDHHC16,LRRK2,UCHL5,EIF2B5,SEMA7A,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0002706	0.67	0.51	5	92	regulation of lymphocyte mediated immunity	BP	1	MALT1,GATA3,RIF1,NDFIP1,THOC1	darkolivegreen	VSMC_M9
GO:0034764	0.67	0.46	9	155	positive regulation of transmembrane transport	BP	1	AZIN1,AKAP9,ITGB1,KIF5B,OSBPL8,APPL1,ANK3,STIM2,KCNMB1	darkolivegreen	VSMC_M9
GO:0001654	0.67	0.43	17	280	eye development	BP	1	AHI1,TOPORS,INHBA,GATA3,RAB3GAP1,JMJD6,ATP2B1,SOS1,MERTK,RDH10,ZDHHC16,SKIL,WNT5B,MYOM1,BMPR2,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:0032787	0.67	0.41	22	404	monocarboxylic acid metabolic process	BP	1	PLAA,ELOVL5,PNPLA8,CYP27C1,ABHD1,HSD17B12,RDH10,HK2,PGAM4,MRS2,IDH2,GATM,PTGS2,TPI1,HK3,PKM,ETFA,SLC1A3,ACOT7,ENO1,ELOVL4,AKR1D1	darkolivegreen	VSMC_M9
GO:0050777	0.67	0.48	7	128	negative regulation of immune response	BP	1	FYN,NDFIP1,CNOT7,LYN,ITCH,GPATCH3,THOC1	darkolivegreen	VSMC_M9

GO:0006970	0.67	0.53	4	71	response to osmotic stress	BP	1	PTGS2,ITGA2,BDKRB2,EFHD1	darkolivegreen	VSMC_M9
GO:0055017	0.67	0.52	4	72	cardiac muscle tissue growth	BP	1	PDLIM5,MAP2K4,PIN1,VGLL4	darkolivegreen	VSMC_M9
GO:0071219	0.67	0.47	7	133	cellular response to molecule of bacterial origin	BP	1	MALT1,PLAA,STAP1,LYN,TLR2,TLR6,TBXA2R	darkolivegreen	VSMC_M9
GO:0034109	0.67	0.52	4	71	homotypic cell-cell adhesion	BP	1	JAK2,ILK,LYN,ANK3	darkolivegreen	VSMC_M9
GO:0001944	0.67	0.39	37	607	vasculature development	BP	1	THBS2,HDAC9,ROCK2,ITGB1,GPR4,JMJD6,STARD13,SOS1,ITGA5,EIF2AK3,TMED2,SULF1,AGTR1,HK2,RASA1,THBS1,ACVR1,ADAM12,NRP2,CLEC14A,PTGS2,ITGAV,PRRX1,ACTA2,AKT3,ADAM10,MYO1E,SRPX2,PKM,MYOCD,ROCK1,TBXA2R,VAV2,BMPR2,CTGF,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0048568	0.67	0.41	20	341	embryonic organ development	BP	1	AHI1,LRIG3,MYO6,HOXA9,HOXA11,GATA3,TMED2,MICAL2,RDH10,SHOX2,ACVR1,IRX5,TBX15,FZD2,PRRX1,TBX6,RBBP6,COL11A1,GDNF,CHST11	darkolivegreen	VSMC_M9
GO:0035821	0.67	0.52	4	75	modulation of process of other organism	BP	1	CAV2,CHD1,VAPB,VAPA	darkolivegreen	VSMC_M9
GO:0099536	0.67	0.40	30	494	synaptic signaling	BP	1	STXBP5,EXT1,PTPRD,AKAP9,JAK2,CHRM2,RAB3B,ITGB1,FYN,SYPL1,KIF5B,RAB3GAP1,MAP1B,ATP2A2,GPR176,LRRK2,EIF4E,KPNA1,PTGS2,SORCS2,SEPT5,ATAD1,KCNMB1,SLC1A3,PAFAH1B1,KIF1B,CDH11,GDNF,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0000725	0.67	0.47	7	126	recombinational repair	BP	1	RMI1,ACTR2,RIF1,BRCA2,INO80,RBBP8,RFWD3	darkolivegreen	VSMC_M9
GO:0071482	0.67	0.50	5	94	cellular response to light stimulus	BP	1	RPL26,USP47,DHX36,INO80,PTGS2	darkolivegreen	VSMC_M9
GO:0022408	0.68	0.47	7	130	negative regulation of cell-cell adhesion	BP	1	SOCS6,JAK2,LRRC32,NDFIP1,ITCH,CBLB,FXYD5	darkolivegreen	VSMC_M9
GO:1905954	0.68	0.52	4	73	positive regulation of lipid localization	BP	1	ABCB4,TMF1,OSBPL11,CIDEA	darkolivegreen	VSMC_M9
GO:0051261	0.68	0.48	6	99	protein depolymerization	BP	1	MICAL2,MAP1B,SPTBN5,CAMSAP2,HDGFL3,CFL2	darkolivegreen	VSMC_M9
GO:0002685	0.68	0.46	8	152	regulation of leukocyte migration	BP	1	STAP1,CAMK1D,LYN,THBS1,ADAM10,MSN,ITGA2,NOV	darkolivegreen	VSMC_M9
GO:0019216	0.68	0.43	14	251	regulation of lipid metabolic process	BP	1	ELOVL5,ZMPSTE24,PIK3R4,PLPP1,LYN,RDH10,AGTR1,ATP1A1,MBTPS2,PTGS2,TNFAIP8L3,SAMD8,CIDEA,VAV2	darkolivegreen	VSMC_M9
GO:0099537	0.68	0.39	29	477	trans-synaptic signaling	BP	1	STXBP5,EXT1,PTPRD,AKAP9,JAK2,CHRM2,RAB3B,ITGB1,FYN,SYPL1,KIF5B,RAB3GAP1,MAP1B,ATP2A2,GPR176,LRRK2,EIF4E,PTGS2,SORCS2,SEPT5,ATAD1,KCNMB1,SLC1A3,PAFAH1B1,KIF1B,CDH11,GDNF,SHISA7,WNT7A	darkolivegreen	VSMC_M9
GO:0010942	0.68	0.40	26	470	positive regulation of cell death	BP	1	JAK2,INHBA,ITGB1,FYN,NOX4,PICALM,CAMK1D,RPL26,LYN,THBS1,LRRK2,EIF2B5,ATF3,PTGS2,SKIL,DKK1,FAS,TLR6,ADAM10,MAP2K4,PIN1,ITGA1,CD40LG,GADD45B,CTGF,E2F3	darkolivegreen	VSMC_M9
GO:0032259	0.68	0.42	16	290	methylation	BP	1	ETF1,TRMO,ZMPSTE24,PIWIL4,ZC3H13,TRDMT1,GATA3,SETD5,NDUFAF5,RIF1,FAM98A,LARP7,PPM1D,GSPT1,RAB6A,TFB2M	darkolivegreen	VSMC_M9
GO:0007601	0.68	0.47	7	123	visual perception	BP	1	RDH10,ARL6,IRX5,SEMA5B,COL11A1,RABGGTB,PDCL	darkolivegreen	VSMC_M9
GO:1905477	0.68	0.49	5	88	positive regulation of protein localization to membrane	BP	1	ITGB1,FYN,KIF5B,ANK3,MYO1C	darkolivegreen	VSMC_M9
GO:0043408	0.68	0.39	29	502	regulation of MAPK cascade	BP	1	CAV2,ROCK2,CBLC,ILK,LYN,ITCH,FFAR4,THBS1,LRRK2,IGF1R,NTRK3,PTPN1,ATF3,IQGAP1,FERMT2,TNIK,TNFAIP8L3,DKK1,FAS,TLR6,SEMA7A,PIN1,ROCK1,PAFAH1B1,GADD45B,CTGF,LAMTOR3,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0001101	0.68	0.48	6	107	response to acid chemical	BP	1	CDO1,FYN,LYN,TOMM20,CTGF,LAMTOR3	darkolivegreen	VSMC_M9
GO:0007204	0.68	0.43	11	194	positive regulation of cytosolic calcium ion concentration	BP	1	JAK2,FYN,GPR4,LYN,FFAR4,AGTR1,ITPR2,ITGAV,GPR65,TBXA2R,BDKRB2	darkolivegreen	VSMC_M9
GO:0051251	0.68	0.44	10	186	positive regulation of lymphocyte activation	BP	1	MALT1,FYN,GATA3,RIF1,HSPH1,LYN,NFKBIZ,SLC39A10,SH3KBP1,CD40LG	darkolivegreen	VSMC_M9
GO:0000079	0.68	0.51	4	80	regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	CCNT2,CCNA1,IPO7,MYOCD	darkolivegreen	VSMC_M9
GO:0098609	0.68	0.38	36	592	cell-cell adhesion	BP	1	SOCS6,MALT1,EXT1,PTPRD,JAK2,PCDH18,ITGB1,FYN,FNDC3A,GATA3,LRRC32,NDFIP1,ILK,ITGA5,DCHS1,HSPH1,LYN,PALLD,ITCH,ACVR1,NFKBIZ,CBLB,PDLIM5,ANK3,ITGAV,KIFAP3,MSN,ADAM19,CYFIP2,SRPX2,ROCK1,GPC4,CD40LG,CDH11,FXYD5,NOV	darkolivegreen	VSMC_M9
GO:0150063	0.68	0.41	17	282	visual system development	BP	1	AHI1,TOPORS,INHBA,GATA3,RAB3GAP1,JMJD6,ATP2B1,SOS1,MERTK,RDH10,ZDHHC16,SKIL,WNT5B,MYOM1,BMPR2,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:1903131	0.68	0.41	17	297	mononuclear cell differentiation	BP	1	MALT1,HDAC9,INHBA,ITGB1,GATA3,JMJD6,AZI2,LIG4,NDFIP1,SOS1,LYN,MERTK,NFKBIZ,GPR89A,CD3G,CD40LG,DNAJB9	darkolivegreen	VSMC_M9
GO:0002376	0.68	0.36	97	1656	immune system process	BP	1	SOCS6,MALT1,TBK1,EXT1,WISP1,PTPRD,JAK2,EXOC1,FBXO9,HDAC9,STAP1,HOXA9,ZMPSTE24,ACTR2,INHBA,DDX1,RAB3B,ITGB1,FYN,KIF5B,EXOSC9,RB1,PICALM,CAMK1D,NUB1,ACTR3,GATA3,JMJD6,LRRC32,DNAJC3,AZI2,RIF1,LIG4,NDFIP1,CUL4A,SOS1,BRCA2,UBA5,HSPH1,TMF1,CNOT7,LYN,MERTK,ATP6V0A2,IPO7,ITCH,LNPEP,PDE12,APPL1,TLR2,DHX36,THBS1,NFKBIZ,CBLB,LRRK2,SLC39A10,TROVE2,EPRS,IGF1R,GPR89A,PTPN1,ABCB10,EIF2B5,LTB4R,GPATCH3,CD3G,SH3KBP1,PITHD1,SKIL,FAS,ADSS,RBM47,TLR6,ADAM10,MSN,MYO1E,GPR65,MAP2K4,SEMA7A,ROCK1,THOC1,ITGA2,ITGA1,MYSM1,CD40LG,MYO1C,PAFAH1B1,VAV2,CEACAM20,AQP3,CLEC4D,RAB6A,CDK13,DNAJB9,NOV,FCN1,NDUFAF4	darkolivegreen	VSMC_M9
GO:0031570	0.69	0.47	6	111	DNA integrity checkpoint signaling	BP	1	CLOCK,RINT1,RPL26,CUL4A,THOC1,RFWD3	darkolivegreen	VSMC_M9
GO:0032412	0.69	0.43	10	178	regulation of ion transmembrane transporter activity	BP	1	UTRN,UBQLN1,AKAP9,ITGB1,KIF5B,REM1,ANK3,STIM2,FXYD5,SHISA7	darkolivegreen	VSMC_M9

GO:0043588	0.69	0.43	10	171	skin development	BP	1	EXT1,ZMPSTE24,ROCK2,INHBA,SOS1,PALLD,PIP5K1A,ROCK1,ITGA2,AQP3	darkolivegreen	VSMC_M9
GO:0002521	0.69	0.39	22	383	leukocyte differentiation	BP	1	MALT1,WISP1,HDAC9,INHBA,ITGB1,RB1,GATA3,JMJD6,AZI2,LIG4,NDFIP1,CUL4A,SOS1,LYN,MERTK,TLR2,NFKBIZ,GPR89A,CD3G,CD40LG,PAFAH1B1,DNAJB9	darkolivegreen	VSMC_M9
GO:0060562	0.69	0.41	16	269	epithelial tube morphogenesis	BP	1	AHI1,EXT1,HOXA11,GATA3,STARD13,ILK,DCHS1,TMED2,MICAL2,RDH10,ACVR1,FZD2,TBX6,PRKACB,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0048754	0.69	0.45	7	121	branching morphogenesis of an epithelial tube	BP	1	EXT1,HOXA11,ILK,DCHS1,RDH10,ACVR1,GDNF	darkolivegreen	VSMC_M9
GO:0070663	0.69	0.44	8	153	regulation of leukocyte proliferation	BP	1	LRRC32,NDFIP1,SOS1,LYN,ITCH,CBLB,SLC39A10,CD40LG	darkolivegreen	VSMC_M9
GO:0045765	0.69	0.41	13	229	regulation of angiogenesis	BP	1	THBS2,ROCK2,ITGB1,GPR4,ITGA5,SULF1,HK2,THBS1,ADAM12,AKT3,PKM,ROCK1,TBXA2R	darkolivegreen	VSMC_M9
GO:0006672	0.69	0.50	4	78	ceramide metabolic process	BP	1	ST3GAL3,PLPP1,CERS5,SAMD8	darkolivegreen	VSMC_M9
GO:0022618	0.69	0.44	8	163	ribonucleoprotein complex assembly	BP	1	DDX1,RPF2,DHX29,EIF2S2,FASTKD2,EIF3J,DICER1,GEMIN6	darkolivegreen	VSMC_M9
GO:0002443	0.69	0.42	12	221	leukocyte mediated immunity	BP	1	MALT1,STAP1,DDX1,KIF5B,GATA3,RIF1,LIG4,NDFIP1,LYN,DHX36,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0030324	0.69	0.44	8	141	lung development	BP	1	EXT1,JMJD6,RDH10,MAN1A2,EIF4E,MYOCD,BMPR2,CTGF	darkolivegreen	VSMC_M9
GO:0098659	0.69	0.50	4	71	inorganic cation import across plasma membrane	BP	1	FYN,SLC39A14,ATP1A1,SLC39A10	darkolivegreen	VSMC_M9
GO:0099587	0.69	0.50	4	71	inorganic ion import across plasma membrane	BP	1	FYN,SLC39A14,ATP1A1,SLC39A10	darkolivegreen	VSMC_M9
GO:0032204	0.69	0.50	4	74	regulation of telomere maintenance	BP	1	XRN1,DHX36,NEK7,USP7	darkolivegreen	VSMC_M9
GO:0030097	0.69	0.37	36	618	hemopoiesis	BP	1	MALT1,EXT1,WISP1,JAK2,HDAC9,HOXA9,INHBA,ITGB1,RB1,PICALM,GATA3,JMJD6,AZI2,LIG4,NDFIP1,CUL4A,SOS1,BRCA2,UBA5,LYN,MERTK,ITCH,TLR2,DHX36,NFKBIZ,GPR89A,ABCB10,CD3G,PITHD1,RBM47,MYO1E,MYSM1,CD40LG,PAFAH1B1,CDK13,DNAJB9	darkolivegreen	VSMC_M9
GO:0051341	0.69	0.50	4	79	regulation of oxidoreductase activity	BP	1	AGTR1,PDP1,LRRK2,GDNF	darkolivegreen	VSMC_M9
GO:0006400	0.69	0.50	4	85	tRNA modification	BP	1	TRMO,TRDMT1,PUS3,DTWD1	darkolivegreen	VSMC_M9
GO:2000779	0.69	0.50	4	76	regulation of double-strand break repair	BP	1	ACTR2,RIF1,FMN2,SPIRE1	darkolivegreen	VSMC_M9
GO:0008284	0.69	0.37	39	681	positive regulation of cell population proliferation	BP	1	WISP1,JAK2,CAV2,ITGB1,FAM98A,LIG4,CUL4A,ILK,HOXC10,CNOT7,LYN,AGTR1,THBS1,SHOX2,SLC39A10,CUL3,IGF1R,NTRK3,ST8SIA1,ATF3,NRP2,PTGS2,ITGAV,FERMT2,PRRX1,AKT3,ADAM10,TBX6,MYOCD,ITGA2,RICTOR,CD40LG,BMPR2,GDNF,CDK13,CTGF,E2F3,TMEM119,WNT7A	darkolivegreen	VSMC_M9
GO:0002027	0.70	0.50	4	73	regulation of heart rate	BP	1	AKAP9,ATP2A2,SHOX2,TPM1	darkolivegreen	VSMC_M9
GO:0009141	0.70	0.49	4	86	nucleoside triphosphate metabolic process	BP	1	RRM2B,LRRK2,ATP6V1A,ENO1	darkolivegreen	VSMC_M9
GO:1903557	0.70	0.50	4	72	positive regulation of tumor necrosis factor superfamily cytokine production	BP	1	JAK2,TLR2,THBS1,LRRK2	darkolivegreen	VSMC_M9
GO:0046474	0.70	0.42	10	185	glycerophospholipid biosynthetic process	BP	1	SOCS6,ETNK2,BPNT1,ETNK1,PIP5K1A,PLD1,PIGW,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0045598	0.70	0.46	6	109	regulation of fat cell differentiation	BP	1	WISP1,NOCT,GATA3,FFAR4,PTGS2,FERMT2	darkolivegreen	VSMC_M9
GO:0046034	0.70	0.42	10	219	ATP metabolic process	BP	1	PARG,PDE12,HK2,PGAM4,ATP6V1A,TPI1,HK3,CLPX,PKM,ENO1	darkolivegreen	VSMC_M9
GO:0007162	0.70	0.41	12	215	negative regulation of cell adhesion	BP	1	SOCS6,JAK2,LRRC32,NDFIP1,ITCH,RASA1,THBS1,CBLB,PHLDB2,CORO1C,ADAM10,FXYD5	darkolivegreen	VSMC_M9
GO:0048638	0.70	0.40	15	257	regulation of developmental growth	BP	1	CDKL3,PLAA,ZMPSTE24,ILK,RNF6,MAP1B,WWC3,SEMA5B,SMURF1,SEMA7A,PIN1,AFG3L2,PAFAH1B1,BMPR2,VGLL4	darkolivegreen	VSMC_M9
GO:0001838	0.70	0.45	6	107	embryonic epithelial tube formation	BP	1	GATA3,TMED2,FZD2,PRKACB,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0062013	0.70	0.47	5	96	positive regulation of small molecule metabolic process	BP	1	ELOVL5,RDH10,PTGS2,PHKG2,ENO1	darkolivegreen	VSMC_M9
GO:0034654	0.70	0.33	170	2841	nucleobase-containing compound biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,RRM2B,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,GFPT1,TAF1B,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,LIG4,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,HSD17B12,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,STOX2,BDP1,MICAL2,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SLC35B3,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,TROVE2,ATP6V1A,KPNA6,NEK7,WWC3,LARP7,IDH2,TAF5L,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,GNPNAT1,SKIL,PRRX1,DKK1,PAPSS2,ADSS,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ACOT7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,RFXAP,ELOVL4,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0017157	0.70	0.43	8	147	regulation of exocytosis	BP	1	STXBP5,RAB3B,RAB3GAP1,LYN,ATP2A2,LRRK2,SEPT5,WNT7A	darkolivegreen	VSMC_M9
GO:0045639	0.70	0.49	4	77	positive regulation of myeloid cell differentiation	BP	1	INHBA,RB1,ABCB10,PITHD1	darkolivegreen	VSMC_M9

GO:0035282	0.70	0.49	4	74	segmentation	BP	1	TMED2,NRP2,TBX6,IRX3	darkolivegreen	VSMC_M9
GO:0010948	0.70	0.40	13	237	negative regulation of cell cycle process	BP	1	CLOCK,RINT1,RB1,RPL26,MYO16,CUL4A,USP47,BRD7,TPR,CCP110,THOC1,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0048880	0.70	0.39	17	286	sensory system development	BP	1	AHI1,TOPORS,INHBA,GATA3,RAB3GAP1,JMJD6,ATP2B1,SOS1,MERTK,RDH10,ZDHHC16,SKIL,WNT5B,MYOM1,BMPR2,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:0008654	0.70	0.40	12	222	phospholipid biosynthetic process	BP	1	SOCS6,ETNK2,MBOAT1,BPNT1,ETNK1,PIP5K1A,PLD1,SAMD8,PIGW,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0050953	0.71	0.44	7	126	sensory perception of light stimulus	BP	1	RDH10,ARL6,IRX5,SEMA5B,COL11A1,RABGGTB,PDCL	darkolivegreen	VSMC_M9
GO:0034728	0.71	0.46	5	97	nucleosome organization	BP	1	PSME4,SMARCA5,LIN54,INO80,NAP1L4	darkolivegreen	VSMC_M9
GO:1904029	0.71	0.48	4	83	regulation of cyclin-dependent protein kinase activity	BP	1	CCNT2,CCNA1,IPO7,MYOCD	darkolivegreen	VSMC_M9
GO:0071333	0.71	0.44	6	110	cellular response to glucose stimulus	BP	1	KIF5B,SLC39A14,BRSK2,IGF1R,CCDC186,C2CD2L	darkolivegreen	VSMC_M9
GO:0043270	0.71	0.41	10	182	positive regulation of ion transport	BP	1	AKAP9,RAB3B,ITGB1,KIF5B,RAB3GAP1,ATP2B1,ANK3,STIM2,KCNMB1,GDNF	darkolivegreen	VSMC_M9
GO:0006820	0.71	0.38	18	319	anion transport	BP	1	SLC35B4,ABCB4,PNPLA8,ITGB1,SLC36A4,RAB3GAP1,SLC16A12,SLC39A14,SLC35B3,GPR89A,VDAC2,CLCNKB,SLC1A3,CLCC1,SLC25A24,PLEKHA3,SLC35D1,BDKRB2	darkolivegreen	VSMC_M9
GO:0071345	0.71	0.36	32	574	cellular response to cytokine stimulus	BP	1	TBK1,EXT1,JAK2,STAP1,ACTR2,KIF5B,ACTR3,GATA3,RIF1,SOS1,ILK,CNOT7,SMARCA5,MAT2A,PDE12,APPL1,HK2,TLR2,THBS1,TANK,TROVE2,EPRS,PTPN1,NRP2,TPR,ZC3H15,MYNN,FAS,PLP2,MYO1C,PAFAH1B1,NUP35	darkolivegreen	VSMC_M9
GO:0018130	0.71	0.32	173	2900	heterocycle biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,RRM2B,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,GFPT1,TAF1B,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,SUCLA2,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,LIG4,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,HSD17B12,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,STOX2,BDP1,MICAL2,ACTR8,ALDH18A1,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SLC35B3,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,TROVE2,ATP6V1A,KPNA6,NEK7,WWC3,LARP7,IDH2,TAF5L,ABCB10,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,GNPNAT1,SKIL,PRRX1,DKK1,PAPSS2,ADSS,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ACOT7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,RFXAP,ELOVL4,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0060401	0.71	0.43	7	126	cytosolic calcium ion transport	BP	1	FYN,ATP2B1,LYN,ATP2A2,ITPR2,AFG3L2,CTGF	darkolivegreen	VSMC_M9
GO:1903531	0.71	0.46	5	99	negative regulation of secretion by cell	BP	1	INHBA,FFAR4,IDH2,SRCIN1,NOV	darkolivegreen	VSMC_M9
GO:0070588	0.71	0.40	12	211	calcium ion transmembrane transport	BP	1	UBQLN1,TMEM165,FYN,ATP2B1,REM1,LYN,ATP2A2,ITPR2,ITGAV,STIM2,ANXA6,AFG3L2	darkolivegreen	VSMC_M9
GO:0120162	0.71	0.47	4	78	positive regulation of cold-induced thermogenesis	BP	1	JAK2,FFAR4,IGF1R,GATM	darkolivegreen	VSMC_M9
GO:0060070	0.71	0.39	14	250	canonical Wnt signaling pathway	BP	1	EXT1,GATA3,ILK,SCYL2,USP47,LRRK2,KPNA1,FZD2,DKK1,WNT5B,TLE3,PIN1,WNT9A,WNT7A	darkolivegreen	VSMC_M9
GO:0034220	0.71	0.34	44	765	ion transmembrane transport	BP	1	UTRN,ATP6V1C1,SLC39A7,SLC35B4,UBQLN1,SLC30A9,AKAP9,TMEM165,ZMPSTE24,ITGB1,FYN,KIF5B,SLC36A4,ATP2B1,REM1,LYN,SLC16A12,ATP6V0A2,SLC30A5,ATP2A2,SLC39A14,SLC35B3,ATP1A1,ATP10A,SLC39A10,MRS2,ATP6V1A,GPR89A,ITPR2,ATP11B,ANK3,ATP13A3,ITGAV,VDAC2,PLP2,CLCNKB,STIM2,KCNMB1,ANXA6,SLC1A3,AFG3L2,FXYD5,SLC35D1,SHISA7	darkolivegreen	VSMC_M9
GO:0045732	0.71	0.40	11	203	positive regulation of protein catabolic process	BP	1	UBQLN1,PSMC2,NUB1,NDFIP1,ITCH,CBLB,LRRK2,SMURF1,MSN,OAZ2,VGLL4	darkolivegreen	VSMC_M9
GO:0001889	0.72	0.44	6	116	liver development	BP	1	ZMPSTE24,UPF2,CUL3,GNPNAT1,ITGA2,SEC63	darkolivegreen	VSMC_M9

GO:0019438	0.72	0.31	173	2902	aromatic compound biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,RRM2B,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,GFPT1,TAF1B,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,SUCLA2,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,LIG4,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,HSD17B12,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,STOX2,BDP1,MICAL2,APPL1,ACTR8,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SLC35B3,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,TROVE2,ATP6V1A,KPNA6,NEK7,WWC3,LARP7,IDH2,TAF5L,ABCB10,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,GNPNAT1,SKIL,PRRX1,DKK1,PAPSS2,ADSS,NOTCH3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ACOT7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,RFXAP,ELOVL4,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,UBE2V1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0031058	0.72	0.47	4	75	positive regulation of histone modification	BP	1	GATA3,RIF1,BRD7,LRRK2	darkolivegreen	VSMC_M9
GO:0062012	0.72	0.38	13	243	regulation of small molecule metabolic process	BP	1	SLC35B4,ELOVL5,ZMPSTE24,RDH10,MBTPS2,PTGS2,PHKG2,CLK2,C1QTNF3,USP7,ENO1,RANBP2,PPTC7	darkolivegreen	VSMC_M9
GO:0002682	0.72	0.33	52	915	regulation of immune system process	BP	1	SOCS6,MALT1,TBK1,PTPRD,STAP1,HOXA9,ZMPSTE24,INHBA,DDX1,FYN,RB1,CAMK1D,GATA3,LRRC32,RIF1,NDFIP1,CUL4A,SOS1,HSPH1,CNOT7,LYN,MERTK,ITCH,APPL1,TLR2,DHX36,THBS1,NFKBIZ,CBLB,LRRK2,SLC39A10,PTPN1,ABCB10,EIF2B5,GPATCH3,SH3KBP1,PITHD1,TLR6,ADAM10,MSN,MAP2K4,SEMA7A,THOC1,ITGA2,MYSM1,CD40LG,VAV2,AQP3,CLEC4D,DNAJB9,NOV,FCN1	darkolivegreen	VSMC_M9
GO:0002250	0.72	0.38	13	244	adaptive immune response	BP	1	MALT1,JAK2,FYN,GATA3,RIF1,LIG4,NDFIP1,LYN,NFKBIZ,CD3G,THOC1,CD40LG,CLEC4D	darkolivegreen	VSMC_M9
GO:0030073	0.72	0.41	8	149	insulin secretion	BP	1	JAK2,CLOCK,KIF5B,SNX19,BRSK2,CCDC186,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0030323	0.72	0.41	8	145	respiratory tube development	BP	1	EXT1,JMJD6,RDH10,MAN1A2,EIF4E,MYOCD,BMPR2,CTGF	darkolivegreen	VSMC_M9
GO:0060419	0.72	0.46	4	77	heart growth	BP	1	PDLIM5,MAP2K4,PIN1,VGLL4	darkolivegreen	VSMC_M9
GO:0072593	0.72	0.40	9	176	reactive oxygen species metabolic process	BP	1	FYN,NOX4,AGTR1,HK2,THBS1,LRRK2,TLR6,ARF4,CTGF	darkolivegreen	VSMC_M9
GO:0007269	0.72	0.43	6	110	neurotransmitter secretion	BP	1	STXBP5,RAB3GAP1,ATP2A2,LRRK2,SEPT5,WNT7A	darkolivegreen	VSMC_M9
GO:0099643	0.72	0.43	6	110	signal release from synapse	BP	1	STXBP5,RAB3GAP1,ATP2A2,LRRK2,SEPT5,WNT7A	darkolivegreen	VSMC_M9
GO:1905114	0.72	0.35	26	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	EXT1,WISP1,GATA3,RAB3GAP1,ILK,SCYL2,SULF1,USP47,TLR2,ARL6,BRD7,LRRK2,CUL3,KPNA1,FZD2,FERMT2,SMURF1,TNIK,DKK1,WNT5B,TLE3,PIN1,GPC4,WNT9A,VGLL4,WNT7A	darkolivegreen	VSMC_M9
GO:0031667	0.72	0.36	20	362	response to nutrient levels	BP	1	STK24,PIK3R4,ATP2B1,EIF2AK3,MAP1B,GDAP1,NUCB2,LRRK2,BRSK2,CHSY1,ATF3,PTGS2,FAS,BNIP2,PPM1D,ITGA2,TBXA2R,BMPR2,AQP3,C12orf66	darkolivegreen	VSMC_M9
GO:0071331	0.72	0.43	6	112	cellular response to hexose stimulus	BP	1	KIF5B,SLC39A14,BRSK2,IGF1R,CCDC186,C2CD2L	darkolivegreen	VSMC_M9
GO:1903364	0.72	0.42	7	137	positive regulation of cellular protein catabolic process	BP	1	UBQLN1,PSMC2,NUB1,LRRK2,SMURF1,MSN,VGLL4	darkolivegreen	VSMC_M9
GO:0031960	0.72	0.43	6	117	response to corticosteroid	BP	1	CDO1,ATP2B1,EIF4E,NTRK3,PTGS2,CTGF	darkolivegreen	VSMC_M9
GO:0045637	0.72	0.41	8	152	regulation of myeloid cell differentiation	BP	1	HOXA9,INHBA,RB1,NDFIP1,CUL4A,LYN,ABCB10,PITHD1	darkolivegreen	VSMC_M9
GO:0002221	0.73	0.41	7	134	pattern recognition receptor signaling pathway	BP	1	LYN,ITCH,APPL1,TLR2,GPATCH3,TLR6,FCN1	darkolivegreen	VSMC_M9
GO:0045664	0.73	0.40	8	145	regulation of neuron differentiation	BP	1	ZEB1,MAP1B,LRRK2,EIF4E,DKK1,TBX6,ROCK1,IRX3	darkolivegreen	VSMC_M9
GO:0030072	0.73	0.39	9	168	peptide hormone secretion	BP	1	JAK2,CLOCK,KIF5B,FFAR4,SNX19,BRSK2,CCDC186,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0000165	0.73	0.34	33	579	MAPK cascade	BP	1	CAV2,ROCK2,CBLC,ILK,LYN,ITCH,FFAR4,BRAP,THBS1,LRRK2,IGF1R,NTRK3,PTPN1,ATF3,IQGAP1,MAP4K5,ITGAV,FERMT2,TNIK,TNFAIP8L3,DKK1,FAS,TLR6,MAP2K4,SEMA7A,PIN1,ROCK1,PAFAH1B1,GADD45B,CTGF,LAMTOR3,RAP2A,WNT7A	darkolivegreen	VSMC_M9
GO:0000819	0.73	0.39	9	168	sister chromatid segregation	BP	1	CDC23,CENPC,RB1,PDS5B,RIOK2,INO80,CUL3,TPR,CDC27	darkolivegreen	VSMC_M9
GO:0043242	0.73	0.45	4	70	negative regulation of protein-containing complex disassembly	BP	1	MAP1B,SPTBN5,CAMSAP2,HDGFL3	darkolivegreen	VSMC_M9
GO:0034767	0.73	0.42	6	114	positive regulation of ion transmembrane transport	BP	1	AKAP9,ITGB1,KIF5B,ANK3,STIM2,KCNMB1	darkolivegreen	VSMC_M9
GO:0071326	0.73	0.42	6	113	cellular response to monosaccharide stimulus	BP	1	KIF5B,SLC39A14,BRSK2,IGF1R,CCDC186,C2CD2L	darkolivegreen	VSMC_M9
GO:0022898	0.73	0.38	10	186	regulation of transmembrane transporter activity	BP	1	UTRN,UBQLN1,AKAP9,ITGB1,KIF5B,REM1,ANK3,STIM2,FXYD5,SHISA7	darkolivegreen	VSMC_M9
GO:0044282	0.73	0.36	14	284	small molecule catabolic process	BP	1	CDO1,ABHD1,HK2,GPD2,BPNT1,DERA,NPL,TPI1,HK3,DLST,ETFA,ENO1,IMPA1,AKR1D1	darkolivegreen	VSMC_M9
GO:0045619	0.74	0.41	6	117	regulation of lymphocyte differentiation	BP	1	MALT1,INHBA,GATA3,NDFIP1,SOS1,NFKBIZ	darkolivegreen	VSMC_M9
GO:1902600	0.74	0.42	5	115	proton transmembrane transport	BP	1	ATP6V1C1,ATP6V0A2,SLC30A5,ATP1A1,ATP6V1A	darkolivegreen	VSMC_M9

GO:0006811	0.74	0.31	59	1026	ion transport	BP	1	UTRN,ATP6V1C1,SLC39A7,SLC35B4,UBQLN1,SLC30A9,ABCB4,AKAP9,TMEM165,ZMPSTE24,PNPLA8,RAB3B,ITGB1,FYN,KIF5B,SLC36A4,RAB3GAP1,NDFIP2,ATP2B1,NDFIP1,REM1,LYN,SLC16A12,ATP6V0A2,SLC30A5,ATP2A2,SLC39A14,SLC35B3,ATP1A1,ATP10A,SLC39A10,MRS2,ATP6V1A,GPR89A,ITPR2,ATP11B,ANK3,ATP13A3,PTGS2,ITGAV,VDAC2,PLP2,CLCNKB,STIM2,MAGED2,KCNMB1,CLTC,ANXA6,SLC1A3,AFG3L2,CLCC1,SLC25A24,FXYD5,PLEKHA3,SLC35D1,GDNF,CTGF,BDKRB2,SHISA7	darkolivegreen	VSMC_M9
GO:0045087	0.74	0.33	25	459	innate immune response	BP	1	MALT1,TBK1,JAK2,FBXO9,ACTR2,DDX1,FYN,KIF5B,NUB1,ACTR3,GATA3,CNOT7,LYN,IPO7,ITCH,PDE12,APPL1,TLR2,DHX36,EPRS,PTPN1,TLR6,MYO1C,CLEC4D,FCN1	darkolivegreen	VSMC_M9
GO:0051091	0.74	0.37	11	204	positive regulation of DNA-binding transcription factor activity	BP	1	MALT1,JAK2,CLOCK,CAMK1D,TLR2,MBTPS2,FZD2,TLR6,MYOCD,CD40LG,UBE2V1	darkolivegreen	VSMC_M9
GO:0003279	0.74	0.42	5	88	cardiac septum development	BP	1	GATA3,ACVR1,NRP2,FZD2,BMPR2	darkolivegreen	VSMC_M9
GO:0061008	0.74	0.41	6	119	hepaticobiliary system development	BP	1	ZMPSTE24,UPF2,CUL3,GNPNAT1,ITGA2,SEC63	darkolivegreen	VSMC_M9
GO:0090407	0.74	0.33	24	452	organophosphate biosynthetic process	BP	1	SOCS6,RRM2B,ELOVL5,HSD17B12,SLC35B3,ETNK2,MBOAT1,ATP6V1A,BPNT1,ETNK1,IDH2,PIP5K1A,TPI1,PLD1,SAMD8,PAPSS2,ADSS,PIGW,ACOT7,ENO1,DPM2,IMPA1,DPM1,ELOVL4	darkolivegreen	VSMC_M9
GO:0007584	0.74	0.39	7	137	response to nutrient	BP	1	ATP2B1,MAP1B,GDAP1,PTGS2,ITGA2,TBXA2R,AQP3	darkolivegreen	VSMC_M9
GO:0035335	0.74	0.44	4	77	peptidyl-tyrosine dephosphorylation	BP	1	PTPRD,ACPP,PTPN1,PTPN12	darkolivegreen	VSMC_M9
GO:0002449	0.74	0.38	8	159	lymphocyte mediated immunity	BP	1	MALT1,KIF5B,GATA3,RIF1,LIG4,NDFIP1,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0000723	0.74	0.40	6	118	telomere maintenance	BP	1	RIF1,BRCA2,XRN1,DHX36,NEK7,USP7	darkolivegreen	VSMC_M9
GO:0030001	0.74	0.32	34	587	metal ion transport	BP	1	UTRN,SLC39A7,UBQLN1,SLC30A9,AKAP9,TMEM165,ZMPSTE24,ITGB1,FYN,KIF5B,NDFIP2,ATP2B1,NDFIP1,REM1,LYN,SLC30A5,ATP2A2,SLC39A14,ATP1A1,SLC39A10,MRS2,ITPR2,ANK3,PTGS2,ITGAV,STIM2,MAGED2,KCNMB1,CLTC,ANXA6,SLC1A3,AFG3L2,FXYD5,CTGF	darkolivegreen	VSMC_M9
GO:0031324	0.74	0.29	111	1896	negative regulation of cellular metabolic process	BP	1	PLAA,TFPI2,CLOCK,ZNF451,HDAC9,STAP1,ZMPSTE24,SH3BP5L,THAP5,ROCK2,INHBA,NOCT,FYN,ZEB1,EXOSC9,DNAJC1,RB1,RTN2,PICALM,TRDMT1,CBLC,MGAT5,GATA3,SUPT5H,DNAJC3,RIF1,NR2C1,NDFIP1,BRCA2,ILK,CNOT7,LYN,IPO7,EIF2AK3,TDG,TMED2,HCFC2,USP47,XRN1,PDE12,PI15,HK2,DCP1A,DHX36,THBS1,SHOX2,MTERF3,CBLB,ATP1A1,DYRK1A,BRD7,LRRK2,TBX15,CUL3,EIF4E,TDP2,UCHL5,EPRS,CORO1C,ANOS1,NTRK3,WWC3,PTPN1,LARP7,LRRFIP1,ATF3,RBBP7,TLK2,TPR,PTGS2,NPAT,ITGAV,SKIL,PRRX1,RTN3,CPEB2,BOD1L1,DKK1,SRP9,MAGED2,SRCIN1,CLK2,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,DICER1,MYOCD,PIN1,RBBP8,BAG5,ROCK1,THOC1,C1QTNF3,USP7,GADD45B,ENO1,WFDC1,THAP11,MIR186,BMPR2,FRY,GDNF,BDKRB2,PMEPA1,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0048534	0.74	0.31	37	649	hematopoietic or lymphoid organ development	BP	1	MALT1,EXT1,WISP1,JAK2,HDAC9,HOXA9,ZMPSTE24,INHBA,ITGB1,RB1,PICALM,GATA3,JMJD6,AZI2,LIG4,NDFIP1,CUL4A,SOS1,BRCA2,UBA5,LYN,MERTK,ITCH,TLR2,DHX36,NFKBIZ,GPR89A,ABCB10,CD3G,PITHD1,RBM47,MYO1E,MYSM1,CD40LG,PAFAH1B1,CDK13,DNAJB9	darkolivegreen	VSMC_M9
GO:0001890	0.75	0.40	6	117	placenta development	BP	1	TMED2,STOX2,ETNK2,PTGS2,ADAM19,BMPR2	darkolivegreen	VSMC_M9
GO:0002790	0.75	0.37	9	172	peptide secretion	BP	1	JAK2,CLOCK,KIF5B,FFAR4,SNX19,BRSK2,CCDC186,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0032508	0.75	0.43	4	75	DNA duplex unwinding	BP	1	DDX1,CHD1,DHX36,CHD9	darkolivegreen	VSMC_M9
GO:0006091	0.75	0.33	19	392	generation of precursor metabolites and energy	BP	1	NOA1,UGP2,GFPT1,NOX4,SUCLA2,PDE12,HK2,PGAM4,GPD2,IDH2,DERA,TPI1,HK3,PHKG2,DLST,PKM,ETFA,ENO1,PPP1R2	darkolivegreen	VSMC_M9
GO:0060041	0.75	0.39	6	108	retina development in camera-type eye	BP	1	AHI1,TOPORS,JMJD6,ATP2B1,MERTK,BMPR2	darkolivegreen	VSMC_M9
GO:0035601	0.75	0.41	5	99	protein deacylation	BP	1	HDAC9,ABHD13,DYRK1A,LRRK2,FRY	darkolivegreen	VSMC_M9
GO:0006357	0.75	0.28	106	1784	regulation of transcription by RNA polymerase II	BP	1	AHI1,TBK1,CAND1,PHF20L1,SLC30A9,CLOCK,NPAS2,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,THAP5,INHBA,ZEB1,EXOSC9,RB1,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,SUPT5H,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,TMF1,HOXC10,CNOT7,MYBL1,TDG,HCFC2,SMARCA5,CHD1,STOX2,MICAL2,TLR2,DHX36,SHOX2,ACVR1,IRX5,INO80,BRD7,ERG,TBX15,UBE3A,CUL3,KPNA6,WWC3,LARP7,TRAK2,LRRFIP1,ATF3,RBBP7,BCLAF3,HDGFL3,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,NPAT,MYNN,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ZNF280C,MYSM1,ENO1,ZNF644,THAP11,BMPR2,ZNF654,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZNF34,ZNF773,ZNF655,IRX3,ZNF556,WNT7A	darkolivegreen	VSMC_M9

GO:1901362	0.75	0.28	178	3012	organic cyclic compound biosynthetic process	BP	1	MALT1,AHI1,TBK1,CAND1,RRM2B,PHF20L1,SLC30A9,TOPORS,JAK2,CLOCK,NPAS2,ELOVL5,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ZMPSTE24,ACTR2,THAP5,GFPT1,TAF1B,INHBA,DDX1,NOCT,ZEB1,EXOSC9,RB1,SUCLA2,PICALM,CAMK1D,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,BRPF1,SUPT5H,SETD5,RIF1,PPP1R12A,LIG4,CEBPZ,SUPT20H,SMAD9,NR2C1,BRCA2,ILK,TMF1,HOXC10,HSD17B12,CNOT7,RNF6,MYBL1,EIF2AK3,TDG,HCFC2,SBNO1,SMARCA5,ITCH,CHD1,USP47,XRN1,STOX2,BDP1,MICAL2,APPL1,ACTR8,ALDH18A1,TLR2,DHX36,SHOX2,LIN54,ACVR1,WDR75,IRX5,MTERF3,INO80,SLC35B3,ATP1A1,DYRK1A,BRD7,ERG,TBX15,UBE3A,CUL3,TDP2,TROVE2,ATP6V1A,KPNA6,NEK7,WWC3,LARP7,IDH2,TAF5L,ABCB10,TRAK2,GPATCH3,LRRFIP1,ATF3,RBBP7,EDRF1,BCLAF3,HDGFL3,PITHD1,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,FZD2,NPAT,MYNN,GNPNAT1,SKIL,PRRX1,DKK1,PAPSS2,ADSS,NOTCH3,ACBD3,TLR6,MAGED2,TRIP4,TBX6,RLIM,MAGEE2,TLE3,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,THOC1,ZNF280C,MYSM1,CD40LG,USP7,ACOT7,ENO1,ZNF644,ZNF326,GTF2B,THAP11,BMPR2,ZNF654,ANKRD49,ARF4,GDNF,CDK13,CTGF,FOXN2,RFXAP,ELOVL4,ZNF789,E2F3,GLIS3,ZPR1,ZNF34,VGLL4,ZNF773,ZNF655,NUP35,SRD5A2,UBE2V1,AKR1D1,IRX3,BCL7A,ZNF556,WNT7A,TFB2M	darkolivegreen	VSMC_M9
GO:0061351	0.75	0.39	6	111	neural precursor cell proliferation	BP	1	CEP120,ILK,LYN,LRRK2,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0070304	0.75	0.40	5	99	positive regulation of stress-activated protein kinase signaling cascade	BP	1	LYN,TNIK,GADD45B,CTGF,WNT7A	darkolivegreen	VSMC_M9
GO:0007264	0.76	0.31	26	437	small GTPase mediated signal transduction	BP	1	PLEKHG1,DENND4C,CAVIN4,CCDC88A,ROCK2,ITGB1,GPR4,RB1,CYTH1,STARD13,SOS1,CCDC125,AGTR1,RASA1,USO1,BRAP,NUCB2,CUL3,ITGAV,PLD1,GPR65,ROCK1,VAV2,RAPGEF1,SSX2IP,RAP2A	darkolivegreen	VSMC_M9
GO:0042886	0.76	0.35	11	210	amide transport	BP	1	JAK2,CLOCK,KIF5B,FFAR4,SNX19,BRSK2,CCDC186,C2CD2L,AQP3,PLEKHA3,NOV	darkolivegreen	VSMC_M9
GO:0051092	0.76	0.39	6	119	positive regulation of NF-kappaB transcription factor activity	BP	1	MALT1,CLOCK,TLR2,TLR6,CD40LG,UBE2V1	darkolivegreen	VSMC_M9
GO:0022411	0.76	0.32	21	375	cellular component disassembly	BP	1	ETF1,UBQLN1,ZMPSTE24,KIF5B,UFM1,UBA5,MICAL2,MAP1B,HK2,ATP2A2,SPTBN5,IGF1R,CAMSAP2,HDGFL3,DKK1,ADAM10,DICER1,CIDEA,GSPT1,PAFAH1B1,CFL2	darkolivegreen	VSMC_M9
GO:0043279	0.76	0.42	4	81	response to alkaloid	BP	1	PPP2R2A,UBE3A,CASP7,SLC1A3	darkolivegreen	VSMC_M9
GO:0045089	0.76	0.42	4	83	positive regulation of innate immune response	BP	1	TBK1,FYN,LYN,FCN1	darkolivegreen	VSMC_M9
GO:0010717	0.76	0.42	4	80	regulation of epithelial to mesenchymal transition	BP	1	GATA3,ACVR1,PHLDB2,FERMT2	darkolivegreen	VSMC_M9
GO:0051302	0.76	0.37	7	138	regulation of cell division	BP	1	PRPF40A,PIK3R4,BRCA2,MAP9,CUL3,PIN1,CCP110	darkolivegreen	VSMC_M9
GO:1903039	0.76	0.37	7	143	positive regulation of leukocyte cell-cell adhesion	BP	1	MALT1,FYN,GATA3,HSPH1,LYN,NFKBIZ,CD40LG	darkolivegreen	VSMC_M9
GO:0032414	0.76	0.41	4	80	positive regulation of ion transmembrane transporter activity	BP	1	AKAP9,KIF5B,ANK3,STIM2	darkolivegreen	VSMC_M9
GO:0071222	0.76	0.38	6	126	cellular response to lipopolysaccharide	BP	1	MALT1,PLAA,STAP1,LYN,TLR2,TBXA2R	darkolivegreen	VSMC_M9
GO:0046942	0.76	0.35	9	173	carboxylic acid transport	BP	1	ABCB4,PNPLA8,ITGB1,SLC36A4,RAB3GAP1,SLC16A12,SLC1A3,SLC35D1,BDKRB2	darkolivegreen	VSMC_M9
GO:0034097	0.76	0.29	36	659	response to cytokine	BP	1	TBK1,EXT1,JAK2,STAP1,ACTR2,KIF5B,NUB1,ACTR3,GATA3,RIF1,SOS1,ILK,CNOT7,SMARCA5,MAT2A,PDE12,APPL1,HK2,TLR2,THBS1,TANK,TROVE2,EPRS,PTPN1,NRP2,TPR,PTGS2,ZC3H15,MYNN,SKIL,FAS,PLP2,ADAM10,MYO1C,PAFAH1B1,NUP35	darkolivegreen	VSMC_M9
GO:0000086	0.76	0.38	6	124	G2/M transition of mitotic cell cycle	BP	1	RINT1,FBXL17,USP47,BRSK2,PPM1D,FBXL7	darkolivegreen	VSMC_M9
GO:0006694	0.76	0.38	6	126	steroid biosynthetic process	BP	1	HSD17B12,ATP1A1,MBTPS2,ACBD3,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0015698	0.77	0.37	6	113	inorganic anion transport	BP	1	SLC39A14,GPR89A,VDAC2,CLCNKB,SLC1A3,CLCC1	darkolivegreen	VSMC_M9
GO:0051384	0.77	0.39	5	104	response to glucocorticoid	BP	1	CDO1,ATP2B1,EIF4E,NTRK3,PTGS2	darkolivegreen	VSMC_M9
GO:0060759	0.77	0.37	6	128	regulation of response to cytokine stimulus	BP	1	TBK1,STAP1,CNOT7,TLR2,PTPN1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0006366	0.77	0.27	110	1862	transcription by RNA polymerase II	BP	1	AHI1,TBK1,CAND1,PHF20L1,SLC30A9,CLOCK,NPAS2,POLR2B,ZNF451,HDAC9,CAVIN4,MYO6,HOXA9,HOXA10,HOXA11,ACTR2,THAP5,INHBA,NOCT,ZEB1,EXOSC9,RB1,ACTR3,GATA3,CCNT2,JMJD6,PAX1,TRAK1,SUPT5H,RIF1,PPP1R12A,CEBPZ,SUPT20H,SMAD9,NR2C1,TMF1,HOXC10,CNOT7,MYBL1,TDG,HCFC2,SMARCA5,CHD1,STOX2,MICAL2,TLR2,DHX36,SHOX2,ACVR1,IRX5,INO80,BRD7,ERG,TBX15,UBE3A,CUL3,KPNA6,WWC3,LARP7,TAF5L,TRAK2,LRRFIP1,ATF3,RBBP7,BCLAF3,HDGFL3,MBTPS2,BAZ1A,ZFX,CREB3L2,TPR,MYEF2,NPAT,MYNN,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,DICER1,ARMCX3,PPM1D,MYOCD,PIN1,SS18,RBBP8,ZNF280C,MYSM1,ENO1,ZNF644,GTF2B,THAP11,BMPR2,ZNF654,ARF4,GDNF,CDK13,FOXN2,RFXAP,ZNF789,E2F3,GLIS3,ZNF34,ZNF773,ZNF655,IRX3,ZNF556,WNT7A	darkolivegreen	VSMC_M9
GO:0007156	0.77	0.39	5	88	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	PCDH18,ITGB1,DCHS1,PALLD,CDH11	darkolivegreen	VSMC_M9
GO:0098732	0.77	0.38	5	102	macromolecule deacylation	BP	1	HDAC9,ABHD13,DYRK1A,LRRK2,FRY	darkolivegreen	VSMC_M9
GO:0098542	0.77	0.29	31	574	defense response to other organism	BP	1	MALT1,TBK1,JAK2,EXOC1,FBXO9,ZMPSTE24,ACTR2,DDX1,FYN,KIF5B,NUB1,ACTR3,GATA3,DNAJC3,TMF1,CNOT7,LYN,IPO7,ITCH,PDE12,APPL1,TLR2,DHX36,EPRS,PTPN1,GPATCH3,TLR6,MYO1C,CLEC4D,FCN1,NDUFAF4	darkolivegreen	VSMC_M9

GO:0015850	0.77	0.34	9	179	organic hydroxy compound transport	BP	1	ABCB4,RAB3B,OSBPL8,TMF1,GRAMD1A,AGTR1,OSBPL11,AQP3,GDNF	darkolivegreen	VSMC_M9
GO:0030900	0.78	0.31	16	282	forebrain development	BP	1	CEP120,EXT1,UBA6,INHBA,FYN,KIF5B,RAB3GAP1,SCYL2,ZDHHC16,LRRK2,UCHL5,EIF2B5,NRP2,SEMA7A,PAFAH1B1,WNT7A	darkolivegreen	VSMC_M9
GO:0090276	0.78	0.35	7	140	regulation of peptide hormone secretion	BP	1	JAK2,CLOCK,KIF5B,FFAR4,BRSK2,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0007600	0.78	0.30	17	320	sensory perception	BP	1	MYO6,FYN,ACPP,FFAR4,RDH10,ARL6,IRX5,SEMA5B,PTGS2,FZD2,ITGA2,SLC1A3,COL11A1,RABGGTB,LHFPL4,NOV,PDCL	darkolivegreen	VSMC_M9
GO:0072175	0.78	0.36	6	116	epithelial tube formation	BP	1	GATA3,TMED2,FZD2,PRKACB,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0046890	0.78	0.35	6	127	regulation of lipid biosynthetic process	BP	1	ELOVL5,RDH10,ATP1A1,MBTPS2,PTGS2,SAMD8	darkolivegreen	VSMC_M9
GO:0006066	0.78	0.31	13	258	alcohol metabolic process	BP	1	CYP27C1,ACPP,PLPP1,RDH10,GPD2,BPNT1,IDH2,MBTPS2,TPI1,DPM2,IMPA1,DPM1,AKR1D1	darkolivegreen	VSMC_M9
GO:0032392	0.78	0.38	4	80	DNA geometric change	BP	1	DDX1,CHD1,DHX36,CHD9	darkolivegreen	VSMC_M9
GO:0050954	0.78	0.35	6	120	sensory perception of mechanical stimulus	BP	1	MYO6,FYN,ITGA2,SLC1A3,COL11A1,LHFPL4	darkolivegreen	VSMC_M9
GO:0002791	0.79	0.34	7	142	regulation of peptide secretion	BP	1	JAK2,CLOCK,KIF5B,FFAR4,BRSK2,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0048511	0.79	0.31	12	223	rhythmic process	BP	1	CLOCK,NPAS2,GFPT1,ROCK2,INHBA,NOCT,CUL4A,FBXL17,GPR176,DYRK1A,UBE3A,USP7	darkolivegreen	VSMC_M9
GO:0009605	0.79	0.24	102	1770	response to external stimulus	BP	1	MALT1,TBK1,EXT1,WISP1,PLAA,JAK2,CLOCK,EXOC1,FBXO9,STAP1,ZMPSTE24,ACTR2,CHRM2,DDX1,NOCT,FYN,KIF5B,GPR4,RB1,CAMK1D,NUB1,ACTR3,GATA3,DNAJC3,STK24,TNFAIP6,PIK3R4,ATP2B1,NDFIP1,SOS1,TMF1,CNOT7,LYN,IPO7,EIF2AK3,FBXL17,PALLD,ITCH,PDE12,FFAR4,MAP1B,APPL1,GDAP1,AGTR1,TLR2,ATP2A2,DHX36,THBS1,NUCB2,NFKBIZ,ATP1A1,LRRK2,BRSK2,PHLDB2,CHSY1,EPRS,CCDC186,ANOS1,NTRK3,PTPN1,SEMA5B,GPATCH3,ATF3,PIP5K1A,NRP2,PTGS2,NCAM1,ITGAV,PLD1,ACTA2,FAS,PLP2,NOTCH3,TLR6,ENAH,ADAM10,BNIP2,PPM1D,MAP2K4,MYOCD,SEMA7A,ITGA2,ITGA1,RICTOR,SLC1A3,AFG3L2,C1QTNF3,MYO1C,TBXA2R,LSM5,ENO1,WFDC1,COL11A1,BMPR2,AQP3,CLEC4D,GDNF,ELOVL4,NOV,FCN1,C12orf66,NDUFAF4	darkolivegreen	VSMC_M9
GO:0002252	0.79	0.29	19	360	immune effector process	BP	1	MALT1,STAP1,DDX1,FYN,KIF5B,GATA3,RIF1,LIG4,NDFIP1,LYN,APPL1,DHX36,NFKBIZ,SEMA7A,THOC1,CD40LG,VAV2,DNAJB9,FCN1	darkolivegreen	VSMC_M9
GO:0046488	0.79	0.33	7	138	phosphatidylinositol metabolic process	BP	1	SOCS6,BPNT1,PIP5K1A,PIGW,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0021953	0.79	0.34	6	116	central nervous system neuron differentiation	BP	1	INHBA,SCYL2,NRP2,PAFAH1B1,CDH11,WNT7A	darkolivegreen	VSMC_M9
GO:1904064	0.79	0.35	5	103	positive regulation of cation transmembrane transport	BP	1	AKAP9,KIF5B,ANK3,STIM2,KCNMB1	darkolivegreen	VSMC_M9
GO:0030595	0.80	0.33	7	150	leukocyte chemotaxis	BP	1	STAP1,CAMK1D,LYN,THBS1,ADAM10,ITGA1,NOV	darkolivegreen	VSMC_M9
GO:0051048	0.80	0.35	5	110	negative regulation of secretion	BP	1	INHBA,FFAR4,IDH2,SRCIN1,NOV	darkolivegreen	VSMC_M9
GO:0006816	0.80	0.29	15	282	calcium ion transport	BP	1	UBQLN1,TMEM165,ZMPSTE24,FYN,ATP2B1,REM1,LYN,ATP2A2,ITPR2,PTGS2,ITGAV,STIM2,ANXA6,AFG3L2,CTGF	darkolivegreen	VSMC_M9
GO:0090087	0.80	0.32	7	144	regulation of peptide transport	BP	1	JAK2,CLOCK,KIF5B,FFAR4,BRSK2,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0045088	0.80	0.32	7	148	regulation of innate immune response	BP	1	TBK1,FYN,CNOT7,LYN,APPL1,PTPN1,FCN1	darkolivegreen	VSMC_M9
GO:0006887	0.80	0.29	14	266	exocytosis	BP	1	STXBP5,EXOC1,RAB3B,RAB3GAP1,LYN,ATP2A2,LRRK2,SNX19,BRSK2,SEPT5,SRCIN1,RAB31,SCAMP1,WNT7A	darkolivegreen	VSMC_M9
GO:0032411	0.80	0.36	4	85	positive regulation of transporter activity	BP	1	AKAP9,KIF5B,ANK3,STIM2	darkolivegreen	VSMC_M9
GO:0002366	0.80	0.31	9	181	leukocyte activation involved in immune response	BP	1	MALT1,GATA3,RIF1,LIG4,NDFIP1,LYN,NFKBIZ,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0071248	0.80	0.32	7	141	cellular response to metal ion	BP	1	LIG4,EIF2AK3,LRRK2,IQGAP1,ANK3,PTGS2,SLC25A24	darkolivegreen	VSMC_M9
GO:0051276	0.80	0.25	38	682	chromosome organization	BP	1	CDC23,SENP6,PSME4,CENPC,ZMPSTE24,DDX1,RB1,GATA3,SETD5,RIF1,LIG4,PDS5B,BRCA2,TDG,HCFC2,SMARCA5,CHD1,RIOK2,XRN1,ACTR8,DHX36,LIN54,INO80,CHD9,CUL3,NAP1L4,KIAA1551,NEK7,SYCP2,RBBP7,TLK2,BAZ1A,TPR,CDC27,NUP155,MYSM1,USP7,RFWD3	darkolivegreen	VSMC_M9
GO:0051100	0.80	0.33	6	129	negative regulation of binding	BP	1	JAK2,ATP2A2,LRRK2,DKK1,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:0050806	0.80	0.34	5	104	positive regulation of synaptic transmission	BP	1	KIF5B,RAB3GAP1,PTGS2,SLC1A3,SHISA7	darkolivegreen	VSMC_M9
GO:0098656	0.80	0.31	8	161	anion transmembrane transport	BP	1	SLC35B4,ITGB1,SLC36A4,SLC16A12,SLC35B3,VDAC2,SLC1A3,SLC35D1	darkolivegreen	VSMC_M9
GO:1903706	0.81	0.28	13	258	regulation of hemopoiesis	BP	1	MALT1,HOXA9,INHBA,RB1,GATA3,NDFIP1,CUL4A,SOS1,LYN,NFKBIZ,ABCB10,PITHD1,MYSM1	darkolivegreen	VSMC_M9
GO:0007052	0.81	0.34	5	109	mitotic spindle organization	BP	1	DCTN6,MAP9,TPR,CLTC,MZT1	darkolivegreen	VSMC_M9
GO:0043207	0.81	0.24	44	820	response to external biotic stimulus	BP	1	MALT1,TBK1,EXT1,PLAA,JAK2,EXOC1,FBXO9,STAP1,ZMPSTE24,ACTR2,CHRM2,DDX1,NOCT,FYN,KIF5B,NUB1,ACTR3,GATA3,DNAJC3,TMF1,CNOT7,LYN,IPO7,ITCH,PDE12,APPL1,TLR2,ATP2A2,DHX36,EPRS,CCDC186,PTPN1,GPATCH3,PTGS2,ACTA2,TLR6,PPM1D,MYO1C,TBXA2R,LSM5,ENO1,CLEC4D,FCN1,NDUFAF4	darkolivegreen	VSMC_M9
GO:0051707	0.81	0.24	44	820	response to other organism	BP	1	MALT1,TBK1,EXT1,PLAA,JAK2,EXOC1,FBXO9,STAP1,ZMPSTE24,ACTR2,CHRM2,DDX1,NOCT,FYN,KIF5B,NUB1,ACTR3,GATA3,DNAJC3,TMF1,CNOT7,LYN,IPO7,ITCH,PDE12,APPL1,TLR2,ATP2A2,DHX36,EPRS,CCDC186,PTPN1,GPATCH3,PTGS2,ACTA2,TLR6,PPM1D,MYO1C,TBXA2R,LSM5,ENO1,CLEC4D,FCN1,NDUFAF4	darkolivegreen	VSMC_M9

GO:0032200	0.81	0.32	6	130	telomere organization	BP	1	RIF1,BRCA2,XRN1,DHX36,NEK7,USP7	darkolivegreen	VSMC_M9
GO:0001508	0.81	0.33	5	99	action potential	BP	1	AKAP9,ATP2A2,ATP1A1,ANK3,NUP155	darkolivegreen	VSMC_M9
GO:0034765	0.81	0.26	17	323	regulation of ion transmembrane transport	BP	1	UTRN,UBQLN1,AKAP9,ZMPSTE24,ITGB1,FYN,KIF5B,REM1,LYN,SLC30A5,GPR89A,ANK3,CLCNKB,STIM2,KCNMB1,FXYD5,SHISA7	darkolivegreen	VSMC_M9
GO:1903169	0.81	0.33	5	110	regulation of calcium ion transmembrane transport	BP	1	UBQLN1,FYN,REM1,LYN,STIM2	darkolivegreen	VSMC_M9
GO:0051056	0.81	0.27	15	259	regulation of small GTPase mediated signal transduction	BP	1	PLEKHG1,DENND4C,CAVIN4,ITGB1,GPR4,CYTH1,STARD13,SOS1,CCDC125,RASA1,CUL3,ITGAV,GPR65,VAV2,SSX2IP	darkolivegreen	VSMC_M9
GO:0044839	0.81	0.31	6	132	cell cycle G2/M phase transition	BP	1	RINT1,FBXL17,USP47,BRSK2,PPM1D,FBXL7	darkolivegreen	VSMC_M9
GO:0098662	0.81	0.24	29	541	inorganic cation transmembrane transport	BP	1	UTRN,ATP6V1C1,SLC39A7,UBQLN1,AKAP9,TMEM165,ITGB1,FYN,KIF5B,ATP2B1,REM1,LYN,ATP6V0A2,SLC30A5,ATP2A2,SLC39A14,ATP1A1,SLC39A10,MRS2,ATP6V1A,ITPR2,ANK3,ITGAV,STIM2,KCNMB1,ANXA6,SLC1A3,AFG3L2,FXYD5	darkolivegreen	VSMC_M9
GO:0045930	0.81	0.29	9	186	negative regulation of mitotic cell cycle	BP	1	RINT1,RB1,RPL26,MYO16,USP47,BRD7,TPR,RFWD3,ZNF655	darkolivegreen	VSMC_M9
GO:0015918	0.81	0.34	4	89	sterol transport	BP	1	ABCB4,OSBPL8,GRAMD1A,OSBPL11	darkolivegreen	VSMC_M9
GO:0009607	0.82	0.23	46	856	response to biotic stimulus	BP	1	MALT1,TBK1,EXT1,PLAA,JAK2,EXOC1,FBXO9,STAP1,ZMPSTE24,ACTR2,CHRM2,DDX1,NOCT,FYN,KIF5B,NUB1,ACTR3,GATA3,DNAJC3,TMF1,CNOT7,LYN,IPO7,EIF2AK3,ITCH,PDE12,APPL1,TLR2,ATP2A2,DHX36,EPRS,CCDC186,PTPN1,GPATCH3,CCDC47,PTGS2,ACTA2,TLR6,PPM1D,MYO1C,TBXA2R,LSM5,ENO1,CLEC4D,FCN1,NDUFAF4	darkolivegreen	VSMC_M9
GO:0050796	0.82	0.31	6	127	regulation of insulin secretion	BP	1	JAK2,CLOCK,KIF5B,BRSK2,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0060840	0.82	0.34	4	81	artery development	BP	1	PRRX1,AKT3,MYOCD,BMPR2	darkolivegreen	VSMC_M9
GO:0002263	0.82	0.28	9	185	cell activation involved in immune response	BP	1	MALT1,GATA3,RIF1,LIG4,NDFIP1,LYN,NFKBIZ,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0006476	0.82	0.33	4	88	protein deacetylation	BP	1	HDAC9,DYRK1A,LRRK2,FRY	darkolivegreen	VSMC_M9
GO:0030099	0.82	0.26	15	293	myeloid cell differentiation	BP	1	WISP1,JAK2,HOXA9,INHBA,RB1,GATA3,JMJD6,NDFIP1,CUL4A,UBA5,LYN,TLR2,ABCB10,PITHD1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0002460	0.82	0.28	8	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	MALT1,GATA3,RIF1,LIG4,NDFIP1,NFKBIZ,THOC1,CD40LG	darkolivegreen	VSMC_M9
GO:0006955	0.82	0.22	55	1012	immune response	BP	1	MALT1,TBK1,EXT1,PTPRD,JAK2,EXOC1,FBXO9,STAP1,ZMPSTE24,ACTR2,DDX1,FYN,KIF5B,EXOSC9,NUB1,ACTR3,GATA3,DNAJC3,RIF1,LIG4,NDFIP1,SOS1,TMF1,CNOT7,LYN,ATP6V0A2,IPO7,ITCH,PDE12,APPL1,TLR2,DHX36,THBS1,NFKBIZ,CBLB,SLC39A10,EPRS,IGF1R,PTPN1,EIF2B5,LTB4R,GPATCH3,CD3G,FAS,TLR6,GPR65,MAP2K4,SEMA7A,THOC1,CD40LG,MYO1C,VAV2,CLEC4D,FCN1,NDUFAF4	darkolivegreen	VSMC_M9
GO:0015833	0.82	0.28	9	186	peptide transport	BP	1	JAK2,CLOCK,KIF5B,FFAR4,SNX19,BRSK2,CCDC186,C2CD2L,NOV	darkolivegreen	VSMC_M9
GO:0042593	0.82	0.28	9	183	glucose homeostasis	BP	1	WISP1,KIF5B,HK2,SLC39A14,BRSK2,IGF1R,CCDC186,C2CD2L,HK3	darkolivegreen	VSMC_M9
GO:0002224	0.83	0.32	4	92	toll-like receptor signaling pathway	BP	1	LYN,APPL1,TLR2,TLR6	darkolivegreen	VSMC_M9
GO:0050905	0.83	0.31	5	103	neuromuscular process	BP	1	ZMPSTE24,UBA5,ATP2A2,SLC1A3,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0006479	0.83	0.28	7	148	protein methylation	BP	1	ETF1,GATA3,SETD5,RIF1,FAM98A,GSPT1,RAB6A	darkolivegreen	VSMC_M9
GO:0008213	0.83	0.28	7	148	protein alkylation	BP	1	ETF1,GATA3,SETD5,RIF1,FAM98A,GSPT1,RAB6A	darkolivegreen	VSMC_M9
GO:0001959	0.83	0.31	5	119	regulation of cytokine-mediated signaling pathway	BP	1	TBK1,STAP1,CNOT7,PTPN1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0006813	0.83	0.28	7	140	potassium ion transport	BP	1	AKAP9,ITGB1,KIF5B,ATP1A1,ANK3,KCNMB1,SLC1A3	darkolivegreen	VSMC_M9
GO:0007188	0.83	0.29	6	129	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	BP	1	CHRM2,GPR4,GPR176,GPR65,TBXA2R,PRKACB	darkolivegreen	VSMC_M9
GO:0033500	0.83	0.27	9	184	carbohydrate homeostasis	BP	1	WISP1,KIF5B,HK2,SLC39A14,BRSK2,IGF1R,CCDC186,C2CD2L,HK3	darkolivegreen	VSMC_M9
GO:0006941	0.83	0.29	6	128	striated muscle contraction	BP	1	AKAP9,ATP2A2,ATP1A1,TPM1,NUP155,CTGF	darkolivegreen	VSMC_M9
GO:0051054	0.84	0.26	8	176	positive regulation of DNA metabolic process	BP	1	NPAS2,ACTR2,RIF1,DHX36,NEK7,FMN2,SPIRE1,USP7	darkolivegreen	VSMC_M9
GO:0000075	0.84	0.27	7	155	cell cycle checkpoint signaling	BP	1	CLOCK,RINT1,RPL26,CUL4A,TPR,THOC1,RFWD3	darkolivegreen	VSMC_M9
GO:0060541	0.84	0.26	8	163	respiratory system development	BP	1	EXT1,JMJD6,RDH10,MAN1A2,EIF4E,MYOCD,BMPR2,CTGF	darkolivegreen	VSMC_M9
GO:0043068	0.84	0.22	21	422	positive regulation of programmed cell death	BP	1	JAK2,INHBA,ITGB1,NOX4,CAMK1D,RPL26,LYN,THBS1,LRRK2,EIF2B5,ATF3,PTGS2,SKIL,FAS,ADAM10,MAP2K4,PIN1,ITGA1,CD40LG,GADD45B,E2F3	darkolivegreen	VSMC_M9
GO:0010565	0.84	0.31	4	95	regulation of cellular ketone metabolic process	BP	1	ELOVL5,RDH10,PTGS2,PPTC7	darkolivegreen	VSMC_M9
GO:0031330	0.84	0.25	10	207	negative regulation of cellular catabolic process	BP	1	NOCT,TRDMT1,DHX36,LRRK2,UCHL5,TLK2,BAG5,ROCK1,USP7,GDNF	darkolivegreen	VSMC_M9
GO:2000060	0.84	0.30	4	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	UBQLN1,NUB1,LRRK2,SMURF1	darkolivegreen	VSMC_M9
GO:0030534	0.84	0.30	4	90	adult behavior	BP	1	ZMPSTE24,SEPT5,PAFAH1B1,GDNF	darkolivegreen	VSMC_M9
GO:1903052	0.84	0.28	5	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	UBQLN1,PSMC2,NUB1,LRRK2,SMURF1	darkolivegreen	VSMC_M9
GO:0043271	0.84	0.30	4	93	negative regulation of ion transport	BP	1	UBQLN1,REM1,ANK3,PTGS2	darkolivegreen	VSMC_M9

GO:0098655	0.85	0.20	33	623	cation transmembrane transport	BP	1	UTRN,ATP6V1C1,SLC39A7,UBQLN1,SLC30A9,AKAP9,TMEM165,ITGB1,FYN,KIF5B,SLC36A4,ATP2B1,REM1,LYN,ATP6V0A2,SLC30A5,ATP2A2,SLC39A14,ATP1A1,SLC39A10,MRS2,ATP6V1A,ITPR2,ANK3,ATP13A3,ITGAV,STIM2,KCNMB1,ANXA6,SLC1A3,AFG3L2,FXYD5,SHISA7	darkolivegreen	VSMC_M9
GO:0002687	0.85	0.29	4	101	positive regulation of leukocyte migration	BP	1	CAMK1D,THBS1,ADAM10,ITGA2	darkolivegreen	VSMC_M9
GO:1902105	0.85	0.24	9	193	regulation of leukocyte differentiation	BP	1	MALT1,INHBA,RB1,GATA3,NDFIP1,CUL4A,SOS1,LYN,NFKBIZ	darkolivegreen	VSMC_M9
GO:0002237	0.85	0.24	11	236	response to molecule of bacterial origin	BP	1	MALT1,PLAA,JAK2,STAP1,NOCT,LYN,TLR2,ATP2A2,PTGS2,TLR6,TBXA2R	darkolivegreen	VSMC_M9
GO:0006979	0.85	0.22	17	357	response to oxidative stress	BP	1	RRM2B,UBQLN1,JAK2,PNPLA8,GPX7,FYN,STK24,ATP2A2,LRRK2,UBE3A,PTGS2,MYEF2,CPEB2,TLR6,TPM1,BAG5,SLC25A24	darkolivegreen	VSMC_M9
GO:0097529	0.85	0.26	6	142	myeloid leukocyte migration	BP	1	STAP1,CAMK1D,LYN,THBS1,ITGA1,NOV	darkolivegreen	VSMC_M9
GO:0035148	0.85	0.26	6	129	tube formation	BP	1	GATA3,TMED2,FZD2,PRKACB,GDNF,IRX3	darkolivegreen	VSMC_M9
GO:0045055	0.85	0.24	8	167	regulated exocytosis	BP	1	STXBP5,RAB3GAP1,LYN,ATP2A2,LRRK2,SEPT5,RAB31,WNT7A	darkolivegreen	VSMC_M9
GO:0045017	0.85	0.23	10	214	glycerolipid biosynthetic process	BP	1	SOCS6,ETNK2,BPNT1,ETNK1,PIP5K1A,PLD1,PIGW,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0090263	0.85	0.28	4	92	positive regulation of canonical Wnt signaling pathway	BP	1	ILK,USP47,LRRK2,PIN1	darkolivegreen	VSMC_M9
GO:0043269	0.85	0.20	23	444	regulation of ion transport	BP	1	UTRN,UBQLN1,AKAP9,ZMPSTE24,RAB3B,ITGB1,FYN,KIF5B,RAB3GAP1,ATP2B1,REM1,LYN,SLC30A5,ATP1A1,GPR89A,ANK3,PTGS2,CLCNKB,STIM2,KCNMB1,FXYD5,GDNF,SHISA7	darkolivegreen	VSMC_M9
GO:0051592	0.85	0.27	5	114	response to calcium ion	BP	1	THBS1,IQGAP1,KCNMB1,SLC25A24,AQP3	darkolivegreen	VSMC_M9
GO:0001837	0.85	0.25	6	131	epithelial to mesenchymal transition	BP	1	ROCK2,GATA3,ACVR1,PHLDB2,FERMT2,ROCK1	darkolivegreen	VSMC_M9
GO:0043065	0.85	0.20	20	410	positive regulation of apoptotic process	BP	1	JAK2,INHBA,ITGB1,NOX4,CAMK1D,RPL26,LYN,THBS1,EIF2B5,ATF3,PTGS2,SKIL,FAS,ADAM10,MAP2K4,PIN1,ITGA1,CD40LG,GADD45B,E2F3	darkolivegreen	VSMC_M9
GO:0048732	0.86	0.21	17	335	gland development	BP	1	CDO1,EXT1,JAK2,HOXA9,ZMPSTE24,UPF2,GATA3,BRCA2,NTN4,SULF1,HK2,UBE3A,CUL3,GNPNAT1,MSN,ITGA2,SEC63	darkolivegreen	VSMC_M9
GO:0050679	0.86	0.24	7	154	positive regulation of epithelial cell proliferation	BP	1	CAV2,AGTR1,NRP2,AKT3,RICTOR,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0051098	0.86	0.21	14	296	regulation of binding	BP	1	JAK2,ZMPSTE24,RB1,GATA3,CLN5,ATP2A2,CBLB,LRRK2,DKK1,MYOCD,PIN1,ROCK1,ITGA2,GTF2B	darkolivegreen	VSMC_M9
GO:0007626	0.86	0.24	6	132	locomotory behavior	BP	1	UBA6,ZMPSTE24,LRRK2,UBE3A,PAFAH1B1,GDNF	darkolivegreen	VSMC_M9
GO:0045580	0.86	0.27	4	98	regulation of T cell differentiation	BP	1	MALT1,GATA3,SOS1,NFKBIZ	darkolivegreen	VSMC_M9
GO:1903008	0.87	0.26	4	101	organelle disassembly	BP	1	KIF5B,UFM1,UBA5,HK2	darkolivegreen	VSMC_M9
GO:0022612	0.87	0.26	4	95	gland morphogenesis	BP	1	NTN4,SULF1,CUL3,MSN	darkolivegreen	VSMC_M9
GO:0032874	0.87	0.26	4	97	positive regulation of stress-activated MAPK cascade	BP	1	TNIK,GADD45B,CTGF,WNT7A	darkolivegreen	VSMC_M9
GO:0071356	0.87	0.23	7	163	cellular response to tumor necrosis factor	BP	1	EXT1,JAK2,GATA3,ILK,THBS1,TANK,FAS	darkolivegreen	VSMC_M9
GO:0071805	0.87	0.23	6	131	potassium ion transmembrane transport	BP	1	AKAP9,ITGB1,ATP1A1,ANK3,KCNMB1,SLC1A3	darkolivegreen	VSMC_M9
GO:0010506	0.87	0.20	13	268	regulation of autophagy	BP	1	TBK1,ATP6V1C1,UBQLN1,EXOC1,ZMPSTE24,RAB3GAP1,SUPT5H,ATP6V0A2,LRRK2,ATP6V1A,RAB3GAP2,TLK2,ROCK1	darkolivegreen	VSMC_M9
GO:0051090	0.87	0.19	16	328	regulation of DNA-binding transcription factor activity	BP	1	MALT1,JAK2,CLOCK,RB1,CAMK1D,ITCH,TLR2,MBTPS2,FZD2,TLR6,TBX6,RLIM,MYOCD,CD40LG,USP7,UBE2V1	darkolivegreen	VSMC_M9
GO:1901800	0.87	0.26	4	104	positive regulation of proteasomal protein catabolic process	BP	1	UBQLN1,PSMC2,NUB1,LRRK2	darkolivegreen	VSMC_M9
GO:0048871	0.87	0.18	19	378	multicellular organismal homeostasis	BP	1	EXT1,JAK2,ITGB1,PIWIL4,RB1,HOXC10,LNPEP,FFAR4,IGF1R,GATM,PTGS2,AKT3,TLE3,CIDEA,PRKACB,AQP3,CTGF,TMEM119,IRX3	darkolivegreen	VSMC_M9
GO:0002833	0.87	0.26	4	101	positive regulation of response to biotic stimulus	BP	1	TBK1,FYN,LYN,FCN1	darkolivegreen	VSMC_M9
GO:2000241	0.87	0.25	4	105	regulation of reproductive process	BP	1	INHBA,SULF1,PGAM4,PRKACB	darkolivegreen	VSMC_M9
GO:0006812	0.88	0.16	42	796	cation transport	BP	1	UTRN,ATP6V1C1,SLC39A7,UBQLN1,SLC30A9,AKAP9,TMEM165,ZMPSTE24,RAB3B,ITGB1,FYN,KIF5B,SLC36A4,NDFIP2,ATP2B1,NDFIP1,REM1,LYN,ATP6V0A2,SLC30A5,ATP2A2,SLC39A14,ATP1A1,SLC39A10,MRS2,ATP6V1A,ITPR2,ANK3,ATP13A3,PTGS2,ITGAV,STIM2,MAGED2,KCNMB1,CLTC,ANXA6,SLC1A3,AFG3L2,FXYD5,GDNF,CTGF,SHISA7	darkolivegreen	VSMC_M9
GO:0032496	0.88	0.20	10	225	response to lipopolysaccharide	BP	1	MALT1,PLAA,JAK2,STAP1,NOCT,LYN,TLR2,ATP2A2,PTGS2,TBXA2R	darkolivegreen	VSMC_M9
GO:0042742	0.88	0.24	4	109	defense response to bacterium	BP	1	TBK1,TMF1,TLR2,TLR6	darkolivegreen	VSMC_M9
GO:0060326	0.88	0.20	9	206	cell chemotaxis	BP	1	STAP1,CAMK1D,LYN,AGTR1,THBS1,PIP5K1A,ADAM10,ITGA1,NOV	darkolivegreen	VSMC_M9
GO:0006865	0.88	0.24	4	99	amino acid transport	BP	1	ITGB1,SLC36A4,RAB3GAP1,SLC1A3	darkolivegreen	VSMC_M9
GO:0002831	0.88	0.19	10	224	regulation of response to biotic stimulus	BP	1	TBK1,ZMPSTE24,FYN,CNOT7,LYN,ITCH,APPL1,PTPN1,GPATCH3,FCN1	darkolivegreen	VSMC_M9
GO:0050678	0.88	0.18	13	275	regulation of epithelial cell proliferation	BP	1	CAV2,RB1,GATA3,BRCA2,SULF1,AGTR1,THBS1,NRP2,AKT3,RICTOR,WFDC1,BMPR2,WNT7A	darkolivegreen	VSMC_M9
GO:0030217	0.88	0.20	8	179	T cell differentiation	BP	1	MALT1,GATA3,JMJD6,LIG4,SOS1,NFKBIZ,GPR89A,CD3G	darkolivegreen	VSMC_M9
GO:0043433	0.88	0.22	5	126	negative regulation of DNA-binding transcription factor activity	BP	1	RB1,ITCH,TBX6,RLIM,USP7	darkolivegreen	VSMC_M9

GO:0046486	0.89	0.17	15	317	glycerolipid metabolic process	BP	1	SOCS6,PNPLA8,OSBPL8,GPCPD1,ETNK2,MBOAT1,BPNT1,ETNK1,PIP5K1A,PLD1,PIGW,PAFAH1B1,DPM2,IMPA1,DPM1	darkolivegreen	VSMC_M9
GO:0050778	0.89	0.17	14	306	positive regulation of immune response	BP	1	MALT1,TBK1,STAP1,FYN,GATA3,RIF1,LYN,APPL1,NFKBIZ,CBLB,SLC39A10,EIF2B5,VAV2,FCN1	darkolivegreen	VSMC_M9
GO:0044255	0.89	0.15	37	743	cellular lipid metabolic process	BP	1	SOCS6,PLAA,ELOVL5,FAM135A,ZMPSTE24,PNPLA8,PDSS1,CYP27C1,ABHD1,ST3GAL3,OSBPL8,GPCPD1,HSD17B12,PLPP1,RDH10,AGTR1,CERS5,ETNK2,MBOAT1,BPNT1,ETNK1,ST8SIA1,PIP5K1A,PTGS2,PLD1,TNFAIP8L3,SAMD8,PIGW,ETFA,DHRS7B,PAFAH1B1,ACOT7,PLPPR5,DPM2,IMPA1,DPM1,ELOVL4	darkolivegreen	VSMC_M9
GO:0070371	0.89	0.18	10	227	ERK1 and ERK2 cascade	BP	1	LYN,FFAR4,PTPN1,ATF3,ITGAV,FERMT2,TNFAIP8L3,SEMA7A,PIN1,CTGF	darkolivegreen	VSMC_M9
GO:0060249	0.89	0.18	10	218	anatomical structure homeostasis	BP	1	EXT1,ITGB1,PIWIL4,RB1,ATP2B1,PTGS2,AKT3,CTGF,TMEM119,CFL2	darkolivegreen	VSMC_M9
GO:1901615	0.89	0.16	18	382	organic hydroxy compound metabolic process	BP	1	CYP27C1,GATA3,ACPP,PLPP1,APPL1,RDH10,GPD2,GCNT4,MRS2,BPNT1,IDH2,MBTPS2,TPI1,DPM2,IMPA1,DPM1,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0006333	0.89	0.22	4	106	chromatin assembly or disassembly	BP	1	SMARCA5,LIN54,NAP1L4,TLK2	darkolivegreen	VSMC_M9
GO:0030111	0.89	0.16	13	277	regulation of Wnt signaling pathway	BP	1	WISP1,ILK,SCYL2,SULF1,USP47,TLR2,LRRK2,KPNA1,DKK1,WNT5B,TLE3,PIN1,VGLL4	darkolivegreen	VSMC_M9
GO:0016570	0.90	0.15	20	399	histone modification	BP	1	PHF20L1,JAK2,CLOCK,ZNF451,HDAC9,ZMPSTE24,GATA3,JMJD6,BRPF1,SETD5,RIF1,BRCA2,PARG,BRD7,LRRK2,TAF5L,MYOCD,MYSM1,USP7,GTF2B	darkolivegreen	VSMC_M9
GO:0070372	0.90	0.17	9	211	regulation of ERK1 and ERK2 cascade	BP	1	LYN,FFAR4,PTPN1,ATF3,FERMT2,TNFAIP8L3,SEMA7A,PIN1,CTGF	darkolivegreen	VSMC_M9
GO:0098660	0.90	0.14	29	574	inorganic ion transmembrane transport	BP	1	UTRN,ATP6V1C1,SLC39A7,UBQLN1,AKAP9,TMEM165,ITGB1,FYN,KIF5B,ATP2B1,REM1,LYN,ATP6V0A2,SLC30A5,ATP2A2,SLC39A14,ATP1A1,SLC39A10,MRS2,ATP6V1A,ITPR2,ANK3,ITGAV,STIM2,KCNMB1,ANXA6,SLC1A3,AFG3L2,FXYD5	darkolivegreen	VSMC_M9
GO:0019932	0.90	0.17	10	218	second-messenger-mediated signaling	BP	1	ZMPSTE24,PDE7A,EIF2AK3,FFAR4,AGTR1,ATP2A2,THBS1,LRRK2,ITPR2,TBXA2R	darkolivegreen	VSMC_M9
GO:0015980	0.90	0.17	10	259	energy derivation by oxidation of organic compounds	BP	1	NOA1,UGP2,GFPT1,SUCLA2,PDE12,GPD2,IDH2,PHKG2,DLST,PPP1R2	darkolivegreen	VSMC_M9
GO:0007605	0.90	0.21	4	102	sensory perception of sound	BP	1	MYO6,SLC1A3,COL11A1,LHFPL4	darkolivegreen	VSMC_M9
GO:1905039	0.90	0.21	4	105	carboxylic acid transmembrane transport	BP	1	ITGB1,SLC36A4,THBS1,SLC1A3	darkolivegreen	VSMC_M9
GO:0071241	0.90	0.17	7	165	cellular response to inorganic substance	BP	1	LIG4,EIF2AK3,LRRK2,IQGAP1,ANK3,PTGS2,SLC25A24	darkolivegreen	VSMC_M9
GO:1903825	0.91	0.20	4	106	organic acid transmembrane transport	BP	1	ITGB1,SLC36A4,THBS1,SLC1A3	darkolivegreen	VSMC_M9
GO:0007420	0.91	0.13	31	587	brain development	BP	1	AHI1,CEP120,EXT1,UBA6,UGP2,INHBA,PCDH18,ITGB1,FYN,KIF5B,RAB3GAP1,CLN5,UFM1,MYO16,ATP2B1,SOS1,BRCA2,SCYL2,ZDHHC16,LRRK2,UBE3A,UCHL5,EIF2B5,NRP2,AKT3,SEMA7A,PAFAH1B1,BMPR2,TMX2,ARF4,WNT7A	darkolivegreen	VSMC_M9
GO:0051924	0.91	0.17	7	172	regulation of calcium ion transport	BP	1	UBQLN1,FYN,ATP2B1,REM1,LYN,PTGS2,STIM2	darkolivegreen	VSMC_M9
GO:0016042	0.91	0.16	9	225	lipid catabolic process	BP	1	PNPLA8,ABHD1,GPCPD1,PLIN1,PLD1,ETFA,CIDEA,PAFAH1B1,AKR1D1	darkolivegreen	VSMC_M9
GO:0090596	0.91	0.16	9	198	sensory organ morphogenesis	BP	1	AHI1,LRIG3,TOPORS,MYO6,GATA3,FZD2,PRRX1,COL11A1,WNT9A	darkolivegreen	VSMC_M9
GO:0009952	0.91	0.17	6	150	anterior/posterior pattern specification	BP	1	HOXA9,HOXA10,HOXA11,TMED2,TBX6,BMPR2	darkolivegreen	VSMC_M9
GO:0048771	0.91	0.18	5	129	tissue remodeling	BP	1	EXT1,ROCK2,ROCK1,BMPR2,TMEM119	darkolivegreen	VSMC_M9
GO:0001894	0.91	0.16	8	189	tissue homeostasis	BP	1	EXT1,ITGB1,PIWIL4,RB1,PTGS2,AKT3,CTGF,TMEM119	darkolivegreen	VSMC_M9
GO:1902107	0.91	0.19	4	110	positive regulation of leukocyte differentiation	BP	1	MALT1,RB1,GATA3,NFKBIZ	darkolivegreen	VSMC_M9
GO:1903708	0.91	0.19	4	110	positive regulation of hemopoiesis	BP	1	MALT1,RB1,GATA3,NFKBIZ	darkolivegreen	VSMC_M9
GO:0042542	0.91	0.18	4	118	response to hydrogen peroxide	BP	1	FYN,STK24,LRRK2,UBE3A	darkolivegreen	VSMC_M9
GO:0042063	0.92	0.14	10	230	gliogenesis	BP	1	STAP1,ILK,LYN,TLR2,DNER,NTRK3,IDH2,EIF2B5,DICER1,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0031327	0.92	0.11	64	1198	negative regulation of cellular biosynthetic process	BP	1	CLOCK,ZNF451,HDAC9,THAP5,ROCK2,NOCT,FYN,ZEB1,EXOSC9,RB1,GATA3,SUPT5H,RIF1,NR2C1,BRCA2,CNOT7,EIF2AK3,TDG,HCFC2,USP47,XRN1,PDE12,DCP1A,DHX36,SHOX2,MTERF3,ATP1A1,BRD7,TBX15,CUL3,EIF4E,TDP2,EPRS,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,CPEB2,DKK1,SRP9,MAGED2,CLK2,TBX6,RLIM,MAGEE2,TLE3,DICER1,MYOCD,RBBP8,ROCK1,C1QTNF3,ENO1,THAP11,BMPR2,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0050776	0.92	0.12	26	538	regulation of immune response	BP	1	MALT1,TBK1,PTPRD,STAP1,ZMPSTE24,FYN,GATA3,RIF1,NDFIP1,SOS1,CNOT7,LYN,ITCH,APPL1,TLR2,NFKBIZ,CBLB,SLC39A10,PTPN1,EIF2B5,GPATCH3,TLR6,MAP2K4,THOC1,VAV2,FCN1	darkolivegreen	VSMC_M9
GO:0021543	0.92	0.17	5	127	pallium development	BP	1	CEP120,UBA6,KIF5B,EIF2B5,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0009617	0.92	0.13	16	362	response to bacterium	BP	1	MALT1,TBK1,PLAA,JAK2,STAP1,NOCT,TMF1,LYN,TLR2,ATP2A2,CCDC186,PTGS2,TLR6,PPM1D,TBXA2R,LSM5	darkolivegreen	VSMC_M9
GO:0035725	0.92	0.16	5	120	sodium ion transmembrane transport	BP	1	UTRN,KIF5B,ATP1A1,ANK3,FXYD5	darkolivegreen	VSMC_M9
GO:0019221	0.92	0.13	13	306	cytokine-mediated signaling pathway	BP	1	TBK1,EXT1,JAK2,STAP1,SOS1,ILK,CNOT7,APPL1,PTPN1,ZC3H15,FAS,PLP2,PAFAH1B1	darkolivegreen	VSMC_M9
GO:0010001	0.92	0.15	7	173	glial cell differentiation	BP	1	ILK,LYN,TLR2,DNER,NTRK3,EIF2B5,DICER1	darkolivegreen	VSMC_M9

GO:0009890	0.92	0.10	65	1222	negative regulation of biosynthetic process	BP	1	CLOCK,ZNF451,HDAC9,THAP5,ROCK2,NOCT,FYN,ZEB1,EXOSC9,RB1,GATA3,SUPT5H,RIF1,NR2C1,BRCA2,CNOT7,EIF2AK3,TDG,HCFC2,USP47,XRN1,PDE12,DCP1A,DHX36,SHOX2,MTERF3,ATP1A1,BRD7,TBX15,CUL3,EIF4E,TDP2,EPRS,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,CPEB2,DKK1,SRP9,MAGED2,CLK2,TBX6,RLIM,MAGEE2,TLE3,CLTC,DICER1,MYOCD,RBBP8,ROCK1,C1QTNF3,ENO1,THAP11,BMPR2,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0007093	0.92	0.17	4	117	mitotic cell cycle checkpoint signaling	BP	1	RINT1,RPL26,TPR,RFWD3	darkolivegreen	VSMC_M9
GO:0006629	0.92	0.10	49	982	lipid metabolic process	BP	1	SOCS6,PLAA,ABCB4,ELOVL5,FAM135A,ZMPSTE24,KBTBD2,PNPLA8,PDSS1,CYP27C1,ABHD1,ST3GAL3,OSBPL8,GPCPD1,PIK3R4,HSD17B12,PLPP1,LYN,RDH10,AGTR1,CERS5,ETNK2,ATP1A1,MBOAT1,BPNT1,ETNK1,ST8SIA1,PLIN1,PIP5K1A,MBTPS2,PTGS2,PLD1,TNFAIP8L3,SAMD8,ACBD3,PIGW,ETFA,DHRS7B,CIDEA,PAFAH1B1,ACOT7,VAV2,PLPPR5,DPM2,IMPA1,DPM1,ELOVL4,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0045333	0.92	0.15	6	191	cellular respiration	BP	1	NOA1,SUCLA2,PDE12,GPD2,IDH2,DLST	darkolivegreen	VSMC_M9
GO:0010558	0.92	0.10	61	1150	negative regulation of macromolecule biosynthetic process	BP	1	CLOCK,ZNF451,HDAC9,THAP5,ROCK2,NOCT,ZEB1,EXOSC9,RB1,GATA3,SUPT5H,RIF1,NR2C1,BRCA2,CNOT7,EIF2AK3,TDG,HCFC2,USP47,XRN1,PDE12,DCP1A,DHX36,SHOX2,MTERF3,BRD7,TBX15,CUL3,EIF4E,TDP2,EPRS,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,CPEB2,DKK1,SRP9,MAGED2,TBX6,RLIM,MAGEE2,TLE3,CLTC,DICER1,MYOCD,RBBP8,ROCK1,ENO1,THAP11,BMPR2,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0010038	0.93	0.12	12	279	response to metal ion	BP	1	LIG4,EIF2AK3,SLC30A5,THBS1,LRRK2,EIF2B5,IQGAP1,ANK3,PTGS2,KCNMB1,SLC25A24,AQP3	darkolivegreen	VSMC_M9
GO:0055088	0.93	0.16	4	116	lipid homeostasis	BP	1	ABCB4,HDAC9,PNPLA8,C1QTNF3	darkolivegreen	VSMC_M9
GO:0098876	0.93	0.15	5	129	vesicle-mediated transport to the plasma membrane	BP	1	EXOC1,EHD4,ANK3,BLZF1,RAB31	darkolivegreen	VSMC_M9
GO:0007417	0.93	0.09	42	795	central nervous system development	BP	1	AHI1,CEP120,EXT1,NPAS2,UBA6,UGP2,INHBA,PCDH18,ITGB1,FYN,KIF5B,RAB3GAP1,CLN5,UFM1,LIG4,MYO16,ATP2B1,SOS1,BRCA2,SCYL2,LYN,TLR2,VCAN,ZDHHC16,LRRK2,UBE3A,DNER,UCHL5,NTRK3,EIF2B5,NRP2,AKT3,TBX6,SEMA7A,PAFAH1B1,CDH11,BMPR2,TMX2,ARF4,GDNF,ZPR1,WNT7A	darkolivegreen	VSMC_M9
GO:0070374	0.93	0.14	5	145	positive regulation of ERK1 and ERK2 cascade	BP	1	FFAR4,FERMT2,TNFAIP8L3,SEMA7A,CTGF	darkolivegreen	VSMC_M9
GO:0050673	0.93	0.11	14	316	epithelial cell proliferation	BP	1	CAV2,RB1,GATA3,BRCA2,SULF1,AGTR1,THBS1,NRP2,AKT3,RICTOR,WFDC1,BMPR2,NOV,WNT7A	darkolivegreen	VSMC_M9
GO:0043393	0.93	0.13	6	162	regulation of protein binding	BP	1	ATP2A2,CBLB,LRRK2,DKK1,PIN1,ROCK1	darkolivegreen	VSMC_M9
GO:2000113	0.94	0.08	60	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	CLOCK,ZNF451,HDAC9,THAP5,ROCK2,NOCT,ZEB1,EXOSC9,RB1,GATA3,SUPT5H,RIF1,NR2C1,BRCA2,CNOT7,EIF2AK3,TDG,HCFC2,USP47,XRN1,PDE12,DCP1A,DHX36,SHOX2,MTERF3,BRD7,TBX15,CUL3,EIF4E,TDP2,EPRS,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,CPEB2,DKK1,SRP9,MAGED2,TBX6,RLIM,MAGEE2,TLE3,DICER1,MYOCD,RBBP8,ROCK1,ENO1,THAP11,BMPR2,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0006323	0.94	0.14	4	119	DNA packaging	BP	1	PSME4,SMARCA5,LIN54,NAP1L4	darkolivegreen	VSMC_M9
GO:0015849	0.94	0.12	8	203	organic acid transport	BP	1	PNPLA8,ITGB1,SLC36A4,RAB3GAP1,THBS1,EPRS,SLC1A3,BDKRB2	darkolivegreen	VSMC_M9
GO:0071103	0.94	0.11	8	200	DNA conformation change	BP	1	PSME4,DDX1,SMARCA5,CHD1,DHX36,LIN54,CHD9,NAP1L4	darkolivegreen	VSMC_M9
GO:0007219	0.94	0.12	5	138	Notch signaling pathway	BP	1	SUSD5,DNER,NOTCH3,ADAM10,NOV	darkolivegreen	VSMC_M9
GO:0010639	0.94	0.10	13	297	negative regulation of organelle organization	BP	1	XRN1,MAP1B,PFN2,DYRK1A,SPTBN5,LRRK2,PHLDB2,CAMSAP2,HDGFL3,TPR,IQCJ-SCHIP1,FHOD3,CCP110	darkolivegreen	VSMC_M9
GO:0046395	0.94	0.11	6	182	carboxylic acid catabolic process	BP	1	CDO1,ABHD1,NPL,DLST,ETFA,AKR1D1	darkolivegreen	VSMC_M9
GO:0009636	0.95	0.11	6	174	response to toxic substance	BP	1	GPX7,LYN,MAP1B,TLR2,PTGS2,MIR186	darkolivegreen	VSMC_M9
GO:0000122	0.95	0.07	34	694	negative regulation of transcription by RNA polymerase II	BP	1	ZNF451,HDAC9,THAP5,ZEB1,RB1,GATA3,SUPT5H,RIF1,NR2C1,TDG,HCFC2,SHOX2,TBX15,CUL3,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,DICER1,MYOCD,ENO1,THAP11,GLIS3,IRX3,ZNF556	darkolivegreen	VSMC_M9
GO:0016054	0.95	0.10	6	186	organic acid catabolic process	BP	1	CDO1,ABHD1,NPL,DLST,ETFA,AKR1D1	darkolivegreen	VSMC_M9
GO:0009060	0.95	0.11	4	161	aerobic respiration	BP	1	SUCLA2,PDE12,IDH2,DLST	darkolivegreen	VSMC_M9
GO:0030902	0.95	0.11	4	116	hindbrain development	BP	1	AHI1,ITGB1,MYO16,WNT7A	darkolivegreen	VSMC_M9
GO:0010035	0.95	0.07	19	435	response to inorganic substance	BP	1	FYN,SELENOV,STK24,LIG4,EIF2AK3,SLC30A5,MAP1B,DHX36,THBS1,LRRK2,UBE3A,EIF2B5,IQGAP1,ANK3,PTGS2,ADSS,KCNMB1,SLC25A24,AQP3	darkolivegreen	VSMC_M9
GO:0060322	0.96	0.06	31	624	head development	BP	1	AHI1,CEP120,EXT1,UBA6,UGP2,INHBA,PCDH18,ITGB1,FYN,KIF5B,RAB3GAP1,CLN5,UFM1,MYO16,ATP2B1,SOS1,BRCA2,SCYL2,ZDHHC16,LRRK2,UBE3A,UCHL5,EIF2B5,NRP2,AKT3,SEMA7A,PAFAH1B1,BMPR2,TMX2,ARF4,WNT7A	darkolivegreen	VSMC_M9
GO:0048167	0.96	0.09	5	143	regulation of synaptic plasticity	BP	1	RAB3GAP1,MAP1B,PTGS2,SORCS2,SHISA7	darkolivegreen	VSMC_M9
GO:0060828	0.96	0.08	8	210	regulation of canonical Wnt signaling pathway	BP	1	ILK,SCYL2,USP47,LRRK2,KPNA1,DKK1,TLE3,PIN1	darkolivegreen	VSMC_M9
GO:0050821	0.96	0.09	5	154	protein stabilization	BP	1	PFN2,C10orf90,PIN1,BAG5,USP7	darkolivegreen	VSMC_M9
GO:0019722	0.96	0.09	5	147	calcium-mediated signaling	BP	1	ZMPSTE24,EIF2AK3,AGTR1,ATP2A2,LRRK2	darkolivegreen	VSMC_M9

GO:0006814	0.96	0.08	6	161	sodium ion transport	BP	1	UTRN,KIF5B,ATP1A1,ANK3,MAGED2,FXYD5	darkolivegreen	VSMC_M9
GO:1901617	0.96	0.08	6	178	organic hydroxy compound biosynthetic process	BP	1	GATA3,APPL1,MBTPS2,IMPA1,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0051260	0.96	0.09	4	128	protein homooligomerization	BP	1	CEP57,JMJD6,KCTD9,EHD4	darkolivegreen	VSMC_M9
GO:0051253	0.96	0.05	52	1032	negative regulation of RNA metabolic process	BP	1	CLOCK,ZNF451,HDAC9,ZMPSTE24,THAP5,NOCT,ZEB1,RB1,TRDMT1,GATA3,SUPT5H,RIF1,NR2C1,CNOT7,TDG,HCFC2,USP47,DHX36,SHOX2,MTERF3,DYRK1A,BRD7,TBX15,CUL3,TDP2,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,DICER1,MYOCD,RBBP8,ENO1,THAP11,GDNF,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0071897	0.96	0.09	5	150	DNA biosynthetic process	BP	1	LIG4,XRN1,NEK7,BMPR2,CTGF	darkolivegreen	VSMC_M9
GO:0031647	0.97	0.06	9	249	regulation of protein stability	BP	1	USP47,PFN2,LRRK2,CUL3,C10orf90,PIN1,BAG5,USP7,DPM2	darkolivegreen	VSMC_M9
GO:0045934	0.97	0.04	56	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	CLOCK,ZNF451,HDAC9,ZMPSTE24,THAP5,NOCT,ZEB1,RB1,TRDMT1,GATA3,SUPT5H,RIF1,NR2C1,NDFIP1,CNOT7,TDG,HCFC2,USP47,XRN1,DHX36,SHOX2,MTERF3,DYRK1A,BRD7,TBX15,CUL3,TDP2,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,ZC3H14,TLE3,DICER1,MYOCD,RBBP8,THOC1,ENO1,THAP11,BMPR2,GDNF,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0021915	0.97	0.07	4	130	neural tube development	BP	1	DCHS1,TMED2,FZD2,PRKACB	darkolivegreen	VSMC_M9
GO:0008202	0.98	0.05	7	217	steroid metabolic process	BP	1	HSD17B12,AGTR1,ATP1A1,MBTPS2,ACBD3,SRD5A2,AKR1D1	darkolivegreen	VSMC_M9
GO:0030258	0.98	0.06	5	171	lipid modification	BP	1	PLPP1,AGTR1,MBOAT1,ETFA,PLPPR5	darkolivegreen	VSMC_M9
GO:0006631	0.98	0.04	9	271	fatty acid metabolic process	BP	1	PLAA,ELOVL5,PNPLA8,ABHD1,HSD17B12,PTGS2,ETFA,ACOT7,ELOVL4	darkolivegreen	VSMC_M9
GO:0000302	0.98	0.05	5	177	response to reactive oxygen species	BP	1	FYN,STK24,LRRK2,UBE3A,TPM1	darkolivegreen	VSMC_M9
GO:0030178	0.98	0.05	4	142	negative regulation of Wnt signaling pathway	BP	1	SCYL2,DKK1,TLE3,VGLL4	darkolivegreen	VSMC_M9
GO:0045892	0.98	0.03	45	943	negative regulation of transcription, DNA-templated	BP	1	CLOCK,ZNF451,HDAC9,THAP5,ZEB1,RB1,GATA3,SUPT5H,RIF1,NR2C1,CNOT7,TDG,HCFC2,USP47,SHOX2,MTERF3,BRD7,TBX15,CUL3,TDP2,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,TLE3,DICER1,MYOCD,RBBP8,ENO1,THAP11,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:1903507	0.98	0.03	45	945	negative regulation of nucleic acid-templated transcription	BP	1	CLOCK,ZNF451,HDAC9,THAP5,ZEB1,RB1,GATA3,SUPT5H,RIF1,NR2C1,CNOT7,TDG,HCFC2,USP47,SHOX2,MTERF3,BRD7,TBX15,CUL3,TDP2,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,TLE3,DICER1,MYOCD,RBBP8,ENO1,THAP11,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:1902679	0.98	0.03	45	946	negative regulation of RNA biosynthetic process	BP	1	CLOCK,ZNF451,HDAC9,THAP5,ZEB1,RB1,GATA3,SUPT5H,RIF1,NR2C1,CNOT7,TDG,HCFC2,USP47,SHOX2,MTERF3,BRD7,TBX15,CUL3,TDP2,WWC3,LARP7,LRRFIP1,ATF3,RBBP7,TPR,NPAT,SKIL,PRRX1,DKK1,MAGED2,TBX6,RLIM,MAGEE2,TLE3,DICER1,MYOCD,RBBP8,ENO1,THAP11,GLIS3,VGLL4,IRX3,BCL7A,ZNF556	darkolivegreen	VSMC_M9
GO:0051259	0.99	0.03	5	174	protein complex oligomerization	BP	1	CEP57,JMJD6,MAT2A,KCTD9,EHD4	darkolivegreen	VSMC_M9
GO:0044242	0.99	0.03	4	164	cellular lipid catabolic process	BP	1	PNPLA8,ABHD1,GPCPD1,ETFA	darkolivegreen	VSMC_M9
GO:0042391	0.99	0.01	10	302	regulation of membrane potential	BP	1	AKAP9,ZMPSTE24,KIF5B,RAB3GAP1,ATP2A2,ATP1A1,LRRK2,ANK3,NUP155,WNT7A	darkolivegreen	VSMC_M9
GO:0051603	0.00	1.00	71	639	proteolysis involved in cellular protein catabolic process	BP	3.8E-09	LATS1,MAPK9,KLHDC10,UBE2H,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,YME1L1,PDCD6IP,FBXL3,NGLY1,BIRC6,PSMD8,TMTC3,VPS37A,CSNK2A1,SGTB,ANAPC10,RNF13,WWP1,RSPRY1,TSG101,KLHL8,CYLD,BTRC,TRIP12,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,USP8,UBE2L5,UBR4,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0019941	0.00	1.00	65	550	modification-dependent protein catabolic process	BP	3.8E-09	LATS1,MAPK9,KLHDC10,UBE2H,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,FBXL3,BIRC6,PSMD8,VPS37A,CSNK2A1,SGTB,ANAPC10,RNF13,WWP1,TSG101,KLHL8,CYLD,BTRC,TRIP12,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,USP8,UBE2L5,UBR4,HUWE1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0006511	0.00	1.00	64	542	ubiquitin-dependent protein catabolic process	BP	4.5E-09	LATS1,MAPK9,KLHDC10,UBE2H,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,UFL1,CUL1,FBXL4,CUL2,FBXL3,BIRC6,PSMD8,VPS37A,CSNK2A1,SGTB,ANAPC10,RNF13,WWP1,TSG101,KLHL8,CYLD,BTRC,TRIP12,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,USP8,UBE2L5,UBR4,HUWE1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5

GO:0043632	0.00	1.00	65	561	modification-dependent macromolecule catabolic process	BP	4.5E-09	LATS1,MAPK9,KLHDC10,UBE2H,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,FBXL3,BIRC6,PSMD8,VPS37A,CSNK2A1,SGTB,ANAPC10,RNF13,WWP1,TSG101,KLHL8,CYLD,BTRC,TRIP12,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,USP8,UBE2L5,UBR4,HUWE1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0044257	0.00	1.00	73	685	cellular protein catabolic process	BP	5.3E-09	LATS1,MAPK9,KLHDC10,UBE2H,VPS13A,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,AFG1L,YME1L1,PDCD6IP,FBXL3,NGLY1,BIRC6,PSMD8,TMTC3,VPS37A,CSNK2A1,SGTB,ANAPC10,RNF13,WWP1,RSPRY1,TSG101,KLHL8,CYLD,BTRC,TRIP12,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,USP8,UBE2L5,UBR4,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0044267	0.00	1.00	242	3725	cellular protein metabolic process	BP	8.2E-09	MEX3C,TAB2,PPIL4,LATS1,PCMT1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBE2H,VPS13A,PCSK5,UBR2,C9orf72,ANXA1,GUF1,VEGFA,ANKIB1,CD2AP,GCLC,RNF38,PTP4A1,FBXO11,ERLEC1,RLF,USP34,UGCG,COMMD1,DPY19L1,TIA1,PCYOX1,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,SRPK2,NCOA1,EPC1,MRE11,PRDM5,POLR2D,MAGI2,YME1L1,MAP3K2,CNOT10,PDCD6IP,PTPN4,KMT2C,FBXL3,FNTA,EPC2,XDH,KAT6A,NGLY1,ZDHHC17,GOLGA7,BIRC6,PSMD8,TMTC3,KITLG,PRKD3,SPRY4,MAP4K3,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,CSNK2A1,MSL2,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ANAPC10,PTCD3,SMAD1,EIF4G2,KCMF1,DIP2B,GFM2,NFS1,RNF13,DPH6,PCGF1,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,COPS4,LXN,GTF2H1,TSG101,HIPK1,UEVLD,PPP3CC,BTG2,KLHL8,ATP2B4,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,BTRC,OGA,NDUFS4,DOCK3,TRIP12,ASB7,CAB39,PPP6R3,PRKAB2,TET2,KMT5B,GSK3B,PUM1,PIK3CA,UBR1,FXR1,MSL3,DCUN1D1,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,PSMC6,ALS2,UBE2F,RPS6KC1,METTL5,UBR3,TLK1,ABI2,HECTD1,JMJD1C,RPS6KA3,CREBL2,ATF2,KLHL15,HERC4,STYXL1,RNF2,TRIM69,KANSL1,FKBP3,UBE2E3,KLHDC2,NEMF,ATM,KDM6A,CUL5,ERO1A,JADE3,PRKCI,COPS2,USP8,TIMP1,CRKL,UBE2L5,UBR4,KAT6B,WNK1,FUT8,HUWE1,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ATRX,ATP7A,CHM,PIAS1,FEM1B,SMAD2,ARIH1,PIK3C3,GSKIP,APPBP2,CCNK,GGNBP2,PTPN9,SMG1,ESCO1,CSNK1A1,USP14,UBE2A,PARP8,XIAP,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,GAN,PKN2,USP33,AC118549.1,ARRDC	pink	VSMC_M5
GO:0006464	0.00	1.00	201	2859	cellular protein modification process	BP	1.7E-08	MEX3C,TAB2,PPIL4,LATS1,PCMT1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBE2H,UBR2,C9orf72,ANXA1,VEGFA,ANKIB1,GCLC,RNF38,PTP4A1,FBXO11,RLF,USP34,UGCG,COMMD1,DPY19L1,ADAM17,UFL1,CUL1,CUL2,PPIL6,SRPK2,NCOA1,EPC1,MRE11,PRDM5,MAGI2,MAP3K2,PTPN4,KMT2C,FBXL3,FNTA,EPC2,XDH,KAT6A,NGLY1,ZDHHC17,GOLGA7,BIRC6,TMTC3,KITLG,PRKD3,SPRY4,MAP4K3,UBA3,MAPK8,PCMTD1,DLC1,RB1CC1,IL6ST,CSNK2A1,MSL2,MTMR6,TNKS2,VCPIP1,CDK5RAP1,PPWD1,PJA2,ARFGEF1,KDM3A,ANAPC10,SMAD1,KCMF1,DIP2B,NFS1,RNF13,DPH6,PCGF1,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,COPS4,GTF2H1,TSG101,HIPK1,UEVLD,PPP3CC,BTG2,KLHL8,ATP2B4,TWF1,IRAK4,PIGP,GXYLT1,CYLD,BTRC,OGA,NDUFS4,DOCK3,TRIP12,ASB7,CAB39,PPP6R3,PRKAB2,TET2,KMT5B,GSK3B,PIK3CA,UBR1,FXR1,MSL3,DCUN1D1,STK39,EGLN1,KDM2A,ALS2,UBE2F,RPS6KC1,UBR3,TLK1,ABI2,HECTD1,JMJD1C,RPS6KA3,CREBL2,ATF2,KLHL15,HERC4,STYXL1,RNF2,TRIM69,KANSL1,FKBP3,UBE2E3,KLHDC2,ATM,KDM6A,CUL5,ERO1A,JADE3,PRKCI,COPS2,USP8,CRKL,UBE2L5,UBR4,KAT6B,WNK1,FUT8,HUWE1,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ATRX,ATP7A,CHM,PIAS1,FEM1B,SMAD2,ARIH1,PIK3C3,GSKIP,APPBP2,CCNK,GGNBP2,PTPN9,SMG1,ESCO1,CSNK1A1,USP14,UBE2A,PARP8,XIAP,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,GAN,PKN2,USP33,AC118549.1,ARRDC5,BIRC2,MINDY3,UBE2D3,USP9X,RNF103,GMFB,UBE2V2,BRMS1L,RNF139,UBE2D2,UBXN2A,BMP2,RNF219,ZDHHC22	pink	VSMC_M5

GO:0036211	0.00	1.00	201	2859	protein modification process	BP	1.7E-08	MEX3C,TAB2,PPIL4,LATS1,PCMT1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBE2H,UBR2,C9orf72,ANXA1,VEGFA,ANKIB1,GCLC,RNF38,PTP4A1,FBXO11,RLF,USP34,UGCG,COMMD1,DPY19L1,ADAM17,UFL1,CUL1,CUL2,PPIL6,SRPK2,NCOA1,EPC1,MRE11,PRDM5,MAGI2,MAP3K2,PTPN4,KMT2C,FBXL3,FNTA,EPC2,XDH,KAT6A,NGLY1,ZDHHC17,GOLGA7,BIRC6,TMTC3,KITLG,PRKD3,SPRY4,MAP4K3,UBA3,MAPK8,PCMTD1,DLC1,RB1CC1,IL6ST,CSNK2A1,MSL2,MTMR6,TNKS2,VCPIP1,CDK5RAP1,PPWD1,PJA2,ARFGEF1,KDM3A,ANAPC10,SMAD1,KCMF1,DIP2B,NFS1,RNF13,DPH6,PCGF1,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,COPS4,GTF2H1,TSG101,HIPK1,UEVLD,PPP3CC,BTG2,KLHL8,ATP2B4,TWF1,IRAK4,PIGP,GXYLT1,CYLD,BTRC,OGA,NDUFS4,DOCK3,TRIP12,ASB7,CAB39,PPP6R3,PRKAB2,TET2,KMT5B,GSK3B,PIK3CA,UBR1,FXR1,MSL3,DCUN1D1,STK39,EGLN1,KDM2A,ALS2,UBE2F,RPS6KC1,UBR3,TLK1,ABI2,HECTD1,JMJD1C,RPS6KA3,CREBL2,ATF2,KLHL15,HERC4,STYXL1,RNF2,TRIM69,KANSL1,FKBP3,UBE2E3,KLHDC2,ATM,KDM6A,CUL5,ERO1A,JADE3,PRKCI,COPS2,USP8,CRKL,UBE2L5,UBR4,KAT6B,WNK1,FUT8,HUWE1,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ATRX,ATP7A,CHM,PIAS1,FEM1B,SMAD2,ARIH1,PIK3C3,GSKIP,APPBP2,CCNK,GGNBP2,PTPN9,SMG1,ESCO1,CSNK1A1,USP14,UBE2A,PARP8,XIAP,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,GAN,PKN2,USP33,AC118549.1,ARRDC5,BIRC2,MINDY3,UBE2D3,USP9X,RNF103,GMFB,UBE2V2,BRMS1L,RNF139,UBE2D2,UBXN2A,BMP2,RNF219,ZDHHC22	pink	VSMC_M5
GO:0044265	0.00	1.00	87	947	cellular macromolecule catabolic process	BP	7.6E-08	LATS1,MAPK9,KLHDC10,UBE2H,VPS13A,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,AFG1L,POLR2D,YME1L1,CNOT10,PDCD6IP,FBXL3,NGLY1,BIRC6,PSMD8,TMTC3,VPS37A,CSNK2A1,YTHDF3,SGTB,ANAPC10,RNF13,WWP1,RSPRY1,TSG101,BTG2,KLHL8,CSDE1,CYLD,BTRC,OGA,TRIP12,GSK3B,PUM1,UBR1,FXR1,ZFAND2A,PSMC6,UBR3,HECTD1,SMG7,KLHL15,KLHDC2,NEMF,ATM,CUL5,USP8,UBE2L5,UBR4,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,DIS3L,PIAS1,FEM1B,ARIH1,APPBP2,SMG1,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,AGO3,UBE2D3,USP9X,RNF103,UBE2V2,NAF1,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0043412	0.00	1.00	205	3029	macromolecule modification	BP	1.2E-07	MEX3C,TAB2,PPIL4,LATS1,PCMT1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBE2H,UBR2,C9orf72,ANXA1,VEGFA,ANKIB1,GCLC,RNF38,PTP4A1,FBXO11,RLF,USP34,UGCG,COMMD1,DPY19L1,ADAM17,UFL1,CUL1,CUL2,PPIL6,SRPK2,NCOA1,EPC1,MRE11,PRDM5,MAGI2,MAP3K2,PTPN4,KMT2C,FBXL3,FNTA,EPC2,XDH,KAT6A,NGLY1,ZDHHC17,GOLGA7,BIRC6,TMTC3,KITLG,PRKD3,SPRY4,MAP4K3,UBA3,MAPK8,PCMTD1,DLC1,RB1CC1,IL6ST,CSNK2A1,MSL2,MTMR6,TNKS2,VCPIP1,CDK5RAP1,PPWD1,PJA2,ARFGEF1,KDM3A,ANAPC10,SMAD1,KCMF1,DIP2B,NFS1,RNF13,DPH6,PCGF1,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,COPS4,GTF2H1,VIRMA,TSG101,HIPK1,UEVLD,PPP3CC,BTG2,KLHL8,ATP2B4,TWF1,IRAK4,PIGP,GXYLT1,CYLD,BTRC,OGA,NDUFS4,DOCK3,TRIP12,ASB7,CAB39,PPP6R3,PRKAB2,TET2,KMT5B,GSK3B,PIK3CA,UBR1,FXR1,MSL3,DCUN1D1,STK39,EGLN1,KDM2A,ALS2,UBE2F,RPS6KC1,METTL5,UBR3,TLK1,ABI2,HECTD1,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,KLHL15,HERC4,STYXL1,RNF2,TRIM69,KANSL1,FKBP3,UBE2E3,KLHDC2,ATM,KDM6A,CUL5,ERO1A,JADE3,PRKCI,COPS2,USP8,CRKL,UBE2L5,UBR4,KAT6B,WNK1,FUT8,HUWE1,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ATRX,ATP7A,CHM,PIAS1,FEM1B,SMAD2,ARIH1,PIK3C3,GSKIP,APPBP2,CCNK,GGNBP2,PTPN9,SMG1,ESCO1,CSNK1A1,USP14,UBE2A,PARP8,XIAP,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,GAN,PKN2,USP33,AC118549.1,ARRDC5,BIRC2,MINDY3,UBE2D3,USP9X,RNF103,GMFB,UBE2V2,NAF1,BRMS1L,RNF139,UBE2D2,UBXN2A,BMP2,RNF219,ZDHHC22	pink	VSMC_M5
GO:0070647	0.00	1.00	77	806	protein modification by small protein conjugation or removal	BP	2.4E-07	MEX3C,MAPK9,UBR5,KLHDC10,UBE2H,UBR2,ANKIB1,GCLC,RNF38,FBXO11,USP34,COMMD1,UFL1,CUL1,CUL2,FBXL3,BIRC6,UBA3,MSL2,TNKS2,VCPIP1,PJA2,ANAPC10,KCMF1,RNF13,PCGF1,WWP1,RSPRY1,COPS4,TSG101,KLHL8,CYLD,BTRC,TRIP12,ASB7,UBR1,DCUN1D1,UBE2F,UBR3,HECTD1,KLHL15,HERC4,RNF2,TRIM69,UBE2E3,KLHDC2,CUL5,COPS2,USP8,UBE2L5,UBR4,HUWE1,UBE2Z,FBXW11,USP3,HERC1,PIAS1,FEM1B,ARIH1,APPBP2,USP14,UBE2A,XIAP,SMAD7,GAN,USP33,ARRDC5,BIRC2,MINDY3,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A,RNF219	pink	VSMC_M5

GO:0019538	0.00	1.00	252	4113	protein metabolic process	BP	5.2E-07	MEX3C,TAB2,PPIL4,LATS1,PCMT1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBE2H,VPS13A,PCSK5,UBR2,C9orf72,ANXA1,GUF1,VEGFA,ANKIB1,CD2AP,GCLC,RNF38,PTP4A1,FBXO11,ERLEC1,RLF,USP34,UGCG,COMMD1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,SRPK2,NCOA1,EPC1,MRE11,PRDM5,POLR2D,MAGI2,YME1L1,MAP3K2,CNOT10,PDCD6IP,PTPN4,KMT2C,FBXL3,FNTA,EPC2,XDH,KAT6A,NGLY1,ZDHHC17,GOLGA7,BIRC6,PSMD8,TMTC3,KITLG,PRKD3,SPRY4,MAP4K3,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ANAPC10,PTCD3,SMAD1,EIF4G2,KCMF1,DIP2B,GFM2,NFS1,RNF13,DPH6,PCGF1,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,COPS4,LXN,GTF2H1,TSG101,HIPK1,UEVLD,PPP3CC,BTG2,KLHL8,ATP2B4,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,RANBP9,BTRC,OGA,TSPAN32,NDUFS4,DOCK3,TRIP12,ASB7,CAB39,PPP6R3,PRKAB2,TET2,KMT5B,GSK3B,PUM1,PIK3CA,UBR1,FXR1,MSL3,DCUN1D1,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,PSMC6,ALS2,UBE2F,RPS6KC1,METTL5,UBR3,TLK1,ABI2,HECTD1,JMJD1C,RPS6KA3,CREBL2,GLRX3,ATF2,KLHL15,HERC4,STYXL1,RNF2,TRIM69,KANSL1,FKBP3,UBE2E3,KLHDC2,NEMF,ATM,KDM6A,CUL5,ERO1A,JADE3,PRKCI,COPS2,USP8,TIMP1,CRKL,UBE2L5,UBR4,KAT6B,NAALADL2,WNK1,FUT8,HUWE1,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ATRX,ATP7A,CHM,PIAS1,FEM1B,SMAD2,ARIH1,PIK3C3,GSKIP,APPBP2,CCNK,GGNBP2,PTPN9,SMG1,ESCO1,CSNK1A1,USP14,UBE2A,PARP8,XIAP,NF1,PRKAA1	pink	VSMC_M5
GO:0030163	0.00	1.00	76	815	protein catabolic process	BP	5.5E-07	LATS1,MAPK9,KLHDC10,UBE2H,VPS13A,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,AFG1L,YME1L1,PDCD6IP,FBXL3,NGLY1,BIRC6,PSMD8,TMTC3,VPS37A,CSNK2A1,SGTB,ANAPC10,RNF13,WWP1,RSPRY1,TIPARP,TSG101,KLHL8,CYLD,BTRC,OGA,TRIP12,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,USP8,TIMP1,UBE2L5,UBR4,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0043161	0.00	1.00	44	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	7.7E-07	MAPK9,KLHDC10,UBE2H,UBR2,ANKIB1,CD2AP,GCLC,ERLEC1,COMMD1,UFL1,CUL1,FBXL4,CUL2,FBXL3,PSMD8,SGTB,ANAPC10,WWP1,BTRC,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,HUWE1,FBXW11,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,BIRC2,UBE2D3,RNF103,UBE2V2,UBXN2A	pink	VSMC_M5
GO:0032446	0.00	1.00	68	703	protein modification by small protein conjugation	BP	8.5E-07	MEX3C,MAPK9,UBR5,KLHDC10,UBE2H,UBR2,ANKIB1,GCLC,RNF38,FBXO11,COMMD1,UFL1,CUL1,CUL2,FBXL3,BIRC6,UBA3,MSL2,TNKS2,VCPIP1,PJA2,ANAPC10,KCMF1,RNF13,PCGF1,WWP1,RSPRY1,TSG101,KLHL8,BTRC,TRIP12,ASB7,UBR1,DCUN1D1,UBE2F,UBR3,HECTD1,KLHL15,HERC4,RNF2,TRIM69,UBE2E3,KLHDC2,CUL5,UBE2L5,UBR4,HUWE1,UBE2Z,FBXW11,HERC1,PIAS1,FEM1B,ARIH1,APPBP2,UBE2A,XIAP,SMAD7,GAN,ARRDC5,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A,RNF219	pink	VSMC_M5
GO:0016567	0.00	1.00	65	656	protein ubiquitination	BP	1.1E-06	MEX3C,MAPK9,UBR5,KLHDC10,UBE2H,UBR2,ANKIB1,GCLC,RNF38,FBXO11,COMMD1,UFL1,CUL1,CUL2,FBXL3,BIRC6,MSL2,TNKS2,VCPIP1,PJA2,ANAPC10,KCMF1,RNF13,PCGF1,WWP1,RSPRY1,TSG101,KLHL8,BTRC,TRIP12,ASB7,UBR1,DCUN1D1,UBR3,HECTD1,KLHL15,HERC4,RNF2,TRIM69,UBE2E3,KLHDC2,CUL5,UBE2L5,UBR4,HUWE1,UBE2Z,FBXW11,HERC1,FEM1B,ARIH1,APPBP2,UBE2A,XIAP,SMAD7,GAN,ARRDC5,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,UBXN2A,RNF219	pink	VSMC_M5
GO:0010498	0.00	1.00	48	434	proteasomal protein catabolic process	BP	1.3E-06	MAPK9,KLHDC10,UBE2H,UBR2,ANKIB1,CD2AP,GCLC,ERLEC1,COMMD1,UFL1,CUL1,FBXL4,CUL2,FBXL3,NGLY1,PSMD8,TMTC3,SGTB,ANAPC10,WWP1,BTRC,GSK3B,UBR1,ZFAND2A,PSMC6,UBR3,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,HUWE1,OPHN1,FBXW11,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,SMAD7,BIRC2,UBE2D3,RNF103,UBE2V2,RNF139,UBXN2A	pink	VSMC_M5

GO:0044260	0.00	1.00	331	5916	cellular macromolecule metabolic process	BP	6.5E-06	MEX3C,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,CSNK1G3,SCAF8,UBR5,DDX17,MKLN1,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CD2AP,GCM1,GCLC,RNF38,PTP4A1,RHOQ,FBXO11,ERLEC1,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,DPY19L1,RAB1A,TIA1,PCYOX1,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,CNOT10,DCLRE1C,PDCD6IP,PTPN4,KMT2C,FBXL3,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,NGLY1,ENDOV,TOP2B,ZDHHC17,GOLGA7,BIRC6,PSMD8,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,KCMF1,DIP2B,GFM2,NFS1,RNF13,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,MLF1,COPS4,LXN,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,UEVLD,ARID2,POLK,PPP3CC,BAZ2B,BTG2,KLHL8,ATP2B4,ZBTB11,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,BBX,BTRC,OGA,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,ASB7,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,GSK3B,DCLRE1A,PUM1,PIK3CA,UBR1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,DCUN1D1,TFIP11,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,TIAL1,PSMC6,ALS2,UBE2F,RPS6KC1,GABPB2,METTL5,UBR3,TLK1,ZNF148,ABI2,HECTD1,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,HERC4,STYX	pink	VSMC_M5
GO:0009057	0.00	1.00	90	1102	macromolecule catabolic process	BP	8E-06	LATS1,MAPK9,KLHDC10,UBE2H,VPS13A,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,AFG1L,POLR2D,YME1L1,CNOT10,PDCD6IP,FBXL3,NGLY1,BIRC6,PSMD8,TMTC3,RB1CC1,VPS37A,CSNK2A1,YTHDF3,SGTB,ANAPC10,RNF13,WWP1,RSPRY1,TIPARP,TSG101,BTG2,KLHL8,CSDE1,CYLD,BTRC,OGA,TRIP12,GSK3B,PUM1,UBR1,FXR1,ZFAND2A,PSMC6,UBR3,HECTD1,SMG7,KLHL15,KLHDC2,NEMF,ATM,CUL5,USP8,TIMP1,UBE2L5,UBR4,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,DIS3L,PIAS1,FEM1B,ARIH1,APPBP2,SMG1,CSNK1A1,USP14,UBE2A,SMAD7,USP33,BIRC2,AGO3,UBE2D3,USP9X,RNF103,UBE2V2,NAF1,RNF139,UBE2D2,UBXN2A	pink	VSMC_M5
GO:1901564	0.00	1.00	273	4789	organonitrogen compound metabolic process	BP	1.5E-05	MEX3C,TAB2,PPIL4,LATS1,PCMT1,MAPK9,MTHFD1L,CSNK1G3,UBR5,SERINC1,LRGUK,KLHDC10,UBE2H,VPS13A,PCSK5,UBR2,C9orf72,ANXA1,GUF1,VEGFA,ANKIB1,CD2AP,ASNS,GCLC,RNF38,PTP4A1,RHOQ,FBXO11,ERLEC1,RLF,USP34,UGCG,COMMD1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,SRPK2,NCOA1,EPC1,MRE11,PRDM5,POLR2D,MAGI2,YME1L1,MAP3K2,CNOT10,PDCD6IP,PTPN4,KMT2C,FBXL3,FNTA,EPC2,XDH,KAT6A,OXSM,NGLY1,ZDHHC17,GOLGA7,BIRC6,PSMD8,TMTC3,KITLG,PRKD3,SPRY4,MAP4K3,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ANAPC10,PTCD3,SMAD1,EIF4G2,KCMF1,DIP2B,FAR1,GFM2,NFS1,RNF13,DPH6,PCGF1,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,COPS4,LXN,GTF2H1,TSG101,HIPK1,UEVLD,PPP3CC,BTG2,KLHL8,ATP2B4,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,RANBP9,BTRC,OGA,TSPAN32,NDUFS4,DOCK3,TRIP12,ASB7,CAB39,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,UBR1,FXR1,MSL3,DCUN1D1,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,ADAL,PSMC6,ALS2,UBE2F,RPS6KC1,METTL5,UBR3,PDE5A,TLK1,ABI2,HECTD1,JMJD1C,RPS6KA3,CREBL2,GLRX3,ATF2,KLHL15,HERC4,STYXL1,RNF2,TRIM69,KANSL1,FKBP3,UBE2E3,KLHDC2,NEMF,ATM,KDM6A,CUL5,ERO1A,JADE3,PRKCI,COPS2,USP8,TIMP1,CRKL,UBE2L5,UBR4,KAT6B,NAALADL2,WNK1,FUT8,HUWE1,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ABCB7,SPTLC2,ATRX,ATP7A,CHM,PIAS1,FEM1B,SMAD2,ARIH1,PIK3C3,GSKIP,APPBP2,C	pink	VSMC_M5
GO:1901565	0.00	1.00	85	1069	organonitrogen compound catabolic process	BP	1.7E-05	LATS1,MAPK9,KLHDC10,UBE2H,VPS13A,UBR2,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,AFG1L,YME1L1,PDCD6IP,FBXL3,XDH,NGLY1,BIRC6,PSMD8,TMTC3,VPS37A,CSNK2A1,SGTB,ANAPC10,RNF13,TET3,WWP1,RSPRY1,TIPARP,TSG101,KLHL8,ATP2B4,CYLD,BTRC,OGA,TRIP12,TET2,GSK3B,UBR1,ZFAND2A,ADAL,PSMC6,UBR3,PDE5A,HECTD1,KLHL15,KLHDC2,NEMF,CUL5,USP8,TIMP1,UBE2L5,UBR4,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,APPBP2,CSNK1A1,USP14,UBE2A,HPRT1,SMAD7,NUDT7,USP33,BIRC2,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,DDAH1,UBE2D2,UBXN2A	pink	VSMC_M5

GO:0044237	0.00	1.00	407	7918	cellular metabolic process	BP	1.9E-05	DGKA,MEX3C,ME2,VTA1,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,MTHFD1L,CSNK1G3,SCAF8,UBR5,SERINC1,EFR3A,SLC25A17,LRGUK,DDX17,MKLN1,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CYP39A1,CD2AP,SDHAF3,ASNS,GCM1,GCLC,RNF38,AGMO,PTP4A1,RHOQ,FBXO11,ERLEC1,FAM126A,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,MDH1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,UFL1,CUL1,FBXL4,CUL2,RAB33B,AFG1L,PPIL6,OSBPL9,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,ACBD5,YME1L1,MED4,MAP3K2,CNOT10,DCLRE1C,PDCD6IP,DGKH,INTS4,PTPN4,RHEB,KMT2C,FBXL3,EMSY,FNTA,ZEB2,EPC2,XDH,ARL8B,KAT6A,OXSM,NGLY1,ENDOV,TOP2B,ZDHHC17,GOLGA7,BIRC6,PSMD8,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,KCMF1,TRPC1,DIP2B,BTBD10,FAR1,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,MLF1,PIP4P2,COPS4,LXN,ARSB,GTF2H1,VIRMA,WDFY3,MED13L,TSG101,HIPK1,ESRP1,UEVLD,ARID2,POLK,PPP3CC,BAZ2B,BTG2,KLHL8,ATP2B4,ZBTB11,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,BBX,BTRC,OGA,NIPSNAP2,SNRPN,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,BICD1,ASB7,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,C2orf69,GSK3	pink	VSMC_M5
GO:0044248	0.00	1.00	121	1755	cellular catabolic process	BP	0.00011	VTA1,TAB2,LATS1,MAPK9,SLC25A17,KLHDC10,UBE2H,VPS13A,UBR2,C9orf72,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,RAB1A,PCYOX1,UFL1,CUL1,FBXL4,CUL2,RAB33B,AFG1L,POLR2D,ACBD5,YME1L1,CNOT10,PDCD6IP,RHEB,FBXL3,XDH,ARL8B,NGLY1,BIRC6,PSMD8,IRS2,TMTC3,MAPK8,RB1CC1,VPS37A,CSNK2A1,YTHDF3,SGTB,ANAPC10,EIF4G2,RNF13,TET3,WWP1,RSPRY1,ARSB,WDFY3,TSG101,BTG2,KLHL8,ATP2B4,CSDE1,CYLD,BTRC,OGA,TRIP12,TET2,ACACB,GSK3B,PUM1,PIK3CA,UBR1,FXR1,ZFAND2A,ADAL,PSMC6,UBR3,PDE5A,SCFD1,HECTD1,PAFAH1B2,SMG7,KLHL15,KLHDC2,NEMF,ATM,ACOX3,CUL5,USP8,TIMP1,UBE2L5,UBR4,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,HERC1,SPTLC2,DIS3L,PIAS1,FEM1B,ARIH1,PIK3C3,APPBP2,SMG1,CSNK1A1,USP14,UBE2A,PRKAA1,HPRT1,SMAD7,NUDT7,USP33,BIRC2,AGO3,UBE2D3,USP9X,RNF103,UBE2V2,NAF1,RNF139,DDAH1,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0006508	0.00	1.00	93	1295	proteolysis	BP	0.00033	LATS1,MAPK9,KLHDC10,UBE2H,PCSK5,UBR2,VEGFA,ANKIB1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,ADAM17,UFL1,CUL1,FBXL4,CUL2,YME1L1,PDCD6IP,FBXL3,XDH,NGLY1,BIRC6,PSMD8,TMTC3,UBA3,APAF1,DLC1,VPS37A,CSNK2A1,VCPIP1,SGTB,ANAPC10,RNF13,WWP1,RSPRY1,COPS4,LXN,TSG101,KLHL8,CYLD,BTRC,TRIP12,GSK3B,UBR1,ZFAND2A,FAM162A,PARL,PSMC6,UBR3,HECTD1,RPS6KA3,KLHL15,KLHDC2,NEMF,CUL5,COPS2,USP8,TIMP1,UBE2L5,UBR4,NAALADL2,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,PIAS1,FEM1B,ARIH1,PIK3C3,APPBP2,CSNK1A1,USP14,UBE2A,XIAP,CPD,SMAD7,PRPF8,USP33,BIRC2,MINDY3,UBE2D3,USP9X,RNF103,UBE2V2,RNF139,UBE2D2,SPINK8,UBXN2A	pink	VSMC_M5
GO:1901575	0.00	1.00	110	1628	organic substance catabolic process	BP	0.00083	LATS1,MAPK9,SLC25A17,KLHDC10,UBE2H,VPS13A,UBR2,ANKIB1,CYP39A1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,PCYOX1,UFL1,CUL1,FBXL4,CUL2,AFG1L,POLR2D,YME1L1,CNOT10,PDCD6IP,FBXL3,XDH,NGLY1,BIRC6,PSMD8,IRS2,TMTC3,RB1CC1,VPS37A,CSNK2A1,IMPAD1,YTHDF3,SGTB,ANAPC10,RNF13,TET3,WWP1,RSPRY1,TIPARP,TSG101,BTG2,KLHL8,ATP2B4,CSDE1,CYLD,BTRC,OGA,TRIP12,TET2,ACACB,GSK3B,PUM1,UBR1,FXR1,ZFAND2A,ADAL,PSMC6,UBR3,PDE5A,HECTD1,PAFAH1B2,SMG7,KLHL15,KLHDC2,NEMF,ATM,ACOX3,CUL5,USP8,TIMP1,UBE2L5,UBR4,FUT8,PGM2,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,DIS3L,PIAS1,FEM1B,ARIH1,APPBP2,SMG1,CSNK1A1,USP14,UBE2A,PRKAA1,HPRT1,SMAD7,NUDT7,USP33,BIRC2,SULT1C4,AGO3,UBE2D3,USP9X,RNF103,UBE2V2,NAF1,RNF139,DDAH1,UBE2D2,UBXN2A	pink	VSMC_M5

GO:0044238	0.00	1.00	387	7641	primary metabolic process	BP	0.00151	DGKA,MEX3C,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,CSNK1G3,SCAF8,UBR5,SERINC1,EFR3A,SLC25A17,LRGUK,DDX17,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CYP39A1,CD2AP,SDHAF3,ASNS,GCM1,GCLC,RNF38,AGMO,PTP4A1,RHOQ,FBXO11,ERLEC1,FAM126A,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,MDH1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,OSBPL9,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,CNOT10,DCLRE1C,PDCD6IP,DGKH,INTS4,PTPN4,KMT2C,FBXL3,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,OXSM,NGLY1,ENDOV,TOP2B,ZDHHC17,GOLGA7,BIRC6,PSMD8,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,KCMF1,DIP2B,FAR1,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,MLF1,PIP4P2,COPS4,LXN,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,ESRP1,UEVLD,ARID2,POLK,PPP3CC,BAZ2B,BTG2,KLHL8,ATP2B4,ZBTB11,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,RANBP9,BBX,BTRC,OGA,TSPAN32,SNRPN,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,BICD1,ASB7,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,GSK3B,DCLRE1A,PUM1,PIK3CA,UBR1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,DCUN1D1,TFIP11,ST	pink	VSMC_M5
GO:0008152	0.00	1.00	419	8467	metabolic process	BP	0.00302	DGKA,MEX3C,ME2,VTA1,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,MTHFD1L,CSNK1G3,SCAF8,UBR5,SERINC1,EFR3A,SLC25A17,LRGUK,DDX17,MKLN1,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CYP39A1,CD2AP,SDHAF3,ASNS,GCM1,GCLC,RNF38,AGMO,PTP4A1,RHOQ,FBXO11,ERLEC1,FAM126A,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,MDH1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,UFL1,CUL1,FBXL4,CUL2,RAB33B,AFG1L,PPIL6,OSBPL9,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,ACBD5,YME1L1,MED4,MAP3K2,CNOT10,DCLRE1C,PDCD6IP,DGKH,INTS4,EPB41L5,PTPN4,RHEB,KMT2C,FBXL3,EMSY,FNTA,ZEB2,EPC2,XDH,ARL8B,KAT6A,OXSM,NGLY1,ENDOV,TOP2B,ZDHHC17,GOLGA7,BIRC6,LTBP1,PSMD8,COG6,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,KCMF1,TRPC1,DIP2B,BTBD10,FAR1,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,MLF1,PIP4P2,COPS4,LXN,ARSB,GTF2H1,VIRMA,WDFY3,MED13L,TSG101,HIPK1,ESRP1,UEVLD,ARID2,POLK,PPP3CC,BAZ2B,BTG2,KLHL8,ATP2B4,ZBTB11,ZC3H11A,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,RANBP9,BBX,BTRC,OGA,NIPSNAP2,TSPAN32,SNRPN,NDUFS4,ID4,DOCK3,ACOT13,NOTCH2,TRIP12,BICD1,ASB7,CAB39,ZMYND	pink	VSMC_M5
GO:0006807	0.00	1.00	370	7284	nitrogen compound metabolic process	BP	0.00544	MEX3C,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,MTHFD1L,CSNK1G3,SCAF8,UBR5,SERINC1,LRGUK,DDX17,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CD2AP,ASNS,GCM1,GCLC,RNF38,PTP4A1,RHOQ,FBXO11,ERLEC1,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,CNOT10,DCLRE1C,PDCD6IP,INTS4,PTPN4,KMT2C,FBXL3,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,OXSM,NGLY1,ENDOV,TOP2B,ZDHHC17,GOLGA7,BIRC6,PSMD8,EAF1,ZNF605,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,KCMF1,DIP2B,FAR1,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,MLF1,COPS4,LXN,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,ESRP1,UEVLD,ARID2,POLK,PPP3CC,BAZ2B,BTG2,KLHL8,ATP2B4,ZBTB11,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,RANBP9,BBX,BTRC,OGA,TSPAN32,SNRPN,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,BICD1,ASB7,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,GSK3B,DCLRE1A,PUM1,PIK3CA,UBR1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,DCUN1D1,TFIP11,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,ADAL,TIAL1,PSMC6,ALS2,UBE2F,RP	pink	VSMC_M5

GO:0009056	0.00	1.00	127	2000	catabolic process	BP	0.00548	VTA1,TAB2,LATS1,MAPK9,SLC25A17,KLHDC10,UBE2H,VPS13A,UBR2,C9orf72,ANKIB1,CYP39A1,CD2AP,GCLC,FBXO11,ERLEC1,USP34,COMMD1,RAB1A,PCYOX1,UFL1,CUL1,FBXL4,CUL2,RAB33B,AFG1L,POLR2D,ACBD5,YME1L1,CNOT10,PDCD6IP,RHEB,FBXL3,XDH,ARL8B,NGLY1,BIRC6,PSMD8,IRS2,TMTC3,MAPK8,RB1CC1,VPS37A,CSNK2A1,IMPAD1,YTHDF3,SGTB,ANAPC10,EIF4G2,RNF13,TET3,WWP1,RSPRY1,TIPARP,ARSB,WDFY3,TSG101,BTG2,KLHL8,ATP2B4,CSDE1,CYLD,BTRC,OGA,TRIP12,TET2,ACACB,GSK3B,PUM1,PIK3CA,UBR1,FXR1,ZFAND2A,ADAL,PSMC6,UBR3,PDE5A,SCFD1,HECTD1,PAFAH1B2,SMG7,KLHL15,KLHDC2,NEMF,ATM,ACOX3,CUL5,USP8,TIMP1,UBE2L5,UBR4,FUT8,PGM2,HUWE1,OPHN1,UBE2Z,FBXW11,USP3,HERC1,SPTLC2,DIS3L,PIAS1,FEM1B,ARIH1,PIK3C3,APPBP2,SMG1,CSNK1A1,USP14,UBE2A,PRKAA1,HPRT1,SMAD7,NUDT7,USP33,BIRC2,SULT1C4,AGO3,UBE2D3,USP9X,RNF103,UBE2V2,NAF1,RNF139,DDAH1,UBE2D2,UBXN2A	pink	VSMC_M5
GO:0034063	0.00	1.00	8	24	stress granule assembly	BP	0.02199	C9orf72,YTHDF3,LSM14A,CSDE1,BICD1,STYXL1,DYNC1H1,PRKAA1	pink	VSMC_M5
GO:0043170	0.00	1.00	358	7034	macromolecule metabolic process	BP	0.0245	MEX3C,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,CSNK1G3,SCAF8,UBR5,DDX17,MKLN1,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CD2AP,GCM1,GCLC,RNF38,PTP4A1,RHOQ,FBXO11,ERLEC1,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,CNOT10,DCLRE1C,PDCD6IP,INTS4,EPB41L5,PTPN4,KMT2C,FBXL3,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,NGLY1,ENDOV,TOP2B,ZDHHC17,GOLGA7,BIRC6,LTBP1,PSMD8,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,KCMF1,DIP2B,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,MLF1,COPS4,LXN,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,ESRP1,UEVLD,ARID2,POLK,PPP3CC,BAZ2B,BTG2,KLHL8,ATP2B4,ZBTB11,ZC3H11A,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,RANBP9,BBX,BTRC,OGA,TSPAN32,SNRPN,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,BICD1,ASB7,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,GSK3B,DCLRE1A,PUM1,PIK3CA,UBR1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,DCUN1D1,TFIP11,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,TIAL1,PSMC6,ALS2,UBE2F,RPS6KC1,GA	pink	VSMC_M5
GO:0016570	0.00	1.00	38	399	histone modification	BP	0.03767	UBR5,UBR2,VEGFA,RLF,UFL1,NCOA1,EPC1,PRDM5,KMT2C,EPC2,KAT6A,MAPK8,MSL2,KDM3A,PCGF1,TET3,TRIP12,TET2,KMT5B,MSL3,KDM2A,JMJD1C,ATF2,RNF2,KANSL1,ATM,KDM6A,JADE3,KAT6B,HUWE1,ASH1L,USP3,ATRX,UBE2A,PRKAA1,NIPBL,AC118549.1,BRMS1L	pink	VSMC_M5
GO:1903050	0.00	1.00	21	192	regulation of proteolysis involved in cellular protein catabolic process	BP	0.04672	LATS1,MAPK9,ANKIB1,GCLC,COMMD1,UFL1,TMTC3,CSNK2A1,BTRC,GSK3B,ZFAND2A,PSMC6,HECTD1,OPHN1,PIAS1,ARIH1,CSNK1A1,USP14,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0071704	0.00	1.00	397	8083	organic substance metabolic process	BP	0.04754	DGKA,MEX3C,ME2,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,MTHFD1L,CSNK1G3,SCAF8,UBR5,SERINC1,EFR3A,SLC25A17,LRGUK,DDX17,MKLN1,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CYP39A1,CD2AP,SDHAF3,ASNS,GCM1,GCLC,RNF38,AGMO,PTP4A1,RHOQ,FBXO11,ERLEC1,FAM126A,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,MDH1,DPY19L1,RAB1A,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,UFL1,CUL1,FBXL4,CUL2,AFG1L,PPIL6,OSBPL9,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,CNOT10,DCLRE1C,PDCD6IP,DGKH,INTS4,EPB41L5,PTPN4,KMT2C,FBXL3,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,OXSM,NGLY1,ENDOV,TOP2B,ZDHHC17,GOLGA7,BIRC6,LTBP1,PSMD8,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,KCMF1,TRPC1,DIP2B,FAR1,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,CPNE3,TIPARP,MLF1,PIP4P2,COPS4,LXN,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,ESRP1,UEVLD,ARID2,POLK,PPP3CC,BAZ2B,BTG2,KLHL8,ATP2B4,ZBTB11,ZC3H11A,CSDE1,TWF1,IRAK4,PIGP,GXYLT1,CYLD,RANBP9,BBX,BTRC,OGA,TSPAN32,SNRPN,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,BICD1,ASB7,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,GSK3B,DCLRE1A,PUM1,PIK3CA,UB	pink	VSMC_M5
GO:0006119	0.00	1.00	13	119	oxidative phosphorylation	BP	0.06169	AFG1L,NIPSNAP2,NDUFS4,C2orf69,GHITM,ATP7A,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5,ATP5PF	pink	VSMC_M5
GO:2000058	0.00	1.00	17	143	regulation of ubiquitin-dependent protein catabolic process	BP	0.07144	LATS1,MAPK9,ANKIB1,GCLC,COMMD1,UFL1,CSNK2A1,GSK3B,ZFAND2A,HECTD1,PIAS1,ARIH1,CSNK1A1,USP14,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0070979	0.00	1.00	6	25	protein K11-linked ubiquitination	BP	0.1058	UBE2H,ANAPC10,UBE2E3,UBE2L5,UBE2A,UBE2D3	pink	VSMC_M5
GO:0061136	0.00	1.00	18	166	regulation of proteasomal protein catabolic process	BP	0.11529	MAPK9,ANKIB1,GCLC,COMMD1,UFL1,TMTC3,BTRC,GSK3B,ZFAND2A,PSMC6,HECTD1,OPHN1,PIAS1,ARIH1,CSNK1A1,USP14,SMAD7,UBE2V2	pink	VSMC_M5
GO:1901800	0.00	1.00	13	104	positive regulation of proteasomal protein catabolic process	BP	0.14257	MAPK9,ANKIB1,GCLC,TMTC3,GSK3B,ZFAND2A,PSMC6,HECTD1,PIAS1,ARIH1,CSNK1A1,SMAD7,UBE2V2	pink	VSMC_M5

GO:1903052	0.00	1.00	14	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	0.15291	MAPK9,ANKIB1,GCLC,TMTC3,GSK3B,ZFAND2A,PSMC6,HECTD1,PIAS1,ARIH1,CSNK1A1,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0018193	0.00	1.00	69	997	peptidyl-amino acid modification	BP	0.15291	PPIL4,LATS1,MAPK9,CSNK1G3,VEGFA,FBXO11,RLF,DPY19L1,ADAM17,PPIL6,SRPK2,NCOA1,EPC1,PRDM5,KMT2C,EPC2,KAT6A,ZDHHC17,GOLGA7,KITLG,MAPK8,IL6ST,CSNK2A1,MSL2,PPWD1,KDM3A,DIP2B,DPH6,TET3,TSG101,HIPK1,ATP2B4,DOCK3,CAB39,TET2,KMT5B,GSK3B,PIK3CA,MSL3,STK39,EGLN1,TLK1,ABI2,RPS6KA3,CREBL2,ATF2,KANSL1,FKBP3,ATM,KDM6A,ERO1A,JADE3,PRKCI,KAT6B,WNK1,FUT8,ASH1L,ATRX,ATP7A,PIAS1,GGNBP2,SMG1,ESCO1,CSNK1A1,PRKAA1,SMAD7,PKN2,AC118549.1,ZDHHC22	pink	VSMC_M5
GO:0000209	0.00	1.00	21	203	protein polyubiquitination	BP	0.19204	UBR5,UBE2H,ANKIB1,CUL1,TNKS2,ANAPC10,WWP1,BTRC,TRIP12,HECTD1,UBE2E3,UBE2L5,HUWE1,FBXW11,ARIH1,UBE2A,XIAP,BIRC2,UBE2D3,UBE2V2,UBE2D2	pink	VSMC_M5
GO:0032434	0.00	1.00	14	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	0.20263	MAPK9,ANKIB1,GCLC,COMMD1,UFL1,GSK3B,ZFAND2A,HECTD1,PIAS1,ARIH1,CSNK1A1,USP14,SMAD7,UBE2V2	pink	VSMC_M5
GO:0018105	0.00	1.00	25	249	peptidyl-serine phosphorylation	BP	0.20263	LATS1,MAPK9,CSNK1G3,VEGFA,SRPK2,MAPK8,CSNK2A1,HIPK1,ATP2B4,CAB39,GSK3B,PIK3CA,STK39,TLK1,RPS6KA3,CREBL2,ATM,PRKCI,WNK1,GGNBP2,SMG1,CSNK1A1,PRKAA1,SMAD7,PKN2	pink	VSMC_M5
GO:0032436	0.00	1.00	11	83	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	0.20263	MAPK9,ANKIB1,GCLC,GSK3B,ZFAND2A,HECTD1,PIAS1,ARIH1,CSNK1A1,SMAD7,UBE2V2	pink	VSMC_M5
GO:2000060	0.00	1.00	12	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	0.20852	MAPK9,ANKIB1,GCLC,GSK3B,ZFAND2A,HECTD1,PIAS1,ARIH1,CSNK1A1,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:1903362	0.00	1.00	21	222	regulation of cellular protein catabolic process	BP	0.24963	LATS1,MAPK9,ANKIB1,GCLC,COMMD1,UFL1,TMTC3,CSNK2A1,BTRC,GSK3B,ZFAND2A,PSMC6,HECTD1,OPHN1,PIAS1,ARIH1,CSNK1A1,USP14,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0009060	0.00	1.00	14	161	aerobic respiration	BP	0.35451	MDH1,AFG1L,NIPSNAP2,NDUFS4,C2orf69,GHITM,ATP7A,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5,ATP5PF	pink	VSMC_M5
GO:0033522	0.00	1.00	6	26	histone H2A ubiquitination	BP	0.35451	UBR5,UBR2,PCGF1,TRIP12,RNF2,UBE2A	pink	VSMC_M5
GO:0070936	0.00	1.00	9	58	protein K48-linked ubiquitination	BP	0.35451	UBR5,UBE2H,CUL1,BTRC,UBE2E3,UBE2A,BIRC2,UBE2D3,UBE2D2	pink	VSMC_M5
GO:0042773	0.00	1.00	9	83	ATP synthesis coupled electron transport	BP	0.35451	AFG1L,NDUFS4,GHITM,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5	pink	VSMC_M5
GO:0042775	0.00	1.00	9	83	mitochondrial ATP synthesis coupled electron transport	BP	0.35451	AFG1L,NDUFS4,GHITM,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5	pink	VSMC_M5
GO:0018209	0.00	1.00	25	267	peptidyl-serine modification	BP	0.37714	LATS1,MAPK9,CSNK1G3,VEGFA,SRPK2,MAPK8,CSNK2A1,HIPK1,ATP2B4,CAB39,GSK3B,PIK3CA,STK39,TLK1,RPS6KA3,CREBL2,ATM,PRKCI,WNK1,GGNBP2,SMG1,CSNK1A1,PRKAA1,SMAD7,PKN2	pink	VSMC_M5
GO:0006367	0.00	1.00	9	65	transcription initiation from RNA polymerase II promoter	BP	0.39816	MED23,TBP,POLR2D,MED4,PSMC6,ATF7IP,GTF2A2,GTF2A1,MED13	pink	VSMC_M5
GO:0006281	0.00	1.00	35	455	DNA repair	BP	0.40342	UBR5,INIP,COMMD1,UFL1,MRE11,DCLRE1C,EMSY,EPC2,ENDOV,VCPIP1,GTF2H1,ARID2,POLK,BTG2,TRIP12,KMT5B,DCLRE1A,GTF2I,TFIP11,KDM2A,KLHL15,ATM,RPAIN,PDS5A,HUWE1,USP3,MLH3,ATRX,SMG1,UBE2A,NIPBL,RAD1,SETX,UBE2D3,UBE2V2	pink	VSMC_M5
GO:0016226	0.00	1.00	5	23	iron-sulfur cluster assembly	BP	0.46926	NFU1,XDH,NFS1,GLRX3,ABCB7	pink	VSMC_M5
GO:0031163	0.00	1.00	5	23	metallo-sulfur cluster assembly	BP	0.46926	NFU1,XDH,NFS1,GLRX3,ABCB7	pink	VSMC_M5
GO:1903364	0.00	1.00	14	137	positive regulation of cellular protein catabolic process	BP	0.49642	MAPK9,ANKIB1,GCLC,TMTC3,GSK3B,ZFAND2A,PSMC6,HECTD1,PIAS1,ARIH1,CSNK1A1,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0019646	0.00	1.00	8	75	aerobic electron transport chain	BP	0.62449	AFG1L,NDUFS4,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5	pink	VSMC_M5
GO:0030902	0.00	1.00	14	116	hindbrain development	BP	0.62511	NCOA1,ATRN,DLC1,SMAD1,ARL13B,PSMG1,ATF2,CRKL,OPHN1,HERC1,ATP7A,MT-CO1,MT-ND4,MTPN	pink	VSMC_M5
GO:0031146	0.00	1.00	7	44	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	BP	0.62511	CUL1,FBXL4,CUL2,FBXL3,BTRC,CUL5,FBXW11	pink	VSMC_M5
GO:0038066	0.00	1.00	7	44	p38MAPK cascade	BP	0.62778	VEGFA,XDH,PJA2,CYLD,STK39,ATF2,BMP2	pink	VSMC_M5
GO:0031323	0.00	1.00	233	4391	regulation of cellular metabolic process	BP	0.65468	TAB2,PPIL4,MED23,LATS1,MAPK9,SCAF8,UBR5,DDX17,MKLN1,ELAVL2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,SDHAF3,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,RAB1A,TIA1,ADAM17,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,MED4,MAP3K2,CNOT10,RHEB,KMT2C,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,BIRC6,EAF1,ZNF605,IRS2,TMTC3,KITLG,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DIP2B,BTBD10,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,LXN,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,TWF1,CYLD,BBX,BTRC,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,CAB39,ZMYND8,MEF2A,PPP6R3,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,DCUN1D1,TFIP11,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,TIAL1,PSMC6,ALS2,GABPB2,METTL5,ZNF148,SCFD1,HECTD1,DLX2,JMJD1C,ATF7IP,RPS6KA3,PAFAH1B2,CREBL2,SMG7,ATF2,KLHL15,STYXL1,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,TIMP1,CRKL,KAT6B,ZNF518B,POGK,WNK1,GHITM,PYGO1,PDS5A,WAPL,RFX7,HUWE1,GTF2A2,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ABCB7,SPTLC2,ATRX,ATP7A,PIAS1,SMAD2,MED13,ARIH1,GSKIP,CCNK,GGNBP2,SMG1,ESCO1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,PTBP2,NFAT5,USP33,MT-CO2,BIRC2,AGO3,UBE2D3,USP9X,UBE2V2,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,HNRNPLL,NAF1,BRM	pink	VSMC_M5

GO:0031324	0.00	1.00	111	1896	negative regulation of cellular metabolic process	BP	0.71386	TAB2,LATS1,SCAF8,UBR5,C9orf72,VEGFA,RUNX2,GCLC,TIA1,UFL1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,ZEB2,XDH,KAT6A,BIRC6,IRS2,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,KDM3A,URI1,EIF4G2,CGGBP1,PCGF1,GABPA,WWP1,LXN,TSG101,BTG2,ATP2B4,BTRC,ID4,NOTCH2,TRIP12,ZMYND8,MEF2A,ACACB,GSK3B,PUM1,PIK3CA,BPTF,FXR1,TFIP11,KDM2A,ZNF148,SCFD1,DLX2,ATF7IP,RPS6KA3,ATF2,KLHL15,STYXL1,RNF2,ATM,COPS2,YWHAQ,TIMP1,CRKL,KAT6B,WNK1,PDS5A,WAPL,OPHN1,CPEB4,UBE2Z,FBXW11,USP3,HERC1,ABCB7,ATRX,PIAS1,SMAD2,GSKIP,GGNBP2,SMG1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,SMAD7,PTBP2,BIRC2,AGO3,UBE2D3,USP9X,PEG3,RBAK,NAF1,BRMS1L,RNF139,SPINK8,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0018205	0.00	1.00	26	313	peptidyl-lysine modification	BP	0.71386	RLF,NCOA1,EPC1,PRDM5,KMT2C,EPC2,KAT6A,MSL2,KDM3A,DIP2B,TET3,TET2,KMT5B,MSL3,ATF2,KANSL1,KDM6A,JADE3,KAT6B,ASH1L,ATRX,ATP7A,PIAS1,ESCO1,PRKAA1,AC118549.1	pink	VSMC_M5
GO:0042176	0.00	1.00	27	342	regulation of protein catabolic process	BP	0.76308	LATS1,MAPK9,ANKIB1,GCLC,COMMD1,UFL1,TMTC3,CSNK2A1,WWP1,TIPARP,BTRC,GSK3B,ZFAND2A,PSMC6,HECTD1,USP8,TIMP1,HUWE1,OPHN1,PIAS1,ARIH1,CSNK1A1,USP14,SMAD7,UBE2V2,RNF139,UBXN2A	pink	VSMC_M5
GO:0016574	0.00	1.00	7	44	histone ubiquitination	BP	0.77632	UBR5,UBR2,PCGF1,TRIP12,RNF2,HUWE1,UBE2A	pink	VSMC_M5
GO:0015980	0.00	1.00	20	259	energy derivation by oxidation of organic compounds	BP	0.77632	MDH1,AFG1L,IRS2,RB1CC1,IL6ST,PPP1CC,NIPSNAP2,NDUFS4,C2orf69,GSK3B,PIK3CA,GHITM,ATP7A,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5,ATP5PF	pink	VSMC_M5
GO:0051346	0.00	1.00	20	242	negative regulation of hydrolase activity	BP	0.81571	ANXA1,VEGFA,BIRC6,CSNK2A1,ARFGEF1,URI1,LXN,BICD1,GSK3B,EGLN1,RPS6KA3,STYXL1,TIMP1,WNK1,UBE2Z,TTC8,USP14,XIAP,BIRC2,SPINK8	pink	VSMC_M5
GO:0045333	0.00	1.00	15	191	cellular respiration	BP	0.85811	MDH1,AFG1L,NIPSNAP2,NDUFS4,C2orf69,PIK3CA,GHITM,ATP7A,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5,ATP5PF	pink	VSMC_M5
GO:0045732	0.00	1.00	18	203	positive regulation of protein catabolic process	BP	0.85811	MAPK9,ANKIB1,GCLC,TMTC3,CSNK2A1,WWP1,TIPARP,GSK3B,ZFAND2A,PSMC6,HECTD1,HUWE1,PIAS1,ARIH1,CSNK1A1,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:1900745	0.00	1.00	5	26	positive regulation of p38MAPK cascade	BP	0.85811	VEGFA,XDH,PJA2,STK39,BMP2	pink	VSMC_M5
GO:0001101	0.00	1.00	12	107	response to acid chemical	BP	0.85811	UBR2,VEGFA,ASNS,GCLC,UFL1,ATP2B4,PIK3CA,UBR1,ATF2,CPEB4,ATP7A,PIK3C3	pink	VSMC_M5
GO:0051171	0.01	1.00	216	4082	regulation of nitrogen compound metabolic process	BP	0.94861	TAB2,PPIL4,MED23,LATS1,MAPK9,SCAF8,UBR5,DDX17,ELAVL2,C9orf72,WASL,GUF1,VEGFA,ANKIB1,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,RAB1A,TIA1,ADAM17,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,MED4,MAP3K2,CNOT10,KMT2C,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,BIRC6,EAF1,ZNF605,TMTC3,KITLG,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DIP2B,DPH6,PCGF1,GABPA,TET3,WWP1,TIPARP,MLF1,LXN,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,TWF1,CYLD,RANBP9,BBX,BTRC,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,CAB39,ZMYND8,MEF2A,PPP6R3,TET2,KMT5B,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,DCUN1D1,TFIP11,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,TIAL1,PSMC6,ALS2,GABPB2,METTL5,ZNF148,HECTD1,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,KLHL15,STYXL1,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,USP8,TIMP1,CRKL,KAT6B,ZNF518B,POGK,WNK1,PYGO1,RFX7,HUWE1,GTF2A2,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,ABCB7,ATRX,PIAS1,SMAD2,MED13,ARIH1,GSKIP,CCNK,GGNBP2,SMG1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,PTBP2,NFAT5,MT-CO2,BIRC2,AGO3,UBE2D3,USP9X,UBE2V2,MTPN,PEG3,EIF5A2,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,RNF139,DDAH1,SPINK8,PAIP2,UBXN2A,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:1900744	0.01	1.00	6	37	regulation of p38MAPK cascade	BP	0.94861	VEGFA,XDH,PJA2,CYLD,STK39,BMP2	pink	VSMC_M5
GO:0051123	0.01	1.00	4	19	RNA polymerase II preinitiation complex assembly	BP	0.97428	TBP,PSMC6,ATF7IP,GTF2A2	pink	VSMC_M5
GO:0030162	0.01	1.00	36	538	regulation of proteolysis	BP	1	LATS1,MAPK9,VEGFA,ANKIB1,GCLC,COMMD1,UFL1,XDH,BIRC6,TMTC3,APAF1,DLC1,CSNK2A1,LXN,BTRC,GSK3B,ZFAND2A,FAM162A,PARL,PSMC6,HECTD1,RPS6KA3,TIMP1,OPHN1,UBE2Z,FBXW11,PIAS1,ARIH1,CSNK1A1,USP14,XIAP,SMAD7,BIRC2,UBE2V2,RNF139,SPINK8	pink	VSMC_M5
GO:0071363	0.01	1.00	41	545	cellular response to growth factor stimulus	BP	1	LATS1,ANXA1,VEGFA,RUNX2,GCLC,ADAM17,RAB14,ZFYVE9,JCAD,MAGI2,EPB41L5,FNTA,ZEB2,FLRT3,XDH,ZDHHC17,LTBP1,SPRY4,NR3C1,APAF1,URI1,SMAD1,CPNE3,ATP2B4,NOTCH2,SHOC2,FSTL1,PIK3CA,BPTF,ACAP2,USP8,CRKL,FUT8,ATP7A,SMAD2,XIAP,SMAD7,SETX,UBE2D3,USP9X,BMP2	pink	VSMC_M5
GO:0018208	0.01	1.00	6	48	peptidyl-proline modification	BP	1	PPIL4,PPIL6,PPWD1,EGLN1,FKBP3,ERO1A	pink	VSMC_M5
GO:0043543	0.01	1.00	18	202	protein acylation	BP	1	NCOA1,EPC1,EPC2,KAT6A,ZDHHC17,GOLGA7,MSL2,DIP2B,GSK3B,MSL3,ATF2,KANSL1,JADE3,KAT6B,ESCO1,PRKAA1,AC118549.1,ZDHHC22	pink	VSMC_M5
GO:0016233	0.01	1.00	6	37	telomere capping	BP	1	MRE11,DCLRE1C,TNKS2,DCLRE1A,TFIP11,ATM	pink	VSMC_M5

GO:0033554	0.01	0.99	90	1561	cellular response to stress	BP	1	MAPK9,UBR5,KLHDC10,ANXA1,TMEM33,VEGFA,ASNS,ERLEC1,INIP,COMMD1,UFL1,MRE11,POLR2D,DCLRE1C,EMSY,EPC2,XDH,KAT6A,NGLY1,ENDOV,TMTC3,MAP4K3,MAPK8,RB1CC1,VCPIP1,PJA2,SGTB,RNF13,GTF2H1,HIPK1,ARID2,POLK,BTG2,IRAK4,CYLD,TRIP12,ANO1,CAB39,KMT5B,GSK3B,DCLRE1A,PIK3CA,GTF2I,FXR1,TFIP11,STK39,EGLN1,KDM2A,FAM162A,PSMC6,TLK1,PLEKHA1,MORC2,RPS6KA3,ATF2,KLHL15,LANCL1,ATM,ERO1A,HP1BP3,CRKL,RPAIN,PDS5A,FUT8,HUWE1,CPEB4,USP3,MLH3,ATRX,ATP7A,FEM1B,PIK3C3,GSKIP,CCNK,SMG1,USP14,UBE2A,XIAP,PRKAA1,NIPBL,RAD1,SETX,USP33,UBE2D3,RNF103,UBE2V2,RNF139,DDAH1,BMT2,BMP2	pink	VSMC_M5
GO:0007062	0.01	1.00	7	47	sister chromatid cohesion	BP	1	MRE11,PDS5A,WAPL,ATRX,ESCO1,STAG2,NIPBL	pink	VSMC_M5
GO:0006513	0.01	1.00	8	61	protein monoubiquitination	BP	1	CUL1,PCGF1,TSG101,RNF2,HUWE1,BIRC2,UBE2D3,RNF219	pink	VSMC_M5
GO:0045104	0.01	1.00	6	30	intermediate filament cytoskeleton organization	BP	1	DST,MACF1,VPS54,ERBIN,ATF2,CSNK1A1	pink	VSMC_M5
GO:0019068	0.01	1.00	5	31	virion assembly	BP	1	VTA1,RAB1A,PDCD6IP,VPS37A,TSG101	pink	VSMC_M5
GO:0071108	0.01	1.00	6	31	protein K48-linked deubiquitination	BP	1	USP34,VCPIP1,USP8,USP33,MINDY3,USP9X	pink	VSMC_M5
GO:0022904	0.01	1.00	9	99	respiratory electron transport chain	BP	1	AFG1L,NDUFS4,GHITM,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5	pink	VSMC_M5
GO:0071539	0.01	1.00	6	31	protein localization to centrosome	BP	1	NEDD1,PCM1,BICD1,GSK3B,GOLGB1,CCDC14	pink	VSMC_M5
GO:0045103	0.01	1.00	6	31	intermediate filament-based process	BP	1	DST,MACF1,VPS54,ERBIN,ATF2,CSNK1A1	pink	VSMC_M5
GO:0071276	0.01	1.00	4	21	cellular response to cadmium ion	BP	1	MAPK9,MAPK8,ATP7A,UBE2D3	pink	VSMC_M5
GO:0043967	0.01	1.00	8	58	histone H4 acetylation	BP	1	NCOA1,EPC1,MSL2,MSL3,ATF2,KANSL1,JADE3,AC118549.1	pink	VSMC_M5
GO:0007049	0.01	0.99	83	1405	cell cycle	BP	1	LATS1,UBR2,WASL,ANXA1,CD2AP,ASNS,PTP4A1,SEPT7,ADAM17,CUL1,CUL2,SRPK2,MRE11,PRDM5,MAGI2,PDCD6IP,CLASP1,RHEB,FBXL3,ARL8B,TOP2B,BIRC6,NR3C1,NEDD1,UBA3,RB1CC1,CSNK2A1,PCM1,VCPIP1,LSM14A,CDK5RAP1,ANAPC10,EIF4G2,PPP1CC,MLF1,GTF2H1,TSG101,POC5,BTG2,ATP2B4,CEP97,CYLD,BTRC,NOTCH2,TET2,DCLRE1A,PUM1,ZBED9,TTC28,TLK1,RPS6KA3,CREBL2,SKA1,ATF2,RNF2,DYNLT3,ATM,CUL5,USP8,PDS5A,WAPL,FBXW11,USP3,MLH3,ATRX,PIAS1,FEM1B,PIK3C3,CCNK,DYNC1H1,ESCO1,CSNK1A1,RAB11FIP4,XIAP,STAG2,NIPBL,RAD1,PKN2,USP33,BIRC2,USP9X,BMP2,RMDN1	pink	VSMC_M5
GO:0046755	0.01	1.00	4	22	viral budding	BP	1	VTA1,PDCD6IP,VPS37A,TSG101	pink	VSMC_M5
GO:0060322	0.01	0.99	46	624	head development	BP	1	NCOA1,FLRT3,TOP2B,IRS2,ATRN,APAF1,DLC1,PCM1,CDK5RAP1,SMAD1,TCTN1,TIPARP,ARL13B,TBC1D23,PPP3CC,BTG2,ATP2B4,PSMG1,NDUFS4,GSK3B,BPTF,CCDC14,PLEKHA1,ZNF148,DLX2,PAFAH1B2,ATF2,YWHAQ,CRKL,OPHN1,FBXW11,HERC1,ATRX,ATP7A,TTC8,NF1,NIPBL,RAD1,HPRT1,STXBP3,MT-CO1,MT-ND4,ATP5PF,RAB18,MTPN,BMP2	pink	VSMC_M5
GO:0018394	0.01	1.00	14	143	peptidyl-lysine acetylation	BP	1	NCOA1,EPC1,EPC2,KAT6A,MSL2,DIP2B,MSL3,ATF2,KANSL1,JADE3,KAT6B,ESCO1,PRKAA1,AC118549.1	pink	VSMC_M5
GO:0022037	0.01	1.00	10	84	metencephalon development	BP	1	NCOA1,ATRN,ATF2,CRKL,OPHN1,HERC1,ATP7A,MT-CO1,MT-ND4,MTPN	pink	VSMC_M5
GO:0080090	0.01	0.99	219	4206	regulation of primary metabolic process	BP	1	TAB2,PPIL4,MED23,LATS1,MAPK9,SCAF8,UBR5,DDX17,ELAVL2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,SDHAF3,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,RAB1A,TIA1,ADAM17,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,MED4,MAP3K2,CNOT10,KMT2C,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,BIRC6,EAF1,ZNF605,IRS2,TMTC3,KITLG,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DIP2B,DPH6,PCGF1,GABPA,TET3,WWP1,TIPARP,MLF1,LXN,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,TWF1,CYLD,RANBP9,BBX,BTRC,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,DCUN1D1,TFIP11,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,TIAL1,PSMC6,ALS2,GABPB2,METTL5,ZNF148,HECTD1,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,KLHL15,STYXL1,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,USP8,TIMP1,CRKL,KAT6B,ZNF518B,POGK,WNK1,PYGO1,RFX7,HUWE1,GTF2A2,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,ARIH1,GSKIP,CCNK,GGNBP2,SMG1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,PTBP2,NFAT5,MT-CO2,BIRC2,AGO3,UBE2D3,USP9X,UBE2V2,MTPN,PEG3,EIF5A2,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,RNF139,SPINK8,PAIP2,UBXN2A,BMP2,ZNF619,ZBTB...	pink	VSMC_M5
GO:0006259	0.01	0.99	47	741	DNA metabolic process	BP	1	UBR5,UBR2,RLF,INIP,COMMD1,UFL1,SRPK2,MRE11,DCLRE1C,EMSY,EPC2,ENDOV,TOP2B,TNKS2,VCPIP1,TET3,GTF2H1,ARID2,POLK,BTG2,TRIP12,TET2,KMT5B,DCLRE1A,PIK3CA,GTF2I,ZBED9,TFIP11,KDM2A,ATF7IP,KLHL15,ATM,RPAIN,PDS5A,HUWE1,USP3,MLH3,ATRX,SMG1,UBE2A,NIPBL,RAD1,SETX,UBE2D3,USP9X,UBE2V2,NAF1	pink	VSMC_M5
GO:1905508	0.01	1.00	6	33	protein localization to microtubule organizing center	BP	1	NEDD1,PCM1,BICD1,GSK3B,GOLGB1,CCDC14	pink	VSMC_M5

GO:0009892	0.01	0.99	125	2254	negative regulation of metabolic process	BP	1	TAB2,LATS1,SCAF8,UBR5,DDX17,C9orf72,ANXA1,VEGFA,RUNX2,CD2AP,GCLC,TIA1,ADAM17,UFL1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,RHEB,ZEB2,XDH,KAT6A,BIRC6,IRS2,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,KDM3A,ERBIN,URI1,SMAD1,EIF4G2,CGGBP1,PCGF1,GABPA,WWP1,TIPARP,LXN,TSG101,BTG2,ATP2B4,CSDE1,CYLD,BTRC,ID4,ACOT13,NOTCH2,TRIP12,ZMYND8,MEF2A,ACACB,GSK3B,PUM1,PIK3CA,BPTF,FXR1,TFIP11,KDM2A,TIAL1,ZNF148,SCFD1,MORC2,DLX2,ATF7IP,RPS6KA3,SMG7,ATF2,KLHL15,STYXL1,RNF2,ATM,COPS2,YWHAQ,TIMP1,CRKL,KAT6B,WNK1,PDS5A,WAPL,OPHN1,CPEB4,UBE2Z,FBXW11,USP3,HERC1,ABCB7,ATRX,PIAS1,SMAD2,GSKIP,GGNBP2,SMG1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,SMAD7,PTBP2,BIRC2,AGO3,UBE2D3,USP9X,PEG3,RBAK,NAF1,BRMS1L,RNF139,SPINK8,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0042752	0.01	1.00	10	89	regulation of circadian rhythm	BP	1	MAPK9,FBXL3,MAPK8,PPP1CC,BTRC,GSK3B,KDM2A,FBXW11,PRKAA1,USP9X	pink	VSMC_M5
GO:0021762	0.01	1.00	5	35	substantia nigra development	BP	1	CCDC14,ZNF148,YWHAQ,RAD1,ATP5PF	pink	VSMC_M5
GO:2000112	0.01	0.99	153	2822	regulation of cellular macromolecule biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,GUF1,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,TIA1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,IRS2,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,PDS5A,WAPL,RFX7,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CCNK,ESCO1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,PAIP2,BMP2,RNF219,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0048857	0.01	1.00	6	46	neural nucleus development	BP	1	CCDC14,ZNF148,ATF2,YWHAQ,RAD1,ATP5PF	pink	VSMC_M5
GO:0006120	0.01	1.00	5	46	mitochondrial electron transport, NADH to ubiquinone	BP	1	NDUFS4,MT-ND3,MT-ND4L,MT-ND4,MT-ND5	pink	VSMC_M5
GO:0007030	0.01	0.99	13	122	Golgi organization	BP	1	SYNE1,RAB1A,RAB33B,CLASP1,VCPIP1,ARFGEF1,GOLGA5,GOLGB1,ATL3,HUWE1,CSNK1A1,GOLPH3L,UBXN2A	pink	VSMC_M5
GO:0070848	0.01	0.99	41	570	response to growth factor	BP	1	LATS1,ANXA1,VEGFA,RUNX2,GCLC,ADAM17,RAB14,ZFYVE9,JCAD,MAGI2,EPB41L5,FNTA,ZEB2,FLRT3,XDH,ZDHHC17,LTBP1,SPRY4,NR3C1,APAF1,URI1,SMAD1,CPNE3,ATP2B4,NOTCH2,SHOC2,FSTL1,PIK3CA,BPTF,ACAP2,USP8,CRKL,FUT8,ATP7A,SMAD2,XIAP,SMAD7,SETX,UBE2D3,USP9X,BMP2	pink	VSMC_M5
GO:0016050	0.01	0.99	20	255	vesicle organization	BP	1	VTA1,WASL,ANXA1,CD2AP,RAB1A,RAB14,PDCD6IP,ZEB2,ARL8B,VPS37A,ZFYVE16,TSG101,LYST,ALS2,PRKCI,USP8,SNX11,PIK3C3,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0007420	0.01	0.99	43	587	brain development	BP	1	NCOA1,TOP2B,IRS2,ATRN,APAF1,DLC1,PCM1,CDK5RAP1,SMAD1,TCTN1,ARL13B,TBC1D23,PPP3CC,BTG2,ATP2B4,PSMG1,NDUFS4,GSK3B,BPTF,CCDC14,ZNF148,DLX2,PAFAH1B2,ATF2,YWHAQ,CRKL,OPHN1,FBXW11,HERC1,ATRX,ATP7A,TTC8,NF1,NIPBL,RAD1,HPRT1,STXBP3,MT-CO1,MT-ND4,ATP5PF,RAB18,MTPN,BMP2	pink	VSMC_M5
GO:0036258	0.01	1.00	4	25	multivesicular body assembly	BP	1	VTA1,PDCD6IP,VPS37A,TSG101	pink	VSMC_M5
GO:0031329	0.01	0.99	45	689	regulation of cellular catabolic process	BP	1	TAB2,LATS1,MAPK9,C9orf72,ANKIB1,GCLC,COMMD1,UFL1,POLR2D,RHEB,IRS2,TMTC3,MAPK8,CSNK2A1,YTHDF3,EIF4G2,BTG2,ATP2B4,BTRC,ACACB,GSK3B,PUM1,PIK3CA,FXR1,ZFAND2A,PSMC6,SCFD1,HECTD1,PAFAH1B2,ATM,TIMP1,OPHN1,HERC1,SPTLC2,PIAS1,ARIH1,SMG1,CSNK1A1,USP14,PRKAA1,SMAD7,USP33,UBE2V2,NAF1,RNF139	pink	VSMC_M5
GO:0031326	0.02	0.99	158	2955	regulation of cellular biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,ANXA1,GUF1,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,TIA1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,IRS2,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,PDS5A,WAPL,RFX7,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ABCB7,ATRX,ATP7A,PIAS1,SMAD2,MED13,CCNK,ESCO1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,AGO3,UBE2D3,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,DDAH1,PAIP2,BMP2,RNF219,ZNF619,ZBTB6,MXD1	pink	VSMC_M5

GO:0060255	0.02	0.99	230	4468	regulation of macromolecule metabolic process	BP	1	TAB2,PPIL4,MED23,LATS1,MAPK9,SCAF8,UBR5,DDX17,MKLN1,ELAVL2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CD2AP,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,RAB1A,TIA1,ADAM17,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,MED4,MAP3K2,CNOT10,EPB41L5,KMT2C,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,BIRC6,LTBP1,EAF1,ZNF605,IRS2,TMTC3,KITLG,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DIP2B,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,TIPARP,MLF1,LXN,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,TWF1,CYLD,RANBP9,BBX,BTRC,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,CAB39,ZMYND8,MEF2A,PPP6R3,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,DCUN1D1,TFIP11,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,TIAL1,PSMC6,ALS2,GABPB2,METTL5,ZNF148,MORC2,HECTD1,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,STYXL1,RNF2,NEMF,ATM,KDM6A,PRKCI,COPS2,YWHAQ,HP1BP3,USP8,TIMP1,CRKL,KAT6B,ZNF518B,POGK,WNK1,PYGO1,PDS5A,WAPL,RFX7,FUT8,HUWE1,GTF2A2,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,ATRX,ATP7A,PIAS1,SMAD2,MED13,ARIH1,GSKIP,CCNK,GGNBP2,SMG1,ESCO1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,PTBP2,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,UBE2V2,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,RNF139,SPINK8,PAIP2,UBX	pink	VSMC_M5
GO:1902914	0.02	1.00	4	23	regulation of protein polyubiquitination	BP	1	UBR5,TRIP12,XIAP,BIRC2	pink	VSMC_M5
GO:0010591	0.02	1.00	5	34	regulation of lamellipodium assembly	BP	1	TWF1,PIK3CA,ABI2,ARPC2,ATP7A	pink	VSMC_M5
GO:0045197	0.02	1.00	6	37	establishment or maintenance of epithelial cell apical/basal polarity	BP	1	PDCD6IP,FAT1,ERBIN,PRKCI,OPHN1,TTC8	pink	VSMC_M5
GO:0006479	0.02	0.99	14	148	protein methylation	BP	1	PCMT1,FBXO11,RLF,PRDM5,KMT2C,PCMTD1,KDM3A,TET3,BTG2,TET2,KMT5B,KDM6A,ASH1L,ATRX	pink	VSMC_M5
GO:0008213	0.02	0.99	14	148	protein alkylation	BP	1	PCMT1,FBXO11,RLF,PRDM5,KMT2C,PCMTD1,KDM3A,TET3,BTG2,TET2,KMT5B,KDM6A,ASH1L,ATRX	pink	VSMC_M5
GO:0006473	0.02	0.99	15	168	protein acetylation	BP	1	NCOA1,EPC1,EPC2,KAT6A,MSL2,DIP2B,GSK3B,MSL3,ATF2,KANSL1,JADE3,KAT6B,ESCO1,PRKAA1,AC118549.1	pink	VSMC_M5
GO:0021549	0.02	0.99	9	77	cerebellum development	BP	1	NCOA1,ATRN,CRKL,OPHN1,HERC1,ATP7A,MT-CO1,MT-ND4,MTPN	pink	VSMC_M5
GO:0010556	0.02	0.99	153	2846	regulation of macromolecule biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,GUF1,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,TIA1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,IRS2,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,PDS5A,WAPL,RFX7,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CCNK,ESCO1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,PAIP2,BMP2,RNF219,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0036257	0.02	1.00	4	26	multivesicular body organization	BP	1	VTA1,PDCD6IP,VPS37A,TSG101	pink	VSMC_M5
GO:0001701	0.02	0.99	24	314	in utero embryonic development	BP	1	LATS1,VEGFA,GCM1,NCOA1,EPB41L5,BIRC6,N4BP2L2,TCTN1,GABPA,NOTCH2,BPTF,ALS2,HECTD1,ATF2,COPS2,FUT8,ATP7A,SMAD2,GGNBP2,UBE2A,PHF6,MT-ND4,SMIM14,BMP2	pink	VSMC_M5
GO:0030177	0.02	0.99	12	124	positive regulation of Wnt signaling pathway	BP	1	CSNK1G3,UBR5,USP34,MACF1,ZEB2,CSNK2A1,TNKS2,USP8,WNK1,GSKIP,XIAP,BMP2	pink	VSMC_M5
GO:0019222	0.02	0.99	247	4858	regulation of metabolic process	BP	1	ME2,TAB2,PPIL4,MED23,LATS1,MAPK9,SCAF8,UBR5,DDX17,MKLN1,ELAVL2,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,CD2AP,SDHAF3,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,RAB1A,TIA1,ADAM17,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,MED4,MAP3K2,CNOT10,EPB41L5,RHEB,KMT2C,EMSY,FNTA,ZEB2,EPC2,XDH,KAT6A,BIRC6,LTBP1,EAF1,ZNF605,IRS2,TMTC3,KITLG,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DIP2B,BTBD10,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,TIPARP,MLF1,LXN,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,TWF1,CYLD,RANBP9,BBX,BTRC,NDUFS4,ID4,DOCK3,ACOT13,NOTCH2,TRIP12,CAB39,ZMYND8,MEF2A,PPP6R3,PRKAB2,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,DCUN1D1,TFIP11,EGLN1,ZFAND2A,KDM2A,FAM162A,PARL,TIAL1,PSMC6,ALS2,GABPB2,METTL5,ZNF148,SCFD1,MORC2,HECTD1,DLX2,JMJD1C,ATF7IP,RPS6KA3,PAFAH1B2,CREBL2,SMG7,ATF2,KLHL15,STYXL1,RNF2,NEMF,ATM,KDM6A,PRKCI,COPS2,YWHAQ,HP1BP3,USP8,TIMP1,CRKL,KAT6B,ZNF518B,POGK,WNK1,GHITM,PYGO1,PDS5A,WAPL,RFX7,FUT8,HUWE1,GTF2A2,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ABCB7,SPTLC2,ATRX,ATP7A,PIAS1,SMAD2,MED13,ARIH1,GSKIP,CCNK,GGNBP2,DYNC1H1,SMG1,ESCO1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,PTBP2,NFAT5,USP33,MT-	pink	VSMC_M5

GO:0006417	0.02	0.99	24	341	regulation of translation	BP	1	GUF1,TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,EIF4G2,DPH6,BTG2,CSDE1,PUM1,FXR1,METTL5,RPS6KA3,NEMF,CPEB4,AGO3,MTPN,EIF5A2,RNF139,PAIP2	pink	VSMC_M5
GO:2000142	0.02	1.00	5	32	regulation of DNA-templated transcription, initiation	BP	1	MED4,PSMC6,ATF7IP,MED13,SETX	pink	VSMC_M5
GO:0006303	0.02	0.99	7	59	double-strand break repair via nonhomologous end joining	BP	1	MRE11,DCLRE1C,KMT5B,DCLRE1A,TFIP11,KDM2A,ATM	pink	VSMC_M5
GO:0006352	0.02	0.99	10	105	DNA-templated transcription, initiation	BP	1	MED23,TBP,POLR2D,MED4,PSMC6,ATF7IP,GTF2A2,GTF2A1,MED13,SETX	pink	VSMC_M5
GO:0008543	0.02	0.99	7	59	fibroblast growth factor receptor signaling pathway	BP	1	RUNX2,RAB14,FLRT3,SPRY4,SHOC2,CRKL,SETX	pink	VSMC_M5
GO:0021533	0.02	1.00	4	17	cell differentiation in hindbrain	BP	1	OPHN1,HERC1,ATP7A,MTPN	pink	VSMC_M5
GO:0010592	0.02	1.00	4	23	positive regulation of lamellipodium assembly	BP	1	PIK3CA,ABI2,ARPC2,ATP7A	pink	VSMC_M5
GO:0051172	0.02	0.99	99	1770	negative regulation of nitrogen compound metabolic process	BP	1	LATS1,SCAF8,UBR5,C9orf72,VEGFA,RUNX2,GCLC,TIA1,UFL1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,ZEB2,XDH,KAT6A,BIRC6,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,KDM3A,URI1,CGGBP1,PCGF1,GABPA,WWP1,LXN,TSG101,BTG2,ATP2B4,BTRC,ID4,NOTCH2,TRIP12,ZMYND8,MEF2A,GSK3B,PUM1,BPTF,FXR1,TFIP11,KDM2A,ZNF148,DLX2,ATF7IP,RPS6KA3,ATF2,KLHL15,STYXL1,RNF2,ATM,COPS2,YWHAQ,TIMP1,CRKL,KAT6B,OPHN1,CPEB4,UBE2Z,FBXW11,USP3,ATRX,PIAS1,SMAD2,GSKIP,GGNBP2,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,SMAD7,PTBP2,BIRC2,AGO3,UBE2D3,USP9X,PEG3,RBAK,NAF1,BRM S1L,RNF139,SPINK8,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0032268	0.02	0.99	100	1819	regulation of cellular protein metabolic process	BP	1	TAB2,PPIL4,LATS1,MAPK9,UBR5,C9orf72,GUF1,VEGFA,ANKIB1,GCLC,COMMD1,TIA1,ADAM17,UFL1,MRE11,POLR2D,MAGI2,CNOT10,FNTA,XDH,BIRC6,TMTC3,KITLG,SPRY4,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,ARFGEF1,KDM3A,PTCD3,EIF4G2,DIP2B,DPH6,LXN,GTF2H1,TSG101,BTG2,ATP2B4,CSDE1,TWF1,BTRC,NDUFS4,DOCK3,TRIP12,CAB39,PPP6R3,GSK3B,PUM1,PIK3CA,FXR1,DCUN1D1,ZFAND2A,FAM162A,PSMC6,ALS2,METTL5,HECTD1,RPS6KA3,CREBL2,ATF2,STYXL1,NEMF,TIMP1,CRKL,WNK1,HUWE1,OPHN1,CPEB4,UBE2Z,FBXW11,ATRX,PIAS1,ARIH1,GSKIP,CCNK,GGNBP2,CSNK1A1,USP14,XIAP,NF1,PRKAA1,NIPBL,SMAD7,BIRC2,AGO3,UBE2V2,MTPN,EIF5A2,RNF139,SPINK8,PAIP2,UBXN2A,BMP2	pink	VSMC_M5
GO:0006517	0.02	1.00	4	24	protein deglycosylation	BP	1	NGLY1,OGA,RNF103,RNF139	pink	VSMC_M5
GO:1902110	0.02	1.00	4	29	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	GCLC,MAPK8,GSK3B,ATF2	pink	VSMC_M5
GO:0051246	0.02	0.98	106	1953	regulation of protein metabolic process	BP	1	TAB2,PPIL4,LATS1,MAPK9,UBR5,C9orf72,GUF1,VEGFA,ANKIB1,GCLC,COMMD1,RAB1A,TIA1,ADAM17,UFL1,MRE11,POLR2D,MAGI2,CNOT10,FNTA,XDH,BIRC6,TMTC3,KITLG,SPRY4,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,ARFGEF1,KDM3A,PTCD3,EIF4G2,DIP2B,DPH6,WWP1,TIPARP,LXN,GTF2H1,TSG101,BTG2,ATP2B4,CSDE1,TWF1,RANBP9,BTRC,NDUFS4,DOCK3,TRIP12,CAB39,PPP6R3,GSK3B,PUM1,PIK3CA,FXR1,DCUN1D1,ZFAND2A,FAM162A,PARL,PSMC6,ALS2,METTL5,HECTD1,RPS6KA3,CREBL2,ATF2,STYXL1,NEMF,USP8,TIMP1,CRKL,WNK1,HUWE1,OPHN1,CPEB4,UBE2Z,FBXW11,ATRX,PIAS1,ARIH1,GSKIP,CCNK,GGNBP2,CSNK1A1,USP14,XIAP,NF1,PRKAA1,NIPBL,SMAD7,BIRC2,AGO3,UBE2V2,MTPN,EIF5A2,RNF139,SPINK8,PAIP2,UBXN2A,BMP2	pink	VSMC_M5
GO:0006612	0.02	0.99	9	97	protein targeting to membrane	BP	1	SRP72,GOLGA7,VPS37A,SGTB,SSR1,SRP54,PRKCI,CHM,ZDHHC22	pink	VSMC_M5
GO:0006996	0.02	0.98	160	2943	organelle organization	BP	1	ARFGEF3,VTA1,LATS1,MAPK9,SYNE1,LRGUK,MKLN1,VPS13A,UBR2,C9orf72,WASL,ANXA1,TMEM33,CD2AP,SDHAF3,GCLC,DST,RHOQ,LCA5,MACF1,VPS54,RAB1A,SEPT7,CAPZA2,UFL1,ZMYM4,RAB14,RAB33B,AFG1L,SCLT1,BBS12,SRPK2,MRE11,YME1L1,AKAP11,DCLRE1C,PDCD6IP,CLASP1,EPB41L5,EMSY,ZEB2,ARL8B,KAT6A,TOP2B,NR3C1,MAPK8,DLC1,RB1CC1,VPS37A,PCM1,YTHDF3,FAT1,TNKS2,VCPIP1,LSM14A,ARFGEF1,KDM3A,ERBIN,RHOBTB3,GFM2,TCTN1,ZFYVE16,ARL13B,FAM92A,ARSB,TSG101,ARID2,BAZ2B,CEP97,CSDE1,TWF1,CYLD,RANBP9,NIPSNAP2,TSPAN32,NDUFS4,NOTCH2,BICD1,ZMYND8,MEF2A,GOLGA5,GSK3B,DCLRE1A,PIK3CA,LYST,DNAAF5,BPTF,GOLGB1,TFIP11,FAM162A,PARL,ALS2,TLK1,SCFD1,ABI2,MORC2,ATF7IP,SKA1,ATF2,MTX2,STYXL1,ATM,KDM6A,ARPC2,PRKCI,HP1BP3,ATL3,USP8,KAT6B,ZNF518B,GHITM,PYGO1,CCSER2,PDS5A,WAPL,HUWE1,OPHN1,SNX11,FBXW11,MLH3,ATRX,ATP7A,SPATA7,NAP1L3,TTC8,DIAPH2,KATNAL2,PSTPIP2,PIK3C3,DYNC1H1,SMG1,ESCO1,CSNK1A1,WDR78,STAG2,NF1,PRKAA1,CPLANE1,NIPBL,BCORL1,RAD1,SETX,GAN,USP33,MT-ND4,MT-ND5,UBE2D3,TMEM38B,FAM206A,GMFB,RAB18,MTPN,NAF1,SLC25A36,GOLPH3L,TIMM9,UBXN2A,RMDN1,SAR1B,DENR	pink	VSMC_M5
GO:0046326	0.02	1.00	5	31	positive regulation of glucose import	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI	pink	VSMC_M5
GO:0006605	0.02	0.99	19	262	protein targeting	BP	1	VPS13A,SRP72,GOLGA7,VPS37A,SGTB,ERBIN,ZFYVE16,SSR1,ZFAND2A,PARL,SRP54,PRKCI,YWHAQ,HUWE1,CHM,PRKAA1,UBE2D3,TIMM9,ZDHHC22	pink	VSMC_M5
GO:0070423	0.02	1.00	4	22	nucleotide-binding oligomerization domain containing signaling pathway	BP	1	ERBIN,CYLD,XIAP,BIRC2	pink	VSMC_M5

GO:0009889	0.02	0.98	159	3010	regulation of biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,ANXA1,GUF1,VEGFA,RUNX2,SDHAF3,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,TIA1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,IRS2,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,PDS5A,WAPL,RFX7,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ABCB7,ATRX,ATP7A,PIAS1,SMAD2,MED13,CCNK,ESCO1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,AGO3,UBE2D3,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,DDAH1,PAIP2,BMP2,RNF219,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0070534	0.02	0.99	6	50	protein K63-linked ubiquitination	BP	1	UBR5,TRIP12,HECTD1,UBE2E3,BIRC2,UBE2V2	pink	VSMC_M5
GO:1901522	0.02	1.00	4	21	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	BP	1	VEGFA,RUNX2,SMAD1,BMP2	pink	VSMC_M5
GO:0046854	0.02	0.99	7	54	phosphatidylinositol phosphate biosynthetic process	BP	1	EFR3A,FAM126A,IMPAD1,PIK3CA,ATM,PIK3C3,SMG1	pink	VSMC_M5
GO:0046324	0.02	0.99	6	44	regulation of glucose import	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3	pink	VSMC_M5
GO:0032007	0.02	0.99	5	33	negative regulation of TOR signaling	BP	1	UBR2,UBR1,ATM,PRKAA1,BMT2	pink	VSMC_M5
GO:0009894	0.02	0.98	50	806	regulation of catabolic process	BP	1	TAB2,LATS1,MAPK9,C9orf72,ANKIB1,GCLC,COMMD1,UFL1,POLR2D,RHEB,IRS2,TMTC3,MAPK8,CSNK2A1,YTHDF3,EIF4G2,WWP1,TIPARP,BTG2,ATP2B4,BTRC,ACACB,GSK3B,PUM1,PIK3CA,FXR1,ZFAND2A,PSMC6,SCFD1,HECTD1,PAFAH1B2,ATM,USP8,TIMP1,HUWE1,OPHN1,HERC1,SPTLC2,PIAS1,ARIH1,SMG1,CSNK1A1,USP14,PRKAA1,SMAD7,USP33,UBE2V2,NAF1,RNF139,UBXN2A	pink	VSMC_M5
GO:0000413	0.02	1.00	4	32	protein peptidyl-prolyl isomerization	BP	1	PPIL4,PPIL6,PPWD1,FKBP3	pink	VSMC_M5
GO:0014013	0.02	0.99	8	73	regulation of gliogenesis	BP	1	UFL1,RHEB,IL6ST,PPP1CC,DLX2,PRKCI,NF1,BMP2	pink	VSMC_M5
GO:0035872	0.02	1.00	4	23	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	BP	1	ERBIN,CYLD,XIAP,BIRC2	pink	VSMC_M5
GO:2000113	0.03	0.98	67	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	SCAF8,VEGFA,RUNX2,GCLC,TIA1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,ZEB2,KAT6A,NR3C1,N4BP2L2,UBA3,CAPRIN1,YTHDF3,LSM14A,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,GSK3B,PUM1,BPTF,FXR1,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,PDS5A,WAPL,CPEB4,FBXW11,USP3,ATRX,PIAS1,SMAD2,NIPBL,PHF6,SMAD7,AGO3,UBE2D3,USP9X,PEG3,RBAK,BRMS1L,RNF139,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:1902686	0.03	1.00	4	31	mitochondrial outer membrane permeabilization involved in programmed cell death	BP	1	GCLC,MAPK8,GSK3B,ATF2	pink	VSMC_M5
GO:0044092	0.03	0.98	48	806	negative regulation of molecular function	BP	1	LATS1,C9orf72,ANXA1,VEGFA,TAX1BP1,COMMD1,UFL1,EPB41L5,BIRC6,IRS2,SPRY4,MAPK8,CSNK2A1,CDK5RAP1,ARFGEF1,ERBIN,URI1,LXN,TSG101,ATP2B4,CYLD,BTRC,BICD1,CAB39,ACACB,GSK3B,TFIP11,STK39,EGLN1,RPS6KA3,STYXL1,RNF2,TIMP1,WNK1,WAPL,UBE2Z,TTC8,GSKIP,GGNBP2,USP14,XIAP,NF1,SMAD7,USP33,BIRC2,GMFB,SPINK8,BMP2	pink	VSMC_M5
GO:0007595	0.03	0.99	5	37	lactation	BP	1	VEGFA,NCOA1,XDH,ATP7A,MT-CO2	pink	VSMC_M5
GO:0016236	0.03	0.99	20	265	macroautophagy	BP	1	VTA1,C9orf72,RAB1A,UFL1,RAB33B,RHEB,ARL8B,MAPK8,RB1CC1,VPS37A,WDFY3,TSG101,PIK3CA,SCFD1,PAFAH1B2,HUWE1,SPTLC2,PIK3C3,SMG1,UBXN2A	pink	VSMC_M5
GO:0051247	0.03	0.98	65	1140	positive regulation of protein metabolic process	BP	1	TAB2,LATS1,MAPK9,GUF1,VEGFA,ANKIB1,GCLC,COMMD1,RAB1A,ADAM17,MRE11,POLR2D,MAGI2,FNTA,XDH,TMTC3,KITLG,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,YTHDF3,CDK5RAP1,ARFGEF1,EIF4G2,DIP2B,WWP1,TIPARP,ATP2B4,RANBP9,BTRC,DOCK3,CAB39,GSK3B,PIK3CA,FXR1,DCUN1D1,ZFAND2A,FAM162A,PSMC6,ALS2,METTL5,HECTD1,CREBL2,ATF2,CRKL,WNK1,HUWE1,FBXW11,PIAS1,ARIH1,CCNK,CSNK1A1,XIAP,PRKAA1,NIPBL,SMAD7,BIRC2,UBE2V2,MTPN,EIF5A2,RNF139,BMP2	pink	VSMC_M5
GO:0070988	0.03	0.99	7	52	demethylation	BP	1	KDM3A,TET3,TET2,KDM2A,JMJD1C,KDM6A,USP9X	pink	VSMC_M5
GO:2000404	0.03	0.99	4	28	regulation of T cell migration	BP	1	ADAM17,STK39,CRKL,WNK1	pink	VSMC_M5

GO:0051173	0.03	0.98	126	2331	positive regulation of nitrogen compound metabolic process	BP	1	TAB2,MED23,LATS1,MAPK9,SCAF8,DDX17,WASL,GUF1,VEGFA,ANKIB1,RUNX2,GCM1,GCLC,RHOQ,RLF,ZNF292,COMMD1,RAB1A,ADAM17,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2D,MAGI2,MED4,MAP3K2,KMT2C,FNTA,ZEB2,XDH,KAT6A,EAF1,TMTC3,KITLG,NR3C1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,YTHDF3,TNKS2,CDK5RAP1,ARFGEF1,KDM3A,ZNF507,SMAD1,EIF4G2,DIP2B,GABPA,TET3,WWP1,TIPARP,GTF2H1,TSG101,ARID2,BTG2,ATP2B4,RANBP9,BTRC,DOCK3,CAB39,MEF2A,TET2,KMT5B,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,DCUN1D1,ZFAND2A,FAM162A,PSMC6,ALS2,GABPB2,METTL5,ZNF148,HECTD1,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,CRKL,KAT6B,WNK1,PYGO1,HUWE1,GTF2A2,FBXW11,ASH1L,ABCB7,ATRX,PIAS1,SMAD2,MED13,ARIH1,CCNK,CSNK1A1,XIAP,PRKAA1,NIPBL,HPRT1,SMAD7,SETX,NFAT5,MT-CO2,BIRC2,USP9X,UBE2V2,MTPN,PEG3,EIF5A2,ZNF770,HNRNPLL,NAF1,RNF139,DDAH1,BMP2	pink	VSMC_M5
GO:0021697	0.03	0.99	4	20	cerebellar cortex formation	BP	1	OPHN1,HERC1,ATP7A,MTPN	pink	VSMC_M5
GO:0035088	0.03	0.99	6	42	establishment or maintenance of apical/basal cell polarity	BP	1	PDCD6IP,FAT1,ERBIN,PRKCI,OPHN1,TTC8	pink	VSMC_M5
GO:0061245	0.03	0.99	6	42	establishment or maintenance of bipolar cell polarity	BP	1	PDCD6IP,FAT1,ERBIN,PRKCI,OPHN1,TTC8	pink	VSMC_M5
GO:0045862	0.03	0.98	20	297	positive regulation of proteolysis	BP	1	MAPK9,ANKIB1,GCLC,XDH,TMTC3,APAF1,DLC1,BTRC,GSK3B,ZFAND2A,FAM162A,PSMC6,HECTD1,FBXW11,PIAS1,ARIH1,CSNK1A1,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0010558	0.03	0.98	67	1150	negative regulation of macromolecule biosynthetic process	BP	1	SCAF8,VEGFA,RUNX2,GCLC,TIA1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,ZEB2,KAT6A,NR3C1,N4BP2L2,UBA3,CAPRIN1,YTHDF3,LSM14A,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,GSK3B,PUM1,BPTF,FXR1,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,PDS5A,WAPL,CPEB4,FBXW11,USP3,ATRX,PIAS1,SMAD2,NIPBL,PHF6,SMAD7,AGO3,UBE2D3,USP9X,PEG3,RBAK,BRMS1L,RNF139,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0006974	0.03	0.98	43	699	cellular response to DNA damage stimulus	BP	1	UBR5,INIP,COMMD1,UFL1,MRE11,DCLRE1C,EMSY,EPC2,ENDOV,VCPIP1,GTF2H1,HIPK1,ARID2,POLK,BTG2,TRIP12,KMT5B,DCLRE1A,GTF2I,FXR1,TFIP11,KDM2A,TLK1,MORC2,ATF2,KLHL15,ATM,RPAIN,PDS5A,HUWE1,USP3,MLH3,ATRX,FEM1B,CCNK,SMG1,UBE2A,XIAP,NIPBL,RAD1,SETX,UBE2D3,UBE2V2	pink	VSMC_M5
GO:0010605	0.03	0.98	114	2090	negative regulation of macromolecule metabolic process	BP	1	LATS1,SCAF8,UBR5,DDX17,C9orf72,ANXA1,VEGFA,RUNX2,CD2AP,GCLC,TIA1,UFL1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,ZEB2,XDH,KAT6A,BIRC6,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,CSNK2A1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,KDM3A,ERBIN,URI1,SMAD1,CGGBP1,PCGF1,GABPA,WWP1,TIPARP,LXN,TSG101,BTG2,ATP2B4,CSDE1,CYLD,BTRC,ID4,NOTCH2,TRIP12,ZMYND8,MEF2A,ACACB,GSK3B,PUM1,BPTF,FXR1,TFIP11,KDM2A,TIAL1,ZNF148,MORC2,DLX2,ATF7IP,RPS6KA3,SMG7,ATF2,KLHL15,STYXL1,RNF2,ATM,COPS2,YWHAQ,TIMP1,CRKL,KAT6B,PDS5A,WAPL,OPHN1,CPEB4,UBE2Z,FBXW11,USP3,ATRX,PIAS1,SMAD2,GSKIP,GGNBP2,SMG1,USP14,XIAP,NF1,PRKAA1,NIPBL,PHF6,SMAD7,PTBP2,BIRC2,AGO3,UBE2D3,USP9X,PEG3,RBAK,NAF1,BRMS1L,RNF139,SPINK8,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0007623	0.03	0.99	14	160	circadian rhythm	BP	1	MAPK9,FBXL3,MAPK8,PPP1CC,BTRC,ID4,GSK3B,KDM2A,HUWE1,FBXW11,PRKAA1,SETX,NMS,USP9X	pink	VSMC_M5
GO:2000401	0.03	0.99	5	41	regulation of lymphocyte migration	BP	1	WASL,ADAM17,STK39,CRKL,WNK1	pink	VSMC_M5
GO:0014015	0.03	0.99	6	48	positive regulation of gliogenesis	BP	1	UFL1,RHEB,IL6ST,PPP1CC,PRKCI,BMP2	pink	VSMC_M5
GO:0031327	0.03	0.98	69	1198	negative regulation of cellular biosynthetic process	BP	1	SCAF8,VEGFA,RUNX2,GCLC,TIA1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,ZEB2,KAT6A,NR3C1,N4BP2L2,UBA3,CAPRIN1,YTHDF3,LSM14A,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,ATP2B4,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,GSK3B,PUM1,BPTF,FXR1,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,PDS5A,WAPL,CPEB4,FBXW11,USP3,ATRX,PIAS1,SMAD2,PRKAA1,NIPBL,PHF6,SMAD7,AGO3,UBE2D3,USP9X,PEG3,RBAK,BRMS1L,RNF139,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0009890	0.03	0.98	70	1222	negative regulation of biosynthetic process	BP	1	SCAF8,VEGFA,RUNX2,GCLC,TIA1,EPC1,PRDM5,SAP130,POLR2D,CNOT10,ZEB2,KAT6A,NR3C1,N4BP2L2,UBA3,CAPRIN1,YTHDF3,LSM14A,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,ATP2B4,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,GSK3B,PUM1,BPTF,FXR1,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,PDS5A,WAPL,CPEB4,FBXW11,USP3,ABCB7,ATRX,PIAS1,SMAD2,PRKAA1,NIPBL,PHF6,SMAD7,AGO3,UBE2D3,USP9X,PEG3,RBAK,BRMS1L,RNF139,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0010613	0.03	0.99	4	26	positive regulation of cardiac muscle hypertrophy	BP	1	IL6ST,TWF1,MEF2A,MTPN	pink	VSMC_M5
GO:0014742	0.03	0.99	4	26	positive regulation of muscle hypertrophy	BP	1	IL6ST,TWF1,MEF2A,MTPN	pink	VSMC_M5
GO:0035089	0.03	0.99	4	20	establishment of apical/basal cell polarity	BP	1	FAT1,PRKCI,OPHN1,TTC8	pink	VSMC_M5
GO:0006839	0.03	0.99	14	210	mitochondrial transport	BP	1	GCLC,MAPK8,GSK3B,PARL,ATF2,MTX2,HUWE1,SFXN1,ABCB7,PRKAA1,UBE2D3,ATP5PF,SLC25A36,TIMM9	pink	VSMC_M5
GO:0060260	0.03	0.99	4	27	regulation of transcription initiation from RNA polymerase II promoter	BP	1	MED4,PSMC6,ATF7IP,MED13	pink	VSMC_M5
GO:0007589	0.03	0.99	7	68	body fluid secretion	BP	1	VEGFA,NCOA1,XDH,STK39,WNK1,ATP7A,MT-CO2	pink	VSMC_M5
GO:0010951	0.03	0.99	11	137	negative regulation of endopeptidase activity	BP	1	VEGFA,BIRC6,CSNK2A1,LXN,RPS6KA3,TIMP1,UBE2Z,USP14,XIAP,BIRC2,SPINK8	pink	VSMC_M5

GO:0032269	0.03	0.98	46	760	negative regulation of cellular protein metabolic process	BP	1	LATS1,UBR5,C9orf72,VEGFA,GCLC,TIA1,UFL1,POLR2D,CNOT10,XDH,BIRC6,SPRY4,CSNK2A1,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,KDM3A,LXN,TSG101,BTG2,ATP2B4,TRIP12,GSK3B,PUM1,FXR1,RPS6KA3,STYXL1,TIMP1,CRKL,OPHN1,CPEB4,UBE2Z,GSKIP,GGNBP2,USP14,XIAP,NF1,PRKAA1,SMAD7,BIRC2,AGO3,RNF139,SPINK8,PAIP2,BMP2	pink	VSMC_M5
GO:0010828	0.03	0.99	5	35	positive regulation of glucose transmembrane transport	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI	pink	VSMC_M5
GO:0035794	0.03	0.99	4	34	positive regulation of mitochondrial membrane permeability	BP	1	GCLC,MAPK8,GSK3B,ATF2	pink	VSMC_M5
GO:0061036	0.03	0.99	4	25	positive regulation of cartilage development	BP	1	RUNX2,SMAD1,SMAD7,BMP2	pink	VSMC_M5
GO:0031098	0.03	0.98	15	197	stress-activated protein kinase signaling cascade	BP	1	MAPK9,KLHDC10,VEGFA,XDH,MAP4K3,MAPK8,RB1CC1,PJA2,RNF13,IRAK4,CYLD,STK39,ATF2,CRKL,BMP2	pink	VSMC_M5
GO:0010611	0.03	0.99	6	51	regulation of cardiac muscle hypertrophy	BP	1	IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,MTPN	pink	VSMC_M5
GO:0009791	0.03	0.99	8	68	post-embryonic development	BP	1	VEGFA,IMPAD1,TIPARP,SCN9A,PLEKHA1,ASH1L,ATRX,SMAD2	pink	VSMC_M5
GO:0007006	0.03	0.99	8	99	mitochondrial membrane organization	BP	1	GCLC,MAPK8,FAM92A,GSK3B,ATF2,MTX2,GHITM,TIMM9	pink	VSMC_M5
GO:0045047	0.03	0.99	4	30	protein targeting to ER	BP	1	SRP72,SGTB,ZFAND2A,SRP54	pink	VSMC_M5
GO:0007007	0.03	0.99	4	35	inner mitochondrial membrane organization	BP	1	FAM92A,MTX2,GHITM,TIMM9	pink	VSMC_M5
GO:0072523	0.03	0.99	5	43	purine-containing compound catabolic process	BP	1	XDH,ADAL,PDE5A,HPRT1,NUDT7	pink	VSMC_M5
GO:0030522	0.04	0.98	17	217	intracellular receptor signaling pathway	BP	1	LATS1,UBR5,DDX17,UFL1,NCOA1,ASXL2,NR3C1,LSM14A,KDM3A,ERBIN,NR3C2,CYLD,PUM1,CRKL,XIAP,BIRC2,BMP2	pink	VSMC_M5
GO:0006950	0.04	0.97	140	2715	response to stress	BP	1	DGKA,MAPK9,UBR5,DDX17,KLHDC10,ANXA1,TMEM33,VEGFA,ASNS,GCLC,DST,ERLEC1,INIP,COMMD1,MACF1,RAB1A,ADAM17,UFL1,RAB14,HSPA4L,SRPK2,MRE11,POLR2D,DCLRE1C,DGKH,CLASP1,EMSY,FLRT3,EPC2,XDH,ARL8B,KAT6A,NGLY1,ENDOV,TMTC3,ATRN,MAP4K3,MAPK8,APAF1,RB1CC1,IL6ST,IFIT5,YTHDF3,VCPIP1,LSM14A,PJA2,SGTB,ARFGEF1,SMAD1,RNF13,LXN,GTF2H1,HIPK1,ARID2,POLK,BTG2,ATP2B4,IRAK4,CYLD,TSPAN32,NOTCH2,TRIP12,ANO1,CAB39,KMT5B,GSK3B,DCLRE1A,PUM1,PIK3CA,LYST,SCN9A,GTF2I,BPTF,FXR1,TFIP11,STK39,EGLN1,KDM2A,FAM162A,TIAL1,PSMC6,ALS2,TLK1,PLEKHA1,ZNF148,SCFD1,MORC2,JMJD1C,RPS6KA3,ATF2,KLHL15,LANCL1,ATM,ERO1A,HP1BP3,TIMP1,CRKL,RPAIN,PDS5A,FUT8,HUWE1,CPEB4,ASH1L,USP3,MLH3,ATRX,ATP7A,FEM1B,SMAD2,PIK3C3,GSKIP,CCNK,SMG1,USP14,UBE2A,XIAP,NF1,PRKAA1,NIPBL,RAD1,SMAD7,F8,SETX,STXBP3,NFAT5,USP33,MT-CO1,MT-CO2,MT-ND3,MT-ND4,MT-ND5,BIRC2,UBE2D3,RNF103,UBE2V2,ELMOD2,RNF139,DDAH1,BMT2,BMP2	pink	VSMC_M5
GO:0021575	0.04	0.99	5	34	hindbrain morphogenesis	BP	1	DLC1,OPHN1,HERC1,ATP7A,MTPN	pink	VSMC_M5
GO:0009896	0.04	0.98	28	420	positive regulation of catabolic process	BP	1	MAPK9,C9orf72,ANKIB1,GCLC,UFL1,POLR2D,IRS2,TMTC3,CSNK2A1,YTHDF3,WWP1,TIPARP,BTG2,GSK3B,PUM1,ZFAND2A,PSMC6,HECTD1,PAFAH1B2,HUWE1,SPTLC2,PIAS1,ARIH1,CSNK1A1,PRKAA1,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0014743	0.04	0.99	6	52	regulation of muscle hypertrophy	BP	1	IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,MTPN	pink	VSMC_M5
GO:0017148	0.04	0.98	13	158	negative regulation of translation	BP	1	TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,BTG2,PUM1,FXR1,CPEB4,AGO3,RNF139,PAIP2	pink	VSMC_M5
GO:0043086	0.04	0.98	34	555	negative regulation of catalytic activity	BP	1	LATS1,ANXA1,VEGFA,BIRC6,IRS2,SPRY4,CSNK2A1,CDK5RAP1,ARFGEF1,URI1,LXN,TSG101,ATP2B4,BICD1,ACACB,GSK3B,TFIP11,EGLN1,RPS6KA3,STYXL1,TIMP1,WNK1,UBE2Z,TTC8,GSKIP,GGNBP2,USP14,XIAP,NF1,SMAD7,BIRC2,GMFB,SPINK8,BMP2	pink	VSMC_M5
GO:1902108	0.04	0.99	4	34	regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	GCLC,MAPK8,GSK3B,ATF2	pink	VSMC_M5
GO:0034968	0.04	0.98	10	98	histone lysine methylation	BP	1	RLF,PRDM5,KMT2C,KDM3A,TET3,TET2,KMT5B,KDM6A,ASH1L,ATRX	pink	VSMC_M5
GO:0002753	0.04	0.99	6	53	cytoplasmic pattern recognition receptor signaling pathway	BP	1	LSM14A,ERBIN,CYLD,PUM1,XIAP,BIRC2	pink	VSMC_M5
GO:2000144	0.04	0.99	4	25	positive regulation of DNA-templated transcription, initiation	BP	1	MED4,PSMC6,MED13,SETX	pink	VSMC_M5
GO:0006914	0.04	0.98	30	450	autophagy	BP	1	VTA1,TAB2,VPS13A,C9orf72,RAB1A,UFL1,RAB33B,ACBD5,RHEB,ARL8B,MAPK8,RB1CC1,VPS37A,EIF4G2,ARSB,WDFY3,TSG101,GSK3B,PIK3CA,SCFD1,PAFAH1B2,ATM,HUWE1,HERC1,SPTLC2,PIK3C3,SMG1,PRKAA1,USP33,UBXN2A	pink	VSMC_M5
GO:0061919	0.04	0.98	30	450	process utilizing autophagic mechanism	BP	1	VTA1,TAB2,VPS13A,C9orf72,RAB1A,UFL1,RAB33B,ACBD5,RHEB,ARL8B,MAPK8,RB1CC1,VPS37A,EIF4G2,ARSB,WDFY3,TSG101,GSK3B,PIK3CA,SCFD1,PAFAH1B2,ATM,HUWE1,HERC1,SPTLC2,PIK3C3,SMG1,PRKAA1,USP33,UBXN2A	pink	VSMC_M5
GO:0046686	0.04	0.99	5	47	response to cadmium ion	BP	1	MAPK9,GCLC,MAPK8,ATP7A,UBE2D3	pink	VSMC_M5
GO:0090263	0.04	0.98	9	92	positive regulation of canonical Wnt signaling pathway	BP	1	CSNK1G3,UBR5,USP34,ZEB2,TNKS2,USP8,WNK1,GSKIP,XIAP	pink	VSMC_M5
GO:0008654	0.04	0.98	16	222	phospholipid biosynthetic process	BP	1	DGKA,SERINC1,EFR3A,FAM126A,DGKH,IMPAD1,MTMR6,FAR1,PIGP,PIK3CA,ATM,SPTLC2,PIK3C3,SMG1,CEPT1,TMEM38B	pink	VSMC_M5
GO:0022900	0.04	0.98	10	149	electron transport chain	BP	1	ME2,AFG1L,NDUFS4,GHITM,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5	pink	VSMC_M5
GO:0007059	0.04	0.98	20	288	chromosome segregation	BP	1	LATS1,MRE11,ARL8B,TOP2B,NR3C1,CSNK2A1,PUM1,TLK1,SKA1,ATM,PDS5A,WAPL,MLH3,ATRX,DYNC1H1,ESCO1,STAG2,NIPBL,USP9X,RMDN1	pink	VSMC_M5
GO:0046034	0.04	0.98	14	219	ATP metabolic process	BP	1	AFG1L,NIPSNAP2,NDUFS4,C2orf69,GHITM,ATP7A,PRKAA1,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5,ATP5PF	pink	VSMC_M5
GO:0120032	0.04	0.98	13	158	regulation of plasma membrane bounded cell projection assembly	BP	1	WASL,RHOQ,SEPT7,CEP97,TWF1,CYLD,ZMYND8,PIK3CA,FXR1,ABI2,ARPC2,ATP7A,FAM206A	pink	VSMC_M5
GO:1905710	0.04	0.99	4	36	positive regulation of membrane permeability	BP	1	GCLC,MAPK8,GSK3B,ATF2	pink	VSMC_M5
GO:0044344	0.04	0.98	8	86	cellular response to fibroblast growth factor stimulus	BP	1	RUNX2,GCLC,RAB14,FLRT3,SPRY4,SHOC2,CRKL,SETX	pink	VSMC_M5
GO:1903747	0.04	0.99	5	43	regulation of establishment of protein localization to mitochondrion	BP	1	MAPK8,PARL,HUWE1,PRKAA1,UBE2D3	pink	VSMC_M5

GO:0060491	0.04	0.98	13	159	regulation of cell projection assembly	BP	1	WASL,RHOQ,SEPT7,CEP97,TWF1,CYLD,ZMYND8,PIK3CA,FXR1,ABI2,ARPC2,ATP7A,FAM206A	pink	VSMC_M5
GO:0031396	0.04	0.98	13	180	regulation of protein ubiquitination	BP	1	MAPK9,UBR5,GCLC,COMMD1,UFL1,BTRC,TRIP12,DCUN1D1,HUWE1,XIAP,SMAD7,BIRC2,UBXN2A	pink	VSMC_M5
GO:0070897	0.04	0.99	4	31	transcription preinitiation complex assembly	BP	1	TBP,PSMC6,ATF7IP,GTF2A2	pink	VSMC_M5
GO:0010466	0.04	0.98	11	145	negative regulation of peptidase activity	BP	1	VEGFA,BIRC6,CSNK2A1,LXN,RPS6KA3,TIMP1,UBE2Z,USP14,XIAP,BIRC2,SPINK8	pink	VSMC_M5
GO:2001252	0.05	0.98	7	72	positive regulation of chromosome organization	BP	1	MRE11,TNKS2,MORC2,ATF7IP,ATM,ATRX,NAF1	pink	VSMC_M5
GO:0031648	0.05	0.99	5	42	protein destabilization	BP	1	FBXL3,BTRC,FBXW11,RNF139,BMP2	pink	VSMC_M5
GO:0007032	0.05	0.98	7	71	endosome organization	BP	1	VTA1,PDCD6IP,VPS37A,TSG101,ALS2,USP8,PIK3C3	pink	VSMC_M5
GO:1903749	0.05	0.99	4	30	positive regulation of establishment of protein localization to mitochondrion	BP	1	MAPK8,HUWE1,PRKAA1,UBE2D3	pink	VSMC_M5
GO:0019748	0.05	0.99	4	30	secondary metabolic process	BP	1	ZEB2,TRPC1,ATP7A,SULT1C4	pink	VSMC_M5
GO:0032006	0.05	0.98	8	84	regulation of TOR signaling	BP	1	UBR2,C9orf72,RHEB,PIK3CA,UBR1,ATM,PRKAA1,BMT2	pink	VSMC_M5
GO:0034453	0.05	0.99	4	25	microtubule anchoring	BP	1	CLASP1,PCM1,BICD1,GSK3B	pink	VSMC_M5
GO:0043414	0.05	0.97	18	254	macromolecule methylation	BP	1	PCMT1,FBXO11,RLF,PRDM5,KMT2C,PCMTD1,KDM3A,TET3,VIRMA,BTG2,TET2,KMT5B,PIK3CA,METTL5,ATF7IP,KDM6A,ASH1L,ATRX	pink	VSMC_M5
GO:0070646	0.05	0.98	11	125	protein modification by small protein removal	BP	1	USP34,VCPIP1,COPS4,CYLD,COPS2,USP8,USP3,USP14,USP33,MINDY3,USP9X	pink	VSMC_M5
GO:0034248	0.05	0.97	25	395	regulation of cellular amide metabolic process	BP	1	GUF1,TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,EIF4G2,DPH6,BTG2,CSDE1,PUM1,FXR1,METTL5,RPS6KA3,NEMF,CPEB4,PRKAA1,AGO3,MTPN,EIF5A2,RNF139,PAIP2	pink	VSMC_M5
GO:0071229	0.05	0.98	7	65	cellular response to acid chemical	BP	1	UBR2,VEGFA,GCLC,PIK3CA,UBR1,CPEB4,ATP7A	pink	VSMC_M5
GO:0002063	0.05	0.99	4	27	chondrocyte development	BP	1	MEX3C,RUNX2,IMPAD1,SMAD7	pink	VSMC_M5
GO:0007131	0.05	0.99	5	44	reciprocal meiotic recombination	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3	pink	VSMC_M5
GO:0140527	0.05	0.99	5	44	reciprocal homologous recombination	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3	pink	VSMC_M5
GO:0034249	0.05	0.97	14	183	negative regulation of cellular amide metabolic process	BP	1	TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,BTG2,PUM1,FXR1,CPEB4,PRKAA1,AGO3,RNF139,PAIP2	pink	VSMC_M5
GO:0008104	0.05	0.96	110	2028	protein localization	BP	1	VTA1,LATS1,MAPK9,SYNE1,VPS13B,SNX2,UBR5,SFT2D1,KPNA5,EFR3A,VPS13A,PCSK5,WASL,ANXA1,CD2AP,SRP72,RHOQ,ERLEC1,FAM126A,LCA5,COMMD1,MACF1,VPS54,RAB1A,SEPT7,TIA1,UFL1,RAB14,RAB33B,MAGI2,AKAP11,PDCD6IP,EPB41L5,FNTA,ARL8B,ZDHHC17,GOLGA7,LTBP1,COG6,IRS2,NBEA,NEDD1,MAPK8,VPS37A,PCM1,TNKS2,VCPIP1,SGTB,ARFGEF1,ERBIN,LRBA,VPS29,TCTN1,ZFYVE16,ARL13B,TSG101,UEVLD,SSR1,ATP2B4,TWF1,TSPAN32,BICD1,ANO1,ZMYND8,IPO8,GSK3B,LYST,GOLGB1,ZFAND2A,PARL,CCDC14,ALS2,TLK1,PLEKHA1,SCFD1,HECTD1,SRP54,MTX2,ODR4,PRKCI,YWHAQ,USP8,CRKL,RPAIN,PYGO1,WAPL,HUWE1,SNX11,MLH3,ATRX,SPATA7,CHM,TTC8,SMAD2,PIK3C3,APPBP2,PTPN9,PRKAA1,NIPBL,SMAD7,STXBP3,ARRDC5,UBE2D3,USP9X,RAB18,EIF5A2,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0051403	0.05	0.97	14	190	stress-activated MAPK cascade	BP	1	MAPK9,KLHDC10,VEGFA,XDH,MAP4K3,MAPK8,RB1CC1,PJA2,IRAK4,CYLD,STK39,ATF2,CRKL,BMP2	pink	VSMC_M5
GO:0034314	0.05	0.99	4	33	Arp2/3 complex-mediated actin nucleation	BP	1	WASL,ABI2,ARPC2,GMFB	pink	VSMC_M5
GO:0016573	0.05	0.98	11	131	histone acetylation	BP	1	NCOA1,EPC1,EPC2,KAT6A,MSL2,MSL3,ATF2,KANSL1,JADE3,KAT6B,AC118549.1	pink	VSMC_M5
GO:0007005	0.05	0.97	25	436	mitochondrion organization	BP	1	VPS13A,SDHAF3,GCLC,AFG1L,YME1L1,MAPK8,RB1CC1,FAM92A,NIPSNAP2,NDUFS4,MEF2A,GSK3B,FAM162A,PARL,ATF2,MTX2,GHITM,HUWE1,ATP7A,PRKAA1,MT-ND4,MT-ND5,UBE2D3,SLC25A36,TIMM9	pink	VSMC_M5
GO:0044728	0.05	0.98	7	67	DNA methylation or demethylation	BP	1	RLF,TET3,TET2,PIK3CA,ATF7IP,ATRX,USP9X	pink	VSMC_M5
GO:0018022	0.05	0.98	10	108	peptidyl-lysine methylation	BP	1	RLF,PRDM5,KMT2C,KDM3A,TET3,TET2,KMT5B,KDM6A,ASH1L,ATRX	pink	VSMC_M5
GO:0031331	0.05	0.97	24	366	positive regulation of cellular catabolic process	BP	1	MAPK9,C9orf72,ANKIB1,GCLC,UFL1,POLR2D,IRS2,TMTC3,YTHDF3,BTG2,GSK3B,PUM1,ZFAND2A,PSMC6,HECTD1,PAFAH1B2,SPTLC2,PIAS1,ARIH1,CSNK1A1,PRKAA1,SMAD7,UBE2V2,RNF139	pink	VSMC_M5
GO:0061162	0.05	0.99	4	22	establishment of monopolar cell polarity	BP	1	FAT1,PRKCI,OPHN1,TTC8	pink	VSMC_M5
GO:0046323	0.05	0.98	6	54	glucose import	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3	pink	VSMC_M5
GO:0010608	0.05	0.96	29	480	posttranscriptional regulation of gene expression	BP	1	GUF1,TIA1,POLR2D,CNOT10,EPB41L5,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,SMAD1,EIF4G2,DPH6,BTG2,CSDE1,PUM1,FXR1,TIAL1,METTL5,RPS6KA3,NEMF,CPEB4,SMAD2,AGO3,MTPN,EIF5A2,NAF1,RNF139,PAIP2	pink	VSMC_M5
GO:0071774	0.05	0.98	8	91	response to fibroblast growth factor	BP	1	RUNX2,GCLC,RAB14,FLRT3,SPRY4,SHOC2,CRKL,SETX	pink	VSMC_M5
GO:2000780	0.05	0.99	4	29	negative regulation of double-strand break repair	BP	1	UBR5,TRIP12,TFIP11,KLHL15	pink	VSMC_M5
GO:0007033	0.06	0.97	12	157	vacuole organization	BP	1	C9orf72,RAB1A,RAB14,RAB33B,ARL8B,RB1CC1,ARSB,LYST,SCFD1,ATF2,PIK3C3,UBXN2A	pink	VSMC_M5
GO:1902745	0.06	0.99	4	30	positive regulation of lamellipodium organization	BP	1	PIK3CA,ABI2,ARPC2,ATP7A	pink	VSMC_M5
GO:0035825	0.06	0.98	5	46	homologous recombination	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3	pink	VSMC_M5
GO:0018393	0.06	0.97	11	134	internal peptidyl-lysine acetylation	BP	1	NCOA1,EPC1,EPC2,KAT6A,MSL2,MSL3,ATF2,KANSL1,JADE3,KAT6B,AC118549.1	pink	VSMC_M5
GO:0048701	0.06	0.98	5	40	embryonic cranial skeleton morphogenesis	BP	1	MTHFD1L,RUNX2,DLX2,SMAD2,NIPBL	pink	VSMC_M5
GO:1902743	0.06	0.98	5	45	regulation of lamellipodium organization	BP	1	TWF1,PIK3CA,ABI2,ARPC2,ATP7A	pink	VSMC_M5

GO:0010468	0.06	0.95	175	3428	regulation of gene expression	BP	1	PPIL4,MED23,MAPK9,SCAF8,UBR5,DDX17,ELAVL2,WASL,ANXA1,GUF1,VEGFA,RUNX2,CD2AP,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,RAB1A,TIA1,ADAM17,UFL1,SRPK2,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,EPB41L5,KMT2C,EMSY,ZEB2,EPC2,XDH,KAT6A,LTBP1,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,IL6ST,GPBP1,CAPRIN1,YTHDF3,LSM14A,ZMYM5,CDK5RAP1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,TIPARP,MLF1,GTF2H1,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,MORC2,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,RNF2,NEMF,ATM,KDM6A,PRKCI,COPS2,YWHAQ,HP1BP3,CRKL,KAT6B,ZNF518B,POGK,PYGO1,RFX7,FUT8,HUWE1,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ATRX,ATP7A,PIAS1,SMAD2,MED13,CCNK,GGNBP2,SMG1,XIAP,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,PTBP2,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,MTPN,PEG3,EIF5A2,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,RNF139,PAIP2,UBXN2A,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0033036	0.06	0.95	125	2356	macromolecule localization	BP	1	RELCH,VTA1,LATS1,MAPK9,SYNE1,VPS13B,SNX2,UBR5,SFT2D1,KPNA5,EFR3A,SLC25A17,VPS13A,PCSK5,WASL,ANXA1,CD2AP,SRP72,RHOQ,ERLEC1,FAM126A,LCA5,UGCG,COMMD1,MACF1,VPS54,RAB1A,SEPT7,TIA1,UFL1,RAB14,RAB33B,OSBPL9,ASXL2,POLR2D,MAGI2,AKAP11,PDCD6IP,EPB41L5,FNTA,ARL8B,ZDHHC17,GOLGA7,LTBP1,COG6,IRS2,NBEA,SHQ1,NEDD1,MAPK8,VPS37A,PCM1,TNKS2,VCPIP1,SGTB,ARFGEF1,ERBIN,LRBA,VPS29,TCTN1,ZFYVE16,ARL13B,TSG101,UEVLD,SSR1,ATP2B4,ZC3H11A,TWF1,TSPAN32,BICD1,ANO1,DENND5B,ZMYND8,IPO8,ACACB,GSK3B,LYST,GOLGB1,ZFAND2A,PARL,CCDC14,ALS2,TLK1,PLEKHA1,SCFD1,HECTD1,SMG7,SRP54,MTX2,ODR4,ATM,PRKCI,YWHAQ,USP8,CRKL,RPAIN,PYGO1,WAPL,HUWE1,SNX11,MLH3,ATRX,SPATA7,CHM,TTC8,SMAD2,PIK3C3,APPBP2,PTPN9,SMG1,PRKAA1,NIPBL,SMAD7,STXBP3,ARRDC5,UBE2D3,ATP5PF,USP9X,RAB18,EIF5A2,NAF1,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0061339	0.06	0.98	4	23	establishment or maintenance of monopolar cell polarity	BP	1	FAT1,PRKCI,OPHN1,TTC8	pink	VSMC_M5
GO:0043200	0.06	0.97	8	93	response to amino acid	BP	1	UBR2,ASNS,GCLC,UFL1,UBR1,CPEB4,ATP7A,PIK3C3	pink	VSMC_M5
GO:0031325	0.06	0.95	130	2483	positive regulation of cellular metabolic process	BP	1	TAB2,MED23,LATS1,MAPK9,SCAF8,DDX17,C9orf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,GCM1,GCLC,RHOQ,RLF,ZNF292,COMMD1,RAB1A,ADAM17,UFL1,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2D,MAGI2,MED4,MAP3K2,KMT2C,FNTA,ZEB2,XDH,KAT6A,EAF1,IRS2,TMTC3,KITLG,NR3C1,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,YTHDF3,TNKS2,CDK5RAP1,ARFGEF1,KDM3A,ZNF507,SMAD1,EIF4G2,DIP2B,BTBD10,GABPA,TET3,GTF2H1,TSG101,ARID2,BTG2,ATP2B4,BTRC,DOCK3,CAB39,MEF2A,TET2,KMT5B,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,DCUN1D1,ZFAND2A,FAM162A,PSMC6,ALS2,GABPB2,METTL5,ZNF148,HECTD1,DLX2,ATF7IP,RPS6KA3,PAFAH1B2,CREBL2,ATF2,ATM,CRKL,KAT6B,WNK1,GHITM,PYGO1,HUWE1,GTF2A2,FBXW11,ASH1L,ABCB7,SPTLC2,ATRX,ATP7A,PIAS1,SMAD2,MED13,ARIH1,CCNK,CSNK1A1,XIAP,PRKAA1,NIPBL,HPRT1,SMAD7,SETX,NFAT5,MT-CO2,BIRC2,USP9X,UBE2V2,CACYBP,PEG3,EIF5A2,ZNF770,HNRNPLL,NAF1,RNF139,DDAH1,BMP2	pink	VSMC_M5
GO:0032206	0.06	0.98	5	48	positive regulation of telomere maintenance	BP	1	MRE11,TNKS2,ATM,ATRX,NAF1	pink	VSMC_M5
GO:0007264	0.06	0.96	30	437	small GTPase mediated signal transduction	BP	1	ARFGEF3,KRIT1,CD2AP,RHOQ,RAB33B,ARHGAP42,RHEB,KITLG,SPRY4,DLC1,ARFGEF1,ERBIN,RHOBTB3,RALGAPB,DNMBP,DOCK3,NOTCH2,SHOC2,ALS2,ABI2,ARHGAP5,RALGPS2,SOS2,YWHAQ,USP8,CRKL,OPHN1,CHM,NF1,RAB18	pink	VSMC_M5
GO:0006475	0.06	0.97	11	136	internal protein amino acid acetylation	BP	1	NCOA1,EPC1,EPC2,KAT6A,MSL2,MSL3,ATF2,KANSL1,JADE3,KAT6B,AC118549.1	pink	VSMC_M5
GO:1904888	0.06	0.98	6	54	cranial skeletal system development	BP	1	MTHFD1L,RUNX2,DLX2,CRKL,SMAD2,NIPBL	pink	VSMC_M5
GO:0045738	0.06	0.98	4	31	negative regulation of DNA repair	BP	1	UBR5,TRIP12,TFIP11,KLHL15	pink	VSMC_M5
GO:0070076	0.06	0.98	4	25	histone lysine demethylation	BP	1	KDM3A,KDM2A,JMJD1C,KDM6A	pink	VSMC_M5
GO:0007566	0.06	0.98	4	36	embryo implantation	BP	1	PCSK5,VEGFA,YTHDF3,TIMP1	pink	VSMC_M5

GO:0044249	0.06	0.95	207	4271	cellular biosynthetic process	BP	1	DGKA,PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,SERINC1,EFR3A,DDX17,ELAVL2,PCSK5,WASL,ANXA1,GUF1,VEGFA,RUNX2,CYP39A1,ASNS,GCM1,GCLC,AGMO,RHOQ,FAM126A,TAX1BP1,RLF,UGCG,ZNF292,COMMD1,DPY19L1,TIA1,UFL1,OSBPL9,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DGKH,KMT2C,EMSY,ZEB2,EPC2,KAT6A,OXSM,ZDHHC17,GOLGA7,EAF1,ZNF605,IRS2,TMTC3,PRKD3,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,TRPC1,FAR1,GFM2,NFS1,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,PIGP,GXYLT1,CYLD,BBX,BTRC,OGA,ID4,NOTCH2,ZMYND8,MEF2A,PRKAB2,TET2,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,WAPL,RFX7,FUT8,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ABCB7,SPTLC2,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,PIK3C3,CCNK,SMG1,ESCO1,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,CEPT1,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,AGO3,UBE2D3,ATP5PF,TMEM38B,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,DDAH1,PAIP2,BMP2,RNF219,ZDHHC22,DENR,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:1903320	0.06	0.97	14	211	regulation of protein modification by small protein conjugation or removal	BP	1	MAPK9,UBR5,GCLC,COMMD1,UFL1,BTRC,TRIP12,DCUN1D1,HUWE1,PIAS1,XIAP,SMAD7,BIRC2,UBXN2A	pink	VSMC_M5
GO:0048511	0.06	0.96	17	223	rhythmic process	BP	1	MAPK9,NCOA1,FBXL3,MAPK8,CSNK2A1,PPP1CC,BTRC,ID4,GSK3B,KDM2A,PLEKHA1,HUWE1,FBXW11,PRKAA1,SETX,NMS,USP9X	pink	VSMC_M5
GO:0065004	0.06	0.97	10	132	protein-DNA complex assembly	BP	1	TBP,KAT6A,PSMC6,ATF7IP,HP1BP3,KAT6B,GTF2A2,ATRX,PIAS1,NAP1L3	pink	VSMC_M5
GO:0051057	0.06	0.98	6	55	positive regulation of small GTPase mediated signal transduction	BP	1	KITLG,ERBIN,NOTCH2,SHOC2,ALS2,SOS2	pink	VSMC_M5
GO:0010827	0.06	0.98	6	58	regulation of glucose transmembrane transport	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3	pink	VSMC_M5
GO:0071824	0.07	0.97	12	163	protein-DNA complex subunit organization	BP	1	TBP,KAT6A,ARID2,BPTF,PSMC6,ATF7IP,HP1BP3,KAT6B,GTF2A2,ATRX,PIAS1,NAP1L3	pink	VSMC_M5
GO:0051568	0.07	0.98	6	51	histone H3-K4 methylation	BP	1	RLF,KMT2C,TET3,TET2,KDM6A,ASH1L	pink	VSMC_M5
GO:0007417	0.07	0.95	50	795	central nervous system development	BP	1	GCM1,NCOA1,RHEB,TOP2B,IRS2,ATRN,APAF1,DLC1,IL6ST,PCM1,CDK5RAP1,SMAD1,TCTN1,WWP1,ARL13B,ARSB,TBC1D23,PPP3CC,BTG2,ATP2B4,PSMG1,NDUFS4,GSK3B,BPTF,CCDC14,ZNF148,DLX2,RPS6KA3,PAFAH1B2,ATF2,YWHAQ,CRKL,OPHN1,FBXW11,HERC1,ATRX,ATP7A,TTC8,NF1,NIPBL,RAD1,HPRT1,STXBP3,MT-CO1,MT-ND4,ATP5PF,RNF103,RAB18,MTPN,BMP2	pink	VSMC_M5
GO:0071560	0.07	0.96	16	199	cellular response to transforming growth factor beta stimulus	BP	1	LATS1,ADAM17,ZFYVE9,EPB41L5,FNTA,ZEB2,LTBP1,NR3C1,APAF1,SMAD1,CRKL,FUT8,SMAD2,SMAD7,USP9X,BMP2	pink	VSMC_M5
GO:0009154	0.07	0.98	4	35	purine ribonucleotide catabolic process	BP	1	XDH,PDE5A,HPRT1,NUDT7	pink	VSMC_M5
GO:0006476	0.07	0.97	8	88	protein deacetylation	BP	1	VEGFA,PRDM5,FNTA,MAPK8,MSL3,PRKAA1,NIPBL,BRMS1L	pink	VSMC_M5
GO:0051865	0.07	0.98	6	62	protein autoubiquitination	BP	1	RNF13,HECTD1,UBE2A,UBE2D3,UBE2D2,RNF219	pink	VSMC_M5
GO:0043154	0.07	0.98	5	55	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	VEGFA,CSNK2A1,RPS6KA3,XIAP,BIRC2	pink	VSMC_M5
GO:0032270	0.07	0.95	58	1066	positive regulation of cellular protein metabolic process	BP	1	TAB2,LATS1,MAPK9,GUF1,VEGFA,ANKIB1,GCLC,COMMD1,ADAM17,MRE11,POLR2D,MAGI2,FNTA,XDH,TMTC3,KITLG,APAF1,DLC1,RB1CC1,IL6ST,YTHDF3,CDK5RAP1,ARFGEF1,EIF4G2,DIP2B,ATP2B4,BTRC,DOCK3,CAB39,GSK3B,PIK3CA,FXR1,DCUN1D1,ZFAND2A,FAM162A,PSMC6,ALS2,METTL5,HECTD1,CREBL2,ATF2,CRKL,WNK1,HUWE1,FBXW11,PIAS1,ARIH1,CCNK,CSNK1A1,XIAP,PRKAA1,NIPBL,SMAD7,BIRC2,UBE2V2,EIF5A2,RNF139,BMP2	pink	VSMC_M5
GO:0021696	0.07	0.98	4	28	cerebellar cortex morphogenesis	BP	1	OPHN1,HERC1,ATP7A,MTPN	pink	VSMC_M5
GO:0032259	0.07	0.96	19	290	methylation	BP	1	PCMT1,FBXO11,RLF,PRDM5,KMT2C,PCMTD1,KDM3A,TET3,VIRMA,BTG2,TET2,KMT5B,PIK3CA,METTL5,ATF7IP,KDM6A,ASH1L,ATRX,BMT2	pink	VSMC_M5
GO:0031929	0.07	0.97	9	105	TOR signaling	BP	1	UBR2,C9orf72,RHEB,PIK3CA,UBR1,ATM,SMG1,PRKAA1,BMT2	pink	VSMC_M5
GO:0009798	0.07	0.97	6	59	axis specification	BP	1	EPB41L5,ARL13B,NOTCH2,RNF2,TTC8,SMAD2	pink	VSMC_M5
GO:0090311	0.07	0.98	5	42	regulation of protein deacetylation	BP	1	VEGFA,FNTA,MAPK8,PRKAA1,NIPBL	pink	VSMC_M5
GO:0010256	0.07	0.95	27	422	endomembrane system organization	BP	1	VTA1,SYNE1,WASL,TMEM33,UGCG,RAB1A,RAB33B,PDCD6IP,CLASP1,ARL8B,VPS37A,VCPIP1,ARFGEF1,TSG101,GOLGA5,LYST,GOLGB1,ALS2,ATL3,USP8,HUWE1,PIK3C3,CSNK1A1,TMEM38B,RAB18,GOLPH3L,UBXN2A	pink	VSMC_M5
GO:0051489	0.07	0.98	5	44	regulation of filopodium assembly	BP	1	WASL,RHOQ,ZMYND8,FXR1,FAM206A	pink	VSMC_M5
GO:0046474	0.07	0.96	13	185	glycerophospholipid biosynthetic process	BP	1	DGKA,EFR3A,FAM126A,DGKH,IMPAD1,MTMR6,FAR1,PIGP,PIK3CA,ATM,PIK3C3,SMG1,CEPT1	pink	VSMC_M5
GO:1903322	0.07	0.97	9	121	positive regulation of protein modification by small protein conjugation or removal	BP	1	MAPK9,COMMD1,BTRC,DCUN1D1,HUWE1,PIAS1,XIAP,SMAD7,BIRC2	pink	VSMC_M5
GO:0001937	0.07	0.98	4	34	negative regulation of endothelial cell proliferation	BP	1	KRIT1,XDH,NF1,PTPRM	pink	VSMC_M5
GO:0051567	0.07	0.98	4	29	histone H3-K9 methylation	BP	1	PRDM5,KDM3A,ASH1L,ATRX	pink	VSMC_M5
GO:0006091	0.08	0.95	22	392	generation of precursor metabolites and energy	BP	1	ME2,MDH1,AFG1L,IRS2,RB1CC1,IL6ST,PPP1CC,NIPSNAP2,NDUFS4,C2orf69,GSK3B,PIK3CA,GHITM,ATP7A,PRKAA1,MT-CO1,MT-CO2,MT-ND3,MT-ND4L,MT-ND4,MT-ND5,ATP5PF	pink	VSMC_M5
GO:0072698	0.08	0.97	6	52	protein localization to microtubule cytoskeleton	BP	1	NEDD1,PCM1,BICD1,GSK3B,GOLGB1,CCDC14	pink	VSMC_M5

GO:0048522	0.08	0.94	212	4212	positive regulation of cellular process	BP	1	TAB2,MED23,LATS1,MAPK9,CSNK1G3,SCAF8,UBR5,DDX17,KLHDC10,C9orf72,WASL,ANXA1,TMEM33,GUF1,VEGFA,ANKIB1,RUNX2,CD2AP,ASNS,GCM1,GCLC,PTP4A1,RHOQ,RLF,USP34,ZNF292,COMMD1,MACF1,RAB1A,SEPT7,TIA1,ADAM17,UFL1,JCAD,SRPK2,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2D,MAGI2,MED4,MAP3K2,PDCD6IP,CLASP1,EPB41L5,RHEB,KMT2C,FNTA,ZEB2,MBD5,FLRT3,XDH,KAT6A,ZDHHC17,BIRC6,EAF1,IRS2,TMTC3,KITLG,NR3C1,N4BP2L2,SHQ1,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,PCM1,IFIT5,YTHDF3,TNKS2,LSM14A,CDK5RAP1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ZNF507,SMAD1,EIF4G2,SLC4A8,NR3C2,TRPC1,DIP2B,BTBD10,RNF13,GABPA,PPP1CC,TET3,CPNE3,FAM92A,ARSB,GTF2H1,TSG101,HIPK1,ARID2,PPP3CC,BTG2,SSR1,ATP2B4,TWF1,IRAK4,CYLD,BTRC,NIPSNAP2,NDUFS4,DOCK3,NOTCH2,BICD1,ANO1,CAB39,ZMYND8,MEF2A,SHOC2,TET2,KMT5B,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,ZBED9,DCUN1D1,STK39,ZFAND2A,FAM162A,TIAL1,PSMC6,ALS2,GABPB2,METTL5,ZNF148,ABI2,MORC2,HECTD1,DLX2,ATF7IP,RPS6KA3,PAFAH1B2,CREBL2,ATF2,STYXL1,DYNLT3,SOS2,ATM,ARPC2,PRKCI,ATL3,USP8,TIMP1,CRKL,KAT6B,WNK1,GHITM,PYGO1,WAPL,HUWE1,GTF2A2,UBE2Z,FBXW11,ASH1L,ABCB7,SPTLC2,ATRX,ATP7A,PIAS1,SMAD2,MED13,ARIH1,GSKIP,CCNK,DYNC1H1,PTPN9,CSNK1A1,UBE2A,XIAP,NF1,PRKAA1,NIPBL,HPRT1,SMAD7,SETX,PKN2,NFAT5,MT-CO2,BIRC2,AGO3,UBE2D3,USP9X,GMFB,UBE2V2,MTPN,CACYBP,PEG3,EIF5A2,ZNF770,HNRNPLL,NAF1,RNF139,DDAH1,GOLPH3L,PAIP2,BMP2,SAR1B	pink	VSMC_M5
GO:0043473	0.08	0.97	7	75	pigmentation	BP	1	RAB1A,ZEB2,KITLG,ATRN,LYST,ATP7A,NF1	pink	VSMC_M5
GO:0031398	0.08	0.97	8	102	positive regulation of protein ubiquitination	BP	1	MAPK9,COMMD1,BTRC,DCUN1D1,HUWE1,XIAP,SMAD7,BIRC2	pink	VSMC_M5
GO:0090162	0.08	0.98	4	27	establishment of epithelial cell polarity	BP	1	CLASP1,FAT1,OPHN1,TTC8	pink	VSMC_M5
GO:0009628	0.08	0.94	50	891	response to abiotic stimulus	BP	1	ANXA1,VEGFA,ASNS,GCLC,INIP,ADAM17,POLR2D,MAP3K2,DCLRE1C,FBXL3,MAP4K3,MAPK8,APAF1,PPP1CC,LXN,ARSB,POLK,BTG2,ATP2B4,ANO1,CAB39,GSK3B,PIK3CA,STK39,EGLN1,FAM162A,SCFD1,ATF2,ATM,ERO1A,HP1BP3,TIMP1,CPEB4,ATP7A,PIAS1,UBE2A,NF1,PRKAA1,NIPBL,RAD1,NFAT5,MT-CO1,MT-CO2,MT-ND3,MT-ND4,MT-ND5,BIRC2,MTPN,DDAH1,BMP2	pink	VSMC_M5
GO:0072599	0.08	0.98	4	34	establishment of protein localization to endoplasmic reticulum	BP	1	SRP72,SGTB,ZFAND2A,SRP54	pink	VSMC_M5
GO:0051248	0.08	0.94	46	813	negative regulation of protein metabolic process	BP	1	LATS1,UBR5,C9orf72,VEGFA,GCLC,TIA1,UFL1,POLR2D,CNOT10,XDH,BIRC6,SPRY4,CSNK2A1,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,KDM3A,LXN,TSG101,BTG2,ATP2B4,TRIP12,GSK3B,PUM1,FXR1,RPS6KA3,STYXL1,TIMP1,CRKL,OPHN1,CPEB4,UBE2Z,GSKIP,GGNBP2,USP14,XIAP,NF1,PRKAA1,SMAD7,BIRC2,AGO3,RNF139,SPINK8,PAIP2,BMP2	pink	VSMC_M5
GO:0001824	0.08	0.97	7	86	blastocyst development	BP	1	LATS1,N4BP2L2,GABPA,COPS2,UBE2A,PHF6,SMIM14	pink	VSMC_M5
GO:0006195	0.08	0.98	4	38	purine nucleotide catabolic process	BP	1	XDH,PDE5A,HPRT1,NUDT7	pink	VSMC_M5
GO:0046148	0.08	0.97	5	52	pigment biosynthetic process	BP	1	ZEB2,TRPC1,ABCB7,ATP7A,HPRT1	pink	VSMC_M5
GO:0030901	0.08	0.97	6	69	midbrain development	BP	1	SMAD1,CCDC14,ZNF148,YWHAQ,RAD1,ATP5PF	pink	VSMC_M5
GO:0003006	0.08	0.94	40	685	developmental process involved in reproduction	BP	1	SYNE1,LRGUK,UBR2,ANXA1,VEGFA,GCM1,RNF38,SEPT7,NCOA1,TBP,BIRC6,KITLG,KDM3A,RHOBTB3,TIPARP,ATP2B4,CSDE1,NOTCH2,PUM1,BPTF,TIAL1,PLEKHA1,HECTD1,PAFAH1B2,HERC4,RNF2,CRKL,PYGO1,FBXW11,ASH1L,ATRX,PIAS1,FEM1B,DIAPH2,GGNBP2,NIPBL,SETX,BIRC2,EIF5A2,PAIP2	pink	VSMC_M5
GO:0051668	0.08	0.94	32	537	localization within membrane	BP	1	EFR3A,SRP72,RHOQ,FAM126A,COMMD1,MACF1,RAB14,KIAA1109,MAGI2,FNTA,GOLGA7,MAPK8,VPS37A,SGTB,VPS29,ARL13B,SSR1,ATP2B4,TSPAN32,ZMYND8,HECTD1,SRP54,ACAP2,PRKCI,CRKL,CHM,TTC8,PTPN9,RAB11FIP4,GOLPH3L,TIMM9,ZDHHC22	pink	VSMC_M5
GO:0035264	0.08	0.96	9	108	multicellular organism growth	BP	1	MBD5,ATRN,TNKS2,NOTCH2,PIK3CA,PLEKHA1,ATRX,TTC8,NIPBL	pink	VSMC_M5
GO:0040014	0.08	0.97	5	47	regulation of multicellular organism growth	BP	1	MBD5,ATRN,TNKS2,PIK3CA,NIPBL	pink	VSMC_M5
GO:0090559	0.08	0.97	5	59	regulation of membrane permeability	BP	1	GCLC,PDCD6IP,MAPK8,GSK3B,ATF2	pink	VSMC_M5
GO:0021766	0.08	0.97	6	59	hippocampus development	BP	1	NCOA1,BTG2,ATP2B4,GSK3B,DLX2,CRKL	pink	VSMC_M5
GO:0097009	0.08	0.98	4	32	energy homeostasis	BP	1	MEX3C,ACACB,PIK3CA,PRKAA1	pink	VSMC_M5
GO:0060711	0.08	0.98	4	37	labyrinthine layer development	BP	1	GCM1,NCOA1,BIRC6,GGNBP2	pink	VSMC_M5
GO:0035924	0.08	0.97	6	62	cellular response to vascular endothelial growth factor stimulus	BP	1	ANXA1,VEGFA,JCAD,XDH,ATP2B4,PIK3CA	pink	VSMC_M5
GO:0016577	0.09	0.98	4	28	histone demethylation	BP	1	KDM3A,KDM2A,JMJD1C,KDM6A	pink	VSMC_M5
GO:0120034	0.09	0.96	8	92	positive regulation of plasma membrane bounded cell projection assembly	BP	1	WASL,RHOQ,SEPT7,ZMYND8,PIK3CA,ABI2,ARPC2,ATP7A	pink	VSMC_M5
GO:0031016	0.09	0.97	5	50	pancreas development	BP	1	ANXA1,RHEB,GSK3B,SRP54,SMAD2	pink	VSMC_M5
GO:0070304	0.09	0.96	8	99	positive regulation of stress-activated protein kinase signaling cascade	BP	1	KLHDC10,VEGFA,XDH,RB1CC1,PJA2,RNF13,STK39,BMP2	pink	VSMC_M5
GO:0034763	0.09	0.96	7	88	negative regulation of transmembrane transport	BP	1	COMMD1,IRS2,CAB39,STK39,YWHAQ,ATP7A,STXBP3	pink	VSMC_M5
GO:0045934	0.09	0.93	61	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	SCAF8,UBR5,VEGFA,RUNX2,GCLC,EPC1,PRDM5,SAP130,ZEB2,KAT6A,NR3C1,N4BP2L2,SHQ1,UBA3,TNKS2,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,BTRC,ID4,NOTCH2,TRIP12,ZMYND8,MEF2A,BPTF,TFIP11,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,KLHL15,RNF2,ATM,COPS2,YWHAQ,KAT6B,FBXW11,USP3,ATRX,PIAS1,SMAD2,NIPBL,PHF6,SMAD7,PTBP2,UBE2D3,USP9X,PEG3,RBAK,NAF1,BRMS1L,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0051438	0.09	0.97	4	43	regulation of ubiquitin-protein transferase activity	BP	1	BTRC,DCUN1D1,FEM1B,SMAD7	pink	VSMC_M5
GO:0045727	0.09	0.96	8	109	positive regulation of translation	BP	1	GUF1,POLR2D,YTHDF3,CDK5RAP1,EIF4G2,FXR1,METTL5,EIF5A2	pink	VSMC_M5
GO:0061458	0.09	0.94	22	333	reproductive system development	BP	1	ANXA1,VEGFA,GCM1,RNF38,NCOA1,BIRC6,KITLG,RHOBTB3,TIPARP,CSDE1,NOTCH2,BPTF,PLEKHA5,PLEKHA1,HECTD1,CRKL,ASH1L,ATRX,FEM1B,GGNBP2,NIPBL,BIRC2	pink	VSMC_M5

GO:0048732	0.09	0.94	22	335	gland development	BP	1	LATS1,ANXA1,VEGFA,ASNS,NCOA1,XDH,IRS2,RB1CC1,BTRC,NOTCH2,PIK3CA,ARHGAP5,SRP54,ATF2,CRKL,ASH1L,ATP7A,FEM1B,SMAD2,NF1,MT-CO2,BMP2	pink	VSMC_M5
GO:0016197	0.09	0.95	15	209	endosomal transport	BP	1	VTA1,SNX2,VPS54,RAB14,ZFYVE9,KIAA1109,ARL8B,RHOBTB3,VPS29,ZFYVE16,TBC1D23,LYST,ALS2,ACAP2,RAB11FIP4	pink	VSMC_M5
GO:0007034	0.09	0.95	11	137	vacuolar transport	BP	1	VTA1,VPS13A,C9orf72,VPS54,ARL8B,VPS37A,ZFYVE16,ARSB,TSG101,LYST,ALS2	pink	VSMC_M5
GO:0070727	0.09	0.93	79	1462	cellular macromolecule localization	BP	1	LATS1,SYNE1,SNX2,UBR5,KPNA5,EFR3A,VPS13A,WASL,CD2AP,SRP72,RHOQ,ERLEC1,FAM126A,COMMD1,MACF1,RAB1A,SEPT7,TIA1,RAB14,RAB33B,MAGI2,AKAP11,FNTA,GOLGA7,NEDD1,MAPK8,VPS37A,PCM1,TNKS2,VCPIP1,SGTB,ERBIN,VPS29,TCTN1,ZFYVE16,ARL13B,TSG101,SSR1,ATP2B4,TWF1,TSPAN32,BICD1,ZMYND8,IPO8,GSK3B,GOLGB1,ZFAND2A,PARL,CCDC14,TLK1,SCFD1,HECTD1,SRP54,ATM,PRKCI,YWHAQ,CRKL,RPAIN,PYGO1,WAPL,HUWE1,SNX11,ATRX,SPATA7,CHM,TTC8,PIK3C3,APPBP2,PTPN9,PRKAA1,NIPBL,SMAD7,STXBP3,UBE2D3,RAB18,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0060828	0.09	0.95	15	210	regulation of canonical Wnt signaling pathway	BP	1	LATS1,CSNK1G3,UBR5,USP34,ZEB2,TNKS2,CYLD,BTRC,GSK3B,USP8,WNK1,GSKIP,CSNK1A1,XIAP,BMP2	pink	VSMC_M5
GO:2000117	0.09	0.97	5	60	negative regulation of cysteine-type endopeptidase activity	BP	1	VEGFA,CSNK2A1,RPS6KA3,XIAP,BIRC2	pink	VSMC_M5
GO:0006900	0.09	0.97	5	55	vesicle budding from membrane	BP	1	WASL,RAB1A,PRKCI,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0018198	0.09	0.97	4	43	peptidyl-cysteine modification	BP	1	ZDHHC17,GOLGA7,ATP2B4,ZDHHC22	pink	VSMC_M5
GO:0044380	0.09	0.96	6	55	protein localization to cytoskeleton	BP	1	NEDD1,PCM1,BICD1,GSK3B,GOLGB1,CCDC14	pink	VSMC_M5
GO:0033043	0.09	0.93	55	950	regulation of organelle organization	BP	1	LATS1,MAPK9,C9orf72,WASL,ANXA1,TMEM33,CD2AP,GCLC,RHOQ,SEPT7,CAPZA2,RAB33B,MRE11,PDCD6IP,CLASP1,ZEB2,MAPK8,DLC1,TNKS2,ARFGEF1,RHOBTB3,TSG101,CEP97,TWF1,CYLD,NOTCH2,BICD1,ZMYND8,GSK3B,PIK3CA,FAM162A,PARL,SCFD1,ABI2,MORC2,ATF7IP,SKA1,STYXL1,ATM,ARPC2,ATL3,GHITM,WAPL,HUWE1,ATRX,TTC8,DYNC1H1,SMG1,PRKAA1,RAD1,FAM206A,GMFB,MTPN,NAF1,SAR1B	pink	VSMC_M5
GO:0046579	0.09	0.97	5	49	positive regulation of Ras protein signal transduction	BP	1	KITLG,ERBIN,NOTCH2,SHOC2,ALS2	pink	VSMC_M5
GO:0016571	0.09	0.95	10	118	histone methylation	BP	1	RLF,PRDM5,KMT2C,KDM3A,TET3,TET2,KMT5B,KDM6A,ASH1L,ATRX	pink	VSMC_M5
GO:1903214	0.09	0.97	4	39	regulation of protein targeting to mitochondrion	BP	1	PARL,HUWE1,PRKAA1,UBE2D3	pink	VSMC_M5
GO:1901576	0.09	0.92	207	4324	organic substance biosynthetic process	BP	1	DGKA,PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,SERINC1,EFR3A,DDX17,ELAVL2,PCSK5,WASL,ANXA1,GUF1,VEGFA,RUNX2,CYP39A1,SDHAF3,ASNS,GCM1,GCLC,AGMO,RHOQ,FAM126A,TAX1BP1,RLF,UGCG,ZNF292,COMMD1,DPY19L1,TIA1,UFL1,OSBPL9,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DGKH,KMT2C,EMSY,ZEB2,EPC2,KAT6A,OXSM,ZDHHC17,GOLGA7,EAF1,ZNF605,IRS2,TMTC3,PRKD3,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,TRPC1,FAR1,GFM2,NFS1,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,PIGP,GXYLT1,CYLD,BBX,BTRC,OGA,ID4,NOTCH2,ZMYND8,MEF2A,PRKAB2,TET2,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,WAPL,RFX7,FUT8,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ABCB7,SPTLC2,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,PIK3C3,CCNK,SMG1,ESCO1,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,CEPT1,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,AGO3,UBE2D3,ATP5PF,TMEM38B,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,PAIP2,BMP2,RNF219,ZDHHC22,DENR,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0071559	0.09	0.94	16	205	response to transforming growth factor beta	BP	1	LATS1,ADAM17,ZFYVE9,EPB41L5,FNTA,ZEB2,LTBP1,NR3C1,APAF1,SMAD1,CRKL,FUT8,SMAD2,SMAD7,USP9X,BMP2	pink	VSMC_M5
GO:0002244	0.10	0.96	8	96	hematopoietic progenitor cell differentiation	BP	1	UFL1,KITLG,N4BP2L2,MLF1,ATF2,SOS2,PYGO1,WDR78	pink	VSMC_M5
GO:0006482	0.10	0.97	4	30	protein demethylation	BP	1	KDM3A,KDM2A,JMJD1C,KDM6A	pink	VSMC_M5
GO:0008214	0.10	0.97	4	30	protein dealkylation	BP	1	KDM3A,KDM2A,JMJD1C,KDM6A	pink	VSMC_M5
GO:0045892	0.10	0.93	52	943	negative regulation of transcription, DNA-templated	BP	1	SCAF8,VEGFA,RUNX2,GCLC,EPC1,PRDM5,SAP130,ZEB2,KAT6A,NR3C1,N4BP2L2,UBA3,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,BPTF,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,FBXW11,USP3,ATRX,PIAS1,SMAD2,NIPBL,PHF6,SMAD7,UBE2D3,USP9X,PEG3,RBAK,BRMS1L,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0034613	0.10	0.92	78	1451	cellular protein localization	BP	1	LATS1,SYNE1,SNX2,UBR5,KPNA5,EFR3A,VPS13A,WASL,CD2AP,SRP72,RHOQ,ERLEC1,FAM126A,COMMD1,MACF1,RAB1A,SEPT7,TIA1,RAB14,RAB33B,MAGI2,AKAP11,FNTA,GOLGA7,NEDD1,MAPK8,VPS37A,PCM1,TNKS2,VCPIP1,SGTB,ERBIN,VPS29,TCTN1,ZFYVE16,ARL13B,TSG101,SSR1,ATP2B4,TWF1,TSPAN32,BICD1,ZMYND8,IPO8,GSK3B,GOLGB1,ZFAND2A,PARL,CCDC14,TLK1,SCFD1,HECTD1,SRP54,PRKCI,YWHAQ,CRKL,RPAIN,PYGO1,WAPL,HUWE1,SNX11,ATRX,SPATA7,CHM,TTC8,PIK3C3,APPBP2,PTPN9,PRKAA1,NIPBL,SMAD7,STXBP3,UBE2D3,RAB18,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5

GO:1903507	0.10	0.93	52	945	negative regulation of nucleic acid-templated transcription	BP	1	SCAF8,VEGFA,RUNX2,GCLC,EPC1,PRDM5,SAP130,ZEB2,KAT6A,NR3C1,N4BP2L2,UBA3,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,BPTF,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,FBXW11,USP3,ATRX,PIAS1,SMAD2,NIPBL,PHF6,SMAD7,UBE2D3,USP9X,PEG3,RBAK,BRMS1L,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0002066	0.10	0.97	4	35	columnar/cuboidal epithelial cell development	BP	1	RHEB,IL6ST,GSK3B,YIPF6	pink	VSMC_M5
GO:0090150	0.10	0.94	13	210	establishment of protein localization to membrane	BP	1	SRP72,MACF1,GOLGA7,MAPK8,VPS37A,SGTB,SSR1,SRP54,PRKCI,CHM,GOLPH3L,TIMM9,ZDHHC22	pink	VSMC_M5
GO:0021587	0.10	0.97	4	33	cerebellum morphogenesis	BP	1	OPHN1,HERC1,ATP7A,MTPN	pink	VSMC_M5
GO:1902679	0.10	0.92	52	946	negative regulation of RNA biosynthetic process	BP	1	SCAF8,VEGFA,RUNX2,GCLC,EPC1,PRDM5,SAP130,ZEB2,KAT6A,NR3C1,N4BP2L2,UBA3,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,BPTF,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,FBXW11,USP3,ATRX,PIAS1,SMAD2,NIPBL,PHF6,SMAD7,UBE2D3,USP9X,PEG3,RBAK,BRMS1L,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0045017	0.10	0.94	14	214	glycerolipid biosynthetic process	BP	1	DGKA,EFR3A,AGMO,FAM126A,DGKH,IMPAD1,MTMR6,FAR1,PIGP,PIK3CA,ATM,PIK3C3,SMG1,CEPT1	pink	VSMC_M5
GO:0010629	0.10	0.93	43	766	negative regulation of gene expression	BP	1	DDX17,ANXA1,VEGFA,CD2AP,TIA1,EPC1,POLR2D,CNOT10,XDH,SHQ1,CAPRIN1,YTHDF3,LSM14A,ERBIN,SMAD1,TIPARP,BTG2,ATP2B4,CSDE1,CYLD,NOTCH2,ACACB,PUM1,FXR1,TIAL1,ZNF148,MORC2,ATF7IP,SMG7,ATM,CRKL,CPEB4,SMAD2,GGNBP2,SMG1,XIAP,PRKAA1,SMAD7,PTBP2,AGO3,RNF139,PAIP2,BMP2	pink	VSMC_M5
GO:0006661	0.10	0.95	9	115	phosphatidylinositol biosynthetic process	BP	1	EFR3A,FAM126A,IMPAD1,MTMR6,PIGP,PIK3CA,ATM,PIK3C3,SMG1	pink	VSMC_M5
GO:0009261	0.10	0.97	4	40	ribonucleotide catabolic process	BP	1	XDH,PDE5A,HPRT1,NUDT7	pink	VSMC_M5
GO:0035601	0.10	0.95	8	99	protein deacylation	BP	1	VEGFA,PRDM5,FNTA,MAPK8,MSL3,PRKAA1,NIPBL,BRMS1L	pink	VSMC_M5
GO:0019219	0.10	0.91	145	2852	regulation of nucleobase-containing compound metabolic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,UBR5,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,TIA1,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,YTHDF3,TNKS2,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,TRIP12,ZMYND8,MEF2A,TET2,KMT5B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,TFIP11,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,KLHL15,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CCNK,SMG1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,PTBP2,NFAT5,MT-CO2,BIRC2,UBE2D3,USP9X,UBE2V2,MTPN,PEG3,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0090287	0.10	0.94	17	230	regulation of cellular response to growth factor stimulus	BP	1	LATS1,RUNX2,ADAM17,JCAD,ZEB2,XDH,ZDHHC17,LTBP1,SPRY4,ATP2B4,NOTCH2,FSTL1,SMAD2,XIAP,SMAD7,UBE2D3,BMP2	pink	VSMC_M5
GO:0035556	0.10	0.92	110	2063	intracellular signal transduction	BP	1	DGKA,ARFGEF3,TAB2,LATS1,MAPK9,KLHDC10,UBR2,C9orf72,VEGFA,KRIT1,CD2AP,RHOQ,UFL1,CUL1,CUL2,RAB33B,JCAD,ARHGAP42,SRPK2,MRE11,MAGI2,MAP3K2,AKAP11,DGKH,RHEB,XDH,KAT6A,ZDHHC17,NKIRAS1,KITLG,PRKD3,SPRY4,MAP4K3,MAPK8,APAF1,DLC1,RB1CC1,IFIT5,LSM14A,PJA2,ARFGEF1,ERBIN,URI1,SMAD1,NR3C2,RHOBTB3,RNF13,PPP1CC,RALGAPB,HIPK1,PPP3CC,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,DOCK3,NOTCH2,ASB7,CAB39,MEF2A,SHOC2,GSK3B,PUM1,PIK3CA,UBR1,STK39,TIAL1,ALS2,TLK1,PLEKHA1,ABI2,ARHGAP5,RPS6KA3,ATF2,STYXL1,RALGPS2,SOS2,ATM,CUL5,ERO1A,PRKCI,YWHAQ,USP8,CRKL,WNK1,OPHN1,ASH1L,ATRX,CHM,FEM1B,SMAD2,PIK3C3,GSKIP,SMG1,XIAP,NF1,PRKAA1,RAD1,SETX,PKN2,NFAT5,BIRC2,AGO3,TMEM38B,RAB18,DDAH1,BMT2,BMP2	pink	VSMC_M5
GO:0022607	0.10	0.91	117	2230	cellular component assembly	BP	1	VTA1,LATS1,MAPK9,LRGUK,C9orf72,WASL,VEGFA,CD2AP,SDHAF3,DST,RHOQ,UGCG,MACF1,RAB1A,SEPT7,NFU1,CAPZA2,RAB14,RAB33B,SCLT1,WDCP,BBS12,SRPK2,TBP,POLR2D,YME1L1,PDCD6IP,CLASP1,EPB41L5,FLRT3,XDH,ARL8B,KAT6A,SHQ1,MAGI1,DLC1,RB1CC1,VPS37A,PCM1,YTHDF3,VCPIP1,LSM14A,ARFGEF1,SMAD1,NFS1,TCTN1,ARL13B,FAM92A,TSG101,HIPK1,CEP97,CSDE1,TWF1,CYLD,RANBP9,PSMG1,NDUFS4,ACOT13,BICD1,KCTD3,ZMYND8,MEF2A,ACACB,GSK3B,PIK3CA,DNAAF5,FXR1,TFIP11,PSMC6,ALS2,ZNF148,SCFD1,ABI2,ATF7IP,GLRX3,SRP54,STYXL1,ATM,ARPC2,HP1BP3,ATL3,CRKL,KAT6B,GTF2A2,OPHN1,MLH3,ABCB7,ATRX,ATP7A,PIAS1,NAP1L3,TTC8,SMAD2,PSTPIP2,PIK3C3,DYNC1H1,WDR78,STAG2,PRKAA1,CPLANE1,HPRT1,SMAD7,PRPF8,SETX,PKN2,MT-ND4,MT-ND5,BIRC2,AGO3,FAM206A,GMFB,UBE2V2,MTPN,NAF1,UBXN2A,SAR1B,DENR	pink	VSMC_M5
GO:0016579	0.10	0.95	9	108	protein deubiquitination	BP	1	USP34,VCPIP1,CYLD,USP8,USP3,USP14,USP33,MINDY3,USP9X	pink	VSMC_M5
GO:0006497	0.10	0.96	6	81	protein lipidation	BP	1	UGCG,ZDHHC17,GOLGA7,PIGP,PIK3C3,ZDHHC22	pink	VSMC_M5

GO:0034645	0.10	0.91	173	3533	cellular macromolecule biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,GUF1,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,UGCG,ZNF292,COMMD1,DPY19L1,TIA1,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,KMT2C,EMSY,ZEB2,EPC2,KAT6A,ZDHHC17,GOLGA7,EAF1,ZNF605,IRS2,TMTC3,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,GFM2,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,PIGP,GXYLT1,CYLD,BBX,BTRC,OGA,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,WAPL,RFX7,FUT8,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,PIK3C3,CCNK,ESCO1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,PAIP2,BMP2,RNF219,ZDHHC22,DENR,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0006304	0.11	0.95	7	84	DNA modification	BP	1	RLF,TET3,TET2,PIK3CA,ATF7IP,ATRX,USP9X	pink	VSMC_M5
GO:0048193	0.11	0.94	17	259	Golgi vesicle transport	BP	1	SNX2,VPS13A,COMMD1,MACF1,VPS54,RAB1A,RAB14,RAB33B,GOLGA7,COG6,GOLGA5,SCFD1,PRKCI,TRAPPC2L,RNF139,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0033135	0.11	0.95	8	104	regulation of peptidyl-serine phosphorylation	BP	1	LATS1,VEGFA,ATP2B4,PIK3CA,CREBL2,GGNBP2,PRKAA1,SMAD7	pink	VSMC_M5
GO:0000045	0.11	0.95	7	88	autophagosome assembly	BP	1	C9orf72,RAB1A,RAB33B,RB1CC1,SCFD1,PIK3C3,UBXN2A	pink	VSMC_M5
GO:0048592	0.11	0.94	10	118	eye morphogenesis	BP	1	VEGFA,FAT1,HIPK1,NOTCH2,ABI2,PRKCI,TTC8,NF1,PTPRM,NIPBL	pink	VSMC_M5
GO:0030509	0.11	0.94	10	116	BMP signaling pathway	BP	1	RUNX2,SMAD1,NOTCH2,FSTL1,SMAD2,XIAP,SMAD7,UBE2D3,USP9X,BMP2	pink	VSMC_M5
GO:0046907	0.11	0.91	68	1261	intracellular transport	BP	1	RELCH,VTA1,SNX2,UBR5,KPNA5,VPS13A,WASL,SRP72,DST,ERLEC1,LCA5,VPS54,RAB1A,RAB14,ZFYVE9,BBS12,KIAA1109,POLR2D,ARL8B,GOLGA7,MAPK8,VPS37A,PCM1,SGTB,ERBIN,RHOBTB3,VPS29,PPP1CC,ZFYVE16,TBC1D23,TSG101,SSR1,ZC3H11A,BICD1,IPO8,GSK3B,LYST,ZFAND2A,PARL,ALS2,TLK1,SCFD1,SMG7,SRP54,ACAP2,NEMF,PRKCI,YWHAQ,RPAIN,HUWE1,SNX11,FBXW11,CHM,PIK3C3,APPBP2,DYNC1H1,SMG1,RAB11FIP4,PRKAA1,TRAPPC2L,STXBP3,UBE2D3,ATP5PF,RAB18,RNF139,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0006305	0.11	0.96	5	53	DNA alkylation	BP	1	RLF,TET3,PIK3CA,ATF7IP,ATRX	pink	VSMC_M5
GO:0006306	0.11	0.96	5	53	DNA methylation	BP	1	RLF,TET3,PIK3CA,ATF7IP,ATRX	pink	VSMC_M5
GO:0001892	0.11	0.95	6	67	embryonic placenta development	BP	1	GCM1,NCOA1,BIRC6,BPTF,HECTD1,GGNBP2	pink	VSMC_M5
GO:0030879	0.11	0.95	9	114	mammary gland development	BP	1	LATS1,VEGFA,NCOA1,XDH,IRS2,BTRC,ARHGAP5,ATP7A,MT-CO2	pink	VSMC_M5
GO:0016575	0.11	0.95	6	71	histone deacetylation	BP	1	VEGFA,PRDM5,MAPK8,MSL3,NIPBL,BRMS1L	pink	VSMC_M5
GO:0000122	0.11	0.92	39	694	negative regulation of transcription by RNA polymerase II	BP	1	SCAF8,VEGFA,EPC1,PRDM5,SAP130,ZEB2,NR3C1,N4BP2L2,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,TSG101,BTG2,ID4,NOTCH2,MEF2A,BPTF,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,USP3,ATRX,PIAS1,NIPBL,PHF6,SMAD7,UBE2D3,USP9X,PEG3,BRMS1L,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0001890	0.11	0.94	9	117	placenta development	BP	1	GCM1,NCOA1,BIRC6,NOTCH2,BPTF,HECTD1,ASH1L,GGNBP2,BIRC2	pink	VSMC_M5
GO:0098732	0.11	0.95	8	102	macromolecule deacylation	BP	1	VEGFA,PRDM5,FNTA,MAPK8,MSL3,PRKAA1,NIPBL,BRMS1L	pink	VSMC_M5
GO:0061008	0.12	0.94	9	119	hepaticobiliary system development	BP	1	ANXA1,ASNS,RB1CC1,NOTCH2,PIK3CA,ATF2,ATP7A,NF1,NIPBL	pink	VSMC_M5
GO:0045010	0.12	0.96	4	44	actin nucleation	BP	1	WASL,ABI2,ARPC2,GMFB	pink	VSMC_M5
GO:0045685	0.12	0.96	5	54	regulation of glial cell differentiation	BP	1	RHEB,IL6ST,DLX2,NF1,BMP2	pink	VSMC_M5
GO:0008637	0.12	0.95	6	87	apoptotic mitochondrial changes	BP	1	GCLC,MAPK8,GSK3B,FAM162A,ATF2,GHITM	pink	VSMC_M5
GO:0035270	0.12	0.95	7	87	endocrine system development	BP	1	ANXA1,RHEB,GSK3B,CRKL,SMAD2,NF1,BMP2	pink	VSMC_M5
GO:0036293	0.12	0.93	17	258	response to decreased oxygen levels	BP	1	VEGFA,ADAM17,APAF1,EGLN1,FAM162A,SCFD1,ERO1A,HP1BP3,CPEB4,ATP7A,NF1,PRKAA1,MT-ND4,MT-ND5,BIRC2,DDAH1,BMP2	pink	VSMC_M5
GO:0043433	0.12	0.94	9	126	negative regulation of DNA-binding transcription factor activity	BP	1	TAX1BP1,COMMD1,UFL1,ERBIN,CYLD,BTRC,EGLN1,RNF2,SMAD7	pink	VSMC_M5
GO:0048259	0.12	0.95	7	85	regulation of receptor-mediated endocytosis	BP	1	MKLN1,WASL,VEGFA,CD2AP,MAGI2,BICD1,OPHN1	pink	VSMC_M5
GO:0003407	0.12	0.95	5	49	neural retina development	BP	1	HIPK1,ATP2B4,DLX2,TTC8,PTPRM	pink	VSMC_M5
GO:0009792	0.12	0.91	32	537	embryo development ending in birth or egg hatching	BP	1	LATS1,MTHFD1L,PCSK5,VEGFA,RUNX2,GCM1,NCOA1,EPB41L5,BIRC6,N4BP2L2,DLC1,TCTN1,GABPA,ARL13B,NOTCH2,BPTF,ALS2,UBR3,HECTD1,DLX2,ATF2,COPS2,FUT8,ATP7A,SMAD2,GGNBP2,UBE2A,NIPBL,PHF6,MT-ND4,SMIM14,BMP2	pink	VSMC_M5
GO:0048593	0.12	0.94	8	96	camera-type eye morphogenesis	BP	1	VEGFA,FAT1,HIPK1,NOTCH2,ABI2,TTC8,NF1,PTPRM	pink	VSMC_M5
GO:0010171	0.12	0.96	4	38	body morphogenesis	BP	1	CLASP1,TIPARP,PLEKHA1,NIPBL	pink	VSMC_M5
GO:0000723	0.12	0.94	9	118	telomere maintenance	BP	1	MRE11,DCLRE1C,TNKS2,DCLRE1A,TFIP11,ATM,ATRX,SMG1,NAF1	pink	VSMC_M5
GO:0036503	0.12	0.94	7	99	ERAD pathway	BP	1	ERLEC1,NGLY1,SGTB,PSMC6,USP14,RNF103,RNF139	pink	VSMC_M5
GO:0048608	0.12	0.92	21	330	reproductive structure development	BP	1	ANXA1,VEGFA,GCM1,RNF38,NCOA1,BIRC6,KITLG,RHOBTB3,TIPARP,CSDE1,NOTCH2,BPTF,PLEKHA1,HECTD1,CRKL,ASH1L,ATRX,FEM1B,GGNBP2,NIPBL,BIRC2	pink	VSMC_M5
GO:0010921	0.12	0.95	6	68	regulation of phosphatase activity	BP	1	MAGI2,URI1,PPP6R3,GSK3B,STYXL1,BMP2	pink	VSMC_M5
GO:0043604	0.12	0.91	34	672	amide biosynthetic process	BP	1	PCSK5,GUF1,ASNS,GCLC,UGCG,TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,EIF4G2,GFM2,DPH6,BTG2,CSDE1,ACACB,PUM1,FXR1,METTL5,RPS6KA3,NEMF,CPEB4,SPTLC2,PRKAA1,HACD1,AGO3,MTPN,EIF5A2,RNF139,PAIP2,DENR	pink	VSMC_M5

GO:0048523	0.12	0.89	183	3647	negative regulation of cellular process	BP	1	TAB2,LATS1,SCAF8,UBR5,UBR2,C9orf72,WASL,ANXA1,VEGFA,KRIT1,RUNX2,CD2AP,ASNS,GCLC,RHOQ,ERLEC1,TAX1BP1,COMMD1,TIA1,ADAM17,CAPZA2,UFL1,RAB33B,ARHGAP42,BBS12,EPC1,MRE11,PRDM5,SAP130,POLR2D,MAGI2,YME1L1,CNOT10,CLASP1,EPB41L5,ZEB2,XDH,KAT6A,BIRC6,LTBP1,IRS2,KITLG,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,DLC1,RB1CC1,IL6ST,CSNK2A1,CAPRIN1,PCM1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,EIF4G2,CGGBP1,TRPC1,DIP2B,BTBD10,PCGF1,GABPA,WWP1,PIP4P2,LXN,TSG101,ARID2,BTG2,ATP2B4,CEP97,TWF1,CYLD,RANBP9,BTRC,TSPAN32,ID4,NOTCH2,TRIP12,BICD1,CAB39,ZMYND8,MEF2A,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,BPTF,FXR1,TFIP11,STK39,KDM2A,TIAL1,PLEKHA1,ZNF148,SCFD1,HECTD1,DLX2,ATF7IP,RPS6KA3,ATF2,KLHL15,HERC4,STYXL1,RNF2,ST7L,ATM,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,KAT6B,WNK1,GHITM,PDS5A,WAPL,HUWE1,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ABCB7,ATRX,ATP7A,PIAS1,FEM1B,SMAD2,GSKIP,GGNBP2,PTPN9,SMG1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,PTPRM,NIPBL,RAD1,PHF6,SMAD7,SETX,STXBP3,PTBP2,BIRC2,AGO3,UBE2D3,ATP5PF,TMEM38B,USP9X,GMFB,UBE2V2,MTPN,CD164,CACYBP,PEG3,RBAK,NAF1,BRMS1L,RNF139,DDAH1,BMT2,SPINK8,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0042158	0.12	0.95	6	84	lipoprotein biosynthetic process	BP	1	UGCG,ZDHHC17,GOLGA7,PIGP,PIK3C3,ZDHHC22	pink	VSMC_M5
GO:0006793	0.12	0.90	110	2169	phosphorus metabolic process	BP	1	DGKA,TAB2,PPIL4,LATS1,MAPK9,CSNK1G3,SERINC1,EFR3A,LRGUK,C9orf72,VEGFA,PTP4A1,RHOQ,FAM126A,ADAM17,SRPK2,MRE11,MAGI2,MAP3K2,DGKH,PTPN4,XDH,OXSM,BIRC6,IRS2,KITLG,PRKD3,SPRY4,MAP4K3,MAPK8,DLC1,RB1CC1,IL6ST,CSNK2A1,IMPAD1,MTMR6,CDK5RAP1,URI1,SMAD1,BTBD10,FAR1,NFS1,PPP1CC,DUSP11,CPNE3,PIP4P2,GTF2H1,TSG101,HIPK1,PPP3CC,ATP2B4,TWF1,IRAK4,PIGP,BTRC,NDUFS4,DOCK3,CAB39,PPP6R3,PRKAB2,ACACB,GSK3B,PIK3CA,FXR1,STK39,ADAL,ALS2,RPS6KC1,PDE5A,TLK1,ABI2,RPS6KA3,CREBL2,SMG7,ATF2,STYXL1,ATM,PRKCI,COPS2,CRKL,WNK1,FUT8,PGM2,FBXW11,SPTLC2,SMAD2,PIK3C3,GSKIP,CCNK,GGNBP2,PTPN9,SMG1,CSNK1A1,NF1,PRKAA1,PTPRM,HPRT1,SMAD7,CEPT1,SLC35A3,NUDT7,PKN2,MT-CO2,SULT1C4,HACD1,ATP5PF,TMEM38B,GMFB,BMP2,DCAKD	pink	VSMC_M5
GO:1905037	0.12	0.94	7	92	autophagosome organization	BP	1	C9orf72,RAB1A,RAB33B,RB1CC1,SCFD1,PIK3C3,UBXN2A	pink	VSMC_M5
GO:0010507	0.13	0.95	6	67	negative regulation of autophagy	BP	1	TAB2,EIF4G2,PIK3CA,SCFD1,HERC1,SMG1	pink	VSMC_M5
GO:0001666	0.13	0.92	16	244	response to hypoxia	BP	1	VEGFA,ADAM17,APAF1,EGLN1,FAM162A,SCFD1,ERO1A,HP1BP3,ATP7A,NF1,PRKAA1,MT-ND4,MT-ND5,BIRC2,DDAH1,BMP2	pink	VSMC_M5
GO:0072678	0.13	0.96	4	42	T cell migration	BP	1	ADAM17,STK39,CRKL,WNK1	pink	VSMC_M5
GO:0033865	0.13	0.94	7	102	nucleoside bisphosphate metabolic process	BP	1	OXSM,FAR1,ACACB,NUDT7,SULT1C4,HACD1,DCAKD	pink	VSMC_M5
GO:0033875	0.13	0.94	7	102	ribonucleoside bisphosphate metabolic process	BP	1	OXSM,FAR1,ACACB,NUDT7,SULT1C4,HACD1,DCAKD	pink	VSMC_M5
GO:0034032	0.13	0.94	7	102	purine nucleoside bisphosphate metabolic process	BP	1	OXSM,FAR1,ACACB,NUDT7,SULT1C4,HACD1,DCAKD	pink	VSMC_M5
GO:0033173	0.13	0.96	4	38	calcineurin-NFAT signaling cascade	BP	1	PPP3CC,ATP2B4,GSK3B,NFAT5	pink	VSMC_M5
GO:0060968	0.13	0.95	5	59	regulation of gene silencing	BP	1	PUM1,FXR1,TIAL1,MORC2,ATF7IP	pink	VSMC_M5
GO:0043009	0.13	0.91	31	522	chordate embryonic development	BP	1	LATS1,MTHFD1L,PCSK5,VEGFA,RUNX2,GCM1,NCOA1,EPB41L5,BIRC6,N4BP2L2,DLC1,TCTN1,GABPA,ARL13B,NOTCH2,BPTF,ALS2,HECTD1,DLX2,ATF2,COPS2,FUT8,ATP7A,SMAD2,GGNBP2,UBE2A,NIPBL,PHF6,MT-ND4,SMIM14,BMP2	pink	VSMC_M5
GO:0055123	0.13	0.94	8	99	digestive system development	BP	1	PCSK5,EPB41L5,IL6ST,SRP54,CRKL,YIPF6,SMAD2,NIPBL	pink	VSMC_M5
GO:0006470	0.13	0.92	15	228	protein dephosphorylation	BP	1	PTP4A1,MAGI2,PTPN4,DLC1,MTMR6,PPP1CC,DUSP11,PPP3CC,BTRC,PPP6R3,GSK3B,STYXL1,FBXW11,PTPN9,PTPRM	pink	VSMC_M5
GO:0022414	0.13	0.90	55	1029	reproductive process	BP	1	SYNE1,LRGUK,VPS13A,PCSK5,UBR2,ANXA1,VEGFA,GCM1,RNF38,SEPT7,NCOA1,TBP,MRE11,TOP2B,BIRC6,KITLG,YTHDF3,KDM3A,SMAD1,RHOBTB3,TIPARP,ATP2B4,CSDE1,NOTCH2,PUM1,BPTF,TIAL1,PLEKHA1,ZNF148,HECTD1,PAFAH1B2,HERC4,RNF2,ATM,TIMP1,CRKL,PYGO1,FBXW11,ASH1L,MLH3,ATRX,ATP7A,PIAS1,FEM1B,DIAPH2,GGNBP2,UBE2A,STAG2,NIPBL,RAD1,SETX,BIRC2,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0051253	0.13	0.90	55	1032	negative regulation of RNA metabolic process	BP	1	SCAF8,VEGFA,RUNX2,GCLC,EPC1,PRDM5,SAP130,ZEB2,KAT6A,NR3C1,N4BP2L2,SHQ1,UBA3,ZMYM5,URI1,CGGBP1,PCGF1,GABPA,WWP1,TSG101,BTG2,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,BPTF,KDM2A,ZNF148,DLX2,ATF7IP,ATF2,RNF2,COPS2,YWHAQ,KAT6B,FBXW11,USP3,ATRX,PIAS1,SMAD2,NIPBL,PHF6,SMAD7,PTBP2,UBE2D3,USP9X,PEG3,RBAK,NAF1,BRMS1L,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0046902	0.13	0.96	4	50	regulation of mitochondrial membrane permeability	BP	1	GCLC,MAPK8,GSK3B,ATF2	pink	VSMC_M5
GO:0046488	0.13	0.93	10	138	phosphatidylinositol metabolic process	BP	1	EFR3A,FAM126A,IMPAD1,MTMR6,PIP4P2,PIGP,PIK3CA,ATM,PIK3C3,SMG1	pink	VSMC_M5

GO:0009058	0.13	0.89	208	4393	biosynthetic process	BP	1	DGKA,PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,SERINC1,EFR3A,DDX17,ELAVL2,PCSK5,WASL,ANXA1,GUF1,VEGFA,RUNX2,CYP39A1,SDHAF3,ASNS,GCM1,GCLC,AGMO,RHOQ,FAM126A,TAX1BP1,RLF,UGCG,ZNF292,COMMD1,DPY19L1,TIA1,UFL1,OSBPL9,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DGKH,KMT2C,EMSY,ZEB2,EPC2,KAT6A,OXSM,ZDHHC17,GOLGA7,EAF1,ZNF605,IRS2,TMTC3,PRKD3,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,IMPAD1,MTMR6,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,TRPC1,FAR1,GFM2,NFS1,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,PIGP,GXYLT1,CYLD,BBX,BTRC,OGA,ID4,NOTCH2,ZMYND8,MEF2A,PRKAB2,TET2,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,WAPL,RFX7,FUT8,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ABCB7,SPTLC2,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,PIK3C3,CCNK,SMG1,ESCO1,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,CEPT1,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,AGO3,UBE2D3,ATP5PF,TMEM38B,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,DDAH1,PAIP2,BMP2,RNF219,ZDHHC22,DENR,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0030041	0.13	0.93	11	160	actin filament polymerization	BP	1	LATS1,WASL,CAPZA2,ARFGEF1,TWF1,ABI2,ARPC2,PSTPIP2,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0043502	0.13	0.94	6	71	regulation of muscle adaptation	BP	1	IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,MTPN	pink	VSMC_M5
GO:0000003	0.13	0.90	55	1031	reproduction	BP	1	SYNE1,LRGUK,VPS13A,PCSK5,UBR2,ANXA1,VEGFA,GCM1,RNF38,SEPT7,NCOA1,TBP,MRE11,TOP2B,BIRC6,KITLG,YTHDF3,KDM3A,SMAD1,RHOBTB3,TIPARP,ATP2B4,CSDE1,NOTCH2,PUM1,BPTF,TIAL1,PLEKHA1,ZNF148,HECTD1,PAFAH1B2,HERC4,RNF2,ATM,TIMP1,CRKL,PYGO1,FBXW11,ASH1L,MLH3,ATRX,ATP7A,PIAS1,FEM1B,DIAPH2,GGNBP2,UBE2A,STAG2,NIPBL,RAD1,SETX,BIRC2,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0009266	0.13	0.93	9	137	response to temperature stimulus	BP	1	GCLC,POLR2D,LXN,ANO1,GSK3B,ATM,ERO1A,PRKAA1,MT-CO2	pink	VSMC_M5
GO:0050878	0.13	0.92	17	273	regulation of body fluid levels	BP	1	DGKA,VEGFA,UGCG,NCOA1,AKAP11,DGKH,XDH,IL6ST,TSPAN32,PIK3CA,STK39,JMJD1C,WNK1,ATP7A,F8,STXBP3,MT-CO2	pink	VSMC_M5
GO:0007276	0.13	0.91	27	469	gamete generation	BP	1	SYNE1,LRGUK,UBR2,SEPT7,TBP,KDM3A,SMAD1,ATP2B4,PUM1,TIAL1,PLEKHA1,ZNF148,PAFAH1B2,HERC4,RNF2,CRKL,PYGO1,FBXW11,MLH3,ATRX,PIAS1,DIAPH2,GGNBP2,SETX,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0043271	0.13	0.94	7	93	negative regulation of ion transport	BP	1	COMMD1,CAB39,STK39,YWHAQ,WNK1,ATP7A,ATP5PF	pink	VSMC_M5
GO:0008610	0.13	0.91	29	544	lipid biosynthetic process	BP	1	DGKA,SERINC1,EFR3A,ANXA1,CYP39A1,AGMO,FAM126A,UGCG,OSBPL9,DGKH,OXSM,PRKD3,IMPAD1,MTMR6,FAR1,PIGP,PRKAB2,ACACB,PIK3CA,CREBL2,ATM,SPTLC2,PIK3C3,SMG1,PRKAA1,CEPT1,HACD1,TMEM38B,BMP2	pink	VSMC_M5
GO:0031328	0.13	0.89	79	1503	positive regulation of cellular biosynthetic process	BP	1	MED23,SCAF8,DDX17,WASL,ANXA1,GUF1,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,ASXL2,POLR2D,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,IRS2,NR3C1,GPBP1,YTHDF3,TNKS2,CDK5RAP1,ARFGEF1,KDM3A,ZNF507,SMAD1,EIF4G2,GABPA,TET3,GTF2H1,TSG101,BTRC,MEF2A,TET2,GTF2I,BPTF,FXR1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ABCB7,ATRX,ATP7A,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,MT-CO2,BIRC2,CACYBP,PEG3,EIF5A2,ZNF770,NAF1,DDAH1,BMP2	pink	VSMC_M5
GO:0009059	0.14	0.88	173	3569	macromolecule biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,GUF1,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,UGCG,ZNF292,COMMD1,DPY19L1,TIA1,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,KMT2C,EMSY,ZEB2,EPC2,KAT6A,ZDHHC17,GOLGA7,EAF1,ZNF605,IRS2,TMTC3,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,GFM2,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,PIGP,GXYLT1,CYLD,BBX,BTRC,OGA,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,WAPL,RFX7,FUT8,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,PIK3C3,CCNK,ESCO1,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,MTPN,CACYBP,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,PAIP2,BMP2,RNF219,ZDHHC22,DENR,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0007163	0.14	0.92	14	189	establishment or maintenance of cell polarity	BP	1	KRIT1,DST,PDCD6IP,CLASP1,FAT1,ARFGEF1,ERBIN,RHOBTB3,GSK3B,PRKCI,CRKL,OPHN1,FBXW11,TTC8	pink	VSMC_M5
GO:0046530	0.14	0.95	4	41	photoreceptor cell differentiation	BP	1	VEGFA,DLX2,PRKCI,TTC8	pink	VSMC_M5
GO:1901136	0.14	0.93	8	126	carbohydrate derivative catabolic process	BP	1	XDH,NGLY1,OGA,ADAL,PDE5A,PGM2,HPRT1,NUDT7	pink	VSMC_M5
GO:0071385	0.14	0.95	4	43	cellular response to glucocorticoid stimulus	BP	1	ANXA1,NR3C1,USP8,MT-ND3	pink	VSMC_M5
GO:1990830	0.14	0.94	6	77	cellular response to leukemia inhibitory factor	BP	1	PRDM5,SPRY4,KDM3A,SMAD7,CACYBP,UBXN2A	pink	VSMC_M5

GO:0007041	0.14	0.93	8	100	lysosomal transport	BP	1	C9orf72,VPS54,ARL8B,ZFYVE16,ARSB,TSG101,LYST,AL S2	pink	VSMC_M5
GO:0008064	0.14	0.92	11	159	regulation of actin polymerization or depolymerization	BP	1	LATS1,WASL,CAPZA2,ARFGEF1,TWF1,PIK3CA,ABI2,AR PC2,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0045995	0.14	0.94	5	50	regulation of embryonic development	BP	1	SEPT7,RAB14,CLASP1,TRIP12,NIPBL	pink	VSMC_M5
GO:2000779	0.14	0.94	6	76	regulation of double-strand break repair	BP	1	UBR5,ARID2,TRIP12,KMT5B,TFIP11,KLHL15	pink	VSMC_M5
GO:0051252	0.14	0.88	134	2654	regulation of RNA metabolic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VE GFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292 ,COMMD1,TIA1,UFL1,SRPK2,NCOA1,EPC1,TBP,PRDM 5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EM SY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,S HQ1,UBA3,MAPK8,GPBP1,YTHDF3,ZMYM5,KDM3A,E RBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,G ABPA,TET3,WWP1,MLF1,GTF2H1,VIRMA,MED13L,TS G101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYL D,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,PUM 1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,TIA L1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS 6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ, HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,RFX7,GTF2A2, FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CC NK,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,PTBP2,N FAT5,BIRC2,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF77 0,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,ZNF619,ZBT B6,MXD1	pink	VSMC_M5
GO:0038202	0.14	0.95	4	40	TORC1 signaling	BP	1	C9orf72,ATM,SMG1,BMT2	pink	VSMC_M5
GO:0006892	0.14	0.93	8	99	post-Golgi vesicle-mediated transport	BP	1	VPS13A,COMMD1,MACF1,VPS54,RAB14,GOLGA7,SC FD1,GOLPH3L	pink	VSMC_M5
GO:0030833	0.14	0.92	10	145	regulation of actin filament polymerization	BP	1	LATS1,WASL,CAPZA2,ARFGEF1,TWF1,ABI2,ARPC2,FA M206A,GMFB,MTPN	pink	VSMC_M5
GO:1990823	0.14	0.94	6	78	response to leukemia inhibitory factor	BP	1	PRDM5,SPRY4,KDM3A,SMAD7,CACYBP,UBXN2A	pink	VSMC_M5
GO:0061647	0.14	0.95	4	38	histone H3-K9 modification	BP	1	PRDM5,KDM3A,ASH1L,ATRX	pink	VSMC_M5
GO:0000819	0.14	0.92	11	168	sister chromatid segregation	BP	1	LATS1,MRE11,TOP2B,ATM,PDS5A,WAPL,ATRX,ESCO1 ,STAG2,NIPBL,RMDN1	pink	VSMC_M5
GO:0007179	0.14	0.92	12	156	transforming growth factor beta receptor signaling pathway	BP	1	LATS1,ADAM17,ZFYVE9,FNTA,ZEB2,LTBP1,SMAD1,FU T8,SMAD2,SMAD7,USP9X,BMP2	pink	VSMC_M5
GO:0030832	0.14	0.92	11	160	regulation of actin filament length	BP	1	LATS1,WASL,CAPZA2,ARFGEF1,TWF1,PIK3CA,ABI2,AR PC2,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0097720	0.14	0.95	4	40	calcineurin-mediated signaling	BP	1	PPP3CC,ATP2B4,GSK3B,NFAT5	pink	VSMC_M5
GO:0046578	0.15	0.92	12	161	regulation of Ras protein signal transduction	BP	1	ARFGEF3,ARHGAP42,KITLG,SPRY4,DLC1,ARFGEF1,ER BIN,NOTCH2,SHOC2,ALS2,RALGPS2,OPHN1	pink	VSMC_M5
GO:0010639	0.15	0.90	19	297	negative regulation of organelle organization	BP	1	GCLC,CAPZA2,CLASP1,DLC1,TNKS2,ARFGEF1,CEP97,T WF1,PIK3CA,SCFD1,STYXL1,ATM,GHITM,WAPL,HUW E1,ATRX,RAD1,GMFB,MTPN	pink	VSMC_M5
GO:0009893	0.15	0.88	141	2815	positive regulation of metabolic process	BP	1	TAB2,MED23,LATS1,MAPK9,SCAF8,UBR5,DDX17,C9o rf72,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,GCM 1,GCLC,RHOQ,RLF,ZNF292,COMMD1,RAB1A,ADAM1 7,UFL1,SRPK2,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2 D,MAGI2,MED4,MAP3K2,KMT2C,FNTA,ZEB2,XDH,KA T6A,EAF1,IRS2,TMTC3,KITLG,NR3C1,MAPK8,APAF1,D LC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,YTHDF3,TNKS2,C DK5RAP1,ARFGEF1,KDM3A,ZNF507,SMAD1,EIF4G2,D IP2B,BTBD10,GABPA,TET3,WWP1,TIPARP,GTF2H1,TS G101,ARID2,BTG2,ATP2B4,RANBP9,BTRC,DOCK3,CAB 39,MEF2A,PRKAB2,TET2,KMT5B,GSK3B,PUM1,PIK3C A,GTF2I,BPTF,FXR1,DCUN1D1,ZFAND2A,FAM162A,PS MC6,ALS2,GABPB2,METTL5,ZNF148,HECTD1,DLX2,A TF7IP,RPS6KA3,PAFAH1B2,CREBL2,ATF2,ATM,CRKL,K AT6B,WNK1,GHITM,PYGO1,HUWE1,GTF2A2,FBXW11 ,ASH1L,ABCB7,SPTLC2,ATRX,ATP7A,PIAS1,SMAD2,M ED13,ARIH1,CCNK,DYNC1H1,CSNK1A1,XIAP,PRKAA1, NIPBL,HPRT1,SMAD7,SETX,NFAT5,MT-CO2,BIRC2,AGO3,USP9X,UBE2V2,MTPN,CACYBP,PEG 3,EIF5A2,ZNF770,HNRNPLL,NAF1,RNF139,DDAH1,B MP2	pink	VSMC_M5
GO:0009891	0.15	0.88	80	1533	positive regulation of biosynthetic process	BP	1	MED23,SCAF8,DDX17,WASL,ANXA1,GUF1,VEGFA,RU NX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,ASX L2,POLR2D,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1 ,IRS2,NR3C1,GPBP1,YTHDF3,TNKS2,CDK5RAP1,ARFG EF1,KDM3A,ZNF507,SMAD1,EIF4G2,GABPA,TET3,GTF 2H1,TSG101,BTRC,MEF2A,TET2,GTF2I,BPTF,FXR1,PS MC6,GABPB2,METTL5,ZNF148,DLX2,ATF7IP,RPS6KA3 ,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,A SH1L,ABCB7,ATRX,ATP7A,PIAS1,SMAD2,MED13,CCN K,PRKAA1,NIPBL,SETX,NFAT5,MT-CO2,BIRC2,MTPN,CACYBP,PEG3,EIF5A2,ZNF770,NAF 1,DDAH1,BMP2	pink	VSMC_M5
GO:0034622	0.15	0.89	43	830	cellular protein-containing complex assembly	BP	1	LATS1,WASL,SDHAF3,CAPZA2,BBS12,SRPK2,TBP,POL R2D,CLASP1,KAT6A,SHQ1,ARFGEF1,SMAD1,TWF1,RA NBP9,PSMG1,NDUFS4,DNAAF5,PSMC6,ABI2,ATF7IP,S RP54,ATM,ARPC2,HP1BP3,KAT6B,GTF2A2,ATRX,PIAS 1,NAP1L3,SMAD2,PSTPIP2,WDR78,PRPF8,SETX,MT-ND4,MT-ND5,AGO3,FAM206A,GMFB,MTPN,NAF1,DENR	pink	VSMC_M5

GO:0006355	0.15	0.87	122	2411	regulation of transcription, DNA-templated	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0032984	0.15	0.91	14	195	protein-containing complex disassembly	BP	1	VTA1,SCAF8,CAPZA2,CLASP1,GFM2,TSG101,ARID2,TWF1,GSK3B,PIK3CA,TFIP11,SETX,MTPN,EIF5A2	pink	VSMC_M5
GO:0051301	0.15	0.89	30	525	cell division	BP	1	LATS1,WASL,VEGFA,CD2AP,SEPT7,PDCD6IP,CLASP1,ARL8B,BIRC6,NR3C1,NEDD1,ANAPC10,PPP1CC,TSG101,DCLRE1A,TTC28,TIAL1,SKA1,DYNLT3,USP8,PDS5A,WAPL,PIK3C3,CCNK,DYNC1H1,CSNK1A1,RAB11FIP4,STAG2,PKN2,USP9X	pink	VSMC_M5
GO:0071772	0.15	0.92	10	126	response to BMP	BP	1	RUNX2,SMAD1,NOTCH2,FSTL1,SMAD2,XIAP,SMAD7,UBE2D3,USP9X,BMP2	pink	VSMC_M5
GO:0071773	0.15	0.92	10	126	cellular response to BMP stimulus	BP	1	RUNX2,SMAD1,NOTCH2,FSTL1,SMAD2,XIAP,SMAD7,UBE2D3,USP9X,BMP2	pink	VSMC_M5
GO:1903506	0.15	0.87	122	2412	regulation of nucleic acid-templated transcription	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0005977	0.15	0.94	5	57	glycogen metabolic process	BP	1	IRS2,RB1CC1,IL6ST,PPP1CC,GSK3B	pink	VSMC_M5
GO:0044271	0.15	0.87	165	3436	cellular nitrogen compound biosynthetic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,DDX17,ELAVL2,PCSK5,WASL,GUF1,VEGFA,RUNX2,ASNS,GCM1,GCLC,RHOQ,TAX1BP1,RLF,UGCG,ZNF292,COMMD1,TIA1,UFL1,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,GFM2,DPH6,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,ACACB,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,ABCB7,SPTLC2,ATRX,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,AGO3,UBE2D3,ATP5PF,USP9X,MTPN,PEG3,EIF5A2,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,RNF139,DDAH1,PAIP2,BMP2,DENR,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0040007	0.15	0.89	42	742	growth	BP	1	MEX3C,LATS1,C9orf72,ANXA1,VEGFA,MACF1,VPS54,ADAM17,KIAA1109,EPC1,MAGI2,EPB41L5,MBD5,FLRT3,ATRN,CSNK2A1,TNKS2,URI1,SMAD1,EIF4G2,DIP2B,TSG101,ARID2,NOTCH2,ACACB,GSK3B,PIK3CA,PLEKHA1,RPS6KA3,ST7L,UBE2E3,COPS2,CRKL,ATRX,TTC8,SMAD2,NIPBL,SMAD7,TMEM38B,USP9X,MTPN,BRMS1L	pink	VSMC_M5
GO:0071495	0.15	0.88	58	1018	cellular response to endogenous stimulus	BP	1	LATS1,UBR5,DDX17,UBR2,ANXA1,RUNX2,ASNS,GCLC,RHOQ,UGCG,ADAM17,UFL1,RAB14,ZFYVE9,NCOA1,MAGI2,EPB41L5,FNTA,ZEB2,MBD5,FLRT3,LTBP1,IRS2,SPRY4,NR3C1,APAF1,KDM3A,URI1,SMAD1,NR3C2,GABPA,GTF2H1,ATP2B4,NOTCH2,ANO1,SHOC2,GSK3B,FSTL1,PIK3CA,UBR1,BPTF,ACAP2,PRKCI,USP8,CRKL,FUT8,CPEB4,ATP7A,SMAD2,XIAP,PRKAA1,SMAD7,SETX,MT-ND3,UBE2D3,TMEM38B,USP9X,BMP2	pink	VSMC_M5
GO:0006446	0.15	0.94	5	66	regulation of translational initiation	BP	1	POLR2D,YTHDF3,EIF4G2,CSDE1,PAIP2	pink	VSMC_M5
GO:0002221	0.15	0.92	9	134	pattern recognition receptor signaling pathway	BP	1	LSM14A,PJA2,ERBIN,IRAK4,CYLD,PUM1,RPS6KA3,XIAP,BIRC2	pink	VSMC_M5
GO:0035303	0.15	0.92	8	106	regulation of dephosphorylation	BP	1	MAGI2,DLC1,URI1,PPP6R3,GSK3B,SMG7,STYXL1,BMP2	pink	VSMC_M5
GO:0030010	0.15	0.92	10	123	establishment of cell polarity	BP	1	KRIT1,CLASP1,FAT1,ARFGEF1,GSK3B,PRKCI,CRKL,OPHN1,FBXW11,TTC8	pink	VSMC_M5
GO:0030032	0.15	0.94	5	61	lamellipodium assembly	BP	1	TWF1,PIK3CA,ABI2,ARPC2,ATP7A	pink	VSMC_M5
GO:0048260	0.15	0.95	4	41	positive regulation of receptor-mediated endocytosis	BP	1	WASL,VEGFA,MAGI2,BICD1	pink	VSMC_M5
GO:0016032	0.15	0.90	19	325	viral process	BP	1	VTA1,PCSK5,RAB1A,SRPK2,PDCD6IP,ARL8B,TOP2B,VPS37A,IFIT5,WWP1,TSG101,CSDE1,BICD1,GSK3B,MORC2,FUT8,CCNK,PKN2,DENR	pink	VSMC_M5

GO:0038084	0.15	0.95	4	41	vascular endothelial growth factor signaling pathway	BP	1	VEGFA,JCAD,XDH,PIK3CA	pink	VSMC_M5
GO:0060070	0.15	0.90	16	250	canonical Wnt signaling pathway	BP	1	LATS1,CSNK1G3,UBR5,USP34,ZEB2,TNKS2,CYLD,BTRC,GSK3B,USP8,WNK1,PYGO1,GSKIP,CSNK1A1,XIAP,BMP2	pink	VSMC_M5
GO:0002090	0.15	0.94	4	43	regulation of receptor internalization	BP	1	MKLN1,VEGFA,MAGI2,OPHN1	pink	VSMC_M5
GO:2001141	0.15	0.87	122	2416	regulation of RNA biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0006796	0.15	0.87	108	2150	phosphate-containing compound metabolic process	BP	1	DGKA,TAB2,PPIL4,LATS1,MAPK9,CSNK1G3,SERINC1,EFR3A,LRGUK,C9orf72,VEGFA,PTP4A1,RHOQ,FAM126A,ADAM17,SRPK2,MRE11,MAGI2,MAP3K2,DGKH,PTPN4,XDH,OXSM,BIRC6,IRS2,KITLG,PRKD3,SPRY4,MAP4K3,MAPK8,DLC1,RB1CC1,IL6ST,CSNK2A1,IMPAD1,MTMR6,CDK5RAP1,URI1,SMAD1,BTBD10,FAR1,NFS1,PPP1CC,DUSP11,CPNE3,PIP4P2,GTF2H1,TSG101,HIPK1,PPP3CC,ATP2B4,TWF1,IRAK4,PIGP,BTRC,NDUFS4,DOCK3,CAB39,PPP6R3,PRKAB2,ACACB,GSK3B,PIK3CA,FXR1,STK39,ADAL,ALS2,RPS6KC1,PDE5A,TLK1,ABI2,RPS6KA3,CREBL2,SMG7,ATF2,STYXL1,ATM,PRKCI,COPS2,CRKL,WNK1,PGM2,FBXW11,SPTLC2,SMAD2,PIK3C3,GSKIP,CCNK,GGNBP2,PTPN9,SMG1,CSNK1A1,NF1,PRKAA1,PTPRM,HPRT1,SMAD7,CEPT1,NUDT7,PKN2,MT-CO2,SULT1C4,HACD1,ATP5PF,TMEM38B,GMFB,BMP2,DCAKD	pink	VSMC_M5
GO:0043648	0.15	0.94	5	73	dicarboxylic acid metabolic process	BP	1	ME2,MTHFD1L,SDHAF3,GCLC,MDH1	pink	VSMC_M5
GO:0018107	0.15	0.92	8	98	peptidyl-threonine phosphorylation	BP	1	MAPK8,CSNK2A1,HIPK1,CAB39,GSK3B,STK39,WNK1,SMAD7	pink	VSMC_M5
GO:0071277	0.16	0.93	6	63	cellular response to calcium ion	BP	1	CPNE3,CPNE8,MEF2A,WNK1,PRKAA1,CACYBP	pink	VSMC_M5
GO:1901657	0.16	0.94	4	60	glycosyl compound metabolic process	BP	1	XDH,ADAL,HPRT1,SULT1C4	pink	VSMC_M5
GO:0006073	0.16	0.94	5	58	cellular glucan metabolic process	BP	1	IRS2,RB1CC1,IL6ST,PPP1CC,GSK3B	pink	VSMC_M5
GO:0044042	0.16	0.94	5	58	glucan metabolic process	BP	1	IRS2,RB1CC1,IL6ST,PPP1CC,GSK3B	pink	VSMC_M5
GO:0006302	0.16	0.90	14	225	double-strand break repair	BP	1	UBR5,MRE11,DCLRE1C,ARID2,TRIP12,KMT5B,DCLRE1A,TFIP11,KDM2A,KLHL15,ATM,NIPBL,SETX,UBE2V2	pink	VSMC_M5
GO:0034728	0.16	0.92	7	97	nucleosome organization	BP	1	KAT6A,ARID2,BPTF,HP1BP3,KAT6B,ATRX,NAP1L3	pink	VSMC_M5
GO:0071384	0.16	0.94	4	46	cellular response to corticosteroid stimulus	BP	1	ANXA1,NR3C1,USP8,MT-ND3	pink	VSMC_M5
GO:0046847	0.16	0.93	5	56	filopodium assembly	BP	1	WASL,RHOQ,ZMYND8,FXR1,FAM206A	pink	VSMC_M5
GO:0018958	0.16	0.93	5	65	phenol-containing compound metabolic process	BP	1	ZEB2,TRPC1,ATP7A,HPRT1,MTPN	pink	VSMC_M5
GO:0036294	0.16	0.91	9	129	cellular response to decreased oxygen levels	BP	1	VEGFA,EGLN1,FAM162A,ERO1A,HP1BP3,CPEB4,ATP7A,PRKAA1,DDAH1	pink	VSMC_M5
GO:0021695	0.16	0.94	4	39	cerebellar cortex development	BP	1	OPHN1,HERC1,ATP7A,MTPN	pink	VSMC_M5
GO:0018023	0.16	0.94	4	39	peptidyl-lysine trimethylation	BP	1	TET3,TET2,KMT5B,ATRX	pink	VSMC_M5
GO:0008154	0.16	0.91	12	183	actin polymerization or depolymerization	BP	1	LATS1,WASL,CAPZA2,ARFGEF1,TWF1,PIK3CA,ABI2,ARPC2,PSTPIP2,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0016311	0.16	0.89	20	342	dephosphorylation	BP	1	PTP4A1,MAGI2,PTPN4,DLC1,IMPAD1,MTMR6,URI1,PPP1CC,DUSP11,PIP4P2,PPP3CC,BTRC,PPP6R3,GSK3B,SMG7,STYXL1,FBXW11,PTPN9,PTPRM,BMP2	pink	VSMC_M5
GO:0045069	0.16	0.93	5	62	regulation of viral genome replication	BP	1	SRPK2,TOP2B,IFIT5,MORC2,PKN2	pink	VSMC_M5
GO:0032874	0.16	0.92	7	97	positive regulation of stress-activated MAPK cascade	BP	1	KLHDC10,VEGFA,XDH,RB1CC1,PJA2,STK39,BMP2	pink	VSMC_M5
GO:0071230	0.16	0.93	5	59	cellular response to amino acid stimulus	BP	1	UBR2,GCLC,UBR1,CPEB4,ATP7A	pink	VSMC_M5
GO:0002065	0.16	0.93	5	61	columnar/cuboidal epithelial cell differentiation	BP	1	RHEB,IL6ST,GSK3B,YIPF6,BMP2	pink	VSMC_M5
GO:0097581	0.16	0.92	6	78	lamellipodium organization	BP	1	SNX2,TWF1,PIK3CA,ABI2,ARPC2,ATP7A	pink	VSMC_M5
GO:0015031	0.17	0.87	66	1301	protein transport	BP	1	VTA1,VPS13B,SNX2,UBR5,SFT2D1,KPNA5,VPS13A,PCSK5,ANXA1,CD2AP,SRP72,ERLEC1,LCA5,COMMD1,MACF1,VPS54,RAB1A,RAB14,RAB33B,PDCD6IP,ARL8B,ZDHHC17,GOLGA7,COG6,IRS2,MAPK8,VPS37A,PCM1,SGTB,ARFGEF1,ERBIN,VPS29,ZFYVE16,TSG101,UEVLD,SSR1,ANO1,IPO8,GSK3B,LYST,ZFAND2A,PARL,TLK1,SCFD1,SRP54,MTX2,PRKCI,YWHAQ,RPAIN,HUWE1,SNX11,CHM,TTC8,SMAD2,PIK3C3,APPBP2,PRKAA1,STXBP3,ARRDC5,UBE2D3,RAB18,EIF5A2,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0008584	0.17	0.91	8	111	male gonad development	BP	1	RNF38,NCOA1,KITLG,RHOBTB3,CSDE1,PLEKHA1,CRKL,ATRX	pink	VSMC_M5
GO:0032535	0.17	0.89	20	325	regulation of cellular component size	BP	1	LATS1,WASL,VEGFA,MACF1,CAPZA2,RB1CC1,ARFGEF1,EIF4G2,DIP2B,TWF1,GSK3B,PIK3CA,ALS2,ABI2,ARPC2,HP1BP3,ATP7A,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0032200	0.17	0.91	9	130	telomere organization	BP	1	MRE11,DCLRE1C,TNKS2,DCLRE1A,TFIP11,ATM,ATRX,SMG1,NAF1	pink	VSMC_M5
GO:0006334	0.17	0.93	5	68	nucleosome assembly	BP	1	KAT6A,HP1BP3,KAT6B,ATRX,NAP1L3	pink	VSMC_M5
GO:0001936	0.17	0.91	8	111	regulation of endothelial cell proliferation	BP	1	VEGFA,KRIT1,ADAM17,JCAD,XDH,NF1,PTPRM,BMP2	pink	VSMC_M5

GO:0010557	0.17	0.86	75	1433	positive regulation of macromolecule biosynthetic process	BP	1	MED23,SCAF8,DDX17,WASL,GUF1,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,ASXL2,POLR2D,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,IRS2,NR3C1,GPBP1,YTHDF3,TNKS2,CDK5RAP1,ARFGEF1,KDM3A,ZNF507,SMAD1,EIF4G2,GABPA,TET3,GTF2H1,TSG101,BTRC,MEF2A,TET2,GTF2I,BPTF,FXR1,PSMC6,GABPB2,METTL5,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,BIRC2,MTPN,CACYBP,PEG3,EIF5A2,ZNF770,NAF1,BMP2	pink	VSMC_M5
GO:0042060	0.17	0.89	20	329	wound healing	BP	1	DGKA,ANXA1,VEGFA,DST,MACF1,ADAM17,DGKH,CLASP1,ARL8B,IL6ST,ARFGEF1,TSPAN32,NOTCH2,PIK3CA,JMJD1C,TIMP1,SMAD2,NF1,F8,STXBP3	pink	VSMC_M5
GO:0048518	0.17	0.85	221	4533	positive regulation of biological process	BP	1	TAB2,MED23,LATS1,MAPK9,CSNK1G3,SCAF8,UBR5,DDX17,KLHDC10,C9orf72,WASL,ANXA1,TMEM33,GUF1,VEGFA,ANKIB1,RUNX2,CD2AP,ASNS,GCM1,GCLC,PTP4A1,RHOQ,RLF,USP34,ZNF292,COMMD1,MACF1,RAB1A,SEPT7,TIA1,ADAM17,UFL1,JCAD,SRPK2,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2D,MAGI2,MED4,MAP3K2,PDCD6IP,CLASP1,EPB41L5,RHEB,KMT2C,FNTA,ZEB2,MBD5,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,BIRC6,EAF1,IRS2,TMTC3,KITLG,NR3C1,N4BP2L2,SHQ1,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,PCM1,IFIT5,YTHDF3,TNKS2,LSM14A,CDK5RAP1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ZNF507,SMAD1,EIF4G2,SLC4A8,NR3C2,TRPC1,DIP2B,BTBD10,RNF13,GABPA,PPP1CC,TET3,WWP1,CPNE3,TIPARP,FAM92A,ARSB,GTF2H1,TSG101,HIPK1,ARID2,PPP3CC,BTG2,SSR1,ATP2B4,TWF1,IRAK4,CYLD,RANBP9,BTRC,NIPSNAP2,NDUFS4,DOCK3,NOTCH2,BICD1,ANO1,DENND5B,CAB39,ZMYND8,MEF2A,SHOC2,PRKAB2,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,ZBED9,DCUN1D1,STK39,ZFAND2A,FAM162A,TIAL1,PSMC6,ALS2,GABPB2,METTL5,PLEKHA1,ZNF148,ABI2,MORC2,HECTD1,DLX2,ATF7IP,RPS6KA3,PAFAH1B2,CREBL2,ATF2,STYXL1,DYNLT3,SOS2,ATM,ARPC2,PRKCI,ATL3,USP8,TIMP1,CRKL,KAT6B,WNK1,GHITM,PYGO1,WAPL,HUWE1,GTF2A2,UBE2Z,FBXW11,ASH1L,ABCB7,SPTLC2,ATRX,ATP7A,PIAS1,SMAD2,MED13,ARIH1,GSKIP,CCNK,DYNC1H1,PTPN9,CSNK1A1,UBE2A,XIAP,NF1,PRKAA1,NIPBL,HPRT1,SMAD7,SETX,PKN2,NFAT5,MT-CO2,BIRC2,AGO3,UBE2D3,ATP5PF,USP9X,GMFB,UBE2V2,MTPN,CACYBP,PEG3,EIF5A2,ZNF770,HNRNPLL,N	pink	VSMC_M5
GO:0030111	0.17	0.89	17	277	regulation of Wnt signaling pathway	BP	1	LATS1,CSNK1G3,UBR5,USP34,MACF1,ZEB2,CSNK2A1,TNKS2,CYLD,BTRC,GSK3B,USP8,WNK1,GSKIP,CSNK1A1,XIAP,BMP2	pink	VSMC_M5
GO:0052548	0.17	0.89	15	270	regulation of endopeptidase activity	BP	1	VEGFA,XDH,BIRC6,APAF1,DLC1,CSNK2A1,LXN,FAM162A,RPS6KA3,TIMP1,UBE2Z,USP14,XIAP,BIRC2,SPINK8	pink	VSMC_M5
GO:0032956	0.17	0.88	19	304	regulation of actin cytoskeleton organization	BP	1	LATS1,C9orf72,WASL,CD2AP,RHOQ,CAPZA2,CLASP1,DLC1,ARFGEF1,RHOBTB3,TWF1,NOTCH2,PIK3CA,ABI2,ARPC2,TTC8,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0006650	0.17	0.89	15	257	glycerophospholipid metabolic process	BP	1	DGKA,SERINC1,EFR3A,FAM126A,DGKH,IMPAD1,MTMR6,FAR1,PIP4P2,PIGP,PIK3CA,ATM,PIK3C3,SMG1,CEPT1	pink	VSMC_M5
GO:0003300	0.17	0.92	6	75	cardiac muscle hypertrophy	BP	1	IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,MTPN	pink	VSMC_M5
GO:0034766	0.17	0.93	5	68	negative regulation of ion transmembrane transport	BP	1	COMMD1,CAB39,STK39,YWHAQ,ATP7A	pink	VSMC_M5
GO:0072657	0.17	0.88	26	466	protein localization to membrane	BP	1	EFR3A,SRP72,RHOQ,FAM126A,MACF1,MAGI2,FNTA,GOLGA7,MAPK8,VPS37A,SGTB,ARL13B,SSR1,ATP2B4,TSPAN32,ZMYND8,HECTD1,SRP54,PRKCI,CRKL,CHM,TTC8,PTPN9,GOLPH3L,TIMM9,ZDHHC22	pink	VSMC_M5
GO:0071383	0.17	0.90	11	163	cellular response to steroid hormone stimulus	BP	1	LATS1,UBR5,DDX17,ANXA1,UFL1,NR3C1,KDM3A,URI1,NR3C2,USP8,MT-ND3	pink	VSMC_M5
GO:0046546	0.17	0.91	8	112	development of primary male sexual characteristics	BP	1	RNF38,NCOA1,KITLG,RHOBTB3,CSDE1,PLEKHA1,CRKL,ATRX	pink	VSMC_M5
GO:0031397	0.17	0.92	5	72	negative regulation of protein ubiquitination	BP	1	UBR5,GCLC,UFL1,TRIP12,SMAD7	pink	VSMC_M5
GO:0098876	0.18	0.90	9	129	vesicle-mediated transport to the plasma membrane	BP	1	COMMD1,MACF1,RAB14,KIAA1109,GOLGA7,VPS29,ACAP2,RAB11FIP4,GOLPH3L	pink	VSMC_M5
GO:0042440	0.18	0.92	5	65	pigment metabolic process	BP	1	ZEB2,TRPC1,ABCB7,ATP7A,HPRT1	pink	VSMC_M5
GO:0034250	0.18	0.91	8	130	positive regulation of cellular amide metabolic process	BP	1	GUF1,POLR2D,YTHDF3,CDK5RAP1,EIF4G2,FXR1,METTL5,EIF5A2	pink	VSMC_M5
GO:0010631	0.18	0.89	16	261	epithelial cell migration	BP	1	ANXA1,VEGFA,KRIT1,MACF1,ADAM17,JCAD,CLASP1,EPB41L5,ZEB2,ARSB,ATP2B4,FSTL1,PIK3CA,NF1,PTPRM,PKN2	pink	VSMC_M5
GO:0043043	0.18	0.87	28	566	peptide biosynthetic process	BP	1	PCSK5,GUF1,GCLC,TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,EIF4G2,GFM2,DPH6,BTG2,CSDE1,PUM1,FXR1,METTL5,RPS6KA3,NEMF,CPEB4,AGO3,MTPN,EIF5A2,RNF139,PAIP2,DENR	pink	VSMC_M5
GO:0042149	0.18	0.93	4	44	cellular response to glucose starvation	BP	1	ASNS,CPEB4,PIK3C3,PRKAA1	pink	VSMC_M5
GO:0021761	0.18	0.92	6	75	limbic system development	BP	1	NCOA1,BTG2,ATP2B4,GSK3B,DLX2,CRKL	pink	VSMC_M5
GO:0032204	0.18	0.92	6	74	regulation of telomere maintenance	BP	1	MRE11,TNKS2,ATM,ATRX,SMG1,NAF1	pink	VSMC_M5
GO:0007254	0.18	0.90	9	134	JNK cascade	BP	1	MAPK9,MAP4K3,MAPK8,RB1CC1,PJA2,IRAK4,CYLD,ATF2,CRKL	pink	VSMC_M5
GO:0032088	0.18	0.92	5	67	negative regulation of NF-kappaB transcription factor activity	BP	1	TAX1BP1,COMMD1,UFL1,ERBIN,CYLD	pink	VSMC_M5
GO:0019058	0.18	0.89	14	239	viral life cycle	BP	1	VTA1,PCSK5,RAB1A,SRPK2,PDCD6IP,ARL8B,TOP2B,VPS37A,IFIT5,WWP1,TSG101,MORC2,CCNK,PKN2	pink	VSMC_M5

GO:0006366	0.18	0.85	95	1862	transcription by RNA polymerase II	BP	1	PPIL4,MED23,SCAF8,DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,KMT2C,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,ZMYM5,KDM3A,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,GTF2H1,MED13L,TSG101,BAZ2B,BTG2,ATP2B4,ZBTB11,BBX,ID4,NOTCH2,MEF2A,TET2,GTF2I,BPTF,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,COPS2,KAT6B,ZNF518B,SNAPC1,PYGO1,RFX7,GTF2A2,ASH1L,USP3,ATRX,GTF2A1,PIAS1,SMAD2,MED13,CCNK,NIPBL,PHF6,SMAD7,SETX,NFAT5,UBE2D3,USP9X,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:1902115	0.18	0.89	11	161	regulation of organelle assembly	BP	1	MAPK9,C9orf72,SEPT7,PDCD6IP,TSG101,CEP97,CYLD,SCFD1,STYXL1,DYNC1H1,PRKAA1	pink	VSMC_M5
GO:0030835	0.18	0.93	4	38	negative regulation of actin filament depolymerization	BP	1	CAPZA2,TWF1,PIK3CA,MTPN	pink	VSMC_M5
GO:0071248	0.18	0.90	10	141	cellular response to metal ion	BP	1	MAPK9,MAPK8,CPNE3,CPNE8,MEF2A,WNK1,ATP7A,PRKAA1,UBE2D3,CACYBP	pink	VSMC_M5
GO:0090132	0.18	0.88	16	262	epithelium migration	BP	1	ANXA1,VEGFA,KRIT1,MACF1,ADAM17,JCAD,CLASP1,EPB41L5,ZEB2,ARSB,ATP2B4,FSTL1,PIK3CA,NF1,PTPRM,PKN2	pink	VSMC_M5
GO:0001889	0.18	0.90	8	116	liver development	BP	1	ANXA1,ASNS,RB1CC1,NOTCH2,PIK3CA,ATF2,ATP7A,NF1	pink	VSMC_M5
GO:0110053	0.18	0.88	15	237	regulation of actin filament organization	BP	1	LATS1,C9orf72,WASL,CAPZA2,CLASP1,DLC1,ARFGEF1,TWF1,PIK3CA,ABI2,ARPC2,TTC8,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0018210	0.18	0.90	8	104	peptidyl-threonine modification	BP	1	MAPK8,CSNK2A1,HIPK1,CAB39,GSK3B,STK39,WNK1,SMAD7	pink	VSMC_M5
GO:0071456	0.18	0.90	8	119	cellular response to hypoxia	BP	1	VEGFA,EGLN1,FAM162A,ERO1A,HP1BP3,ATP7A,PRKAA1,DDAH1	pink	VSMC_M5
GO:0007178	0.18	0.88	18	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	LATS1,RUNX2,ADAM17,ZFYVE9,MAGI2,FNTA,ZEB2,LTBP1,SMAD1,NOTCH2,FSTL1,FUT8,SMAD2,XIAP,SMAD7,UBE2D3,USP9X,BMP2	pink	VSMC_M5
GO:0014897	0.18	0.91	6	77	striated muscle hypertrophy	BP	1	IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,MTPN	pink	VSMC_M5
GO:0048589	0.18	0.86	30	501	developmental growth	BP	1	MEX3C,LATS1,C9orf72,ANXA1,VEGFA,MACF1,MAGI2,EPB41L5,MBD5,FLRT3,ATRN,TNKS2,SMAD1,EIF4G2,DIP2B,ARID2,NOTCH2,ACACB,GSK3B,PIK3CA,PLEKHA1,COPS2,ATRX,TTC8,SMAD2,NIPBL,SMAD7,TMEM38B,USP9X,MTPN	pink	VSMC_M5
GO:0051402	0.18	0.89	12	198	neuron apoptotic process	BP	1	GCLC,SRPK2,BTG2,PIK3CA,FAM162A,ATF2,LANCL1,PRKCI,CPEB4,XIAP,NF1,UBE2V2	pink	VSMC_M5
GO:0046700	0.19	0.87	20	357	heterocycle catabolic process	BP	1	POLR2D,CNOT10,XDH,YTHDF3,TET3,BTG2,CSDE1,TET2,PUM1,FXR1,ADAL,PDE5A,SMG7,ATM,DIS3L,SMG1,HPRT1,NUDT7,AGO3,NAF1	pink	VSMC_M5
GO:0035335	0.19	0.91	6	77	peptidyl-tyrosine dephosphorylation	BP	1	PTP4A1,PTPN4,MTMR6,DUSP11,PTPN9,PTPRM	pink	VSMC_M5
GO:0071826	0.19	0.89	10	170	ribonucleoprotein complex subunit organization	BP	1	SRPK2,POLR2D,SHQ1,TFIP11,ATM,PRPF8,SETX,AGO3,NAF1,DENR	pink	VSMC_M5
GO:0070482	0.19	0.88	17	280	response to oxygen levels	BP	1	VEGFA,ADAM17,APAF1,EGLN1,FAM162A,SCFD1,ERO1A,HP1BP3,CPEB4,ATP7A,NF1,PRKAA1,MT-ND4,MT-ND5,BIRC2,DDAH1,BMP2	pink	VSMC_M5
GO:0031050	0.19	0.93	4	46	dsRNA processing	BP	1	SMAD1,PUM1,SMAD2,AGO3	pink	VSMC_M5
GO:0035196	0.19	0.93	4	46	production of miRNAs involved in gene silencing by miRNA	BP	1	SMAD1,PUM1,SMAD2,AGO3	pink	VSMC_M5
GO:0070918	0.19	0.93	4	46	production of small RNA involved in gene silencing by RNA	BP	1	SMAD1,PUM1,SMAD2,AGO3	pink	VSMC_M5
GO:0048519	0.19	0.84	195	3961	negative regulation of biological process	BP	1	TAB2,LATS1,SCAF8,UBR5,DDX17,UBR2,C9orf72,WASL,ANXA1,VEGFA,KRIT1,RUNX2,CD2AP,ASNS,GCLC,RHOQ,ERLEC1,TAX1BP1,COMMD1,TIA1,ADAM17,CAPZA2,UFL1,RAB33B,ARHGAP42,BBS12,SRPK2,EPC1,MRE11,PRDM5,SAP130,POLR2D,MAGI2,YME1L1,CNOT10,CLASP1,EPB41L5,RHEB,ZEB2,XDH,KAT6A,BIRC6,LTBP1,IRS2,KITLG,SPRY4,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,DLC1,RB1CC1,IL6ST,CSNK2A1,CAPRIN1,PCM1,IFIT5,YTHDF3,TNKS2,LSM14A,ZMYM5,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,EIF4G2,CGGBP1,TRPC1,DIP2B,BTBD10,PCGF1,GABPA,WWP1,TIPARP,PIP4P2,LXN,TSG101,ARID2,BTG2,ATP2B4,CEP97,CSDE1,TWF1,CYLD,RANBP9,BTRC,TSPAN32,ID4,ACOT13,NOTCH2,TRIP12,BICD1,CAB39,ZMYND8,MEF2A,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,GTF2I,BPTF,FXR1,TFIP11,STK39,KDM2A,TIAL1,PLEKHA1,ZNF148,SCFD1,MORC2,HECTD1,DLX2,ATF7IP,RPS6KA3,SMG7,GLRX3,ATF2,KLHL15,HERC4,STYXL1,RNF2,ST7L,ATM,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,KAT6B,WNK1,GHITM,PDS5A,WAPL,HUWE1,OPHN1,CPEB4,UBE2Z,FBXW11,ASH1L,USP3,HERC1,ABCB7,ATRX,ATP7A,PIAS1,FEM1B,TTC8,SMAD2,GSKIP,GGNBP2,PTPN9,SMG1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,PTPRM,NIPBL,RAD1,PHF6,SMAD7,SETX,STXBP3,PTBP2,BIRC2,AGO3,UBE2D3,ATP5PF,TMEM38B,USP9X,GMFB,UBE2V2,MTPN,CD164,CACYBP,PEG3,RBAK,NAF1,BRMS1L,RNF139,DDAH1,BMT2,SPINK8,PAIP2,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0014896	0.19	0.91	6	78	muscle hypertrophy	BP	1	IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,MTPN	pink	VSMC_M5
GO:0065003	0.19	0.85	61	1210	protein-containing complex assembly	BP	1	LATS1,MAPK9,WASL,VEGFA,CD2AP,SDHAF3,CAPZA2,WDCP,BBS12,SRPK2,TBP,POLR2D,YME1L1,PDCD6IP,CLASP1,KAT6A,SHQ1,MAGI1,ARFGEF1,SMAD1,TWF1,RANBP9,PSMG1,NDUFS4,ACOT13,KCTD3,ACACB,GSK3B,DNAAF5,TFIP11,PSMC6,ALS2,ZNF148,ABI2,ATF7IP,SRP54,ATM,ARPC2,HP1BP3,ATL3,KAT6B,GTF2A2,ATRX,PIAS1,NAP1L3,SMAD2,PSTPIP2,WDR78,HPRT1,PRPF8,SETX,MT-ND4,MT-ND5,BIRC2,AGO3,FAM206A,GMFB,MTPN,NAF1,SAR1B,DENR	pink	VSMC_M5
GO:0090130	0.19	0.87	16	266	tissue migration	BP	1	ANXA1,VEGFA,KRIT1,MACF1,ADAM17,JCAD,CLASP1,EPB41L5,ZEB2,ARSB,ATP2B4,FSTL1,PIK3CA,NF1,PTPRM,PKN2	pink	VSMC_M5
GO:0044270	0.19	0.86	20	361	cellular nitrogen compound catabolic process	BP	1	POLR2D,CNOT10,XDH,YTHDF3,TET3,BTG2,CSDE1,TET2,PUM1,FXR1,ADAL,PDE5A,SMG7,ATM,DIS3L,SMG1,HPRT1,NUDT7,AGO3,NAF1	pink	VSMC_M5

GO:0006351	0.19	0.83	125	2521	transcription, DNA-templated	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0043066	0.20	0.85	34	662	negative regulation of apoptotic process	BP	1	ANXA1,VEGFA,KRIT1,ASNS,GCLC,TAX1BP1,UFL1,MRE11,YME1L1,BIRC6,IRS2,KITLG,MAPK8,RB1CC1,IL6ST,CSNK2A1,URI1,BTG2,NOTCH2,GSK3B,FSTL1,PIK3CA,RPS6KA3,PRKCI,TIMP1,GHITM,CPEB4,UBE2Z,PIAS1,XIAP,PRKAA1,SETX,BIRC2,UBE2V2	pink	VSMC_M5
GO:0097659	0.20	0.83	125	2522	nucleic acid-templated transcription	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0048565	0.20	0.90	7	92	digestive tract development	BP	1	PCSK5,EPB41L5,IL6ST,CRKL,YIPF6,SMAD2,NIPBL	pink	VSMC_M5
GO:0071241	0.20	0.88	11	165	cellular response to inorganic substance	BP	1	MAPK9,MAPK8,CPNE3,CPNE8,MEF2A,WNK1,ATRX,ATP7A,PRKAA1,UBE2D3,CACYBP	pink	VSMC_M5
GO:0043281	0.20	0.89	9	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	VEGFA,XDH,APAF1,DLC1,CSNK2A1,FAM162A,RPS6KA3,XIAP,BIRC2	pink	VSMC_M5
GO:0031330	0.20	0.88	13	207	negative regulation of cellular catabolic process	BP	1	TAB2,CSNK2A1,EIF4G2,ATP2B4,ACACB,PIK3CA,SCFD1,TIMP1,OPHN1,HERC1,SMG1,USP14,NAF1	pink	VSMC_M5
GO:0006397	0.20	0.86	21	407	mRNA processing	BP	1	SCAF8,DDX17,TIA1,CPSF3,CDC40,SRPK2,POLR2D,PPWD1,AQR,VIRMA,ESRP1,SNRPN,FXR1,TFIP11,SCNM1,TSEN15,WDR83,PRPF8,SETX,PTBP2,HNRNPLL	pink	VSMC_M5
GO:0010604	0.20	0.83	128	2586	positive regulation of macromolecule metabolic process	BP	1	TAB2,MED23,LATS1,MAPK9,SCAF8,UBR5,DDX17,WASL,ANXA1,GUF1,VEGFA,ANKIB1,RUNX2,GCM1,GCLC,RHOQ,RLF,ZNF292,COMMD1,RAB1A,ADAM17,SRPK2,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2D,MAGI2,MED4,MAP3K2,KMT2C,FNTA,ZEB2,XDH,KAT6A,EAF1,IRS2,TMTC3,KITLG,NR3C1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,YTHDF3,TNKS2,CDK5RAP1,ARFGEF1,KDM3A,ZNF507,SMAD1,EIF4G2,DIP2B,GABPA,TET3,WWP1,TIPARP,GTF2H1,TSG101,ARID2,BTG2,ATP2B4,RANBP9,BTRC,DOCK3,CAB39,MEF2A,TET2,KMT5B,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,DCUN1D1,ZFAND2A,FAM162A,PSMC6,ALS2,GABPB2,METTL5,ZNF148,HECTD1,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,CRKL,KAT6B,WNK1,PYGO1,HUWE1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,ARIH1,CCNK,CSNK1A1,XIAP,PRKAA1,NIPBL,SMAD7,SETX,NFAT5,BIRC2,AGO3,USP9X,UBE2V2,MTPN,CACYBP,PEG3,EIF5A2,ZNF770,HNRNPLL,NAF1,RNF139,BMP2	pink	VSMC_M5
GO:0051056	0.20	0.86	18	259	regulation of small GTPase mediated signal transduction	BP	1	ARFGEF3,CD2AP,ARHGAP42,KITLG,SPRY4,DLC1,ARFGEF1,ERBIN,RALGAPB,DNMBP,DOCK3,NOTCH2,SHOC2,ALS2,ARHGAP5,RALGPS2,SOS2,OPHN1	pink	VSMC_M5
GO:0051893	0.20	0.91	5	60	regulation of focal adhesion assembly	BP	1	VEGFA,MACF1,CLASP1,EPB41L5,DLC1	pink	VSMC_M5
GO:0090109	0.20	0.91	5	60	regulation of cell-substrate junction assembly	BP	1	VEGFA,MACF1,CLASP1,EPB41L5,DLC1	pink	VSMC_M5

GO:0050794	0.21	0.82	361	7581	regulation of cellular process	BP	1	DGKA,MEX3C,ARFGEF3,TAB2,PPIL4,MED23,LATS1,MAPK9,CSNK1G3,SCAF8,UBR5,DDX17,MKLN1,KLHDC10,ELAVL2,UBR2,C9orf72,WASL,ANXA1,TMEM33,GUF1,VEGFA,KRIT1,ANKIB1,RUNX2,CD2AP,SDHAF3,ASNS,GCM1,GCLC,DST,PTP4A1,RHOQ,FBXO11,ERLEC1,TAX1BP1,RLF,USP34,UGCG,ZNF292,COMMD1,MACF1,RAB1A,SEPT7,TIA1,ADAM17,CAPZA2,UFL1,CUL1,RAB14,CUL2,RAB33B,ZFYVE9,JCAD,ARHGAP42,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,AKAP11,CNOT10,PDCD6IP,DGKH,CLASP1,EPB41L5,RHEB,KMT2C,FBXL3,EMSY,FNTA,ZEB2,MBD5,FLRT3,EPC2,XDH,KAT6A,MEMO1,ZDHHC17,NKIRAS1,BIRC6,LTBP1,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,PCM1,IFIT5,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,CDK5RAP1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,SLC4A8,CGGBP1,NR3C2,RHOBTB3,TRPC1,DIP2B,BTBD10,RNF13,DPH6,PCGF1,TCTN1,GABPA,PPP1CC,TET3,WWP1,ZFYVE16,CPNE3,TIPARP,MLF1,RALGAPB,ARL13B,PIP4P2,LXN,FAM92A,ARSB,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BAZ2B,BTG2,SSR1,DNMBP,ATP2B4,ZBTB11,CEP97,CSDE1,TWF1,IRAK4,CYLD,RANBP9,BBX,BTRC,NIPSNAP2,TSPAN32,NDUFS4,ID4,DOCK3,NOTCH2,TRIP12,BICD1,ANO1,ASB7,CAB39,ZMYND8,IPO8,MEF2A,PPP6R3,SHOC2,PRKAB2,TET2,KMT5B,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,SCN9A,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,DCUN1D1,TFIP11,STK39,EGLN1,ZFAND2A,KDM2A,TTC28,FAM162A,PARL,TIAL1,PS	pink	VSMC_M5
GO:0072676	0.21	0.91	5	72	lymphocyte migration	BP	1	WASL,ADAM17,STK39,CRKL,WNK1	pink	VSMC_M5
GO:0006915	0.21	0.83	70	1436	apoptotic process	BP	1	LATS1,MAPK9,ANXA1,VEGFA,KRIT1,ASNS,GCLC,FBXO11,TAX1BP1,TIA1,ADAM17,UFL1,CUL1,CUL2,SRPK2,NCOA1,MRE11,YME1L1,PDCD6IP,BIRC6,IRS2,KITLG,NR3C1,SHQ1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,URI1,HIPK1,BTG2,CYLD,NOTCH2,MEF2A,GSK3B,FSTL1,PIK3CA,FXR1,FAM162A,TIAL1,RPS6KA3,ATF2,STYXL1,TRIM69,LANCL1,ATM,CUL5,ERO1A,PRKCI,TIMP1,CRKL,GHITM,CPEB4,UBE2Z,PIAS1,FEM1B,GSKIP,XIAP,NF1,PRKAA1,SETX,PKN2,BIRC2,MINDY3,UBE2D3,UBE2V2,PEG3,BMP2	pink	VSMC_M5
GO:1904659	0.21	0.90	6	80	glucose transmembrane transport	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3	pink	VSMC_M5
GO:0043666	0.21	0.92	4	47	regulation of phosphoprotein phosphatase activity	BP	1	MAGI2,PPP6R3,GSK3B,STYXL1	pink	VSMC_M5
GO:0090407	0.21	0.85	23	452	organophosphate biosynthetic process	BP	1	DGKA,SERINC1,EFR3A,FAM126A,DGKH,IMPAD1,MTMR6,FAR1,NFS1,PIGP,ACACB,PIK3CA,ATM,SPTLC2,PIK3C3,SMG1,HPRT1,CEPT1,MT-CO2,HACD1,ATP5PF,TMEM38B,DCAKD	pink	VSMC_M5
GO:0043933	0.21	0.83	69	1370	protein-containing complex subunit organization	BP	1	VTA1,LATS1,MAPK9,SCAF8,WASL,VEGFA,CD2AP,SDHAF3,CAPZA2,WDCP,BBS12,SRPK2,TBP,POLR2D,YME1L1,PDCD6IP,CLASP1,KAT6A,SHQ1,MAGI1,ARFGEF1,SMAD1,GFM2,TSG101,ARID2,TWF1,RANBP9,PSMG1,NDUFS4,ACOT13,KCTD3,ACACB,GSK3B,PIK3CA,DNAAF5,BPTF,TFIP11,PSMC6,ALS2,ZNF148,ABI2,ATF7IP,SRP54,ATM,ARPC2,HP1BP3,ATL3,KAT6B,GTF2A2,ATRX,PIAS1,NAP1L3,SMAD2,PSTPIP2,WDR78,HPRT1,PRPF8,SETX,MT-ND4,MT-ND5,BIRC2,AGO3,FAM206A,GMFB,MTPN,EIF5A2,NAF1,SAR1B,DENR	pink	VSMC_M5
GO:0009719	0.21	0.83	65	1202	response to endogenous stimulus	BP	1	LATS1,UBR5,DDX17,UBR2,ANXA1,RUNX2,ASNS,GCLC,RHOQ,UGCG,ADAM17,UFL1,RAB14,ZFYVE9,NCOA1,MAGI2,EPB41L5,FNTA,ZEB2,MBD5,FLRT3,LTBP1,IRS2,SPRY4,NR3C1,APAF1,KDM3A,URI1,SMAD1,NR3C2,GABPA,ARSB,GTF2H1,BTG2,ATP2B4,SNRPN,NOTCH2,ANO1,CAB39,SHOC2,GSK3B,FSTL1,PIK3CA,UBR1,BPTF,ACAP2,PRKCI,USP8,TIMP1,CRKL,FUT8,CPEB4,ATP7A,SMAD2,XIAP,PRKAA1,SMAD7,SETX,STXBP3,MT-ND3,UBE2D3,TMEM38B,USP9X,CACYBP,BMP2	pink	VSMC_M5
GO:0006333	0.21	0.89	7	106	chromatin assembly or disassembly	BP	1	KAT6A,ARID2,TLK1,HP1BP3,KAT6B,ATRX,NAP1L3	pink	VSMC_M5
GO:0032774	0.21	0.82	125	2534	RNA biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,SMAD7,LRIF1,SETX,NFAT5,BIRC2,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0006886	0.21	0.84	38	739	intracellular protein transport	BP	1	SNX2,UBR5,KPNA5,VPS13A,SRP72,ERLEC1,RAB1A,RAB14,GOLGA7,MAPK8,VPS37A,PCM1,SGTB,ERBIN,VPS29,ZFYVE16,SSR1,IPO8,GSK3B,ZFAND2A,PARL,TLK1,SCFD1,SRP54,PRKCI,YWHAQ,RPAIN,HUWE1,SNX11,CHM,APPBP2,PRKAA1,STXBP3,UBE2D3,RAB18,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0034605	0.21	0.91	4	53	cellular response to heat	BP	1	POLR2D,ANO1,GSK3B,ATM	pink	VSMC_M5
GO:0007265	0.21	0.85	18	296	Ras protein signal transduction	BP	1	ARFGEF3,RAB33B,ARHGAP42,KITLG,SPRY4,DLC1,ARFGEF1,ERBIN,NOTCH2,SHOC2,ALS2,ABI2,ARHGAP5,RALGPS2,USP8,CRKL,OPHN1,NF1	pink	VSMC_M5
GO:0015908	0.21	0.91	4	60	fatty acid transport	BP	1	SLC25A17,ANXA1,IRS2,ATP5PF	pink	VSMC_M5
GO:0006637	0.21	0.90	5	78	acyl-CoA metabolic process	BP	1	OXSM,FAR1,ACACB,NUDT7,HACD1	pink	VSMC_M5
GO:0035383	0.21	0.90	5	78	thioester metabolic process	BP	1	OXSM,FAR1,ACACB,NUDT7,HACD1	pink	VSMC_M5

GO:0007167	0.22	0.83	43	752	enzyme linked receptor protein signaling pathway	BP	1	LATS1,VEGFA,RUNX2,RHOQ,ADAM17,RAB14,ZFYVE9,JCAD,MAGI2,FNTA,ZEB2,MBD5,FLRT3,XDH,ZDHHC17,LTBP1,IRS2,SPRY4,IL6ST,ERBIN,SMAD1,CPNE3,TIPARP,TSG101,NOTCH2,SHOC2,GSK3B,FSTL1,PIK3CA,PLEKHA1,MUC20,CUL5,CRKL,FUT8,SMAD2,XIAP,PRKAA1,SMAD7,SETX,UBE2D3,USP9X,MPZL1,BMP2	pink	VSMC_M5
GO:0072655	0.22	0.89	6	103	establishment of protein localization to mitochondrion	BP	1	MAPK8,PARL,HUWE1,PRKAA1,UBE2D3,TIMM9	pink	VSMC_M5
GO:0043536	0.22	0.91	4	53	positive regulation of blood vessel endothelial cell migration	BP	1	ANXA1,VEGFA,ADAM17,JCAD	pink	VSMC_M5
GO:0006406	0.22	0.91	4	53	mRNA export from nucleus	BP	1	POLR2D,ZC3H11A,SMG7,SMG1	pink	VSMC_M5
GO:0071427	0.22	0.91	4	53	mRNA-containing ribonucleoprotein complex export from nucleus	BP	1	POLR2D,ZC3H11A,SMG7,SMG1	pink	VSMC_M5
GO:0006112	0.22	0.90	5	65	energy reserve metabolic process	BP	1	IRS2,RB1CC1,IL6ST,PPP1CC,GSK3B	pink	VSMC_M5
GO:0006644	0.22	0.85	17	314	phospholipid metabolic process	BP	1	DGKA,SERINC1,EFR3A,FAM126A,DGKH,IMPAD1,MTMR6,FAR1,PIP4P2,PIGP,PIK3CA,ATM,SPTLC2,PIK3C3,SMG1,CEPT1,TMEM38B	pink	VSMC_M5
GO:0031047	0.22	0.88	8	129	gene silencing by RNA	BP	1	DDX17,CNOT10,SMAD1,PUM1,FXR1,TIAL1,SMAD2,AGO3	pink	VSMC_M5
GO:0006919	0.22	0.91	4	57	activation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	XDH,APAF1,DLC1,FAM162A	pink	VSMC_M5
GO:0044087	0.22	0.83	44	801	regulation of cellular component biogenesis	BP	1	LATS1,MAPK9,C9orf72,WASL,VEGFA,RHOQ,MACF1,SEPT7,CAPZA2,PDCD6IP,CLASP1,EPB41L5,FLRT3,SHQ1,DLC1,ARFGEF1,TSG101,CEP97,TWF1,CYLD,ZMYND8,GSK3B,PIK3CA,FXR1,TFIP11,PSMC6,SCFD1,ABI2,MORC2,ATF7IP,STYXL1,ATM,ARPC2,ABCB7,ATP7A,TTC8,DYNC1H1,PRKAA1,BIRC2,FAM206A,GMFB,UBE2V2,MTPN,SAR1B	pink	VSMC_M5
GO:1901361	0.22	0.84	21	395	organic cyclic compound catabolic process	BP	1	CYP39A1,POLR2D,CNOT10,XDH,YTHDF3,TET3,BTG2,CSDE1,TET2,PUM1,FXR1,ADAL,PDE5A,SMG7,ATM,DIS3L,SMG1,HPRT1,NUDT7,AGO3,NAF1	pink	VSMC_M5
GO:0030518	0.22	0.88	7	96	intracellular steroid hormone receptor signaling pathway	BP	1	LATS1,UBR5,DDX17,UFL1,NR3C1,KDM3A,NR3C2	pink	VSMC_M5
GO:0016071	0.22	0.83	30	586	mRNA metabolic process	BP	1	SCAF8,DDX17,TIA1,CPSF3,CDC40,SRPK2,POLR2D,CNOT10,YTHDF3,PPWD1,AQR,VIRMA,ESRP1,BTG2,CSDE1,SNRPN,PUM1,FXR1,TFIP11,SCNM1,SMG7,TSEN15,ATM,WDR83,SMG1,PRPF8,SETX,PTBP2,AGO3,HNRNPLL	pink	VSMC_M5
GO:0045807	0.22	0.89	6	82	positive regulation of endocytosis	BP	1	WASL,VEGFA,MAGI2,TSG101,PPP3CC,BICD1	pink	VSMC_M5
GO:0071453	0.22	0.87	9	142	cellular response to oxygen levels	BP	1	VEGFA,EGLN1,FAM162A,ERO1A,HP1BP3,CPEB4,ATP7A,PRKAA1,DDAH1	pink	VSMC_M5
GO:0120031	0.22	0.84	25	435	plasma membrane bounded cell projection assembly	BP	1	LRGUK,WASL,CD2AP,RHOQ,SEPT7,SCLT1,PCM1,TCTN1,ARL13B,FAM92A,CEP97,TWF1,CYLD,ZMYND8,PIK3CA,DNAAF5,FXR1,ABI2,ARPC2,OPHN1,ATP7A,TTC8,WDR78,CPLANE1,FAM206A	pink	VSMC_M5
GO:0045861	0.22	0.86	12	213	negative regulation of proteolysis	BP	1	VEGFA,BIRC6,CSNK2A1,LXN,RPS6KA3,TIMP1,OPHN1,UBE2Z,USP14,XIAP,BIRC2,SPINK8	pink	VSMC_M5
GO:0060395	0.22	0.89	5	62	SMAD protein signal transduction	BP	1	MAGI2,SMAD1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0008645	0.22	0.89	6	83	hexose transmembrane transport	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3	pink	VSMC_M5
GO:0048609	0.23	0.83	30	563	multicellular organismal reproductive process	BP	1	SYNE1,LRGUK,UBR2,SEPT7,NCOA1,TBP,KDM3A,SMAD1,ATP2B4,PUM1,TIAL1,PLEKHA1,ZNF148,PAFAH1B2,HERC4,RNF2,CRKL,PYGO1,FBXW11,ASH1L,MLH3,ATRX,PIAS1,DIAPH2,GGNBP2,UBE2A,SETX,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0043535	0.23	0.88	6	87	regulation of blood vessel endothelial cell migration	BP	1	ANXA1,VEGFA,ADAM17,JCAD,ATP2B4,NF1	pink	VSMC_M5
GO:0031346	0.23	0.84	19	302	positive regulation of cell projection organization	BP	1	WASL,VEGFA,RHOQ,MACF1,SEPT7,MAGI2,CAPRIN1,EIF4G2,ARSB,TWF1,ZMYND8,PIK3CA,ABI2,STYXL1,ARPC2,PRKCI,ATP7A,SETX,UBE2V2	pink	VSMC_M5
GO:0043500	0.23	0.88	6	88	muscle adaptation	BP	1	IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,MTPN	pink	VSMC_M5
GO:0048232	0.23	0.84	20	371	male gamete generation	BP	1	SYNE1,LRGUK,UBR2,SEPT7,TBP,KDM3A,ATP2B4,PUM1,PLEKHA1,PAFAH1B2,HERC4,CRKL,PYGO1,MLH3,ATRX,PIAS1,GGNBP2,SETX,EIF5A2,PAIP2	pink	VSMC_M5
GO:0006357	0.23	0.81	90	1784	regulation of transcription by RNA polymerase II	BP	1	PPIL4,MED23,SCAF8,DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,PRDM5,ASXL2,SAP130,MED4,KMT2C,ZEB2,EPC2,KAT6A,ZNF605,NR3C1,N4BP2L2,ZMYM5,KDM3A,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,GTF2H1,MED13L,TSG101,BAZ2B,BTG2,ATP2B4,ZBTB11,BBX,ID4,NOTCH2,MEF2A,TET2,GTF2I,BPTF,KDM2A,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,COPS2,KAT6B,ZNF518B,PYGO1,RFX7,GTF2A2,ASH1L,USP3,ATRX,PIAS1,SMAD2,MED13,CCNK,NIPBL,PHF6,SMAD7,SETX,NFAT5,UBE2D3,USP9X,PEG3,RBAK,ZNF770,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0033138	0.23	0.89	5	74	positive regulation of peptidyl-serine phosphorylation	BP	1	LATS1,VEGFA,ATP2B4,PIK3CA,CREBL2	pink	VSMC_M5
GO:0033365	0.23	0.82	39	737	protein localization to organelle	BP	1	LATS1,SYNE1,UBR5,KPNA5,VPS13A,CD2AP,SRP72,TIA1,RAB33B,AKAP11,NEDD1,MAPK8,VPS37A,PCM1,TNKS2,VCPIP1,SGTB,TCTN1,ZFYVE16,ARL13B,TSG101,BICD1,IPO8,GSK3B,GOLGB1,ZFAND2A,PARL,CCDC14,SRP54,RPAIN,PYGO1,WAPL,HUWE1,ATRX,SPATA7,PRKAA1,NIPBL,UBE2D3,TIMM9	pink	VSMC_M5
GO:0001935	0.23	0.87	8	123	endothelial cell proliferation	BP	1	VEGFA,KRIT1,ADAM17,JCAD,XDH,NF1,PTPRM,BMP2	pink	VSMC_M5
GO:0008380	0.23	0.84	18	356	RNA splicing	BP	1	DDX17,TIA1,CDC40,SRPK2,PPWD1,AQR,VIRMA,ESRP1,SNRPN,FXR1,TFIP11,SCNM1,TSEN15,WDR83,PRPF8,SETX,PTBP2,HNRNPLL	pink	VSMC_M5
GO:0000377	0.23	0.85	13	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1	DDX17,TIA1,CDC40,SRPK2,PPWD1,AQR,SNRPN,FXR1,TFIP11,SCNM1,WDR83,PRPF8,SETX	pink	VSMC_M5
GO:0000398	0.23	0.85	13	255	mRNA splicing, via spliceosome	BP	1	DDX17,TIA1,CDC40,SRPK2,PPWD1,AQR,SNRPN,FXR1,TFIP11,SCNM1,WDR83,PRPF8,SETX	pink	VSMC_M5
GO:0019439	0.23	0.83	20	375	aromatic compound catabolic process	BP	1	POLR2D,CNOT10,XDH,YTHDF3,TET3,BTG2,CSDE1,TET2,PUM1,FXR1,ADAL,PDE5A,SMG7,ATM,DIS3L,SMG1,HPRT1,NUDT7,AGO3,NAF1	pink	VSMC_M5
GO:0006413	0.23	0.88	6	99	translational initiation	BP	1	POLR2D,YTHDF3,EIF4G2,CSDE1,PAIP2,DENR	pink	VSMC_M5
GO:0043523	0.24	0.86	10	169	regulation of neuron apoptotic process	BP	1	GCLC,SRPK2,BTG2,PIK3CA,ATF2,LANCL1,PRKCI,CPEB4,NF1,UBE2V2	pink	VSMC_M5

GO:0045444	0.24	0.85	11	188	fat cell differentiation	BP	1	MEX3C,BBS12,ASXL2,CREBL2,ATF2,ERO1A,PIAS1,TTC8,NIPBL,NUDT7,BMP2	pink	VSMC_M5
GO:1990090	0.24	0.90	4	46	cellular response to nerve growth factor stimulus	BP	1	MAGI2,BPTF,ACAP2,USP8	pink	VSMC_M5
GO:0030433	0.24	0.89	5	78	ubiquitin-dependent ERAD pathway	BP	1	ERLEC1,SGTB,PSMC6,USP14,RNF103	pink	VSMC_M5
GO:0032091	0.24	0.89	5	76	negative regulation of protein binding	BP	1	EPB41L5,MAPK8,GSK3B,TFIP11,USP33	pink	VSMC_M5
GO:0035967	0.24	0.88	6	103	cellular response to topologically incorrect protein	BP	1	TMEM33,ERLEC1,UFL1,NGLY1,KLHL15,ERO1A	pink	VSMC_M5
GO:0009064	0.24	0.90	4	59	glutamine family amino acid metabolic process	BP	1	ASNS,GCLC,ATP2B4,DDAH1	pink	VSMC_M5
GO:0019438	0.24	0.79	140	2902	aromatic compound biosynthetic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,TNKS2,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,TRPC1,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,ACACB,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ABCB7,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,UBE2D3,ATP5PF,USP9X,MTPN,PEG3,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0006493	0.24	0.89	5	74	protein O-linked glycosylation	BP	1	TMTC3,TET3,GXYLT1,OGA,TET2	pink	VSMC_M5
GO:0045184	0.24	0.80	69	1395	establishment of protein localization	BP	1	VTA1,VPS13B,SNX2,UBR5,SFT2D1,KPNA5,VPS13A,PCSK5,ANXA1,CD2AP,SRP72,ERLEC1,LCA5,COMMD1,MACF1,VPS54,RAB1A,RAB14,RAB33B,PDCD6IP,EPB41L5,ARL8B,ZDHHC17,GOLGA7,COG6,IRS2,MAPK8,VPS37A,PCM1,SGTB,ARFGEF1,ERBIN,VPS29,ZFYVE16,TSG101,UEVLD,SSR1,ANO1,IPO8,GSK3B,LYST,ZFAND2A,PARL,TLK1,PLEKHA1,SCFD1,SRP54,MTX2,PRKCI,YWHAQ,RPAIN,HUWE1,SNX11,CHM,TTC8,SMAD2,PIK3C3,APPBP2,PRKAA1,NIPBL,STXBP3,ARRDC5,UBE2D3,RAB18,EIF5A2,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0006626	0.24	0.88	5	86	protein targeting to mitochondrion	BP	1	PARL,HUWE1,PRKAA1,UBE2D3,TIMM9	pink	VSMC_M5
GO:0015749	0.24	0.88	6	84	monosaccharide transmembrane transport	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3	pink	VSMC_M5
GO:0048524	0.24	0.90	4	55	positive regulation of viral process	BP	1	SRPK2,TOP2B,TSG101,PKN2	pink	VSMC_M5
GO:0042981	0.24	0.80	53	1092	regulation of apoptotic process	BP	1	LATS1,MAPK9,ANXA1,VEGFA,KRIT1,ASNS,GCLC,FBXO11,TAX1BP1,TIA1,ADAM17,UFL1,SRPK2,NCOA1,MRE11,YME1L1,BIRC6,IRS2,KITLG,SHQ1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,URI1,BTG2,CYLD,NOTCH2,GSK3B,FSTL1,PIK3CA,FAM162A,RPS6KA3,ATF2,STYXL1,LANCL1,ATM,PRKCI,TIMP1,GHITM,CPEB4,UBE2Z,PIAS1,FEM1B,XIAP,NF1,PRKAA1,SETX,BIRC2,UBE2V2,BMP2	pink	VSMC_M5
GO:0002064	0.24	0.84	12	173	epithelial cell development	BP	1	VEGFA,MAGI2,EPB41L5,RHEB,IL6ST,FAT1,NOTCH2,GSK3B,ABI2,YIPF6,ATRX,FEM1B	pink	VSMC_M5
GO:0006139	0.24	0.79	197	4274	nucleobase-containing compound metabolic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,UBR5,LRGUK,DDX17,ELAVL2,UBR2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,INIP,COMMD1,TIA1,CPSF3,UFL1,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DCLRE1C,INTS4,KMT2C,EMSY,ZEB2,EPC2,XDH,KAT6A,OXSM,ENDOV,TOP2B,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,YTHDF3,TNKS2,VCPIP1,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,FAR1,AQR,PCGF1,GABPA,TET3,WWP1,DUSP11,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,SNRPN,ID4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,DCLRE1A,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,TFIP11,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,PDE5A,SCNM1,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,TSEN15,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,RFX7,FUT8,HUWE1,GTF2A2,FBXW11,ASH1L,USP3,MLH3,WDR83,ATRX,DIS3L,GTF2A1,PIAS1,SMAD2,MED13,CCNK,SMG1,UBE2A,PRKAA1,NIPBL,RAD1,PHF6,HPRT1,SMAD7,PRPF8,LRIF1,SETX,SLC35A3,NUDT7,PTBP2,NFAT5,MT-CO2,BIRC2,SULT1C4,HACD1,AGO3,UBE2D3,ATP5PF,USP9X,UBE2V2,MTPN,PEG3,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0006412	0.24	0.82	26	548	translation	BP	1	GUF1,TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,EIF4G2,GFM2,DPH6,BTG2,CSDE1,PUM1,FXR1,METTL5,RPS6KA3,NEMF,CPEB4,AGO3,MTPN,EIF5A2,RNF139,PAIP2,DENR	pink	VSMC_M5
GO:0072594	0.24	0.83	19	355	establishment of protein localization to organelle	BP	1	UBR5,KPNA5,VPS13A,SRP72,MAPK8,VPS37A,SGTB,ZFYVE16,TSG101,IPO8,ZFAND2A,PARL,SRP54,RPAIN,HUWE1,PRKAA1,NIPBL,UBE2D3,TIMM9	pink	VSMC_M5
GO:1990089	0.24	0.89	4	47	response to nerve growth factor	BP	1	MAGI2,BPTF,ACAP2,USP8	pink	VSMC_M5
GO:0030510	0.24	0.87	6	74	regulation of BMP signaling pathway	BP	1	NOTCH2,FSTL1,SMAD2,XIAP,SMAD7,UBE2D3	pink	VSMC_M5
GO:1903321	0.24	0.88	5	82	negative regulation of protein modification by small protein conjugation or removal	BP	1	UBR5,GCLC,UFL1,TRIP12,SMAD7	pink	VSMC_M5
GO:0034976	0.24	0.84	12	222	response to endoplasmic reticulum stress	BP	1	TMEM33,ERLEC1,UFL1,NGLY1,TMTC3,SGTB,GSK3B,PSMC6,ERO1A,USP14,RNF103,RNF139	pink	VSMC_M5
GO:0071675	0.24	0.88	5	81	regulation of mononuclear cell migration	BP	1	WASL,ADAM17,STK39,CRKL,WNK1	pink	VSMC_M5
GO:0009166	0.24	0.89	4	61	nucleotide catabolic process	BP	1	XDH,PDE5A,HPRT1,NUDT7	pink	VSMC_M5

GO:0009790	0.25	0.80	46	841	embryo development	BP	1	LATS1,MTHFD1L,PCSK5,VEGFA,RUNX2,GCM1,SEPT7,RAB14,NCOA1,CLASP1,EPB41L5,FLRT3,BIRC6,KITLG,N4BP2L2,DLC1,IMPAD1,SMAD1,TCTN1,GABPA,TET3,ARL13B,TBC1D23,HIPK1,ARID2,NOTCH2,TRIP12,BPTF,ALS2,UBR3,HECTD1,DLX2,ATF2,RNF2,COPS2,WNK1,FUT8,ATP7A,SMAD2,GGNBP2,UBE2A,NIPBL,PHF6,MT-ND4,SMIM14,BMP2	pink	VSMC_M5
GO:0032504	0.25	0.81	30	571	multicellular organism reproduction	BP	1	SYNE1,LRGUK,UBR2,SEPT7,NCOA1,TBP,KDM3A,SMAD1,ATP2B4,PUM1,TIAL1,PLEKHA1,ZNF148,PAFAH1B2,HERC4,RNF2,CRKL,PYGO1,FBXW11,ASH1L,MLH3,ATRX,PIAS1,DIAPH2,GGNBP2,UBE2A,SETX,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0070585	0.25	0.87	6	107	protein localization to mitochondrion	BP	1	MAPK8,PARL,HUWE1,PRKAA1,UBE2D3,TIMM9	pink	VSMC_M5
GO:1901222	0.25	0.88	5	75	regulation of NIK/NF-kappaB signaling	BP	1	NR3C2,CYLD,NFAT5,BIRC2,AGO3	pink	VSMC_M5
GO:0009987	0.25	0.80	528	11676	cellular process	BP	1	DGKA,RELCH,MEX3C,DMXL1,ME2,ARFGEF3,VTA1,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,MTHFD1L,SYNE1,SNX2,CSNK1G3,SCAF8,UBR5,SFT2D1,KPNA5,SERINC1,EFR3A,SLC25A17,LRGUK,DDX17,MKLN1,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,TMEM33,GUF1,VEGFA,KRIT1,ANKIB1,FRYL,RUNX2,CYP39A1,CD2AP,SDHAF3,ASNS,SRP72,GCM1,GCLC,RNF38,DST,AGMO,PTP4A1,RHOQ,FBXO11,ERLEC1,FAM126A,LCA5,TAX1BP1,RLF,USP34,UGCG,ZNF292,INIP,COMMD1,MACF1,MDH1,VPS54,DPY19L1,RAB1A,SEPT7,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,CAPZA2,UFL1,CUL1,FBXL4,ZMYM4,RAB14,CUL2,RAB33B,ZFYVE9,SLC41A3,AFG1L,SCLT1,PPIL6,OSBPL9,CDC40,HSPA4L,WDCP,JCAD,ARHGAP42,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,ACBD5,YME1L1,MED4,MAP3K2,AKAP11,CNOT10,DCLRE1C,PDCD6IP,DGKH,CLASP1,INTS4,EPB41L5,PTPN4,RHEB,KMT2C,FBXL3,EMSY,FNTA,ZEB2,MBD5,FLRT3,EPC2,XDH,ARL8B,KAT6A,OXSM,NGLY1,ENDOV,MEMO1,TOP2B,ZDHHC17,GOLGA7,SLC30A6,NKIRAS1,BIRC6,LTBP1,PSMD8,COG6,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,ATRN,NR3C1,N4BP2L2,MAP4K3,SHQ1,NEDD1,UBA3,MAPK8,APAF1,MAGI1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,PCM1,IFIT5,YTHDF3,FAT1,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,SLC4A8,CGGBP1,NR3C2,KCMF1,RHOBTB3,TRPC1,DIP2B,BTBD10,FAR1,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,VPS29,TCTN1,GABPA,PPP1CC,TET3,WWP1,RSPRY1,DUSP11,ZFYVE16,CRMP2,TIPARP,AMFR,PALM2AKAP2,ARHGAP32,PIP4K2A	pink	VSMC_M5
GO:0000079	0.25	0.88	5	80	regulation of cyclin-dependent protein serine/threonine kinase activity	BP	1	LATS1,ADAM17,CDK5RAP1,GTF2H1,CCNK	pink	VSMC_M5
GO:0043242	0.25	0.87	6	70	negative regulation of protein-containing complex disassembly	BP	1	SCAF8,CAPZA2,CLASP1,TWF1,PIK3CA,MTPN	pink	VSMC_M5
GO:0030031	0.25	0.82	25	443	cell projection assembly	BP	1	LRGUK,WASL,CD2AP,RHOQ,SEPT7,SCLT1,PCM1,TCTN1,ARL13B,FAM92A,CEP97,TWF1,CYLD,ZMYND8,PIK3CA,DNAAF5,FXR1,ABI2,ARPC2,OPHN1,ATP7A,TTC8,WDR78,CPLANE1,FAM206A	pink	VSMC_M5
GO:0010506	0.25	0.83	16	268	regulation of autophagy	BP	1	TAB2,C9orf72,UFL1,RHEB,MAPK8,EIF4G2,GSK3B,PIK3CA,SCFD1,PAFAH1B2,ATM,HERC1,SPTLC2,SMG1,PRKAA1,USP33	pink	VSMC_M5
GO:0007283	0.25	0.82	19	357	spermatogenesis	BP	1	SYNE1,LRGUK,UBR2,SEPT7,TBP,KDM3A,ATP2B4,PUM1,PLEKHA1,PAFAH1B2,HERC4,CRKL,PYGO1,ATRX,PIAS1,GGNBP2,SETX,EIF5A2,PAIP2	pink	VSMC_M5
GO:0046483	0.25	0.78	201	4376	heterocycle metabolic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,UBR5,LRGUK,DDX17,ELAVL2,UBR2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,INIP,COMMD1,TIA1,CPSF3,UFL1,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DCLRE1C,INTS4,KMT2C,EMSY,ZEB2,EPC2,XDH,KAT6A,OXSM,ENDOV,TOP2B,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,YTHDF3,TNKS2,VCPIP1,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,FAR1,AQR,NFS1,PCGF1,GABPA,TET3,WWP1,DUSP11,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,SNRPN,ID4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,DCLRE1A,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,TFIP11,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,PDE5A,SCNM1,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,TSEN15,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,RFX7,FUT8,HUWE1,GTF2A2,FBXW11,ASH1L,USP3,MLH3,ABCB7,WDR83,ATRX,ATP7A,DIS3L,GTF2A1,PIAS1,SMAD2,MED13,CCNK,SMG1,UBE2A,PRKAA1,NIPBL,RAD1,PHF6,HPRT1,SMAD7,PRPF8,LRIF1,SETX,SLC35A3,NUDT7,PTBP2,NFAT5,MT-CO2,BIRC2,SULT1C4,HACD1,AGO3,UBE2D3,ATP5PF,USP9X,UBE2V2,MTPN,PEG3,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0043069	0.25	0.81	34	681	negative regulation of programmed cell death	BP	1	ANXA1,VEGFA,KRIT1,ASNS,GCLC,TAX1BP1,UFL1,MRE11,YME1L1,BIRC6,IRS2,KITLG,MAPK8,RB1CC1,IL6ST,CSNK2A1,URI1,BTG2,NOTCH2,GSK3B,FSTL1,PIK3CA,RPS6KA3,PRKCI,TIMP1,GHITM,CPEB4,UBE2Z,PIAS1,XIAP,PRKAA1,SETX,BIRC2,UBE2V2	pink	VSMC_M5
GO:0000375	0.25	0.84	13	259	RNA splicing, via transesterification reactions	BP	1	DDX17,TIA1,CDC40,SRPK2,PPWD1,AQR,SNRPN,FXR1,TFIP11,SCNM1,WDR83,PRPF8,SETX	pink	VSMC_M5
GO:0043254	0.25	0.82	20	361	regulation of protein-containing complex assembly	BP	1	LATS1,MAPK9,WASL,VEGFA,CAPZA2,CLASP1,ARFGEF1,TWF1,GSK3B,TFIP11,PSMC6,ABI2,ATF7IP,ATM,ARPC2,BIRC2,FAM206A,GMFB,MTPN,SAR1B	pink	VSMC_M5

GO:0044085	0.25	0.78	121	2454	cellular component biogenesis	BP	1	VTA1,LATS1,MAPK9,SERINC1,LRGUK,DDX17,C9orf72,WASL,VEGFA,CD2AP,SDHAF3,DST,RHOQ,UGCG,MACF1,RAB1A,SEPT7,NFU1,CAPZA2,RAB14,RAB33B,SCLT1,WDCP,BBS12,SRPK2,TBP,POLR2D,YME1L1,PDCD6IP,CLASP1,EPB41L5,FLRT3,XDH,ARL8B,KAT6A,SHQ1,MAGI1,DLC1,RB1CC1,VPS37A,PCM1,YTHDF3,VCPIP1,LSM14A,ARFGEF1,SMAD1,NFS1,TCTN1,ARL13B,FAM92A,TSG101,HIPK1,CEP97,CSDE1,TWF1,CYLD,RANBP9,PSMG1,NDUFS4,ACOT13,BICD1,KCTD3,ZMYND8,MEF2A,ACACB,GSK3B,PIK3CA,DNAAF5,FXR1,TFIP11,PSMC6,ALS2,METTL5,ZNF148,SCFD1,ABI2,MORC2,ATF7IP,GLRX3,SRP54,STYXL1,ATM,ARPC2,HP1BP3,ATL3,CRKL,KAT6B,GTF2A2,OPHN1,MLH3,ABCB7,ATRX,ATP7A,PIAS1,NAP1L3,TTC8,SMAD2,PSTPIP2,PIK3C3,DYNC1H1,WDR78,STAG2,PRKAA1,CPLANE1,HPRT1,SMAD7,PRPF8,SETX,PKN2,MT-ND4,MT-ND5,BIRC2,AGO3,FAM206A,GMFB,UBE2V2,MTPN,NAF1,UBXN2A,SAR1B,DENR	pink	VSMC_M5
GO:0034655	0.25	0.82	18	335	nucleobase-containing compound catabolic process	BP	1	POLR2D,CNOT10,XDH,YTHDF3,BTG2,CSDE1,PUM1,FXR1,ADAL,PDE5A,SMG7,ATM,DIS3L,SMG1,HPRT1,NUDT7,AGO3,NAF1	pink	VSMC_M5
GO:1902305	0.25	0.89	4	50	regulation of sodium ion transmembrane transport	BP	1	COMMD1,ATP2B4,STK39,WNK1	pink	VSMC_M5
GO:0072330	0.25	0.85	8	144	monocarboxylic acid biosynthetic process	BP	1	ANXA1,CYP39A1,OSBPL9,OXSM,PRKAB2,ACACB,PRKAA1,HACD1	pink	VSMC_M5
GO:0150116	0.25	0.88	5	65	regulation of cell-substrate junction organization	BP	1	VEGFA,MACF1,CLASP1,EPB41L5,DLC1	pink	VSMC_M5
GO:0060627	0.25	0.82	22	403	regulation of vesicle-mediated transport	BP	1	MKLN1,WASL,ANXA1,VEGFA,CD2AP,RAB33B,MAGI2,PDCD6IP,CLASP1,SLC4A8,ZFYVE16,PIP4P2,TSG101,PPP3CC,BICD1,GSK3B,SCFD1,OPHN1,PRKAA1,STXBP3,RNF139,SAR1B	pink	VSMC_M5
GO:0098813	0.25	0.83	13	230	nuclear chromosome segregation	BP	1	LATS1,MRE11,TOP2B,ATM,PDS5A,WAPL,MLH3,ATRX,DYNC1H1,ESCO1,STAG2,NIPBL,RMDN1	pink	VSMC_M5
GO:0051604	0.25	0.84	12	230	protein maturation	BP	1	PCSK5,NFU1,ADAM17,YME1L1,TSPAN32,PARL,GLRX3,ERO1A,PIK3C3,XIAP,CPD,RNF139	pink	VSMC_M5
GO:0046394	0.25	0.84	11	213	carboxylic acid biosynthetic process	BP	1	MTHFD1L,ANXA1,CYP39A1,ASNS,OSBPL9,OXSM,ATP2B4,PRKAB2,ACACB,PRKAA1,HACD1	pink	VSMC_M5
GO:0034219	0.25	0.87	6	86	carbohydrate transmembrane transport	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3	pink	VSMC_M5
GO:0051726	0.25	0.80	42	827	regulation of cell cycle	BP	1	LATS1,ANXA1,ASNS,ADAM17,SRPK2,MRE11,MAGI2,PDCD6IP,RHEB,FBXL3,BIRC6,UBA3,CSNK2A1,CDK5RAP1,EIF4G2,MLF1,GTF2H1,TSG101,BTG2,ATP2B4,CEP97,CYLD,BTRC,NOTCH2,PUM1,ZBED9,TTC28,ATF2,DYNLT3,ATM,WAPL,ATRX,FEM1B,PIK3C3,CCNK,DYNC1H1,RAB11FIP4,XIAP,RAD1,PKN2,BIRC2,BMP2	pink	VSMC_M5
GO:0051641	0.25	0.78	115	2295	cellular localization	BP	1	RELCH,VTA1,LATS1,SYNE1,SNX2,UBR5,KPNA5,EFR3A,VPS13A,WASL,CD2AP,SRP72,DST,RHOQ,ERLEC1,FAM126A,LCA5,COMMD1,MACF1,VPS54,RAB1A,SEPT7,TIA1,RAB14,RAB33B,ZFYVE9,BBS12,KIAA1109,POLR2D,MAGI2,AKAP11,CLASP1,FNTA,ARL8B,GOLGA7,NEDD1,MAPK8,VPS37A,PCM1,TNKS2,VCPIP1,SGTB,ERBIN,SLC4A8,RHOBTB3,TRPC1,VPS29,TCTN1,PPP1CC,ZFYVE16,ARL13B,TBC1D23,TSG101,PPP3CC,SSR1,ATP2B4,ZC3H11A,TWF1,TSPAN32,BICD1,ANO1,ZMYND8,IPO8,MEF2A,GSK3B,LYST,GOLGB1,ZFAND2A,PARL,CCDC14,ALS2,TLK1,SCFD1,HECTD1,SMG7,SRP54,ACAP2,NEMF,ATM,ERO1A,PRKCI,YWHAQ,CRKL,RPAIN,PYGO1,WAPL,HUWE1,OPHN1,SNX11,FBXW11,ATRX,SPATA7,CHM,TTC8,PIK3C3,APPBP2,DYNC1H1,PTPN9,SMG1,RAB11FIP4,PRKAA1,NIPBL,SMAD7,TRAPPC2L,STXBP3,UBE2D3,ATP5PF,TMEM38B,RAB18,RNF139,GOLPH3L,TIMM9,RMDN1,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0016458	0.25	0.84	10	169	gene silencing	BP	1	DDX17,CNOT10,SMAD1,PUM1,FXR1,TIAL1,MORC2,ATF7IP,SMAD2,AGO3	pink	VSMC_M5
GO:0006979	0.25	0.82	18	357	response to oxidative stress	BP	1	MAPK9,ANXA1,GCLC,ATRN,MAPK8,ALS2,PLEKHA1,ATF2,LANCL1,ERO1A,FUT8,ATP7A,GSKIP,PRKAA1,SETX,MT-CO1,MT-ND3,MT-ND5	pink	VSMC_M5
GO:0022618	0.26	0.84	9	163	ribonucleoprotein complex assembly	BP	1	SRPK2,POLR2D,SHQ1,ATM,PRPF8,SETX,AGO3,NAF1,DENR	pink	VSMC_M5
GO:0021537	0.26	0.83	12	184	telencephalon development	BP	1	NCOA1,TCTN1,ARL13B,BTG2,ATP2B4,GSK3B,DLX2,CRKL,TTC8,NF1,HPRT1,BMP2	pink	VSMC_M5
GO:0030900	0.26	0.82	18	282	forebrain development	BP	1	NCOA1,TOP2B,DLC1,PCM1,TCTN1,ARL13B,BTG2,ATP2B4,GSK3B,DLX2,CRKL,OPHN1,ATRX,ATP7A,TTC8,NF1,HPRT1,BMP2	pink	VSMC_M5
GO:0071887	0.26	0.87	5	79	leukocyte apoptotic process	BP	1	ANXA1,ADAM17,IRS2,KITLG,CRKL	pink	VSMC_M5
GO:0044703	0.26	0.80	35	688	multi-organism reproductive process	BP	1	SYNE1,LRGUK,PCSK5,UBR2,VEGFA,SEPT7,NCOA1,TBP,YTHDF3,KDM3A,SMAD1,ATP2B4,PUM1,TIAL1,PLEKHA1,ZNF148,PAFAH1B2,HERC4,RNF2,TIMP1,CRKL,PYGO1,FBXW11,ASH1L,MLH3,ATRX,ATP7A,PIAS1,DIAPH2,GGNBP2,UBE2A,SETX,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0009150	0.26	0.82	15	286	purine ribonucleotide metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,PDE5A,PRKAA1,HPRT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0052547	0.26	0.82	15	294	regulation of peptidase activity	BP	1	VEGFA,XDH,BIRC6,APAF1,DLC1,CSNK2A1,LXN,FAM162A,RPS6KA3,TIMP1,UBE2Z,USP14,XIAP,BIRC2,SPINK8	pink	VSMC_M5
GO:0034614	0.26	0.85	7	124	cellular response to reactive oxygen species	BP	1	MAPK9,ANXA1,MAPK8,PLEKHA1,ATP7A,PRKAA1,SETX	pink	VSMC_M5
GO:0016053	0.26	0.83	11	215	organic acid biosynthetic process	BP	1	MTHFD1L,ANXA1,CYP39A1,ASNS,OSBPL9,OXSM,ATP2B4,PRKAB2,ACACB,PRKAA1,HACD1	pink	VSMC_M5

GO:0018130	0.26	0.77	139	2900	heterocycle biosynthetic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,TNKS2,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,NFS1,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,ACACB,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ABCB7,ATRX,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,UBE2D3,ATP5PF,USP9X,MTPN,PEG3,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0030148	0.26	0.87	5	83	sphingolipid biosynthetic process	BP	1	UGCG,PRKD3,SPTLC2,PRKAA1,HACD1	pink	VSMC_M5
GO:0043484	0.26	0.85	8	126	regulation of RNA splicing	BP	1	DDX17,TIA1,SRPK2,ESRP1,FXR1,SETX,PTBP2,HNRNPLL	pink	VSMC_M5
GO:0032456	0.26	0.87	5	70	endocytic recycling	BP	1	RAB14,KIAA1109,VPS29,ACAP2,RAB11FIP4	pink	VSMC_M5
GO:0051653	0.26	0.88	4	49	spindle localization	BP	1	WASL,CLASP1,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0090307	0.26	0.88	4	57	mitotic spindle assembly	BP	1	CLASP1,LSM14A,CEP97,STAG2	pink	VSMC_M5
GO:0006275	0.26	0.86	6	92	regulation of DNA replication	BP	1	PDS5A,WAPL,ATRX,ESCO1,CACYBP,RNF219	pink	VSMC_M5
GO:0007029	0.26	0.87	5	80	endoplasmic reticulum organization	BP	1	TMEM33,VCPIP1,ATL3,TMEM38B,RAB18	pink	VSMC_M5
GO:0009755	0.26	0.84	9	142	hormone-mediated signaling pathway	BP	1	LATS1,UBR5,DDX17,UFL1,NCOA1,NR3C1,KDM3A,NR3C2,GTF2H1	pink	VSMC_M5
GO:0008643	0.26	0.85	7	112	carbohydrate transport	BP	1	RHOQ,IRS2,MEF2A,CREBL2,PRKCI,STXBP3,SLC35A3	pink	VSMC_M5
GO:0031124	0.26	0.88	4	56	mRNA 3'-end processing	BP	1	SCAF8,CPSF3,POLR2D,VIRMA	pink	VSMC_M5
GO:0070302	0.27	0.84	9	151	regulation of stress-activated protein kinase signaling cascade	BP	1	KLHDC10,VEGFA,XDH,RB1CC1,PJA2,RNF13,CYLD,STK39,BMP2	pink	VSMC_M5
GO:1904029	0.27	0.87	5	83	regulation of cyclin-dependent protein kinase activity	BP	1	LATS1,ADAM17,CDK5RAP1,GTF2H1,CCNK	pink	VSMC_M5
GO:0061912	0.27	0.87	5	63	selective autophagy	BP	1	UFL1,RB1CC1,WDFY3,HUWE1,SPTLC2	pink	VSMC_M5
GO:0046661	0.27	0.84	8	128	male sex differentiation	BP	1	RNF38,NCOA1,KITLG,RHOBTB3,CSDE1,PLEKHA1,CRKL,ATRX	pink	VSMC_M5
GO:0009062	0.27	0.87	5	86	fatty acid catabolic process	BP	1	SLC25A17,IRS2,ACACB,ACOX3,NUDT7	pink	VSMC_M5
GO:0062207	0.27	0.87	5	77	regulation of pattern recognition receptor signaling pathway	BP	1	PJA2,ERBIN,PUM1,XIAP,BIRC2	pink	VSMC_M5
GO:2000116	0.27	0.84	9	167	regulation of cysteine-type endopeptidase activity	BP	1	VEGFA,XDH,APAF1,DLC1,CSNK2A1,FAM162A,RPS6KA3,XIAP,BIRC2	pink	VSMC_M5
GO:0051058	0.27	0.88	4	49	negative regulation of small GTPase mediated signal transduction	BP	1	CD2AP,ARHGAP42,SPRY4,DLC1	pink	VSMC_M5
GO:0006635	0.27	0.88	4	64	fatty acid beta-oxidation	BP	1	SLC25A17,IRS2,ACACB,ACOX3	pink	VSMC_M5
GO:0061448	0.27	0.82	12	203	connective tissue development	BP	1	MEX3C,RUNX2,IMPAD1,SMAD1,PIK3CA,DLX2,ATF2,TIMP1,SPTLC2,ATP7A,SMAD7,BMP2	pink	VSMC_M5
GO:0032880	0.27	0.79	36	693	regulation of protein localization	BP	1	LATS1,UBR5,WASL,ANXA1,CD2AP,RHOQ,ERLEC1,COMMD1,UFL1,RAB14,EPB41L5,IRS2,MAPK8,PCM1,VCPIP1,TSG101,ATP2B4,BICD1,ANO1,ZMYND8,GSK3B,PARL,SCFD1,HECTD1,PRKCI,USP8,CRKL,WAPL,HUWE1,TTC8,PIK3C3,PTPN9,PRKAA1,UBE2D3,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0033108	0.27	0.88	4	83	mitochondrial respiratory chain complex assembly	BP	1	SDHAF3,NDUFS4,MT-ND4,MT-ND5	pink	VSMC_M5
GO:0002764	0.27	0.81	15	278	immune response-regulating signaling pathway	BP	1	MAPK9,MAPK8,LSM14A,PJA2,ERBIN,JRAK4,CYLD,PUM1,PIK3CA,PLEKHA1,RPS6KA3,CRKL,WNK1,XIAP,BIRC2	pink	VSMC_M5
GO:0006282	0.27	0.84	7	118	regulation of DNA repair	BP	1	UBR5,ARID2,TRIP12,KMT5B,TFIP11,KLHL15,UBE2V2	pink	VSMC_M5
GO:0009611	0.27	0.79	23	422	response to wounding	BP	1	DGKA,ANXA1,VEGFA,DST,MACF1,ADAM17,DGKH,CLASP1,FLRT3,ARL8B,IL6ST,ARFGEF1,TSPAN32,NOTCH2,PIK3CA,BPTF,JMJD1C,TIMP1,ATP7A,SMAD2,NF1,F8,STXBP3	pink	VSMC_M5
GO:1901566	0.27	0.77	59	1317	organonitrogen compound biosynthetic process	BP	1	MTHFD1L,PCSK5,GUF1,ASNS,GCLC,UGCG,DPY19L1,TIA1,POLR2D,CNOT10,ZDHHC17,GOLGA7,TMTC3,PRKD3,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,ARFGEF1,PTCD3,EIF4G2,GFM2,NFS1,DPH6,TET3,BTG2,ATP2B4,CSDE1,PIGP,GXYLT1,OGA,TET2,ACACB,PUM1,FXR1,ADAL,METTL5,RPS6KA3,NEMF,FUT8,CPEB4,ABCB7,SPTLC2,ATP7A,PIK3C3,PRKAA1,HPRT1,CEPT1,MT-CO2,HACD1,AGO3,ATP5PF,MTPN,EIF5A2,RNF139,PAIP2,ZDHHC22,DENR,DCAKD	pink	VSMC_M5
GO:0062197	0.27	0.81	15	282	cellular response to chemical stress	BP	1	MAPK9,ANXA1,MAPK8,CAB39,PIK3CA,STK39,PLEKHA1,ATF2,LANCL1,ATM,FUT8,ATP7A,GSKIP,PRKAA1,SETX	pink	VSMC_M5
GO:0016055	0.28	0.80	21	373	Wnt signaling pathway	BP	1	LATS1,CSNK1G3,UBR5,USP34,MACF1,MAGI2,ZEB2,CSNK2A1,TNKS2,CYLD,BTRC,GSK3B,USP8,WNK1,PYGO1,FBXW11,GSKIP,CSNK1A1,XIAP,PRKAA1,BMP2	pink	VSMC_M5
GO:1902600	0.28	0.85	6	115	proton transmembrane transport	BP	1	ATP7A,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF	pink	VSMC_M5
GO:0030834	0.28	0.87	4	46	regulation of actin filament depolymerization	BP	1	CAPZA2,TWF1,PIK3CA,MTPN	pink	VSMC_M5
GO:0012501	0.28	0.76	70	1474	programmed cell death	BP	1	LATS1,MAPK9,ANXA1,VEGFA,KRIT1,ASNS,GCLC,FBXO11,TAX1BP1,TIA1,ADAM17,UFL1,CUL1,CUL2,SRPK2,NCOA1,MRE11,YME1L1,PDCD6IP,BIRC6,IRS2,KITLG,NR3C1,SHQ1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,URI1,HIPK1,BTG2,CYLD,NOTCH2,MEF2A,GSK3B,FSTL1,PIK3CA,FXR1,FAM162A,TIAL1,RPS6KA3,ATF2,STYXL1,TRIM69,LANCL1,ATM,CUL5,ERO1A,PRKCI,TIMP1,CRKL,GHITM,CPEB4,UBE2Z,PIAS1,FEM1B,GSKIP,XIAP,NF1,PRKAA1,SETX,PKN2,BIRC2,MINDY3,UBE2D3,UBE2V2,PEG3,BMP2	pink	VSMC_M5
GO:0048016	0.28	0.87	4	48	inositol phosphate-mediated signaling	BP	1	PPP3CC,ATP2B4,GSK3B,NFAT5	pink	VSMC_M5
GO:0002685	0.28	0.83	8	152	regulation of leukocyte migration	BP	1	WASL,ANXA1,VEGFA,ADAM17,KITLG,STK39,CRKL,WNK1	pink	VSMC_M5

GO:0010632	0.28	0.81	12	208	regulation of epithelial cell migration	BP	1	ANXA1,VEGFA,KRIT1,MACF1,ADAM17,JCAD,CLASP1,EPB41L5,ARSB,ATP2B4,NF1,PTPRM	pink	VSMC_M5
GO:2000106	0.28	0.87	4	59	regulation of leukocyte apoptotic process	BP	1	ANXA1,ADAM17,IRS2,KITLG	pink	VSMC_M5
GO:0198738	0.28	0.79	21	374	cell-cell signaling by wnt	BP	1	LATS1,CSNK1G3,UBR5,USP34,MACF1,MAGI2,ZEB2,CSNK2A1,TNKS2,CYLD,BTRC,GSK3B,USP8,WNK1,PYGO1,FBXW11,GSKIP,CSNK1A1,XIAP,PRKAA1,BMP2	pink	VSMC_M5
GO:0019953	0.28	0.78	29	565	sexual reproduction	BP	1	SYNE1,LRGUK,UBR2,SEPT7,NCOA1,TBP,KDM3A,SMAD1,ATP2B4,PUM1,TIAL1,PLEKHA1,ZNF148,PAFAH1B2,HERC4,RNF2,CRKL,PYGO1,FBXW11,ASH1L,MLH3,ATRX,PIAS1,DIAPH2,GGNBP2,SETX,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0010035	0.28	0.79	23	435	response to inorganic substance	BP	1	MAPK9,ANXA1,GCLC,MAPK8,TRPC1,CPNE3,ARL13B,ATP2B4,CPNE8,MEF2A,PIK3CA,EGLN1,PLEKHA1,ATF2,WNK1,ATRX,ATP7A,PRKAA1,SETX,MT-CO1,MT-ND5,UBE2D3,CACYBP	pink	VSMC_M5
GO:0019079	0.28	0.85	6	99	viral genome replication	BP	1	SRPK2,TOP2B,IFIT5,MORC2,CCNK,PKN2	pink	VSMC_M5
GO:0034654	0.28	0.75	136	2841	nucleobase-containing compound biosynthetic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,TNKS2,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,ACACB,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ATRX,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,UBE2D3,ATP5PF,USP9X,MTPN,PEG3,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0001655	0.28	0.80	17	283	urogenital system development	BP	1	PCSK5,ANXA1,VEGFA,MAGI2,APAF1,SMAD1,TIPARP,NOTCH2,CRKL,PYGO1,FEM1B,TTC8,SMAD2,NF1,NIPBL,SMAD7,BMP2	pink	VSMC_M5
GO:0006893	0.28	0.87	4	56	Golgi to plasma membrane transport	BP	1	COMMD1,MACF1,GOLGA7,GOLPH3L	pink	VSMC_M5
GO:1904063	0.28	0.87	4	62	negative regulation of cation transmembrane transport	BP	1	COMMD1,CAB39,STK39,ATP7A	pink	VSMC_M5
GO:0002011	0.28	0.87	4	50	morphogenesis of an epithelial sheet	BP	1	ADAM17,CLASP1,FLRT3,NOTCH2	pink	VSMC_M5
GO:0010970	0.28	0.82	9	139	transport along microtubule	BP	1	DST,LCA5,RAB1A,BBS12,ARL8B,PCM1,BICD1,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0030855	0.28	0.79	24	430	epithelial cell differentiation	BP	1	LATS1,ANXA1,VEGFA,UGCG,KIAA1109,MAGI2,EPB41L5,RHEB,XDH,IL6ST,FAT1,TSG101,ESRP1,NOTCH2,GSK3B,FSTL1,ABI2,OPHN1,YIPF6,ATRX,FEM1B,TTC8,TMEM38B,BMP2	pink	VSMC_M5
GO:0045669	0.28	0.87	4	56	positive regulation of osteoblast differentiation	BP	1	RUNX2,IL6ST,SMAD1,BMP2	pink	VSMC_M5
GO:0090304	0.28	0.75	181	3916	nucleic acid metabolic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,UBR5,DDX17,ELAVL2,UBR2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,INIP,COMMD1,TIA1,CPSF3,UFL1,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DCLRE1C,INTS4,KMT2C,EMSY,ZEB2,EPC2,KAT6A,ENDOV,TOP2B,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,YTHDF3,TNKS2,VCPIP1,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,AQR,PCGF1,GABPA,TET3,WWP1,DUSP11,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,SNRPN,ID4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,DCLRE1A,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,TFIP11,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,SCNM1,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,TSEN15,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,RFX7,HUWE1,GTF2A2,FBXW11,ASH1L,USP3,MLH3,WDR83,ATRX,DIS3L,GTF2A1,PIAS1,SMAD2,MED13,CCNK,SMG1,UBE2A,PRKAA1,NIPBL,RAD1,PHF6,SMAD7,PRPF8,LRIF1,SETX,PTBP2,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,UBE2V2,MTPN,PEG3,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0030258	0.28	0.82	9	171	lipid modification	BP	1	DGKA,SLC25A17,DGKH,IRS2,MTMR6,PIP4P2,ACACB,ACOX3,PRKAA1	pink	VSMC_M5
GO:0008406	0.28	0.82	10	166	gonad development	BP	1	VEGFA,RNF38,NCOA1,KITLG,RHOBTB3,TIPARP,CSDE1,PLEKHA1,CRKL,ATRX	pink	VSMC_M5
GO:0031399	0.28	0.76	59	1182	regulation of protein modification process	BP	1	TAB2,PPIL4,LATS1,MAPK9,UBR5,C9orf72,VEGFA,GCLC,COMMD1,ADAM17,UFL1,MRE11,MAGI2,FNTA,XDH,KITLG,SPRY4,MAPK8,DLC1,RB1CC1,IL6ST,CDK5RAP1,ARFGEF1,KDM3A,DIP2B,GTF2H1,TSG101,ATP2B4,TWF1,BTRC,NDUFS4,DOCK3,TRIP12,CAB39,PPP6R3,GSK3B,PIK3CA,FXR1,DCUN1D1,ALS2,CREBL2,ATF2,STYXL1,CRKL,WNK1,HUWE1,ATRX,PIAS1,GSKIP,CCNK,GGNBP2,XIAP,NF1,PRKAA1,NIPBL,SMAD7,BIRC2,UBXN2A,BMP2	pink	VSMC_M5

GO:0050789	0.29	0.74	372	7907	regulation of biological process	BP	1	DGKA,MEX3C,ME2,ARFGEF3,TAB2,PPIL4,MED23,LATS1,MAPK9,CSNK1G3,SCAF8,UBR5,DDX17,MKLN1,KLHDC10,ELAVL2,UBR2,C9orf72,WASL,ANXA1,TMEM33,GUF1,VEGFA,KRIT1,ANKIB1,RUNX2,CD2AP,SDHAF3,ASNS,GCM1,GCLC,DST,PTP4A1,RHOQ,FBXO11,ERLEC1,TAX1BP1,RLF,USP34,UGCG,ZNF292,COMMD1,MACF1,VPS54,RAB1A,SEPT7,TIA1,ADAM17,CAPZA2,UFL1,CUL1,ZMYM4,RAB14,CUL2,RAB33B,ZFYVE9,JCAD,ARHGAP42,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,AKAP11,CNOT10,PDCD6IP,DGKH,CLASP1,EPB41L5,RHEB,KMT2C,FBXL3,EMSY,FNTA,ZEB2,MBD5,FLRT3,EPC2,XDH,KAT6A,MEMO1,TOP2B,ZDHHC17,NKIRAS1,BIRC6,LTBP1,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,ATRN,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,PCM1,IFIT5,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,CDK5RAP1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,SLC4A8,CGGBP1,NR3C2,RHOBTB3,TRPC1,DIP2B,BTBD10,RNF13,DPH6,PCGF1,TCTN1,GABPA,PPP1CC,TET3,WWP1,ZFYVE16,CPNE3,TIPARP,MLF1,RALGAPB,ARL13B,PIP4P2,LXN,FAM92A,ARSB,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BAZ2B,BTG2,SSR1,DNMBP,ATP2B4,ZBTB11,CEP97,CSDE1,TWF1,IRAK4,CYLD,RANBP9,BBX,BTRC,NIPSNAP2,TSPAN32,NDUFS4,ID4,DOCK3,ACOT13,NOTCH2,TRIP12,BICD1,ANO1,ASB7,DENND5B,CAB39,ZMYND8,IPO8,MEF2A,PPP6R3,SHOC2,PRKAB2,TET2,KMT5B,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,SCN9A,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,DCUN1D1,TFIP11,STK39,EGL	pink	VSMC_M5
GO:0034641	0.29	0.74	220	4878	cellular nitrogen compound metabolic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,UBR5,LRGUK,DDX17,ELAVL2,PCSK5,UBR2,WASL,GUF1,VEGFA,RUNX2,ASNS,GCM1,GCLC,RHOQ,TAX1BP1,RLF,UGCG,ZNF292,INIP,COMMD1,TIA1,CPSF3,UFL1,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DCLRE1C,INTS4,KMT2C,EMSY,ZEB2,EPC2,XDH,KAT6A,OXSM,ENDOV,TOP2B,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,CAPRIN1,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,FAR1,GFM2,AQR,DPH6,PCGF1,GABPA,TET3,WWP1,DUSP11,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,SNRPN,ID4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,DCLRE1A,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,TFIP11,EGLN1,KDM2A,PARL,ADAL,TIAL1,PSMC6,GABPB2,METTL5,PDE5A,SCNM1,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,TSEN15,RNF2,NEMF,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,RFX7,FUT8,HUWE1,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,MLH3,ABCB7,SPTLC2,WDR83,ATRX,ATP7A,DIS3L,GTF2A1,PIAS1,SMAD2,MED13,CCNK,SMG1,UBE2A,PRKAA1,NIPBL,RAD1,PHF6,HPRT1,CPD,SMAD7,PRPF8,LRIF1,SETX,SLC35A3,NUDT7,PTBP2,NFAT5,MT-CO2,BIRC2,SULT1C4,HACD1,AGO3,UBE2D3,ATP5PF,USP9X,UBE2V2,MTPN,PEG3,EIF5A2,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,RNF139,DDAH1,PAIP2,BMP2,DENR,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:2001020	0.29	0.81	11	200	regulation of response to DNA damage stimulus	BP	1	UBR5,ARID2,TRIP12,KMT5B,FXR1,TFIP11,KLHL15,ATM,FEM1B,SMG1,UBE2V2	pink	VSMC_M5
GO:1905515	0.29	0.87	4	53	non-motile cilium assembly	BP	1	SEPT7,PCM1,ARL13B,TTC8	pink	VSMC_M5
GO:0072521	0.29	0.80	16	319	purine-containing compound metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,ADAL,PDE5A,PRKAA1,HPRT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:1903827	0.29	0.78	24	454	regulation of cellular protein localization	BP	1	LATS1,UBR5,CD2AP,RHOQ,ERLEC1,COMMD1,MAPK8,PCM1,VCPIP1,TSG101,ATP2B4,BICD1,ZMYND8,GSK3B,PARL,HECTD1,PRKCI,CRKL,WAPL,HUWE1,PTPN9,PRKAA1,UBE2D3,SAR1B	pink	VSMC_M5
GO:1901362	0.29	0.75	143	3012	organic cyclic compound biosynthetic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,CYP39A1,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,UFL1,OSBPL9,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,KMT2C,EMSY,ZEB2,EPC2,KAT6A,EAF1,ZNF605,NR3C1,N4BP2L2,UBA3,MAPK8,GPBP1,TNKS2,ZMYM5,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,TRPC1,NFS1,PCGF1,GABPA,TET3,WWP1,MLF1,GTF2H1,MED13L,TSG101,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CYLD,BBX,BTRC,ID4,NOTCH2,ZMYND8,MEF2A,TET2,ACACB,GTF2I,BPTF,MSL3,GOLGB1,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,ATF2,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,ABCB7,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,PHF6,HPRT1,SMAD7,LRIF1,SETX,NFAT5,MT-CO2,BIRC2,HACD1,UBE2D3,ATP5PF,USP9X,MTPN,PEG3,RBAK,ZNF770,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0009408	0.29	0.85	5	84	response to heat	BP	1	GCLC,POLR2D,ANO1,GSK3B,ATM	pink	VSMC_M5
GO:1903828	0.29	0.84	6	99	negative regulation of cellular protein localization	BP	1	LATS1,RHOQ,ERLEC1,COMMD1,GSK3B,HECTD1	pink	VSMC_M5
GO:0031503	0.29	0.81	11	186	protein-containing complex localization	BP	1	WASL,LCA5,BBS12,POLR2D,PCM1,ZC3H11A,SMG7,ATM,OPHN1,SMG1,SMAD7	pink	VSMC_M5
GO:0007015	0.29	0.78	21	373	actin filament organization	BP	1	LATS1,C9orf72,WASL,CD2AP,CAPZA2,CLASP1,DLC1,FAT1,ARFGEF1,RHOBTB3,TWF1,PIK3CA,ABI2,ARPC2,PRKCI,TTC8,DIAPH2,PSTPIP2,FAM206A,GMFB,MTPN	pink	VSMC_M5

GO:0008219	0.29	0.75	75	1587	cell death	BP	1	LATS1,MAPK9,ANXA1,VEGFA,KRIT1,ASNS,GCLC,FBXO11,TAX1BP1,TIA1,ADAM17,UFL1,CUL1,CUL2,SRPK2,NCOA1,MRE11,YME1L1,PDCD6IP,BIRC6,IRS2,KITLG,NR3C1,SHQ1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,URI1,EIF4G2,BTBD10,HIPK1,BTG2,CYLD,NOTCH2,MEF2A,GSK3B,FSTL1,PIK3CA,FXR1,FAM162A,TIAL1,ALS2,RPS6KA3,ATF2,STYXL1,TRIM69,LANCL1,ATM,CUL5,ERO1A,PRKCI,TIMP1,CRKL,GHITM,CPEB4,UBE2Z,PIAS1,FEM1B,GSKIP,XIAP,NF1,PRKAA1,SETX,PKN2,MT-CO2,BIRC2,MINDY3,UBE2D3,UBE2V2,CACYBP,PEG3,BMP2	pink	VSMC_M5
GO:0019395	0.29	0.85	5	87	fatty acid oxidation	BP	1	SLC25A17,IRS2,ACACB,ACOX3,PRKAA1	pink	VSMC_M5
GO:0044264	0.29	0.85	5	75	cellular polysaccharide metabolic process	BP	1	IRS2,RB1CC1,IL6ST,PPP1CC,GSK3B	pink	VSMC_M5
GO:0010467	0.29	0.74	204	4455	gene expression	BP	1	PPIL4,MED23,MAPK9,SCAF8,UBR5,DDX17,ELAVL2,PCSK5,WASL,ANXA1,GUF1,VEGFA,RUNX2,CD2AP,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,RAB1A,NFU1,TIA1,CPSF3,ADAM17,UFL1,CDC40,SRPK2,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,YME1L1,MED4,MAP3K2,CNOT10,INTS4,EPB41L5,KMT2C,EMSY,ZEB2,EPC2,XDH,KAT6A,LTBP1,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,IL6ST,GPBP1,CAPRIN1,YTHDF3,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,CGGBP1,NR3C2,GFM2,AQR,DPH6,PCGF1,GABPA,PPP1CC,TET3,WWP1,DUSP11,TIPARP,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,ZC3H11A,CSDE1,CYLD,BBX,BTRC,TSPAN32,SNRPN,ID4,NOTCH2,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,GSK3B,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,TFIP11,EGLN1,KDM2A,PARL,TIAL1,PSMC6,GABPB2,METTL5,SCNM1,ZNF148,MORC2,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,GLRX3,ATF2,TSEN15,RNF2,NEMF,ATM,KDM6A,ERO1A,PRKCI,COPS2,YWHAQ,HP1BP3,CRKL,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,FUT8,HUWE1,GTF2A2,CPEB4,FBXW11,ASH1L,USP3,WDR83,ATRX,ATP7A,GTF2A1,PIAS1,SMAD2,MED13,PIK3C3,CCNK,GGNBP2,SMG1,XIAP,PRKAA1,NIPBL,PHF6,CPD,SMAD7,PRPF8,LRIF1,SETX,PTBP2,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,MTPN,PEG3,EIF5A2,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,RNF139,PAIP2,UBXN2A,BMP2,DENR,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0003073	0.29	0.86	4	60	regulation of systemic arterial blood pressure	BP	1	PCSK5,ARHGAP42,WNK1,DDAH1	pink	VSMC_M5
GO:0051052	0.29	0.79	16	297	regulation of DNA metabolic process	BP	1	UBR5,RLF,MRE11,TNKS2,ARID2,TRIP12,KMT5B,PIK3CA,TFIP11,KLHL15,ATM,ATRX,SMG1,USP9X,UBE2V2,NAF1	pink	VSMC_M5
GO:0006725	0.29	0.74	201	4410	cellular aromatic compound metabolic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,UBR5,LRGUK,DDX17,ELAVL2,UBR2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,INIP,COMMD1,TIA1,CPSF3,UFL1,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DCLRE1C,INTS4,KMT2C,EMSY,ZEB2,EPC2,XDH,KAT6A,OXSM,ENDOV,TOP2B,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,YTHDF3,TNKS2,VCPIP1,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,TRPC1,FAR1,AQR,PCGF1,GABPA,TET3,WWP1,DUSP11,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,SNRPN,ID4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,DCLRE1A,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,TFIP11,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,PDE5A,SCNM1,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,TSEN15,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,RFX7,FUT8,HUWE1,GTF2A2,FBXW11,ASH1L,USP3,MLH3,ABCB7,WDR83,ATRX,ATP7A,DIS3L,GTF2A1,PIAS1,SMAD2,MED13,CCNK,SMG1,UBE2A,PRKAA1,NIPBL,RAD1,PHF6,HPRT1,SMAD7,PRPF8,LRIF1,SETX,SLC35A3,NUDT7,PTBP2,NFAT5,MT-CO2,BIRC2,SULT1C4,HACD1,AGO3,UBE2D3,ATP5PF,USP9X,UBE2V2,MTPN,PEG3,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0048568	0.29	0.78	19	341	embryonic organ development	BP	1	MTHFD1L,PCSK5,VEGFA,RUNX2,GCM1,NCOA1,BIRC6,KITLG,ARL13B,TBC1D23,HIPK1,ARID2,NOTCH2,BPTF,HECTD1,DLX2,SMAD2,GGNBP2,NIPBL	pink	VSMC_M5
GO:0035304	0.30	0.85	5	74	regulation of protein dephosphorylation	BP	1	MAGI2,DLC1,PPP6R3,GSK3B,STYXL1	pink	VSMC_M5
GO:0021953	0.30	0.82	8	116	central nervous system neuron differentiation	BP	1	TCTN1,BTG2,DLX2,OPHN1,HERC1,ATP7A,HPRT1,MTPN	pink	VSMC_M5
GO:0043244	0.30	0.82	8	107	regulation of protein-containing complex disassembly	BP	1	SCAF8,CAPZA2,CLASP1,TWF1,PIK3CA,SETX,MTPN,EIF5A2	pink	VSMC_M5
GO:0006468	0.30	0.74	63	1223	protein phosphorylation	BP	1	TAB2,PPIL4,LATS1,MAPK9,CSNK1G3,C9orf72,VEGFA,ADAM17,SRPK2,MRE11,MAP3K2,XDH,BIRC6,KITLG,PRKD3,SPRY4,MAP4K3,MAPK8,RB1CC1,IL6ST,CSNK2A1,CDK5RAP1,SMAD1,CPNE3,GTF2H1,TSG101,HIPK1,ATP2B4,TWF1,IRAK4,NDUFS4,DOCK3,CAB39,PRKAB2,GSK3B,PIK3CA,FXR1,STK39,ALS2,RPS6KC1,TLK1,ABI2,RPS6KA3,CREBL2,ATF2,ATM,PRKCI,COPS2,CRKL,WNK1,SMAD2,PIK3C3,GSKIP,CCNK,GGNBP2,SMG1,CSNK1A1,NF1,PRKAA1,SMAD7,PKN2,GMFB,BMP2	pink	VSMC_M5
GO:0006633	0.30	0.83	6	107	fatty acid biosynthetic process	BP	1	ANXA1,OXSM,PRKAB2,ACACB,PRKAA1,HACD1	pink	VSMC_M5
GO:0040008	0.30	0.77	27	518	regulation of growth	BP	1	LATS1,VEGFA,MACF1,VPS54,ADAM17,KIAA1109,EPC1,MBD5,ATRN,CSNK2A1,TNKS2,URI1,EIF4G2,DIP2B,TSG101,NOTCH2,ACACB,GSK3B,PIK3CA,RPS6KA3,ST7L,UBE2E3,CRKL,NIPBL,SMAD7,MTPN,BRMS1L	pink	VSMC_M5
GO:0001952	0.30	0.82	7	105	regulation of cell-matrix adhesion	BP	1	VEGFA,MACF1,CLASP1,EPB41L5,DLC1,GSK3B,NF1	pink	VSMC_M5

GO:0043067	0.30	0.75	53	1119	regulation of programmed cell death	BP	1	LATS1,MAPK9,ANXA1,VEGFA,KRIT1,ASNS,GCLC,FBXO11,TAX1BP1,TIA1,ADAM17,UFL1,SRPK2,NCOA1,MRE11,YME1L1,BIRC6,IRS2,KITLG,SHQ1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,URI1,BTG2,CYLD,NOTCH2,GSK3B,FSTL1,PIK3CA,FAM162A,RPS6KA3,ATF2,STYXL1,LANCL1,ATM,PRKCI,TIMP1,GHITM,CPEB4,UBE2Z,PIAS1,FEM1B,XIAP,NF1,PRKAA1,SETX,BIRC2,UBE2V2,BMP2	pink	VSMC_M5
GO:0051130	0.30	0.75	46	870	positive regulation of cellular component organization	BP	1	MAPK9,WASL,ANXA1,VEGFA,GCM1,RHOQ,MACF1,SEPT7,MRE11,MAGI2,PDCD6IP,CLASP1,EPB41L5,FLRT3,MAPK8,CAPRIN1,TNKS2,EIF4G2,ARSB,TSG101,PPP3CC,TWF1,BICD1,ZMYND8,GSK3B,PIK3CA,FAM162A,PSMC6,ABI2,MORC2,ATF7IP,STYXL1,ATM,ARPC2,PRKCI,ATL3,ABCB7,ATRX,ATP7A,DYNC1H1,SETX,GMFB,UBE2V2,EIF5A2,NAF1,BMP2	pink	VSMC_M5
GO:0090502	0.30	0.85	4	62	RNA phosphodiester bond hydrolysis, endonucleolytic	BP	1	CPSF3,ENDOV,RPP14,AGO3	pink	VSMC_M5
GO:0016241	0.31	0.81	8	128	regulation of macroautophagy	BP	1	C9orf72,RHEB,MAPK8,PIK3CA,SCFD1,PAFAH1B2,SPTLC2,SMG1	pink	VSMC_M5
GO:0045137	0.31	0.80	10	170	development of primary sexual characteristics	BP	1	VEGFA,RNF38,NCOA1,KITLG,RHOBTB3,TIPARP,CSDE1,PLEKHA1,CRKL,ATRX	pink	VSMC_M5
GO:0042157	0.31	0.83	6	111	lipoprotein metabolic process	BP	1	UGCG,ZDHHC17,GOLGA7,PIGP,PIK3C3,ZDHHC22	pink	VSMC_M5
GO:0030168	0.31	0.83	6	96	platelet activation	BP	1	DGKA,DGKH,IL6ST,TSPAN32,PIK3CA,STXBP3	pink	VSMC_M5
GO:0061035	0.31	0.85	4	61	regulation of cartilage development	BP	1	RUNX2,SMAD1,SMAD7,BMP2	pink	VSMC_M5
GO:0030837	0.31	0.85	4	53	negative regulation of actin filament polymerization	BP	1	CAPZA2,ARFGEF1,TWF1,MTPN	pink	VSMC_M5
GO:0030100	0.31	0.80	10	174	regulation of endocytosis	BP	1	MKLN1,WASL,VEGFA,CD2AP,MAGI2,ZFYVE16,TSG101,PPP3CC,BICD1,OPHN1	pink	VSMC_M5
GO:0014823	0.31	0.85	4	57	response to activity	BP	1	GCLC,CAB39,PRKAA1,ATP5PF	pink	VSMC_M5
GO:0090316	0.31	0.81	8	136	positive regulation of intracellular protein transport	BP	1	UBR5,MAPK8,PCM1,GSK3B,HUWE1,PRKAA1,UBE2D3,SAR1B	pink	VSMC_M5
GO:0051216	0.31	0.80	9	154	cartilage development	BP	1	MEX3C,RUNX2,IMPAD1,SMAD1,DLX2,TIMP1,ATP7A,SMAD7,BMP2	pink	VSMC_M5
GO:0034440	0.31	0.84	5	90	lipid oxidation	BP	1	SLC25A17,IRS2,ACACB,ACOX3,PRKAA1	pink	VSMC_M5
GO:0008589	0.31	0.84	5	71	regulation of smoothened signaling pathway	BP	1	RUNX2,TCTN1,FAM92A,BTRC,HERC4	pink	VSMC_M5
GO:0031497	0.31	0.84	5	84	chromatin assembly	BP	1	KAT6A,HP1BP3,KAT6B,ATRX,NAP1L3	pink	VSMC_M5
GO:0051348	0.31	0.79	12	219	negative regulation of transferase activity	BP	1	LATS1,IRS2,SPRY4,CDK5RAP1,TSG101,GSK3B,WNK1,GSKIP,GGNBP2,NF1,SMAD7,BMP2	pink	VSMC_M5
GO:0002690	0.31	0.85	4	71	positive regulation of leukocyte chemotaxis	BP	1	VEGFA,ADAM17,STK39,WNK1	pink	VSMC_M5
GO:0030865	0.31	0.85	4	55	cortical cytoskeleton organization	BP	1	RHOQ,AKAP11,PDCD6IP,RHOBTB3	pink	VSMC_M5
GO:0007586	0.31	0.85	4	63	digestion	BP	1	CYP39A1,UGCG,STK39,WNK1	pink	VSMC_M5
GO:0098586	0.31	0.85	4	63	cellular response to virus	BP	1	LSM14A,PUM1,ATF2,BIRC2	pink	VSMC_M5
GO:0035195	0.31	0.82	6	107	gene silencing by miRNA	BP	1	SMAD1,PUM1,FXR1,TIAL1,SMAD2,AGO3	pink	VSMC_M5
GO:0009259	0.32	0.77	15	302	ribonucleotide metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,PDE5A,PRKAA1,HPRT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0051704	0.32	0.74	35	709	multi-organism process	BP	1	SYNE1,LRGUK,PCSK5,UBR2,VEGFA,SEPT7,NCOA1,TBP,YTHDF3,KDM3A,SMAD1,ATP2B4,PUM1,TIAL1,PLEKHA1,ZNF148,PAFAH1B2,HERC4,RNF2,TIMP1,CRKL,PYGO1,FBXW11,ASH1L,MLH3,ATRX,ATP7A,PIAS1,DIAPH2,GGNBP2,UBE2A,SETX,USP9X,EIF5A2,PAIP2	pink	VSMC_M5
GO:0051493	0.32	0.75	26	457	regulation of cytoskeleton organization	BP	1	LATS1,C9orf72,WASL,CD2AP,RHOQ,CAPZA2,CLASP1,DLC1,ARFGEF1,RHOBTB3,CEP97,TWF1,CYLD,NOTCH2,BICD1,GSK3B,PIK3CA,ABI2,SKA1,ARPC2,TTC8,DYNC1H1,PRKAA1,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0051053	0.32	0.82	6	94	negative regulation of DNA metabolic process	BP	1	UBR5,TNKS2,TRIP12,TFIP11,KLHL15,ATM	pink	VSMC_M5
GO:0001657	0.32	0.83	5	78	ureteric bud development	BP	1	VEGFA,SMAD1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0051716	0.32	0.71	241	5042	cellular response to stimulus	BP	1	DGKA,ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,DDX17,MKLN1,KLHDC10,UBR2,C9orf72,ANXA1,TMEM33,VEGFA,KRIT1,RUNX2,CD2AP,ASNS,GCLC,DST,RHOQ,ERLEC1,USP34,UGCG,INIP,COMMD1,MACF1,ADAM17,UFL1,CUL1,RAB14,CUL2,RAB33B,ZFYVE9,JCAD,ARHGAP42,SRPK2,NCOA1,MRE11,PRDM5,ASXL2,POLR2D,MAGI2,MAP3K2,AKAP11,DCLRE1C,DGKH,EPB41L5,RHEB,EMSY,FNTA,ZEB2,MBD5,FLRT3,EPC2,XDH,KAT6A,NGLY1,ENDOV,ZDHHC17,NKIRAS1,BIRC6,LTBP1,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NR3C1,MAP4K3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,TNKS2,VCPIP1,LSM14A,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,NR3C2,RHOBTB3,RNF13,TCTN1,GABPA,PPP1CC,WWP1,ZFYVE16,CPNE3,TIPARP,RALGAPB,ARL13B,FAM92A,GTF2H1,TSG101,HIPK1,ARID2,POLK,PPP3CC,BTG2,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,TSPAN32,DOCK3,CPNE8,NOTCH2,TRIP12,BICD1,ANO1,ASB7,CAB39,ZMYND8,IPO8,MEF2A,SHOC2,PRKAB2,KMT5B,GSK3B,FSTL1,DCLRE1A,PUM1,PIK3CA,LYST,UBR1,GTF2I,BPTF,FXR1,TFIP11,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,TIAL1,PSMC6,ALS2,RPS6KC1,PDE5A,TLK1,PLEKHA1,MUC20,ABI2,MORC2,DLX2,ARHGAP5,RPS6KA3,CREBL2,SRP54,ATF2,KLHL15,ACAP2,HERC4,STYXL1,RALGPS2,LANCL1,SOS2,ATM,CUL5,ERO1A,PRKCI,COPS2,YWHAQ,HP1BP3,USP8,TIMP1,CRKL,RPAIN,WNK1,GHITM,PYGO1,PDS5A,FUT8,HUWE1,OPHN1,CPEB4,FBXW11,ASH1L,USP3,MLH3,ATRX,ATP7A,CHM,PIAS1,FEM1B,SMAD2,PIK3C3,GSKIP,CCNK,GGNBP2,SMG1,CSNK1A1,USP14,UBE2A,XIAP,NF1,PRKAA1,PTPRM,NIPBL,RAD1,SMAD7,PRPF8,SETX,STXBP3,PKN2,NFAT5,USP33,MT-ND2,BIRC2,NMI,CUL1,C1GA1,AGO3,UBE2D3,TMEM43,PPM1A,ZNF292,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2D,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,NR3C1,GPBP1,YTHDF3,TNKS2,KDM3A,ZNF507,SMAD1,GABPA,TET3,GTF2H1,TSG101,ARID2,BTG2,BTRC,MEF2A,TET2,KMT5B,PUM1,GTF2I,BPTF,PSMC6,GABPB2,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,MT-CO2,BIRC2,USP9X,UBE2V2,PEG3,ZNF770,HNRNPLL,NAF1,BMP2	pink	VSMC_M5
GO:0070972	0.32	0.84	4	60	protein localization to endoplasmic reticulum	BP	1	SRP72,SGTB,ZFAND2A,SRP54	pink	VSMC_M5
GO:0007568	0.32	0.78	13	252	aging	BP	1	MAPK9,GCLC,KAT6A,MAPK8,APAF1,BAZ2B,DNMBP,ATM,ERO1A,TIMP1,MT-CO1,MT-ND4,CACYBP	pink	VSMC_M5
GO:0045935	0.32	0.73	74	1489	positive regulation of nucleobase-containing compound metabolic process	BP	1	MED23,SCAF8,DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,MRE11,ASXL2,POLR2D,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,NR3C1,GPBP1,YTHDF3,TNKS2,KDM3A,ZNF507,SMAD1,GABPA,TET3,GTF2H1,TSG101,ARID2,BTG2,BTRC,MEF2A,TET2,KMT5B,PUM1,GTF2I,BPTF,PSMC6,GABPB2,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,MT-CO2,BIRC2,USP9X,UBE2V2,PEG3,ZNF770,HNRNPLL,NAF1,BMP2	pink	VSMC_M5

GO:0010033	0.32	0.72	110	2273	response to organic substance	BP	1	TAB2,LATS1,UBR5,DDX17,UBR2,ANXA1,TMEM33,VEGFA,RUNX2,ASNS,GCLC,RHOQ,ERLEC1,UGCG,ADAM17,UFL1,RAB14,ZFYVE9,HSPA4L,JCAD,NCOA1,PRDM5,MAGI2,EPB41L5,FNTA,ZEB2,MBD5,FLRT3,XDH,NGLY1,ZDHHC17,LTBP1,IRS2,SPRY4,NR3C1,MAP4K3,MAPK8,APAF1,IL6ST,YTHDF3,LSM14A,SGTB,KDM3A,ERBIN,URI1,SMAD1,NR3C2,GABPA,CPNE3,TIPARP,ARSB,GTF2H1,HIPK1,BTG2,ATP2B4,IRAK4,CYLD,BTRC,SNRPN,NDUFS4,NOTCH2,ANO1,CAB39,SHOC2,TET2,ACACB,GSK3B,FSTL1,PIK3CA,UBR1,BPTF,STK39,PSMC6,RPS6KA3,KLHL15,ACAP2,ATM,ERO1A,PRKCI,USP8,TIMP1,CRKL,WNK1,FUT8,CPEB4,ATRX,ATP7A,SMAD2,PIK3C3,USP14,XIAP,PRKAA1,HPRT1,SMAD7,PRPF8,SETX,STXBP3,NFAT5,MT-ND3,MT-ND4,MT-ND5,BIRC2,UBE2D3,TMEM38B,USP9X,RNF103,CACYBP,RNF139,UBXN2A,BMP2	pink	VSMC_M5
GO:0070925	0.32	0.74	37	705	organelle assembly	BP	1	VTA1,MAPK9,LRGUK,C9orf72,RAB1A,SEPT7,RAB14,RAB33B,SCLT1,PDCD6IP,CLASP1,ARL8B,RB1CC1,VPS37A,PCM1,YTHDF3,LSM14A,TCTN1,ARL13B,FAM92A,TSG101,CEP97,CSDE1,CYLD,BICD1,MEF2A,DNAAF5,SCFD1,STYXL1,TTC8,PIK3C3,DYNC1H1,WDR78,STAG2,PRKAA1,CPLANE1,UBXN2A	pink	VSMC_M5
GO:0006163	0.32	0.77	15	302	purine nucleotide metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,PDE5A,PRKAA1,HPRT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0009952	0.32	0.79	9	150	anterior/posterior pattern specification	BP	1	PCSK5,EPB41L5,HIPK1,BTG2,BPTF,RNF2,CRKL,SMAD2,BMP2	pink	VSMC_M5
GO:0030042	0.32	0.84	4	51	actin filament depolymerization	BP	1	CAPZA2,TWF1,PIK3CA,MTPN	pink	VSMC_M5
GO:0007040	0.32	0.84	4	61	lysosome organization	BP	1	RAB14,ARL8B,ARSB,LYST	pink	VSMC_M5
GO:0080171	0.32	0.84	4	61	lytic vacuole organization	BP	1	RAB14,ARL8B,ARSB,LYST	pink	VSMC_M5
GO:0006401	0.32	0.78	13	237	RNA catabolic process	BP	1	POLR2D,CNOT10,YTHDF3,BTG2,CSDE1,PUM1,FXR1,SMG7,ATM,DIS3L,SMG1,AGO3,NAF1	pink	VSMC_M5
GO:0042475	0.33	0.84	4	63	odontogenesis of dentin-containing tooth	BP	1	RUNX2,DLX2,ATF2,BMP2	pink	VSMC_M5
GO:0030968	0.33	0.84	4	69	endoplasmic reticulum unfolded protein response	BP	1	TMEM33,ERLEC1,UFL1,ERO1A	pink	VSMC_M5
GO:0016525	0.33	0.82	5	82	negative regulation of angiogenesis	BP	1	KRIT1,ATP2B4,GTF2I,ATF2,PTPRM	pink	VSMC_M5
GO:1901880	0.33	0.82	5	62	negative regulation of protein depolymerization	BP	1	CAPZA2,CLASP1,TWF1,PIK3CA,MTPN	pink	VSMC_M5
GO:0051222	0.33	0.77	13	241	positive regulation of protein transport	BP	1	UBR5,CD2AP,IRS2,MAPK8,PCM1,TSG101,ANO1,GSK3B,HUWE1,PRKAA1,UBE2D3,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0007169	0.33	0.74	27	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	VEGFA,RUNX2,RHOQ,ADAM17,RAB14,JCAD,MBD5,FLRT3,XDH,ZDHHC17,IRS2,SPRY4,ERBIN,CPNE3,TIPARP,TSG101,SHOC2,GSK3B,PIK3CA,PLEKHA1,MUC20,CUL5,CRKL,PRKAA1,SETX,MPZL1,BMP2	pink	VSMC_M5
GO:0048708	0.33	0.84	4	60	astrocyte differentiation	BP	1	GCM1,IL6ST,NF1,BMP2	pink	VSMC_M5
GO:0010821	0.33	0.80	7	124	regulation of mitochondrion organization	BP	1	GCLC,MAPK8,GSK3B,FAM162A,PARL,GHITM,HUWE1	pink	VSMC_M5
GO:0045921	0.33	0.84	4	63	positive regulation of exocytosis	BP	1	PDCD6IP,CLASP1,SLC4A8,TSG101	pink	VSMC_M5
GO:1901292	0.33	0.84	4	69	nucleoside phosphate catabolic process	BP	1	XDH,PDE5A,HPRT1,NUDT7	pink	VSMC_M5
GO:0051276	0.33	0.73	35	682	chromosome organization	BP	1	LATS1,ANXA1,MRE11,DCLRE1C,EMSY,KAT6A,TOP2B,NR3C1,TNKS2,ARID2,BAZ2B,DCLRE1A,BPTF,TFIP11,TLK1,MORC2,ATF7IP,ATM,KDM6A,HP1BP3,KAT6B,ZNF518B,PDS5A,WAPL,MLH3,ATRX,NAP1L3,SMG1,ESCO1,STAG2,NIPBL,BCORL1,SETX,NAF1,RMDN1	pink	VSMC_M5
GO:0009895	0.33	0.76	14	254	negative regulation of catabolic process	BP	1	TAB2,CSNK2A1,EIF4G2,ATP2B4,ACACB,PIK3CA,SCFD1,TIMP1,OPHN1,HERC1,SMG1,USP14,PRKAA1,NAF1	pink	VSMC_M5
GO:0043603	0.33	0.73	40	897	cellular amide metabolic process	BP	1	PCSK5,GUF1,ASNS,GCLC,UGCG,TIA1,POLR2D,CNOT10,XDH,OXSM,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,EIF4G2,FAR1,GFM2,DPH6,BTG2,CSDE1,ACACB,PUM1,FXR1,PARL,METTL5,RPS6KA3,NEMF,CPEB4,SPTLC2,PRKAA1,CPD,NUDT7,HACD1,AGO3,MTPN,EIF5A2,RNF139,PAIP2,DENR	pink	VSMC_M5
GO:2000181	0.33	0.82	5	83	negative regulation of blood vessel morphogenesis	BP	1	KRIT1,ATP2B4,GTF2I,ATF2,PTPRM	pink	VSMC_M5
GO:1903900	0.33	0.81	6	104	regulation of viral life cycle	BP	1	SRPK2,TOP2B,IFIT5,TSG101,MORC2,PKN2	pink	VSMC_M5
GO:0072329	0.33	0.82	5	95	monocarboxylic acid catabolic process	BP	1	SLC25A17,IRS2,ACACB,ACOX3,NUDT7	pink	VSMC_M5
GO:0043401	0.33	0.80	7	111	steroid hormone mediated signaling pathway	BP	1	LATS1,UBR5,DDX17,UFL1,NR3C1,KDM3A,NR3C2	pink	VSMC_M5
GO:0030307	0.33	0.79	8	134	positive regulation of cell growth	BP	1	VEGFA,MACF1,ADAM17,CSNK2A1,EIF4G2,RPS6KA3,SMAD7,MTPN	pink	VSMC_M5
GO:0060548	0.33	0.73	36	754	negative regulation of cell death	BP	1	ANXA1,VEGFA,KRIT1,ASNS,GCLC,TAX1BP1,UFL1,MRE11,YME1L1,BIRC6,IRS2,KITLG,MAPK8,RB1CC1,IL6ST,CSNK2A1,URI1,BTBD10,BTG2,NOTCH2,GSK3B,FSTL1,PIK3CA,RPS6KA3,PRKCI,TIMP1,GHITM,CPEB4,UBE2Z,PIAS1,XIAP,PRKAA1,SETX,BIRC2,UBE2V2,CACYBP	pink	VSMC_M5
GO:0032970	0.34	0.75	19	337	regulation of actin filament-based process	BP	1	LATS1,C9orf72,WASL,CD2AP,RHOQ,CAPZA2,CLASP1,DLC1,ARFGEF1,RHOBTB3,TWF1,NOTCH2,PIK3CA,ABI2,ARPC2,TTC8,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0031647	0.34	0.76	13	249	regulation of protein stability	BP	1	FBXL3,GOLGA7,BTRC,ATF7IP,CREBL2,USP8,FBXW11,USP3,SMAD7,USP33,USP9X,RNF139,BMP2	pink	VSMC_M5
GO:0090092	0.34	0.77	12	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	LATS1,ADAM17,MAGI2,ZEB2,LTBP1,NOTCH2,FSTL1,SMAD2,XIAP,SMAD7,UBE2D3,BMP2	pink	VSMC_M5
GO:0048675	0.34	0.80	7	106	axon extension	BP	1	C9orf72,VEGFA,MACF1,EIF4G2,DIP2B,GSK3B,USP9X	pink	VSMC_M5
GO:0051100	0.34	0.79	7	129	negative regulation of binding	BP	1	C9orf72,EPB41L5,MAPK8,GSK3B,TFIP11,WAPL,USP33	pink	VSMC_M5
GO:0051048	0.34	0.80	6	110	negative regulation of secretion	BP	1	ANXA1,RAB33B,STK39,WNK1,STXBP3,ATP5PF	pink	VSMC_M5
GO:1901343	0.34	0.81	5	84	negative regulation of vasculature development	BP	1	KRIT1,ATP2B4,GTF2I,ATF2,PTPRM	pink	VSMC_M5
GO:0000278	0.34	0.72	36	729	mitotic cell cycle	BP	1	LATS1,ANXA1,ASNS,ADAM17,CUL1,CUL2,MRE11,PRDM5,PDCD6IP,CLASP1,FBXL3,UBA3,VCPIP1,LSM14A,BTG2,CEP97,CYLD,TTC28,SKA1,ATF2,RNF2,DYNLT3,ATM,CUL5,USP8,PDS5A,WAPL,FBXW11,USP3,ATRX,PIAS1,DYNC1H1,STAG2,NIPBL,PKN2,RMDN1	pink	VSMC_M5
GO:0044282	0.34	0.76	13	284	small molecule catabolic process	BP	1	SLC25A17,CYP39A1,XDH,IRS2,IMPAD1,ATP2B4,ACACB,ADAL,ACOX3,FUT8,NUDT7,SULT1C4,DDAH1	pink	VSMC_M5
GO:0035966	0.34	0.79	7	143	response to topologically incorrect protein	BP	1	TMEM33,ERLEC1,UFL1,HSPA4L,NGLY1,KLHL15,ERO1A	pink	VSMC_M5
GO:0043065	0.34	0.74	20	410	positive regulation of apoptotic process	BP	1	LATS1,MAPK9,ANXA1,TIA1,SRPK2,NCOA1,SHQ1,MAPK8,APAF1,DLC1,CYLD,NOTCH2,FAM162A,ATF2,STYXL1,ATM,PRKCI,UBE2Z,NF1,BMP2	pink	VSMC_M5

GO:0006790	0.34	0.76	13	270	sulfur compound metabolic process	BP	1	GCLC,NFU1,XDH,OXSM,IMPAD1,FAR1,NFS1,ACACB,GLRX3,ABCB7,NUDT7,SULT1C4,HACD1	pink	VSMC_M5
GO:0071426	0.34	0.83	4	66	ribonucleoprotein complex export from nucleus	BP	1	POLR2D,ZC3H11A,SMG7,SMG1	pink	VSMC_M5
GO:0006403	0.34	0.78	9	171	RNA localization	BP	1	POLR2D,SHQ1,ZC3H11A,BICD1,SMG7,ATM,SMG1,EIF5A2,NAF1	pink	VSMC_M5
GO:0048704	0.34	0.81	5	83	embryonic skeletal system morphogenesis	BP	1	MTHFD1L,RUNX2,DLX2,SMAD2,NIPBL	pink	VSMC_M5
GO:0090066	0.35	0.73	22	418	regulation of anatomical structure size	BP	1	LATS1,WASL,VEGFA,GCLC,MACF1,CAPZA2,ARHGAP42,RB1CC1,ARFGEF1,EIF4G2,DIP2B,TWF1,GSK3B,PIK3CA,ALS2,ABI2,ARPC2,HP1BP3,ATP7A,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0006338	0.35	0.77	10	175	chromatin remodeling	BP	1	KAT6A,ARID2,BAZ2B,BPTF,MORC2,KDM6A,HP1BP3,KAT6B,ATRX,NAP1L3	pink	VSMC_M5
GO:0031401	0.35	0.72	37	747	positive regulation of protein modification process	BP	1	TAB2,LATS1,MAPK9,VEGFA,COMMD1,ADAM17,MRE11,MAGI2,FNTA,KITLG,DLC1,RB1CC1,IL6ST,CDK5RAP1,ARFGEF1,DIP2B,ATP2B4,BTRC,DOCK3,CAB39,PIK3CA,FXR1,DCUN1D1,ALS2,CREBL2,ATF2,CRKL,WNK1,HUWE1,PIAS1,CCNK,XIAP,PRKAA1,NIPBL,SMAD7,BIRC2,BMP2	pink	VSMC_M5
GO:0009314	0.35	0.74	18	359	response to radiation	BP	1	ANXA1,ASNS,INIP,DCLRE1C,FBXL3,MAP4K3,MAPK8,PPP1CC,POLK,ATM,TIMP1,PIAS1,UBE2A,NF1,PRKAA1,NIPBL,RAD1,MT-ND3	pink	VSMC_M5
GO:0017015	0.35	0.79	7	102	regulation of transforming growth factor beta receptor signaling pathway	BP	1	LATS1,ADAM17,ZEB2,LTBP1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0017157	0.35	0.78	8	147	regulation of exocytosis	BP	1	ANXA1,RAB33B,PDCD6IP,CLASP1,SLC4A8,TSG101,GSK3B,STXBP3	pink	VSMC_M5
GO:0071166	0.35	0.82	4	67	ribonucleoprotein complex localization	BP	1	POLR2D,ZC3H11A,SMG7,SMG1	pink	VSMC_M5
GO:0046486	0.35	0.74	16	317	glycerolipid metabolic process	BP	1	DGKA,SERINC1,EFR3A,AGMO,FAM126A,DGKH,IMPAD1,MTMR6,FAR1,PIP4P2,PIGP,PIK3CA,ATM,PIK3C3,SMG1,CEPT1	pink	VSMC_M5
GO:0034764	0.35	0.77	9	155	positive regulation of transmembrane transport	BP	1	RHOQ,IRS2,TRPC1,NIPSNAP2,MEF2A,STK39,CREBL2,PRKCI,WNK1	pink	VSMC_M5
GO:0019693	0.35	0.74	15	312	ribose phosphate metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,PDE5A,PRKAA1,HPRT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0009100	0.35	0.74	15	299	glycoprotein metabolic process	BP	1	DPY19L1,RAB1A,NGLY1,TMTC3,IMPAD1,ARFGEF1,TET3,GXYLT1,OGA,TET2,FUT8,ATP7A,RNF103,RNF139,BMP2	pink	VSMC_M5
GO:0043467	0.35	0.79	6	104	regulation of generation of precursor metabolites and energy	BP	1	IRS2,GSK3B,PIK3CA,GHITM,ATP7A,PRKAA1	pink	VSMC_M5
GO:1901360	0.35	0.68	206	4575	organic cyclic compound metabolic process	BP	1	PPIL4,MED23,MAPK9,MTHFD1L,SCAF8,UBR5,LRGUK,DDX17,ELAVL2,UBR2,WASL,VEGFA,RUNX2,CYP39A1,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,INIP,COMMD1,TIA1,CPSF3,UFL1,OSBPL9,CDC40,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,DCLRE1C,INTS4,KMT2C,EMSY,ZEB2,EPC2,XDH,KAT6A,OXSM,ENDOV,TOP2B,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,YTHDF3,TNKS2,VCPIP1,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,TRPC1,FAR1,AQR,NFS1,PCGF1,GABPA,TET3,WWP1,DUSP11,TIPARP,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,POLK,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,SNRPN,ID4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,DCLRE1A,PUM1,PIK3CA,GTF2I,BPTF,FXR1,MSL3,GOLGB1,ZBED9,TFIP11,EGLN1,KDM2A,ADAL,TIAL1,PSMC6,GABPB2,METTL5,PDE5A,SCNM1,PLEKHA1,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,KLHL15,TSEN15,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,RPAIN,POGK,SNAPC1,PYGO1,PDS5A,RFX7,FUT8,HUWE1,GTF2A2,FBXW11,ASH1L,USP3,MLH3,ABCB7,WDR83,ATRX,ATP7A,DIS3L,GTF2A1,PIAS1,SMAD2,MED13,CCNK,SMG1,UBE2A,PRKAA1,NIPBL,RAD1,PHF6,HPRT1,SMAD7,PRPF8,LRIF1,SETX,SLC35A3,NUDT7,PTBP2,NFAT5,MT-CO2,BIRC2,SULT1C4,HACD1,AGO3,UBE2D3,ATP5PF,USP9X,UBE2V2,MTPN,PEG3,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,DCAKD,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0031333	0.35	0.78	7	115	negative regulation of protein-containing complex assembly	BP	1	CAPZA2,ARFGEF1,TWF1,GSK3B,TFIP11,BIRC2,MTPN	pink	VSMC_M5
GO:0072659	0.36	0.75	13	239	protein localization to plasma membrane	BP	1	EFR3A,RHOQ,FAM126A,MACF1,GOLGA7,ATP2B4,TSPAN32,HECTD1,PRKCI,TTC8,PTPN9,GOLPH3L,ZDHHC22	pink	VSMC_M5
GO:0071310	0.36	0.69	88	1784	cellular response to organic substance	BP	1	LATS1,UBR5,DDX17,UBR2,ANXA1,TMEM33,VEGFA,RUNX2,ASNS,GCLC,RHOQ,ERLEC1,UGCG,ADAM17,UFL1,RAB14,ZFYVE9,JCAD,NCOA1,PRDM5,MAGI2,EPB41L5,FNTA,ZEB2,MBD5,FLRT3,XDH,NGLY1,ZDHHC17,LTBP1,IRS2,SPRY4,NR3C1,MAPK8,APAF1,IL6ST,YTHDF3,LSM14A,KDM3A,ERBIN,URI1,SMAD1,NR3C2,GABPA,CPNE3,TIPARP,GTF2H1,HIPK1,ATP2B4,IRAK4,CYLD,BTRC,NOTCH2,ANO1,SHOC2,GSK3B,FSTL1,PIK3CA,UBR1,BPTF,STK39,KLHL15,ACAP2,ATM,ERO1A,PRKCI,USP8,CRKL,WNK1,FUT8,CPEB4,ATP7A,SMAD2,XIAP,PRKAA1,SMAD7,PRPF8,SETX,STXBP3,NFAT5,MT-ND3,BIRC2,UBE2D3,TMEM38B,USP9X,CACYBP,UBXN2A,BMP2	pink	VSMC_M5
GO:0072163	0.36	0.80	5	79	mesonephric epithelium development	BP	1	VEGFA,SMAD1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0072164	0.36	0.80	5	79	mesonephric tubule development	BP	1	VEGFA,SMAD1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:1902532	0.36	0.73	21	407	negative regulation of intracellular signal transduction	BP	1	UBR2,CD2AP,ARHGAP42,MAGI2,XDH,SPRY4,DLC1,ERBIN,URI1,ATP2B4,CYLD,RANBP9,GSK3B,UBR1,PLEKHA1,ATM,ASH1L,NF1,PRKAA1,BMT2,BMP2	pink	VSMC_M5
GO:1990542	0.36	0.82	4	84	mitochondrial transmembrane transport	BP	1	SFXN1,ABCB7,ATP5PF,SLC25A36	pink	VSMC_M5
GO:0080135	0.36	0.72	27	553	regulation of cellular response to stress	BP	1	UBR5,KLHDC10,TMEM33,VEGFA,UFL1,XDH,RB1CC1,PJA2,RNF13,ARID2,CYLD,TRIP12,KMT5B,GSK3B,FXR1,TFIP11,STK39,KLHL15,LANCL1,ATM,FUT8,FEM1B,SMG1,USP14,UBE2V2,DDAH1,BMP2	pink	VSMC_M5
GO:0019637	0.36	0.71	34	743	organophosphate metabolic process	BP	1	DGKA,SERINC1,EFR3A,LRGUK,RHOQ,FAM126A,DGKH,XDH,OXSM,IMPAD1,MTMR6,FAR1,NFS1,PIP4P2,PIGP,ACACB,PIK3CA,ADAL,PDE5A,ATM,PGM2,SPTLC2,PIK3C3,SMG1,PRKAA1,HPRT1,CEPT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,TMEM38B,DCAKD	pink	VSMC_M5

GO:0090398	0.36	0.82	4	68	cellular senescence	BP	1	MAPK9,KAT6A,MAPK8,ATM	pink	VSMC_M5
GO:0008360	0.36	0.77	8	134	regulation of cell shape	BP	1	MKLN1,ANXA1,VEGFA,RHOQ,SEPT7,DLC1,RHOBTB3,DNMBP	pink	VSMC_M5
GO:0044106	0.36	0.81	4	74	cellular amine metabolic process	BP	1	ATP2B4,ATP7A,HPRT1,MTPN	pink	VSMC_M5
GO:0032271	0.36	0.75	11	199	regulation of protein polymerization	BP	1	LATS1,WASL,CAPZA2,CLASP1,ARFGEF1,TWF1,ABI2,ARPC2,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:1903844	0.36	0.78	7	104	regulation of cellular response to transforming growth factor beta stimulus	BP	1	LATS1,ADAM17,ZEB2,LTBP1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0001667	0.36	0.73	19	360	ameboidal-type cell migration	BP	1	ANXA1,VEGFA,KRIT1,MACF1,ADAM17,JCAD,CLASP1,EPB41L5,ZEB2,KITLG,YTHDF3,ARSB,ATP2B4,FSTL1,PIK3CA,TIMP1,NF1,PTPRM,PKN2	pink	VSMC_M5
GO:0032922	0.36	0.81	4	55	circadian regulation of gene expression	BP	1	PPP1CC,ID4,KDM2A,HUWE1	pink	VSMC_M5
GO:0042147	0.36	0.80	5	80	retrograde transport, endosome to Golgi	BP	1	SNX2,VPS54,RHOBTB3,VPS29,TBC1D23	pink	VSMC_M5
GO:0046467	0.36	0.78	6	120	membrane lipid biosynthetic process	BP	1	UGCG,PRKD3,PIGP,SPTLC2,PRKAA1,HACD1	pink	VSMC_M5
GO:0071705	0.36	0.68	75	1609	nitrogen compound transport	BP	1	VTA1,VPS13B,SNX2,UBR5,SFT2D1,KPNA5,SLC25A17,VPS13A,PCSK5,ANXA1,CD2AP,SRP72,ERLEC1,LCA5,COMMD1,MACF1,VPS54,RAB1A,RAB14,RAB33B,POLR2D,PDCD6IP,ARL8B,ZDHHC17,GOLGA7,COG6,IRS2,MAPK8,VPS37A,PCM1,SGTB,ARFGEF1,ERBIN,VPS29,ZFYVE16,TSG101,UEVLD,SSR1,ZC3H11A,ANO1,IPO8,GSK3B,LYST,ZFAND2A,PARL,TLK1,SCFD1,SMG7,SRP54,MTX2,PRKCI,YWHAQ,RPAIN,HUWE1,SFXN1,SNX11,ABCB7,CHM,TTC8,SMAD2,PIK3C3,APPBP2,SMG1,PRKAA1,STXBP3,SLC35A3,ARRDC5,UBE2D3,RAB18,EIF5A2,SLC25A36,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0006643	0.36	0.76	8	164	membrane lipid metabolic process	BP	1	SERINC1,AGMO,UGCG,PRKD3,PIGP,SPTLC2,PRKAA1,HACD1	pink	VSMC_M5
GO:0007004	0.36	0.81	4	63	telomere maintenance via telomerase	BP	1	MRE11,TNKS2,ATM,NAF1	pink	VSMC_M5
GO:0000904	0.37	0.70	32	562	cell morphogenesis involved in differentiation	BP	1	LATS1,C9orf72,WASL,VEGFA,MACF1,RAB1A,EPB41L5,FLRT3,TOP2B,ZDHHC17,SPRY4,ATRN,CAPRIN1,FAT1,EIF4G2,DIP2B,TCTN1,ARL13B,NOTCH2,MEF2A,GSK3B,ALS2,ABI2,ARPC2,CRKL,OPHN1,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5
GO:0006402	0.37	0.75	11	201	mRNA catabolic process	BP	1	POLR2D,CNOT10,YTHDF3,BTG2,CSDE1,PUM1,FXR1,SMG7,ATM,SMG1,AGO3	pink	VSMC_M5
GO:0051054	0.37	0.76	9	176	positive regulation of DNA metabolic process	BP	1	MRE11,TNKS2,ARID2,KMT5B,ATM,ATRX,USP9X,UBE2V2,NAF1	pink	VSMC_M5
GO:0007010	0.37	0.68	62	1177	cytoskeleton organization	BP	1	ARFGEF3,LATS1,LRGUK,MKLN1,C9orf72,WASL,ANXA1,CD2AP,DST,RHOQ,MACF1,VPS54,CAPZA2,ZMYM4,AKAP11,PDCD6IP,CLASP1,EPB41L5,DLC1,PCM1,FAT1,LSM14A,ARFGEF1,ERBIN,RHOBTB3,CEP97,TWF1,CYLD,RANBP9,TSPAN32,NOTCH2,BICD1,MEF2A,GSK3B,PIK3CA,DNAAF5,ABI2,SKA1,ATF2,ARPC2,PRKCI,CCSER2,OPHN1,FBXW11,ATRX,SPATA7,TTC8,DIAPH2,KATNAL2,PSTPIP2,DYNC1H1,CSNK1A1,WDR78,STAG2,NF1,PRKAA1,GAN,USP33,FAM206A,GMFB,MTPN,RMDN1	pink	VSMC_M5
GO:0034502	0.37	0.79	5	86	protein localization to chromosome	BP	1	TNKS2,VCPIP1,WAPL,ATRX,NIPBL	pink	VSMC_M5
GO:0001823	0.37	0.79	5	81	mesonephros development	BP	1	VEGFA,SMAD1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0071260	0.37	0.81	4	69	cellular response to mechanical stimulus	BP	1	GCLC,MAP3K2,MAPK8,MTPN	pink	VSMC_M5
GO:0098930	0.37	0.81	4	58	axonal transport	BP	1	DST,ARL8B,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0005976	0.37	0.79	5	83	polysaccharide metabolic process	BP	1	IRS2,RB1CC1,IL6ST,PPP1CC,GSK3B	pink	VSMC_M5
GO:0031122	0.37	0.81	4	52	cytoplasmic microtubule organization	BP	1	DST,CLASP1,PCM1,DYNC1H1	pink	VSMC_M5
GO:0038127	0.37	0.78	6	102	ERBB signaling pathway	BP	1	ADAM17,ERBIN,CPNE3,TSG101,PIK3CA,CUL5	pink	VSMC_M5
GO:0035194	0.37	0.77	6	112	post-transcriptional gene silencing by RNA	BP	1	SMAD1,PUM1,FXR1,TIAL1,SMAD2,AGO3	pink	VSMC_M5
GO:1903533	0.37	0.80	4	69	regulation of protein targeting	BP	1	PARL,HUWE1,PRKAA1,UBE2D3	pink	VSMC_M5
GO:0048706	0.37	0.77	6	105	embryonic skeletal system development	BP	1	MTHFD1L,PCSK5,RUNX2,DLX2,SMAD2,NIPBL	pink	VSMC_M5
GO:1905475	0.38	0.75	8	147	regulation of protein localization to membrane	BP	1	RHOQ,MAPK8,ATP2B4,ZMYND8,HECTD1,PRKCI,CRKL,PTPN9	pink	VSMC_M5
GO:0016070	0.38	0.66	159	3480	RNA metabolic process	BP	1	PPIL4,MED23,MAPK9,SCAF8,DDX17,ELAVL2,WASL,VEGFA,RUNX2,GCM1,GCLC,RHOQ,TAX1BP1,RLF,ZNF292,COMMD1,TIA1,CPSF3,UFL1,CDC40,SRPK2,NCOA1,EPC1,TBP,PRDM5,ASXL2,SAP130,POLR2D,MED4,MAP3K2,CNOT10,INTS4,KMT2C,EMSY,ZEB2,EPC2,KAT6A,ENDOV,EAF1,ZNF605,NR3C1,N4BP2L2,SHQ1,UBA3,MAPK8,GPBP1,YTHDF3,ZMYM5,RPP14,CDK5RAP1,PPWD1,KDM3A,ERBIN,ZNF507,URI1,SMAD1,CGGBP1,NR3C2,AQR,PCGF1,GABPA,TET3,WWP1,DUSP11,MLF1,GTF2H1,VIRMA,MED13L,TSG101,ESRP1,ARID2,BAZ2B,BTG2,ATP2B4,ZBTB11,CSDE1,CYLD,BBX,BTRC,SNRPN,ID4,NOTCH2,BICD1,ZMYND8,MEF2A,TET2,PUM1,GTF2I,BPTF,FXR1,MSL3,GOLGB1,TFIP11,EGLN1,KDM2A,TIAL1,PSMC6,GABPB2,METTL5,SCNM1,ZNF148,DLX2,JMJD1C,ATF7IP,RPS6KA3,CREBL2,SMG7,ATF2,TSEN15,RNF2,ATM,PRKCI,COPS2,YWHAQ,HP1BP3,KAT6B,ZNF518B,POGK,SNAPC1,PYGO1,RFX7,GTF2A2,FBXW11,ASH1L,USP3,WDR83,ATRX,DIS3L,GTF2A1,PIAS1,SMAD2,MED13,CCNK,SMG1,PRKAA1,NIPBL,PHF6,SMAD7,PRPF8,LRIF1,SETX,PTBP2,NFAT5,BIRC2,AGO3,UBE2D3,USP9X,MTPN,PEG3,RBAK,ZNF770,HNRNPLL,NAF1,BRMS1L,ZNF45,BMP2,ZNF619,ZBTB6,MXD1	pink	VSMC_M5
GO:0048844	0.38	0.80	4	57	artery morphogenesis	BP	1	VEGFA,ARID2,NF1,SMAD7	pink	VSMC_M5
GO:0051592	0.38	0.76	7	114	response to calcium ion	BP	1	TRPC1,CPNE3,CPNE8,MEF2A,WNK1,PRKAA1,CACYBP	pink	VSMC_M5
GO:0032872	0.38	0.75	8	148	regulation of stress-activated MAPK cascade	BP	1	KLHDC10,VEGFA,XDH,RB1CC1,PJA2,CYLD,STK39,BMP2	pink	VSMC_M5
GO:0072073	0.38	0.76	7	115	kidney epithelium development	BP	1	VEGFA,MAGI2,SMAD1,NOTCH2,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0106106	0.38	0.76	7	123	cold-induced thermogenesis	BP	1	VEGFA,ADAM17,RHEB,KDM3A,ACOT13,PRKAB2,DYNC1H1	pink	VSMC_M5
GO:0120161	0.38	0.76	7	123	regulation of cold-induced thermogenesis	BP	1	VEGFA,ADAM17,RHEB,KDM3A,ACOT13,PRKAB2,DYNC1H1	pink	VSMC_M5
GO:0031056	0.38	0.76	7	124	regulation of histone modification	BP	1	UBR5,VEGFA,MAPK8,KDM3A,TRIP12,ATRX,NIPBL	pink	VSMC_M5
GO:0097190	0.39	0.70	22	471	apoptotic signaling pathway	BP	1	MAPK9,GCLC,CUL1,CUL2,BIRC6,KITLG,MAPK8,APAF1,RB1CC1,CSNK2A1,URI1,HIPK1,CYLD,GSK3B,FAM162A,STYXL1,ATM,CUL5,ERO1A,GHITM,FEM1B,GSKIP	pink	VSMC_M5
GO:0033157	0.39	0.73	10	196	regulation of intracellular protein transport	BP	1	UBR5,ERLEC1,MAPK8,PCM1,GSK3B,PARL,HUWE1,PRKAA1,UBE2D3,SAR1B	pink	VSMC_M5

GO:0001776	0.39	0.79	4	70	leukocyte homeostasis	BP	1	ANXA1,ADAM17,KITLG,SOS2	pink	VSMC_M5
GO:0009416	0.39	0.72	12	239	response to light stimulus	BP	1	ASNS,FBXL3,MAP4K3,MAPK8,PPP1CC,POLK,TIMP1,PIAS1,UBE2A,NF1,PRKAA1,MT-ND3	pink	VSMC_M5
GO:2001021	0.39	0.79	4	72	negative regulation of response to DNA damage stimulus	BP	1	UBR5,TRIP12,TFIP11,KLHL15	pink	VSMC_M5
GO:0043068	0.39	0.70	20	422	positive regulation of programmed cell death	BP	1	LATS1,MAPK9,ANXA1,TIA1,SRPK2,NCOA1,SHQ1,MAPK8,APAF1,DLC1,CYLD,NOTCH2,FAM162A,ATF2,STYXL1,ATM,PRKCI,UBE2Z,NF1,BMP2	pink	VSMC_M5
GO:0009308	0.39	0.79	4	77	amine metabolic process	BP	1	ATP2B4,ATP7A,HPRT1,MTPN	pink	VSMC_M5
GO:0010720	0.39	0.72	13	231	positive regulation of cell development	BP	1	VEGFA,MACF1,UFL1,RHEB,IL6ST,CAPRIN1,EIF4G2,PPP1CC,ARPC2,PRKCI,CRKL,SMAD7,BMP2	pink	VSMC_M5
GO:0010942	0.39	0.69	22	470	positive regulation of cell death	BP	1	LATS1,MAPK9,ANXA1,TIA1,SRPK2,NCOA1,SHQ1,MAPK8,APAF1,DLC1,CYLD,NOTCH2,GSK3B,FAM162A,ATF2,STYXL1,ATM,PRKCI,UBE2Z,NF1,MT-CO2,BMP2	pink	VSMC_M5
GO:0002687	0.39	0.77	5	101	positive regulation of leukocyte migration	BP	1	VEGFA,ADAM17,KITLG,STK39,WNK1	pink	VSMC_M5
GO:0006278	0.39	0.79	4	64	RNA-dependent DNA biosynthetic process	BP	1	MRE11,TNKS2,ATM,NAF1	pink	VSMC_M5
GO:0006405	0.39	0.79	4	69	RNA export from nucleus	BP	1	POLR2D,ZC3H11A,SMG7,SMG1	pink	VSMC_M5
GO:0051260	0.39	0.75	7	128	protein homooligomerization	BP	1	PDCD6IP,ACOT13,KCTD3,ACACB,ALS2,ATL3,HPRT1	pink	VSMC_M5
GO:1903076	0.39	0.77	5	90	regulation of protein localization to plasma membrane	BP	1	RHOQ,ATP2B4,HECTD1,PRKCI,PTPN9	pink	VSMC_M5
GO:0010941	0.39	0.66	56	1223	regulation of cell death	BP	1	LATS1,MAPK9,ANXA1,VEGFA,KRIT1,ASNS,GCLC,FBXO11,TAX1BP1,TIA1,ADAM17,UFL1,SRPK2,NCOA1,MRE11,YME1L1,BIRC6,IRS2,KITLG,SHQ1,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,CSNK2A1,URI1,BTBD10,BTG2,CYLD,NOTCH2,GSK3B,FSTL1,PIK3CA,FAM162A,RPS6KA3,ATF2,STYXL1,LANCL1,ATM,PRKCI,TIMP1,GHITM,CPEB4,UBE2Z,PIAS1,FEM1B,XIAP,NF1,PRKAA1,SETX,MT-CO2,BIRC2,UBE2V2,CACYBP,BMP2	pink	VSMC_M5
GO:0006665	0.40	0.76	6	120	sphingolipid metabolic process	BP	1	SERINC1,UGCG,PRKD3,SPTLC2,PRKAA1,HACD1	pink	VSMC_M5
GO:0033209	0.40	0.79	4	75	tumor necrosis factor-mediated signaling pathway	BP	1	ADAM17,HIPK1,CYLD,BIRC2	pink	VSMC_M5
GO:0010976	0.40	0.74	8	140	positive regulation of neuron projection development	BP	1	MAGI2,CAPRIN1,ARSB,TWF1,STYXL1,PRKCI,SETX,UBE2V2	pink	VSMC_M5
GO:0051050	0.40	0.67	33	660	positive regulation of transport	BP	1	UBR5,WASL,ANXA1,VEGFA,CD2AP,RHOQ,MAGI2,PDCD6IP,CLASP1,IRS2,MAPK8,PCM1,SLC4A8,TRPC1,TSG101,PPP3CC,NIPSNAP2,BICD1,ANO1,DENND5B,MEF2A,GSK3B,STK39,CREBL2,PRKCI,WNK1,HUWE1,DYNC1H1,PRKAA1,UBE2D3,GOLPH3L,BMP2,SAR1B	pink	VSMC_M5
GO:0006325	0.40	0.70	16	301	chromatin organization	BP	1	EMSY,KAT6A,NR3C1,ARID2,BAZ2B,BPTF,TLK1,MORC2,ATF7IP,KDM6A,HP1BP3,KAT6B,ZNF518B,ATRX,NAP1L3,BCORL1	pink	VSMC_M5
GO:0090288	0.40	0.77	5	78	negative regulation of cellular response to growth factor stimulus	BP	1	XDH,SPRY4,ATP2B4,SMAD7,UBE2D3	pink	VSMC_M5
GO:0051258	0.40	0.71	13	250	protein polymerization	BP	1	LATS1,WASL,CAPZA2,CLASP1,ARFGEF1,TWF1,RANBP9,ABI2,ARPC2,PSTPIP2,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0040029	0.40	0.77	5	86	regulation of gene expression, epigenetic	BP	1	EPC1,CGGBP1,MORC2,ATF7IP,LRIF1	pink	VSMC_M5
GO:0043534	0.40	0.75	6	108	blood vessel endothelial cell migration	BP	1	ANXA1,VEGFA,ADAM17,JCAD,ATP2B4,NF1	pink	VSMC_M5
GO:0007127	0.40	0.76	5	94	meiosis I	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3	pink	VSMC_M5
GO:0016441	0.40	0.75	6	115	posttranscriptional gene silencing	BP	1	SMAD1,PUM1,FXR1,TIAL1,SMAD2,AGO3	pink	VSMC_M5
GO:0106027	0.40	0.76	5	78	neuron projection organization	BP	1	WASL,CAPRIN1,ZMYND8,GSK3B,ABI2	pink	VSMC_M5
GO:0003151	0.40	0.78	4	59	outflow tract morphogenesis	BP	1	VEGFA,ATF2,CRKL,NIPBL	pink	VSMC_M5
GO:0030336	0.40	0.71	12	223	negative regulation of cell migration	BP	1	WASL,KRIT1,MAGI2,CLASP1,DLC1,ARID2,ATP2B4,ZMYND8,TIMP1,NF1,PTPRM,SMAD7	pink	VSMC_M5
GO:0016482	0.40	0.72	9	153	cytosolic transport	BP	1	SNX2,VPS13A,VPS54,RAB14,ARL8B,RHOBTB3,VPS29,TBC1D23,PIK3C3	pink	VSMC_M5
GO:0006518	0.40	0.67	30	688	peptide metabolic process	BP	1	PCSK5,GUF1,GCLC,TIA1,POLR2D,CNOT10,CAPRIN1,YTHDF3,LSM14A,CDK5RAP1,PTCD3,EIF4G2,GFM2,DPH6,BTG2,CSDE1,PUM1,FXR1,PARL,METTL5,RPS6KA3,NEMF,CPEB4,CPD,AGO3,MTPN,EIF5A2,RNF139,PAIP2,DENR	pink	VSMC_M5
GO:0010810	0.40	0.72	10	175	regulation of cell-substrate adhesion	BP	1	VEGFA,MACF1,CLASP1,EPB41L5,SPRY4,DLC1,GSK3B,ARPC2,CRKL,NF1	pink	VSMC_M5
GO:0002028	0.40	0.78	4	66	regulation of sodium ion transport	BP	1	COMMD1,ATP2B4,STK39,WNK1	pink	VSMC_M5
GO:0007224	0.41	0.74	7	119	smoothened signaling pathway	BP	1	RUNX2,TCTN1,ARL13B,FAM92A,HIPK1,BTRC,HERC4	pink	VSMC_M5
GO:1904951	0.41	0.70	13	257	positive regulation of establishment of protein localization	BP	1	UBR5,CD2AP,IRS2,MAPK8,PCM1,TSG101,ANO1,GSK3B,HUWE1,PRKAA1,UBE2D3,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0000902	0.41	0.65	44	799	cell morphogenesis	BP	1	LATS1,SNX2,MKLN1,C9orf72,WASL,ANXA1,VEGFA,FRYL,RHOQ,MACF1,RAB1A,SEPT7,ZMYM4,EPB41L5,FLRT3,TOP2B,ZDHHC17,SPRY4,ATRN,DLC1,CAPRIN1,FAT1,EIF4G2,RHOBTB3,DIP2B,TCTN1,ARL13B,DNMBP,NOTCH2,MEF2A,GSK3B,ALS2,SCFD1,ABI2,ARPC2,CRKL,OPHN1,ATP7A,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5
GO:0009267	0.41	0.74	7	130	cellular response to starvation	BP	1	ASNS,MAPK8,CPEB4,PIK3C3,PRKAA1,USP33,BMT2	pink	VSMC_M5
GO:0021954	0.41	0.78	4	61	central nervous system neuron development	BP	1	TCTN1,BTG2,ATP7A,HPRT1	pink	VSMC_M5
GO:0007044	0.41	0.74	6	89	cell-substrate junction assembly	BP	1	VEGFA,DST,MACF1,CLASP1,EPB41L5,DLC1	pink	VSMC_M5
GO:0010565	0.41	0.76	5	95	regulation of cellular ketone metabolic process	BP	1	ANXA1,IRS2,ATP2B4,ACACB,BMP2	pink	VSMC_M5
GO:0001906	0.41	0.77	4	78	cell killing	BP	1	ARL8B,MAPK8,LYST,HPRT1	pink	VSMC_M5
GO:0044089	0.41	0.67	23	441	positive regulation of cellular component biogenesis	BP	1	MAPK9,WASL,VEGFA,RHOQ,SEPT7,PDCD6IP,CLASP1,EPB41L5,FLRT3,TSG101,ZMYND8,GSK3B,PIK3CA,PSMC6,ABI2,MORC2,ATF7IP,ATM,ARPC2,ATP7A,DYNC1H1,GMFB,UBE2V2	pink	VSMC_M5
GO:0045893	0.41	0.64	61	1244	positive regulation of transcription, DNA-templated	BP	1	MED23,SCAF8,DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,ASXL2,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,NR3C1,GPBP1,KDM3A,ZNF507,SMAD1,GABPA,TET3,GTF2H1,TSG101,BTRC,MEF2A,TET2,GTF2I,BPTF,PSMC6,GABPB2,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,BIRC2,PEG3,ZNF770,BMP2	pink	VSMC_M5

GO:1903508	0.41	0.64	61	1244	positive regulation of nucleic acid-templated transcription	BP	1	MED23,SCAF8,DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,ASXL2,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,NR3C1,GPBP1,KDM3A,ZNF507,SMAD1,GABPA,TET3,GTF2H1,TSG101,BTRC,MEF2A,TET2,GTF2I,BPTF,PSMC6,GABPB2,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,BIRC2,PEG3,ZNF770,BMP2	pink	VSMC_M5
GO:0030036	0.41	0.66	32	600	actin cytoskeleton organization	BP	1	ARFGEF3,LATS1,MKLN1,C9orf72,WASL,ANXA1,CD2AP,RHOQ,CAPZA2,AKAP11,PDCD6IP,CLASP1,EPB41L5,DLC1,FAT1,ARFGEF1,RHOBTB3,TWF1,NOTCH2,MEF2A,PIK3CA,ABI2,ARPC2,PRKCI,OPHN1,TTC8,DIAPH2,PSTPIP2,NF1,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0043542	0.42	0.71	10	195	endothelial cell migration	BP	1	ANXA1,VEGFA,KRIT1,ADAM17,JCAD,ATP2B4,FSTL1,PIK3CA,NF1,PTPRM	pink	VSMC_M5
GO:0045765	0.42	0.70	12	229	regulation of angiogenesis	BP	1	VEGFA,KRIT1,JCAD,SMAD1,HIPK1,ATP2B4,GTF2I,EGLN1,ATF2,NF1,PTPRM,DDAH1	pink	VSMC_M5
GO:0045944	0.42	0.65	45	904	positive regulation of transcription by RNA polymerase II	BP	1	DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,ASXL2,MED4,KMT2C,ZEB2,KAT6A,NR3C1,KDM3A,ZNF507,SMAD1,GABPA,TET3,MEF2A,TET2,GTF2I,BPTF,PSMC6,GABPB2,ZNF148,DLX2,RPS6KA3,ATF2,ATM,KAT6B,PYGO1,GTF2A2,ASH1L,ATRX,SMAD2,MED13,NIPBL,SETX,NFAT5,PEG3,ZNF770,BMP2	pink	VSMC_M5
GO:1902680	0.42	0.64	61	1246	positive regulation of RNA biosynthetic process	BP	1	MED23,SCAF8,DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,ASXL2,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,NR3C1,GPBP1,KDM3A,ZNF507,SMAD1,GABPA,TET3,GTF2H1,TSG101,BTRC,MEF2A,TET2,GTF2I,BPTF,PSMC6,GABPB2,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,BIRC2,PEG3,ZNF770,BMP2	pink	VSMC_M5
GO:2001022	0.42	0.75	5	95	positive regulation of response to DNA damage stimulus	BP	1	ARID2,KMT5B,FXR1,ATM,UBE2V2	pink	VSMC_M5
GO:0048041	0.42	0.75	5	81	focal adhesion assembly	BP	1	VEGFA,MACF1,CLASP1,EPB41L5,DLC1	pink	VSMC_M5
GO:0010508	0.42	0.74	6	105	positive regulation of autophagy	BP	1	C9orf72,UFL1,GSK3B,PAFAH1B2,SPTLC2,PRKAA1	pink	VSMC_M5
GO:0045931	0.42	0.75	5	97	positive regulation of mitotic cell cycle	BP	1	ANXA1,ASNS,ADAM17,DYNLT3,PKN2	pink	VSMC_M5
GO:0051254	0.42	0.63	66	1357	positive regulation of RNA metabolic process	BP	1	MED23,SCAF8,DDX17,WASL,VEGFA,RUNX2,GCM1,RHOQ,RLF,ZNF292,NCOA1,EPC1,TBP,ASXL2,POLR2D,MED4,MAP3K2,KMT2C,ZEB2,KAT6A,EAF1,NR3C1,GPBP1,YTHDF3,KDM3A,ZNF507,SMAD1,GABPA,TET3,GTF2H1,TSG101,BTG2,BTRC,MEF2A,TET2,PUM1,GTF2I,BPTF,PSMC6,GABPB2,ZNF148,DLX2,ATF7IP,RPS6KA3,CREBL2,ATF2,ATM,KAT6B,PYGO1,GTF2A2,FBXW11,ASH1L,ATRX,PIAS1,SMAD2,MED13,CCNK,PRKAA1,NIPBL,SETX,NFAT5,BIRC2,PEG3,ZNF770,HNRNPLL,BMP2	pink	VSMC_M5
GO:0016485	0.42	0.72	8	170	protein processing	BP	1	PCSK5,ADAM17,YME1L1,PARL,PIK3C3,XIAP,CPD,RNF139	pink	VSMC_M5
GO:0031400	0.42	0.67	21	426	negative regulation of protein modification process	BP	1	LATS1,UBR5,C9orf72,GCLC,UFL1,XDH,SPRY4,CDK5RAP1,KDM3A,TSG101,ATP2B4,TRIP12,GSK3B,STYXL1,CRKL,GSKIP,GGNBP2,NF1,PRKAA1,SMAD7,BMP2	pink	VSMC_M5
GO:0007548	0.42	0.70	11	206	sex differentiation	BP	1	VEGFA,RNF38,NCOA1,KITLG,RHOBTB3,TIPARP,CSDE1,PLEKHA1,CRKL,ATRX,NIPBL	pink	VSMC_M5
GO:0071902	0.42	0.71	9	170	positive regulation of protein serine/threonine kinase activity	BP	1	VEGFA,ADAM17,KITLG,CDK5RAP1,ATP2B4,CAB39,ALS2,CCNK,BMP2	pink	VSMC_M5
GO:0033673	0.42	0.70	10	191	negative regulation of kinase activity	BP	1	LATS1,IRS2,SPRY4,CDK5RAP1,TSG101,WNK1,GSKIP,GGNBP2,NF1,BMP2	pink	VSMC_M5
GO:0000956	0.42	0.74	6	102	nuclear-transcribed mRNA catabolic process	BP	1	POLR2D,BTG2,CSDE1,SMG7,ATM,SMG1	pink	VSMC_M5
GO:1904019	0.42	0.75	5	86	epithelial cell apoptotic process	BP	1	KRIT1,TIA1,HIPK1,ATF2,PRKCI	pink	VSMC_M5
GO:0007052	0.42	0.73	6	109	mitotic spindle organization	BP	1	CLASP1,LSM14A,CEP97,DYNC1H1,STAG2,RMDN1	pink	VSMC_M5
GO:0070301	0.42	0.76	4	79	cellular response to hydrogen peroxide	BP	1	ANXA1,PLEKHA1,PRKAA1,SETX	pink	VSMC_M5
GO:1901342	0.43	0.69	12	232	regulation of vasculature development	BP	1	VEGFA,KRIT1,JCAD,SMAD1,HIPK1,ATP2B4,GTF2I,EGLN1,ATF2,NF1,PTPRM,DDAH1	pink	VSMC_M5
GO:0061097	0.43	0.76	4	74	regulation of protein tyrosine kinase activity	BP	1	ADAM17,TSG101,DOCK3,GGNBP2	pink	VSMC_M5
GO:0043524	0.43	0.73	6	115	negative regulation of neuron apoptotic process	BP	1	GCLC,BTG2,PIK3CA,PRKCI,CPEB4,UBE2V2	pink	VSMC_M5
GO:0051259	0.43	0.70	9	174	protein complex oligomerization	BP	1	WDCP,YME1L1,PDCD6IP,ACOT13,KCTD3,ACACB,ALS2,ATL3,HPRT1	pink	VSMC_M5
GO:0033044	0.43	0.70	9	168	regulation of chromosome organization	BP	1	MRE11,TNKS2,MORC2,ATF7IP,ATM,WAPL,ATRX,SMG1,NAF1	pink	VSMC_M5
GO:0044782	0.43	0.67	15	288	cilium organization	BP	1	LRGUK,LCA5,SEPT7,SCLT1,BBS12,PCM1,TCTN1,ARL13B,FAM92A,CEP97,CYLD,DNAAF5,TTC8,WDR78,CPLANE1	pink	VSMC_M5
GO:0030516	0.43	0.74	5	83	regulation of axon extension	BP	1	VEGFA,MACF1,EIF4G2,DIP2B,GSK3B	pink	VSMC_M5
GO:0035107	0.43	0.72	7	115	appendage morphogenesis	BP	1	PCSK5,RUNX2,IMPAD1,FAM92A,NOTCH2,ATRX,NIPBL	pink	VSMC_M5
GO:0035108	0.43	0.72	7	115	limb morphogenesis	BP	1	PCSK5,RUNX2,IMPAD1,FAM92A,NOTCH2,ATRX,NIPBL	pink	VSMC_M5
GO:1901135	0.43	0.64	35	791	carbohydrate derivative metabolic process	BP	1	LRGUK,RHOQ,UGCG,DPY19L1,RAB1A,XDH,OXSM,NGLY1,TMTC3,IMPAD1,ARFGEF1,FAR1,TET3,PIGP,GXYLT1,OGA,TET2,ACACB,ADAL,PDE5A,FUT8,PGM2,ATP7A,PRKAA1,HPRT1,SLC35A3,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,RNF103,RNF139,BMP2,DCAKD	pink	VSMC_M5
GO:0007565	0.43	0.71	7	139	female pregnancy	BP	1	PCSK5,VEGFA,YTHDF3,TIMP1,ASH1L,ATP7A,UBE2A	pink	VSMC_M5

GO:0016043	0.43	0.60	223	4652	cellular component organization	BP	1	ARFGEF3,VTA1,LATS1,MAPK9,SYNE1,SNX2,SCAF8,LRGUK,MKLN1,VPS13A,UBR2,C9orf72,WASL,ANXA1,TMEM33,VEGFA,FRYL,CD2AP,SDHAF3,GCM1,GCLC,DST,RHOQ,LCA5,UGCG,MACF1,VPS54,RAB1A,SEPT7,NFU1,ADAM17,CAPZA2,UFL1,ZMYM4,RAB14,RAB33B,AFG1L,SCLT1,WDCP,BBS12,KIAA1109,SRPK2,TBP,MRE11,POLR2D,MAGI2,YME1L1,AKAP11,DCLRE1C,PDCD6IP,CLASP1,EPB41L5,EMSY,FNTA,ZEB2,FLRT3,XDH,ARL8B,KAT6A,TOP2B,ZDHHC17,NR3C1,SHQ1,MAPK8,MAGI1,DLC1,RB1CC1,VPS37A,CSNK2A1,CAPRIN1,PCM1,YTHDF3,FAT1,TNKS2,VCPIP1,LSM14A,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,EIF4G2,RHOBTB3,DIP2B,GFM2,NFS1,TCTN1,ZFYVE16,ARL13B,FAM92A,ARSB,TBC1D23,TSG101,HIPK1,ARID2,PPP3CC,BAZ2B,BTG2,OPTC,CEP97,CSDE1,TWF1,CYLD,RANBP9,PSMG1,NIPSNAP2,TSPAN32,NDUFS4,ACOT13,NOTCH2,BICD1,KCTD3,ZMYND8,MEF2A,ACACB,GOLGA5,GSK3B,DCLRE1A,PIK3CA,LYST,DNAAF5,BPTF,FXR1,GOLGB1,TFIP11,FAM162A,PARL,PSMC6,ALS2,TLK1,PLEKHA1,ZNF148,SCFD1,ABI2,MORC2,ATF7IP,RPS6KA3,GLRX3,SKA1,SRP54,ATF2,MTX2,STYXL1,ST7L,ATM,KDM6A,ARPC2,ERO1A,PRKCI,HP1BP3,ATL3,USP8,CRKL,KAT6B,ZNF518B,GHITM,PYGO1,CCSER2,PDS5A,WAPL,HUWE1,GTF2A2,OPHN1,SNX11,FBXW11,HERC1,MLH3,ABCB7,ATRX,ATP7A,SPATA7,PIAS1,NAP1L3,TTC8,DIAPH2,SMAD2,KATNAL2,PSTPIP2,PIK3C3,DYNC1H1,PTPN9,SMG1,ESCO1,CSNK1A1,WDR78,STAG2,NF1,PRKAA1,PTPRM,CPLANE1,NIPBL,BCORL1,RAD1,HPRT1,SMAD7,PRPF8,SETX,GAN,PKN2,GFOD2,USP33,MT-ND4,MT-ND5,BIRC2,AGO3,UBE2D3,TMEM38B,USP9X,FAM206A,GMFB,UBE2V2,RAB18,MTPN,EIF5A2,NAF1,SLC25A	pink	VSMC_M5
GO:0006310	0.43	0.68	12	245	DNA recombination	BP	1	UBR2,MRE11,DCLRE1C,TOP2B,ARID2,KMT5B,KLHL15,ATM,RPAIN,MLH3,NIPBL,SETX	pink	VSMC_M5
GO:0061982	0.43	0.74	5	99	meiosis I cell cycle process	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3	pink	VSMC_M5
GO:0006457	0.44	0.71	7	166	protein folding	BP	1	PPIL6,HSPA4L,NGLY1,CSNK2A1,SGTB,ERO1A,TTC1	pink	VSMC_M5
GO:0034599	0.44	0.68	11	234	cellular response to oxidative stress	BP	1	MAPK9,ANXA1,MAPK8,PLEKHA1,ATF2,LANCL1,FUT8,ATP7A,GSKIP,PRKAA1,SETX	pink	VSMC_M5
GO:0032870	0.44	0.65	23	450	cellular response to hormone stimulus	BP	1	LATS1,UBR5,DDX17,ANXA1,ASNS,GCLC,RHOQ,UGCG,UFL1,NCOA1,MBD5,IRS2,NR3C1,KDM3A,URI1,NR3C2,GTF2H1,GSK3B,PIK3CA,PRKCI,USP8,PRKAA1,MT-ND3	pink	VSMC_M5
GO:1902117	0.44	0.75	4	61	positive regulation of organelle assembly	BP	1	MAPK9,SEPT7,PDCD6IP,DYNC1H1	pink	VSMC_M5
GO:0051962	0.44	0.68	12	216	positive regulation of nervous system development	BP	1	VEGFA,MACF1,UFL1,RHEB,FLRT3,IL6ST,CAPRIN1,EIF4G2,PPP1CC,PRKCI,UBE2V2,BMP2	pink	VSMC_M5
GO:0071901	0.44	0.73	5	93	negative regulation of protein serine/threonine kinase activity	BP	1	LATS1,SPRY4,CDK5RAP1,NF1,BMP2	pink	VSMC_M5
GO:0010038	0.44	0.67	14	279	response to metal ion	BP	1	MAPK9,GCLC,MAPK8,TRPC1,CPNE3,ARL13B,CPNE8,MEF2A,WNK1,ATP7A,PRKAA1,MT-CO1,UBE2D3,CACYBP	pink	VSMC_M5
GO:0070997	0.44	0.67	14	288	neuron death	BP	1	GCLC,SRPK2,BTBD10,BTG2,GSK3B,PIK3CA,FAM162A,ATF2,LANCL1,PRKCI,CPEB4,XIAP,NF1,UBE2V2	pink	VSMC_M5
GO:0010212	0.44	0.71	7	137	response to ionizing radiation	BP	1	ANXA1,INIP,DCLRE1C,ATM,PRKAA1,NIPBL,RAD1	pink	VSMC_M5
GO:0050792	0.44	0.72	6	119	regulation of viral process	BP	1	SRPK2,TOP2B,IFIT5,TSG101,MORC2,PKN2	pink	VSMC_M5
GO:0032272	0.44	0.75	4	66	negative regulation of protein polymerization	BP	1	CAPZA2,ARFGEF1,TWF1,MTPN	pink	VSMC_M5
GO:0002062	0.44	0.73	5	91	chondrocyte differentiation	BP	1	MEX3C,RUNX2,IMPAD1,SMAD7,BMP2	pink	VSMC_M5
GO:0043112	0.44	0.71	7	131	receptor metabolic process	BP	1	MKLN1,VEGFA,MAGI2,FNTA,ALS2,FUT8,OPHN1	pink	VSMC_M5
GO:2000241	0.44	0.73	5	105	regulation of reproductive process	BP	1	VEGFA,GCM1,YTHDF3,TIMP1,RAD1	pink	VSMC_M5
GO:0038061	0.44	0.73	5	99	NIK/NF-kappaB signaling	BP	1	NR3C2,CYLD,NFAT5,BIRC2,AGO3	pink	VSMC_M5
GO:0070085	0.44	0.69	9	194	glycosylation	BP	1	DPY19L1,COG6,TMTC3,ARFGEF1,TET3,GXYLT1,OGA,TET2,FUT8	pink	VSMC_M5
GO:0031334	0.45	0.68	10	199	positive regulation of protein-containing complex assembly	BP	1	MAPK9,WASL,VEGFA,CLASP1,GSK3B,PSMC6,ABI2,ATM,ARPC2,GMFB	pink	VSMC_M5
GO:0006970	0.45	0.75	4	71	response to osmotic stress	BP	1	CAB39,STK39,ATF2,NFAT5	pink	VSMC_M5
GO:0072522	0.45	0.70	7	157	purine-containing compound biosynthetic process	BP	1	ACACB,ADAL,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:1902904	0.45	0.69	8	139	negative regulation of supramolecular fiber organization	BP	1	CAPZA2,CLASP1,DLC1,ARFGEF1,TWF1,PIK3CA,GMFB,MTPN	pink	VSMC_M5
GO:1990778	0.45	0.66	14	279	protein localization to cell periphery	BP	1	EFR3A,RHOQ,FAM126A,MACF1,GOLGA7,ARL13B,ATP2B4,TSPAN32,HECTD1,PRKCI,TTC8,PTPN9,GOLPH3L,ZDHHC22	pink	VSMC_M5
GO:0000302	0.45	0.69	8	177	response to reactive oxygen species	BP	1	MAPK9,ANXA1,MAPK8,PLEKHA1,ATP7A,PRKAA1,SETX,MT-ND5	pink	VSMC_M5
GO:0008217	0.45	0.71	6	122	regulation of blood pressure	BP	1	PCSK5,ARHGAP42,STK39,WNK1,ATP5PF,DDAH1	pink	VSMC_M5
GO:0048871	0.45	0.64	19	378	multicellular organismal homeostasis	BP	1	MEX3C,VEGFA,LCA5,UGCG,VPS54,ADAM17,BBS12,AKAP11,RHEB,KDM3A,ACOT13,PRKAB2,ACACB,PIK3CA,STK39,SPATA7,DYNC1H1,NF1,PRKAA1	pink	VSMC_M5
GO:0003002	0.45	0.66	13	251	regionalization	BP	1	PCSK5,EPB41L5,TCTN1,ARL13B,HIPK1,BTG2,NOTCH2,BPTF,DLX2,RNF2,CRKL,SMAD2,BMP2	pink	VSMC_M5
GO:0051336	0.45	0.62	36	754	regulation of hydrolase activity	BP	1	PCSK5,ANXA1,VEGFA,ARHGAP42,MAGI2,FNTA,XDH,BIRC6,MAPK8,APAF1,DLC1,CSNK2A1,ARFGEF1,URI1,RALGAPB,LXN,BICD1,PPP6R3,GSK3B,EGLN1,FAM162A,ALS2,RPS6KA3,STYXL1,TIMP1,CRKL,WNK1,UBE2Z,TTC8,USP14,XIAP,NF1,BIRC2,ELMOD2,SPINK8,BMP2	pink	VSMC_M5
GO:0044843	0.45	0.68	9	180	cell cycle G1/S phase transition	BP	1	LATS1,ANXA1,ADAM17,CUL1,CUL2,ATP2B4,ATM,CUL5,PIAS1	pink	VSMC_M5
GO:0046434	0.45	0.71	6	126	organophosphate catabolic process	BP	1	XDH,IMPAD1,PDE5A,PGM2,HPRT1,NUDT7	pink	VSMC_M5
GO:0071674	0.45	0.71	6	126	mononuclear cell migration	BP	1	WASL,ANXA1,ADAM17,STK39,CRKL,WNK1	pink	VSMC_M5
GO:0010594	0.45	0.69	8	157	regulation of endothelial cell migration	BP	1	ANXA1,VEGFA,KRIT1,ADAM17,JCAD,ATP2B4,NF1,PTPRM	pink	VSMC_M5
GO:2000146	0.45	0.66	12	234	negative regulation of cell motility	BP	1	WASL,KRIT1,MAGI2,CLASP1,DLC1,ARID2,ATP2B4,ZMYND8,TIMP1,NF1,PTPRM,SMAD7	pink	VSMC_M5
GO:0001578	0.45	0.72	5	86	microtubule bundle formation	BP	1	LRGUK,CLASP1,DNAAF5,CCSER2,WDR78	pink	VSMC_M5
GO:1901216	0.45	0.74	4	78	positive regulation of neuron death	BP	1	SRPK2,GSK3B,ATF2,NF1	pink	VSMC_M5
GO:0032388	0.46	0.68	9	173	positive regulation of intracellular transport	BP	1	UBR5,MAPK8,PCM1,GSK3B,HUWE1,DYNC1H1,PRKAA1,UBE2D3,SAR1B	pink	VSMC_M5
GO:0072001	0.46	0.65	14	256	renal system development	BP	1	PCSK5,VEGFA,MAGI2,APAF1,SMAD1,TIPARP,NOTCH2,PYGO1,TTC8,SMAD2,NF1,NIPBL,SMAD7,BMP2	pink	VSMC_M5
GO:2001236	0.46	0.70	6	121	regulation of extrinsic apoptotic signaling pathway	BP	1	GCLC,BIRC6,RB1CC1,CYLD,GSK3B,FEM1B	pink	VSMC_M5

GO:0120035	0.46	0.62	27	524	regulation of plasma membrane bounded cell projection organization	BP	1	WASL,VEGFA,RHOQ,MACF1,SEPT7,MAGI2,CAPRIN1,EIF4G2,DIP2B,ARSB,CEP97,TWF1,CYLD,ZMYND8,GSK3B,PIK3CA,FXR1,ABI2,STYXL1,ARPC2,PRKCI,CRKL,ATP7A,PTPN9,SETX,FAM206A,UBE2V2	pink	VSMC_M5
GO:0032092	0.46	0.73	4	73	positive regulation of protein binding	BP	1	EPB41L5,GSK3B,USP33,BMP2	pink	VSMC_M5
GO:0000082	0.46	0.68	8	160	G1/S transition of mitotic cell cycle	BP	1	LATS1,ANXA1,ADAM17,CUL1,CUL2,ATM,CUL5,PIAS1	pink	VSMC_M5
GO:0006323	0.46	0.70	6	119	DNA packaging	BP	1	KAT6A,HP1BP3,KAT6B,WAPL,ATRX,NAP1L3	pink	VSMC_M5
GO:0051090	0.46	0.64	16	328	regulation of DNA-binding transcription factor activity	BP	1	MAPK9,VEGFA,TAX1BP1,COMMD1,UFL1,MAPK8,ERBIN,CYLD,BTRC,EGLN1,ATF2,RNF2,PRKCI,SMAD7,MTPN,BMP2	pink	VSMC_M5
GO:0051494	0.46	0.68	8	138	negative regulation of cytoskeleton organization	BP	1	CAPZA2,CLASP1,DLC1,ARFGEF1,TWF1,PIK3CA,GMFB,MTPN	pink	VSMC_M5
GO:0070507	0.46	0.68	8	135	regulation of microtubule cytoskeleton organization	BP	1	CLASP1,CEP97,CYLD,BICD1,GSK3B,SKA1,DYNC1H1,PRKAA1	pink	VSMC_M5
GO:0010833	0.46	0.73	4	73	telomere maintenance via telomere lengthening	BP	1	MRE11,TNKS2,ATM,NAF1	pink	VSMC_M5
GO:0150115	0.46	0.70	6	95	cell-substrate junction organization	BP	1	VEGFA,DST,MACF1,CLASP1,EPB41L5,DLC1	pink	VSMC_M5
GO:0001837	0.46	0.69	7	131	epithelial to mesenchymal transition	BP	1	DDX17,CLASP1,EPB41L5,GSK3B,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0001501	0.46	0.62	21	413	skeletal system development	BP	1	MEX3C,MTHFD1L,PCSK5,RUNX2,RAB33B,IMPAD1,SMAD1,TIPARP,BBX,NOTCH2,PLEKHA1,DLX2,RPS6KA3,TIMP1,ASH1L,ATP7A,SMAD2,NIPBL,SMAD7,TMEM38B,BMP2	pink	VSMC_M5
GO:0090305	0.47	0.66	10	213	nucleic acid phosphodiester bond hydrolysis	BP	1	CPSF3,MRE11,DCLRE1C,ENDOV,RPP14,DCLRE1A,TSEN15,DIS3L,RAD1,AGO3	pink	VSMC_M5
GO:0030705	0.47	0.66	10	173	cytoskeleton-dependent intracellular transport	BP	1	WASL,DST,LCA5,RAB1A,BBS12,ARL8B,PCM1,BICD1,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0032386	0.47	0.64	14	290	regulation of intracellular transport	BP	1	UBR5,ERLEC1,MAPK8,PCM1,PPP1CC,GSK3B,PARL,SCFD1,HUWE1,DYNC1H1,PRKAA1,UBE2D3,RNF139,SAR1B	pink	VSMC_M5
GO:0016049	0.47	0.62	20	399	cell growth	BP	1	MEX3C,C9orf72,VEGFA,MACF1,ADAM17,KIAA1109,EPB41L5,FLRT3,CSNK2A1,URI1,EIF4G2,DIP2B,TSG101,GSK3B,RPS6KA3,ST7L,CRKL,SMAD7,USP9X,MTPN	pink	VSMC_M5
GO:0050896	0.47	0.57	273	5876	response to stimulus	BP	1	DGKA,ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,DDX17,MKLN1,KLHDC10,UBR2,C9orf72,WASL,ANXA1,TMEM33,VEGFA,KRIT1,RUNX2,CD2AP,ASNS,GCLC,DST,RHOQ,ERLEC1,USP34,UGCG,INIP,COMMD1,MACF1,RAB1A,ADAM17,UFL1,CUL1,RAB14,CUL2,RAB33B,ZFYVE9,HSPA4L,JCAD,ARHGAP42,SRPK2,NCOA1,MRE11,PRDM5,ASXL2,POLR2D,MAGI2,MAP3K2,AKAP11,DCLRE1C,DGKH,CLASP1,EPB41L5,RHEB,FBXL3,EMSY,FNTA,ZEB2,MBD5,FLRT3,EPC2,XDH,ARL8B,KAT6A,NGLY1,ENDOV,ZDHHC17,NKIRAS1,BIRC6,LTBP1,IRS2,TMTC3,KITLG,PRKD3,SPRY4,ATRN,NR3C1,MAP4K3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,TNKS2,VCPIP1,LSM14A,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,NR3C2,RHOBTB3,TRPC1,RNF13,TCTN1,GABPA,PPP1CC,WWP1,ZFYVE16,CPNE3,TIPARP,RALGAPB,ARL13B,LXN,FAM92A,ARSB,GTF2H1,TSG101,HIPK1,ARID2,POLK,PPP3CC,BTG2,DNMBP,ATP2B4,TWF1,IRAK4,CYLD,RANBP9,BTRC,TSPAN32,SNRPN,NDUFS4,DOCK3,CPNE8,NOTCH2,TRIP12,BICD1,ANO1,ASB7,CAB39,ZMYND8,IPO8,MEF2A,SHOC2,PRKAB2,TET2,KMT5B,ACACB,GSK3B,FSTL1,DCLRE1A,PUM1,PIK3CA,LYST,UBR1,SCN9A,GTF2I,BPTF,FXR1,TFIP11,STK39,EGLN1,ZFAND2A,KDM2A,FAM162A,TIAL1,PSMC6,ALS2,RPS6KC1,PDE5A,TLK1,PLEKHA1,ZNF148,SCFD1,MUC20,ABI2,MORC2,DLX2,JMJD1C,ARHGAP5,RPS6KA3,CREBL2,GLRX3,SRP54,ATF2,KLHL15,ACAP2,HERC4,STYXL1,RALGPS2,LANCL1,SOS2,ATM,CUL5,ERO1A,PRKCI,COPS2,YWHAQ,HP1BP3,USP8,TIMP1,CRKL,NAALADL2,RPAIN,WNK1,GHITM,PYGO1,PDS5A,WAPL,FUT8,HUWE1,OPHN1,CPEB4,FBXW11,ASH1L,USP3,MLH3,ATRX,ATP7A,SPATA7,CHM,PIAS1,FEM1B,TTC8,SM	pink	VSMC_M5
GO:0046632	0.47	0.73	4	74	alpha-beta T cell differentiation	BP	1	ANXA1,ATF2,ATP7A,SMAD7	pink	VSMC_M5
GO:0060840	0.47	0.71	5	81	artery development	BP	1	VEGFA,ARID2,HECTD1,NF1,SMAD7	pink	VSMC_M5
GO:0055076	0.47	0.71	5	107	transition metal ion homeostasis	BP	1	COMMD1,GLRX3,ABCB7,ATP7A,XIAP	pink	VSMC_M5
GO:0007596	0.47	0.67	8	164	blood coagulation	BP	1	DGKA,DGKH,IL6ST,TSPAN32,PIK3CA,JMJD1C,F8,STXBP3	pink	VSMC_M5
GO:0070887	0.47	0.58	105	2230	cellular response to chemical stimulus	BP	1	LATS1,MAPK9,UBR5,DDX17,UBR2,ANXA1,TMEM33,VEGFA,RUNX2,ASNS,GCLC,RHOQ,ERLEC1,UGCG,ADAM17,UFL1,RAB14,ZFYVE9,JCAD,NCOA1,PRDM5,MAGI2,EPB41L5,FNTA,ZEB2,MBD5,FLRT3,XDH,NGLY1,ZDHHC17,LTBP1,IRS2,SPRY4,NR3C1,MAPK8,APAF1,IL6ST,YTHDF3,LSM14A,KDM3A,ERBIN,URI1,SMAD1,NR3C2,GABPA,CPNE3,TIPARP,GTF2H1,HIPK1,ATP2B4,IRAK4,CYLD,BTRC,CPNE8,NOTCH2,ANO1,CAB39,MEF2A,SHOC2,GSK3B,FSTL1,PIK3CA,LYST,UBR1,BPTF,STK39,EGLN1,ZFAND2A,FAM162A,PLEKHA1,SRP54,ATF2,KLHL15,ACAP2,LANCL1,ATM,ERO1A,PRKCI,HP1BP3,USP8,CRKL,WNK1,FUT8,CPEB4,ATRX,ATP7A,SMAD2,GSKIP,XIAP,PRKAA1,SMAD7,PRPF8,SETX,STXBP3,NFAT5,MT-ND3,BIRC2,SULT1C4,UBE2D3,TMEM38B,USP9X,CACYBP,DDAH1,UBXN2A,BMP2	pink	VSMC_M5
GO:0021543	0.47	0.68	7	127	pallium development	BP	1	NCOA1,BTG2,ATP2B4,GSK3B,DLX2,CRKL,NF1	pink	VSMC_M5
GO:0050769	0.47	0.66	10	181	positive regulation of neurogenesis	BP	1	VEGFA,MACF1,UFL1,RHEB,IL6ST,CAPRIN1,EIF4G2,PPP1CC,PRKCI,BMP2	pink	VSMC_M5
GO:0099111	0.47	0.66	9	165	microtubule-based transport	BP	1	DST,LCA5,RAB1A,BBS12,ARL8B,PCM1,BICD1,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0034620	0.47	0.72	4	86	cellular response to unfolded protein	BP	1	TMEM33,ERLEC1,UFL1,ERO1A	pink	VSMC_M5
GO:1990845	0.47	0.68	7	132	adaptive thermogenesis	BP	1	VEGFA,ADAM17,RHEB,KDM3A,ACOT13,PRKAB2,DYNC1H1	pink	VSMC_M5
GO:0030512	0.48	0.72	4	64	negative regulation of transforming growth factor beta receptor signaling pathway	BP	1	ADAM17,LTBP1,SMAD7,BMP2	pink	VSMC_M5
GO:0060996	0.48	0.70	5	87	dendritic spine development	BP	1	WASL,CAPRIN1,EIF4G2,ZMYND8,ABI2	pink	VSMC_M5
GO:0007018	0.48	0.63	15	283	microtubule-based movement	BP	1	VPS13A,DST,LCA5,RAB1A,BBS12,ARL8B,PCM1,ATP2B4,BICD1,DNAAF5,DYNLT3,FBXW11,ASH1L,DYNC1H1,WDR78	pink	VSMC_M5
GO:0008585	0.48	0.72	4	72	female gonad development	BP	1	VEGFA,KITLG,TIPARP,PLEKHA1	pink	VSMC_M5
GO:0034446	0.48	0.70	5	89	substrate adhesion-dependent cell spreading	BP	1	RAB1A,SPRY4,ATRN,ARPC2,CRKL	pink	VSMC_M5

GO:0010638	0.48	0.61	21	428	positive regulation of organelle organization	BP	1	MAPK9,WASL,ANXA1,SEPT7,MRE11,PDCD6IP,CLASP1,MAPK8,TNKS2,GSK3B,FAM162A,ABI2,MORC2,ATF7IP,ATM,ARPC2,ATL3,ATRX,DYNC1H1,GMFB,NAF1	pink	VSMC_M5
GO:0022604	0.48	0.63	14	261	regulation of cell morphogenesis	BP	1	MKLN1,ANXA1,VEGFA,RHOQ,MACF1,SEPT7,ZMYM4,SPRY4,DLC1,CAPRIN1,RHOBTB3,DNMBP,ARPC2,CRKL	pink	VSMC_M5
GO:0045165	0.48	0.66	9	172	cell fate commitment	BP	1	LATS1,RUNX2,GCM1,SMAD1,ESRP1,NOTCH2,DLX2,SMAD2,BMP2	pink	VSMC_M5
GO:0050817	0.48	0.66	8	166	coagulation	BP	1	DGKA,DGKH,IL6ST,TSPAN32,PIK3CA,JMJD1C,F8,STXBP3	pink	VSMC_M5
GO:1901214	0.48	0.64	12	251	regulation of neuron death	BP	1	GCLC,SRPK2,BTBD10,BTG2,GSK3B,PIK3CA,ATF2,LANCL1,PRKCI,CPEB4,NF1,UBE2V2	pink	VSMC_M5
GO:1901215	0.48	0.66	8	161	negative regulation of neuron death	BP	1	GCLC,BTBD10,BTG2,GSK3B,PIK3CA,PRKCI,CPEB4,UBE2V2	pink	VSMC_M5
GO:0007599	0.48	0.66	8	166	hemostasis	BP	1	DGKA,DGKH,IL6ST,TSPAN32,PIK3CA,JMJD1C,F8,STXBP3	pink	VSMC_M5
GO:1901879	0.48	0.70	5	75	regulation of protein depolymerization	BP	1	CAPZA2,CLASP1,TWF1,PIK3CA,MTPN	pink	VSMC_M5
GO:0030838	0.48	0.72	4	82	positive regulation of actin filament polymerization	BP	1	WASL,ABI2,ARPC2,GMFB	pink	VSMC_M5
GO:0051128	0.48	0.57	91	1877	regulation of cellular component organization	BP	1	LATS1,MAPK9,SCAF8,MKLN1,C9orf72,WASL,ANXA1,TMEM33,VEGFA,CD2AP,GCM1,GCLC,RHOQ,MACF1,SEPT7,ADAM17,CAPZA2,RAB33B,KIAA1109,MRE11,MAGI2,PDCD6IP,CLASP1,EPB41L5,ZEB2,FLRT3,MAPK8,DLC1,CSNK2A1,CAPRIN1,TNKS2,ARFGEF1,URI1,EIF4G2,RHOBTB3,DIP2B,ZFYVE16,ARSB,TSG101,PPP3CC,CEP97,TWF1,CYLD,NOTCH2,BICD1,ZMYND8,GSK3B,PIK3CA,FXR1,TFIP11,FAM162A,PARL,PSMC6,TLK1,SCFD1,ABI2,MORC2,ATF7IP,RPS6KA3,SKA1,STYXL1,ST7L,ATM,ARPC2,PRKCI,ATL3,CRKL,GHITM,WAPL,HUWE1,OPHN1,ABCB7,ATRX,ATP7A,TTC8,DYNC1H1,PTPN9,SMG1,PRKAA1,RAD1,SMAD7,SETX,BIRC2,FAM206A,GMFB,UBE2V2,MTPN,EIF5A2,NAF1,BMP2,SAR1B	pink	VSMC_M5
GO:0048513	0.48	0.56	123	2529	animal organ development	BP	1	MEX3C,TAB2,LATS1,MTHFD1L,DDX17,PCSK5,ANXA1,VEGFA,RUNX2,ASNS,GCM1,RNF38,UGCG,ADAM17,UFL1,CUL1,RAB33B,NCOA1,ASXL2,MAGI2,DCLRE1C,CLASP1,EPB41L5,RHEB,FLRT3,XDH,KAT6A,TOP2B,BIRC6,IRS2,KITLG,SPRY4,ATRN,N4BP2L2,APAF1,DLC1,RB1CC1,IMPAD1,PCM1,FAT1,CDK5RAP1,SMAD1,EIF4G2,RHOBTB3,TCTN1,GABPA,TIPARP,MLF1,ARL13B,TBC1D23,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BTG2,ATP2B4,CSDE1,BBX,BTRC,PSMG1,NDUFS4,NOTCH2,MEF2A,TET2,KMT5B,ACACB,GSK3B,PIK3CA,BPTF,FXR1,TFIP11,CCDC14,PLEKHA1,ZNF148,ABI2,HECTD1,DLX2,ARHGAP5,PAFAH1B2,SRP54,ATF2,SOS2,ATM,KDM6A,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,PYGO1,OPHN1,FBXW11,ASH1L,HERC1,SPTLC2,ATRX,ATP7A,FEM1B,TTC8,SMAD2,GGNBP2,WDR78,NF1,PRKAA1,PTPRM,NIPBL,RAD1,HPRT1,SMAD7,STXBP3,MT-CO1,MT-CO2,MT-ND4,BIRC2,ATP5PF,TMEM38B,RAB18,MTPN,CD164,CACYBP,BMP2	pink	VSMC_M5
GO:1902850	0.48	0.67	7	133	microtubule cytoskeleton organization involved in mitosis	BP	1	CLASP1,LSM14A,CEP97,FBXW11,DYNC1H1,STAG2,RMDN1	pink	VSMC_M5
GO:0071103	0.48	0.65	10	200	DNA conformation change	BP	1	ANXA1,MRE11,KAT6A,TOP2B,HP1BP3,KAT6B,WAPL,ATRX,NAP1L3,SETX	pink	VSMC_M5
GO:0090257	0.48	0.65	9	179	regulation of muscle system process	BP	1	ARHGAP42,IL6ST,ATP2B4,TWF1,MEF2A,GLRX3,SMAD7,TMEM38B,MTPN	pink	VSMC_M5
GO:0008088	0.49	0.71	4	68	axo-dendritic transport	BP	1	DST,ARL8B,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0051983	0.49	0.71	4	78	regulation of chromosome segregation	BP	1	CSNK2A1,PUM1,ATM,WAPL	pink	VSMC_M5
GO:0009152	0.49	0.67	6	137	purine ribonucleotide biosynthetic process	BP	1	ACACB,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0044255	0.49	0.59	32	743	cellular lipid metabolic process	BP	1	DGKA,SERINC1,EFR3A,SLC25A17,ANXA1,AGMO,FAM126A,UGCG,DGKH,OXSM,IRS2,PRKD3,IMPAD1,MTMR6,FAR1,PIP4P2,PIGP,PRKAB2,ACACB,PIK3CA,MORC2,ATF2,ATM,ACOX3,SPTLC2,PIK3C3,SMG1,PRKAA1,CEPT1,NUDT7,HACD1,TMEM38B	pink	VSMC_M5
GO:0016192	0.49	0.57	57	1192	vesicle-mediated transport	BP	1	VTA1,SNX2,CSNK1G3,SFT2D1,MKLN1,VPS13A,C9orf72,WASL,ANXA1,VEGFA,CD2AP,RHOQ,COMMD1,MACF1,VPS54,RAB1A,RAB14,RAB33B,ZFYVE9,KIAA1109,MAGI2,PDCD6IP,CLASP1,ARL8B,GOLGA7,COG6,MTMR6,ARFGEF1,SLC4A8,RHOBTB3,VPS29,ZFYVE16,PIP4P2,TBC1D23,TSG101,PPP3CC,BICD1,GOLGA5,GSK3B,PIK3CA,LYST,ALS2,SCFD1,ACAP2,PRKCI,CCZ1B,OPHN1,CHM,PIK3C3,RAB11FIP4,PRKAA1,TRAPPC2L,STXBP3,USP33,RNF139,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0090100	0.49	0.69	5	85	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ADAM17,ZEB2,NOTCH2,SMAD2,BMP2	pink	VSMC_M5
GO:0090101	0.49	0.67	6	101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ADAM17,MAGI2,LTBP1,SMAD7,UBE2D3,BMP2	pink	VSMC_M5
GO:0045185	0.49	0.69	5	80	maintenance of protein location	BP	1	LATS1,SYNE1,VPS13A,LTBP1,TWF1	pink	VSMC_M5
GO:0000077	0.49	0.69	5	105	DNA damage checkpoint signaling	BP	1	MRE11,ATF2,ATM,FEM1B,RAD1	pink	VSMC_M5
GO:0016310	0.49	0.56	69	1440	phosphorylation	BP	1	DGKA,TAB2,PPIL4,LATS1,MAPK9,CSNK1G3,LRGUK,C9orf72,VEGFA,ADAM17,SRPK2,MRE11,MAP3K2,DGKH,XDH,BIRC6,IRS2,KITLG,PRKD3,SPRY4,MAP4K3,MAPK8,RB1CC1,IL6ST,CSNK2A1,CDK5RAP1,SMAD1,BTBD10,CPNE3,GTF2H1,TSG101,HIPK1,ATP2B4,TWF1,IRAK4,NDUFS4,DOCK3,CAB39,PRKAB2,GSK3B,PIK3CA,FXR1,STK39,ALS2,RPS6KC1,TLK1,ABI2,RPS6KA3,CREBL2,ATF2,ATM,PRKCI,COPS2,CRKL,WNK1,SMAD2,PIK3C3,GSKIP,CCNK,GGNBP2,SMG1,CSNK1A1,NF1,PRKAA1,SMAD7,PKN2,GMFB,BMP2,DCAKD	pink	VSMC_M5
GO:0051271	0.49	0.62	12	241	negative regulation of cellular component movement	BP	1	WASL,KRIT1,MAGI2,CLASP1,DLC1,ARID2,ATP2B4,ZMYND8,TIMP1,NF1,PTPRM,SMAD7	pink	VSMC_M5
GO:0030595	0.49	0.66	7	150	leukocyte chemotaxis	BP	1	ANXA1,VEGFA,ADAM17,LYST,STK39,SRP54,WNK1	pink	VSMC_M5

GO:0010563	0.49	0.61	17	356	negative regulation of phosphorus metabolic process	BP	1	LATS1,C9orf72,XDH,IRS2,SPRY4,CDK5RAP1,URI1,TSG101,GSK3B,STYXL1,CRKL,WNK1,GSKIP,GGNBP2,NF1,SMAD7,BMP2	pink	VSMC_M5
GO:0045936	0.49	0.61	17	356	negative regulation of phosphate metabolic process	BP	1	LATS1,C9orf72,XDH,IRS2,SPRY4,CDK5RAP1,URI1,TSG101,GSK3B,STYXL1,CRKL,WNK1,GSKIP,GGNBP2,NF1,SMAD7,BMP2	pink	VSMC_M5
GO:0032886	0.49	0.63	11	202	regulation of microtubule-based process	BP	1	MACF1,PDCD6IP,CLASP1,MEMO1,CEP97,CYLD,BICD1,GSK3B,SKA1,DYNC1H1,PRKAA1	pink	VSMC_M5
GO:0043624	0.49	0.66	7	119	cellular protein complex disassembly	BP	1	CAPZA2,CLASP1,GFM2,TWF1,PIK3CA,MTPN,EIF5A2	pink	VSMC_M5
GO:0051607	0.49	0.65	8	174	defense response to virus	BP	1	DDX17,IFIT5,LSM14A,TSPAN32,PUM1,LYST,BIRC2,ELMOD2	pink	VSMC_M5
GO:0140546	0.49	0.65	8	174	defense response to symbiont	BP	1	DDX17,IFIT5,LSM14A,TSPAN32,PUM1,LYST,BIRC2,ELMOD2	pink	VSMC_M5
GO:1901617	0.50	0.65	8	178	organic hydroxy compound biosynthetic process	BP	1	CYP39A1,OSBPL9,ZEB2,TRPC1,SPTLC2,ATP7A,PRKAA1,BMP2	pink	VSMC_M5
GO:0097193	0.50	0.63	11	242	intrinsic apoptotic signaling pathway	BP	1	CUL1,CUL2,APAF1,URI1,HIPK1,CYLD,STYXL1,ATM,CUL5,ERO1A,GSKIP	pink	VSMC_M5
GO:0060284	0.50	0.60	20	384	regulation of cell development	BP	1	VEGFA,MACF1,UFL1,RHEB,SPRY4,IL6ST,CAPRIN1,PCM1,EIF4G2,DIP2B,PPP1CC,NOTCH2,GSK3B,DLX2,ARPC2,PRKCI,CRKL,NF1,SMAD7,BMP2	pink	VSMC_M5
GO:2001237	0.50	0.70	4	79	negative regulation of extrinsic apoptotic signaling pathway	BP	1	GCLC,BIRC6,RB1CC1,GSK3B	pink	VSMC_M5
GO:0048813	0.50	0.65	7	126	dendrite morphogenesis	BP	1	WASL,CAPRIN1,MEF2A,GSK3B,ABI2,HPRT1,FAM206A	pink	VSMC_M5
GO:1903829	0.50	0.62	12	241	positive regulation of cellular protein localization	BP	1	UBR5,CD2AP,MAPK8,TSG101,ATP2B4,BICD1,GSK3B,PRKCI,HUWE1,PTPN9,PRKAA1,UBE2D3	pink	VSMC_M5
GO:0097191	0.50	0.64	8	173	extrinsic apoptotic signaling pathway	BP	1	GCLC,BIRC6,KITLG,RB1CC1,HIPK1,CYLD,GSK3B,FEM1B	pink	VSMC_M5
GO:0009967	0.50	0.56	53	1127	positive regulation of signal transduction	BP	1	TAB2,MAPK9,CSNK1G3,UBR5,KLHDC10,TMEM33,VEGFA,USP34,MACF1,ADAM17,JCAD,ASXL2,RHEB,ZEB2,MBD5,XDH,ZDHHC17,KITLG,RB1CC1,IL6ST,CSNK2A1,IFIT5,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,NR3C2,RNF13,FAM92A,IRAK4,CYLD,NOTCH2,SHOC2,PUM1,PIK3CA,STK39,TIAL1,ALS2,STYXL1,SOS2,ATM,PRKCI,USP8,CRKL,WNK1,SMAD2,GSKIP,XIAP,NFAT5,BIRC2,AGO3,BMP2	pink	VSMC_M5
GO:0051225	0.50	0.68	5	101	spindle assembly	BP	1	CLASP1,LSM14A,CEP97,DYNC1H1,STAG2	pink	VSMC_M5
GO:0050900	0.50	0.62	11	245	leukocyte migration	BP	1	WASL,ANXA1,VEGFA,ADAM17,KITLG,IRAK4,LYST,STK39,SRP54,CRKL,WNK1	pink	VSMC_M5
GO:0002688	0.50	0.69	4	92	regulation of leukocyte chemotaxis	BP	1	VEGFA,ADAM17,STK39,WNK1	pink	VSMC_M5
GO:0009411	0.51	0.66	6	127	response to UV	BP	1	MAP4K3,MAPK8,POLK,TIMP1,UBE2A,PRKAA1	pink	VSMC_M5
GO:0046545	0.51	0.69	4	75	development of primary female sexual characteristics	BP	1	VEGFA,KITLG,TIPARP,PLEKHA1	pink	VSMC_M5
GO:0042742	0.51	0.67	5	109	defense response to bacterium	BP	1	RAB1A,ADAM17,RAB14,NOTCH2,LYST	pink	VSMC_M5
GO:0099518	0.51	0.69	4	65	vesicle cytoskeletal trafficking	BP	1	WASL,RAB1A,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0061157	0.51	0.69	4	79	mRNA destabilization	BP	1	POLR2D,YTHDF3,BTG2,PUM1	pink	VSMC_M5
GO:1905114	0.51	0.58	22	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	LATS1,CSNK1G3,UBR5,USP34,MACF1,MAGI2,ZEB2,CSNK2A1,TNKS2,CYLD,BTRC,ZMYND8,GSK3B,USP8,WNK1,PYGO1,FBXW11,GSKIP,CSNK1A1,XIAP,PRKAA1,BMP2	pink	VSMC_M5
GO:0048024	0.51	0.69	4	85	regulation of mRNA splicing, via spliceosome	BP	1	DDX17,TIA1,SRPK2,FXR1	pink	VSMC_M5
GO:0120162	0.51	0.69	4	78	positive regulation of cold-induced thermogenesis	BP	1	VEGFA,KDM3A,PRKAB2,DYNC1H1	pink	VSMC_M5
GO:0006888	0.51	0.67	5	106	endoplasmic reticulum to Golgi vesicle-mediated transport	BP	1	RAB1A,SCFD1,TRAPPC2L,RNF139,SAR1B	pink	VSMC_M5
GO:0097061	0.51	0.69	4	70	dendritic spine organization	BP	1	WASL,CAPRIN1,ZMYND8,ABI2	pink	VSMC_M5
GO:0000041	0.51	0.68	4	86	transition metal ion transport	BP	1	SLC30A6,TRPC1,ABCB7,ATP7A	pink	VSMC_M5
GO:0032465	0.52	0.68	4	72	regulation of cytokinesis	BP	1	BIRC6,PIK3C3,RAB11FIP4,PKN2	pink	VSMC_M5
GO:0000018	0.52	0.68	4	83	regulation of DNA recombination	BP	1	MRE11,ARID2,KMT5B,KLHL15	pink	VSMC_M5
GO:0000165	0.52	0.56	27	579	MAPK cascade	BP	1	MAPK9,KLHDC10,VEGFA,JCAD,MAP3K2,XDH,ZDHHC17,KITLG,SPRY4,MAP4K3,MAPK8,RB1CC1,PJA2,SMAD1,PPP1CC,IRAK4,CYLD,RANBP9,NOTCH2,MEF2A,STK39,ATF2,CRKL,ASH1L,NF1,SETX,BMP2	pink	VSMC_M5
GO:0001659	0.52	0.63	7	141	temperature homeostasis	BP	1	VEGFA,ADAM17,RHEB,KDM3A,ACOT13,PRKAB2,DYNC1H1	pink	VSMC_M5
GO:0042221	0.52	0.52	135	2921	response to chemical	BP	1	TAB2,LATS1,MAPK9,UBR5,DDX17,UBR2,ANXA1,TMEM33,VEGFA,RUNX2,ASNS,GCLC,RHOQ,ERLEC1,UGCG,ADAM17,UFL1,RAB14,ZFYVE9,HSPA4L,JCAD,NCOA1,PRDM5,MAGI2,EPB41L5,FNTA,ZEB2,MBD5,FLRT3,XDH,NGLY1,ZDHHC17,LTBP1,IRS2,SPRY4,NR3C1,MAP4K3,MAPK8,APAF1,IL6ST,YTHDF3,LSM14A,SGTB,KDM3A,ERBIN,URI1,SMAD1,NR3C2,TRPC1,GABPA,CPNE3,TIPARP,ARL13B,ARSB,GTF2H1,HIPK1,BTG2,ATP2B4,IRAK4,CYLD,BTRC,SNRPN,NDUFS4,CPNE8,NOTCH2,ANO1,CAB39,MEF2A,SHOC2,TET2,ACACB,GSK3B,FSTL1,PIK3CA,LYST,UBR1,SCN9A,BPTF,STK39,EGLN1,ZFAND2A,FAM162A,PSMC6,PLEKHA1,SCFD1,RPS6KA3,SRP54,ATF2,KLHL15,ACAP2,LANCL1,ATM,ERO1A,PRKCI,HP1BP3,USP8,TIMP1,CRKL,WNK1,WAPL,FUT8,OPHN1,CPEB4,ATRX,ATP7A,TTC8,SMAD2,PIK3C3,GSKIP,USP14,XIAP,PRKAA1,PTPRM,HPRT1,SMAD7,PRPF8,SETX,STXBP3,NFAT5,USP33,MT-CO1,MT-ND3,MT-ND4,MT-ND5,BIRC2,SULT1C4,UBE2D3,TMEM38B,USP9X,RNF103,CACYBP,RNF139,DDAH1,UBXN2A,BMP2	pink	VSMC_M5
GO:0140053	0.52	0.68	4	101	mitochondrial gene expression	BP	1	CDK5RAP1,PTCD3,GFM2,PRKAA1	pink	VSMC_M5
GO:1903046	0.52	0.63	7	153	meiotic cell cycle process	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3,ATRX,RAD1	pink	VSMC_M5
GO:0006486	0.52	0.62	8	182	protein glycosylation	BP	1	DPY19L1,TMTC3,ARFGEF1,TET3,GXYLT1,OGA,TET2,FUT8	pink	VSMC_M5
GO:0043413	0.52	0.62	8	182	macromolecule glycosylation	BP	1	DPY19L1,TMTC3,ARFGEF1,TET3,GXYLT1,OGA,TET2,FUT8	pink	VSMC_M5
GO:0048638	0.52	0.59	13	257	regulation of developmental growth	BP	1	LATS1,VEGFA,MACF1,MBD5,ATRN,TNKS2,EIF4G2,DIP2B,ACACB,GSK3B,PIK3CA,NIPBL,SMAD7	pink	VSMC_M5
GO:0031344	0.52	0.56	27	538	regulation of cell projection organization	BP	1	WASL,VEGFA,RHOQ,MACF1,SEPT7,MAGI2,CAPRIN1,EIF4G2,DIP2B,ARSB,CEP97,TWF1,CYLD,ZMYND8,GSK3B,PIK3CA,FXR1,ABI2,STYXL1,ARPC2,PRKCI,CRKL,ATP7A,PTPN9,SETX,FAM206A,UBE2V2	pink	VSMC_M5
GO:0045927	0.52	0.60	10	199	positive regulation of growth	BP	1	VEGFA,MACF1,ADAM17,CSNK2A1,EIF4G2,ACACB,RPS6KA3,NIPBL,SMAD7,MTPN	pink	VSMC_M5
GO:0022408	0.52	0.64	6	130	negative regulation of cell-cell adhesion	BP	1	ANXA1,VEGFA,EPB41L5,WNK1,SMAD7,BMP2	pink	VSMC_M5

GO:0009117	0.53	0.58	16	381	nucleotide metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,ADAL,PDE5A,PRKAA1,HPRT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:1903532	0.53	0.61	9	196	positive regulation of secretion by cell	BP	1	CD2AP,PDCD6IP,CLASP1,IRS2,SLC4A8,TSG101,ANO1,GOLPH3L,BMP2	pink	VSMC_M5
GO:0015931	0.53	0.62	8	181	nucleobase-containing compound transport	BP	1	SLC25A17,POLR2D,ZC3H11A,SMG7,SMG1,SLC35A3,EIF5A2,SLC25A36	pink	VSMC_M5
GO:0044283	0.53	0.57	17	414	small molecule biosynthetic process	BP	1	MTHFD1L,ANXA1,CYP39A1,SDHAF3,ASNS,OSBPL9,OXSM,KDM3A,ATP2B4,PRKAB2,ACACB,ADAL,SPTLC2,PRKAA1,HPRT1,HACD1,BMP2	pink	VSMC_M5
GO:0001822	0.53	0.58	13	248	kidney development	BP	1	PCSK5,VEGFA,MAGI2,APAF1,SMAD1,TIPARP,NOTCH2,PYGO1,SMAD2,NF1,NIPBL,SMAD7,BMP2	pink	VSMC_M5
GO:0010811	0.53	0.65	5	100	positive regulation of cell-substrate adhesion	BP	1	VEGFA,EPB41L5,GSK3B,ARPC2,CRKL	pink	VSMC_M5
GO:0007399	0.53	0.52	94	1867	nervous system development	BP	1	MTHFD1L,VPS13A,C9orf72,WASL,ANXA1,VEGFA,FRYL,RUNX2,GCM1,FAM126A,UGCG,MACF1,UFL1,SCLT1,NCOA1,MAGI2,RHEB,ZEB2,MBD5,FLRT3,TOP2B,ZDHHC17,IRS2,ATRN,APAF1,DLC1,IL6ST,CAPRIN1,PCM1,CDK5RAP1,ARFGEF1,SMAD1,EIF4G2,DIP2B,TCTN1,PPP1CC,WWP1,ARL13B,ARSB,TBC1D23,HIPK1,ESRP1,PPP3CC,BTG2,ATP2B4,TWF1,PSMG1,NDUFS4,NOTCH2,ZMYND8,MEF2A,GSK3B,BPTF,CCDC14,ALS2,ZNF148,ABI2,HECTD1,DLX2,RPS6KA3,PAFAH1B2,ATF2,STYXL1,PRKCI,COPS2,YWHAQ,CRKL,WNK1,OPHN1,FBXW11,HERC1,ATRX,ATP7A,TTC8,PTPN9,NF1,PTPRM,NIPBL,RAD1,HPRT1,SETX,STXBP3,USP33,MT-CO1,MT-ND4,ATP5PF,USP9X,FAM206A,RNF103,GMFB,UBE2V2,RAB18,MTPN,BMP2	pink	VSMC_M5
GO:0008361	0.53	0.61	8	157	regulation of cell size	BP	1	VEGFA,MACF1,RB1CC1,EIF4G2,DIP2B,GSK3B,ATP7A,MTPN	pink	VSMC_M5
GO:0005996	0.53	0.60	9	199	monosaccharide metabolic process	BP	1	SDHAF3,GCLC,IRS2,ACACB,GSK3B,PIK3CA,FUT8,PGM2,PRKAA1	pink	VSMC_M5
GO:0001678	0.53	0.63	6	124	cellular glucose homeostasis	BP	1	GCLC,IRS2,ANO1,PIK3CA,PRKAA1,STXBP3	pink	VSMC_M5
GO:0007165	0.53	0.50	184	3919	signal transduction	BP	1	DGKA,ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,DDX17,MKLN1,KLHDC10,UBR2,C9orf72,ANXA1,TMEM33,VEGFA,KRIT1,RUNX2,CD2AP,GCLC,DST,RHOQ,ERLEC1,USP34,UGCG,MACF1,ADAM17,UFL1,CUL1,RAB14,CUL2,RAB33B,ZFYVE9,JCAD,ARHGAP42,SRPK2,NCOA1,MRE11,ASXL2,MAGI2,MAP3K2,AKAP11,DGKH,RHEB,FNTA,ZEB2,MBD5,FLRT3,XDH,KAT6A,ZDHHC17,NKIRAS1,BIRC6,LTBP1,IRS2,KITLG,PRKD3,SPRY4,NR3C1,MAP4K3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,TNKS2,LSM14A,PJA2,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,NR3C2,RHOBTB3,RNF13,TCTN1,PPP1CC,WWP1,ZFYVE16,CPNE3,TIPARP,RALGAPB,ARL13B,FAM92A,GTF2H1,TSG101,HIPK1,PPP3CC,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,TSPAN32,DOCK3,NOTCH2,BICD1,ANO1,ASB7,CAB39,ZMYND8,IPO8,MEF2A,SHOC2,PRKAB2,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,STK39,FAM162A,TIAL1,ALS2,RPS6KC1,PDE5A,TLK1,PLEKHA1,MUC20,ABI2,DLX2,ARHGAP5,RPS6KA3,CREBL2,ATF2,HERC4,STYXL1,RALGPS2,SOS2,ATM,CUL5,ERO1A,PRKCI,COPS2,YWHAQ,USP8,TIMP1,CRKL,WNK1,GHITM,PYGO1,FUT8,OPHN1,CPEB4,FBXW11,ASH1L,ATRX,CHM,PIAS1,FEM1B,SMAD2,PIK3C3,GSKIP,GGNBP2,SMG1,CSNK1A1,XIAP,NF1,PRKAA1,PTPRM,RAD1,SMAD7,SETX,PKN2,NFAT5,USP33,BIRC2,NMS,AGO3,UBE2D3,TMEM38B,USP9X,GMFB,RAB18,CD164,DDAH1,BMT2,MPZL1,BMP2	pink	VSMC_M5
GO:0070665	0.53	0.67	4	93	positive regulation of leukocyte proliferation	BP	1	ANXA1,IRS2,KITLG,IL6ST	pink	VSMC_M5
GO:0050779	0.54	0.66	4	82	RNA destabilization	BP	1	POLR2D,YTHDF3,BTG2,PUM1	pink	VSMC_M5
GO:0001938	0.54	0.66	4	78	positive regulation of endothelial cell proliferation	BP	1	VEGFA,ADAM17,JCAD,BMP2	pink	VSMC_M5
GO:0031570	0.54	0.64	5	111	DNA integrity checkpoint signaling	BP	1	MRE11,ATF2,ATM,FEM1B,RAD1	pink	VSMC_M5
GO:0071900	0.54	0.57	14	300	regulation of protein serine/threonine kinase activity	BP	1	LATS1,VEGFA,ADAM17,KITLG,SPRY4,CDK5RAP1,GTF2H1,TSG101,ATP2B4,CAB39,ALS2,CCNK,NF1,BMP2	pink	VSMC_M5
GO:2001251	0.54	0.66	4	77	negative regulation of chromosome organization	BP	1	TNKS2,ATM,WAPL,ATRX	pink	VSMC_M5
GO:1904375	0.54	0.64	5	107	regulation of protein localization to cell periphery	BP	1	RHOQ,ATP2B4,HECTD1,PRKCI,PTPN9	pink	VSMC_M5
GO:0008286	0.54	0.64	5	93	insulin receptor signaling pathway	BP	1	RHOQ,IRS2,GSK3B,PIK3CA,PRKAA1	pink	VSMC_M5
GO:0072384	0.54	0.66	4	78	organelle transport along microtubule	BP	1	RAB1A,BICD1,FBXW11,DYNC1H1	pink	VSMC_M5
GO:0042063	0.54	0.58	11	230	gliogenesis	BP	1	ANXA1,GCM1,UFL1,RHEB,IL6ST,PPP1CC,DLX2,PRKCI,CRKL,NF1,BMP2	pink	VSMC_M5
GO:0010721	0.54	0.61	7	130	negative regulation of cell development	BP	1	VEGFA,SPRY4,PCM1,DIP2B,GSK3B,DLX2,NF1	pink	VSMC_M5
GO:1901698	0.54	0.53	39	845	response to nitrogen compound	BP	1	UBR2,ANXA1,ASNS,GCLC,RHOQ,ERLEC1,UFL1,MBD5,NGLY1,IRS2,SGTB,ERBIN,GABPA,BTG2,ATP2B4,NDUFS4,ANO1,GSK3B,PIK3CA,UBR1,EGLN1,PSMC6,PRKCI,TIMP1,CRKL,CPEB4,ATRX,ATP7A,PIK3C3,USP14,PRKAA1,HPRT1,STXBP3,MT-ND5,BIRC2,TMEM38B,RNF103,CACYBP,RNF139	pink	VSMC_M5
GO:1990138	0.54	0.60	8	147	neuron projection extension	BP	1	C9orf72,VEGFA,MACF1,FLRT3,EIF4G2,DIP2B,GSK3B,USP9X	pink	VSMC_M5
GO:0060271	0.54	0.57	13	266	cilium assembly	BP	1	LRGUK,SEPT7,SCLT1,PCM1,TCTN1,ARL13B,FAM92A,CEP97,CYLD,DNAAF5,TTC8,WDR78,CPLANE1	pink	VSMC_M5
GO:0071214	0.54	0.57	12	267	cellular response to abiotic stimulus	BP	1	GCLC,MAP3K2,MAPK8,POLK,CAB39,PIK3CA,STK39,ATM,TIMP1,NIPBL,RAD1,MTPN	pink	VSMC_M5
GO:0104004	0.54	0.57	12	267	cellular response to environmental stimulus	BP	1	GCLC,MAP3K2,MAPK8,POLK,CAB39,PIK3CA,STK39,ATM,TIMP1,NIPBL,RAD1,MTPN	pink	VSMC_M5
GO:0006631	0.54	0.58	11	271	fatty acid metabolic process	BP	1	SLC25A17,ANXA1,OXSM,IRS2,PRKAB2,ACACB,MORC2,ACOX3,PRKAA1,NUDT7,HACD1	pink	VSMC_M5
GO:0042542	0.54	0.64	5	118	response to hydrogen peroxide	BP	1	ANXA1,PLEKHA1,PRKAA1,SETX,MT-ND5	pink	VSMC_M5
GO:0010647	0.55	0.51	58	1251	positive regulation of cell communication	BP	1	TAB2,MAPK9,CSNK1G3,UBR5,KLHDC10,TMEM33,VEGFA,USP34,MACF1,ADAM17,JCAD,ASXL2,RHEB,ZEB2,MBD5,XDH,ZDHHC17,IRS2,KITLG,RB1CC1,IL6ST,CSNK2A1,IFIT5,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,SLC4A8,NR3C2,RNF13,FAM92A,IRAK4,CYLD,NOTCH2,ANO1,SHOC2,GSK3B,PUM1,PIK3CA,STK39,TIAL1,ALS2,STYXL1,SOS2,ATM,PRKCI,USP8,CRKL,WNK1,SMAD2,GSKIP,XIAP,NFAT5,BIRC2,AGO3,PAIP2,BMP2	pink	VSMC_M5
GO:0048705	0.55	0.59	9	186	skeletal system morphogenesis	BP	1	MTHFD1L,RUNX2,RAB33B,IMPAD1,TIPARP,PLEKHA1,DLX2,SMAD2,NIPBL	pink	VSMC_M5

GO:0061014	0.55	0.65	4	82	positive regulation of mRNA catabolic process	BP	1	POLR2D,YTHDF3,BTG2,PUM1	pink	VSMC_M5
GO:0048545	0.55	0.57	12	258	response to steroid hormone	BP	1	LATS1,UBR5,DDX17,ANXA1,UFL1,NCOA1,NR3C1,KDM3A,URI1,NR3C2,USP8,MT-ND3	pink	VSMC_M5
GO:0055086	0.55	0.55	18	439	nucleobase-containing small molecule metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,ADAL,PDE5A,FUT8,PRKAA1,HPRT1,SLC35A3,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0007229	0.55	0.63	5	92	integrin-mediated signaling pathway	BP	1	DST,ERBIN,TSPAN32,TIMP1,FUT8	pink	VSMC_M5
GO:0051028	0.55	0.63	5	109	mRNA transport	BP	1	POLR2D,ZC3H11A,SMG7,SMG1,EIF5A2	pink	VSMC_M5
GO:0061387	0.55	0.63	5	95	regulation of extent of cell growth	BP	1	VEGFA,MACF1,EIF4G2,DIP2B,GSK3B	pink	VSMC_M5
GO:0016477	0.55	0.51	55	1120	cell migration	BP	1	WASL,ANXA1,VEGFA,KRIT1,CD2AP,PTP4A1,RHOQ,MACF1,RAB1A,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,ZEB2,FLRT3,TOP2B,IRS2,KITLG,ATRN,DLC1,PCM1,YTHDF3,FAT1,RHOBTB3,CPNE3,ARL13B,ARSB,ARID2,ATP2B4,IRAK4,ZMYND8,FSTL1,PIK3CA,LYST,STK39,ABI2,SRP54,ATM,PRKCI,TIMP1,CRKL,WNK1,FUT8,OPHN1,ATP7A,PSTPIP2,NF1,PTPRM,NIPBL,SMAD7,PKN2,USP33,USP9X,BMP2	pink	VSMC_M5
GO:0003341	0.55	0.63	5	103	cilium movement	BP	1	VPS13A,ATP2B4,DNAAF5,ASH1L,WDR78	pink	VSMC_M5
GO:0006753	0.55	0.55	16	387	nucleoside phosphate metabolic process	BP	1	LRGUK,RHOQ,XDH,OXSM,FAR1,ACACB,ADAL,PDE5A,PRKAA1,HPRT1,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:1903008	0.55	0.63	5	101	organelle disassembly	BP	1	UFL1,RB1CC1,GFM2,HUWE1,DENR	pink	VSMC_M5
GO:0019080	0.56	0.65	4	86	viral gene expression	BP	1	CSDE1,GSK3B,FUT8,DENR	pink	VSMC_M5
GO:0090596	0.56	0.57	10	198	sensory organ morphogenesis	BP	1	VEGFA,FAT1,HIPK1,NOTCH2,ABI2,PRKCI,TTC8,NF1,PTPRM,NIPBL	pink	VSMC_M5
GO:0065007	0.56	0.48	384	8375	biological regulation	BP	1	DGKA,MEX3C,DMXL1,ME2,ARFGEF3,TAB2,PPIL4,MED23,LATS1,MAPK9,CSNK1G3,SCAF8,UBR5,SERINC1,DDX17,MKLN1,KLHDC10,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,TMEM33,GUF1,VEGFA,KRIT1,ANKIB1,RUNX2,CYP39A1,CD2AP,SDHAF3,ASNS,GCM1,GCLC,DST,PTP4A1,RHOQ,FBXO11,ERLEC1,LCA5,SMAP2,TAX1BP1,RLF,USP34,UGCG,ZNF292,COMMD1,MACF1,VPS54,RAB1A,SEPT7,TIA1,ADAM17,CAPZA2,UFL1,CUL1,ZMYM4,RAB14,CUL2,RAB33B,ZFYVE9,JCAD,ARHGAP42,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,YME1L1,MED4,MAP3K2,AKAP11,CNOT10,PDCD6IP,DGKH,CLASP1,EPB41L5,RHEB,KMT2C,FBXL3,EMSY,FNTA,ZEB2,MBD5,FLRT3,EPC2,XDH,KAT6A,MEMO1,TOP2B,ZDHHC17,GOLGA7,NKIRAS1,BIRC6,LTBP1,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,ATRN,NR3C1,N4BP2L2,MAP4K3,SHQ1,UBA3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,GPBP1,CSNK2A1,CAPRIN1,PCM1,IFIT5,YTHDF3,TNKS2,VCPIP1,LSM14A,ZMYM5,CDK5RAP1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,SLC4A8,CGGBP1,NR3C2,RHOBTB3,TRPC1,DIP2B,BTBD10,RNF13,DPH6,PCGF1,TCTN1,GABPA,PPP1CC,TET3,WWP1,ZFYVE16,CPNE3,TIPARP,MLF1,RALGAPB,ARL13B,PIP4P2,LXN,FAM92A,ARSB,GTF2H1,VIRMA,MED13L,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BAZ2B,BTG2,SSR1,DNMBP,ATP2B4,ZBTB11,CEP97,CSDE1,TWF1,IRAK4,CYLD,RANBP9,BBX,BTRC,NIPSNAP2,TSPAN32,NDUFS4,ID4,DOCK3,ACOT13,NOTCH2,TRIP12,BICD1,ANO1,ASB7,DENND5B,CAB39,ZMYND8,IPO8,MEF2A,PPP6R3,SHOC2,PRKAB2,TET2,KMT5B,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,SCN9A,GTF2I,BPTF	pink	VSMC_M5
GO:0030216	0.56	0.64	4	74	keratinocyte differentiation	BP	1	LATS1,ANXA1,UGCG,TSG101	pink	VSMC_M5
GO:0045598	0.56	0.62	5	109	regulation of fat cell differentiation	BP	1	MEX3C,BBS12,ASXL2,CREBL2,BMP2	pink	VSMC_M5
GO:0099173	0.56	0.59	7	137	postsynapse organization	BP	1	WASL,FNTA,CAPRIN1,ZMYND8,ABI2,CRKL,OPHN1	pink	VSMC_M5
GO:0032508	0.56	0.64	4	75	DNA duplex unwinding	BP	1	ANXA1,MRE11,ATRX,SETX	pink	VSMC_M5
GO:0051129	0.56	0.52	27	569	negative regulation of cellular component organization	BP	1	SCAF8,WASL,VEGFA,GCLC,CAPZA2,CLASP1,DLC1,TNKS2,ARFGEF1,DIP2B,CEP97,TWF1,GSK3B,PIK3CA,TFIP11,SCFD1,STYXL1,ATM,GHITM,WAPL,HUWE1,ATRX,PTPN9,RAD1,BIRC2,GMFB,MTPN	pink	VSMC_M5
GO:0000910	0.56	0.59	7	141	cytokinesis	BP	1	SEPT7,PDCD6IP,BIRC6,USP8,PIK3C3,RAB11FIP4,PKN2	pink	VSMC_M5
GO:0006986	0.56	0.62	5	124	response to unfolded protein	BP	1	TMEM33,ERLEC1,UFL1,HSPA4L,ERO1A	pink	VSMC_M5
GO:0009260	0.56	0.60	6	149	ribonucleotide biosynthetic process	BP	1	ACACB,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0061326	0.56	0.64	4	77	renal tubule development	BP	1	VEGFA,NOTCH2,TTC8,BMP2	pink	VSMC_M5
GO:0046903	0.56	0.51	30	673	secretion	BP	1	PCSK5,ANXA1,VEGFA,CD2AP,RAB1A,RAB33B,NCOA1,PDCD6IP,CLASP1,XDH,ARL8B,IRS2,ARFGEF1,SLC4A8,TSG101,ANO1,GSK3B,STK39,PRKCI,WNK1,ATP7A,SMAD2,PIK3C3,PRKAA1,STXBP3,MT-CO2,ATP5PF,TMEM38B,GOLPH3L,BMP2	pink	VSMC_M5
GO:0071702	0.56	0.48	84	1891	organic substance transport	BP	1	RELCH,VTA1,VPS13B,SNX2,UBR5,SFT2D1,KPNA5,SLC25A17,VPS13A,PCSK5,ANXA1,CD2AP,SRP72,RHOQ,ERLEC1,LCA5,UGCG,COMMD1,MACF1,VPS54,RAB1A,RAB14,RAB33B,OSBPL9,POLR2D,PDCD6IP,ARL8B,ZDHHC17,GOLGA7,COG6,IRS2,MAPK8,VPS37A,PCM1,SGTB,ARFGEF1,ERBIN,SLC4A8,VPS29,ZFYVE16,TSG101,UEVLD,SSR1,ZC3H11A,ANO1,DENND5B,IPO8,MEF2A,GSK3B,LYST,ZFAND2A,PARL,TLK1,SCFD1,CREBL2,SMG7,SRP54,MTX2,PRKCI,YWHAQ,RPAIN,HUWE1,SFXN1,SNX11,ABCB7,CHM,TTC8,SMAD2,PIK3C3,APPBP2,SMG1,PRKAA1,STXBP3,SLC35A3,ARRDC5,UBE2D3,ATP5PF,RAB18,EIF5A2,SLC25A36,GOLPH3L,TIMM9,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0010717	0.56	0.64	4	80	regulation of epithelial to mesenchymal transition	BP	1	CLASP1,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0046395	0.57	0.59	7	182	carboxylic acid catabolic process	BP	1	SLC25A17,IRS2,ATP2B4,ACACB,ACOX3,NUDT7,DDAH1	pink	VSMC_M5
GO:0044706	0.57	0.59	7	159	multi-multicellular organism process	BP	1	PCSK5,VEGFA,YTHDF3,TIMP1,ASH1L,ATP7A,UBE2A	pink	VSMC_M5
GO:0006164	0.57	0.60	6	149	purine nucleotide biosynthetic process	BP	1	ACACB,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0023056	0.57	0.49	58	1258	positive regulation of signaling	BP	1	TAB2,MAPK9,CSNK1G3,UBR5,KLHDC10,TMEM33,VEGFA,USP34,MACF1,ADAM17,JCAD,ASXL2,RHEB,ZEB2,MBD5,XDH,ZDHHC17,IRS2,KITLG,RB1CC1,IL6ST,CSNK2A1,IFIT5,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,SLC4A8,NR3C2,RNF13,FAM92A,IRAK4,CYLD,NOTCH2,ANO1,SHOC2,GSK3B,PUM1,PIK3CA,STK39,TIAL1,ALS2,STYXL1,SOS2,ATM,PRKCI,USP8,CRKL,WNK1,SMAD2,GSKIP,XIAP,NFAT5,BIRC2,AGO3,PAIP2,BMP2	pink	VSMC_M5

GO:0051650	0.57	0.59	7	143	establishment of vesicle localization	BP	1	WASL,RAB1A,CLASP1,TBC1D23,FBXW11,DYNC1H1,SAR1B	pink	VSMC_M5
GO:0071466	0.57	0.63	4	92	cellular response to xenobiotic stimulus	BP	1	NCOA1,CRKL,PRKAA1,SULT1C4	pink	VSMC_M5
GO:0006469	0.57	0.57	8	172	negative regulation of protein kinase activity	BP	1	LATS1,SPRY4,CDK5RAP1,TSG101,GSKIP,GGNBP2,NF1,BMP2	pink	VSMC_M5
GO:0002224	0.57	0.63	4	92	toll-like receptor signaling pathway	BP	1	PJA2,IRAK4,RPS6KA3,BIRC2	pink	VSMC_M5
GO:0071840	0.57	0.46	226	4827	cellular component organization or biogenesis	BP	1	ARFGEF3,VTA1,LATS1,MAPK9,SYNE1,SNX2,SCAF8,SERINC1,LRGUK,DDX17,MKLN1,VPS13A,UBR2,C9orf72,WASL,ANXA1,TMEM33,VEGFA,FRYL,CD2AP,SDHAF3,GCM1,GCLC,DST,RHOQ,LCA5,UGCG,MACF1,VPS54,RAB1A,SEPT7,NFU1,ADAM17,CAPZA2,UFL1,ZMYM4,RAB14,RAB33B,AFG1L,SCLT1,WDCP,BBS12,KIAA1109,SRPK2,TBP,MRE11,POLR2D,MAGI2,YME1L1,AKAP11,DCLRE1C,PDCD6IP,CLASP1,EPB41L5,EMSY,FNTA,ZEB2,FLRT3,XDH,ARL8B,KAT6A,TOP2B,ZDHHC17,NR3C1,SHQ1,MAPK8,MAGI1,DLC1,RB1CC1,VPS37A,CSNK2A1,CAPRIN1,PCM1,YTHDF3,FAT1,TNKS2,VCPIP1,LSM14A,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,EIF4G2,RHOBTB3,DIP2B,GFM2,NFS1,TCTN1,ZFYVE16,ARL13B,FAM92A,ARSB,TBC1D23,TSG101,HIPK1,ARID2,PPP3CC,BAZ2B,BTG2,OPTC,CEP97,CSDE1,TWF1,CYLD,RANBP9,PSMG1,NIPSNAP2,TSPAN32,NDUFS4,ACOT13,NOTCH2,BICD1,KCTD3,ZMYND8,MEF2A,ACACB,GOLGA5,GSK3B,DCLRE1A,PIK3CA,LYST,DNAAF5,BPTF,FXR1,GOLGB1,TFIP11,FAM162A,PARL,PSMC6,ALS2,METTL5,TLK1,PLEKHA1,ZNF148,SCFD1,ABI2,MORC2,ATF7IP,RPS6KA3,GLRX3,SKA1,SRP54,ATF2,MTX2,STYXL1,ST7L,ATM,KDM6A,ARPC2,ERO1A,PRKCI,HP1BP3,ATL3,USP8,CRKL,KAT6B,ZNF518B,GHITM,PYGO1,CCSER2,PDS5A,WAPL,HUWE1,GTF2A2,OPHN1,SNX11,FBXW11,HERC1,MLH3,ABCB7,ATRX,ATP7A,SPATA7,PIAS1,NAP1L3,TTC8,DIAPH2,SMAD2,KATNAL2,PSTPIP2,PIK3C3,DYNC1H1,PTPN9,SMG1,ESCO1,CSNK1A1,WDR78,STAG2,NF1,PRKAA1,PTPRM,CPLANE1,NIPBL,BCORL1,RAD1,HPRT1,SMAD7,PRPF8,SETX,GAN,PKN2,GFOD2,USP33,MT-ND4,MT-ND5,BIRC2,AGO3,UBE2D3,TMEM38B,USP9X,FAM206	pink	VSMC_M5
GO:0008150	0.57	0.49	543	12183	biological_process	BP	1	DGKA,RELCH,MEX3C,DMXL1,ME2,ARFGEF3,VTA1,TAB2,PPIL4,MED23,LATS1,PCMT1,MAPK9,MTHFD1L,SYNE1,PSORS1C2,VPS13B,SNX2,CSNK1G3,SCAF8,UBR5,SFT2D1,KPNA5,SERINC1,EFR3A,SLC25A17,LRGUK,DDX17,MKLN1,KLHDC10,UBE2H,VPS13A,ELAVL2,PCSK5,UBR2,C9orf72,WASL,ANXA1,TMEM33,GUF1,VEGFA,KRIT1,ANKIB1,FRYL,RUNX2,CYP39A1,CD2AP,SDHAF3,ASNS,SRP72,GCM1,GCLC,RNF38,DST,AGMO,PTP4A1,RHOQ,FBXO11,ERLEC1,FAM126A,LCA5,SMAP2,TAX1BP1,RLF,USP34,UGCG,HSDL2,ZNF292,INIP,COMMD1,MACF1,MDH1,VPS54,DPY19L1,RAB1A,SEPT7,NFU1,TIA1,PCYOX1,CPSF3,ADAM17,CAPZA2,UFL1,CUL1,FBXL4,ZMYM4,RAB14,CUL2,RAB33B,ZFYVE9,SLC41A3,AFG1L,SCLT1,PPIL6,OSBPL9,CDC40,HSPA4L,WDCP,JCAD,ARHGAP42,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,TBP,MRE11,PRDM5,ASXL2,SAP130,POLR2D,MAGI2,ACBD5,YME1L1,MED4,MAP3K2,AKAP11,CNOT10,DCLRE1C,PDCD6IP,DGKH,CLASP1,INTS4,EPB41L5,PTPN4,RHEB,KMT2C,FBXL3,EMSY,FNTA,ZEB2,MBD5,FLRT3,EPC2,XDH,ARL8B,KAT6A,OXSM,NGLY1,ENDOV,MEMO1,TOP2B,ZDHHC17,GOLGA7,SLC30A6,NKIRAS1,BIRC6,LTBP1,PSMD8,COG6,EAF1,ZNF605,IRS2,TMTC3,KITLG,PRKD3,SPRY4,NBEA,ATRN,NR3C1,N4BP2L2,MAP4K3,SHQ1,NEDD1,UBA3,MAPK8,APAF1,MAGI1,PCMTD1,DLC1,RB1CC1,IL6ST,VPS37A,GPBP1,CSNK2A1,MSL2,IMPAD1,MTMR6,CAPRIN1,PCM1,IFIT5,YTHDF3,FAT1,TNKS2,VCPIP1,LSM14A,ZMYM5,RPP14,CDK5RAP1,PPWD1,PJA2,SGTB,ARFGEF1,KDM3A,ERBIN,ANAPC10,PTCD3,ZNF507,URI1,SMAD1,EIF4G2,SLC4A8,CGGBP1,NR3C2,KCMF1,LRBA,RHOBTB3,TRPC1,DIP2B,BTBD10,FAR1,GFM2,AQR,NFS1,RNF13,DPH6,PCGF1,VPS29,TCTN1,	pink	VSMC_M5
GO:0060341	0.57	0.50	31	675	regulation of cellular localization	BP	1	LATS1,UBR5,CD2AP,RHOQ,ERLEC1,COMMD1,MAPK8,PCM1,VCPIP1,TRPC1,PPP1CC,TSG101,ATP2B4,BICD1,ANO1,ZMYND8,GSK3B,PARL,SCFD1,HECTD1,PRKCI,CRKL,WAPL,HUWE1,DYNC1H1,PTPN9,PRKAA1,UBE2D3,TMEM38B,RNF139,SAR1B	pink	VSMC_M5
GO:0031623	0.57	0.63	4	85	receptor internalization	BP	1	MKLN1,VEGFA,MAGI2,OPHN1	pink	VSMC_M5
GO:0008016	0.58	0.58	7	144	regulation of heart contraction	BP	1	TRPC1,ATP2B4,MEF2A,GLRX3,SMAD7,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0006006	0.58	0.58	7	155	glucose metabolic process	BP	1	SDHAF3,IRS2,ACACB,GSK3B,PIK3CA,PGM2,PRKAA1	pink	VSMC_M5
GO:0051649	0.58	0.47	78	1679	establishment of localization in cell	BP	1	RELCH,VTA1,SNX2,UBR5,KPNA5,VPS13A,WASL,SRP72,DST,ERLEC1,LCA5,VPS54,RAB1A,RAB14,ZFYVE9,BBS12,KIAA1109,POLR2D,CLASP1,ARL8B,GOLGA7,MAPK8,VPS37A,PCM1,SGTB,ERBIN,SLC4A8,RHOBTB3,TRPC1,VPS29,PPP1CC,ZFYVE16,TBC1D23,TSG101,PPP3CC,SSR1,ATP2B4,ZC3H11A,BICD1,ANO1,IPO8,GSK3B,LYST,ZFAND2A,PARL,ALS2,TLK1,SCFD1,SMG7,SRP54,ACAP2,NEMF,ERO1A,PRKCI,YWHAQ,RPAIN,HUWE1,OPHN1,SNX11,FBXW11,CHM,PIK3C3,APPBP2,DYNC1H1,SMG1,RAB11FIP4,PRKAA1,TRAPPC2L,STXBP3,UBE2D3,ATP5PF,TMEM38B,RAB18,RNF139,TIMM9,RMDN1,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0001959	0.58	0.60	5	119	regulation of cytokine-mediated signaling pathway	BP	1	ADAM17,YTHDF3,LSM14A,HIPK1,CYLD	pink	VSMC_M5
GO:0051168	0.58	0.59	6	131	nuclear export	BP	1	POLR2D,ZC3H11A,GSK3B,SMG7,NEMF,SMG1	pink	VSMC_M5
GO:0010769	0.58	0.62	4	80	regulation of cell morphogenesis involved in differentiation	BP	1	SPRY4,CAPRIN1,ARPC2,CRKL	pink	VSMC_M5
GO:0016054	0.58	0.57	7	186	organic acid catabolic process	BP	1	SLC25A17,IRS2,ATP2B4,ACACB,ACOX3,NUDT7,DDAH1	pink	VSMC_M5
GO:0048588	0.58	0.54	10	195	developmental cell growth	BP	1	MEX3C,C9orf72,VEGFA,MACF1,FLRT3,EIF4G2,DIP2B,GSK3B,SMAD7,USP9X	pink	VSMC_M5

GO:1902531	0.58	0.47	61	1309	regulation of intracellular signal transduction	BP	1	ARFGEF3,TAB2,KLHDC10,UBR2,C9orf72,VEGFA,CD2AP,UFL1,JCAD,ARHGAP42,MAGI2,RHEB,XDH,KAT6A,ZDHHC17,KITLG,SPRY4,DLC1,RB1CC1,IFIT5,PJA2,ARFGEF1,ERBIN,URI1,NR3C2,RNF13,RALGAPB,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,DOCK3,NOTCH2,SHOC2,GSK3B,PUM1,PIK3CA,UBR1,STK39,TIAL1,ALS2,PLEKHA1,ARHGAP5,STYXL1,RALGPS2,SOS2,ATM,CRKL,OPHN1,ASH1L,FEM1B,XIAP,NF1,PRKAA1,NFAT5,BIRC2,AGO3,BMT2,BMP2	pink	VSMC_M5
GO:0051223	0.58	0.51	18	412	regulation of protein transport	BP	1	UBR5,ANXA1,CD2AP,ERLEC1,IRS2,MAPK8,PCM1,TSG101,ANO1,GSK3B,PARL,SCFD1,HUWE1,PIK3C3,PRKAA1,UBE2D3,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0043409	0.59	0.58	6	131	negative regulation of MAPK cascade	BP	1	SPRY4,CYLD,RANBP9,ASH1L,NF1,BMP2	pink	VSMC_M5
GO:0140013	0.59	0.58	6	139	meiotic nuclear division	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3,RAD1	pink	VSMC_M5
GO:0045787	0.59	0.54	11	243	positive regulation of cell cycle	BP	1	ANXA1,ASNS,ADAM17,SRPK2,CDK5RAP1,ZBED9,DYNLT3,ATRX,CCNK,DYNC1H1,PKN2	pink	VSMC_M5
GO:2000377	0.59	0.59	5	120	regulation of reactive oxygen species metabolic process	BP	1	XDH,PARL,ABCB7,MT-CO2,BIRC2	pink	VSMC_M5
GO:0071333	0.59	0.59	5	110	cellular response to glucose stimulus	BP	1	GCLC,IRS2,ANO1,PIK3CA,PRKAA1	pink	VSMC_M5
GO:0050684	0.59	0.59	5	118	regulation of mRNA processing	BP	1	DDX17,TIA1,SRPK2,VIRMA,FXR1	pink	VSMC_M5
GO:0007017	0.59	0.48	34	715	microtubule-based process	BP	1	LRGUK,VPS13A,DST,LCA5,MACF1,RAB1A,BBS12,PDCD6IP,CLASP1,ARL8B,MEMO1,PCM1,LSM14A,ATP2B4,CEP97,CYLD,RANBP9,BICD1,GSK3B,DNAAF5,SKA1,DYNLT3,CCSER2,FBXW11,ASH1L,ATRX,SPATA7,KATNAL2,DYNC1H1,WDR78,STAG2,PRKAA1,USP33,RMDN1	pink	VSMC_M5
GO:0007219	0.59	0.57	6	138	Notch signaling pathway	BP	1	ADAM17,IL6ST,NOTCH2,DLX2,PRKCI,BMP2	pink	VSMC_M5
GO:0008283	0.59	0.46	64	1442	cell population proliferation	BP	1	ANXA1,VEGFA,KRIT1,RUNX2,ADAM17,UFL1,CUL1,JCAD,SRPK2,MRE11,MAGI2,YME1L1,XDH,BIRC6,IRS2,KITLG,N4BP2L2,DLC1,IL6ST,CSNK2A1,PCM1,SMAD1,BTBD10,PPP1CC,TSG101,HIPK1,ARID2,BTG2,SSR1,IRAK4,BTRC,PSMG1,TSPAN32,NDUFS4,NOTCH2,GOLGB1,ZBED9,TIAL1,ATF2,SOS2,ATM,PRKCI,COPS2,HP1BP3,TIMP1,CRKL,WAPL,ATP7A,PIAS1,SMAD2,GGNBP2,UBE2A,XIAP,NF1,PRKAA1,PTPRM,HPRT1,SMAD7,BIRC2,AGO3,CD164,RNF139,DDAH1,BMP2	pink	VSMC_M5
GO:0001764	0.60	0.57	6	113	neuron migration	BP	1	VEGFA,TOP2B,PCM1,CRKL,NIPBL,USP9X	pink	VSMC_M5
GO:0070201	0.60	0.50	19	436	regulation of establishment of protein localization	BP	1	UBR5,ANXA1,CD2AP,ERLEC1,EPB41L5,IRS2,MAPK8,PCM1,TSG101,ANO1,GSK3B,PARL,SCFD1,HUWE1,PIK3C3,PRKAA1,UBE2D3,GOLPH3L,SAR1B	pink	VSMC_M5
GO:0009725	0.60	0.48	30	652	response to hormone	BP	1	LATS1,UBR5,DDX17,ANXA1,ASNS,GCLC,RHOQ,UGCG,UFL1,NCOA1,MBD5,IRS2,NR3C1,KDM3A,URI1,NR3C2,ARSB,GTF2H1,BTG2,SNRPN,CAB39,GSK3B,PIK3CA,PRKCI,USP8,TIMP1,PRKAA1,STXBP3,MT-ND3,CACYBP	pink	VSMC_M5
GO:0003007	0.60	0.53	10	197	heart morphogenesis	BP	1	VEGFA,DLC1,ARL13B,ARID2,NOTCH2,ATF2,CRKL,NIPBL,SMAD7,BMP2	pink	VSMC_M5
GO:0032392	0.60	0.60	4	80	DNA geometric change	BP	1	ANXA1,MRE11,ATRX,SETX	pink	VSMC_M5
GO:0043280	0.60	0.60	4	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	XDH,APAF1,DLC1,FAM162A	pink	VSMC_M5
GO:0050679	0.60	0.56	7	154	positive regulation of epithelial cell proliferation	BP	1	VEGFA,ADAM17,JCAD,NOTCH2,ZBED9,ATP7A,BMP2	pink	VSMC_M5
GO:0050680	0.60	0.58	5	108	negative regulation of epithelial cell proliferation	BP	1	KRIT1,XDH,ATF2,NF1,PTPRM	pink	VSMC_M5
GO:0009966	0.60	0.45	104	2237	regulation of signal transduction	BP	1	ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBR2,C9orf72,TMEM33,VEGFA,RUNX2,CD2AP,GCLC,USP34,UGCG,MACF1,ADAM17,UFL1,JCAD,ARHGAP42,NCOA1,ASXL2,MAGI2,RHEB,ZEB2,MBD5,XDH,KAT6A,ZDHHC17,BIRC6,LTBP1,KITLG,SPRY4,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,URI1,NR3C2,RNF13,TCTN1,RALGAPB,FAM92A,TSG101,HIPK1,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,DOCK3,NOTCH2,BICD1,ZMYND8,SHOC2,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,STK39,TIAL1,ALS2,PLEKHA1,DLX2,ARHGAP5,HERC4,STYXL1,RALGPS2,SOS2,ATM,PRKCI,USP8,TIMP1,CRKL,WNK1,GHITM,OPHN1,ASH1L,FEM1B,SMAD2,GSKIP,GGNBP2,CSNK1A1,XIAP,NF1,PRKAA1,SMAD7,NFAT5,USP33,BIRC2,AGO3,UBE2D3,BMT2,BMP2	pink	VSMC_M5
GO:0008284	0.60	0.48	30	681	positive regulation of cell population proliferation	BP	1	ANXA1,VEGFA,RUNX2,ADAM17,UFL1,JCAD,SRPK2,BIRC6,IRS2,KITLG,N4BP2L2,IL6ST,CSNK2A1,PPP1CC,HIPK1,SSR1,IRAK4,NDUFS4,NOTCH2,ZBED9,TIAL1,ATF2,PRKCI,TIMP1,CRKL,WAPL,ATP7A,UBE2A,PRKAA1,BMP2	pink	VSMC_M5
GO:0051236	0.60	0.57	6	138	establishment of RNA localization	BP	1	POLR2D,ZC3H11A,SMG7,ATM,SMG1,EIF5A2	pink	VSMC_M5
GO:0019318	0.60	0.54	8	185	hexose metabolic process	BP	1	SDHAF3,IRS2,ACACB,GSK3B,PIK3CA,FUT8,PGM2,PRKAA1	pink	VSMC_M5
GO:0031123	0.60	0.60	4	94	RNA 3'-end processing	BP	1	SCAF8,CPSF3,POLR2D,VIRMA	pink	VSMC_M5
GO:0010243	0.60	0.47	36	793	response to organonitrogen compound	BP	1	UBR2,ANXA1,ASNS,GCLC,RHOQ,ERLEC1,UFL1,MBD5,NGLY1,IRS2,SGTB,ERBIN,GABPA,BTG2,ATP2B4,NDUFS4,ANO1,GSK3B,PIK3CA,UBR1,PSMC6,PRKCI,TIMP1,CPEB4,ATP7A,PIK3C3,USP14,PRKAA1,HPRT1,STXBP3,MT-ND5,BIRC2,TMEM38B,RNF103,CACYBP,RNF139	pink	VSMC_M5
GO:0046390	0.60	0.56	6	156	ribose phosphate biosynthetic process	BP	1	ACACB,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0042180	0.60	0.56	6	150	cellular ketone metabolic process	BP	1	ANXA1,IRS2,ATP2B4,ACACB,SULT1C4,BMP2	pink	VSMC_M5
GO:0120036	0.60	0.45	59	1193	plasma membrane bounded cell projection organization	BP	1	SNX2,LRGUK,C9orf72,WASL,VEGFA,FRYL,CD2AP,RHOQ,LCA5,MACF1,SEPT7,SCLT1,BBS12,MAGI2,FLRT3,TOP2B,ZDHHC17,CAPRIN1,PCM1,ARFGEF1,EIF4G2,DIP2B,TCTN1,ARL13B,FAM92A,ARSB,TBC1D23,BTG2,CEP97,TWF1,CYLD,NOTCH2,ZMYND8,MEF2A,GSK3B,PIK3CA,DNAAF5,FXR1,ALS2,PLEKHA1,ABI2,STYXL1,ARPC2,PRKCI,CRKL,OPHN1,HERC1,ATP7A,TTC8,PTPN9,WDR78,PTPRM,CPLANE1,HPRT1,SETX,USP33,USP9X,FAM206A,UBE2V2	pink	VSMC_M5
GO:0071331	0.60	0.58	5	112	cellular response to hexose stimulus	BP	1	GCLC,IRS2,ANO1,PIK3CA,PRKAA1	pink	VSMC_M5
GO:0034097	0.60	0.47	28	659	response to cytokine	BP	1	ANXA1,GCLC,UGCG,ADAM17,PRDM5,SPRY4,MAP4K3,IL6ST,YTHDF3,LSM14A,KDM3A,ERBIN,HIPK1,IRAK4,CYLD,GSK3B,STK39,PRKCI,TIMP1,CRKL,WNK1,SMAD7,PRPF8,STXBP3,NFAT5,BIRC2,CACYBP,UBXN2A	pink	VSMC_M5

GO:0042594	0.60	0.55	7	158	response to starvation	BP	1	ASNS,MAPK8,CPEB4,PIK3C3,PRKAA1,USP33,BMT2	pink	VSMC_M5
GO:0007498	0.61	0.59	4	89	mesoderm development	BP	1	VEGFA,EPB41L5,SMAD1,SMAD2	pink	VSMC_M5
GO:0042326	0.61	0.50	14	311	negative regulation of phosphorylation	BP	1	LATS1,C9orf72,XDH,IRS2,SPRY4,CDK5RAP1,TSG101,CRKL,WNK1,GSKIP,GGNBP2,NF1,SMAD7,BMP2	pink	VSMC_M5
GO:0048667	0.61	0.48	23	446	cell morphogenesis involved in neuron differentiation	BP	1	C9orf72,WASL,VEGFA,MACF1,FLRT3,TOP2B,ZDHHC17,CAPRIN1,EIF4G2,DIP2B,TCTN1,NOTCH2,MEF2A,GSK3B,ALS2,ABI2,OPHN1,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5
GO:0051047	0.61	0.53	9	211	positive regulation of secretion	BP	1	CD2AP,PDCD6IP,CLASP1,IRS2,SLC4A8,TSG101,ANO1,GOLPH3L,BMP2	pink	VSMC_M5
GO:0042127	0.61	0.45	54	1230	regulation of cell population proliferation	BP	1	ANXA1,VEGFA,KRIT1,RUNX2,ADAM17,UFL1,JCAD,SRPK2,MAGI2,XDH,BIRC6,IRS2,KITLG,N4BP2L2,DLC1,IL6ST,CSNK2A1,SMAD1,PPP1CC,TSG101,HIPK1,ARID2,BTG2,SSR1,IRAK4,TSPAN32,NDUFS4,NOTCH2,ZBED9,TIAL1,ATF2,SOS2,ATM,PRKCI,HP1BP3,TIMP1,CRKL,WAPL,ATP7A,PIAS1,SMAD2,GGNBP2,UBE2A,XIAP,NF1,PRKAA1,PTPRM,SMAD7,BIRC2,AGO3,CD164,RNF139,DDAH1,BMP2	pink	VSMC_M5
GO:1901890	0.61	0.59	4	82	positive regulation of cell junction assembly	BP	1	VEGFA,EPB41L5,FLRT3,UBE2V2	pink	VSMC_M5
GO:0071326	0.61	0.57	5	113	cellular response to monosaccharide stimulus	BP	1	GCLC,IRS2,ANO1,PIK3CA,PRKAA1	pink	VSMC_M5
GO:0030029	0.61	0.46	33	662	actin filament-based process	BP	1	ARFGEF3,LATS1,MKLN1,C9orf72,WASL,ANXA1,CD2AP,RHOQ,CAPZA2,AKAP11,PDCD6IP,CLASP1,EPB41L5,DLC1,FAT1,ARFGEF1,RHOBTB3,TWF1,NOTCH2,MEF2A,PIK3CA,ABI2,ACAP2,ARPC2,PRKCI,OPHN1,TTC8,DIAPH2,PSTPIP2,NF1,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:1903531	0.61	0.59	4	99	negative regulation of secretion by cell	BP	1	ANXA1,RAB33B,STXBP3,ATP5PF	pink	VSMC_M5
GO:0002009	0.61	0.48	20	412	morphogenesis of an epithelium	BP	1	MTHFD1L,VEGFA,GCM1,ADAM17,MAGI2,CLASP1,EPB41L5,FLRT3,DLC1,FAT1,TCTN1,ARL13B,BTRC,NOTCH2,HECTD1,OPHN1,ATP7A,FEM1B,TTC8,BMP2	pink	VSMC_M5
GO:0040013	0.61	0.50	12	261	negative regulation of locomotion	BP	1	WASL,KRIT1,MAGI2,CLASP1,DLC1,ARID2,ATP2B4,ZMYND8,TIMP1,NF1,PTPRM,SMAD7	pink	VSMC_M5
GO:0060047	0.62	0.53	8	172	heart contraction	BP	1	TRPC1,ATP2B4,MEF2A,PIK3CA,GLRX3,SMAD7,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0030030	0.62	0.44	60	1226	cell projection organization	BP	1	SNX2,LRGUK,C9orf72,WASL,VEGFA,FRYL,CD2AP,RHOQ,LCA5,MACF1,SEPT7,SCLT1,BBS12,MAGI2,FLRT3,TOP2B,ZDHHC17,CAPRIN1,PCM1,ARFGEF1,EIF4G2,DIP2B,TCTN1,ARL13B,FAM92A,ARSB,TBC1D23,BTG2,CEP97,TWF1,CYLD,NOTCH2,ZMYND8,MEF2A,GSK3B,PIK3CA,DNAAF5,FXR1,ALS2,PLEKHA1,ABI2,STYXL1,ARPC2,PRKCI,CRKL,OPHN1,HERC1,ATP7A,TTC8,PTPN9,WDR78,PTPRM,CPLANE1,HPRT1,SETX,PKN2,USP33,USP9X,FAM206A,UBE2V2	pink	VSMC_M5
GO:0051051	0.62	0.49	13	314	negative regulation of transport	BP	1	ANXA1,ERLEC1,COMMD1,RAB33B,IRS2,PIP4P2,CAB39,STK39,YWHAQ,WNK1,ATP7A,STXBP3,ATP5PF	pink	VSMC_M5
GO:0022411	0.62	0.48	18	375	cellular component disassembly	BP	1	VTA1,SCAF8,CAPZA2,UFL1,CLASP1,RB1CC1,GFM2,TSG101,ARID2,TWF1,GSK3B,PIK3CA,TFIP11,HUWE1,SETX,MTPN,EIF5A2,DENR	pink	VSMC_M5
GO:0006909	0.62	0.53	7	163	phagocytosis	BP	1	ANXA1,RAB14,KIAA1109,ARL8B,PIP4P2,PIK3CA,LYST	pink	VSMC_M5
GO:0060560	0.62	0.50	10	200	developmental growth involved in morphogenesis	BP	1	C9orf72,VEGFA,MACF1,MAGI2,EPB41L5,FLRT3,EIF4G2,DIP2B,GSK3B,USP9X	pink	VSMC_M5
GO:0048736	0.62	0.53	7	140	appendage development	BP	1	PCSK5,RUNX2,IMPAD1,FAM92A,NOTCH2,ATRX,NIPBL	pink	VSMC_M5
GO:0060173	0.62	0.53	7	140	limb development	BP	1	PCSK5,RUNX2,IMPAD1,FAM92A,NOTCH2,ATRX,NIPBL	pink	VSMC_M5
GO:0051321	0.62	0.52	8	192	meiotic cell cycle	BP	1	UBR2,MRE11,TOP2B,ATM,MLH3,ATRX,STAG2,RAD1	pink	VSMC_M5
GO:0006260	0.62	0.50	10	230	DNA replication	BP	1	SRPK2,MRE11,POLK,RPAIN,PDS5A,WAPL,ATRX,ESCO1,CACYBP,RNF219	pink	VSMC_M5
GO:1905477	0.63	0.57	4	88	positive regulation of protein localization to membrane	BP	1	MAPK8,ATP2B4,PRKCI,PTPN9	pink	VSMC_M5
GO:0031175	0.63	0.44	39	784	neuron projection development	BP	1	C9orf72,WASL,VEGFA,FRYL,MACF1,MAGI2,FLRT3,TOP2B,ZDHHC17,CAPRIN1,ARFGEF1,EIF4G2,DIP2B,TCTN1,ARSB,TBC1D23,BTG2,TWF1,NOTCH2,ZMYND8,MEF2A,GSK3B,ALS2,ABI2,STYXL1,PRKCI,CRKL,OPHN1,HERC1,ATP7A,TTC8,PTPN9,PTPRM,HPRT1,SETX,USP33,USP9X,FAM206A,UBE2V2	pink	VSMC_M5
GO:0016358	0.63	0.50	10	204	dendrite development	BP	1	WASL,CAPRIN1,EIF4G2,ZMYND8,MEF2A,GSK3B,ABI2,CRKL,HPRT1,FAM206A	pink	VSMC_M5
GO:0062013	0.63	0.57	4	96	positive regulation of small molecule metabolic process	BP	1	ANXA1,IRS2,PRKAA1,MT-CO2	pink	VSMC_M5
GO:0001558	0.63	0.47	15	339	regulation of cell growth	BP	1	VEGFA,MACF1,ADAM17,KIAA1109,CSNK2A1,URI1,EIF4G2,DIP2B,TSG101,GSK3B,RPS6KA3,ST7L,CRKL,SMAD7,MTPN	pink	VSMC_M5
GO:0006913	0.63	0.49	11	257	nucleocytoplasmic transport	BP	1	UBR5,KPNA5,POLR2D,PPP1CC,ZC3H11A,IPO8,GSK3B,SMG7,NEMF,RPAIN,SMG1	pink	VSMC_M5
GO:0051169	0.63	0.49	11	257	nuclear transport	BP	1	UBR5,KPNA5,POLR2D,PPP1CC,ZC3H11A,IPO8,GSK3B,SMG7,NEMF,RPAIN,SMG1	pink	VSMC_M5
GO:0090090	0.63	0.55	5	113	negative regulation of canonical Wnt signaling pathway	BP	1	LATS1,CYLD,GSK3B,CSNK1A1,BMP2	pink	VSMC_M5
GO:0042476	0.63	0.57	4	95	odontogenesis	BP	1	RUNX2,DLX2,ATF2,BMP2	pink	VSMC_M5
GO:0030098	0.63	0.49	11	259	lymphocyte differentiation	BP	1	ANXA1,RUNX2,ADAM17,DCLRE1C,NOTCH2,HECTD1,ATF2,SOS2,ATM,ATP7A,SMAD7	pink	VSMC_M5
GO:0035265	0.63	0.53	6	134	organ growth	BP	1	LATS1,SMAD1,ARID2,ACACB,SMAD2,TMEM38B	pink	VSMC_M5
GO:0031669	0.63	0.51	8	182	cellular response to nutrient levels	BP	1	ASNS,NCOA1,MAPK8,CPEB4,PIK3C3,PRKAA1,USP33,BMT2	pink	VSMC_M5
GO:0050767	0.63	0.48	14	285	regulation of neurogenesis	BP	1	VEGFA,MACF1,UFL1,RHEB,IL6ST,CAPRIN1,PCM1,EIF4G2,DIP2B,PPP1CC,DLX2,PRKCI,NF1,BMP2	pink	VSMC_M5
GO:0050673	0.63	0.47	14	316	epithelial cell proliferation	BP	1	VEGFA,KRIT1,ADAM17,JCAD,XDH,BTBD10,BTRC,NOTCH2,ZBED9,ATF2,ATP7A,NF1,PTPRM,BMP2	pink	VSMC_M5
GO:0097435	0.63	0.44	30	622	supramolecular fiber organization	BP	1	LATS1,C9orf72,WASL,CD2AP,DST,CAPZA2,CLASP1,DLC1,PCM1,FAT1,ARFGEF1,RHOBTB3,OPTC,TWF1,RANBP9,MEF2A,PIK3CA,ABI2,ARPC2,PRKCI,ATP7A,TTC8,DIAPH2,PSTPIP2,DYNC1H1,NF1,USP9X,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0070663	0.63	0.53	6	153	regulation of leukocyte proliferation	BP	1	ANXA1,IRS2,KITLG,IL6ST,SOS2,ATM	pink	VSMC_M5
GO:0030183	0.64	0.56	4	96	B cell differentiation	BP	1	ADAM17,DCLRE1C,NOTCH2,ATM	pink	VSMC_M5

GO:0072593	0.64	0.51	7	176	reactive oxygen species metabolic process	BP	1	XDH,NDUFS4,PARL,ABCB7,ATP7A,MT-CO2,BIRC2	pink	VSMC_M5
GO:0006629	0.64	0.42	40	982	lipid metabolic process	BP	1	DGKA,SERINC1,EFR3A,SLC25A17,ANXA1,CYP39A1,AGMO,FAM126A,UGCG,OSBPL9,DGKH,OXSM,IRS2,PRKD3,IMPAD1,MTMR6,FAR1,TIPARP,PIP4P2,PIGP,PRKAB2,ACACB,PIK3CA,PLEKHA1,MORC2,PAFAH1B2,CREBL2,ATF2,ATM,ACOX3,CRKL,SPTLC2,PIK3C3,SMG1,PRKAA1,CEPT1,NUDT7,HACD1,TMEM38B,BMP2	pink	VSMC_M5
GO:0035725	0.64	0.52	6	120	sodium ion transmembrane transport	BP	1	COMMD1,SLC4A8,ATP2B4,SCN9A,STK39,WNK1	pink	VSMC_M5
GO:0007173	0.64	0.56	4	90	epidermal growth factor receptor signaling pathway	BP	1	ADAM17,ERBIN,TSG101,PIK3CA	pink	VSMC_M5
GO:0007249	0.64	0.49	9	222	I-kappaB kinase/NF-kappaB signaling	BP	1	TAB2,UFL1,ZDHHC17,NKIRAS1,IFIT5,IRAK4,BTRC,ASH1L,BIRC2	pink	VSMC_M5
GO:0032273	0.64	0.53	5	116	positive regulation of protein polymerization	BP	1	WASL,CLASP1,ABI2,ARPC2,GMFB	pink	VSMC_M5
GO:0051648	0.64	0.51	7	154	vesicle localization	BP	1	WASL,RAB1A,CLASP1,TBC1D23,FBXW11,DYNC1H1,SAR1B	pink	VSMC_M5
GO:0061025	0.64	0.53	5	125	membrane fusion	BP	1	ANXA1,ARL8B,VCPIP1,HUWE1,UBXN2A	pink	VSMC_M5
GO:0043122	0.65	0.49	8	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	TAB2,UFL1,ZDHHC17,IFIT5,IRAK4,BTRC,ASH1L,BIRC2	pink	VSMC_M5
GO:0060759	0.65	0.53	5	128	regulation of response to cytokine stimulus	BP	1	ADAM17,YTHDF3,LSM14A,HIPK1,CYLD	pink	VSMC_M5
GO:0001933	0.65	0.47	12	276	negative regulation of protein phosphorylation	BP	1	LATS1,C9orf72,XDH,SPRY4,CDK5RAP1,TSG101,CRKL,GSKIP,GGNBP2,NF1,SMAD7,BMP2	pink	VSMC_M5
GO:0046660	0.65	0.55	4	88	female sex differentiation	BP	1	VEGFA,KITLG,TIPARP,PLEKHA1	pink	VSMC_M5
GO:1903522	0.65	0.49	8	179	regulation of blood circulation	BP	1	ARHGAP42,TRPC1,ATP2B4,MEF2A,GLRX3,SMAD7,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0070555	0.65	0.55	4	98	response to interleukin-1	BP	1	ANXA1,GCLC,IRAK4,PRKCI	pink	VSMC_M5
GO:0000226	0.65	0.43	24	522	microtubule cytoskeleton organization	BP	1	LRGUK,DST,PDCD6IP,CLASP1,PCM1,LSM14A,CEP97,CYLD,RANBP9,BICD1,GSK3B,DNAAF5,SKA1,CCSER2,FBXW11,ATRX,SPATA7,KATNAL2,DYNC1H1,WDR78,STAG2,PRKAA1,USP33,RMDN1	pink	VSMC_M5
GO:1905952	0.65	0.52	5	118	regulation of lipid localization	BP	1	ASXL2,IRS2,DENND5B,ACACB,ATP5PF	pink	VSMC_M5
GO:0021987	0.65	0.54	4	87	cerebral cortex development	BP	1	NCOA1,GSK3B,CRKL,NF1	pink	VSMC_M5
GO:0010634	0.65	0.51	6	143	positive regulation of epithelial cell migration	BP	1	ANXA1,VEGFA,ADAM17,JCAD,CLASP1,EPB41L5	pink	VSMC_M5
GO:0007051	0.65	0.49	7	165	spindle organization	BP	1	CLASP1,LSM14A,CEP97,ATRX,DYNC1H1,STAG2,RMDN1	pink	VSMC_M5
GO:0046631	0.66	0.54	4	97	alpha-beta T cell activation	BP	1	ANXA1,ATF2,ATP7A,SMAD7	pink	VSMC_M5
GO:2001233	0.66	0.46	11	292	regulation of apoptotic signaling pathway	BP	1	MAPK9,GCLC,BIRC6,RB1CC1,CSNK2A1,URI1,CYLD,GSK3B,STYXL1,GHITM,FEM1B	pink	VSMC_M5
GO:0048870	0.66	0.40	59	1234	cell motility	BP	1	VPS13A,WASL,ANXA1,VEGFA,KRIT1,CD2AP,DST,PTP4A1,RHOQ,MACF1,RAB1A,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,ZEB2,FLRT3,TOP2B,IRS2,KITLG,ATRN,DLC1,PCM1,YTHDF3,FAT1,RHOBTB3,CPNE3,ARL13B,ARSB,ARID2,ATP2B4,IRAK4,ZMYND8,FSTL1,PIK3CA,LYST,STK39,ABI2,SRP54,ATM,ARPC2,PRKCI,TIMP1,CRKL,WNK1,FUT8,OPHN1,ASH1L,ATP7A,PSTPIP2,NF1,PTPRM,NIPBL,SMAD7,PKN2,USP33,USP9X,BMP2	pink	VSMC_M5
GO:0051674	0.66	0.40	59	1234	localization of cell	BP	1	VPS13A,WASL,ANXA1,VEGFA,KRIT1,CD2AP,DST,PTP4A1,RHOQ,MACF1,RAB1A,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,ZEB2,FLRT3,TOP2B,IRS2,KITLG,ATRN,DLC1,PCM1,YTHDF3,FAT1,RHOBTB3,CPNE3,ARL13B,ARSB,ARID2,ATP2B4,IRAK4,ZMYND8,FSTL1,PIK3CA,LYST,STK39,ABI2,SRP54,ATM,ARPC2,PRKCI,TIMP1,CRKL,WNK1,FUT8,OPHN1,ASH1L,ATP7A,PSTPIP2,NF1,PTPRM,NIPBL,SMAD7,PKN2,USP33,USP9X,BMP2	pink	VSMC_M5
GO:0007409	0.66	0.44	17	341	axonogenesis	BP	1	C9orf72,VEGFA,MACF1,FLRT3,TOP2B,ZDHHC17,EIF4G2,DIP2B,TCTN1,NOTCH2,GSK3B,ALS2,OPHN1,TTC8,PTPRM,USP33,USP9X	pink	VSMC_M5
GO:0045860	0.66	0.45	13	305	positive regulation of protein kinase activity	BP	1	TAB2,VEGFA,ADAM17,KITLG,CDK5RAP1,ATP2B4,DOCK3,CAB39,PIK3CA,ALS2,WNK1,CCNK,BMP2	pink	VSMC_M5
GO:0051179	0.66	0.37	210	4586	localization	BP	1	RELCH,VTA1,LATS1,MAPK9,SYNE1,VPS13B,SNX2,CSNK1G3,UBR5,SFT2D1,KPNA5,EFR3A,SLC25A17,MKLN1,VPS13A,PCSK5,C9orf72,WASL,ANXA1,VEGFA,KRIT1,CD2AP,SRP72,GCLC,DST,PTP4A1,RHOQ,ERLEC1,FAM126A,LCA5,UGCG,COMMD1,MACF1,VPS54,RAB1A,SEPT7,TIA1,PCYOX1,ADAM17,UFL1,RAB14,RAB33B,ZFYVE9,SLC41A3,OSBPL9,JCAD,BBS12,KIAA1109,NCOA1,ASXL2,POLR2D,MAGI2,AKAP11,PDCD6IP,CLASP1,EPB41L5,FNTA,ZEB2,FLRT3,XDH,ARL8B,TOP2B,ZDHHC17,GOLGA7,SLC30A6,LTBP1,COG6,IRS2,KITLG,NBEA,ATRN,SHQ1,NEDD1,MAPK8,DLC1,VPS37A,MTMR6,PCM1,YTHDF3,FAT1,TNKS2,VCPIP1,SGTB,ARFGEF1,ERBIN,SLC4A8,LRBA,RHOBTB3,TRPC1,VPS29,TCTN1,PPP1CC,WWP1,ZFYVE16,CPNE3,ANTXR2,ARL13B,PIP4P2,ARSB,TBC1D23,TSG101,UEVLD,ARID2,PPP3CC,SSR1,ATP2B4,ZC3H11A,TWF1,IRAK4,NIPSNAP2,TSPAN32,BICD1,ANO1,DENND5B,CAB39,ZMYND8,IPO8,MEF2A,ACACB,GOLGA5,GSK3B,FSTL1,PIK3CA,LYST,SCN9A,GOLGB1,STK39,ZFAND2A,PARL,CCDC14,ALS2,TLK1,PLEKHA1,SCFD1,ABI2,HECTD1,CREBL2,SMG7,SRP54,ATF2,MTX2,ACAP2,ODR4,NEMF,ATM,CUL5,ARPC2,ERO1A,PRKCI,YWHAQ,USP8,TIMP1,CRKL,CCZ1B,RPAIN,WNK1,PYGO1,WAPL,FUT8,HUWE1,OPHN1,SFXN1,SNX11,FBXW11,ASH1L,MLH3,ABCB7,ATRX,ATP7A,SPATA7,CHM,TTC8,SMAD2,PSTPIP2,PIK3C3,APPBP2,DYNC1H1,PTPN9,SMG1,RAB11FIP4,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,TRAPPC2L,STXBP3,SLC35A3,PKN2,USP33,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ARRDC5,UBE2D3,ATP5PF,TMEM38B,USP9X,RAB18,EIF5A2,NAF1,SLC25A36,RNF139,GOLPH3L,TIMM9,BMP2,RMDN1,SAR1B,ZDHHC22	pink	VSMC_M5
GO:1901605	0.66	0.51	5	146	alpha-amino acid metabolic process	BP	1	ASNS,GCLC,ATP2B4,ATP7A,DDAH1	pink	VSMC_M5
GO:0001841	0.66	0.53	4	92	neural tube formation	BP	1	MTHFD1L,DLC1,TCTN1,HECTD1	pink	VSMC_M5
GO:2001056	0.66	0.53	4	105	positive regulation of cysteine-type endopeptidase activity	BP	1	XDH,APAF1,DLC1,FAM162A	pink	VSMC_M5
GO:0071322	0.66	0.51	5	121	cellular response to carbohydrate stimulus	BP	1	GCLC,IRS2,ANO1,PIK3CA,PRKAA1	pink	VSMC_M5
GO:0007626	0.66	0.49	6	132	locomotory behavior	BP	1	VPS13A,PUM1,ALS2,ATP7A,HPRT1,NMS	pink	VSMC_M5
GO:0060429	0.67	0.40	38	810	epithelium development	BP	1	LATS1,MTHFD1L,ANXA1,VEGFA,GCM1,UGCG,ADAM17,KIAA1109,MAGI2,CLASP1,EPB41L5,RHEB,FLRT3,XDH,DLC1,IL6ST,FAT1,SMAD1,TCTN1,ARL13B,TSG101,ESRP1,BTRC,NOTCH2,GSK3B,FSTL1,ABI2,HECTD1,OPHN1,YIPF6,ATRX,ATP7A,FEM1B,TTC8,SMAD2,SMAD7,TMEM38B,BMP2	pink	VSMC_M5

GO:2001234	0.67	0.48	7	187	negative regulation of apoptotic signaling pathway	BP	1	GCLC,BIRC6,RB1CC1,CSNK2A1,URI1,GSK3B,GHITM	pink	VSMC_M5
GO:0007389	0.67	0.43	15	329	pattern specification process	BP	1	PCSK5,EPB41L5,SMAD1,TCTN1,ARL13B,HIPK1,BTG2,NOTCH2,BPTF,DLX2,RNF2,CRKL,TTC8,SMAD2,BMP2	pink	VSMC_M5
GO:0050776	0.67	0.41	22	538	regulation of immune response	BP	1	MAPK9,ANXA1,MAPK8,IL6ST,YTHDF3,LSM14A,PJA2,ERBIN,IRAK4,CYLD,TSPAN32,KMT5B,PUM1,PIK3CA,PLEKHA1,RPS6KA3,CRKL,WNK1,XIAP,SMAD7,BIRC2,ELMOD2	pink	VSMC_M5
GO:0051046	0.67	0.42	18	434	regulation of secretion	BP	1	ANXA1,CD2AP,RAB33B,PDCD6IP,CLASP1,IRS2,SLC4A8,TSG101,ANO1,GSK3B,STK39,WNK1,PIK3C3,PRKAA1,STXBP3,ATP5PF,GOLPH3L,BMP2	pink	VSMC_M5
GO:0010906	0.67	0.52	4	96	regulation of glucose metabolic process	BP	1	SDHAF3,IRS2,ACACB,GSK3B	pink	VSMC_M5
GO:0050678	0.67	0.44	12	275	regulation of epithelial cell proliferation	BP	1	VEGFA,KRIT1,ADAM17,JCAD,XDH,NOTCH2,ZBED9,ATF2,ATP7A,NF1,PTPRM,BMP2	pink	VSMC_M5
GO:0048699	0.67	0.38	58	1177	generation of neurons	BP	1	C9orf72,WASL,VEGFA,FRYL,RUNX2,UGCG,MACF1,UFL1,SCLT1,NCOA1,MAGI2,RHEB,FLRT3,TOP2B,ZDHHC17,IL6ST,CAPRIN1,PCM1,CDK5RAP1,ARFGEF1,EIF4G2,DIP2B,TCTN1,PPP1CC,ARSB,TBC1D23,HIPK1,ESRP1,BTG2,TWF1,NOTCH2,ZMYND8,MEF2A,GSK3B,ALS2,ABI2,DLX2,STYXL1,PRKCI,COPS2,CRKL,WNK1,OPHN1,HERC1,ATP7A,TTC8,PTPN9,NF1,PTPRM,NIPBL,HPRT1,SETX,USP33,USP9X,FAM206A,UBE2V2,MTPN,BMP2	pink	VSMC_M5
GO:1902903	0.67	0.43	15	327	regulation of supramolecular fiber organization	BP	1	LATS1,C9orf72,WASL,CAPZA2,CLASP1,DLC1,ARFGEF1,TWF1,PIK3CA,ABI2,ARPC2,TTC8,FAM206A,GMFB,MTPN	pink	VSMC_M5
GO:0050790	0.67	0.37	81	1823	regulation of catalytic activity	BP	1	ARFGEF3,TAB2,LATS1,SERINC1,PCSK5,C9orf72,WASL,ANXA1,VEGFA,KRIT1,SMAP2,ADAM17,ARHGAP42,MRE11,MAGI2,FNTA,ZEB2,XDH,BIRC6,IRS2,KITLG,SPRY4,MAPK8,APAF1,DLC1,CSNK2A1,CDK5RAP1,ARFGEF1,URI1,RALGAPB,LXN,GTF2H1,TSG101,DNMBP,ATP2B4,BTRC,DOCK3,BICD1,DENND5B,CAB39,PPP6R3,SHOC2,PRKAB2,ACACB,GSK3B,PIK3CA,DCUN1D1,TFIP11,EGLN1,FAM162A,ALS2,ARHGAP5,RPS6KA3,ACAP2,STYXL1,RALGPS2,SOS2,TIMP1,CRKL,WNK1,OPHN1,UBE2Z,HERC1,ATP7A,CHM,FEM1B,TTC8,GSKIP,CCNK,GGNBP2,USP14,XIAP,NF1,SMAD7,BIRC2,GMFB,NAF1,ELMOD2,DDAH1,SPINK8,BMP2	pink	VSMC_M5
GO:0003015	0.68	0.46	8	180	heart process	BP	1	TRPC1,ATP2B4,MEF2A,PIK3CA,GLRX3,SMAD7,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0007569	0.68	0.52	4	98	cell aging	BP	1	MAPK9,KAT6A,MAPK8,ATM	pink	VSMC_M5
GO:0090501	0.68	0.50	5	124	RNA phosphodiester bond hydrolysis	BP	1	CPSF3,ENDOV,RPP14,DIS3L,AGO3	pink	VSMC_M5
GO:0061024	0.68	0.40	25	599	membrane organization	BP	1	WASL,ANXA1,TMEM33,GCLC,UGCG,RAB1A,SCLT1,PDCD6IP,FNTA,ARL8B,MAPK8,VCPIP1,FAM92A,ZMYND8,GSK3B,ATF2,MTX2,PRKCI,CRKL,GHITM,HUWE1,GOLPH3L,TIMM9,UBXN2A,SAR1B	pink	VSMC_M5
GO:0030182	0.68	0.38	52	1067	neuron differentiation	BP	1	C9orf72,WASL,VEGFA,FRYL,RUNX2,UGCG,MACF1,SCLT1,NCOA1,MAGI2,FLRT3,TOP2B,ZDHHC17,CAPRIN1,CDK5RAP1,ARFGEF1,EIF4G2,DIP2B,TCTN1,PPP1CC,ARSB,TBC1D23,HIPK1,ESRP1,BTG2,TWF1,NOTCH2,ZMYND8,MEF2A,GSK3B,ALS2,ABI2,DLX2,STYXL1,PRKCI,COPS2,CRKL,WNK1,OPHN1,HERC1,ATP7A,TTC8,PTPN9,PTPRM,HPRT1,SETX,USP33,USP9X,FAM206A,UBE2V2,MTPN,BMP2	pink	VSMC_M5
GO:0043487	0.68	0.48	6	148	regulation of RNA stability	BP	1	POLR2D,YTHDF3,BTG2,PUM1,FXR1,NAF1	pink	VSMC_M5
GO:0051384	0.68	0.52	4	104	response to glucocorticoid	BP	1	ANXA1,NR3C1,USP8,MT-ND3	pink	VSMC_M5
GO:0009615	0.68	0.44	10	253	response to virus	BP	1	DDX17,IFIT5,LSM14A,URI1,TSPAN32,PUM1,LYST,ATF2,BIRC2,ELMOD2	pink	VSMC_M5
GO:0051261	0.68	0.49	5	99	protein depolymerization	BP	1	CAPZA2,CLASP1,TWF1,PIK3CA,MTPN	pink	VSMC_M5
GO:0050714	0.68	0.51	4	100	positive regulation of protein secretion	BP	1	CD2AP,IRS2,ANO1,GOLPH3L	pink	VSMC_M5
GO:0048729	0.68	0.40	23	490	tissue morphogenesis	BP	1	MTHFD1L,VEGFA,GCM1,ADAM17,MAGI2,CLASP1,EPB41L5,FLRT3,DLC1,FAT1,SMAD1,TCTN1,ARL13B,BTRC,NOTCH2,HECTD1,OPHN1,ATP7A,FEM1B,TTC8,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0006897	0.68	0.40	20	444	endocytosis	BP	1	SNX2,CSNK1G3,MKLN1,C9orf72,WASL,VEGFA,CD2AP,RHOQ,RAB1A,ZFYVE9,KIAA1109,MAGI2,MTMR6,ZFYVE16,TSG101,PPP3CC,BICD1,OPHN1,PIK3C3,USP33	pink	VSMC_M5
GO:0034612	0.68	0.46	7	181	response to tumor necrosis factor	BP	1	ADAM17,MAP4K3,ERBIN,HIPK1,CYLD,PRPF8,BIRC2	pink	VSMC_M5
GO:0060537	0.69	0.41	15	323	muscle tissue development	BP	1	DDX17,VEGFA,SMAD1,TIPARP,ARID2,BTG2,NOTCH2,MEF2A,COPS2,NF1,PRKAA1,SMAD7,MTPN,CACYBP,BMP2	pink	VSMC_M5
GO:0072009	0.69	0.50	4	89	nephron epithelium development	BP	1	VEGFA,MAGI2,NOTCH2,BMP2	pink	VSMC_M5
GO:0001738	0.69	0.50	4	84	morphogenesis of a polarized epithelium	BP	1	MAGI2,FAT1,OPHN1,TTC8	pink	VSMC_M5
GO:0061351	0.69	0.48	5	111	neural precursor cell proliferation	BP	1	VEGFA,PCM1,BTG2,PSMG1,NF1	pink	VSMC_M5
GO:0007162	0.69	0.44	9	215	negative regulation of cell adhesion	BP	1	ANXA1,VEGFA,EPB41L5,SPRY4,DLC1,WNK1,SMAD7,CD164,BMP2	pink	VSMC_M5
GO:0032869	0.69	0.45	7	161	cellular response to insulin stimulus	BP	1	GCLC,RHOQ,IRS2,GSK3B,PIK3CA,PRKCI,PRKAA1	pink	VSMC_M5
GO:0050866	0.69	0.48	5	136	negative regulation of cell activation	BP	1	ANXA1,GCLC,TSPAN32,ATM,SMAD7	pink	VSMC_M5
GO:0032787	0.69	0.40	15	404	monocarboxylic acid metabolic process	BP	1	ME2,MTHFD1L,SLC25A17,ANXA1,CYP39A1,OSBPL9,OXSM,IRS2,PRKAB2,ACACB,MORC2,ACOX3,PRKAA1,NUDT7,HACD1	pink	VSMC_M5
GO:0002285	0.69	0.48	5	127	lymphocyte activation involved in immune response	BP	1	ANXA1,NOTCH2,KMT5B,ATP7A,SMAD7	pink	VSMC_M5
GO:0071407	0.69	0.39	20	448	cellular response to organic cyclic compound	BP	1	LATS1,UBR5,DDX17,ANXA1,GCLC,UFL1,NR3C1,KDM3A,URI1,SMAD1,NR3C2,GABPA,TIPARP,ATP2B4,BTRC,GSK3B,USP8,MT-ND3,TMEM38B,BMP2	pink	VSMC_M5
GO:0050821	0.69	0.46	6	154	protein stabilization	BP	1	GOLGA7,ATF7IP,CREBL2,SMAD7,USP33,USP9X	pink	VSMC_M5

GO:0007275	0.69	0.34	180	3815	multicellular organism development	BP	1	MEX3C,TAB2,LATS1,MTHFD1L,DDX17,VPS13A,PCSK5,C9orf72,WASL,ANXA1,VEGFA,KRIT1,FRYL,RUNX2,ASNS,GCM1,RNF38,FAM126A,UGCG,MACF1,SEPT7,ADAM17,UFL1,CUL1,ZMYM4,RAB14,RAB33B,SCLT1,JCAD,KIAA1109,SRPK2,NCOA1,EPC1,ASXL2,MAGI2,DCLRE1C,CLASP1,EPB41L5,RHEB,ZEB2,MBD5,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,BIRC6,IRS2,KITLG,SPRY4,ATRN,N4BP2L2,APAF1,DLC1,RB1CC1,IL6ST,IMPAD1,CAPRIN1,PCM1,YTHDF3,FAT1,CDK5RAP1,ARFGEF1,SMAD1,EIF4G2,RHOBTB3,DIP2B,TCTN1,GABPA,PPP1CC,TET3,WWP1,TIPARP,MLF1,ARL13B,FAM92A,ARSB,TBC1D23,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BTG2,ATP2B4,CSDE1,TWF1,BBX,BTRC,PSMG1,NDUFS4,NOTCH2,TRIP12,ZMYND8,MEF2A,TET2,KMT5B,ACACB,GSK3B,FSTL1,PIK3CA,SCN9A,GTF2I,BPTF,FXR1,TFIP11,EGLN1,CCDC14,ALS2,UBR3,PLEKHA5,PLEKHA1,ZNF148,ABI2,HECTD1,DLX2,ARHGAP5,RPS6KA3,PAFAH1B2,SRP54,ATF2,STYXL1,RNF2,SOS2,ATM,KDM6A,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,WNK1,PYGO1,FUT8,OPHN1,YIPF6,FBXW11,ASH1L,HERC1,SPTLC2,ATRX,ATP7A,FEM1B,TTC8,SMAD2,GGNBP2,PTPN9,UBE2A,WDR78,NF1,PRKAA1,PTPRM,NIPBL,RAD1,PHF6,HPRT1,SMAD7,SETX,STXBP3,USP33,MT-CO1,MT-CO2,MT-ND4,BIRC2,SMIM14,ATP5PF,TMEM38B,USP9X,FAM206A,RNF103,GMFB,UBE2V2,RAB18,MTPN,CD164,CACYBP,ZNF45,DDAH1,BMP2	pink	VSMC_M5
GO:0007507	0.70	0.38	23	474	heart development	BP	1	TAB2,PCSK5,VEGFA,FLRT3,DLC1,RB1CC1,SMAD1,EIF4G2,ARL13B,ARID2,NOTCH2,MEF2A,ACACB,HECTD1,ATF2,KDM6A,CRKL,SMAD2,NF1,NIPBL,SMAD7,CACYBP,BMP2	pink	VSMC_M5
GO:0050670	0.70	0.47	5	137	regulation of lymphocyte proliferation	BP	1	ANXA1,IRS2,IL6ST,SOS2,ATM	pink	VSMC_M5
GO:0010595	0.70	0.49	4	105	positive regulation of endothelial cell migration	BP	1	ANXA1,VEGFA,ADAM17,JCAD	pink	VSMC_M5
GO:0060041	0.70	0.47	5	108	retina development in camera-type eye	BP	1	HIPK1,ATP2B4,DLX2,TTC8,PTPRM	pink	VSMC_M5
GO:0043491	0.70	0.45	6	147	protein kinase B signaling	BP	1	MAGI2,XDH,ARFGEF1,PIK3CA,PLEKHA1,SETX	pink	VSMC_M5
GO:0071496	0.70	0.41	11	267	cellular response to external stimulus	BP	1	ASNS,GCLC,NCOA1,MAP3K2,MAPK8,CPEB4,PIK3C3,PRKAA1,USP33,MTPN,BMT2	pink	VSMC_M5
GO:0032147	0.70	0.49	4	105	activation of protein kinase activity	BP	1	VEGFA,CAB39,PIK3CA,WNK1	pink	VSMC_M5
GO:0002819	0.70	0.49	4	111	regulation of adaptive immune response	BP	1	ANXA1,IL6ST,KMT5B,SMAD7	pink	VSMC_M5
GO:1903313	0.70	0.49	4	105	positive regulation of mRNA metabolic process	BP	1	POLR2D,YTHDF3,BTG2,PUM1	pink	VSMC_M5
GO:0032944	0.70	0.47	5	138	regulation of mononuclear cell proliferation	BP	1	ANXA1,IRS2,IL6ST,SOS2,ATM	pink	VSMC_M5
GO:0051960	0.70	0.39	16	344	regulation of nervous system development	BP	1	VEGFA,MACF1,UFL1,RHEB,FLRT3,IL6ST,CAPRIN1,PCM1,EIF4G2,DIP2B,PPP1CC,DLX2,PRKCI,NF1,UBE2V2,BMP2	pink	VSMC_M5
GO:0030278	0.70	0.49	4	91	regulation of ossification	BP	1	RUNX2,NIPBL,SMAD7,BMP2	pink	VSMC_M5
GO:1902533	0.70	0.36	31	731	positive regulation of intracellular signal transduction	BP	1	TAB2,KLHDC10,VEGFA,JCAD,RHEB,XDH,ZDHHC17,KITLG,RB1CC1,IFIT5,PJA2,ARFGEF1,ERBIN,NR3C2,RNF13,IRAK4,NOTCH2,SHOC2,PUM1,PIK3CA,STK39,TIAL1,ALS2,STYXL1,SOS2,ATM,CRKL,NFAT5,BIRC2,AGO3,BMP2	pink	VSMC_M5
GO:0043405	0.70	0.45	6	146	regulation of MAP kinase activity	BP	1	VEGFA,KITLG,SPRY4,TSG101,NF1,BMP2	pink	VSMC_M5
GO:1903131	0.70	0.40	12	297	mononuclear cell differentiation	BP	1	ANXA1,VEGFA,RUNX2,ADAM17,DCLRE1C,NOTCH2,HECTD1,ATF2,SOS2,ATM,ATP7A,SMAD7	pink	VSMC_M5
GO:0009749	0.70	0.45	6	153	response to glucose	BP	1	GCLC,IRS2,ANO1,PIK3CA,SMAD2,PRKAA1	pink	VSMC_M5
GO:0030217	0.70	0.44	7	179	T cell differentiation	BP	1	ANXA1,RUNX2,ADAM17,ATF2,SOS2,ATP7A,SMAD7	pink	VSMC_M5
GO:0001654	0.71	0.40	13	280	eye development	BP	1	VEGFA,FAT1,HIPK1,ATP2B4,NOTCH2,ABI2,DLX2,PRKCI,TTC8,NF1,PTPRM,NIPBL,RAB18	pink	VSMC_M5
GO:1901137	0.71	0.38	19	494	carbohydrate derivative biosynthetic process	BP	1	UGCG,DPY19L1,TMTC3,ARFGEF1,TET3,PIGP,GXYLT1,OGA,TET2,ACACB,ADAL,FUT8,ATP7A,PRKAA1,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0002768	0.71	0.44	6	158	immune response-regulating cell surface receptor signaling pathway	BP	1	MAPK9,MAPK8,PIK3CA,PLEKHA1,CRKL,WNK1	pink	VSMC_M5
GO:0042177	0.71	0.48	4	101	negative regulation of protein catabolic process	BP	1	CSNK2A1,TIMP1,OPHN1,USP14	pink	VSMC_M5
GO:0016042	0.71	0.42	8	225	lipid catabolic process	BP	1	SLC25A17,CYP39A1,IRS2,ACACB,PAFAH1B2,ACOX3,PRKAA1,NUDT7	pink	VSMC_M5
GO:0050921	0.71	0.48	4	109	positive regulation of chemotaxis	BP	1	VEGFA,ADAM17,STK39,WNK1	pink	VSMC_M5
GO:0042770	0.71	0.44	6	155	signal transduction in response to DNA damage	BP	1	MRE11,ATF2,ATM,ATRX,FEM1B,RAD1	pink	VSMC_M5
GO:0048639	0.71	0.44	6	134	positive regulation of developmental growth	BP	1	VEGFA,MACF1,EIF4G2,ACACB,NIPBL,SMAD7	pink	VSMC_M5
GO:0048583	0.71	0.32	127	2834	regulation of response to stimulus	BP	1	ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBR2,C9orf72,ANXA1,TMEM33,VEGFA,RUNX2,CD2AP,GCLC,USP34,UGCG,MACF1,ADAM17,UFL1,JCAD,ARHGAP42,NCOA1,ASXL2,MAGI2,CLASP1,RHEB,ZEB2,MBD5,XDH,KAT6A,ZDHHC17,BIRC6,LTBP1,KITLG,SPRY4,MAPK8,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,URI1,NR3C2,RNF13,TCTN1,RALGAPB,FAM92A,TSG101,HIPK1,ARID2,DNMBP,ATP2B4,TWF1,IRAK4,CYLD,RANBP9,BTRC,TSPAN32,DOCK3,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,SHOC2,KMT5B,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,FXR1,TFIP11,STK39,TIAL1,ALS2,PLEKHA1,DLX2,ARHGAP5,RPS6KA3,GLRX3,KLHL15,HERC4,STYXL1,RALGPS2,LANCL1,SOS2,ATM,PRKCI,USP8,TIMP1,CRKL,WNK1,GHITM,FUT8,OPHN1,ASH1L,ATP7A,FEM1B,SMAD2,GSKIP,GGNBP2,SMG1,CSNK1A1,USP14,XIAP,NF1,PRKAA1,SMAD7,NFAT5,USP33,BIRC2,AGO3,UBE2D3,UBE2V2,MTPN,ELMOD2,DDAH1,BMT2,BMP2	pink	VSMC_M5
GO:0051896	0.71	0.45	5	125	regulation of protein kinase B signaling	BP	1	MAGI2,XDH,ARFGEF1,PIK3CA,PLEKHA1	pink	VSMC_M5
GO:0045834	0.71	0.47	4	109	positive regulation of lipid metabolic process	BP	1	ANXA1,IRS2,CREBL2,PRKAA1	pink	VSMC_M5
GO:0060326	0.72	0.41	8	206	cell chemotaxis	BP	1	ANXA1,VEGFA,ADAM17,LYST,STK39,SRP54,CRKL,WNK1	pink	VSMC_M5
GO:0043434	0.72	0.39	13	308	response to peptide hormone	BP	1	ANXA1,GCLC,RHOQ,MBD5,IRS2,BTG2,GSK3B,PIK3CA,PRKCI,TIMP1,PRKAA1,STXBP3,CACYBP	pink	VSMC_M5
GO:0150063	0.72	0.39	13	282	visual system development	BP	1	VEGFA,FAT1,HIPK1,ATP2B4,NOTCH2,ABI2,DLX2,PRKCI,TTC8,NF1,PTPRM,NIPBL,RAB18	pink	VSMC_M5
GO:0031532	0.72	0.47	4	94	actin cytoskeleton reorganization	BP	1	MKLN1,ANXA1,CD2AP,NOTCH2	pink	VSMC_M5

GO:0048666	0.72	0.34	42	877	neuron development	BP	1	C9orf72,WASL,VEGFA,FRYL,UGCG,MACF1,SCLT1,MAGI2,FLRT3,TOP2B,ZDHHC17,CAPRIN1,ARFGEF1,EIF4G2,DIP2B,TCTN1,ARSB,TBC1D23,BTG2,TWF1,NOTCH2,ZMYND8,MEF2A,GSK3B,ALS2,ABI2,STYXL1,PRKCI,CRKL,WNK1,OPHN1,HERC1,ATP7A,TTC8,PTPN9,PTPRM,HPRT1,SETX,USP33,USP9X,FAM206A,UBE2V2	pink	VSMC_M5
GO:0006997	0.72	0.45	5	112	nucleus organization	BP	1	SYNE1,SRPK2,KDM3A,PYGO1,UBXN2A	pink	VSMC_M5
GO:0071345	0.72	0.36	23	574	cellular response to cytokine stimulus	BP	1	UGCG,ADAM17,PRDM5,SPRY4,IL6ST,YTHDF3,LSM14A,KDM3A,ERBIN,HIPK1,IRAK4,CYLD,GSK3B,STK39,CRKL,WNK1,SMAD7,PRPF8,STXBP3,NFAT5,BIRC2,CACYBP,UBXN2A	pink	VSMC_M5
GO:0050657	0.72	0.44	5	135	nucleic acid transport	BP	1	POLR2D,ZC3H11A,SMG7,SMG1,EIF5A2	pink	VSMC_M5
GO:0050658	0.72	0.44	5	135	RNA transport	BP	1	POLR2D,ZC3H11A,SMG7,SMG1,EIF5A2	pink	VSMC_M5
GO:0048863	0.72	0.42	7	171	stem cell differentiation	BP	1	RUNX2,UFL1,KITLG,N4BP2L2,KDM3A,PUM1,METTL5	pink	VSMC_M5
GO:0007369	0.72	0.43	6	138	gastrulation	BP	1	CLASP1,EPB41L5,SMAD1,RNF2,WNK1,SMAD2	pink	VSMC_M5
GO:0010628	0.72	0.34	33	803	positive regulation of gene expression	BP	1	MED23,MAPK9,UBR5,ANXA1,GUF1,VEGFA,RUNX2,RAB1A,ADAM17,SRPK2,POLR2D,MAPK8,IL6ST,YTHDF3,CDK5RAP1,SMAD1,EIF4G2,GABPA,MEF2A,KMT5B,GSK3B,FXR1,METTL5,ATF2,ATM,SMAD2,PRKAA1,SETX,NFAT5,AGO3,EIF5A2,HNRNPLL,BMP2	pink	VSMC_M5
GO:0034762	0.72	0.36	17	396	regulation of transmembrane transport	BP	1	RHOQ,COMMD1,IRS2,TRPC1,ATP2B4,NIPSNAP2,CAB39,MEF2A,SCN9A,STK39,CREBL2,PRKCI,YWHAQ,WNK1,ATP7A,STXBP3,TMEM38B	pink	VSMC_M5
GO:0009913	0.73	0.43	5	120	epidermal cell differentiation	BP	1	LATS1,ANXA1,UGCG,TSG101,ESRP1	pink	VSMC_M5
GO:0045664	0.73	0.42	6	145	regulation of neuron differentiation	BP	1	NCOA1,CDK5RAP1,ESRP1,GSK3B,DLX2,BMP2	pink	VSMC_M5
GO:0048880	0.73	0.37	13	286	sensory system development	BP	1	VEGFA,FAT1,HIPK1,ATP2B4,NOTCH2,ABI2,DLX2,PRKCI,TTC8,NF1,PTPRM,NIPBL,RAB18	pink	VSMC_M5
GO:0009746	0.73	0.41	6	159	response to hexose	BP	1	GCLC,IRS2,ANO1,PIK3CA,SMAD2,PRKAA1	pink	VSMC_M5
GO:0002443	0.73	0.39	8	221	leukocyte mediated immunity	BP	1	ADAM17,ARL8B,IRAK4,KMT5B,LYST,HPRT1,SMAD7,STXBP3	pink	VSMC_M5
GO:0032501	0.73	0.30	232	5003	multicellular organismal process	BP	1	DGKA,MEX3C,TAB2,LATS1,MTHFD1L,SYNE1,LRGUK,DDX17,VPS13A,PCSK5,UBR2,C9orf72,WASL,ANXA1,VEGFA,KRIT1,FRYL,RUNX2,CYP39A1,CD2AP,ASNS,GCM1,GCLC,RNF38,FBXO11,FAM126A,LCA5,UGCG,MACF1,VPS54,RAB1A,SEPT7,TIA1,ADAM17,UFL1,CUL1,ZMYM4,RAB14,RAB33B,SCLT1,JCAD,ARHGAP42,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,TBP,ASXL2,MAGI2,AKAP11,DCLRE1C,DGKH,CLASP1,EPB41L5,RHEB,ZEB2,MBD5,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,BIRC6,LTBP1,IRS2,KITLG,SPRY4,ATRN,N4BP2L2,APAF1,DLC1,RB1CC1,IL6ST,IMPAD1,CAPRIN1,PCM1,YTHDF3,FAT1,TNKS2,CDK5RAP1,PJA2,ARFGEF1,KDM3A,ERBIN,SMAD1,EIF4G2,SLC4A8,RHOBTB3,TRPC1,DIP2B,TCTN1,GABPA,PPP1CC,TET3,WWP1,TIPARP,MLF1,ARL13B,LXN,FAM92A,ARSB,TBC1D23,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BTG2,ATP2B4,CSDE1,TWF1,CYLD,BBX,BTRC,PSMG1,TSPAN32,NDUFS4,ID4,ACOT13,NOTCH2,TRIP12,ANO1,ZMYND8,MEF2A,PRKAB2,TET2,KMT5B,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,SCN9A,GTF2I,BPTF,FXR1,TFIP11,STK39,EGLN1,KDM2A,TIAL1,CCDC14,ALS2,UBR3,PLEKHA5,PLEKHA1,ZNF148,ABI2,HECTD1,DLX2,JMJD1C,ARHGAP5,RPS6KA3,PAFAH1B2,GLRX3,SRP54,ATF2,HERC4,STYXL1,RNF2,CCDC50,SOS2,ATM,KDM6A,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,WNK1,PYGO1,FUT8,HUWE1,OPHN1,YIPF6,FBXW11,ASH1L,HERC1,MLH3,SPTLC2,ATRX,ATP7A,SPATA7,CHM,PIAS1,FEM1B,TTC8,DIAPH2,SMAD2,GGNBP2,DYNC1H1,PTPN9,UBE2A,WDR78,NF1,PRKAA1,PTPRM,NIPBL,RAD1,PHF6,HPRT1,SMAD7,F8,SETX,STXBP3,PKN2,NFAT5,USP33,MT-CO1,MT-CO2,MT-ND4,BIRC2,SMIM14,ATP5PF,TMEM38B,USP9X,FAM2	pink	VSMC_M5
GO:0071356	0.73	0.41	6	163	cellular response to tumor necrosis factor	BP	1	ADAM17,ERBIN,HIPK1,CYLD,PRPF8,BIRC2	pink	VSMC_M5
GO:0002695	0.73	0.45	4	118	negative regulation of leukocyte activation	BP	1	ANXA1,TSPAN32,ATM,SMAD7	pink	VSMC_M5
GO:0080134	0.74	0.32	40	970	regulation of response to stress	BP	1	UBR5,KLHDC10,ANXA1,TMEM33,VEGFA,UFL1,CLASP1,XDH,RB1CC1,IL6ST,YTHDF3,LSM14A,PJA2,ARFGEF1,RNF13,ARID2,ATP2B4,CYLD,TSPAN32,TRIP12,KMT5B,GSK3B,FXR1,TFIP11,STK39,KLHL15,LANCL1,ATM,FUT8,ASH1L,ATP7A,FEM1B,SMG1,USP14,XIAP,BIRC2,UBE2V2,ELMOD2,DDAH1,BMP2	pink	VSMC_M5
GO:0019722	0.74	0.41	6	147	calcium-mediated signaling	BP	1	PPP3CC,ATP2B4,GSK3B,PRKAA1,NFAT5,TMEM38B	pink	VSMC_M5
GO:0000280	0.74	0.36	14	355	nuclear division	BP	1	UBR2,MRE11,CLASP1,TOP2B,LSM14A,CEP97,ATM,PDS5A,MLH3,ATRX,STAG2,NIPBL,RAD1,RMDN1	pink	VSMC_M5
GO:0007166	0.74	0.30	87	1935	cell surface receptor signaling pathway	BP	1	LATS1,MAPK9,CSNK1G3,UBR5,ANXA1,VEGFA,RUNX2,GCLC,DST,RHOQ,USP34,UGCG,MACF1,ADAM17,RAB14,ZFYVE9,JCAD,MAGI2,FNTA,ZEB2,MBD5,FLRT3,XDH,ZDHHC17,BIRC6,LTBP1,IRS2,KITLG,SPRY4,MAPK8,MAGI1,RB1CC1,IL6ST,CSNK2A1,YTHDF3,TNKS2,LSM14A,ERBIN,SMAD1,TCTN1,CPNE3,TIPARP,ARL13B,FAM92A,TSG101,HIPK1,IRAK4,CYLD,RANBP9,BTRC,TSPAN32,NOTCH2,ZMYND8,SHOC2,GSK3B,FSTL1,PIK3CA,STK39,PLEKHA1,MUC20,DLX2,HERC4,CUL5,PRKCI,USP8,TIMP1,CRKL,WNK1,PYGO1,FUT8,CPEB4,FBXW11,PIAS1,FEM1B,SMAD2,GSKIP,GGNBP2,CSNK1A1,XIAP,PRKAA1,SMAD7,SETX,BIRC2,UBE2D3,USP9X,MPZL1,BMP2	pink	VSMC_M5
GO:0140694	0.74	0.36	13	305	non-membrane-bounded organelle assembly	BP	1	MAPK9,C9orf72,CLASP1,YTHDF3,LSM14A,CEP97,CSDE1,BICD1,MEF2A,STYXL1,DYNC1H1,STAG2,PRKAA1	pink	VSMC_M5
GO:0048598	0.74	0.33	21	469	embryonic morphogenesis	BP	1	LATS1,MTHFD1L,RUNX2,GCM1,NCOA1,CLASP1,EPB41L5,FLRT3,DLC1,IMPAD1,SMAD1,TCTN1,ARL13B,HIPK1,NOTCH2,HECTD1,DLX2,RNF2,WNK1,SMAD2,NIPBL	pink	VSMC_M5
GO:0045597	0.74	0.32	27	639	positive regulation of cell differentiation	BP	1	MAPK9,ANXA1,VEGFA,RUNX2,MACF1,UFL1,NCOA1,ASXL2,RHEB,ZEB2,KITLG,IL6ST,CAPRIN1,SMAD1,EIF4G2,PPP1CC,NOTCH2,DLX2,RPS6KA3,CREBL2,ARPC2,PRKCI,CRKL,PIAS1,SMAD2,SMAD7,BMP2	pink	VSMC_M5

GO:0009607	0.74	0.32	34	856	response to biotic stimulus	BP	1	TAB2,DDX17,WASL,ANXA1,RAB1A,ADAM17,RAB14,SRPK2,ARL8B,MAPK8,APAF1,IFIT5,YTHDF3,LSM14A,PJA2,ERBIN,URI1,IRAK4,CYLD,TSPAN32,NOTCH2,GSK3B,PUM1,LYST,RPS6KA3,ATF2,NAALADL2,USP14,XIAP,PRPF8,STXBP3,BIRC2,ELMOD2,BMP2	pink	VSMC_M5
GO:0030856	0.74	0.43	4	106	regulation of epithelial cell differentiation	BP	1	VEGFA,KIAA1109,XDH,ESRP1	pink	VSMC_M5
GO:0007043	0.74	0.43	4	99	cell-cell junction assembly	BP	1	PDCD6IP,HIPK1,SMAD7,PKN2	pink	VSMC_M5
GO:0031589	0.74	0.35	13	294	cell-substrate adhesion	BP	1	MKLN1,VEGFA,MACF1,RAB1A,CLASP1,EPB41L5,SPRY4,ATRN,DLC1,GSK3B,ARPC2,CRKL,NF1	pink	VSMC_M5
GO:0120039	0.75	0.32	25	517	plasma membrane bounded cell projection morphogenesis	BP	1	SNX2,C9orf72,WASL,VEGFA,MACF1,FLRT3,TOP2B,ZDHHC17,CAPRIN1,EIF4G2,DIP2B,TCTN1,NOTCH2,MEF2A,GSK3B,ALS2,ABI2,OPHN1,ATP7A,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5
GO:0098542	0.75	0.33	22	574	defense response to other organism	BP	1	DDX17,ANXA1,RAB1A,ADAM17,RAB14,SRPK2,ARL8B,IFIT5,YTHDF3,LSM14A,PJA2,IRAK4,CYLD,TSPAN32,NOTCH2,PUM1,LYST,USP14,XIAP,STXBP3,BIRC2,ELMOD2	pink	VSMC_M5
GO:0070661	0.75	0.39	7	201	leukocyte proliferation	BP	1	ANXA1,IRS2,KITLG,IL6ST,SOS2,ATM,HPRT1	pink	VSMC_M5
GO:0016331	0.75	0.41	5	127	morphogenesis of embryonic epithelium	BP	1	MTHFD1L,EPB41L5,DLC1,TCTN1,HECTD1	pink	VSMC_M5
GO:0035295	0.75	0.31	38	849	tube development	BP	1	MTHFD1L,PCSK5,ANXA1,VEGFA,KRIT1,JCAD,SRPK2,EPB41L5,XDH,DLC1,IL6ST,SMAD1,TCTN1,TIPARP,ARL13B,HIPK1,ARID2,ATP2B4,BTRC,NOTCH2,PIK3CA,GTF2I,EGLN1,HECTD1,ATF2,CRKL,YIPF6,ATRX,ATP7A,TTC8,SMAD2,NF1,PTPRM,NIPBL,SMAD7,TMEM38B,DDAH1,BMP2	pink	VSMC_M5
GO:0055007	0.75	0.43	4	96	cardiac muscle cell differentiation	BP	1	VEGFA,MEF2A,CACYBP,BMP2	pink	VSMC_M5
GO:0050851	0.75	0.43	4	117	antigen receptor-mediated signaling pathway	BP	1	PIK3CA,PLEKHA1,CRKL,WNK1	pink	VSMC_M5
GO:0007517	0.75	0.36	11	259	muscle organ development	BP	1	DDX17,BTG2,MEF2A,KMT5B,FXR1,COPS2,PRKAA1,SMAD7,MTPN,CD164,BMP2	pink	VSMC_M5
GO:0042593	0.75	0.38	7	183	glucose homeostasis	BP	1	GCLC,MBD5,IRS2,ANO1,PIK3CA,PRKAA1,STXBP3	pink	VSMC_M5
GO:0098656	0.75	0.39	6	161	anion transmembrane transport	BP	1	SLC25A17,PCYOX1,SLC4A8,ANO1,SFXN1,SLC35A3	pink	VSMC_M5
GO:1900180	0.75	0.43	4	116	regulation of protein localization to nucleus	BP	1	LATS1,UBR5,CD2AP,GSK3B	pink	VSMC_M5
GO:0035148	0.75	0.40	5	129	tube formation	BP	1	MTHFD1L,VEGFA,DLC1,TCTN1,HECTD1	pink	VSMC_M5
GO:0048858	0.75	0.32	25	520	cell projection morphogenesis	BP	1	SNX2,C9orf72,WASL,VEGFA,MACF1,FLRT3,TOP2B,ZDHHC17,CAPRIN1,EIF4G2,DIP2B,TCTN1,NOTCH2,MEF2A,GSK3B,ALS2,ABI2,OPHN1,ATP7A,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5
GO:0050731	0.75	0.40	5	136	positive regulation of peptidyl-tyrosine phosphorylation	BP	1	VEGFA,ADAM17,KITLG,IL6ST,DOCK3	pink	VSMC_M5
GO:0022402	0.75	0.30	40	951	cell cycle process	BP	1	LATS1,UBR2,WASL,ANXA1,SEPT7,ADAM17,CUL1,CUL2,MRE11,PDCD6IP,CLASP1,FBXL3,TOP2B,BIRC6,CSNK2A1,PCM1,LSM14A,ATP2B4,CEP97,ATF2,ATM,CUL5,USP8,PDS5A,WAPL,FBXW11,MLH3,ATRX,PIAS1,FEM1B,PIK3C3,DYNC1H1,ESCO1,RAB11FIP4,STAG2,NIPBL,RAD1,PKN2,USP33,RMDN1	pink	VSMC_M5
GO:0009612	0.76	0.37	7	176	response to mechanical stimulus	BP	1	ASNS,GCLC,MAP3K2,MAPK8,BTG2,PIK3CA,MTPN	pink	VSMC_M5
GO:0023052	0.76	0.27	194	4258	signaling	BP	1	DGKA,ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,DDX17,MKLN1,KLHDC10,PCSK5,UBR2,C9orf72,ANXA1,TMEM33,VEGFA,KRIT1,RUNX2,CD2AP,GCLC,DST,RHOQ,ERLEC1,USP34,UGCG,MACF1,RAB1A,ADAM17,UFL1,CUL1,RAB14,CUL2,RAB33B,ZFYVE9,JCAD,ARHGAP42,SRPK2,NCOA1,MRE11,ASXL2,MAGI2,MAP3K2,AKAP11,DGKH,RHEB,FNTA,ZEB2,MBD5,FLRT3,XDH,KAT6A,ZDHHC17,NKIRAS1,BIRC6,LTBP1,IRS2,KITLG,PRKD3,SPRY4,NR3C1,MAP4K3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,FAT1,TNKS2,LSM14A,PJA2,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,SLC4A8,NR3C2,KCMF1,RHOBTB3,TRPC1,RNF13,TCTN1,PPP1CC,WWP1,ZFYVE16,CPNE3,TIPARP,RALGAPB,ARL13B,FAM92A,GTF2H1,TSG101,HIPK1,PPP3CC,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,TSPAN32,DOCK3,NOTCH2,BICD1,ANO1,ASB7,CAB39,ZMYND8,IPO8,MEF2A,SHOC2,PRKAB2,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,SCN9A,STK39,FAM162A,TIAL1,ALS2,RPS6KC1,PDE5A,TLK1,PLEKHA1,MUC20,ABI2,DLX2,ARHGAP5,RPS6KA3,CREBL2,ATF2,HERC4,STYXL1,RALGPS2,SOS2,ATM,CUL5,ERO1A,PRKCI,COPS2,YWHAQ,USP8,TIMP1,CRKL,WNK1,GHITM,PYGO1,FUT8,OPHN1,CPEB4,FBXW11,ASH1L,ATRX,CHM,PIAS1,FEM1B,SMAD2,PIK3C3,GSKIP,GGNBP2,SMG1,CSNK1A1,XIAP,NF1,PRKAA1,PTPRM,RAD1,SMAD7,SETX,STXBP3,PKN2,NFAT5,USP33,BIRC2,NMS,AGO3,UBE2D3,ATP5PF,TMEM38B,USP9X,GMFB,RAB18,CD164,DDAH1,BMT2,PAIP2,MPZL1,BMP2	pink	VSMC_M5
GO:0033500	0.76	0.37	7	184	carbohydrate homeostasis	BP	1	GCLC,MBD5,IRS2,ANO1,PIK3CA,PRKAA1,STXBP3	pink	VSMC_M5
GO:0046651	0.76	0.38	6	177	lymphocyte proliferation	BP	1	ANXA1,IRS2,IL6ST,SOS2,ATM,HPRT1	pink	VSMC_M5
GO:0002262	0.76	0.39	5	134	myeloid cell homeostasis	BP	1	ANXA1,VEGFA,ADAM17,UFL1,KITLG	pink	VSMC_M5
GO:0051347	0.76	0.32	18	441	positive regulation of transferase activity	BP	1	TAB2,SERINC1,VEGFA,ADAM17,MRE11,KITLG,CDK5RAP1,ATP2B4,BTRC,DOCK3,CAB39,PIK3CA,DCUN1D1,ALS2,WNK1,CCNK,NAF1,BMP2	pink	VSMC_M5
GO:0043393	0.76	0.38	6	162	regulation of protein binding	BP	1	EPB41L5,MAPK8,GSK3B,TFIP11,USP33,BMP2	pink	VSMC_M5
GO:2000027	0.76	0.41	4	108	regulation of animal organ morphogenesis	BP	1	VEGFA,RUNX2,MAGI2,BMP2	pink	VSMC_M5
GO:0048762	0.76	0.36	8	198	mesenchymal cell differentiation	BP	1	DDX17,CLASP1,EPB41L5,KITLG,GSK3B,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0048284	0.76	0.41	4	120	organelle fusion	BP	1	ANXA1,ARL8B,VCPIP1,HUWE1	pink	VSMC_M5
GO:0062012	0.76	0.35	9	243	regulation of small molecule metabolic process	BP	1	ANXA1,SDHAF3,IRS2,ATP2B4,ACACB,GSK3B,PRKAA1,MT-CO2,BMP2	pink	VSMC_M5
GO:0034284	0.76	0.38	6	164	response to monosaccharide	BP	1	GCLC,IRS2,ANO1,PIK3CA,SMAD2,PRKAA1	pink	VSMC_M5
GO:1901888	0.76	0.37	7	165	regulation of cell junction assembly	BP	1	VEGFA,MACF1,CLASP1,EPB41L5,FLRT3,DLC1,UBE2V2	pink	VSMC_M5
GO:0001838	0.76	0.41	4	107	embryonic epithelial tube formation	BP	1	MTHFD1L,DLC1,TCTN1,HECTD1	pink	VSMC_M5
GO:0048812	0.76	0.31	24	503	neuron projection morphogenesis	BP	1	C9orf72,WASL,VEGFA,MACF1,FLRT3,TOP2B,ZDHHC17,CAPRIN1,EIF4G2,DIP2B,TCTN1,NOTCH2,MEF2A,GSK3B,ALS2,ABI2,OPHN1,ATP7A,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5

GO:0043207	0.76	0.30	32	820	response to external biotic stimulus	BP	1	TAB2,DDX17,WASL,ANXA1,RAB1A,ADAM17,RAB14,SRPK2,ARL8B,MAPK8,IFIT5,YTHDF3,LSM14A,PJA2,ERBIN,URI1,IRAK4,CYLD,TSPAN32,NOTCH2,PUM1,LYST,RPS6KA3,ATF2,NAALADL2,USP14,XIAP,PRPF8,STXBP3,BIRC2,ELMOD2,BMP2	pink	VSMC_M5
GO:0051707	0.76	0.30	32	820	response to other organism	BP	1	TAB2,DDX17,WASL,ANXA1,RAB1A,ADAM17,RAB14,SRPK2,ARL8B,MAPK8,IFIT5,YTHDF3,LSM14A,PJA2,ERBIN,URI1,IRAK4,CYLD,TSPAN32,NOTCH2,PUM1,LYST,RPS6KA3,ATF2,NAALADL2,USP14,XIAP,PRPF8,STXBP3,BIRC2,ELMOD2,BMP2	pink	VSMC_M5
GO:0060538	0.77	0.39	5	132	skeletal muscle organ development	BP	1	DDX17,BTG2,FXR1,COPS2,PRKAA1	pink	VSMC_M5
GO:0009101	0.77	0.35	9	245	glycoprotein biosynthetic process	BP	1	DPY19L1,TMTC3,ARFGEF1,TET3,GXYLT1,OGA,TET2,FUT8,ATP7A	pink	VSMC_M5
GO:0031668	0.77	0.35	8	205	cellular response to extracellular stimulus	BP	1	ASNS,NCOA1,MAPK8,CPEB4,PIK3C3,PRKAA1,USP33,BMT2	pink	VSMC_M5
GO:0045667	0.77	0.40	4	109	regulation of osteoblast differentiation	BP	1	RUNX2,IL6ST,SMAD1,BMP2	pink	VSMC_M5
GO:0045785	0.77	0.33	12	306	positive regulation of cell adhesion	BP	1	ANXA1,VEGFA,EPB41L5,MAGI1,IL6ST,GSK3B,PIK3CA,ATM,ARPC2,CRKL,SMAD7,NFAT5	pink	VSMC_M5
GO:0007610	0.77	0.31	18	406	behavior	BP	1	VPS13A,BBS12,NCOA1,MBD5,PCM1,PJA2,BTG2,PUM1,SCN9A,ALS2,UBR3,ATP7A,PIAS1,NF1,PRKAA1,HPRT1,NMS,PAIP2	pink	VSMC_M5
GO:0032943	0.77	0.37	6	179	mononuclear cell proliferation	BP	1	ANXA1,IRS2,IL6ST,SOS2,ATM,HPRT1	pink	VSMC_M5
GO:0030072	0.77	0.37	6	168	peptide hormone secretion	BP	1	ANXA1,RAB1A,IRS2,ANO1,SMAD2,STXBP3	pink	VSMC_M5
GO:0031023	0.77	0.38	5	127	microtubule organizing center organization	BP	1	PDCD6IP,CLASP1,PCM1,FBXW11,USP33	pink	VSMC_M5
GO:0043488	0.77	0.38	5	137	regulation of mRNA stability	BP	1	POLR2D,YTHDF3,BTG2,PUM1,FXR1	pink	VSMC_M5
GO:0019221	0.77	0.33	11	306	cytokine-mediated signaling pathway	BP	1	UGCG,ADAM17,IL6ST,YTHDF3,LSM14A,HIPK1,IRAK4,CYLD,STK39,WNK1,BIRC2	pink	VSMC_M5
GO:0031960	0.77	0.40	4	117	response to corticosteroid	BP	1	ANXA1,NR3C1,USP8,MT-ND3	pink	VSMC_M5
GO:0045766	0.77	0.38	5	133	positive regulation of angiogenesis	BP	1	VEGFA,JCAD,SMAD1,HIPK1,DDAH1	pink	VSMC_M5
GO:1904018	0.77	0.38	5	133	positive regulation of vasculature development	BP	1	VEGFA,JCAD,SMAD1,HIPK1,DDAH1	pink	VSMC_M5
GO:0040011	0.77	0.27	62	1349	locomotion	BP	1	VPS13A,WASL,ANXA1,VEGFA,KRIT1,CD2AP,DST,PTP4A1,RHOQ,MACF1,RAB1A,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,ZEB2,FLRT3,TOP2B,IRS2,KITLG,ATRN,DLC1,PCM1,YTHDF3,FAT1,RHOBTB3,CPNE3,ARL13B,ARSB,ARID2,ATP2B4,IRAK4,NOTCH2,ZMYND8,FSTL1,PIK3CA,LYST,STK39,ABI2,SRP54,ATM,ARPC2,PRKCI,TIMP1,CRKL,WNK1,FUT8,OPHN1,ASH1L,ATP7A,TTC8,PSTPIP2,USP14,NF1,PTPRM,NIPBL,SMAD7,PKN2,USP33,USP9X,BMP2	pink	VSMC_M5
GO:0043436	0.77	0.30	24	677	oxoacid metabolic process	BP	1	ME2,MTHFD1L,SLC25A17,ANXA1,CYP39A1,SDHAF3,ASNS,GCLC,MDH1,OSBPL9,OXSM,IRS2,UEVLD,ATP2B4,PRKAB2,ACACB,MORC2,ACOX3,ATP7A,PRKAA1,NUDT7,SULT1C4,HACD1,DDAH1	pink	VSMC_M5
GO:0045216	0.77	0.37	6	146	cell-cell junction organization	BP	1	VEGFA,PDCD6IP,HIPK1,PRKCI,SMAD7,PKN2	pink	VSMC_M5
GO:0050730	0.77	0.35	7	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	VEGFA,ADAM17,KITLG,IL6ST,TSG101,DOCK3,GGNBP2	pink	VSMC_M5
GO:0006575	0.77	0.40	4	136	cellular modified amino acid metabolic process	BP	1	MTHFD1L,SERINC1,GCLC,PCYOX1	pink	VSMC_M5
GO:0030326	0.78	0.39	4	96	embryonic limb morphogenesis	BP	1	RUNX2,IMPAD1,NOTCH2,NIPBL	pink	VSMC_M5
GO:0035113	0.78	0.39	4	96	embryonic appendage morphogenesis	BP	1	RUNX2,IMPAD1,NOTCH2,NIPBL	pink	VSMC_M5
GO:0006694	0.78	0.39	4	126	steroid biosynthetic process	BP	1	CYP39A1,OSBPL9,PRKAA1,BMP2	pink	VSMC_M5
GO:0010675	0.78	0.39	4	114	regulation of cellular carbohydrate metabolic process	BP	1	SDHAF3,IRS2,ACACB,GSK3B	pink	VSMC_M5
GO:0051338	0.78	0.28	29	706	regulation of transferase activity	BP	1	TAB2,LATS1,SERINC1,VEGFA,ADAM17,MRE11,IRS2,KITLG,SPRY4,CDK5RAP1,GTF2H1,TSG101,ATP2B4,BTRC,DOCK3,CAB39,GSK3B,PIK3CA,DCUN1D1,ALS2,WNK1,FEM1B,GSKIP,CCNK,GGNBP2,NF1,SMAD7,NAF1,BMP2	pink	VSMC_M5
GO:0055088	0.78	0.39	4	116	lipid homeostasis	BP	1	CYP39A1,IRS2,ACOX3,PRKAA1	pink	VSMC_M5
GO:0007160	0.78	0.34	8	192	cell-matrix adhesion	BP	1	MKLN1,VEGFA,MACF1,CLASP1,EPB41L5,DLC1,GSK3B,NF1	pink	VSMC_M5
GO:0032502	0.78	0.24	211	4589	developmental process	BP	1	MEX3C,TAB2,LATS1,MAPK9,MTHFD1L,SYNE1,SNX2,LRGUK,DDX17,MKLN1,VPS13A,PCSK5,UBR2,C9orf72,WASL,ANXA1,VEGFA,KRIT1,FRYL,RUNX2,ASNS,GCM1,GCLC,RNF38,RHOQ,FAM126A,UGCG,MACF1,RAB1A,SEPT7,ADAM17,UFL1,CUL1,ZMYM4,RAB14,RAB33B,SCLT1,JCAD,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,TBP,ASXL2,MAGI2,DCLRE1C,CLASP1,EPB41L5,RHEB,ZEB2,MBD5,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,BIRC6,IRS2,KITLG,SPRY4,ATRN,N4BP2L2,MAPK8,APAF1,DLC1,RB1CC1,IL6ST,IMPAD1,CAPRIN1,PCM1,YTHDF3,FAT1,TNKS2,CDK5RAP1,ARFGEF1,KDM3A,SMAD1,EIF4G2,RHOBTB3,DIP2B,TCTN1,GABPA,PPP1CC,TET3,WWP1,TIPARP,MLF1,ARL13B,FAM92A,ARSB,TBC1D23,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BAZ2B,BTG2,DNMBP,ATP2B4,CSDE1,TWF1,BBX,BTRC,PSMG1,NDUFS4,ID4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,SCN9A,GTF2I,BPTF,FXR1,TFIP11,EGLN1,TIAL1,CCDC14,ALS2,METTL5,UBR3,PLEKHA5,PLEKHA1,ZNF148,SCFD1,ABI2,HECTD1,DLX2,ARHGAP5,RPS6KA3,PAFAH1B2,CREBL2,SRP54,ATF2,HERC4,STYXL1,RNF2,SOS2,ATM,KDM6A,ARPC2,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,WNK1,PYGO1,FUT8,HUWE1,OPHN1,YIPF6,FBXW11,ASH1L,HERC1,SPTLC2,ATRX,ATP7A,PIAS1,FEM1B,TTC8,DIAPH2,SMAD2,GGNBP2,PTPN9,UBE2A,WDR78,NF1,PRKAA1,PTPRM,NIPBL,RAD1,PHF6,HPRT1,SMAD7,SETX,STXBP3,NUDT7,USP33,MT-CO1,MT-CO2,MT-ND4,BIRC2,SMIM14,ATP5PF,TMEM38B,USP9X,FAM206A,RNF103,GMFB,UBE2V2,RAB18,MTPN,CD164,CACYBP,EIF5A2,ZNF45,DDAH1,PAIP2,BMP2	pink	VSMC_M5

GO:0065008	0.78	0.25	123	2770	regulation of biological quality	BP	1	DGKA,MEX3C,DMXL1,LATS1,MKLN1,PCSK5,WASL,ANXA1,VEGFA,KRIT1,CYP39A1,GCLC,RHOQ,LCA5,UGCG,COMMD1,MACF1,VPS54,RAB1A,SEPT7,ADAM17,CAPZA2,UFL1,ARHGAP42,BBS12,NCOA1,POLR2D,AKAP11,PDCD6IP,DGKH,RHEB,FBXL3,MBD5,FLRT3,XDH,GOLGA7,IRS2,KITLG,MAPK8,DLC1,RB1CC1,IL6ST,CAPRIN1,YTHDF3,CDK5RAP1,ARFGEF1,KDM3A,ERBIN,SMAD1,EIF4G2,SLC4A8,RHOBTB3,TRPC1,DIP2B,TIPARP,ARID2,BAZ2B,BTG2,DNMBP,ATP2B4,TWF1,BTRC,TSPAN32,ACOT13,ANO1,ZMYND8,PRKAB2,ACACB,GSK3B,FSTL1,PUM1,PIK3CA,SCN9A,GTF2I,FXR1,STK39,EGLN1,ALS2,PLEKHA1,ABI2,JMJD1C,ATF7IP,CREBL2,GLRX3,ATF2,SOS2,ACOX3,ARPC2,ERO1A,PRKCI,HP1BP3,USP8,WNK1,OPHN1,FBXW11,USP3,ABCB7,ATP7A,SPATA7,SMAD2,DYNC1H1,XIAP,NF1,PRKAA1,SMAD7,F8,STXBP3,USP33,MT-CO2,ATP5PF,TMEM38B,USP9X,FAM206A,GMFB,UBE2V2,MTPN,EIF5A2,NAF1,SLC25A36,RNF139,DDAH1,PAIP2,BMP2	pink	VSMC_M5
GO:0022603	0.78	0.27	34	761	regulation of anatomical structure morphogenesis	BP	1	MKLN1,ANXA1,VEGFA,KRIT1,RUNX2,RHOQ,MACF1,SEPT7,ZMYM4,JCAD,MAGI2,CLASP1,SPRY4,DLC1,CAPRIN1,SMAD1,EIF4G2,RHOBTB3,DIP2B,HIPK1,DNMBP,ATP2B4,GSK3B,GTF2I,EGLN1,ABI2,ATF2,ARPC2,CRKL,HUWE1,NF1,PTPRM,DDAH1,BMP2	pink	VSMC_M5
GO:0000070	0.78	0.36	5	143	mitotic sister chromatid segregation	BP	1	ATM,PDS5A,ATRX,NIPBL,RMDN1	pink	VSMC_M5
GO:0021915	0.78	0.36	5	130	neural tube development	BP	1	MTHFD1L,DLC1,TCTN1,ARL13B,HECTD1	pink	VSMC_M5
GO:0008015	0.78	0.30	15	369	blood circulation	BP	1	PCSK5,VEGFA,GCLC,ARHGAP42,TRPC1,ATP2B4,MEF2A,PIK3CA,STK39,GLRX3,WNK1,SMAD7,ATP5PF,TMEM38B,DDAH1	pink	VSMC_M5
GO:0071692	0.78	0.32	10	271	protein localization to extracellular region	BP	1	PCSK5,ANXA1,CD2AP,LTBP1,IRS2,ANO1,SMAD2,PIK3C3,STXBP3,GOLPH3L	pink	VSMC_M5
GO:0010876	0.78	0.31	12	311	lipid localization	BP	1	RELCH,SLC25A17,ANXA1,UGCG,OSBPL9,ASXL2,ARL8B,IRS2,DENND5B,ACACB,PRKAA1,ATP5PF	pink	VSMC_M5
GO:0002790	0.78	0.35	6	172	peptide secretion	BP	1	ANXA1,RAB1A,IRS2,ANO1,SMAD2,STXBP3	pink	VSMC_M5
GO:0030097	0.78	0.28	25	618	hemopoiesis	BP	1	ANXA1,VEGFA,RUNX2,ADAM17,UFL1,DCLRE1C,KAT6A,KITLG,N4BP2L2,GABPA,TIPARP,MLF1,HIPK1,NOTCH2,TET2,HECTD1,SRP54,ATF2,SOS2,ATM,PYGO1,ATP7A,WDR78,SMAD7,CD164	pink	VSMC_M5
GO:0010950	0.78	0.38	4	127	positive regulation of endopeptidase activity	BP	1	XDH,APAF1,DLC1,FAM162A	pink	VSMC_M5
GO:1901652	0.78	0.30	15	375	response to peptide	BP	1	ANXA1,GCLC,RHOQ,MBD5,IRS2,ERBIN,BTG2,ANO1,GSK3B,PIK3CA,PRKCI,TIMP1,PRKAA1,STXBP3,CACYBP	pink	VSMC_M5
GO:0048738	0.78	0.33	8	186	cardiac muscle tissue development	BP	1	VEGFA,SMAD1,ARID2,NOTCH2,MEF2A,SMAD7,CACYBP,BMP2	pink	VSMC_M5
GO:0000086	0.79	0.38	4	124	G2/M transition of mitotic cell cycle	BP	1	LATS1,MRE11,FBXL3,ATM	pink	VSMC_M5
GO:0051302	0.79	0.36	5	138	regulation of cell division	BP	1	VEGFA,BIRC6,PIK3C3,RAB11FIP4,PKN2	pink	VSMC_M5
GO:0051049	0.79	0.26	54	1276	regulation of transport	BP	1	UBR5,MKLN1,WASL,ANXA1,VEGFA,CD2AP,GCLC,RHOQ,ERLEC1,COMMD1,RAB33B,MAGI2,PDCD6IP,CLASP1,IRS2,MAPK8,PCM1,SLC4A8,TRPC1,PPP1CC,ZFYVE16,PIP4P2,TSG101,PPP3CC,ATP2B4,NIPSNAP2,BICD1,ANO1,DENND5B,CAB39,MEF2A,GSK3B,SCN9A,STK39,PARL,SCFD1,CREBL2,PRKCI,YWHAQ,WNK1,HUWE1,OPHN1,ATP7A,PIK3C3,DYNC1H1,PRKAA1,STXBP3,UBE2D3,ATP5PF,TMEM38B,RNF139,GOLPH3L,BMP2,SAR1B	pink	VSMC_M5
GO:1902806	0.79	0.38	4	115	regulation of cell cycle G1/S phase transition	BP	1	ANXA1,ADAM17,ATP2B4,ATM	pink	VSMC_M5
GO:0022008	0.79	0.25	60	1272	neurogenesis	BP	1	C9orf72,WASL,ANXA1,VEGFA,FRYL,RUNX2,GCM1,UGCG,MACF1,UFL1,SCLT1,NCOA1,MAGI2,RHEB,FLRT3,TOP2B,ZDHHC17,IL6ST,CAPRIN1,PCM1,CDK5RAP1,ARFGEF1,EIF4G2,DIP2B,TCTN1,PPP1CC,ARSB,TBC1D23,HIPK1,ESRP1,BTG2,TWF1,NOTCH2,ZMYND8,MEF2A,GSK3B,ALS2,ABI2,DLX2,STYXL1,PRKCI,COPS2,CRKL,WNK1,OPHN1,HERC1,ATP7A,TTC8,PTPN9,NF1,PTPRM,NIPBL,HPRT1,SETX,USP33,USP9X,FAM206A,UBE2V2,MTPN,BMP2	pink	VSMC_M5
GO:0140014	0.79	0.32	9	244	mitotic nuclear division	BP	1	CLASP1,LSM14A,CEP97,ATM,PDS5A,ATRX,STAG2,NIPBL,RMDN1	pink	VSMC_M5
GO:0014706	0.79	0.30	13	307	striated muscle tissue development	BP	1	DDX17,VEGFA,SMAD1,ARID2,BTG2,NOTCH2,MEF2A,COPS2,PRKAA1,SMAD7,MTPN,CACYBP,BMP2	pink	VSMC_M5
GO:0001894	0.79	0.33	7	189	tissue homeostasis	BP	1	VEGFA,LCA5,VPS54,BBS12,STK39,SPATA7,NF1	pink	VSMC_M5
GO:0046890	0.79	0.37	4	127	regulation of lipid biosynthetic process	BP	1	ANXA1,CREBL2,PRKAA1,BMP2	pink	VSMC_M5
GO:0022409	0.79	0.34	6	176	positive regulation of cell-cell adhesion	BP	1	ANXA1,MAGI1,IL6ST,PIK3CA,SMAD7,NFAT5	pink	VSMC_M5
GO:1903311	0.79	0.32	9	247	regulation of mRNA metabolic process	BP	1	DDX17,TIA1,SRPK2,POLR2D,YTHDF3,VIRMA,BTG2,PUM1,FXR1	pink	VSMC_M5
GO:0006109	0.79	0.35	5	139	regulation of carbohydrate metabolic process	BP	1	SDHAF3,IRS2,ACACB,GSK3B,PRKAA1	pink	VSMC_M5
GO:0032868	0.79	0.32	8	206	response to insulin	BP	1	GCLC,RHOQ,IRS2,GSK3B,PIK3CA,PRKCI,PRKAA1,STXBP3	pink	VSMC_M5
GO:0045786	0.79	0.30	11	306	negative regulation of cell cycle	BP	1	LATS1,MRE11,CDK5RAP1,BTG2,ATF2,ATM,WAPL,ATRX,FEM1B,RAD1,BMP2	pink	VSMC_M5
GO:0009968	0.79	0.26	41	973	negative regulation of signal transduction	BP	1	LATS1,UBR2,RUNX2,CD2AP,GCLC,ADAM17,UFL1,ARHGAP42,MAGI2,XDH,BIRC6,LTBP1,SPRY4,DLC1,RB1CC1,CSNK2A1,YTHDF3,ERBIN,URI1,TSG101,ATP2B4,CYLD,RANBP9,BTRC,BICD1,GSK3B,UBR1,PLEKHA1,DLX2,HERC4,ATM,GHITM,ASH1L,GGNBP2,CSNK1A1,NF1,PRKAA1,SMAD7,UBE2D3,BMT2,BMP2	pink	VSMC_M5
GO:0019752	0.79	0.27	23	659	carboxylic acid metabolic process	BP	1	ME2,MTHFD1L,SLC25A17,ANXA1,CYP39A1,SDHAF3,ASNS,GCLC,MDH1,OSBPL9,OXSM,IRS2,UEVLD,ATP2B4,PRKAB2,ACACB,MORC2,ACOX3,ATP7A,PRKAA1,NUDT7,HACD1,DDAH1	pink	VSMC_M5
GO:0034504	0.79	0.31	9	244	protein localization to nucleus	BP	1	LATS1,SYNE1,UBR5,KPNA5,CD2AP,IPO8,GSK3B,RPAIN,PYGO1	pink	VSMC_M5
GO:0061564	0.79	0.28	17	380	axon development	BP	1	C9orf72,VEGFA,MACF1,FLRT3,TOP2B,ZDHHC17,EIF4G2,DIP2B,TCTN1,NOTCH2,GSK3B,ALS2,OPHN1,TTC8,PTPRM,USP33,USP9X	pink	VSMC_M5
GO:0060348	0.79	0.33	7	172	bone development	BP	1	RUNX2,IMPAD1,SMAD1,BBX,NOTCH2,TMEM38B,BMP2	pink	VSMC_M5
GO:1903530	0.80	0.29	15	399	regulation of secretion by cell	BP	1	ANXA1,CD2AP,RAB33B,PDCD6IP,CLASP1,IRS2,SLC4A8,TSG101,ANO1,GSK3B,PIK3C3,STXBP3,ATP5PF,GOLPH3L,BMP2	pink	VSMC_M5

GO:0048856	0.80	0.23	194	4193	anatomical structure development	BP	1	MEX3C,TAB2,LATS1,MTHFD1L,SYNE1,SNX2,DDX17,MKLN1,VPS13A,PCSK5,C9orf72,WASL,ANXA1,VEGFA,KRIT1,FRYL,RUNX2,ASNS,GCM1,RNF38,RHOQ,FAM126A,UGCG,MACF1,RAB1A,SEPT7,ADAM17,UFL1,CUL1,ZMYM4,RAB14,RAB33B,SCLT1,JCAD,KIAA1109,SRPK2,NCOA1,EPC1,ASXL2,MAGI2,DCLRE1C,CLASP1,EPB41L5,RHEB,ZEB2,MBD5,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,BIRC6,IRS2,KITLG,SPRY4,ATRN,N4BP2L2,APAF1,DLC1,RB1CC1,IL6ST,IMPAD1,CAPRIN1,PCM1,YTHDF3,FAT1,CDK5RAP1,ARFGEF1,KDM3A,SMAD1,EIF4G2,RHOBTB3,DIP2B,TCTN1,GABPA,PPP1CC,TET3,WWP1,TIPARP,MLF1,ARL13B,FAM92A,ARSB,TBC1D23,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BTG2,DNMBP,ATP2B4,CSDE1,TWF1,BBX,BTRC,PSMG1,NDUFS4,NOTCH2,TRIP12,BICD1,ZMYND8,MEF2A,TET2,KMT5B,ACACB,GSK3B,FSTL1,PIK3CA,SCN9A,GTF2I,BPTF,FXR1,TFIP11,EGLN1,TIAL1,CCDC14,ALS2,UBR3,PLEKHA5,PLEKHA1,ZNF148,SCFD1,ABI2,HECTD1,DLX2,ARHGAP5,RPS6KA3,PAFAH1B2,SRP54,ATF2,STYXL1,RNF2,SOS2,ATM,KDM6A,ARPC2,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,WNK1,PYGO1,FUT8,HUWE1,OPHN1,YIPF6,FBXW11,ASH1L,HERC1,SPTLC2,ATRX,ATP7A,PIAS1,FEM1B,TTC8,DIAPH2,SMAD2,GGNBP2,PTPN9,UBE2A,WDR78,NF1,PRKAA1,PTPRM,NIPBL,RAD1,PHF6,HPRT1,SMAD7,SETX,STXBP3,USP33,MT-CO1,MT-CO2,MT-ND4,BIRC2,SMIM14,ATP5PF,TMEM38B,USP9X,FAM206A,RNF103,GMFB,UBE2V2,RAB18,MTPN,CD164,CACYBP,ZNF45,DDAH1,BMP2	pink	VSMC_M5
GO:0043123	0.80	0.35	5	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	TAB2,ZDHHC17,IFIT5,IRAK4,BIRC2	pink	VSMC_M5
GO:0010975	0.80	0.28	16	376	regulation of neuron projection development	BP	1	VEGFA,MACF1,MAGI2,CAPRIN1,EIF4G2,DIP2B,ARSB,TWF1,GSK3B,ABI2,STYXL1,PRKCI,CRKL,PTPN9,SETX,UBE2V2	pink	VSMC_M5
GO:0008285	0.80	0.27	21	548	negative regulation of cell population proliferation	BP	1	KRIT1,MAGI2,XDH,DLC1,SMAD1,TSG101,ARID2,BTG2,TSPAN32,TIAL1,ATF2,ATM,SMAD2,GGNBP2,NF1,PTPRM,SMAD7,CD164,RNF139,DDAH1,BMP2	pink	VSMC_M5
GO:0032990	0.80	0.26	25	536	cell part morphogenesis	BP	1	SNX2,C9orf72,WASL,VEGFA,MACF1,FLRT3,TOP2B,ZDHHC17,CAPRIN1,EIF4G2,DIP2B,TCTN1,NOTCH2,MEF2A,GSK3B,ALS2,ABI2,OPHN1,ATP7A,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5
GO:0002449	0.80	0.34	5	159	lymphocyte mediated immunity	BP	1	ARL8B,KMT5B,LYST,HPRT1,SMAD7	pink	VSMC_M5
GO:0071478	0.80	0.34	5	150	cellular response to radiation	BP	1	POLK,ATM,TIMP1,NIPBL,RAD1	pink	VSMC_M5
GO:0014070	0.80	0.26	29	703	response to organic cyclic compound	BP	1	LATS1,UBR5,DDX17,ANXA1,ASNS,GCLC,UFL1,NCOA1,NR3C1,KDM3A,URI1,SMAD1,NR3C2,GABPA,TIPARP,BTG2,ATP2B4,BTRC,NDUFS4,TET2,ACACB,GSK3B,USP8,SMAD2,PRKAA1,MT-ND3,BIRC2,TMEM38B,BMP2	pink	VSMC_M5
GO:0048534	0.80	0.26	26	649	hematopoietic or lymphoid organ development	BP	1	ANXA1,VEGFA,RUNX2,ADAM17,UFL1,DCLRE1C,KAT6A,KITLG,N4BP2L2,GABPA,TIPARP,MLF1,HIPK1,NOTCH2,TET2,HECTD1,SRP54,ATF2,SOS2,ATM,CRKL,PYGO1,ATP7A,WDR78,SMAD7,CD164	pink	VSMC_M5
GO:0009451	0.80	0.36	4	141	RNA modification	BP	1	CDK5RAP1,VIRMA,METTL5,NAF1	pink	VSMC_M5
GO:0006082	0.80	0.26	24	689	organic acid metabolic process	BP	1	ME2,MTHFD1L,SLC25A17,ANXA1,CYP39A1,SDHAF3,ASNS,GCLC,MDH1,OSBPL9,OXSM,IRS2,UEVLD,ATP2B4,PRKAB2,ACACB,MORC2,ACOX3,ATP7A,PRKAA1,NUDT7,SULT1C4,HACD1,DDAH1	pink	VSMC_M5
GO:0007154	0.80	0.22	194	4300	cell communication	BP	1	DGKA,ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,DDX17,MKLN1,KLHDC10,PCSK5,UBR2,C9orf72,ANXA1,TMEM33,VEGFA,KRIT1,RUNX2,CD2AP,ASNS,GCLC,DST,RHOQ,ERLEC1,USP34,UGCG,MACF1,RAB1A,ADAM17,UFL1,CUL1,RAB14,CUL2,RAB33B,ZFYVE9,JCAD,ARHGAP42,SRPK2,NCOA1,MRE11,ASXL2,MAGI2,MAP3K2,AKAP11,DGKH,RHEB,FNTA,ZEB2,MBD5,FLRT3,XDH,KAT6A,ZDHHC17,NKIRAS1,BIRC6,LTBP1,IRS2,KITLG,PRKD3,SPRY4,NR3C1,MAP4K3,MAPK8,APAF1,MAGI1,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,FAT1,TNKS2,LSM14A,PJA2,ARFGEF1,KDM3A,ERBIN,URI1,SMAD1,SLC4A8,NR3C2,KCMF1,RHOBTB3,RNF13,TCTN1,PPP1CC,WWP1,ZFYVE16,CPNE3,TIPARP,RALGAPB,ARL13B,FAM92A,GTF2H1,TSG101,HIPK1,PPP3CC,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,TSPAN32,DOCK3,NOTCH2,BICD1,ANO1,ASB7,CAB39,ZMYND8,IPO8,MEF2A,SHOC2,PRKAB2,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,SCN9A,STK39,FAM162A,TIAL1,ALS2,RPS6KC1,PDE5A,TLK1,PLEKHA1,MUC20,ABI2,DLX2,ARHGAP5,RPS6KA3,CREBL2,ATF2,HERC4,STYXL1,RALGPS2,SOS2,ATM,CUL5,ERO1A,PRKCI,COPS2,YWHAQ,USP8,TIMP1,CRKL,WNK1,GHITM,PYGO1,FUT8,OPHN1,CPEB4,FBXW11,ASH1L,ATRX,CHM,PIAS1,FEM1B,SMAD2,PIK3C3,GSKIP,GGNBP2,SMG1,CSNK1A1,XIAP,NF1,PRKAA1,PTPRM,RAD1,SMAD7,SETX,STXBP3,PKN2,NFAT5,USP33,BIRC2,NMS,AGO3,UBE2D3,ATP5PF,TMEM38B,USP9X,GMFB,RAB18,CD164,DDAH1,BMT2,PAIP2,MPZL1,BMP2	pink	VSMC_M5
GO:0002040	0.80	0.36	4	114	sprouting angiogenesis	BP	1	ANXA1,VEGFA,JCAD,SMAD1	pink	VSMC_M5
GO:0030073	0.80	0.34	5	149	insulin secretion	BP	1	ANXA1,IRS2,ANO1,SMAD2,STXBP3	pink	VSMC_M5
GO:0030178	0.80	0.34	5	142	negative regulation of Wnt signaling pathway	BP	1	LATS1,CYLD,GSK3B,CSNK1A1,BMP2	pink	VSMC_M5
GO:0006887	0.81	0.29	10	266	exocytosis	BP	1	ANXA1,RAB33B,PDCD6IP,CLASP1,ARL8B,ARFGEF1,SLC4A8,TSG101,GSK3B,STXBP3	pink	VSMC_M5
GO:0048469	0.81	0.35	4	116	cell maturation	BP	1	VEGFA,RUNX2,SCLT1,FEM1B	pink	VSMC_M5
GO:0009617	0.81	0.28	13	362	response to bacterium	BP	1	TAB2,WASL,RAB1A,ADAM17,RAB14,MAPK8,ERBIN,NOTCH2,LYST,RPS6KA3,NAALADL2,PRPF8,BMP2	pink	VSMC_M5
GO:0061013	0.81	0.33	5	144	regulation of mRNA catabolic process	BP	1	POLR2D,YTHDF3,BTG2,PUM1,FXR1	pink	VSMC_M5
GO:0001763	0.81	0.32	6	157	morphogenesis of a branching structure	BP	1	VEGFA,GCM1,BTRC,DLX2,FEM1B,BMP2	pink	VSMC_M5
GO:0000075	0.81	0.33	5	155	cell cycle checkpoint signaling	BP	1	MRE11,ATF2,ATM,FEM1B,RAD1	pink	VSMC_M5
GO:0043010	0.81	0.29	10	242	camera-type eye development	BP	1	VEGFA,FAT1,HIPK1,ATP2B4,NOTCH2,ABI2,DLX2,TTC8,NF1,PTPRM	pink	VSMC_M5
GO:1903034	0.81	0.35	4	123	regulation of response to wounding	BP	1	ANXA1,CLASP1,ARFGEF1,ATP7A	pink	VSMC_M5

GO:0009165	0.81	0.32	6	198	nucleotide biosynthetic process	BP	1	ACACB,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:1904062	0.81	0.29	9	241	regulation of cation transmembrane transport	BP	1	COMMD1,TRPC1,ATP2B4,NIPSNAP2,CAB39,STK39,WNK1,ATP7A,TMEM38B	pink	VSMC_M5
GO:0034767	0.81	0.34	4	114	positive regulation of ion transmembrane transport	BP	1	TRPC1,NIPSNAP2,STK39,WNK1	pink	VSMC_M5
GO:0097553	0.81	0.34	4	95	calcium ion transmembrane import into cytosol	BP	1	TRPC1,ATP2B4,ERO1A,TMEM38B	pink	VSMC_M5
GO:1901293	0.81	0.31	6	199	nucleoside phosphate biosynthetic process	BP	1	ACACB,HPRT1,MT-CO2,HACD1,ATP5PF,DCAKD	pink	VSMC_M5
GO:0019827	0.81	0.34	4	106	stem cell population maintenance	BP	1	PCM1,KDM3A,NOTCH2,NIPBL	pink	VSMC_M5
GO:0050768	0.81	0.34	4	102	negative regulation of neurogenesis	BP	1	PCM1,DIP2B,DLX2,NF1	pink	VSMC_M5
GO:0044242	0.82	0.32	5	164	cellular lipid catabolic process	BP	1	SLC25A17,IRS2,ACACB,ACOX3,NUDT7	pink	VSMC_M5
GO:0006869	0.82	0.28	10	273	lipid transport	BP	1	RELCH,SLC25A17,ANXA1,UGCG,OSBPL9,ARL8B,IRS2,DENND5B,PRKAA1,ATP5PF	pink	VSMC_M5
GO:0060249	0.82	0.29	8	218	anatomical structure homeostasis	BP	1	VEGFA,LCA5,VPS54,BBS12,STK39,SPATA7,NF1,PRKAA1	pink	VSMC_M5
GO:0050727	0.82	0.29	8	239	regulation of inflammatory response	BP	1	ANXA1,UFL1,IL6ST,CYLD,STK39,ASH1L,XIAP,BIRC2	pink	VSMC_M5
GO:0044262	0.82	0.29	8	229	cellular carbohydrate metabolic process	BP	1	SDHAF3,IRS2,RB1CC1,IL6ST,IMPAD1,PPP1CC,ACACB,GSK3B	pink	VSMC_M5
GO:0007605	0.82	0.33	4	102	sensory perception of sound	BP	1	FBXO11,CCDC50,NIPBL,TIMM9	pink	VSMC_M5
GO:0098727	0.82	0.33	4	108	maintenance of cell number	BP	1	PCM1,KDM3A,NOTCH2,NIPBL	pink	VSMC_M5
GO:0042445	0.82	0.33	4	133	hormone metabolic process	BP	1	PCSK5,TIPARP,PLEKHA1,BMP2	pink	VSMC_M5
GO:0006952	0.82	0.23	36	949	defense response	BP	1	DDX17,ANXA1,RAB1A,ADAM17,UFL1,RAB14,SRPK2,ARL8B,ATRN,IL6ST,IFIT5,YTHDF3,LSM14A,PJA2,SMAD1,LXN,IRAK4,CYLD,TSPAN32,NOTCH2,PUM1,LYST,SCN9A,STK39,TIAL1,ALS2,ZNF148,TIMP1,ASH1L,USP14,XIAP,F8,STXBP3,BIRC2,ELMOD2,BMP2	pink	VSMC_M5
GO:0072175	0.82	0.33	4	116	epithelial tube formation	BP	1	MTHFD1L,DLC1,TCTN1,HECTD1	pink	VSMC_M5
GO:0098742	0.82	0.29	7	152	cell-cell adhesion via plasma-membrane adhesion molecules	BP	1	FLRT3,FAT1,WNK1,PTPRM,CD164,BMP2,PCDHGB1	pink	VSMC_M5
GO:0099504	0.82	0.31	5	138	synaptic vesicle cycle	BP	1	KIAA1109,SLC4A8,PPP3CC,GSK3B,OPHN1	pink	VSMC_M5
GO:0048872	0.82	0.28	8	229	homeostasis of number of cells	BP	1	ANXA1,VEGFA,VPS54,ADAM17,UFL1,KITLG,FSTL1,SOS2	pink	VSMC_M5
GO:0045859	0.82	0.24	20	513	regulation of protein kinase activity	BP	1	TAB2,LATS1,VEGFA,ADAM17,KITLG,SPRY4,CDK5RAP1,GTF2H1,TSG101,ATP2B4,DOCK3,CAB39,PIK3CA,ALS2,WNK1,GSKIP,CCNK,GGNBP2,NF1,BMP2	pink	VSMC_M5
GO:0044839	0.82	0.32	4	132	cell cycle G2/M phase transition	BP	1	LATS1,MRE11,FBXL3,ATM	pink	VSMC_M5
GO:0001934	0.83	0.23	21	543	positive regulation of protein phosphorylation	BP	1	TAB2,LATS1,VEGFA,ADAM17,MRE11,KITLG,RB1CC1,IL6ST,CDK5RAP1,ATP2B4,DOCK3,CAB39,PIK3CA,FXR1,ALS2,CREBL2,ATF2,CRKL,WNK1,CCNK,BMP2	pink	VSMC_M5
GO:0007281	0.83	0.29	6	177	germ cell development	BP	1	KDM3A,TIAL1,RNF2,PYGO1,FBXW11,DIAPH2	pink	VSMC_M5
GO:0035239	0.83	0.22	30	699	tube morphogenesis	BP	1	MTHFD1L,ANXA1,VEGFA,KRIT1,JCAD,SRPK2,EPB41L5,XDH,DLC1,SMAD1,TCTN1,TIPARP,ARL13B,HIPK1,ARID2,ATP2B4,BTRC,NOTCH2,PIK3CA,GTF2I,EGLN1,HECTD1,ATF2,SMAD2,NF1,PTPRM,NIPBL,SMAD7,DDAH1,BMP2	pink	VSMC_M5
GO:0002366	0.83	0.28	6	181	leukocyte activation involved in immune response	BP	1	ANXA1,NOTCH2,KMT5B,ATP7A,SMAD7,STXBP3	pink	VSMC_M5
GO:0030334	0.83	0.22	31	735	regulation of cell migration	BP	1	WASL,ANXA1,VEGFA,KRIT1,PTP4A1,MACF1,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,IRS2,KITLG,DLC1,YTHDF3,CPNE3,ARSB,ARID2,ATP2B4,ZMYND8,STK39,ATM,TIMP1,CRKL,WNK1,ATP7A,NF1,PTPRM,NIPBL,SMAD7,BMP2	pink	VSMC_M5
GO:0098660	0.83	0.22	23	574	inorganic ion transmembrane transport	BP	1	COMMD1,PCYOX1,ZDHHC17,SLC30A6,SLC4A8,TRPC1,ATP2B4,NIPSNAP2,ANO1,CAB39,SCN9A,STK39,CUL5,ERO1A,WNK1,ABCB7,ATP7A,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0034329	0.83	0.24	14	318	cell junction assembly	BP	1	VEGFA,DST,MACF1,PDCD6IP,CLASP1,EPB41L5,FLRT3,DLC1,HIPK1,CRKL,OPHN1,SMAD7,PKN2,UBE2V2	pink	VSMC_M5
GO:0007266	0.83	0.31	4	116	Rho protein signal transduction	BP	1	ARHGAP42,DLC1,ARHGAP5,OPHN1	pink	VSMC_M5
GO:0002521	0.84	0.24	14	383	leukocyte differentiation	BP	1	ANXA1,VEGFA,RUNX2,ADAM17,DCLRE1C,KITLG,NOTCH2,HECTD1,SRP54,ATF2,SOS2,ATM,ATP7A,SMAD7	pink	VSMC_M5
GO:0014074	0.84	0.31	4	109	response to purine-containing compound	BP	1	NDUFS4,PRKAA1,BIRC2,TMEM38B	pink	VSMC_M5
GO:0001932	0.84	0.21	34	845	regulation of protein phosphorylation	BP	1	TAB2,PPIL4,LATS1,C9orf72,VEGFA,ADAM17,MRE11,XDH,KITLG,SPRY4,RB1CC1,IL6ST,CDK5RAP1,GTF2H1,TSG101,ATP2B4,TWF1,NDUFS4,DOCK3,CAB39,PIK3CA,FXR1,ALS2,CREBL2,ATF2,CRKL,WNK1,GSKIP,CCNK,GGNBP2,NF1,PRKAA1,SMAD7,BMP2	pink	VSMC_M5
GO:0009306	0.84	0.25	9	266	protein secretion	BP	1	PCSK5,ANXA1,CD2AP,IRS2,ANO1,SMAD2,PIK3C3,STXBP3,GOLPH3L	pink	VSMC_M5
GO:0035592	0.84	0.25	9	266	establishment of protein localization to extracellular region	BP	1	PCSK5,ANXA1,CD2AP,IRS2,ANO1,SMAD2,PIK3C3,STXBP3,GOLPH3L	pink	VSMC_M5
GO:0006898	0.84	0.27	7	192	receptor-mediated endocytosis	BP	1	MKLN1,WASL,VEGFA,CD2AP,MAGI2,BICD1,OPHN1	pink	VSMC_M5
GO:0006396	0.84	0.21	33	950	RNA processing	BP	1	SCAF8,DDX17,TIA1,CPSF3,CDC40,SRPK2,POLR2D,INTS4,SHQ1,RPP14,CDK5RAP1,PPWD1,SMAD1,AQR,DUSP11,VIRMA,ESRP1,SNRPN,BICD1,PUM1,FXR1,TFIP11,METTL5,SCNM1,TSEN15,WDR83,SMAD2,PRPF8,SETX,PTBP2,AGO3,HNRNPLL,NAF1	pink	VSMC_M5
GO:0051961	0.84	0.30	4	106	negative regulation of nervous system development	BP	1	PCM1,DIP2B,DLX2,NF1	pink	VSMC_M5
GO:0097529	0.84	0.30	4	142	myeloid leukocyte migration	BP	1	ANXA1,VEGFA,IRAK4,SRP54	pink	VSMC_M5

GO:0048731	0.84	0.18	163	3556	system development	BP	1	MEX3C,TAB2,LATS1,MTHFD1L,DDX17,VPS13A,PCSK5,C9orf72,WASL,ANXA1,VEGFA,KRIT1,FRYL,RUNX2,ASNS,GCM1,RNF38,FAM126A,UGCG,MACF1,ADAM17,UFL1,CUL1,RAB33B,SCLT1,JCAD,SRPK2,NCOA1,EPC1,ASXL2,MAGI2,DCLRE1C,CLASP1,EPB41L5,RHEB,ZEB2,MBD5,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,BIRC6,IRS2,KITLG,SPRY4,ATRN,N4BP2L2,APAF1,DLC1,RB1CC1,IL6ST,IMPAD1,CAPRIN1,PCM1,FAT1,CDK5RAP1,ARFGEF1,SMAD1,EIF4G2,RHOBTB3,DIP2B,TCTN1,GABPA,PPP1CC,WWP1,TIPARP,MLF1,ARL13B,ARSB,TBC1D23,TSG101,HIPK1,ESRP1,ARID2,PPP3CC,BTG2,ATP2B4,CSDE1,TWF1,BBX,BTRC,PSMG1,NDUFS4,NOTCH2,ZMYND8,MEF2A,TET2,KMT5B,ACACB,GSK3B,PIK3CA,GTF2I,BPTF,FXR1,TFIP11,EGLN1,CCDC14,ALS2,PLEKHA5,PLEKHA1,ZNF148,ABI2,HECTD1,DLX2,ARHGAP5,RPS6KA3,PAFAH1B2,SRP54,ATF2,STYXL1,SOS2,ATM,KDM6A,ERO1A,PRKCI,COPS2,YWHAQ,TIMP1,CRKL,WNK1,PYGO1,OPHN1,YIPF6,FBXW11,ASH1L,HERC1,SPTLC2,ATRX,ATP7A,FEM1B,TTC8,SMAD2,GGNBP2,PTPN9,WDR78,NF1,PRKAA1,PTPRM,NIPBL,RAD1,HPRT1,SMAD7,SETX,STXBP3,USP33,MT-CO1,MT-CO2,MT-ND4,BIRC2,ATP5PF,TMEM38B,USP9X,FAM206A,RNF103,GMFB,UBE2V2,RAB18,MTPN,CD164,CACYBP,DDAH1,BMP2	pink	VSMC_M5
GO:0071375	0.84	0.26	8	219	cellular response to peptide hormone stimulus	BP	1	GCLC,RHOQ,MBD5,IRS2,GSK3B,PIK3CA,PRKCI,PRKAA1	pink	VSMC_M5
GO:0071897	0.84	0.28	5	150	DNA biosynthetic process	BP	1	MRE11,TNKS2,POLK,ATM,NAF1	pink	VSMC_M5
GO:0001568	0.85	0.21	24	576	blood vessel development	BP	1	ANXA1,VEGFA,KRIT1,JCAD,SRPK2,XDH,SMAD1,TIPARP,HIPK1,ARID2,ATP2B4,NOTCH2,PIK3CA,GTF2I,EGLN1,HECTD1,ATF2,CRKL,ATP7A,GGNBP2,NF1,PTPRM,SMAD7,DDAH1	pink	VSMC_M5
GO:0006606	0.85	0.29	4	129	protein import into nucleus	BP	1	UBR5,KPNA5,IPO8,RPAIN	pink	VSMC_M5
GO:0005975	0.85	0.22	16	458	carbohydrate metabolic process	BP	1	SDHAF3,GCLC,MDH1,IRS2,RB1CC1,IL6ST,IMPAD1,PPP1CC,UEVLD,ACACB,GSK3B,PIK3CA,LANCL1,FUT8,PGM2,PRKAA1	pink	VSMC_M5
GO:0006814	0.85	0.27	6	161	sodium ion transport	BP	1	COMMD1,SLC4A8,ATP2B4,SCN9A,STK39,WNK1	pink	VSMC_M5
GO:0015833	0.85	0.27	6	186	peptide transport	BP	1	ANXA1,RAB1A,IRS2,ANO1,SMAD2,STXBP3	pink	VSMC_M5
GO:0000724	0.85	0.29	4	124	double-strand break repair via homologous recombination	BP	1	MRE11,ARID2,KLHL15,NIPBL	pink	VSMC_M5
GO:0010001	0.85	0.26	6	173	glial cell differentiation	BP	1	GCM1,RHEB,IL6ST,DLX2,NF1,BMP2	pink	VSMC_M5
GO:0001818	0.85	0.26	6	195	negative regulation of cytokine production	BP	1	ANXA1,CD2AP,TIA1,ERBIN,CYLD,SMAD7	pink	VSMC_M5
GO:0002263	0.85	0.26	6	185	cell activation involved in immune response	BP	1	ANXA1,NOTCH2,KMT5B,ATP7A,SMAD7,STXBP3	pink	VSMC_M5
GO:0034470	0.85	0.23	11	345	ncRNA processing	BP	1	DDX17,INTS4,SHQ1,RPP14,CDK5RAP1,SMAD1,METTL5,TSEN15,SMAD2,AGO3,NAF1	pink	VSMC_M5
GO:0010952	0.85	0.29	4	142	positive regulation of peptidase activity	BP	1	XDH,APAF1,DLC1,FAM162A	pink	VSMC_M5
GO:0002520	0.85	0.20	27	694	immune system development	BP	1	ANXA1,VEGFA,RUNX2,ADAM17,UFL1,DCLRE1C,KAT6A,KITLG,N4BP2L2,GABPA,TIPARP,MLF1,HIPK1,NOTCH2,TET2,KMT5B,HECTD1,SRP54,ATF2,SOS2,ATM,CRKL,PYGO1,ATP7A,WDR78,SMAD7,CD164	pink	VSMC_M5
GO:0065009	0.85	0.18	98	2307	regulation of molecular function	BP	1	ARFGEF3,TAB2,LATS1,MAPK9,SERINC1,PCSK5,C9orf72,WASL,ANXA1,VEGFA,KRIT1,SMAP2,TAX1BP1,COMMD1,ADAM17,UFL1,ARHGAP42,MRE11,MAGI2,EPB41L5,FNTA,ZEB2,XDH,BIRC6,IRS2,KITLG,SPRY4,MAPK8,APAF1,DLC1,CSNK2A1,CDK5RAP1,ARFGEF1,ERBIN,URI1,RALGAPB,LXN,GTF2H1,TSG101,DNMBP,ATP2B4,CYLD,BTRC,NIPSNAP2,DOCK3,BICD1,DENND5B,CAB39,PPP6R3,SHOC2,PRKAB2,ACACB,GSK3B,PIK3CA,DCUN1D1,TFIP11,STK39,EGLN1,FAM162A,ALS2,ARHGAP5,RPS6KA3,ATF2,ACAP2,STYXL1,RNF2,RALGPS2,SOS2,PRKCI,TIMP1,CRKL,WNK1,WAPL,OPHN1,UBE2Z,HERC1,ATP7A,CHM,FEM1B,TTC8,SMAD2,GSKIP,CCNK,GGNBP2,CSNK1A1,USP14,XIAP,NF1,SMAD7,USP33,BIRC2,GMFB,MTPN,NAF1,ELMOD2,DDAH1,SPINK8,BMP2	pink	VSMC_M5
GO:0000725	0.85	0.28	4	126	recombinational repair	BP	1	MRE11,ARID2,KLHL15,NIPBL	pink	VSMC_M5
GO:0019220	0.85	0.19	44	1074	regulation of phosphate metabolic process	BP	1	TAB2,PPIL4,LATS1,C9orf72,VEGFA,ADAM17,MRE11,MAGI2,XDH,IRS2,KITLG,SPRY4,DLC1,RB1CC1,IL6ST,CDK5RAP1,URI1,BTBD10,GTF2H1,TSG101,ATP2B4,TWF1,NDUFS4,DOCK3,CAB39,PPP6R3,GSK3B,PIK3CA,FXR1,ALS2,CREBL2,SMG7,ATF2,STYXL1,CRKL,WNK1,GSKIP,CCNK,GGNBP2,NF1,PRKAA1,SMAD7,MT-CO2,BMP2	pink	VSMC_M5
GO:0051174	0.85	0.19	44	1074	regulation of phosphorus metabolic process	BP	1	TAB2,PPIL4,LATS1,C9orf72,VEGFA,ADAM17,MRE11,MAGI2,XDH,IRS2,KITLG,SPRY4,DLC1,RB1CC1,IL6ST,CDK5RAP1,URI1,BTBD10,GTF2H1,TSG101,ATP2B4,TWF1,NDUFS4,DOCK3,CAB39,PPP6R3,GSK3B,PIK3CA,FXR1,ALS2,CREBL2,SMG7,ATF2,STYXL1,CRKL,WNK1,GSKIP,CCNK,GGNBP2,NF1,PRKAA1,SMAD7,MT-CO2,BMP2	pink	VSMC_M5
GO:0044770	0.85	0.21	15	426	cell cycle phase transition	BP	1	LATS1,ANXA1,ADAM17,CUL1,CUL2,MRE11,CLASP1,FBXL3,ATP2B4,ATF2,ATM,CUL5,PIAS1,FEM1B,RAD1	pink	VSMC_M5
GO:1903039	0.85	0.28	4	143	positive regulation of leukocyte cell-cell adhesion	BP	1	ANXA1,IL6ST,PIK3CA,NFAT5	pink	VSMC_M5
GO:0007519	0.85	0.28	4	122	skeletal muscle tissue development	BP	1	DDX17,BTG2,COPS2,PRKAA1	pink	VSMC_M5
GO:0048468	0.85	0.18	72	1587	cell development	BP	1	MEX3C,LATS1,C9orf72,WASL,VEGFA,FRYL,RUNX2,UGCG,MACF1,RAB1A,UFL1,SCLT1,MAGI2,EPB41L5,RHEB,FLRT3,TOP2B,ZDHHC17,KITLG,SPRY4,ATRN,IL6ST,IMPAD1,CAPRIN1,PCM1,FAT1,ARFGEF1,KDM3A,EIF4G2,DIP2B,TCTN1,PPP1CC,ARL13B,ARSB,TBC1D23,BTG2,TWF1,NOTCH2,ZMYND8,MEF2A,GSK3B,TIAL1,ALS2,ABI2,DLX2,STYXL1,RNF2,ARPC2,PRKCI,CRKL,WNK1,PYGO1,OPHN1,YIPF6,FBXW11,HERC1,ATRX,ATP7A,FEM1B,TTC8,DIAPH2,PTPN9,NF1,PTPRM,HPRT1,SMAD7,SETX,USP33,USP9X,FAM206A,UBE2V2,BMP2	pink	VSMC_M5
GO:0051170	0.85	0.28	4	132	import into nucleus	BP	1	UBR5,KPNA5,IPO8,RPAIN	pink	VSMC_M5

GO:0006810	0.86	0.17	141	3300	transport	BP	1	RELCH,VTA1,VPS13B,SNX2,CSNK1G3,UBR5,SFT2D1,KPNA5,SLC25A17,MKLN1,VPS13A,PCSK5,C9orf72,WASL,ANXA1,VEGFA,CD2AP,SRP72,GCLC,DST,RHOQ,ERLEC1,LCA5,UGCG,COMMD1,MACF1,VPS54,RAB1A,PCYOX1,RAB14,RAB33B,ZFYVE9,SLC41A3,OSBPL9,BBS12,KIAA1109,NCOA1,POLR2D,MAGI2,PDCD6IP,CLASP1,XDH,ARL8B,ZDHHC17,GOLGA7,SLC30A6,COG6,IRS2,MAPK8,VPS37A,MTMR6,PCM1,SGTB,ARFGEF1,ERBIN,SLC4A8,RHOBTB3,TRPC1,VPS29,PPP1CC,WWP1,ZFYVE16,ANTXR2,PIP4P2,ARSB,TBC1D23,TSG101,UEVLD,PPP3CC,SSR1,ATP2B4,ZC3H11A,NIPSNAP2,BICD1,ANO1,DENND5B,CAB39,IPO8,MEF2A,GOLGA5,GSK3B,PIK3CA,LYST,SCN9A,STK39,ZFAND2A,PARL,ALS2,TLK1,SCFD1,CREBL2,SMG7,SRP54,ATF2,MTX2,ACAP2,NEMF,CUL5,ERO1A,PRKCI,YWHAQ,CCZ1B,RPAIN,WNK1,HUWE1,OPHN1,SFXN1,SNX11,FBXW11,ABCB7,ATP7A,CHM,TTC8,SMAD2,PIK3C3,APPBP2,DYNC1H1,SMG1,RAB11FIP4,PRKAA1,TRAPPC2L,STXBP3,SLC35A3,USP33,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ARRDC5,UBE2D3,ATP5PF,TMEM38B,RAB18,EIF5A2,SLC25A36,RNF139,GOLPH3L,TIMM9,BMP2,SAR1B,ZDHHC22	pink	VSMC_M5
GO:0050770	0.86	0.26	5	132	regulation of axonogenesis	BP	1	VEGFA,MACF1,EIF4G2,DIP2B,GSK3B	pink	VSMC_M5
GO:0030323	0.86	0.26	5	145	respiratory tube development	BP	1	PCSK5,VEGFA,ATP7A,SMAD2,TMEM38B	pink	VSMC_M5
GO:0019932	0.86	0.24	8	218	second-messenger-mediated signaling	BP	1	VEGFA,PPP3CC,ATP2B4,GSK3B,PRKAA1,NFAT5,TMEM38B,DDAH1	pink	VSMC_M5
GO:1903047	0.86	0.20	23	608	mitotic cell cycle process	BP	1	LATS1,ANXA1,ADAM17,CUL1,CUL2,MRE11,PDCD6IP,CLASP1,FBXL3,LSM14A,CEP97,ATF2,ATM,CUL5,USP8,PDS5A,FBXW11,ATRX,PIAS1,DYNC1H1,STAG2,NIPBL,RMDN1	pink	VSMC_M5
GO:2000145	0.86	0.19	32	772	regulation of cell motility	BP	1	WASL,ANXA1,VEGFA,KRIT1,PTP4A1,MACF1,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,IRS2,KITLG,DLC1,YTHDF3,CPNE3,ARSB,ARID2,ATP2B4,ZMYND8,STK39,ATM,TIMP1,CRKL,WNK1,ATP7A,NF1,PTPRM,NIPBL,SMAD7,PKN2,BMP2	pink	VSMC_M5
GO:0030335	0.86	0.20	17	443	positive regulation of cell migration	BP	1	ANXA1,VEGFA,PTP4A1,ADAM17,JCAD,CLASP1,EPB41L5,IRS2,KITLG,CPNE3,STK39,ATM,CRKL,WNK1,ATP7A,NIPBL,BMP2	pink	VSMC_M5
GO:0007584	0.86	0.27	4	137	response to nutrient	BP	1	GCLC,NCOA1,APAF1,ARSB	pink	VSMC_M5
GO:0048771	0.86	0.27	4	129	tissue remodeling	BP	1	NOTCH2,TIMP1,ATP7A,NF1	pink	VSMC_M5
GO:0051098	0.86	0.22	10	296	regulation of binding	BP	1	C9orf72,EPB41L5,MAPK8,GSK3B,TFIP11,WAPL,SMAD2,CSNK1A1,USP33,BMP2	pink	VSMC_M5
GO:0009888	0.86	0.17	61	1389	tissue development	BP	1	MEX3C,LATS1,MTHFD1L,DDX17,ANXA1,VEGFA,RUNX2,GCM1,UGCG,ADAM17,KIAA1109,MAGI2,CLASP1,EPB41L5,RHEB,FLRT3,XDH,KITLG,ATRN,DLC1,IL6ST,IMPAD1,FAT1,SMAD1,TCTN1,TIPARP,ARL13B,TSG101,ESRP1,ARID2,BTG2,BTRC,NOTCH2,MEF2A,GSK3B,FSTL1,PIK3CA,BPTF,TFIP11,ABI2,HECTD1,DLX2,ATF2,COPS2,TIMP1,OPHN1,YIPF6,ASH1L,SPTLC2,ATRX,ATP7A,FEM1B,TTC8,SMAD2,NF1,PRKAA1,SMAD7,TMEM38B,MTPN,CACYBP,BMP2	pink	VSMC_M5
GO:0009743	0.86	0.24	6	186	response to carbohydrate	BP	1	GCLC,IRS2,ANO1,PIK3CA,SMAD2,PRKAA1	pink	VSMC_M5
GO:0033674	0.86	0.21	14	373	positive regulation of kinase activity	BP	1	TAB2,VEGFA,ADAM17,MRE11,KITLG,CDK5RAP1,ATP2B4,DOCK3,CAB39,PIK3CA,ALS2,WNK1,CCNK,BMP2	pink	VSMC_M5
GO:0098662	0.86	0.19	21	541	inorganic cation transmembrane transport	BP	1	COMMD1,ZDHHC17,SLC30A6,SLC4A8,TRPC1,ATP2B4,NIPSNAP2,CAB39,SCN9A,STK39,CUL5,ERO1A,WNK1,ABCB7,ATP7A,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0061138	0.86	0.25	5	147	morphogenesis of a branching epithelium	BP	1	VEGFA,GCM1,BTRC,FEM1B,BMP2	pink	VSMC_M5
GO:0001944	0.86	0.19	25	607	vasculature development	BP	1	ANXA1,VEGFA,KRIT1,JCAD,SRPK2,EPC1,XDH,SMAD1,TIPARP,HIPK1,ARID2,ATP2B4,NOTCH2,PIK3CA,GTF2I,EGLN1,HECTD1,ATF2,CRKL,ATP7A,GGNBP2,NF1,PTPRM,SMAD7,DDAH1	pink	VSMC_M5
GO:0042113	0.86	0.24	6	193	B cell activation	BP	1	ADAM17,DCLRE1C,IRS2,NOTCH2,KMT5B,ATM	pink	VSMC_M5
GO:0060402	0.86	0.27	4	107	calcium ion transport into cytosol	BP	1	TRPC1,ATP2B4,ERO1A,TMEM38B	pink	VSMC_M5
GO:0040012	0.87	0.18	33	796	regulation of locomotion	BP	1	WASL,ANXA1,VEGFA,KRIT1,PTP4A1,MACF1,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,IRS2,KITLG,DLC1,YTHDF3,CPNE3,ARSB,ARID2,ATP2B4,ZMYND8,STK39,ATM,TIMP1,CRKL,WNK1,ATP7A,USP14,NF1,PTPRM,NIPBL,SMAD7,PKN2,BMP2	pink	VSMC_M5
GO:0048285	0.87	0.20	14	401	organelle fission	BP	1	UBR2,MRE11,CLASP1,TOP2B,LSM14A,CEP97,ATM,PDS5A,MLH3,ATRX,STAG2,NIPBL,RAD1,RMDN1	pink	VSMC_M5
GO:0051345	0.87	0.19	16	440	positive regulation of hydrolase activity	BP	1	VEGFA,ARHGAP42,MAGI2,FNTA,XDH,MAPK8,APAF1,DLC1,RALGAPB,GSK3B,FAM162A,ALS2,CRKL,NF1,ELMOD2,BMP2	pink	VSMC_M5
GO:0022407	0.87	0.21	10	293	regulation of cell-cell adhesion	BP	1	ANXA1,VEGFA,EPB41L5,MAGI1,IL6ST,PIK3CA,WNK1,SMAD7,NFAT5,BMP2	pink	VSMC_M5
GO:0048584	0.87	0.16	60	1488	positive regulation of response to stimulus	BP	1	TAB2,MAPK9,CSNK1G3,UBR5,KLHDC10,ANXA1,TMEM33,VEGFA,USP34,MACF1,ADAM17,JCAD,ASXL2,RHEB,ZEB2,MBD5,XDH,ZDHHC17,KITLG,RB1CC1,IL6ST,CSNK2A1,IFIT5,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,NR3C2,RNF13,FAM92A,ARID2,IRAK4,CYLD,NOTCH2,SHOC2,KMT5B,PUM1,PIK3CA,FXR1,STK39,TIAL1,ALS2,PLEKHA1,STYXL1,SOS2,ATM,PRKCI,USP8,CRKL,WNK1,ATP7A,SMAD2,GSKIP,XIAP,NFAT5,BIRC2,AGO3,UBE2V2,BMP2	pink	VSMC_M5
GO:0002831	0.87	0.23	7	224	regulation of response to biotic stimulus	BP	1	YTHDF3,LSM14A,TSPAN32,PUM1,XIAP,BIRC2,ELMOD2	pink	VSMC_M5
GO:0006954	0.87	0.19	17	497	inflammatory response	BP	1	ANXA1,UFL1,ATRN,IL6ST,PJA2,SMAD1,LXN,CYLD,NOTCH2,SCN9A,STK39,TIMP1,ASH1L,XIAP,F8,BIRC2,BMP2	pink	VSMC_M5
GO:0015711	0.87	0.22	7	228	organic anion transport	BP	1	SLC25A17,ANXA1,SLC4A8,SFXN1,PRKAA1,SLC35A3,ATP5PF	pink	VSMC_M5
GO:0002460	0.87	0.24	5	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	ANXA1,ADAM17,KMT5B,HPRT1,SMAD7	pink	VSMC_M5
GO:0048562	0.87	0.22	8	225	embryonic organ morphogenesis	BP	1	MTHFD1L,RUNX2,ARL13B,HIPK1,NOTCH2,DLX2,SMAD2,NIPBL	pink	VSMC_M5
GO:0051099	0.87	0.25	4	141	positive regulation of binding	BP	1	EPB41L5,GSK3B,USP33,BMP2	pink	VSMC_M5

GO:0051235	0.87	0.20	10	248	maintenance of location	BP	1	LATS1,SYNE1,VPS13A,ASXL2,LTBP1,TRPC1,TWF1,ACACB,ERO1A,TMEM38B	pink	VSMC_M5
GO:0010959	0.87	0.21	9	263	regulation of metal ion transport	BP	1	COMMD1,TRPC1,ATP2B4,NIPSNAP2,CAB39,STK39,WNK1,ATP7A,TMEM38B	pink	VSMC_M5
GO:0032940	0.87	0.18	21	574	secretion by cell	BP	1	PCSK5,ANXA1,CD2AP,RAB1A,RAB33B,PDCD6IP,CLASP1,ARL8B,IRS2,ARFGEF1,SLC4A8,TSG101,ANO1,GSK3B,SMAD2,PIK3C3,STXBP3,ATP5PF,TMEM38B,GOLPH3L,BMP2	pink	VSMC_M5
GO:0009636	0.87	0.24	5	174	response to toxic substance	BP	1	ASNS,SCN9A,SCFD1,WAPL,ATP7A	pink	VSMC_M5
GO:0010562	0.87	0.17	26	669	positive regulation of phosphorus metabolic process	BP	1	TAB2,LATS1,VEGFA,ADAM17,MRE11,MAGI2,KITLG,DLC1,RB1CC1,IL6ST,CDK5RAP1,BTBD10,ATP2B4,DOCK3,CAB39,PIK3CA,FXR1,ALS2,CREBL2,ATF2,CRKL,WNK1,CCNK,PRKAA1,MT-CO2,BMP2	pink	VSMC_M5
GO:0045937	0.87	0.17	26	669	positive regulation of phosphate metabolic process	BP	1	TAB2,LATS1,VEGFA,ADAM17,MRE11,MAGI2,KITLG,DLC1,RB1CC1,IL6ST,CDK5RAP1,BTBD10,ATP2B4,DOCK3,CAB39,PIK3CA,FXR1,ALS2,CREBL2,ATF2,CRKL,WNK1,CCNK,PRKAA1,MT-CO2,BMP2	pink	VSMC_M5
GO:0023051	0.87	0.15	110	2524	regulation of signaling	BP	1	ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBR2,C9orf72,ANXA1,TMEM33,VEGFA,RUNX2,CD2AP,GCLC,USP34,UGCG,MACF1,ADAM17,UFL1,JCAD,ARHGAP42,NCOA1,ASXL2,MAGI2,RHEB,ZEB2,MBD5,XDH,KAT6A,ZDHHC17,BIRC6,LTBP1,IRS2,KITLG,SPRY4,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,URI1,SLC4A8,NR3C2,TRPC1,RNF13,TCTN1,RALGAPB,FAM92A,TSG101,HIPK1,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,DOCK3,NOTCH2,BICD1,ANO1,ZMYND8,SHOC2,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,STK39,TIAL1,ALS2,PLEKHA1,DLX2,ARHGAP5,HERC4,STYXL1,RALGPS2,SOS2,ATM,PRKCI,USP8,TIMP1,CRKL,WNK1,GHITM,OPHN1,ASH1L,FEM1B,SMAD2,GSKIP,GGNBP2,CSNK1A1,XIAP,NF1,PRKAA1,SMAD7,NFAT5,USP33,BIRC2,AGO3,UBE2D3,BMT2,PAIP2,BMP2	pink	VSMC_M5
GO:0051234	0.87	0.15	146	3429	establishment of localization	BP	1	RELCH,VTA1,VPS13B,SNX2,CSNK1G3,UBR5,SFT2D1,KPNA5,SLC25A17,MKLN1,VPS13A,PCSK5,C9orf72,WASL,ANXA1,VEGFA,CD2AP,SRP72,GCLC,DST,RHOQ,ERLEC1,LCA5,UGCG,COMMD1,MACF1,VPS54,RAB1A,PCYOX1,RAB14,RAB33B,ZFYVE9,SLC41A3,OSBPL9,BBS12,KIAA1109,NCOA1,POLR2D,MAGI2,PDCD6IP,CLASP1,EPB41L5,XDH,ARL8B,ZDHHC17,GOLGA7,SLC30A6,COG6,IRS2,MAPK8,VPS37A,MTMR6,PCM1,SGTB,ARFGEF1,ERBIN,SLC4A8,RHOBTB3,TRPC1,VPS29,PPP1CC,WWP1,ZFYVE16,ANTXR2,PIP4P2,ARSB,TBC1D23,TSG101,UEVLD,PPP3CC,SSR1,ATP2B4,ZC3H11A,NIPSNAP2,BICD1,ANO1,DENND5B,CAB39,IPO8,MEF2A,GOLGA5,GSK3B,PIK3CA,LYST,SCN9A,STK39,ZFAND2A,PARL,ALS2,TLK1,PLEKHA1,SCFD1,CREBL2,SMG7,SRP54,ATF2,MTX2,ACAP2,NEMF,ATM,CUL5,ERO1A,PRKCI,YWHAQ,CCZ1B,RPAIN,WNK1,HUWE1,OPHN1,SFXN1,SNX11,FBXW11,ABCB7,ATP7A,CHM,TTC8,SMAD2,PIK3C3,APPBP2,DYNC1H1,SMG1,RAB11FIP4,PRKAA1,NIPBL,TRAPPC2L,STXBP3,SLC35A3,USP33,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ARRDC5,UBE2D3,ATP5PF,TMEM38B,RAB18,EIF5A2,SLC25A36,RNF139,GOLPH3L,TIMM9,BMP2,RMDN1,SAR1B,ZDHHC22	pink	VSMC_M5
GO:1903037	0.87	0.22	6	206	regulation of leukocyte cell-cell adhesion	BP	1	ANXA1,IL6ST,PIK3CA,WNK1,SMAD7,NFAT5	pink	VSMC_M5
GO:0043547	0.88	0.21	7	202	positive regulation of GTPase activity	BP	1	ARHGAP42,RALGAPB,GSK3B,ALS2,CRKL,NF1,ELMOD2	pink	VSMC_M5
GO:0072006	0.88	0.25	4	118	nephron development	BP	1	VEGFA,MAGI2,NOTCH2,BMP2	pink	VSMC_M5
GO:0006928	0.88	0.15	70	1565	movement of cell or subcellular component	BP	1	VPS13A,WASL,ANXA1,VEGFA,KRIT1,CD2AP,DST,PTP4A1,RHOQ,LCA5,MACF1,RAB1A,ADAM17,JCAD,BBS12,MAGI2,CLASP1,EPB41L5,ZEB2,FLRT3,ARL8B,TOP2B,IRS2,KITLG,ATRN,DLC1,PCM1,YTHDF3,FAT1,RHOBTB3,CPNE3,ARL13B,ARSB,ARID2,ATP2B4,IRAK4,NOTCH2,BICD1,ZMYND8,FSTL1,PIK3CA,LYST,DNAAF5,STK39,ABI2,SRP54,DYNLT3,ATM,ARPC2,PRKCI,TIMP1,CRKL,WNK1,FUT8,OPHN1,FBXW11,ASH1L,ATP7A,TTC8,PSTPIP2,DYNC1H1,WDR78,NF1,PTPRM,NIPBL,SMAD7,PKN2,USP33,USP9X,BMP2	pink	VSMC_M5
GO:0009887	0.88	0.16	33	784	animal organ morphogenesis	BP	1	MTHFD1L,VEGFA,RUNX2,CUL1,RAB33B,ASXL2,MAGI2,ATRN,DLC1,IMPAD1,FAT1,TIPARP,ARL13B,HIPK1,ARID2,BTRC,NOTCH2,PLEKHA1,ABI2,DLX2,ATF2,PRKCI,CRKL,FBXW11,ASH1L,FEM1B,TTC8,SMAD2,NF1,PTPRM,NIPBL,SMAD7,BMP2	pink	VSMC_M5
GO:0098655	0.88	0.17	24	623	cation transmembrane transport	BP	1	COMMD1,SLC41A3,ZDHHC17,SLC30A6,SLC4A8,TRPC1,ATP2B4,NIPSNAP2,ANO1,CAB39,SCN9A,STK39,CUL5,ERO1A,WNK1,SFXN1,ABCB7,ATP7A,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0048514	0.88	0.17	20	508	blood vessel morphogenesis	BP	1	ANXA1,VEGFA,KRIT1,JCAD,SRPK2,XDH,SMAD1,TIPARP,HIPK1,ARID2,ATP2B4,NOTCH2,PIK3CA,GTF2I,EGLN1,ATF2,NF1,PTPRM,SMAD7,DDAH1	pink	VSMC_M5
GO:2000026	0.88	0.16	42	1014	regulation of multicellular organismal development	BP	1	ANXA1,VEGFA,KRIT1,RUNX2,MACF1,SEPT7,UFL1,RAB14,JCAD,KIAA1109,CLASP1,RHEB,FLRT3,XDH,KITLG,IL6ST,CAPRIN1,PCM1,SMAD1,EIF4G2,DIP2B,GABPA,PP1CC,HIPK1,ESRP1,ATP2B4,NOTCH2,TRIP12,ACACB,GTF2I,EGLN1,DLX2,ATF2,SOS2,PRKCI,NF1,PTPRM,NIPBL,SMAD7,UBE2V2,DDAH1,BMP2	pink	VSMC_M5
GO:0072359	0.88	0.16	39	902	circulatory system development	BP	1	TAB2,PCSK5,ANXA1,VEGFA,KRIT1,JCAD,SRPK2,EPC1,FLRT3,XDH,DLC1,RB1CC1,SMAD1,EIF4G2,TIPARP,ARL13B,HIPK1,ARID2,ATP2B4,NOTCH2,MEF2A,ACACB,PIK3CA,GTF2I,EGLN1,HECTD1,ATF2,KDM6A,CRKL,ATP7A,SMAD2,GGNBP2,NF1,PTPRM,NIPBL,SMAD7,CACYBP,DDAH1,BMP2	pink	VSMC_M5

GO:0050793	0.88	0.15	80	1852	regulation of developmental process	BP	1	MEX3C,LATS1,MAPK9,DDX17,MKLN1,ANXA1,VEGFA,KRIT1,RUNX2,GCM1,RHOQ,MACF1,SEPT7,UFL1,ZMYM4,RAB14,JCAD,BBS12,KIAA1109,NCOA1,ASXL2,MAGI2,CLASP1,RHEB,ZEB2,MBD5,FLRT3,XDH,KITLG,SPRY4,ATRN,N4BP2L2,DLC1,IL6ST,CAPRIN1,PCM1,TNKS2,CDK5RAP1,KDM3A,SMAD1,EIF4G2,RHOBTB3,DIP2B,GABPA,PPP1CC,HIPK1,ESRP1,DNMBP,ATP2B4,NOTCH2,TRIP12,ZMYND8,KMT5B,ACACB,GSK3B,PIK3CA,GTF2I,EGLN1,ABI2,DLX2,RPS6KA3,CREBL2,ATF2,SOS2,ARPC2,PRKCI,CRKL,HUWE1,PIAS1,SMAD2,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,BIRC2,UBE2V2,MTPN,DDAH1,BMP2	pink	VSMC_M5
GO:0035051	0.88	0.24	4	119	cardiocyte differentiation	BP	1	VEGFA,MEF2A,CACYBP,BMP2	pink	VSMC_M5
GO:0044419	0.88	0.16	35	948	biological process involved in interspecies interaction between organisms	BP	1	TAB2,DDX17,WASL,ANXA1,RAB1A,ADAM17,RAB14,SRPK2,ARL8B,MAPK8,IFIT5,YTHDF3,LSM14A,PJA2,ERBIN,URI1,WWP1,TSG101,IRAK4,CYLD,TSPAN32,NOTCH2,PUM1,LYST,RPS6KA3,ATF2,NAALADL2,CCNK,USP14,XIAP,PRPF8,STXBP3,BIRC2,ELMOD2,BMP2	pink	VSMC_M5
GO:0015849	0.88	0.22	6	203	organic acid transport	BP	1	SLC25A17,ANXA1,IRS2,SFXN1,PRKAA1,ATP5PF	pink	VSMC_M5
GO:0032879	0.88	0.14	89	2074	regulation of localization	BP	1	LATS1,UBR5,MKLN1,WASL,ANXA1,VEGFA,KRIT1,CD2AP,GCLC,PTP4A1,RHOQ,ERLEC1,COMMD1,MACF1,ADAM17,UFL1,RAB14,RAB33B,JCAD,ASXL2,MAGI2,PDCD6IP,CLASP1,EPB41L5,IRS2,KITLG,SHQ1,MAPK8,DLC1,PCM1,YTHDF3,VCPIP1,SLC4A8,TRPC1,PPP1CC,ZFYVE16,CPNE3,PIP4P2,ARSB,TSG101,ARID2,PPP3CC,ATP2B4,NIPSNAP2,BICD1,ANO1,DENND5B,CAB39,ZMYND8,MEF2A,ACACB,GSK3B,SCN9A,STK39,PARL,SCFD1,HECTD1,CREBL2,ATM,ERO1A,PRKCI,YWHAQ,USP8,TIMP1,CRKL,WNK1,WAPL,HUWE1,OPHN1,ATP7A,TTC8,PIK3C3,DYNC1H1,PTPN9,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,STXBP3,PKN2,UBE2D3,ATP5PF,TMEM38B,NAF1,RNF139,GOLPH3L,BMP2,SAR1B	pink	VSMC_M5
GO:0099003	0.88	0.22	5	151	vesicle-mediated transport in synapse	BP	1	KIAA1109,SLC4A8,PPP3CC,GSK3B,OPHN1	pink	VSMC_M5
GO:0071805	0.88	0.24	4	131	potassium ion transmembrane transport	BP	1	CAB39,STK39,WNK1,TMEM38B	pink	VSMC_M5
GO:0007411	0.88	0.21	7	181	axon guidance	BP	1	VEGFA,FLRT3,NOTCH2,OPHN1,TTC8,PTPRM,USP33	pink	VSMC_M5
GO:0010646	0.88	0.14	109	2513	regulation of cell communication	BP	1	ARFGEF3,TAB2,LATS1,MAPK9,CSNK1G3,UBR5,KLHDC10,UBR2,C9orf72,ANXA1,TMEM33,VEGFA,RUNX2,CD2AP,GCLC,USP34,UGCG,MACF1,ADAM17,UFL1,JCAD,ARHGAP42,NCOA1,ASXL2,MAGI2,RHEB,ZEB2,MBD5,XDH,KAT6A,ZDHHC17,BIRC6,LTBP1,IRS2,KITLG,SPRY4,DLC1,RB1CC1,IL6ST,CSNK2A1,IFIT5,YTHDF3,TNKS2,LSM14A,PJA2,ARFGEF1,ERBIN,URI1,SLC4A8,NR3C2,RNF13,TCTN1,RALGAPB,FAM92A,TSG101,HIPK1,DNMBP,ATP2B4,IRAK4,CYLD,RANBP9,BTRC,DOCK3,NOTCH2,BICD1,ANO1,ZMYND8,SHOC2,GSK3B,FSTL1,PUM1,PIK3CA,UBR1,STK39,TIAL1,ALS2,PLEKHA1,DLX2,ARHGAP5,HERC4,STYXL1,RALGPS2,SOS2,ATM,PRKCI,USP8,TIMP1,CRKL,WNK1,GHITM,OPHN1,ASH1L,FEM1B,SMAD2,GSKIP,GGNBP2,CSNK1A1,XIAP,NF1,PRKAA1,SMAD7,NFAT5,USP33,BIRC2,AGO3,UBE2D3,BMT2,PAIP2,BMP2	pink	VSMC_M5
GO:2000147	0.88	0.17	17	455	positive regulation of cell motility	BP	1	ANXA1,VEGFA,PTP4A1,ADAM17,JCAD,CLASP1,EPB41L5,IRS2,KITLG,CPNE3,STK39,ATM,CRKL,WNK1,ATP7A,NIPBL,BMP2	pink	VSMC_M5
GO:0006261	0.88	0.24	4	137	DNA-dependent DNA replication	BP	1	SRPK2,MRE11,RPAIN,ATRX	pink	VSMC_M5
GO:0046649	0.88	0.17	16	470	lymphocyte activation	BP	1	ANXA1,RUNX2,ADAM17,DCLRE1C,IRS2,IL6ST,NOTCH2,KMT5B,PIK3CA,HECTD1,ATF2,SOS2,ATM,ATP7A,HPRT1,SMAD7	pink	VSMC_M5
GO:0097485	0.88	0.20	7	182	neuron projection guidance	BP	1	VEGFA,FLRT3,NOTCH2,OPHN1,TTC8,PTPRM,USP33	pink	VSMC_M5
GO:0050920	0.88	0.22	5	167	regulation of chemotaxis	BP	1	VEGFA,ADAM17,STK39,WNK1,USP14	pink	VSMC_M5
GO:0045088	0.89	0.23	4	148	regulation of innate immune response	BP	1	YTHDF3,LSM14A,XIAP,BIRC2	pink	VSMC_M5
GO:0001525	0.89	0.17	16	428	angiogenesis	BP	1	ANXA1,VEGFA,KRIT1,JCAD,SRPK2,SMAD1,HIPK1,ATP2B4,NOTCH2,PIK3CA,GTF2I,EGLN1,ATF2,NF1,PTPRM,DDAH1	pink	VSMC_M5
GO:0022412	0.89	0.19	8	247	cellular process involved in reproduction in multicellular organism	BP	1	UBR2,KDM3A,TIAL1,RNF2,PYGO1,FBXW11,MLH3,DIAPH2	pink	VSMC_M5
GO:0001649	0.89	0.20	6	190	osteoblast differentiation	BP	1	RUNX2,UFL1,IL6ST,SMAD1,NF1,BMP2	pink	VSMC_M5
GO:0043588	0.89	0.20	6	171	skin development	BP	1	LATS1,ANXA1,UGCG,TSG101,ASH1L,ATP7A	pink	VSMC_M5
GO:0051251	0.89	0.21	5	186	positive regulation of lymphocyte activation	BP	1	ANXA1,IRS2,IL6ST,KMT5B,PIK3CA	pink	VSMC_M5
GO:0050708	0.89	0.20	6	200	regulation of protein secretion	BP	1	ANXA1,CD2AP,IRS2,ANO1,PIK3C3,GOLPH3L	pink	VSMC_M5
GO:0050954	0.89	0.22	4	120	sensory perception of mechanical stimulus	BP	1	FBXO11,CCDC50,NIPBL,TIMM9	pink	VSMC_M5
GO:0002429	0.89	0.22	4	148	immune response-activating cell surface receptor signaling pathway	BP	1	PIK3CA,PLEKHA1,CRKL,WNK1	pink	VSMC_M5
GO:0002757	0.89	0.22	4	148	immune response-activating signal transduction	BP	1	PIK3CA,PLEKHA1,CRKL,WNK1	pink	VSMC_M5
GO:0042327	0.89	0.15	23	612	positive regulation of phosphorylation	BP	1	TAB2,LATS1,VEGFA,ADAM17,MRE11,KITLG,RB1CC1,IL6ST,CDK5RAP1,BTBD10,ATP2B4,DOCK3,CAB39,PIK3CA,FXR1,ALS2,CREBL2,ATF2,CRKL,WNK1,CCNK,PRKAA1,BMP2	pink	VSMC_M5
GO:0060485	0.89	0.18	8	235	mesenchyme development	BP	1	DDX17,CLASP1,EPB41L5,KITLG,GSK3B,SMAD2,SMAD7,BMP2	pink	VSMC_M5
GO:0048585	0.90	0.13	49	1229	negative regulation of response to stimulus	BP	1	LATS1,UBR5,UBR2,ANXA1,RUNX2,CD2AP,GCLC,ADAM17,UFL1,ARHGAP42,MAGI2,CLASP1,XDH,BIRC6,LTBP1,SPRY4,DLC1,RB1CC1,CSNK2A1,YTHDF3,ERBIN,URI1,TSG101,ATP2B4,CYLD,RANBP9,BTRC,TRIP12,BICD1,GSK3B,UBR1,TFIP11,PLEKHA1,DLX2,KLHL15,HERC4,ATM,GHITM,ASH1L,GGNBP2,CSNK1A1,USP14,NF1,PRKAA1,SMAD7,UBE2D3,DDAH1,BMT2,BMP2	pink	VSMC_M5
GO:0072331	0.90	0.21	4	139	signal transduction by p53 class mediator	BP	1	KAT6A,HIPK1,ATM,ATRX	pink	VSMC_M5
GO:0071396	0.90	0.15	15	422	cellular response to lipid	BP	1	LATS1,UBR5,DDX17,ANXA1,UFL1,NR3C1,MAPK8,KDM3A,URI1,NR3C2,ATM,USP8,PRPF8,SETX,MT-ND3	pink	VSMC_M5
GO:0010948	0.90	0.18	7	237	negative regulation of cell cycle process	BP	1	MRE11,ATF2,ATM,WAPL,ATRX,FEM1B,RAD1	pink	VSMC_M5

GO:0006955	0.90	0.13	37	1012	immune response	BP	1	MAPK9,DDX17,ANXA1,RAB1A,ADAM17,RAB14,SRPK2,DCLRE1C,ARL8B,MAPK8,IL6ST,IFIT5,YTHDF3,LSM14A,PJA2,ERBIN,IRAK4,CYLD,TSPAN32,NOTCH2,KMT5B,PUM1,PIK3CA,LYST,PLEKHA1,RPS6KA3,CRKL,WNK1,ATP7A,USP14,XIAP,HPRT1,SMAD7,STXBP3,BIRC2,CD164,ELMOD2	pink	VSMC_M5
GO:0051272	0.90	0.15	17	466	positive regulation of cellular component movement	BP	1	ANXA1,VEGFA,PTP4A1,ADAM17,JCAD,CLASP1,EPB41L5,IRS2,KITLG,CPNE3,STK39,ATM,CRKL,WNK1,ATP7A,NIPBL,BMP2	pink	VSMC_M5
GO:0040017	0.90	0.15	17	462	positive regulation of locomotion	BP	1	ANXA1,VEGFA,PTP4A1,ADAM17,JCAD,CLASP1,EPB41L5,IRS2,KITLG,CPNE3,STK39,ATM,CRKL,WNK1,ATP7A,NIPBL,BMP2	pink	VSMC_M5
GO:1901653	0.90	0.17	9	270	cellular response to peptide	BP	1	GCLC,RHOQ,MBD5,IRS2,ANO1,GSK3B,PIK3CA,PRKCI,PRKAA1	pink	VSMC_M5
GO:0051651	0.90	0.18	6	163	maintenance of location in cell	BP	1	SYNE1,VPS13A,TRPC1,TWF1,ERO1A,TMEM38B	pink	VSMC_M5
GO:0046879	0.90	0.18	6	206	hormone secretion	BP	1	ANXA1,RAB1A,IRS2,ANO1,SMAD2,STXBP3	pink	VSMC_M5
GO:0051094	0.90	0.13	39	982	positive regulation of developmental process	BP	1	MAPK9,ANXA1,VEGFA,RUNX2,GCM1,MACF1,UFL1,JCAD,NCOA1,ASXL2,CLASP1,RHEB,ZEB2,FLRT3,KITLG,IL6ST,CAPRIN1,SMAD1,EIF4G2,PPP1CC,HIPK1,NOTCH2,ZMYND8,KMT5B,ACACB,DLX2,RPS6KA3,CREBL2,ARPC2,PRKCI,CRKL,PIAS1,SMAD2,PRKAA1,NIPBL,SMAD7,UBE2V2,DDAH1,BMP2	pink	VSMC_M5
GO:0046777	0.90	0.17	7	204	protein autophosphorylation	BP	1	VEGFA,MRE11,GSK3B,STK39,ATM,WNK1,SMG1	pink	VSMC_M5
GO:0031032	0.90	0.18	6	172	actomyosin structure organization	BP	1	PDCD6IP,CLASP1,EPB41L5,DLC1,MEF2A,TTC8	pink	VSMC_M5
GO:0070372	0.90	0.18	6	211	regulation of ERK1 and ERK2 cascade	BP	1	ZDHHC17,SPRY4,RANBP9,NOTCH2,CRKL,BMP2	pink	VSMC_M5
GO:1901615	0.90	0.15	12	382	organic hydroxy compound metabolic process	BP	1	CYP39A1,OSBPL9,ZEB2,IMPAD1,TRPC1,SPTLC2,ATP7A,PRKAA1,HPRT1,SULT1C4,MTPN,BMP2	pink	VSMC_M5
GO:0031667	0.90	0.15	12	362	response to nutrient levels	BP	1	ASNS,GCLC,NCOA1,MAPK8,APAF1,ARSB,ACACB,CPEB4,PIK3C3,PRKAA1,USP33,BMT2	pink	VSMC_M5
GO:0044281	0.91	0.12	45	1301	small molecule metabolic process	BP	1	ME2,MTHFD1L,SLC25A17,LRGUK,ANXA1,CYP39A1,SDHAF3,ASNS,GCLC,AGMO,RHOQ,MDH1,OSBPL9,XDH,OXSM,IRS2,IMPAD1,KDM3A,FAR1,UEVLD,ATP2B4,PRKAB2,ACACB,GSK3B,PIK3CA,ADAL,PDE5A,MORC2,ACOX3,FUT8,PGM2,SFXN1,SPTLC2,ATP7A,PRKAA1,HPRT1,SLC35A3,NUDT7,MT-CO2,SULT1C4,HACD1,ATP5PF,DDAH1,BMP2,DCAKD	pink	VSMC_M5
GO:0071216	0.91	0.20	4	157	cellular response to biotic stimulus	BP	1	MAPK8,APAF1,GSK3B,PRPF8	pink	VSMC_M5
GO:0034220	0.91	0.13	29	765	ion transmembrane transport	BP	1	SLC25A17,COMMD1,PCYOX1,SLC41A3,ZDHHC17,SLC30A6,SLC4A8,TRPC1,WWP1,ATP2B4,NIPSNAP2,ANO1,CAB39,SCN9A,STK39,CUL5,ERO1A,YWHAQ,WNK1,SFXN1,ABCB7,ATP7A,SLC35A3,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0044057	0.91	0.15	14	398	regulation of system process	BP	1	ARHGAP42,IL6ST,TRPC1,ATP2B4,TWF1,ZMYND8,MEF2A,STK39,GLRX3,WNK1,SMAD7,ATP5PF,TMEM38B,MTPN	pink	VSMC_M5
GO:0010648	0.91	0.12	41	1047	negative regulation of cell communication	BP	1	LATS1,UBR2,RUNX2,CD2AP,GCLC,ADAM17,UFL1,ARHGAP42,MAGI2,XDH,BIRC6,LTBP1,SPRY4,DLC1,RB1CC1,CSNK2A1,YTHDF3,ERBIN,URI1,TSG101,ATP2B4,CYLD,RANBP9,BTRC,BICD1,GSK3B,UBR1,PLEKHA1,DLX2,HERC4,ATM,GHITM,ASH1L,GGNBP2,CSNK1A1,NF1,PRKAA1,SMAD7,UBE2D3,BMT2,BMP2	pink	VSMC_M5
GO:0007600	0.91	0.15	11	320	sensory perception	BP	1	FBXO11,LXN,ANO1,SCN9A,UBR3,CCDC50,SPATA7,CHM,TTC8,NIPBL,TIMM9	pink	VSMC_M5
GO:0071695	0.91	0.18	5	163	anatomical structure maturation	BP	1	VEGFA,RUNX2,SCLT1,FEM1B,BMP2	pink	VSMC_M5
GO:0023057	0.91	0.12	41	1048	negative regulation of signaling	BP	1	LATS1,UBR2,RUNX2,CD2AP,GCLC,ADAM17,UFL1,ARHGAP42,MAGI2,XDH,BIRC6,LTBP1,SPRY4,DLC1,RB1CC1,CSNK2A1,YTHDF3,ERBIN,URI1,TSG101,ATP2B4,CYLD,RANBP9,BTRC,BICD1,GSK3B,UBR1,PLEKHA1,DLX2,HERC4,ATM,GHITM,ASH1L,GGNBP2,CSNK1A1,NF1,PRKAA1,SMAD7,UBE2D3,BMT2,BMP2	pink	VSMC_M5
GO:0044772	0.91	0.15	11	350	mitotic cell cycle phase transition	BP	1	LATS1,ANXA1,ADAM17,CUL1,CUL2,MRE11,CLASP1,FBXL3,ATM,CUL5,PIAS1	pink	VSMC_M5
GO:0008202	0.91	0.17	6	217	steroid metabolic process	BP	1	CYP39A1,OSBPL9,TIPARP,PLEKHA1,PRKAA1,BMP2	pink	VSMC_M5
GO:0009653	0.91	0.11	92	2050	anatomical structure morphogenesis	BP	1	LATS1,MTHFD1L,SNX2,MKLN1,PCSK5,C9orf72,WASL,ANXA1,VEGFA,KRIT1,FRYL,RUNX2,GCM1,RHOQ,MACF1,RAB1A,SEPT7,ADAM17,CUL1,ZMYM4,RAB33B,JCAD,SRPK2,NCOA1,ASXL2,MAGI2,CLASP1,EPB41L5,FLRT3,XDH,TOP2B,ZDHHC17,SPRY4,ATRN,DLC1,IMPAD1,CAPRIN1,FAT1,SMAD1,EIF4G2,RHOBTB3,DIP2B,TCTN1,GABPA,TIPARP,ARL13B,FAM92A,HIPK1,ARID2,DNMBP,ATP2B4,BTRC,NOTCH2,BICD1,MEF2A,GSK3B,PIK3CA,GTF2I,EGLN1,ALS2,PLEKHA1,SCFD1,ABI2,HECTD1,DLX2,ATF2,RNF2,ARPC2,PRKCI,CRKL,WNK1,HUWE1,OPHN1,FBXW11,ASH1L,HERC1,ATRX,ATP7A,FEM1B,TTC8,SMAD2,NF1,PTPRM,NIPBL,HPRT1,SMAD7,USP33,USP9X,FAM206A,MTPN,DDAH1,BMP2	pink	VSMC_M5
GO:0002250	0.91	0.16	7	244	adaptive immune response	BP	1	ANXA1,ADAM17,DCLRE1C,IL6ST,KMT5B,HPRT1,SMAD7	pink	VSMC_M5
GO:0006813	0.91	0.19	4	140	potassium ion transport	BP	1	CAB39,STK39,WNK1,TMEM38B	pink	VSMC_M5
GO:0035637	0.91	0.19	4	114	multicellular organismal signaling	BP	1	TRPC1,ATP2B4,MEF2A,SCN9A	pink	VSMC_M5
GO:0042886	0.91	0.16	6	210	amide transport	BP	1	ANXA1,RAB1A,IRS2,ANO1,SMAD2,STXBP3	pink	VSMC_M5
GO:0003013	0.92	0.13	16	437	circulatory system process	BP	1	PCSK5,VEGFA,GCLC,ARHGAP42,SLC4A8,TRPC1,ATP2B4,MEF2A,PIK3CA,STK39,GLRX3,WNK1,SMAD7,ATP5PF,TMEM38B,DDAH1	pink	VSMC_M5
GO:0016051	0.92	0.18	4	155	carbohydrate biosynthetic process	BP	1	SDHAF3,IRS2,GSK3B,FUT8	pink	VSMC_M5
GO:0051495	0.92	0.16	6	194	positive regulation of cytoskeleton organization	BP	1	WASL,CLASP1,ABI2,ARPC2,DYNC1H1,GMFB	pink	VSMC_M5
GO:0002274	0.92	0.18	4	156	myeloid leukocyte activation	BP	1	PJA2,TSPAN32,NOTCH2,STXBP3	pink	VSMC_M5
GO:0010564	0.92	0.13	18	515	regulation of cell cycle process	BP	1	ANXA1,ADAM17,MRE11,PDCD6IP,BIRC6,CSNK2A1,ATP2B4,CEP97,ATF2,ATM,WAPL,ATRX,FEM1B,PIK3C3,DYNC1H1,RAB11FIP4,RAD1,PKN2	pink	VSMC_M5
GO:0009914	0.92	0.16	6	212	hormone transport	BP	1	ANXA1,RAB1A,IRS2,ANO1,SMAD2,STXBP3	pink	VSMC_M5
GO:0034765	0.92	0.14	11	323	regulation of ion transmembrane transport	BP	1	COMMD1,TRPC1,ATP2B4,NIPSNAP2,CAB39,SCN9A,STK39,YWHAQ,WNK1,ATP7A,TMEM38B	pink	VSMC_M5
GO:0032989	0.92	0.12	26	609	cellular component morphogenesis	BP	1	SNX2,C9orf72,WASL,VEGFA,MACF1,CLASP1,FLRT3,TOP2B,ZDHHC17,CAPRIN1,EIF4G2,DIP2B,TCTN1,NOTCH2,MEF2A,GSK3B,ALS2,ABI2,OPHN1,ATP7A,TTC8,PTPRM,HPRT1,USP33,USP9X,FAM206A	pink	VSMC_M5

GO:0090068	0.92	0.16	5	180	positive regulation of cell cycle process	BP	1	ANXA1,ADAM17,ATRX,DYNC1H1,PKN2	pink	VSMC_M5
GO:0022613	0.92	0.14	11	376	ribonucleoprotein complex biogenesis	BP	1	DDX17,SRPK2,POLR2D,SHQ1,METTL5,ATM,PRPF8,SETX,AGO3,NAF1,DENR	pink	VSMC_M5
GO:0030198	0.92	0.14	8	250	extracellular matrix organization	BP	1	CLASP1,OPTC,ERO1A,ATP7A,NF1,GFOD2,TMEM38B,BMP2	pink	VSMC_M5
GO:0060401	0.92	0.17	4	126	cytosolic calcium ion transport	BP	1	TRPC1,ATP2B4,ERO1A,TMEM38B	pink	VSMC_M5
GO:0032496	0.92	0.15	6	225	response to lipopolysaccharide	BP	1	TAB2,ADAM17,MAPK8,ERBIN,RPS6KA3,PRPF8	pink	VSMC_M5
GO:0043087	0.92	0.13	10	285	regulation of GTPase activity	BP	1	ARHGAP42,ARFGEF1,RALGAPB,GSK3B,ALS2,CRKL,WNK1,TTC8,NF1,ELMOD2	pink	VSMC_M5
GO:0051249	0.92	0.14	8	287	regulation of lymphocyte activation	BP	1	ANXA1,IRS2,IL6ST,KMT5B,PIK3CA,SOS2,ATM,SMAD7	pink	VSMC_M5
GO:0045229	0.92	0.14	8	251	external encapsulating structure organization	BP	1	CLASP1,OPTC,ERO1A,ATP7A,NF1,GFOD2,TMEM38B,BMP2	pink	VSMC_M5
GO:0048015	0.92	0.17	4	133	phosphatidylinositol-mediated signaling	BP	1	PIK3CA,PLEKHA1,PIK3C3,NF1	pink	VSMC_M5
GO:0043062	0.92	0.14	8	251	extracellular structure organization	BP	1	CLASP1,OPTC,ERO1A,ATP7A,NF1,GFOD2,TMEM38B,BMP2	pink	VSMC_M5
GO:0010817	0.92	0.13	10	331	regulation of hormone levels	BP	1	PCSK5,ANXA1,RAB1A,IRS2,TIPARP,ANO1,PLEKHA1,SMAD2,STXBP3,BMP2	pink	VSMC_M5
GO:0002573	0.92	0.16	4	154	myeloid leukocyte differentiation	BP	1	VEGFA,KITLG,NOTCH2,SRP54	pink	VSMC_M5
GO:0045595	0.92	0.10	46	1153	regulation of cell differentiation	BP	1	MEX3C,MAPK9,DDX17,ANXA1,VEGFA,RUNX2,GCM1,MACF1,UFL1,BBS12,KIAA1109,NCOA1,ASXL2,CLASP1,RHEB,ZEB2,XDH,KITLG,SPRY4,N4BP2L2,IL6ST,CAPRIN1,PCM1,CDK5RAP1,KDM3A,SMAD1,EIF4G2,DIP2B,GABPA,PPP1CC,ESRP1,NOTCH2,GSK3B,DLX2,RPS6KA3,CREBL2,SOS2,ARPC2,PRKCI,CRKL,PIAS1,SMAD2,NF1,SMAD7,BIRC2,BMP2	pink	VSMC_M5
GO:0060562	0.93	0.13	9	269	epithelial tube morphogenesis	BP	1	MTHFD1L,VEGFA,DLC1,TCTN1,ARL13B,BTRC,NOTCH2,HECTD1,BMP2	pink	VSMC_M5
GO:1901654	0.93	0.16	4	151	response to ketone	BP	1	NCOA1,NR3C1,USP8,PRKAA1	pink	VSMC_M5
GO:0050807	0.93	0.15	5	165	regulation of synapse organization	BP	1	FLRT3,CAPRIN1,ZMYND8,ABI2,UBE2V2	pink	VSMC_M5
GO:0002682	0.93	0.10	32	915	regulation of immune system process	BP	1	MAPK9,WASL,ANXA1,VEGFA,ADAM17,IRS2,KITLG,MAPK8,IL6ST,YTHDF3,LSM14A,PJA2,ERBIN,GABPA,IRAK4,CYLD,TSPAN32,NOTCH2,KMT5B,PUM1,PIK3CA,STK39,PLEKHA1,RPS6KA3,SOS2,ATM,CRKL,WNK1,XIAP,SMAD7,BIRC2,ELMOD2	pink	VSMC_M5
GO:0030324	0.93	0.16	4	141	lung development	BP	1	VEGFA,ATP7A,SMAD2,TMEM38B	pink	VSMC_M5
GO:1902105	0.93	0.15	5	193	regulation of leukocyte differentiation	BP	1	ANXA1,KITLG,NOTCH2,SOS2,SMAD7	pink	VSMC_M5
GO:0034660	0.93	0.12	12	412	ncRNA metabolic process	BP	1	DDX17,INTS4,SHQ1,RPP14,CDK5RAP1,SMAD1,METTL5,TSEN15,DIS3L,SMAD2,AGO3,NAF1	pink	VSMC_M5
GO:0023061	0.93	0.12	10	325	signal release	BP	1	PCSK5,ANXA1,RAB1A,IRS2,SLC4A8,ANO1,GSK3B,SMAD2,STXBP3,ATP5PF	pink	VSMC_M5
GO:0042110	0.93	0.12	9	310	T cell activation	BP	1	ANXA1,RUNX2,ADAM17,IL6ST,PIK3CA,ATF2,SOS2,ATP7A,SMAD7	pink	VSMC_M5
GO:0048017	0.93	0.16	4	137	inositol lipid-mediated signaling	BP	1	PIK3CA,PLEKHA1,PIK3C3,NF1	pink	VSMC_M5
GO:0006935	0.93	0.11	15	426	chemotaxis	BP	1	ANXA1,VEGFA,ADAM17,FLRT3,NOTCH2,LYST,STK39,SRP54,CRKL,WNK1,OPHN1,TTC8,USP14,PTPRM,USP33	pink	VSMC_M5
GO:0003018	0.93	0.13	6	200	vascular process in circulatory system	BP	1	VEGFA,GCLC,ARHGAP42,SLC4A8,ATP2B4,DDAH1	pink	VSMC_M5
GO:0002252	0.93	0.11	11	360	immune effector process	BP	1	ANXA1,ADAM17,ARL8B,IRAK4,NOTCH2,KMT5B,LYST,ATP7A,HPRT1,SMAD7,STXBP3	pink	VSMC_M5
GO:0030155	0.93	0.10	20	541	regulation of cell adhesion	BP	1	ANXA1,VEGFA,MACF1,CLASP1,EPB41L5,SPRY4,MAGI1,DLC1,IL6ST,GSK3B,PIK3CA,ATM,ARPC2,CRKL,WNK1,NF1,SMAD7,NFAT5,CD164,BMP2	pink	VSMC_M5
GO:0007423	0.93	0.11	15	415	sensory organ development	BP	1	VEGFA,FAT1,HIPK1,ESRP1,ATP2B4,NOTCH2,ABI2,DLX2,PRKCI,TTC8,NF1,PTPRM,NIPBL,RAB18,BMP2	pink	VSMC_M5
GO:0045321	0.93	0.10	19	586	leukocyte activation	BP	1	ANXA1,RUNX2,ADAM17,DCLRE1C,IRS2,IL6ST,PJA2,TSPAN32,NOTCH2,KMT5B,PIK3CA,HECTD1,ATF2,SOS2,ATM,ATP7A,HPRT1,SMAD7,STXBP3	pink	VSMC_M5
GO:0050863	0.93	0.14	5	206	regulation of T cell activation	BP	1	ANXA1,IL6ST,PIK3CA,SOS2,SMAD7	pink	VSMC_M5
GO:0002694	0.93	0.11	10	352	regulation of leukocyte activation	BP	1	ANXA1,IRS2,IL6ST,PJA2,TSPAN32,KMT5B,PIK3CA,SOS2,ATM,SMAD7	pink	VSMC_M5
GO:0043408	0.93	0.10	17	502	regulation of MAPK cascade	BP	1	KLHDC10,VEGFA,JCAD,XDH,ZDHHC17,KITLG,SPRY4,RB1CC1,PJA2,CYLD,RANBP9,NOTCH2,STK39,CRKL,ASH1L,NF1,BMP2	pink	VSMC_M5
GO:0016072	0.93	0.14	5	206	rRNA metabolic process	BP	1	DDX17,SHQ1,METTL5,DIS3L,NAF1	pink	VSMC_M5
GO:0003205	0.93	0.15	4	135	cardiac chamber development	BP	1	NOTCH2,HECTD1,SMAD7,BMP2	pink	VSMC_M5
GO:0032412	0.93	0.14	5	178	regulation of ion transmembrane transporter activity	BP	1	NIPSNAP2,CAB39,STK39,WNK1,ATP7A	pink	VSMC_M5
GO:0007159	0.93	0.13	6	234	leukocyte cell-cell adhesion	BP	1	ANXA1,IL6ST,PIK3CA,WNK1,SMAD7,NFAT5	pink	VSMC_M5
GO:0042330	0.93	0.10	15	427	taxis	BP	1	ANXA1,VEGFA,ADAM17,FLRT3,NOTCH2,LYST,STK39,SRP54,CRKL,WNK1,OPHN1,TTC8,USP14,PTPRM,USP33	pink	VSMC_M5
GO:0045087	0.94	0.10	14	459	innate immune response	BP	1	ANXA1,SRPK2,ARL8B,IFIT5,YTHDF3,LSM14A,PJA2,IRAK4,CYLD,LYST,USP14,XIAP,STXBP3,BIRC2	pink	VSMC_M5
GO:0043549	0.94	0.10	22	612	regulation of kinase activity	BP	1	TAB2,LATS1,VEGFA,ADAM17,MRE11,IRS2,KITLG,SPRY4,CDK5RAP1,GTF2H1,TSG101,ATP2B4,DOCK3,CAB39,PIK3CA,ALS2,WNK1,GSKIP,CCNK,GGNBP2,NF1,BMP2	pink	VSMC_M5
GO:0008544	0.94	0.13	6	201	epidermis development	BP	1	LATS1,ANXA1,UGCG,TSG101,ESRP1,ATP7A	pink	VSMC_M5
GO:0050803	0.94	0.13	5	170	regulation of synapse structure or activity	BP	1	FLRT3,CAPRIN1,ZMYND8,ABI2,UBE2V2	pink	VSMC_M5
GO:0006520	0.94	0.13	5	224	cellular amino acid metabolic process	BP	1	ASNS,GCLC,ATP2B4,ATP7A,DDAH1	pink	VSMC_M5
GO:0031347	0.94	0.11	12	397	regulation of defense response	BP	1	ANXA1,UFL1,IL6ST,YTHDF3,LSM14A,CYLD,TSPAN32,STK39,ASH1L,XIAP,BIRC2,ELMOD2	pink	VSMC_M5
GO:1902905	0.94	0.13	5	179	positive regulation of supramolecular fiber organization	BP	1	WASL,CLASP1,ABI2,ARPC2,GMFB	pink	VSMC_M5
GO:0018108	0.94	0.11	9	287	peptidyl-tyrosine phosphorylation	BP	1	VEGFA,ADAM17,KITLG,IL6ST,TSG101,HIPK1,DOCK3,ABI2,GGNBP2	pink	VSMC_M5
GO:0070371	0.94	0.12	6	227	ERK1 and ERK2 cascade	BP	1	ZDHHC17,SPRY4,RANBP9,NOTCH2,CRKL,BMP2	pink	VSMC_M5

GO:0030154	0.94	0.08	129	2966	cell differentiation	BP	1	MEX3C,LATS1,MAPK9,SYNE1,LRGUK,DDX17,C9orf72,WASL,ANXA1,VEGFA,FRYL,RUNX2,GCM1,UGCG,MACF1,RAB1A,SEPT7,ADAM17,UFL1,SCLT1,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,ASXL2,MAGI2,DCLRE1C,CLASP1,EPB41L5,RHEB,ZEB2,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,KITLG,SPRY4,ATRN,N4BP2L2,APAF1,IL6ST,IMPAD1,CAPRIN1,PCM1,FAT1,CDK5RAP1,ARFGEF1,KDM3A,SMAD1,EIF4G2,DIP2B,TCTN1,GABPA,PPP1CC,TIPARP,MLF1,ARL13B,ARSB,TBC1D23,TSG101,HIPK1,ESRP1,BTG2,TWF1,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,FSTL1,PUM1,FXR1,TIAL1,ALS2,METTL5,PLEKHA1,ABI2,HECTD1,DLX2,RPS6KA3,CREBL2,SRP54,ATF2,HERC4,STYXL1,RNF2,SOS2,ATM,ARPC2,ERO1A,PRKCI,COPS2,CRKL,WNK1,PYGO1,HUWE1,OPHN1,YIPF6,FBXW11,HERC1,ATRX,ATP7A,PIAS1,FEM1B,TTC8,DIAPH2,SMAD2,GGNBP2,PTPN9,WDR78,NF1,PTPRM,NIPBL,HPRT1,SMAD7,SETX,NUDT7,USP33,BIRC2,TMEM38B,USP9X,FAM206A,UBE2V2,MTPN,CACYBP,BMP2	pink	VSMC_M5
GO:0098657	0.94	0.14	4	155	import into cell	BP	1	IRS2,TSG101,ATP2B4,WNK1	pink	VSMC_M5
GO:0043085	0.94	0.09	32	875	positive regulation of catalytic activity	BP	1	TAB2,SERINC1,VEGFA,ADAM17,ARHGAP42,MRE11,MAGI2,FNTA,XDH,KITLG,MAPK8,APAF1,DLC1,CDK5RAP1,RALGAPB,ATP2B4,BTRC,DOCK3,CAB39,GSK3B,PIK3CA,DCUN1D1,FAM162A,ALS2,CRKL,WNK1,ATP7A,CCNK,NF1,NAF1,ELMOD2,BMP2	pink	VSMC_M5
GO:0009991	0.94	0.10	12	385	response to extracellular stimulus	BP	1	ASNS,GCLC,NCOA1,MAPK8,APAF1,ARSB,ACACB,CPEB4,PIK3C3,PRKAA1,USP33,BMT2	pink	VSMC_M5
GO:0007346	0.94	0.10	11	360	regulation of mitotic cell cycle	BP	1	ANXA1,ASNS,ADAM17,MRE11,BTG2,CYLD,TTC28,ATF2,DYNLT3,ATM,PKN2	pink	VSMC_M5
GO:0140352	0.94	0.09	21	618	export from cell	BP	1	PCSK5,ANXA1,CD2AP,RAB1A,RAB33B,PDCD6IP,CLASP1,ARL8B,IRS2,ARFGEF1,SLC4A8,TSG101,ANO1,GSK3B,SMAD2,PIK3C3,STXBP3,ATP5PF,TMEM38B,GOLPH3L,BMP2	pink	VSMC_M5
GO:0009410	0.94	0.11	9	314	response to xenobiotic stimulus	BP	1	ANXA1,GCLC,ADAM17,NCOA1,ACACB,CRKL,PRKAA1,PTPRM,SULT1C4	pink	VSMC_M5
GO:0043410	0.94	0.10	11	356	positive regulation of MAPK cascade	BP	1	KLHDC10,VEGFA,JCAD,XDH,KITLG,RB1CC1,PJA2,NOTCH2,STK39,CRKL,BMP2	pink	VSMC_M5
GO:0002237	0.94	0.12	6	236	response to molecule of bacterial origin	BP	1	TAB2,ADAM17,MAPK8,ERBIN,RPS6KA3,PRPF8	pink	VSMC_M5
GO:0018212	0.94	0.11	9	290	peptidyl-tyrosine modification	BP	1	VEGFA,ADAM17,KITLG,IL6ST,TSG101,HIPK1,DOCK3,ABI2,GGNBP2	pink	VSMC_M5
GO:0050890	0.94	0.11	7	214	cognition	BP	1	PJA2,BTG2,PIAS1,TTC8,NF1,NIPBL,PAIP2	pink	VSMC_M5
GO:1901699	0.94	0.09	18	508	cellular response to nitrogen compound	BP	1	UBR2,GCLC,RHOQ,MBD5,IRS2,GABPA,ATP2B4,ANO1,GSK3B,PIK3CA,UBR1,PRKCI,CRKL,CPEB4,ATRX,ATP7A,PRKAA1,TMEM38B	pink	VSMC_M5
GO:0050865	0.94	0.10	11	385	regulation of cell activation	BP	1	ANXA1,GCLC,IRS2,IL6ST,PJA2,TSPAN32,KMT5B,PIK3CA,SOS2,ATM,SMAD7	pink	VSMC_M5
GO:1901988	0.94	0.12	5	201	negative regulation of cell cycle phase transition	BP	1	MRE11,ATF2,ATM,FEM1B,RAD1	pink	VSMC_M5
GO:0001775	0.94	0.08	23	692	cell activation	BP	1	DGKA,ANXA1,RUNX2,GCLC,ADAM17,DCLRE1C,DGKH,IRS2,IL6ST,PJA2,TSPAN32,NOTCH2,KMT5B,PIK3CA,HECTD1,ATF2,SOS2,ATM,TIMP1,ATP7A,HPRT1,SMAD7,STXBP3	pink	VSMC_M5
GO:0051270	0.95	0.08	32	830	regulation of cellular component movement	BP	1	WASL,ANXA1,VEGFA,KRIT1,PTP4A1,MACF1,ADAM17,JCAD,MAGI2,CLASP1,EPB41L5,IRS2,KITLG,DLC1,YTHDF3,CPNE3,ARSB,ARID2,ATP2B4,ZMYND8,STK39,ATM,TIMP1,CRKL,WNK1,ATP7A,NF1,PTPRM,NIPBL,SMAD7,PKN2,BMP2	pink	VSMC_M5
GO:0022898	0.95	0.11	5	186	regulation of transmembrane transporter activity	BP	1	NIPSNAP2,CAB39,STK39,WNK1,ATP7A	pink	VSMC_M5
GO:0006820	0.95	0.10	9	319	anion transport	BP	1	SLC25A17,ANXA1,PCYOX1,SLC4A8,ANO1,SFXN1,PRKAA1,SLC35A3,ATP5PF	pink	VSMC_M5
GO:0017038	0.95	0.12	4	174	protein import	BP	1	UBR5,KPNA5,IPO8,RPAIN	pink	VSMC_M5
GO:0042325	0.95	0.07	36	967	regulation of phosphorylation	BP	1	TAB2,PPIL4,LATS1,C9orf72,VEGFA,ADAM17,MRE11,XDH,IRS2,KITLG,SPRY4,RB1CC1,IL6ST,CDK5RAP1,BTBD10,GTF2H1,TSG101,ATP2B4,TWF1,NDUFS4,DOCK3,CAB39,PIK3CA,FXR1,ALS2,CREBL2,ATF2,CRKL,WNK1,GSKIP,CCNK,GGNBP2,NF1,PRKAA1,SMAD7,BMP2	pink	VSMC_M5
GO:0042592	0.95	0.07	50	1295	homeostatic process	BP	1	MEX3C,DMXL1,ANXA1,VEGFA,KRIT1,CYP39A1,GCLC,LCA5,UGCG,COMMD1,VPS54,ADAM17,UFL1,BBS12,AKAP11,RHEB,MBD5,IRS2,KITLG,KDM3A,SMAD1,SLC4A8,TRPC1,ARID2,ATP2B4,ACOT13,ANO1,PRKAB2,ACACB,FSTL1,PIK3CA,GTF2I,STK39,EGLN1,GLRX3,SOS2,ACOX3,ERO1A,WNK1,ABCB7,ATP7A,SPATA7,DYNC1H1,XIAP,NF1,PRKAA1,SMAD7,STXBP3,TMEM38B,EIF5A2	pink	VSMC_M5
GO:0048869	0.95	0.06	131	3033	cellular developmental process	BP	1	MEX3C,LATS1,MAPK9,SYNE1,SNX2,LRGUK,DDX17,C9orf72,WASL,ANXA1,VEGFA,FRYL,RUNX2,GCM1,UGCG,MACF1,RAB1A,SEPT7,ADAM17,UFL1,SCLT1,BBS12,KIAA1109,SRPK2,NCOA1,EPC1,ASXL2,MAGI2,DCLRE1C,CLASP1,EPB41L5,RHEB,ZEB2,FLRT3,XDH,KAT6A,TOP2B,ZDHHC17,KITLG,SPRY4,ATRN,N4BP2L2,MAPK8,APAF1,IL6ST,IMPAD1,CAPRIN1,PCM1,FAT1,CDK5RAP1,ARFGEF1,KDM3A,SMAD1,EIF4G2,DIP2B,TCTN1,GABPA,PPP1CC,TIPARP,MLF1,ARL13B,ARSB,TBC1D23,TSG101,HIPK1,ESRP1,BTG2,TWF1,ID4,NOTCH2,ZMYND8,MEF2A,TET2,GSK3B,FSTL1,PUM1,FXR1,TIAL1,ALS2,METTL5,PLEKHA1,ABI2,HECTD1,DLX2,RPS6KA3,CREBL2,SRP54,ATF2,HERC4,STYXL1,RNF2,SOS2,ATM,ARPC2,ERO1A,PRKCI,COPS2,CRKL,WNK1,PYGO1,HUWE1,OPHN1,YIPF6,FBXW11,HERC1,ATRX,ATP7A,PIAS1,FEM1B,TTC8,DIAPH2,SMAD2,GGNBP2,PTPN9,WDR78,NF1,PTPRM,NIPBL,HPRT1,SMAD7,SETX,NUDT7,USP33,BIRC2,TMEM38B,USP9X,FAM206A,UBE2V2,MTPN,CACYBP,BMP2	pink	VSMC_M5
GO:0002696	0.95	0.11	5	218	positive regulation of leukocyte activation	BP	1	ANXA1,IRS2,IL6ST,KMT5B,PIK3CA	pink	VSMC_M5
GO:0046942	0.95	0.12	4	173	carboxylic acid transport	BP	1	ANXA1,SFXN1,PRKAA1,ATP5PF	pink	VSMC_M5
GO:0034330	0.95	0.07	21	541	cell junction organization	BP	1	WASL,VEGFA,DST,MACF1,PDCD6IP,CLASP1,EPB41L5,FNTA,FLRT3,DLC1,CAPRIN1,HIPK1,ZMYND8,ALS2,ABI2,PRKCI,CRKL,OPHN1,SMAD7,PKN2,UBE2V2	pink	VSMC_M5
GO:0050778	0.95	0.09	8	306	positive regulation of immune response	BP	1	ANXA1,IL6ST,LSM14A,KMT5B,PIK3CA,PLEKHA1,CRKL,WNK1	pink	VSMC_M5

GO:0071417	0.95	0.07	16	466	cellular response to organonitrogen compound	BP	1	UBR2,GCLC,RHOQ,MBD5,IRS2,GABPA,ATP2B4,ANO1,GSK3B,PIK3CA,UBR1,PRKCI,CPEB4,ATP7A,PRKAA1,TMEM38B	pink	VSMC_M5
GO:0033002	0.96	0.11	4	174	muscle cell proliferation	BP	1	SMAD1,ARID2,IRAK4,BMP2	pink	VSMC_M5
GO:0043583	0.96	0.10	4	162	ear development	BP	1	ESRP1,TTC8,NIPBL,BMP2	pink	VSMC_M5
GO:0001503	0.96	0.07	10	328	ossification	BP	1	RUNX2,UFL1,IL6ST,IMPAD1,SMAD1,NF1,NIPBL,SMAD7,TMEM38B,BMP2	pink	VSMC_M5
GO:0050867	0.96	0.09	5	226	positive regulation of cell activation	BP	1	ANXA1,IRS2,IL6ST,KMT5B,PIK3CA	pink	VSMC_M5
GO:0045055	0.96	0.09	4	167	regulated exocytosis	BP	1	ARL8B,SLC4A8,GSK3B,STXBP3	pink	VSMC_M5
GO:0033993	0.96	0.06	22	657	response to lipid	BP	1	TAB2,LATS1,UBR5,DDX17,ANXA1,ADAM17,UFL1,NCOA1,NR3C1,MAPK8,KDM3A,ERBIN,URI1,NR3C2,RPS6KA3,ATM,USP8,SMAD2,PRKAA1,PRPF8,SETX,MT-ND3	pink	VSMC_M5
GO:0003012	0.96	0.07	10	332	muscle system process	BP	1	ARHGAP42,IL6ST,ATP2B4,TWF1,MEF2A,PIK3CA,GLRX3,SMAD7,TMEM38B,MTPN	pink	VSMC_M5
GO:0015850	0.96	0.09	4	179	organic hydroxy compound transport	BP	1	RELCH,OSBPL9,ARL8B,PRKAA1	pink	VSMC_M5
GO:0032409	0.96	0.08	5	198	regulation of transporter activity	BP	1	NIPSNAP2,CAB39,STK39,WNK1,ATP7A	pink	VSMC_M5
GO:0030099	0.96	0.07	8	293	myeloid cell differentiation	BP	1	VEGFA,UFL1,KAT6A,KITLG,GABPA,NOTCH2,TET2,SRP54	pink	VSMC_M5
GO:0051656	0.96	0.07	10	334	establishment of organelle localization	BP	1	WASL,RAB1A,CLASP1,PCM1,TBC1D23,BICD1,FBXW11,DYNC1H1,RMDN1,SAR1B	pink	VSMC_M5
GO:0006364	0.96	0.09	4	198	rRNA processing	BP	1	DDX17,SHQ1,METTL5,NAF1	pink	VSMC_M5
GO:0051091	0.96	0.08	5	204	positive regulation of DNA-binding transcription factor activity	BP	1	VEGFA,ATF2,PRKCI,MTPN,BMP2	pink	VSMC_M5
GO:0045930	0.97	0.08	4	186	negative regulation of mitotic cell cycle	BP	1	MRE11,BTG2,ATF2,ATM	pink	VSMC_M5
GO:0060541	0.97	0.08	4	163	respiratory system development	BP	1	VEGFA,ATP7A,SMAD2,TMEM38B	pink	VSMC_M5
GO:0006066	0.97	0.07	6	258	alcohol metabolic process	BP	1	CYP39A1,IMPAD1,SPTLC2,PRKAA1,SULT1C4,BMP2	pink	VSMC_M5
GO:0032103	0.97	0.07	7	286	positive regulation of response to external stimulus	BP	1	VEGFA,ADAM17,IL6ST,LSM14A,PUM1,STK39,WNK1	pink	VSMC_M5
GO:0002253	0.97	0.08	4	191	activation of immune response	BP	1	PIK3CA,PLEKHA1,CRKL,WNK1	pink	VSMC_M5
GO:0051241	0.97	0.05	25	743	negative regulation of multicellular organismal process	BP	1	ANXA1,KRIT1,CD2AP,TIA1,ADAM17,ARHGAP42,RHEB,PCM1,ERBIN,DIP2B,ATP2B4,CYLD,ACOT13,GSK3B,GTF2I,STK39,DLX2,GLRX3,ATF2,TIMP1,WNK1,NF1,PTPRM,SMAD7,BMP2	pink	VSMC_M5
GO:1901987	0.97	0.06	8	311	regulation of cell cycle phase transition	BP	1	ANXA1,ADAM17,MRE11,ATP2B4,ATF2,ATM,FEM1B,RAD1	pink	VSMC_M5
GO:0019216	0.97	0.07	6	251	regulation of lipid metabolic process	BP	1	ANXA1,IRS2,ACACB,CREBL2,PRKAA1,BMP2	pink	VSMC_M5
GO:0061061	0.97	0.05	17	504	muscle structure development	BP	1	SYNE1,DDX17,VEGFA,EPC1,SMAD1,BTG2,MEF2A,KMT5B,FXR1,COPS2,PIAS1,PRKAA1,SMAD7,MTPN,CD164,CACYBP,BMP2	pink	VSMC_M5
GO:0055085	0.97	0.04	37	1047	transmembrane transport	BP	1	SLC25A17,RHOQ,COMMD1,PCYOX1,SLC41A3,ZDHHC17,SLC30A6,IRS2,SLC4A8,TRPC1,WWP1,ATP2B4,NIPSNAP2,ANO1,CAB39,MEF2A,SCN9A,STK39,CREBL2,SRP54,CUL5,ERO1A,PRKCI,YWHAQ,WNK1,SFXN1,ABCB7,ATP7A,STXBP3,SLC35A3,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF,TMEM38B,SLC25A36	pink	VSMC_M5
GO:0070588	0.97	0.06	6	211	calcium ion transmembrane transport	BP	1	TRPC1,ATP2B4,NIPSNAP2,CUL5,ERO1A,TMEM38B	pink	VSMC_M5
GO:0042692	0.97	0.06	9	303	muscle cell differentiation	BP	1	SYNE1,VEGFA,EPC1,SMAD1,MEF2A,PIAS1,MTPN,CACYBP,BMP2	pink	VSMC_M5
GO:0097305	0.97	0.07	4	174	response to alcohol	BP	1	SMAD2,PRKAA1,MT-ND4,BIRC2	pink	VSMC_M5
GO:0048646	0.97	0.04	33	877	anatomical structure formation involved in morphogenesis	BP	1	LATS1,MTHFD1L,ANXA1,VEGFA,KRIT1,GCM1,ADAM17,JCAD,SRPK2,CLASP1,EPB41L5,DLC1,SMAD1,TCTN1,GABPA,HIPK1,ATP2B4,NOTCH2,MEF2A,PIK3CA,GTF2I,EGLN1,HECTD1,ATF2,OPHN1,HERC1,ATP7A,SMAD2,NF1,PTPRM,MTPN,DDAH1,BMP2	pink	VSMC_M5
GO:1903706	0.97	0.06	6	258	regulation of hemopoiesis	BP	1	ANXA1,KITLG,GABPA,NOTCH2,SOS2,SMAD7	pink	VSMC_M5
GO:0051239	0.97	0.04	76	1937	regulation of multicellular organismal process	BP	1	LATS1,ANXA1,VEGFA,KRIT1,RUNX2,CD2AP,MACF1,RAB1A,SEPT7,TIA1,ADAM17,UFL1,RAB14,JCAD,ARHGAP42,KIAA1109,CLASP1,EPB41L5,RHEB,MBD5,FLRT3,XDH,LTBP1,KITLG,ATRN,IL6ST,CAPRIN1,PCM1,TNKS2,KDM3A,ERBIN,SMAD1,EIF4G2,TRPC1,DIP2B,GABPA,PPP1CC,ARSB,HIPK1,ESRP1,ATP2B4,TWF1,CYLD,ACOT13,NOTCH2,TRIP12,ZMYND8,MEF2A,PRKAB2,KMT5B,ACACB,GSK3B,PIK3CA,GTF2I,STK39,EGLN1,DLX2,GLRX3,ATF2,SOS2,PRKCI,TIMP1,WNK1,SMAD2,DYNC1H1,NF1,PRKAA1,PTPRM,NIPBL,SMAD7,ATP5PF,TMEM38B,UBE2V2,MTPN,DDAH1,BMP2	pink	VSMC_M5
GO:0007611	0.97	0.06	5	183	learning or memory	BP	1	PJA2,BTG2,PIAS1,NF1,PAIP2	pink	VSMC_M5
GO:0002683	0.97	0.06	7	290	negative regulation of immune system process	BP	1	WASL,ANXA1,KITLG,YTHDF3,TSPAN32,ATM,SMAD7	pink	VSMC_M5
GO:0048878	0.97	0.04	29	832	chemical homeostasis	BP	1	DMXL1,VEGFA,CYP39A1,GCLC,UGCG,COMMD1,AKAP11,MBD5,IRS2,SLC4A8,TRPC1,ATP2B4,ANO1,PIK3CA,GTF2I,STK39,EGLN1,GLRX3,ACOX3,ERO1A,WNK1,ABCB7,ATP7A,XIAP,PRKAA1,SMAD7,STXBP3,TMEM38B,EIF5A2	pink	VSMC_M5
GO:0002376	0.98	0.03	59	1656	immune system process	BP	1	MAPK9,DDX17,WASL,ANXA1,VEGFA,RUNX2,RAB1A,ADAM17,UFL1,RAB14,SRPK2,DCLRE1C,ARL8B,KAT6A,IRS2,KITLG,N4BP2L2,MAPK8,IL6ST,IFIT5,YTHDF3,LSM14A,PJA2,ERBIN,GABPA,TIPARP,MLF1,HIPK1,IRAK4,CYLD,TSPAN32,NOTCH2,TET2,KMT5B,PUM1,PIK3CA,LYST,STK39,PLEKHA1,HECTD1,RPS6KA3,SRP54,ATF2,SOS2,ATM,CRKL,WNK1,PYGO1,ATP7A,USP14,WDR78,XIAP,HPRT1,SMAD7,STXBP3,BIRC2,CD164,ELMOD2,SAR1B	pink	VSMC_M5
GO:0043270	0.98	0.06	4	182	positive regulation of ion transport	BP	1	TRPC1,NIPSNAP2,STK39,WNK1	pink	VSMC_M5
GO:1901700	0.98	0.03	44	1234	response to oxygen-containing compound	BP	1	TAB2,MAPK9,UBR2,ANXA1,ASNS,GCLC,RHOQ,ADAM17,UFL1,NCOA1,MBD5,IRS2,NR3C1,MAPK8,ERBIN,GABPA,BTG2,ATP2B4,NDUFS4,ANO1,GSK3B,PIK3CA,UBR1,EGLN1,PLEKHA1,RPS6KA3,ATF2,ATM,PRKCI,USP8,TIMP1,CRKL,CPEB4,ATP7A,SMAD2,PIK3C3,PRKAA1,PRPF8,SETX,STXBP3,MT-ND4,MT-ND5,BIRC2,CACYBP	pink	VSMC_M5
GO:0021700	0.98	0.06	5	204	developmental maturation	BP	1	VEGFA,RUNX2,SCLT1,FEM1B,BMP2	pink	VSMC_M5
GO:0043269	0.98	0.04	13	444	regulation of ion transport	BP	1	COMMD1,TRPC1,ATP2B4,NIPSNAP2,CAB39,SCN9A,STK39,YWHAQ,WNK1,ATP7A,PRKAA1,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0050808	0.98	0.04	10	329	synapse organization	BP	1	WASL,FNTA,FLRT3,CAPRIN1,ZMYND8,ALS2,ABI2,CRKL,OPHN1,UBE2V2	pink	VSMC_M5

GO:0045596	0.98	0.03	15	489	negative regulation of cell differentiation	BP	1	ANXA1,VEGFA,BBS12,XDH,SPRY4,N4BP2L2,PCM1,SMAD1,DIP2B,GABPA,GSK3B,DLX2,NF1,SMAD7,BMP2	pink	VSMC_M5
GO:0051640	0.98	0.03	13	447	organelle localization	BP	1	WASL,RAB1A,CLASP1,ARL8B,PCM1,TBC1D23,BICD1,MEF2A,FBXW11,DYNC1H1,STXBP3,RMDN1,SAR1B	pink	VSMC_M5
GO:0044403	0.98	0.04	4	206	biological process involved in symbiotic interaction	BP	1	ARL8B,WWP1,TSG101,CCNK	pink	VSMC_M5
GO:0002684	0.99	0.03	14	542	positive regulation of immune system process	BP	1	ANXA1,VEGFA,ADAM17,IRS2,KITLG,IL6ST,LSM14A,NOTCH2,KMT5B,PIK3CA,STK39,PLEKHA1,CRKL,WNK1	pink	VSMC_M5
GO:0009605	0.99	0.02	64	1770	response to external stimulus	BP	1	TAB2,DDX17,WASL,ANXA1,VEGFA,ASNS,GCLC,RAB1A,ADAM17,UFL1,RAB14,SRPK2,NCOA1,MAP3K2,CLASP1,FBXL3,FLRT3,ARL8B,MAPK8,APAF1,IL6ST,IFIT5,YTHDF3,LSM14A,PJA2,ERBIN,URI1,PPP1CC,LXN,ARSB,BTG2,IRAK4,CYLD,TSPAN32,NOTCH2,ANO1,ACACB,PUM1,PIK3CA,LYST,STK39,RPS6KA3,SRP54,ATF2,CRKL,NAALADL2,WNK1,OPHN1,CPEB4,ASH1L,TTC8,PIK3C3,USP14,XIAP,PRKAA1,PTPRM,PRPF8,STXBP3,USP33,BIRC2,MTPN,ELMOD2,BMT2,BMP2	pink	VSMC_M5
GO:0051240	0.99	0.02	36	1050	positive regulation of multicellular organismal process	BP	1	ANXA1,VEGFA,RUNX2,MACF1,RAB1A,ADAM17,UFL1,JCAD,RHEB,FLRT3,KITLG,IL6ST,CAPRIN1,KDM3A,SMAD1,EIF4G2,PPP1CC,HIPK1,TWF1,NOTCH2,MEF2A,PRKAB2,KMT5B,ACACB,ATF2,PRKCI,SMAD2,DYNC1H1,PRKAA1,NIPBL,SMAD7,ATP5PF,UBE2V2,MTPN,DDAH1,BMP2	pink	VSMC_M5
GO:0051480	0.99	0.03	5	212	regulation of cytosolic calcium ion concentration	BP	1	TRPC1,ATP2B4,GTF2I,ERO1A,TMEM38B	pink	VSMC_M5
GO:0051146	0.99	0.03	5	220	striated muscle cell differentiation	BP	1	VEGFA,MEF2A,MTPN,CACYBP,BMP2	pink	VSMC_M5
GO:0051093	0.99	0.02	21	676	negative regulation of developmental process	BP	1	ANXA1,VEGFA,KRIT1,BBS12,XDH,SPRY4,N4BP2L2,PCM1,SMAD1,DIP2B,GABPA,ATP2B4,GSK3B,GTF2I,DLX2,ATF2,HUWE1,NF1,PTPRM,SMAD7,BMP2	pink	VSMC_M5
GO:0050801	0.99	0.02	16	542	ion homeostasis	BP	1	DMXL1,GCLC,COMMD1,SLC4A8,TRPC1,ATP2B4,GTF2I,STK39,GLRX3,ERO1A,WNK1,ABCB7,ATP7A,XIAP,SMAD7,TMEM38B	pink	VSMC_M5
GO:0044093	0.99	0.02	39	1151	positive regulation of molecular function	BP	1	TAB2,SERINC1,VEGFA,ADAM17,ARHGAP42,MRE11,MAGI2,EPB41L5,FNTA,XDH,KITLG,MAPK8,APAF1,DLC1,CDK5RAP1,RALGAPB,ATP2B4,BTRC,NIPSNAP2,DOCK3,CAB39,GSK3B,PIK3CA,DCUN1D1,STK39,FAM162A,ALS2,ATF2,PRKCI,CRKL,WNK1,ATP7A,CCNK,NF1,USP33,MTPN,NAF1,ELMOD2,BMP2	pink	VSMC_M5
GO:0007267	0.99	0.02	40	1146	cell-cell signaling	BP	1	LATS1,CSNK1G3,UBR5,PCSK5,ANXA1,USP34,MACF1,RAB1A,MAGI2,ZEB2,IRS2,CSNK2A1,FAT1,TNKS2,SLC4A8,KCMF1,CYLD,BTRC,TSPAN32,ANO1,ZMYND8,GSK3B,ALS2,RPS6KA3,USP8,CRKL,WNK1,PYGO1,OPHN1,FBXW11,SMAD2,GSKIP,CSNK1A1,XIAP,PRKAA1,STXBP3,ATP5PF,PAIP2,MPZL1,BMP2	pink	VSMC_M5
GO:0006812	0.99	0.02	25	796	cation transport	BP	1	SLC25A17,COMMD1,SLC41A3,ZDHHC17,SLC30A6,SLC4A8,TRPC1,ATP2B4,NIPSNAP2,ANO1,CAB39,SCN9A,STK39,CUL5,ERO1A,WNK1,SFXN1,ABCB7,ATP7A,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0098609	0.99	0.02	19	592	cell-cell adhesion	BP	1	ANXA1,VEGFA,CD2AP,EPB41L5,FLRT3,MAGI1,IL6ST,FAT1,TSPAN32,PIK3CA,TMEM47,WNK1,PTPRM,SMAD7,STXBP3,NFAT5,CD164,BMP2,PCDHGB1	pink	VSMC_M5
GO:0001816	0.99	0.02	13	504	cytokine production	BP	1	PCSK5,ANXA1,CD2AP,RAB1A,TIA1,ADAM17,LTBP1,IL6ST,ERBIN,CYLD,ATF2,SMAD7,NFAT5	pink	VSMC_M5
GO:0032101	0.99	0.02	18	646	regulation of response to external stimulus	BP	1	ANXA1,VEGFA,ADAM17,UFL1,CLASP1,IL6ST,YTHDF3,LSM14A,CYLD,TSPAN32,PUM1,STK39,WNK1,ASH1L,USP14,XIAP,BIRC2,ELMOD2	pink	VSMC_M5
GO:0042391	0.99	0.02	7	302	regulation of membrane potential	BP	1	GCLC,SLC4A8,ZMYND8,GSK3B,SCN9A,SMAD7,SLC25A36	pink	VSMC_M5
GO:0007204	0.99	0.02	4	194	positive regulation of cytosolic calcium ion concentration	BP	1	TRPC1,ATP2B4,ERO1A,TMEM38B	pink	VSMC_M5
GO:0055082	0.99	0.01	16	564	cellular chemical homeostasis	BP	1	DMXL1,GCLC,IRS2,SLC4A8,TRPC1,ATP2B4,ANO1,PIK3CA,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,PRKAA1,STXBP3,TMEM38B	pink	VSMC_M5
GO:1901990	0.99	0.02	4	237	regulation of mitotic cell cycle phase transition	BP	1	ANXA1,ADAM17,MRE11,ATM	pink	VSMC_M5
GO:0007155	0.99	0.01	38	1044	cell adhesion	BP	1	MKLN1,ANXA1,VEGFA,CD2AP,DST,MACF1,RAB1A,ADAM17,JCAD,CLASP1,EPB41L5,FLRT3,KITLG,SPRY4,ATRN,MAGI1,DLC1,IL6ST,FAT1,ERBIN,TSPAN32,GSK3B,PIK3CA,ARHGAP5,TMEM47,ATM,ARPC2,CRKL,WNK1,NF1,PTPRM,SMAD7,STXBP3,PKN2,NFAT5,CD164,BMP2,PCDHGB1	pink	VSMC_M5
GO:0042254	0.99	0.02	4	256	ribosome biogenesis	BP	1	DDX17,SHQ1,METTL5,NAF1	pink	VSMC_M5
GO:0022610	0.99	0.01	38	1050	biological adhesion	BP	1	MKLN1,ANXA1,VEGFA,CD2AP,DST,MACF1,RAB1A,ADAM17,JCAD,CLASP1,EPB41L5,FLRT3,KITLG,SPRY4,ATRN,MAGI1,DLC1,IL6ST,FAT1,ERBIN,TSPAN32,GSK3B,PIK3CA,ARHGAP5,TMEM47,ATM,ARPC2,CRKL,WNK1,NF1,PTPRM,SMAD7,STXBP3,PKN2,NFAT5,CD164,BMP2,PCDHGB1	pink	VSMC_M5
GO:0006936	1.00	0.01	5	256	muscle contraction	BP	1	ARHGAP42,ATP2B4,PIK3CA,SMAD7,TMEM38B	pink	VSMC_M5
GO:0006816	1.00	0.01	6	282	calcium ion transport	BP	1	TRPC1,ATP2B4,NIPSNAP2,CUL5,ERO1A,TMEM38B	pink	VSMC_M5
GO:0006811	1.00	0.01	31	1026	ion transport	BP	1	SLC25A17,ANXA1,COMMD1,PCYOX1,SLC41A3,ZDHHC17,SLC30A6,SLC4A8,TRPC1,WWP1,ATP2B4,NIPSNAP2,ANO1,CAB39,SCN9A,STK39,CUL5,ERO1A,YWHAQ,WNK1,SFXN1,ABCB7,ATP7A,PRKAA1,SLC35A3,MT-CO1,MT-CO2,MT-ND4,MT-ND5,ATP5PF,TMEM38B	pink	VSMC_M5
GO:0001817	1.00	0.01	11	492	regulation of cytokine production	BP	1	ANXA1,CD2AP,RAB1A,TIA1,ADAM17,LTBP1,IL6ST,ERBIN,CYLD,ATF2,SMAD7	pink	VSMC_M5
GO:0030001	1.00	0.01	16	587	metal ion transport	BP	1	COMMD1,ZDHHC17,SLC30A6,SLC4A8,TRPC1,ATP2B4,NIPSNAP2,CAB39,SCN9A,STK39,CUL5,ERO1A,WNK1,ABCB7,ATP7A,TMEM38B	pink	VSMC_M5
GO:0055080	1.00	0.01	12	494	cation homeostasis	BP	1	DMXL1,COMMD1,SLC4A8,TRPC1,ATP2B4,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,XIAP,TMEM38B	pink	VSMC_M5
GO:0001819	1.00	0.01	5	304	positive regulation of cytokine production	BP	1	ANXA1,RAB1A,ADAM17,IL6ST,ATF2	pink	VSMC_M5

GO:0003008	1.00	0.00	42	1240	system process	BP	1	PCSK5,VEGFA,GCLC,FBXO11,UGCG,VPS54,ARHGAP42,AKAP11,IL6ST,PJA2,SLC4A8,TRPC1,LXN,BTG2,ATP2B4,TWF1,ANO1,ZMYND8,MEF2A,GSK3B,PIK3CA,SCN9A,STK39,UBR3,GLRX3,CCDC50,WNK1,HERC1,SPATA7,CHM,PIAS1,TTC8,NF1,NIPBL,SMAD7,NFAT5,ATP5PF,TMEM38B,MTPN,DDAH1,TIMM9,PAIP2	pink	VSMC_M5
GO:0050877	1.00	0.00	20	678	nervous system process	BP	1	FBXO11,VPS54,PJA2,LXN,BTG2,ANO1,ZMYND8,GSK3B,SCN9A,UBR3,CCDC50,HERC1,SPATA7,CHM,PIAS1,TTC8,NF1,NIPBL,TIMM9,PAIP2	pink	VSMC_M5
GO:0019725	1.00	0.00	17	638	cellular homeostasis	BP	1	DMXL1,KRIT1,GCLC,IRS2,SLC4A8,TRPC1,ATP2B4,ANO1,PIK3CA,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,PRKAA1,STXBP3,TMEM38B	pink	VSMC_M5
GO:0055065	1.00	0.01	10	438	metal ion homeostasis	BP	1	COMMD1,TRPC1,ATP2B4,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,XIAP,TMEM38B	pink	VSMC_M5
GO:0030003	1.00	0.01	10	434	cellular cation homeostasis	BP	1	DMXL1,SLC4A8,TRPC1,ATP2B4,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,TMEM38B	pink	VSMC_M5
GO:0098771	1.00	0.00	12	502	inorganic ion homeostasis	BP	1	DMXL1,COMMD1,SLC4A8,TRPC1,ATP2B4,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,XIAP,TMEM38B	pink	VSMC_M5
GO:0006875	1.00	0.00	8	381	cellular metal ion homeostasis	BP	1	TRPC1,ATP2B4,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,TMEM38B	pink	VSMC_M5
GO:0007186	1.00	0.00	10	458	G protein-coupled receptor signaling pathway	BP	1	DGKA,ANXA1,DGKH,PRKD3,ATP2B4,BICD1,ANO1,CRKL,USP33,NMS	pink	VSMC_M5
GO:0006873	1.00	0.00	10	444	cellular ion homeostasis	BP	1	DMXL1,SLC4A8,TRPC1,ATP2B4,GTF2I,GLRX3,ERO1A,ABCB7,ATP7A,TMEM38B	pink	VSMC_M5
GO:0006874	1.00	0.00	5	283	cellular calcium ion homeostasis	BP	1	TRPC1,ATP2B4,GTF2I,ERO1A,TMEM38B	pink	VSMC_M5
GO:1901701	1.00	0.00	25	887	cellular response to oxygen-containing compound	BP	1	MAPK9,UBR2,ANXA1,GCLC,RHOQ,MBD5,IRS2,NR3C1,MAPK8,GABPA,ATP2B4,ANO1,GSK3B,PIK3CA,UBR1,PLEKHA1,ATM,PRKCI,USP8,CRKL,CPEB4,ATP7A,PRKAA1,PRPF8,SETX	pink	VSMC_M5
GO:0050804	1.00	0.00	6	317	modulation of chemical synaptic transmission	BP	1	SLC4A8,ZMYND8,GSK3B,USP8,OPHN1,PAIP2	pink	VSMC_M5
GO:0099177	1.00	0.00	6	318	regulation of trans-synaptic signaling	BP	1	SLC4A8,ZMYND8,GSK3B,USP8,OPHN1,PAIP2	pink	VSMC_M5
GO:0055074	1.00	0.00	5	291	calcium ion homeostasis	BP	1	TRPC1,ATP2B4,GTF2I,ERO1A,TMEM38B	pink	VSMC_M5
GO:0099536	1.00	0.00	11	494	synaptic signaling	BP	1	SLC4A8,KCMF1,ZMYND8,GSK3B,ALS2,RPS6KA3,USP8,CRKL,OPHN1,STXBP3,PAIP2	pink	VSMC_M5
GO:0072503	1.00	0.00	5	306	cellular divalent inorganic cation homeostasis	BP	1	TRPC1,ATP2B4,GTF2I,ERO1A,TMEM38B	pink	VSMC_M5
GO:0072507	1.00	0.00	5	323	divalent inorganic cation homeostasis	BP	1	TRPC1,ATP2B4,GTF2I,ERO1A,TMEM38B	pink	VSMC_M5
GO:0007268	1.00	0.00	9	471	chemical synaptic transmission	BP	1	SLC4A8,ZMYND8,GSK3B,ALS2,RPS6KA3,USP8,OPHN1,STXBP3,PAIP2	pink	VSMC_M5
GO:0098916	1.00	0.00	9	471	anterograde trans-synaptic signaling	BP	1	SLC4A8,ZMYND8,GSK3B,ALS2,RPS6KA3,USP8,OPHN1,STXBP3,PAIP2	pink	VSMC_M5
GO:0099537	1.00	0.00	9	477	trans-synaptic signaling	BP	1	SLC4A8,ZMYND8,GSK3B,ALS2,RPS6KA3,USP8,OPHN1,STXBP3,PAIP2	pink	VSMC_M5
GO:0002181	0.00	1.00	16	111	cytoplasmic translation	BP	0.86618	EIF3D,RPS5,RPL28,RPS7,RPS11,RPS3,RPS3A,RPS6,EIF3I,RBM4,RPL35A,RPL18A,FTSJ1,RPS24,DPH5,RPS20	red	VSMC_M1
GO:0042073	0.00	1.00	7	34	intraciliary transport	BP	0.88679	ICK,WDR35,IFT122,IFT57,ARL3,IFT46,DYNC2H1	red	VSMC_M1
GO:0072331	0.00	1.00	15	139	signal transduction by p53 class mediator	BP	0.88679	SGK1,DYRK2,NDRG1,RPS7,KMT5A,SPRED1,SMYD2,KDM1A,USP28,CDK5RAP3,RFFL,YJU2,USP10,WWOX,RPS20	red	VSMC_M1
GO:1901796	0.00	1.00	11	83	regulation of signal transduction by p53 class mediator	BP	0.88679	SGK1,DYRK2,RPS7,KMT5A,SPRED1,SMYD2,KDM1A,CDK5RAP3,RFFL,YJU2,RPS20	red	VSMC_M1
GO:0070647	0.00	1.00	50	806	protein modification by small protein conjugation or removal	BP	0.88679	DCAF13,EGR1,UBE2M,ANKRD39,COPS9,RPS7,IRF2BP1,RPS3,RNF121,HDAC3,SOCS2,TNKS,COPS5,CTR9,FBXW8,TBC1D7,CDC73,PPP1R11,KLHL41,DCAF17,FBXO45,EGR2,KDM1A,USP28,ANAPC16,USP5,TRIM4,UBA1,UVSSA,PELI2,TRRAP,ZMIZ1,KAT2A,ANAPC13,RNF40,CDK5RAP3,RNF138,HMG20A,RFFL,USP22,FBXO4,UBE4B,USP10,MED31,URM1,FKBP1A,RACK1,RPS20,RNF125,RCHY1	red	VSMC_M1
GO:0032446	0.00	1.00	45	703	protein modification by small protein conjugation	BP	0.88679	DCAF13,EGR1,UBE2M,ANKRD39,COPS9,RPS7,IRF2BP1,RPS3,RNF121,HDAC3,SOCS2,TNKS,CTR9,FBXW8,TBC1D7,CDC73,PPP1R11,KLHL41,DCAF17,FBXO45,EGR2,KDM1A,ANAPC16,USP5,TRIM4,UBA1,UVSSA,PELI2,ZMIZ1,ANAPC13,RNF40,CDK5RAP3,RNF138,HMG20A,RFFL,USP22,FBXO4,UBE4B,MED31,URM1,FKBP1A,RACK1,RPS20,RNF125,RCHY1	red	VSMC_M1
GO:0035721	0.00	1.00	4	11	intraciliary retrograde transport	BP	0.88679	ICK,WDR35,IFT122,DYNC2H1	red	VSMC_M1
GO:0048199	0.00	1.00	5	20	vesicle targeting, to, from or within Golgi	BP	1	CSNK1D,TFG,WIPI1,CEP19,GOSR1	red	VSMC_M1
GO:0035308	0.00	1.00	6	30	negative regulation of protein dephosphorylation	BP	1	FKBP1B,PPP1R8,ENSA,PPP1R11,PTPA,FKBP1A	red	VSMC_M1
GO:0060271	0.00	1.00	21	266	cilium assembly	BP	1	ICK,FAM161A,WDR35,ARHGAP35,IFT122,VDAC3,CSNK1D,TBC1D7,IFT57,ARL3,UNC119B,CFAP410,WDR11,IFT46,MAP4,CEP19,RP2,DYNC2H1,DNAL1,B9D1,E2F4	red	VSMC_M1
GO:0034968	0.00	1.00	11	98	histone lysine methylation	BP	1	SMAD4,KMT5C,PIH1D1,KMT5A,CTR9,SMYD5,WDR5B,SMYD2,KDM1A,MECOM,WDR5	red	VSMC_M1
GO:0006413	0.00	1.00	11	99	translational initiation	BP	1	EIF3D,RPS5,EIF2B4,RPS3,MTIF3,COPS5,RPS3A,EIF2A,EIF3I,RBM4,EIF2B2	red	VSMC_M1
GO:0051569	0.00	1.00	5	26	regulation of histone H3-K4 methylation	BP	1	SMAD4,PIH1D1,CTR9,KDM1A,WDR5	red	VSMC_M1
GO:0044782	0.00	1.00	21	288	cilium organization	BP	1	ICK,FAM161A,WDR35,ARHGAP35,IFT122,VDAC3,CSNK1D,TBC1D7,IFT57,ARL3,UNC119B,CFAP410,WDR11,IFT46,MAP4,CEP19,RP2,DYNC2H1,DNAL1,B9D1,E2F4	red	VSMC_M1
GO:0018022	0.00	1.00	11	108	peptidyl-lysine methylation	BP	1	SMAD4,KMT5C,PIH1D1,KMT5A,CTR9,SMYD5,WDR5B,SMYD2,KDM1A,MECOM,WDR5	red	VSMC_M1
GO:0060606	0.00	1.00	9	83	tube closure	BP	1	RPS7,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2,FGF10	red	VSMC_M1
GO:0042026	0.00	1.00	4	16	protein refolding	BP	1	HSPA1L,FKBP1B,HSPA2,FKBP1A	red	VSMC_M1
GO:0016567	0.00	1.00	39	656	protein ubiquitination	BP	1	DCAF13,UBE2M,ANKRD39,RPS7,IRF2BP1,RPS3,RNF121,HDAC3,SOCS2,TNKS,CTR9,FBXW8,TBC1D7,CDC73,PPP1R11,KLHL41,DCAF17,FBXO45,KDM1A,ANAPC16,USP5,TRIM4,UBA1,UVSSA,PELI2,ANAPC13,RNF40,CDK5RAP3,RNF138,RFFL,USP22,FBXO4,UBE4B,MED31,FKBP1A,RACK1,RPS20,RNF125,RCHY1	red	VSMC_M1
GO:0032482	0.00	1.00	4	18	Rab protein signal transduction	BP	1	RAB30,RAB9A,RAB12,RAB39B	red	VSMC_M1
GO:0043392	0.00	1.00	6	40	negative regulation of DNA binding	BP	1	SRI,TNKS,KDM1A,CTNNBIP1,TMSB4X,CPNE1	red	VSMC_M1
GO:1901019	0.00	1.00	8	67	regulation of calcium ion transmembrane transporter activity	BP	1	SRI,FKBP1B,CACNA2D1,STIMATE,HSPA2,CALM2,FKBP1A,AHNAK	red	VSMC_M1
GO:0035305	0.00	1.00	6	40	negative regulation of dephosphorylation	BP	1	FKBP1B,PPP1R8,ENSA,PPP1R11,PTPA,FKBP1A	red	VSMC_M1

GO:0002823	0.00	1.00	5	30	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	ARG1,IL1RL1,AHR,IL20RB,PARP3	red	VSMC_M1
GO:0006903	0.00	1.00	6	42	vesicle targeting	BP	1	CSNK1D,TFG,WIPI1,WDR11,CEP19,GOSR1	red	VSMC_M1
GO:0002704	0.00	1.00	5	30	negative regulation of leukocyte mediated immunity	BP	1	ARG1,AHR,IL20RB,PARP3,IL13RA2	red	VSMC_M1
GO:0034284	0.00	1.00	14	164	response to monosaccharide	BP	1	EGR1,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,EIF2B4,ENSA,NR1D1,EIF2B2,STXBP4,SPARC,RACK1,PTPRN2	red	VSMC_M1
GO:0007224	0.00	1.00	11	119	smoothened signaling pathway	BP	1	DYRK2,CTNNA1,IFT122,IFT57,ARL3,CFAP410,WDR11,DYNC2H1,B9D1,RACK1,FGF10	red	VSMC_M1
GO:0016571	0.00	1.00	11	118	histone methylation	BP	1	SMAD4,KMT5C,PIH1D1,KMT5A,CTR9,SMYD5,WDR5B,SMYD2,KDM1A,MECOM,WDR5	red	VSMC_M1
GO:0043516	0.01	1.00	5	29	regulation of DNA damage response, signal transduction by p53 class mediator	BP	1	KMT5A,SPRED1,SMYD2,KDM1A,YJU2	red	VSMC_M1
GO:0086065	0.01	1.00	6	46	cell communication involved in cardiac conduction	BP	1	SRI,FKBP1B,CACNA2D1,CACNA1D,GJC1,CALM2	red	VSMC_M1
GO:0031058	0.01	1.00	8	75	positive regulation of histone modification	BP	1	SMAD4,PIH1D1,WBP2,CTR9,KDM1A,KAT2A,RNF40,WDR5	red	VSMC_M1
GO:0035304	0.01	1.00	8	74	regulation of protein dephosphorylation	BP	1	CSNK2B,FKBP1B,PPP1R8,ENSA,PPP1R11,CALM2,PTPA,FKBP1A	red	VSMC_M1
GO:0009749	0.01	1.00	13	153	response to glucose	BP	1	EGR1,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,EIF2B4,ENSA,NR1D1,EIF2B2,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0002820	0.01	1.00	5	33	negative regulation of adaptive immune response	BP	1	ARG1,IL1RL1,AHR,IL20RB,PARP3	red	VSMC_M1
GO:0006368	0.01	1.00	7	58	transcription elongation from RNA polymerase II promoter	BP	1	RECQL5,PCID2,CTR9,CDC73,ZMIZ1,SUPT4H1,ELOF1	red	VSMC_M1
GO:0070925	0.01	1.00	40	705	organelle assembly	BP	1	SMAD4,ICK,RPS5,FAM161A,WDR35,ARHGAP35,STAM,IFT122,RPS3,VDAC3,NEB,CSNK1D,HDAC3,TNKS,EIF2A,OGFOD1,AMBRA1,TBC1D7,IFT57,ARL3,UNC119B,NPRL2,CFAP410,WIPI1,AKAP13,KLHL41,WDR11,IFT46,BCCIP,MAP4,CEP19,IL1RAP,RP2,LSM4,DYNC2H1,KAT2A,VPS37C,DNAL1,B9D1,E2F4	red	VSMC_M1
GO:0060314	0.01	1.00	4	20	regulation of ryanodine-sensitive calcium-release channel activity	BP	1	SRI,FKBP1B,CALM2,FKBP1A	red	VSMC_M1
GO:0022613	0.01	1.00	26	376	ribonucleoprotein complex biogenesis	BP	1	DCAF13,EIF3D,RCL1,RPS5,MALSU1,UTP11,RPS7,PIH1D1,SNRPD2,ERI3,EBNA1BP2,SMN2,EIF2A,RPS6,CDC73,EIF3I,RPL35A,PES1,EXOSC7,EMG1,LSM4,RPS24,YJU2,RPF1,NUDT21,NOP10	red	VSMC_M1
GO:0002701	0.01	1.00	4	22	negative regulation of production of molecular mediator of immune response	BP	1	ARG1,PARP3,CUEDC2,IL13RA2	red	VSMC_M1
GO:0009746	0.01	1.00	13	159	response to hexose	BP	1	EGR1,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,EIF2B4,ENSA,NR1D1,EIF2B2,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0001843	0.01	1.00	8	82	neural tube closure	BP	1	RPS7,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2	red	VSMC_M1
GO:0043666	0.01	1.00	6	47	regulation of phosphoprotein phosphatase activity	BP	1	CSNK2B,FKBP1B,PPP1R11,CALM2,PTPA,FKBP1A	red	VSMC_M1
GO:0072175	0.01	1.00	10	116	epithelial tube formation	BP	1	RPS7,FGF2,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2,FGF10	red	VSMC_M1
GO:0086064	0.01	1.00	4	23	cell communication by electrical coupling involved in cardiac conduction	BP	1	SRI,FKBP1B,GJC1,CALM2	red	VSMC_M1
GO:0051101	0.01	1.00	9	91	regulation of DNA binding	BP	1	CSNK2B,SRI,TNKS,CEBPG,KDM1A,CALM2,CTNNBIP1,TMSB4X,CPNE1	red	VSMC_M1
GO:1903320	0.01	1.00	16	211	regulation of protein modification by small protein conjugation or removal	BP	1	EGR1,COPS9,RPS7,RPS3,HDAC3,CTR9,TBC1D7,KDM1A,ZMIZ1,RNF40,CDK5RAP3,HMG20A,FBXO4,FKBP1A,RPS20,RCHY1	red	VSMC_M1
GO:0018205	0.01	1.00	21	313	peptidyl-lysine modification	BP	1	SMAD4,EGR1,KMT5C,PIH1D1,WBP2,KMT5A,CTR9,SMYD5,ACTL6A,WDR5B,SMYD2,EGR2,KDM1A,MECOM,TRRAP,ZMIZ1,KAT2A,HMG20A,USP22,WDR5,DR1	red	VSMC_M1
GO:0032259	0.01	1.00	20	290	methylation	BP	1	SMAD4,KMT5C,COQ3,PIH1D1,KMT5A,CTR9,SMYD5,PRDM10,WDR5B,SMYD2,KDM1A,EMG1,TRMT44,MECOM,FTSJ1,METTL9,CYP1A1,RBM15,WDR5,DPH5	red	VSMC_M1
GO:0032272	0.01	1.00	7	66	negative regulation of protein polymerization	BP	1	TRIOBP,TMSB10,MAP2,PFN1,TUBB4A,KANK4,TMSB4X	red	VSMC_M1
GO:0030330	0.01	1.00	7	63	DNA damage response, signal transduction by p53 class mediator	BP	1	NDRG1,KMT5A,SPRED1,SMYD2,KDM1A,YJU2,USP10	red	VSMC_M1
GO:0048193	0.01	1.00	18	259	Golgi vesicle transport	BP	1	NRBP1,UVRAG,SPAST,CSNK1D,VTI1B,TFG,ARL3,SORCS1,WIPI1,ARFGEF2,CEP19,RP2,COPZ2,TRAPPC1,MYO18A,GOLPH3,GOSR1,RACK1	red	VSMC_M1
GO:0051568	0.01	1.00	6	51	histone H3-K4 methylation	BP	1	SMAD4,PIH1D1,CTR9,WDR5B,KDM1A,WDR5	red	VSMC_M1
GO:0031440	0.01	1.00	4	26	regulation of mRNA 3'-end processing	BP	1	CTR9,CDC73,RNF40,NUDT21	red	VSMC_M1
GO:0000460	0.01	1.00	5	34	maturation of 5.8S rRNA	BP	1	RCL1,ERI3,PES1,EXOSC7,RPF1	red	VSMC_M1
GO:1902532	0.01	0.99	25	407	negative regulation of intracellular signal transduction	BP	1	SMAD4,DYRK2,MAD2L1BP,ARHGAP35,HDAC3,CXCL12,SPRED1,TBC1D7,NPRL2,CRTC3,KDM1A,NDUFA13,MECOM,ITFG2,NR1D1,CDK5RAP3,RFFL,YJU2,ERRFI1,USP10,RACK1,TIMP3,TMSB4X,CPNE1,RNF125	red	VSMC_M1
GO:0032515	0.01	1.00	4	23	negative regulation of phosphoprotein phosphatase activity	BP	1	FKBP1B,PPP1R11,PTPA,FKBP1A	red	VSMC_M1
GO:0014020	0.01	1.00	8	86	primary neural tube formation	BP	1	RPS7,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2	red	VSMC_M1
GO:0002707	0.01	1.00	4	26	negative regulation of lymphocyte mediated immunity	BP	1	ARG1,AHR,IL20RB,PARP3	red	VSMC_M1
GO:0009743	0.01	0.99	14	186	response to carbohydrate	BP	1	EGR1,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,EIF2B4,ENSA,NR1D1,EIF2B2,STXBP4,SPARC,RACK1,PTPRN2	red	VSMC_M1
GO:1901985	0.01	1.00	5	39	positive regulation of protein acetylation	BP	1	SMAD4,FAM161A,PIH1D1,WBP2,KAT2A	red	VSMC_M1
GO:0006412	0.01	0.99	34	548	translation	BP	1	MTRF1L,POLDIP3,EIF3D,RPS5,RPL28,EEF1A1,MALSU1,RPS7,RPS11,EIF2B4,RPS3,MTIF3,COPS5,RPS3A,EIF2A,RPS6,OGFOD1,FARS2,YARS,EIF3I,RBM4,RPL35A,RPL18A,EXOSC7,MRPS14,CHCHD1,FTSJ1,RPS24,RARA,DCP2,EIF2B2,DPH5,RACK1,RPS20	red	VSMC_M1
GO:0010921	0.01	1.00	7	68	regulation of phosphatase activity	BP	1	CSNK2B,FKBP1B,PPP1R11,CDK5RAP3,CALM2,PTPA,FKBP1A	red	VSMC_M1
GO:0032006	0.01	1.00	8	84	regulation of TOR signaling	BP	1	PIH1D1,HDAC3,GPAT3,TBC1D7,NPRL2,ITFG2,RFFL,GOLPH3	red	VSMC_M1
GO:1902904	0.01	0.99	11	139	negative regulation of supramolecular fiber organization	BP	1	SMAD4,PFDN6,TRIOBP,PFDN1,TMSB10,TMEFF2,MAP2,PFN1,TUBB4A,KANK4,TMSB4X	red	VSMC_M1
GO:0043966	0.01	1.00	6	54	histone H3 acetylation	BP	1	SMAD4,PIH1D1,WBP2,KAT2A,WDR5,DR1	red	VSMC_M1

GO:0000466	0.01	1.00	4	24	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	1	RCL1,ERI3,PES1,EXOSC7	red	VSMC_M1
GO:0001889	0.01	0.99	10	116	liver development	BP	1	ARG1,CSNK2B,WDR35,CEBPG,PTCD2,ELK1,RARA,CDK5RAP3,CYP1A1,GFER	red	VSMC_M1
GO:0032922	0.01	1.00	6	55	circadian regulation of gene expression	BP	1	EGR1,AHR,CSNK1D,HDAC3,NR1D1,BHLHE41	red	VSMC_M1
GO:0031398	0.02	0.99	9	102	positive regulation of protein ubiquitination	BP	1	HDAC3,CTR9,TBC1D7,KDM1A,RNF40,CDK5RAP3,FBXO4,FKBP1A,RCHY1	red	VSMC_M1
GO:0061512	0.02	1.00	6	54	protein localization to cilium	BP	1	INVS,WDR35,IFT122,CSNK1D,ARL3,DYNC2H1	red	VSMC_M1
GO:0010644	0.02	1.00	4	27	cell communication by electrical coupling	BP	1	SRI,FKBP1B,GJC1,CALM2	red	VSMC_M1
GO:0035066	0.02	1.00	4	26	positive regulation of histone acetylation	BP	1	SMAD4,PIH1D1,WBP2,KAT2A	red	VSMC_M1
GO:0035303	0.02	0.99	9	106	regulation of dephosphorylation	BP	1	CSNK2B,FKBP1B,PPP1R8,ENSA,PPP1R11,CDK5RAP3,CALM2,PTPA,FKBP1A	red	VSMC_M1
GO:0061008	0.02	0.99	10	119	hepaticobiliary system development	BP	1	ARG1,CSNK2B,WDR35,CEBPG,PTCD2,ELK1,RARA,CDK5RAP3,CYP1A1,GFER	red	VSMC_M1
GO:0010639	0.02	0.99	19	297	negative regulation of organelle organization	BP	1	SMAD4,TRIOBP,MAD2L1BP,PCID2,TNKS,TMSB10,TBC1D7,TMEFF2,MAP4,MAP2,KAT2A,PFN1,DCP2,PRRT2,XRCC3,TUBB4A,KANK4,OMA1,TMSB4X	red	VSMC_M1
GO:0031929	0.02	0.99	9	105	TOR signaling	BP	1	PIH1D1,HDAC3,RPS6,GPAT3,TBC1D7,NPRL2,ITFG2,RFFL,GOLPH3	red	VSMC_M1
GO:0001841	0.02	0.99	8	92	neural tube formation	BP	1	RPS7,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2	red	VSMC_M1
GO:0033554	0.02	0.99	76	1561	cellular response to stress	BP	1	ARG1,DYRK2,KLF10,HSPA1L,NDRG1,HMGA1,EGR1,CTNNA1,MAP4K4,XPA,KMT5C,APLF,FKBP1B,RECQL5,PAK1,UVRAG,RPS3,IL18BP,RNF121,HDAC3,ERLIN2,CXCL12,TNFRSF19,COPS5,CEBPG,KMT5A,SLC12A6,EIF2A,SPRED1,AMBRA1,TMEM117,PARP3,VKORC1L1,NPRL2,CFAP410,WIPI1,ACTL6A,RBM4,SMYD2,BCCIP,FBXO45,INO80D,KDM1A,ETV5,USP28,MECOM,UBA1,UVSSA,TRRAP,ITFG2,HSPA2,CDK5RAP3,INO80E,PARP16,PRDX2,STXBP4,INTS3,INO80C,RNF138,XRCC3,FBXO4,OMA1,YJU2,TBC1D24,ERRFI1,UBE4B,GSTM3,USP10,RACK1,HUS1,SRXN1,NREP,TOMM7,ATP5IF1,RCHY1,FGF10	red	VSMC_M1
GO:1902531	0.02	0.99	64	1309	regulation of intracellular signal transduction	BP	1	SMAD4,SGK1,DYRK2,DYNLT1,TCP11,MAD2L1BP,MAP4K4,NPR2,RPS7,PIH1D1,FGF2,ARHGAP35,PAK1,RPS3,PSD2,HDAC3,PCID2,CXCL12,TNFRSF19,COPS5,KMT5A,RHOF,P2RX4,SPRED1,STIMATE,HPSE,GPAT3,TFG,TBC1D7,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RHOD,CRTC3,SMYD2,ARHGDIB,KDM1A,NDUFA13,MECOM,PELI2,ITFG2,ITPKB,NR1D1,CDK5RAP3,PRDX2,CALM2,XRCC3,RFFL,MIER1,FBXO4,GOLPH3,YJU2,ERRFI1,USP10,GARNL3,FKBP1A,RACK1,TIMP3,RPS20,TMSB4X,CPNE1,RNF125,FGF10	red	VSMC_M1
GO:0051928	0.02	0.99	8	86	positive regulation of calcium ion transport	BP	1	SRI,CACNA2D1,CXCL12,P2RX4,CACNA1D,STIMATE,HSPA2,CALM2	red	VSMC_M1
GO:0007007	0.02	1.00	5	35	inner mitochondrial membrane organization	BP	1	TIMM10,NDUFA13,APOOL,TMEM11,OMA1	red	VSMC_M1
GO:0035148	0.02	0.99	10	129	tube formation	BP	1	RPS7,FGF2,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2,FGF10	red	VSMC_M1
GO:0010614	0.02	1.00	4	27	negative regulation of cardiac muscle hypertrophy	BP	1	SMAD4,PAK1,P2RX4,ERRFI1	red	VSMC_M1
GO:1901798	0.02	1.00	4	24	positive regulation of signal transduction by p53 class mediator	BP	1	RPS7,SPRED1,CDK5RAP3,RPS20	red	VSMC_M1
GO:0043043	0.02	0.99	34	566	peptide biosynthetic process	BP	1	MTRF1L,POLDIP3,EIF3D,RPS5,RPL28,EEF1A1,MALSU1,RPS7,RPS11,EIF2B4,RPS3,MTIF3,COPS5,RPS3A,EIF2A,RPS6,OGFOD1,FARS2,YARS,EIF3I,RBM4,RPL35A,RPL18A,EXOSC7,MRPS14,CHCHD1,FTSJ1,RPS24,RARA,DCP2,EIF2B2,DPH5,RACK1,RPS20	red	VSMC_M1
GO:0120031	0.02	0.99	25	435	plasma membrane bounded cell projection assembly	BP	1	ICK,FAM161A,WDR35,ARHGAP35,IFT122,VDAC3,CSNK1D,TBC1D7,IFT57,ARL3,UNC119B,CFAP410,RHOD,WDR11,IFT46,MAP4,CEP19,RP2,DYNC2H1,PFN1,DNAL1,PMP22,B9D1,GOLPH3,E2F4	red	VSMC_M1
GO:0006974	0.02	0.99	38	699	cellular response to DNA damage stimulus	BP	1	DYRK2,NDRG1,XPA,KMT5C,APLF,RECQL5,PAK1,UVRAG,RPS3,CXCL12,CEBPG,KMT5A,SPRED1,PARP3,CFAP410,ACTL6A,SMYD2,BCCIP,FBXO45,INO80D,KDM1A,USP28,UBA1,UVSSA,TRRAP,CDK5RAP3,INO80E,STXBP4,INTS3,INO80C,RNF138,XRCC3,FBXO4,YJU2,USP10,HUS1,RCHY1,FGF10	red	VSMC_M1
GO:0010467	0.02	0.98	197	4455	gene expression	BP	1	SMAD4,SGK1,ARG1,MTRF1L,KLF10,DCAF13,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,POLR2F,EIF3D,MTERF2,SRI,RPP25L,RCL1,IL1RL1,SPIN1,ZNF584,RPS5,AHR,RPL28,KMT5C,EEF1A1,MALSU1,UTP11,INPP5B,RPS7,YAE1,RPS11,PIH1D1,WDR35,FKBP1B,SF3B6,FGF2,TAL1,PMPCB,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,EBNA1BP2,RPS3,HNRNPL,CSNK1D,HDAC3,PCID2,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,IL20RB,KMT5A,PDCD5,CTR9,SMN2,PTCD2,RPS3A,ELOC,PLRG1,EIF2A,RPS6,MMP16,SMYD5,HPSE,OGFOD1,PKIG,FARS2,CD58,PARP3,PRDM10,CUEDC2,YARS,CDC73,EIF3I,ARFGEF2,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,RAE1,PPP1R11,RBM4,CRTC3,SMYD2,RPL35A,PES1,RPL18A,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,MRPS14,EMG1,TRMT44,PRDX6,MECOM,CHCHD1,LSM4,TRIM4,DYNC2H1,ELK1,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,ARID3B,ZNF287,HMG20A,COQ7,IL13RA2,USP22,MIER1,FBXO4,OMA1,GOLPH3,YJU2,ERRFI1,CTNNBIP1,RBM15,ZNF276,DPH5,CDYL2,WWOX,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,FKBP1A,MYPOP,RACK1,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,NOP10,CPNE1,RNF125,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,PSENEN,LY96,SF3B5,AHNAK,FGF10	red	VSMC_M1
GO:0014741	0.02	1.00	4	28	negative regulation of muscle hypertrophy	BP	1	SMAD4,PAK1,P2RX4,ERRFI1	red	VSMC_M1
GO:0042274	0.02	0.99	7	64	ribosomal small subunit biogenesis	BP	1	DCAF13,RCL1,RPS5,RPS7,RPS6,EMG1,RPS24	red	VSMC_M1
GO:0043967	0.02	0.99	6	58	histone H4 acetylation	BP	1	PIH1D1,ACTL6A,TRRAP,KAT2A,USP22,WDR5	red	VSMC_M1
GO:1902808	0.02	0.99	5	41	positive regulation of cell cycle G1/S phase transition	BP	1	PLRG1,CDC73,STXBP4,CYP1A1,FGF10	red	VSMC_M1

GO:0006778	0.02	0.99	5	40	porphyrin-containing compound metabolic process	BP	1	ALAD,UROS,CYP1A1,HMOX2,ATP5IF1	red	VSMC_M1
GO:0006364	0.02	0.99	15	198	rRNA processing	BP	1	DCAF13,RCL1,UTP11,RPS7,PIH1D1,ERI3,EBNA1BP2,RPS6,RPL35A,PES1,EXOSC7,EMG1,RPS24,RPF1,NOP10	red	VSMC_M1
GO:0016574	0.02	0.99	5	44	histone ubiquitination	BP	1	CTR9,CDC73,KDM1A,RNF40,USP22	red	VSMC_M1
GO:0044085	0.02	0.98	113	2454	cellular component biogenesis	BP	1	SMAD4,CSNK2B,DCAF13,PFDN6,TAF11,CTNNA1,TRIOBP,EIF3D,RCL1,MAP4K4,ICK,CLTA,RPS5,MALSU1,FAM161A,UTP11,ALAD,RPS7,KCNF1,PIH1D1,PARD3,WDR35,TAL1,ARHGAP35,SNRPD2,SDK2,STAM,FAM171A1,IFT122,ERI3,PCDH17,PAK1,UVRAG,EBNA1BP2,RPS3,VDAC3,SPAST,NEB,NDUFA2,CSNK1D,HDAC3,KCTD16,TNKS,CXCL12,COPS5,SMN2,TMSB10,ARFIP1,EIF2A,RPS6,OGFOD1,AMBRA1,TFG,TBC1D7,IFT57,TMEFF2,ARL3,UNC119B,CDC73,NPRL2,EIF3I,CFAP410,WIPI1,COX19,AKAP13,RHOD,KLHL41,WDR11,CRTC3,NDUFA10,IFT46,RPL35A,PES1,BCCIP,MAP4,FBXO45,CEP19,MAP2,CABIN1,IL1RAP,EXOSC7,GJC1,NDUFA13,EMG1,RP2,LSM4,DYNC2H1,RPS24,KAT2A,PFN1,HSPA2,NDUFB7,VPS37C,DNAL1,PRRT2,FLRT2,PMP22,B9D1,XRCC3,TUBB4A,KANK4,OMA1,GOLPH3,YJU2,CTNNBIP1,DR1,RPF1,E2F4,NUDT21,FKBP1A,RACK1,TMSB4X,NOP10	red	VSMC_M1
GO:0042254	0.02	0.99	18	256	ribosome biogenesis	BP	1	DCAF13,RCL1,RPS5,MALSU1,UTP11,RPS7,PIH1D1,ERI3,EBNA1BP2,EIF2A,RPS6,RPL35A,PES1,EXOSC7,EMG1,RPS24,RPF1,NOP10	red	VSMC_M1
GO:2000758	0.02	1.00	4	30	positive regulation of peptidyl-lysine acetylation	BP	1	SMAD4,PIH1D1,WBP2,KAT2A	red	VSMC_M1
GO:0031333	0.02	0.99	9	115	negative regulation of protein-containing complex assembly	BP	1	TRIOBP,TMSB10,MAP2,PFN1,PRRT2,TUBB4A,KANK4,CTNNBIP1,TMSB4X	red	VSMC_M1
GO:0071333	0.02	0.99	9	110	cellular response to glucose stimulus	BP	1	SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,NR1D1,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0035773	0.02	0.99	6	58	insulin secretion involved in cellular response to glucose stimulus	BP	1	SRI,MAP4K4,FKBP1B,NR1D1,STXBP4,PTPRN2	red	VSMC_M1
GO:0001508	0.02	0.99	8	99	action potential	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,SCN3A,GJC1,KCNAB2	red	VSMC_M1
GO:0030031	0.02	0.99	25	443	cell projection assembly	BP	1	ICK,FAM161A,WDR35,ARHGAP35,IFT122,VDAC3,CSNK1D,TBC1D7,IFT57,ARL3,UNC119B,CFAP410,RHOD,WDR11,IFT46,MAP4,CEP19,RP2,DYNC2H1,PFN1,DNAL1,PMP22,B9D1,GOLPH3,E2F4	red	VSMC_M1
GO:0033273	0.02	0.99	7	75	response to vitamin	BP	1	ARG1,ALAD,FKBP1B,HLCS,RARA,SPARC,CYP1A1	red	VSMC_M1
GO:0045666	0.03	0.99	6	61	positive regulation of neuron differentiation	BP	1	CSNK1D,SOCS2,CXCL12,ETV5,RARA,CPNE1	red	VSMC_M1
GO:0071331	0.03	0.99	9	112	cellular response to hexose stimulus	BP	1	SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,NR1D1,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0002698	0.03	0.99	6	62	negative regulation of immune effector process	BP	1	ARG1,AHR,IL20RB,PARP3,CUEDC2,IL13RA2	red	VSMC_M1
GO:0031112	0.03	0.99	4	32	positive regulation of microtubule polymerization or depolymerization	BP	1	PAK1,RPS3,SPAST,ARL3	red	VSMC_M1
GO:0051494	0.03	0.99	10	138	negative regulation of cytoskeleton organization	BP	1	SMAD4,TRIOBP,TMSB10,TMEFF2,MAP2,KAT2A,PFN1,TUBB4A,KANK4,TMSB4X	red	VSMC_M1
GO:0006479	0.03	0.99	11	148	protein methylation	BP	1	SMAD4,KMT5C,PIH1D1,KMT5A,CTR9,SMYD5,WDR5B,SMYD2,KDM1A,MECOM,WDR5	red	VSMC_M1
GO:0008213	0.03	0.99	11	148	protein alkylation	BP	1	SMAD4,KMT5C,PIH1D1,KMT5A,CTR9,SMYD5,WDR5B,SMYD2,KDM1A,MECOM,WDR5	red	VSMC_M1
GO:0071326	0.03	0.99	9	113	cellular response to monosaccharide stimulus	BP	1	SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,NR1D1,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0006892	0.03	0.99	8	99	post-Golgi vesicle-mediated transport	BP	1	VTI1B,ARL3,SORCS1,WIPI1,ARFGEF2,RP2,GOLPH3,RACK1	red	VSMC_M1
GO:0006996	0.03	0.98	131	2943	organelle organization	BP	1	SMAD4,HSPA1L,DYNLT1,FGFR1OP,MEI1,HMGA1,REEP2,CTNNA1,TRIOBP,MAD2L1BP,SPIN1,ICK,RPS5,XPA,CRIPT,MEI4,FAM161A,PIH1D1,PARD3,WDR35,TAL1,PMPCB,ARHGAP35,STAM,RAB30,FAM171A1,IFT122,RECQL5,PAK1,UVRAG,RPS3,VDAC3,SPAST,NEB,NDUFA2,CSNK1D,HDAC3,PCID2,TNKS,MTIF3,CXCL12,MTFR1,KMT5A,PDCD5,VTI1B,TIMM10,TMSB10,PTCD2,ARFIP1,RHOF,EIF2A,OGFOD1,AMBRA1,FBXW8,TFG,ACOT8,TBC1D7,IFT57,PARP3,TMEFF2,ARL3,UNC119B,FAM118B,NPRL2,CFAP410,WIPI1,ARFGEF2,COX19,ACTL6A,AKAP13,RHOD,EMC9,RAE1,KLHL41,WDR11,NDUFA10,IFT46,MTFR1L,BCCIP,ARHGDIB,MAP4,CEP19,MAP2,CABIN1,IL1RAP,NDUFA13,EMG1,MECOM,RP2,LSM4,DYNC2H1,TOP3B,MYO5C,KAT2A,PFN1,HSPA2,CTDNEP1,CECR2,DCP2,NDUFB7,VPS37C,DNAL1,PRRT2,INO80E,MBTD1,APOOL,GATAD2B,SUPT4H1,INO80C,HMG20A,B9D1,XRCC3,TMEM11,FBXO4,TUBB4A,KANK4,MYO18A,OMA1,GOLPH3,GOSR1,DNLZ,PTPA,DR1,ELMO3,E2F4,HUS1,TMSB4X,NOP10,TOMM7,ATP5IF1,FGF10	red	VSMC_M1
GO:0046685	0.03	0.99	4	29	response to arsenic-containing substance	BP	1	ALAD,RBM4,UROS,CYP1A1	red	VSMC_M1
GO:0034470	0.03	0.98	22	345	ncRNA processing	BP	1	DCAF13,RPP25L,RCL1,UTP11,RPS7,PIH1D1,TSEN54,ERI3,EBNA1BP2,RPS6,FARS2,RPL35A,PES1,EXOSC7,EMG1,TRMT44,FTSJ1,RPS24,INTS3,RPF1,URM1,NOP10	red	VSMC_M1
GO:0016072	0.03	0.99	15	206	rRNA metabolic process	BP	1	DCAF13,RCL1,UTP11,RPS7,PIH1D1,ERI3,EBNA1BP2,RPS6,RPL35A,PES1,EXOSC7,EMG1,RPS24,RPF1,NOP10	red	VSMC_M1
GO:0046579	0.03	0.99	5	49	positive regulation of Ras protein signal transduction	BP	1	DYNLT1,MAP4K4,AKAP13,ITPKB,FGF10	red	VSMC_M1
GO:0051493	0.03	0.98	25	457	regulation of cytoskeleton organization	BP	1	SMAD4,DYNLT1,TRIOBP,ARHGAP35,PAK1,RPS3,SPAST,NEB,CXCL12,TMSB10,ARFIP1,RHOF,PARP3,TMEFF2,ARL3,AKAP13,RHOD,RAE1,ARHGDIB,MAP2,KAT2A,PFN1,TUBB4A,KANK4,TMSB4X	red	VSMC_M1
GO:0050684	0.03	0.99	9	118	regulation of mRNA processing	BP	1	HNRNPL,CTR9,PTCD2,CDC73,RBM4,PRDX6,RNF40,RBM15,NUDT21	red	VSMC_M1
GO:1902116	0.03	0.99	4	33	negative regulation of organelle assembly	BP	1	SMAD4,TBC1D7,MAP4,KAT2A	red	VSMC_M1

GO:0044267	0.03	0.98	164	3725	cellular protein metabolic process	BP	1	SMAD4,SGK1,DYRK2,MTRF1L,ACR,CSNK2B,DCAF13,FGFR1OP,POLDIP3,EGR1,NAA35,TRIOBP,EIF3D,UBAP1,MAP4K4,NPR2,ICK,UBE2M,RPS5,ANKRD39,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,PGM3,FAM161A,ALAD,RPS7,PSMB2,RPS11,PIH1D1,PARD3,WDR35,ADCK2,FKBP1B,FGF2,TAL1,PMPCB,IRF2BP1,STAM,EIF2B4,WBP2,PAK1,UVRAG,RPS3,ENGASE,RNF121,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,COPS5,KMT5A,PDCD5,CTR9,RPS3A,ELOC,EIF2A,SPRED1,CCNI,RPS6,SMYD5,OGFOD1,FBXW8,PKIG,FARS2,HLCS,TBC1D7,IFT57,PARP3,VKORC1L1,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ACTL6A,AKAP13,WDR5B,PPP1R8,ENSA,PPP1R11,KLHL41,RBM4,SMYD2,PSMA7,DCAF17,RPL35A,BCCIP,RPL18A,FBXO45,EGR2,KDM1A,USP28,EXOSC7,NDUFA13,MRPS14,ANAPC16,USP5,MECOM,CHCHD1,TRIM4,UBA1,UVSSA,PELI2,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PSMB6,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,VPS37C,ANAPC13,RNF40,CDK5RAP3,EIF2B2,PARP16,CALM2,RNF138,HMG20A,RFFL,USP22,MIER1,FBXO4,RAB12,OMA1,MOB3A,ERRFI1,UBE4B,WDR5,USP10,PTPA,DPH5,ALG14,DR1,MED31,URM1,FKBP1A,RACK1,HUS1,TIMP3,RPS20,ACP1,WFDC3,RNF125,ATP5IF1,PSENEN,PTPRN2,RCHY1,FGF10	red	VSMC_M1
GO:1901976	0.03	0.99	4	31	regulation of cell cycle checkpoint	BP	1	MAD2L1BP,PCID2,XRCC3,FBXO4	red	VSMC_M1
GO:0010907	0.03	0.99	4	32	positive regulation of glucose metabolic process	BP	1	DYRK2,DGAT2,KAT2A,WDR5	red	VSMC_M1
GO:0006626	0.03	0.99	8	86	protein targeting to mitochondrion	BP	1	HSPA1L,PMPCB,PDCD5,TIMM10,NDUFA13,DNLZ,TOMM7,ATP5IF1	red	VSMC_M1
GO:1902903	0.03	0.98	19	327	regulation of supramolecular fiber organization	BP	1	SMAD4,PFDN6,TRIOBP,ARHGAP35,PAK1,RPS3,SPAST,PFDN1,CXCL12,TMSB10,ARFIP1,TMEFF2,ARL3,AKAP13,MAP2,PFN1,TUBB4A,KANK4,TMSB4X	red	VSMC_M1
GO:0031113	0.03	0.99	5	49	regulation of microtubule polymerization	BP	1	PAK1,RPS3,ARL3,MAP2,TUBB4A	red	VSMC_M1
GO:1901661	0.03	0.99	4	28	quinone metabolic process	BP	1	COQ3,VKORC1L1,COQ7,COQ10A	red	VSMC_M1
GO:0010923	0.03	0.99	4	32	negative regulation of phosphatase activity	BP	1	FKBP1B,PPP1R11,PTPA,FKBP1A	red	VSMC_M1
GO:0051899	0.03	0.99	6	66	membrane depolarization	BP	1	CACNA2D1,P2RX4,CACNA1D,SCN3A,RACK1,ATP5IF1	red	VSMC_M1
GO:0042770	0.04	0.98	11	155	signal transduction in response to DNA damage	BP	1	NDRG1,KMT5A,SPRED1,SMYD2,KDM1A,USP28,CDK5RAP3,FBXO4,YJU2,USP10,HUS1	red	VSMC_M1
GO:0006325	0.04	0.98	18	301	chromatin organization	BP	1	HMGA1,SPIN1,PIH1D1,TAL1,PAK1,HDAC3,ACTL6A,CABIN1,MECOM,KAT2A,CECR2,INO80E,MBTD1,GATAD2B,SUPT4H1,INO80C,HMG20A,DR1	red	VSMC_M1
GO:0060562	0.04	0.98	16	269	epithelial tube morphogenesis	BP	1	SMAD4,CSNK2B,RPS7,FGF2,ARHGAP35,IFT122,PAK1,EDNRA,IFT57,KAT2A,PFN1,RARA,CECR2,CTNNBIP1,RBM15,FGF10	red	VSMC_M1
GO:0006354	0.04	0.99	7	80	DNA-templated transcription, elongation	BP	1	RECQL5,PCID2,CTR9,CDC73,ZMIZ1,SUPT4H1,ELOF1	red	VSMC_M1
GO:1905515	0.04	0.99	5	53	non-motile cilium assembly	BP	1	IFT122,CSNK1D,IFT57,MAP4,DYNC2H1	red	VSMC_M1
GO:0043414	0.04	0.98	16	254	macromolecule methylation	BP	1	SMAD4,KMT5C,PIH1D1,KMT5A,CTR9,SMYD5,WDR5B,SMYD2,KDM1A,EMG1,TRMT44,MECOM,FTSJ1,CYP1A1,RBM15,WDR5	red	VSMC_M1
GO:0007507	0.04	0.98	25	474	heart development	BP	1	SMAD4,SRI,FGF2,IFT122,PAK1,NEB,EDNRA,PTCD2,SPRED1,IFT57,AKAP13,MYO18B,WDR11,SMYD2,GJC1,DYNC2H1,ZMIZ1,KAT2A,RARA,MEF2D,FLRT2,SPARC,RBM15,FKBP1A,BORCS8	red	VSMC_M1
GO:2001239	0.04	0.99	4	33	regulation of extrinsic apoptotic signaling pathway in absence of ligand	BP	1	CTNNA1,PRDX2,WWOX,FGF10	red	VSMC_M1
GO:0007584	0.04	0.98	10	137	response to nutrient	BP	1	ARG1,ALAD,FKBP1B,TNKS,HLCS,ENSA,RARA,SPARC,CYP1A1,COX4I1	red	VSMC_M1
GO:0060048	0.04	0.98	8	103	cardiac muscle contraction	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,MYL4,GJC1,CALM2	red	VSMC_M1
GO:0016331	0.04	0.98	9	127	morphogenesis of embryonic epithelium	BP	1	RPS7,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2,FGF10	red	VSMC_M1
GO:0001838	0.04	0.98	8	107	embryonic epithelial tube formation	BP	1	RPS7,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2	red	VSMC_M1
GO:0071322	0.04	0.98	9	121	cellular response to carbohydrate stimulus	BP	1	SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,NR1D1,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0016570	0.04	0.98	22	399	histone modification	BP	1	SMAD4,KMT5C,PIH1D1,WBP2,HDAC3,KMT5A,CTR9,SMYD5,HLCS,CDC73,ACTL6A,WDR5B,SMYD2,KDM1A,MECOM,TRRAP,KAT2A,RNF40,USP22,MIER1,WDR5,DR1	red	VSMC_M1
GO:0030837	0.04	0.99	5	53	negative regulation of actin filament polymerization	BP	1	TRIOBP,TMSB10,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0045664	0.04	0.98	10	145	regulation of neuron differentiation	BP	1	ZHX2,CSNK1D,SOCS2,CXCL12,ETV5,RARA,CDK5RAP3,HMG20A,NREP,CPNE1	red	VSMC_M1
GO:0031060	0.04	0.99	5	52	regulation of histone methylation	BP	1	SMAD4,PIH1D1,CTR9,KDM1A,WDR5	red	VSMC_M1
GO:0006518	0.04	0.97	38	688	peptide metabolic process	BP	1	MTRF1L,POLDIP3,EIF3D,RPS5,RPL28,EEF1A1,MALSU1,RPS7,RPS11,EIF2B4,RPS3,LTA4H,MTIF3,SP1,COPS5,RPS3A,EIF2A,RPS6,OGFOD1,FARS2,YARS,EIF3I,RBM4,RPL35A,RPL18A,EXOSC7,MRPS14,CHCHD1,FTSJ1,RPS24,RARA,DCP2,EIF2B2,GSTM3,DPH5,RACK1,RPS20,PSENEN	red	VSMC_M1
GO:0061647	0.04	0.99	4	38	histone H3-K9 modification	BP	1	SMAD4,PIH1D1,KDM1A,MECOM	red	VSMC_M1
GO:1903322	0.04	0.98	9	121	positive regulation of protein modification by small protein conjugation or removal	BP	1	HDAC3,CTR9,TBC1D7,KDM1A,RNF40,CDK5RAP3,FBXO4,FKBP1A,RCHY1	red	VSMC_M1
GO:0061178	0.04	0.99	5	50	regulation of insulin secretion involved in cellular response to glucose stimulus	BP	1	SRI,MAP4K4,FKBP1B,NR1D1,STXBP4	red	VSMC_M1
GO:0048678	0.04	0.99	6	65	response to axon injury	BP	1	ARG1,CTNNA1,FKBP1B,FGF2,P2RX4,NREP	red	VSMC_M1
GO:0001678	0.04	0.98	9	124	cellular glucose homeostasis	BP	1	SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,NR1D1,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:2001020	0.04	0.98	13	200	regulation of response to DNA damage stimulus	BP	1	KMT5C,RECQL5,RPS3,CXCL12,CEBPG,KMT5A,SPRED1,PARP3,SMYD2,KDM1A,FBXO4,YJU2,FGF10	red	VSMC_M1
GO:0006458	0.04	0.99	4	33	'de novo' protein folding	BP	1	HSPA1L,FKBP1B,HSPA2,FKBP1A	red	VSMC_M1

GO:0019538	0.04	0.96	178	4113	protein metabolic process	BP	1	SMAD4,SGK1,DYRK2,MTRF1L,ACR,CSNK2B,DCAF13,FGFR1OP,PFDN6,POLDIP3,EGR1,NAA35,TRIOBP,EIF3D,UBAP1,MAP4K4,NPR2,ICK,UBE2M,RPS5,ANKRD39,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,PGM3,FAM161A,INPP5B,ALAD,RPS7,PSMB2,YAE1,RPS11,PIH1D1,PARD3,WDR35,ADCK2,FKBP1B,FGF2,TAL1,PMPCB,IRF2BP1,STAM,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,ENGASE,PFDN1,RNF121,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,KMT5A,PDCD5,CTR9,RPS3A,ELOC,EIF2A,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,OGFOD1,FBXW8,PKIG,FARS2,HLCS,ACOT8,TBC1D7,IFT57,PARP3,VKORC1L1,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ACTL6A,AKAP13,WDR5B,PPP1R8,ENSA,PPP1R11,KLHL41,RBM4,SMYD2,PSMA7,DCAF17,RPL35A,BCCIP,RPL18A,FBXO45,EGR2,KDM1A,USP28,EXOSC7,NDUFA13,MRPS14,ANAPC16,USP5,MECOM,CHCHD1,TRIM4,UBA1,DYNC2H1,UVSSA,PELI2,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PSMB6,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,VPS37C,ANAPC13,RNF40,CDK5RAP3,EIF2B2,PARP16,CALM2,RNF138,HMG20A,CHST9,RFFL,USP22,MIER1,FBXO4,RAB12,OMA1,GOLPH3,MOB3A,ERRFI1,UBE4B,WDR5,USP10,PTPA,DPH5,ALG14,DR1,MED31,URM1,FKBP1A,RACK1,HUS1,TIMP3,RPS20,ACP1,CPNE1,WFDC3,RNF125,ATP5IF1,PSENEN,PTPRN2,RCHY1,FGF10	red	VSMC_M1
GO:0043604	0.04	0.97	37	672	amide biosynthetic process	BP	1	ARG1,MTRF1L,POLDIP3,EIF3D,RPS5,RPL28,EEF1A1,MALSU1,RPS7,RPS11,EIF2B4,RPS3,MTIF3,COPS5,RPS3A,EIF2A,RPS6,OGFOD1,FARS2,ELOVL2,YARS,EIF3I,RBM4,RPL35A,RPL18A,EXOSC7,MRPS14,CHCHD1,FTSJ1,RPS24,RARA,DCP2,EIF2B2,DPH5,SLC25A1,RACK1,RPS20	red	VSMC_M1
GO:0051057	0.04	0.99	5	55	positive regulation of small GTPase mediated signal transduction	BP	1	DYNLT1,MAP4K4,AKAP13,ITPKB,FGF10	red	VSMC_M1
GO:0007163	0.04	0.98	12	189	establishment or maintenance of cell polarity	BP	1	DYNLT1,CTNNA1,PARD3,ARHGAP35,PAK1,RHOF,RHOD,MAP4,MYO18A,GOLPH3,RACK1,FGF10	red	VSMC_M1
GO:0007265	0.05	0.98	17	296	Ras protein signal transduction	BP	1	DYNLT1,MAP4K4,FGF2,ARHGAP35,RAB30,PSD2,RRAS2,ARFGEF2,AKAP13,RAB9A,RHOD,ARHGDIB,USP28,ITPKB,RAB12,RAB39B,FGF10	red	VSMC_M1
GO:0044260	0.05	0.96	247	5916	cellular macromolecule metabolic process	BP	1	SMAD4,SGK1,DYRK2,MTRF1L,ACR,CSNK2B,KLF10,DCAF13,FGFR1OP,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,POLR2F,TRIOBP,EIF3D,MTERF2,SRI,UBAP1,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,ANKRD39,AHR,XPA,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,ALAD,APLF,RPS7,PSMB2,RPS11,PIH1D1,PARD3,WDR35,ADCK2,FKBP1B,FGF2,TAL1,PMPCB,IRF2BP1,STAM,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,RPS3,ENGASE,RNF121,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,PDCD5,CTR9,SMN2,RPS3A,ELOC,EIF2A,SPRED1,CCNI,RPS6,SMYD5,HPSE,OGFOD1,FBXW8,PKIG,FARS2,HLCS,ACOT8,TBC1D7,IFT57,PARP3,PRDM10,VKORC1L1,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,TGIF1,WDR5B,NIF3L1,PPP1R8,ENSA,PPP1R11,KLHL41,RBM4,CRTC3,SMYD2,PSMA7,DCAF17,RPL35A,BCCIP,RPL18A,FBXO45,EGR2,INO80D,KDM1A,ETV5,USP28,IL1RAP,EXOSC7,NDUFA13,MRPS14,ANAPC16,EMG1,TRMT44,USP5,MECOM,CHCHD1,LSM4,TRIM4,UBA1,UVSSA,ELK1,PELI2,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,PSMB6,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,CECR2,NR1D1,DCP2,VPS37C,ETV3,SAMD1,ANAPC13,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,CALM2,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,CHST9,XRCC3,RFFL,USP22,MIER1,FBXO4,RAB12,MYO18A,OMA1,GOLPH3,MOB3A,ERRFI1,CTNNBIP1,RBM15,UBE4B,ZNF276,WDR5,USP10,PTPA,DPH5,CDYL2,WWOX,CIZ1,ALG14,DR1,E2F4,IER2,MED31,ZBTB43,URM1,F	red	VSMC_M1
GO:0033013	0.05	0.99	5	49	tetrapyrrole metabolic process	BP	1	ALAD,UROS,CYP1A1,HMOX2,ATP5IF1	red	VSMC_M1
GO:0008589	0.05	0.98	6	71	regulation of smoothened signaling pathway	BP	1	CTNNA1,IFT122,WDR11,DYNC2H1,RACK1,FGF10	red	VSMC_M1
GO:0007017	0.05	0.97	36	715	microtubule-based process	BP	1	DYNLT1,FGFR1OP,DNAL4,DCTN3,ICK,CRIPT,INPP5B,PARD3,WDR35,IFT122,PAK1,UVRAG,RPS3,SPAST,CSNK1D,HDAC3,TNKS,DNAH12,IFT57,PARP3,ARL3,RAE1,IFT46,BCCIP,MAP4,CEP19,MAP2,DYNC2H1,KAT2A,DNAL1,XRCC3,TUBB4A,PTPA,DYNLRB2,E2F4,FGF10	red	VSMC_M1
GO:0033043	0.05	0.97	46	950	regulation of organelle organization	BP	1	SMAD4,DYNLT1,TRIOBP,MAD2L1BP,CRIPT,WDR35,TAL1,ARHGAP35,STAM,PAK1,UVRAG,RPS3,VDAC3,SPAST,NEB,PCID2,TNKS,CXCL12,PDCD5,TMSB10,ARFIP1,RHOF,TBC1D7,PARP3,TMEFF2,ARL3,NPRL2,AKAP13,RHOD,RAE1,ARHGDIB,MAP4,MAP2,IL1RAP,KAT2A,PFN1,DCP2,PRRT2,XRCC3,FBXO4,TUBB4A,KANK4,OMA1,GOLPH3,TMSB4X,ATP5IF1	red	VSMC_M1
GO:1901021	0.05	0.99	4	36	positive regulation of calcium ion transmembrane transporter activity	BP	1	CACNA2D1,STIMATE,HSPA2,CALM2	red	VSMC_M1
GO:0035637	0.05	0.98	8	114	multicellular organismal signaling	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,SCN3A,GJC1,CALM2	red	VSMC_M1
GO:0070588	0.05	0.98	13	211	calcium ion transmembrane transport	BP	1	SRI,FKBP1B,FGF2,PMPCB,CACNA2D1,P2RX4,CACNA1D,STIMATE,HSPA2,CALM2,CACHD1,FKBP1A,AHNAK	red	VSMC_M1
GO:0006941	0.05	0.98	9	128	striated muscle contraction	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,KLHL41,MYL4,GJC1,CALM2	red	VSMC_M1
GO:0006473	0.05	0.98	11	168	protein acetylation	BP	1	SMAD4,NAA35,FAM161A,PIH1D1,WBP2,ACTL6A,TRRAP,KAT2A,USP22,WDR5,DR1	red	VSMC_M1
GO:0061337	0.05	0.98	6	76	cardiac conduction	BP	1	SRI,FKBP1B,CACNA2D1,CACNA1D,GJC1,CALM2	red	VSMC_M1
GO:0006378	0.05	0.99	4	40	mRNA polyadenylation	BP	1	CTR9,CDC73,RNF40,NUDT21	red	VSMC_M1

GO:0097435	0.05	0.97	31	622	supramolecular fiber organization	BP	1	SMAD4,PFDN6,CTNNA1,TRIOBP,CRIPT,ARHGAP35,FAM171A1,PAK1,RPS3,SPAST,NEB,PFDN1,CSNK1D,CXCL12,TMSB10,ARFIP1,RHOF,TLL1,TMEFF2,ARL3,AKAP13,RHOD,KLHL41,MAP2,MYO5C,PFN1,TUBB4A,KANK4,ELMO3,FKBP1A,TMSB4X	red	VSMC_M1
GO:0046785	0.05	0.98	6	74	microtubule polymerization	BP	1	PAK1,RPS3,CSNK1D,ARL3,MAP2,TUBB4A	red	VSMC_M1
GO:0007051	0.05	0.97	11	165	spindle organization	BP	1	UVRAG,RPS3,SPAST,CSNK1D,HDAC3,TNKS,PARP3,RAE1,BCCIP,MAP4,PTPA	red	VSMC_M1
GO:0034641	0.05	0.95	210	4878	cellular nitrogen compound metabolic process	BP	1	SMAD4,SGK1,ARG1,MTRF1L,KLF10,DCAF13,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,TST,EIF3D,MTERF2,SRI,RPP25L,RCL1,SPIN1,NPR2,ZNF584,RPS5,AHR,XPA,RPL28,KMT5C,EEF1A1,MALSU1,MEI4,PGM3,UTP11,ALAD,APLF,RPS7,RPS11,PIH1D1,WDR35,SF3B6,FGF2,TAL1,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,UVRAG,EBNA1BP2,DGAT2,RPS3,HNRNPL,NAXD,HDAC3,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,PTCD2,RPS3A,ELOC,P2RX4,PLRG1,EIF2A,RPS6,OGFOD1,GMDS,PKIG,FARS2,HLCS,ELOVL2,ACOT8,PARP3,PRDM10,YARS,CDC73,EIF3I,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,GMPR2,RBM4,CRTC3,SMYD2,RPL35A,PES1,UROS,BCCIP,RPL18A,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,EMG1,TRMT44,PRDX6,MECOM,CHCHD1,LSM4,UVSSA,ELK1,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CECR2,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,XRCC3,USP22,MIER1,FBXO4,MYO18A,YJU2,HMOX2,CTNNBIP1,RBM15,GSTM3,ZNF276,USP10,DPH5,CDYL2,WWOX,CIZ1,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,MYPOP,SLC25A1,RACK1,HUS1,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,PSENEN,SF3B5,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0031396	0.05	0.97	12	180	regulation of protein ubiquitination	BP	1	RPS7,RPS3,HDAC3,CTR9,TBC1D7,KDM1A,RNF40,CDK5RAP3,FBXO4,FKBP1A,RPS20,RCHY1	red	VSMC_M1
GO:0044271	0.06	0.96	149	3436	cellular nitrogen compound biosynthetic process	BP	1	SMAD4,SGK1,ARG1,MTRF1L,KLF10,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,EIF3D,MTERF2,SRI,SPIN1,NPR2,ZNF584,RPS5,AHR,RPL28,EEF1A1,MALSU1,PGM3,ALAD,RPS7,RPS11,PIH1D1,WDR35,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,RPS3,NAXD,HDAC3,PCID2,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,RPS3A,ELOC,P2RX4,EIF2A,RPS6,OGFOD1,GMDS,PKIG,FARS2,ELOVL2,PARP3,PRDM10,YARS,CDC73,EIF3I,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,RPL35A,UROS,RPL18A,EGR2,KDM1A,ETV5,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,MECOM,CHCHD1,ELK1,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,USP10,DPH5,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,RACK1,ELOF1,ZNF614,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,RCHY1,FGF10	red	VSMC_M1
GO:0016573	0.06	0.98	9	131	histone acetylation	BP	1	SMAD4,PIH1D1,WBP2,ACTL6A,TRRAP,KAT2A,USP22,WDR5,DR1	red	VSMC_M1
GO:0043631	0.06	0.99	4	41	RNA polyadenylation	BP	1	CTR9,CDC73,RNF40,NUDT21	red	VSMC_M1
GO:1903169	0.06	0.98	8	110	regulation of calcium ion transmembrane transport	BP	1	SRI,FKBP1B,CACNA2D1,STIMATE,HSPA2,CALM2,FKBP1A,AHNAK	red	VSMC_M1
GO:0007006	0.06	0.98	8	99	mitochondrial membrane organization	BP	1	DYNLT1,PDCD5,TIMM10,NDUFA13,APOOL,TMEM11,OMA1,ATP5IF1	red	VSMC_M1
GO:0042181	0.06	0.98	4	36	ketone biosynthetic process	BP	1	EGR1,COQ3,COQ7,COQ10A	red	VSMC_M1
GO:0042168	0.06	0.98	4	37	heme metabolic process	BP	1	ALAD,UROS,HMOX2,ATP5IF1	red	VSMC_M1
GO:1904427	0.06	0.98	5	55	positive regulation of calcium ion transmembrane transport	BP	1	SRI,CACNA2D1,STIMATE,HSPA2,CALM2	red	VSMC_M1
GO:0055007	0.06	0.98	7	96	cardiac muscle cell differentiation	BP	1	SMAD4,PAK1,NEB,AKAP13,MYO18B,KAT2A,RARA	red	VSMC_M1
GO:0018023	0.06	0.98	4	39	peptidyl-lysine trimethylation	BP	1	KMT5C,PIH1D1,CTR9,SMYD5	red	VSMC_M1
GO:0051276	0.06	0.96	34	682	chromosome organization	BP	1	HMGA1,MAD2L1BP,SPIN1,XPA,MEI4,PIH1D1,TAL1,RECQL5,PAK1,HDAC3,PCID2,TNKS,KMT5A,PARP3,ACTL6A,RAE1,CABIN1,MECOM,TOP3B,KAT2A,HSPA2,CECR2,DCP2,INO80E,MBTD1,GATAD2B,SUPT4H1,INO80C,HMG20A,XRCC3,FBXO4,DR1,HUS1,NOP10	red	VSMC_M1
GO:0001541	0.06	0.98	4	39	ovarian follicle development	BP	1	SMAD4,CTNNA1,EIF2B4,EIF2B2	red	VSMC_M1
GO:0018393	0.06	0.97	9	134	internal peptidyl-lysine acetylation	BP	1	SMAD4,PIH1D1,WBP2,ACTL6A,TRRAP,KAT2A,USP22,WDR5,DR1	red	VSMC_M1
GO:0030010	0.07	0.97	8	123	establishment of cell polarity	BP	1	DYNLT1,PARD3,PAK1,MAP4,MYO18A,GOLPH3,RACK1,FGF10	red	VSMC_M1
GO:1903214	0.07	0.98	4	39	regulation of protein targeting to mitochondrion	BP	1	HSPA1L,PDCD5,TOMM7,ATP5IF1	red	VSMC_M1
GO:0051924	0.07	0.97	11	172	regulation of calcium ion transport	BP	1	SRI,FKBP1B,CACNA2D1,CXCL12,P2RX4,CACNA1D,STIMATE,HSPA2,CALM2,FKBP1A,AHNAK	red	VSMC_M1
GO:1902850	0.07	0.97	9	133	microtubule cytoskeleton organization involved in mitosis	BP	1	DYNLT1,SPAST,TNKS,PARP3,RAE1,BCCIP,MAP4,PTPA,FGF10	red	VSMC_M1
GO:1901989	0.07	0.97	7	91	positive regulation of cell cycle phase transition	BP	1	MAD2L1BP,PLRG1,CDC73,HSPA2,STXBP4,CYP1A1,FGF10	red	VSMC_M1
GO:0031110	0.07	0.97	6	79	regulation of microtubule polymerization or depolymerization	BP	1	PAK1,RPS3,SPAST,ARL3,MAP2,TUBB4A	red	VSMC_M1
GO:0010676	0.07	0.98	4	40	positive regulation of cellular carbohydrate metabolic process	BP	1	DYRK2,DGAT2,KAT2A,WDR5	red	VSMC_M1
GO:0006475	0.07	0.97	9	136	internal protein amino acid acetylation	BP	1	SMAD4,PIH1D1,WBP2,ACTL6A,TRRAP,KAT2A,USP22,WDR5,DR1	red	VSMC_M1
GO:2001257	0.07	0.97	8	116	regulation of cation channel activity	BP	1	SRI,FKBP1B,CACNA2D1,STIMATE,CALM2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1

GO:0006338	0.07	0.96	11	175	chromatin remodeling	BP	1	HMGA1,PIH1D1,PAK1,ACTL6A,CABIN1,KAT2A,CECR2,INO80E,GATAD2B,INO80C,DR1	red	VSMC_M1
GO:0043170	0.07	0.94	291	7034	macromolecule metabolic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,MTRF1L,ACR,CSNK2B,KLF10,DCAF13,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,POLR2F,TRIOBP,EIF3D,MTERF2,SRI,UBAP1,RPP25L,RCL1,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,ANKRD39,AHR,XPA,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,PSMB2,YAE1,RPS11,PIH1D1,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,FGF2,TAL1,PMPCB,IRF2BP1,SNRPD2,STAM,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,ENGASE,HNRNPL,PFDN1,RNF121,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,IL20RB,KMT5A,PDCD5,CTR9,SMN2,PTCD2,RPS3A,ELOC,PLRG1,EIF2A,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,OGFOD1,FBXW8,PKIG,FARS2,HLCS,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PRDM10,VKORC1L1,CUEDC2,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,TGIF1,WDR5B,NIF3L1,PPP1R8,RAE1,ENSA,PPP1R11,KLHL41,RBM4,CRTC3,SMYD2,PSMA7,DCAF17,RPL35A,PES1,BCCIP,RPL18A,FBXO45,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,IL1RAP,EXOSC7,NDUFA13,MRPS14,ANAPC16,EMG1,TRMT44,PRDX6,USP5,MECOM,CHCHD1,LSM4,TRIM4,UBA1,DYNC2H1,UVSSA,ELK1,PELI2,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,PSMB6,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,CECR2,NR1D1,DCP2,VPS37C,ETV3,SAMD1,ANAPC13,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,CALM2,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,CHST	red	VSMC_M1
GO:0006281	0.07	0.95	24	455	DNA repair	BP	1	XPA,KMT5C,APLF,RECQL5,UVRAG,RPS3,CEBPG,PARP3,ACTL6A,BCCIP,INO80D,KDM1A,USP28,UVSSA,TRRAP,INO80E,INTS3,INO80C,RNF138,XRCC3,USP10,HUS1,RCHY1,FGF10	red	VSMC_M1
GO:0010970	0.07	0.97	9	139	transport along microtubule	BP	1	ICK,WDR35,IFT122,SPAST,IFT57,ARL3,IFT46,MAP2,DYNC2H1	red	VSMC_M1
GO:0034660	0.08	0.95	23	412	ncRNA metabolic process	BP	1	DCAF13,RPP25L,RCL1,UTP11,RPS7,PIH1D1,TSEN54,ERI3,EBNA1BP2,RPS6,FARS2,YARS,RPL35A,PES1,EXOSC7,EMG1,TRMT44,FTSJ1,RPS24,INTS3,RPF1,URM1,NOP10	red	VSMC_M1
GO:0072655	0.08	0.97	8	103	establishment of protein localization to mitochondrion	BP	1	HSPA1L,PMPCB,PDCD5,TIMM10,NDUFA13,DNLZ,TOMM7,ATP5IF1	red	VSMC_M1
GO:0042147	0.08	0.97	6	80	retrograde transport, endosome to Golgi	BP	1	VTI1B,ARFIP1,RAB9A,ERC1,GOSR1,EVI5	red	VSMC_M1
GO:0043462	0.08	0.98	4	37	regulation of ATPase activity	BP	1	MYL4,PFN1,ATP5IF1,FGF10	red	VSMC_M1
GO:0061077	0.08	0.97	5	55	chaperone-mediated protein folding	BP	1	HSPA1L,FKBP1B,PDCD5,HSPA2,FKBP1A	red	VSMC_M1
GO:1902017	0.08	0.98	4	45	regulation of cilium assembly	BP	1	ARHGAP35,VDAC3,TBC1D7,MAP4	red	VSMC_M1
GO:0048738	0.08	0.96	11	186	cardiac muscle tissue development	BP	1	SMAD4,FGF2,PAK1,NEB,PTCD2,AKAP13,MYO18B,GJC1,KAT2A,RARA,FKBP1A	red	VSMC_M1
GO:1901983	0.08	0.97	5	63	regulation of protein acetylation	BP	1	SMAD4,FAM161A,PIH1D1,WBP2,KAT2A	red	VSMC_M1
GO:0090503	0.08	0.98	4	42	RNA phosphodiester bond hydrolysis, exonucleolytic	BP	1	ERI3,REXO2,EXOSC7,DCP2	red	VSMC_M1
GO:0051716	0.08	0.93	207	5042	cellular response to stimulus	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,KLF10,HSPA1L,DYNLT1,NDRG1,HMGA1,GNG5,EGR1,TCP11,RHPN1,CTNNA1,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,AHR,XPA,CORO2A,INVS,KMT5C,EEF1A1,COPS9,INPP5B,ALAD,APLF,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,ADGRF3,STAM,NR2C2,RAB30,IFT122,RECQL5,EIF2B4,WBP2,NRBP1,PAK1,UVRAG,DGAT2,RPS3,PSD2,NRG2,IL18BP,RNF121,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,TNKS,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,CD8B,IL20RB,KMT5A,PDCD5,CTR9,EDNRA,SLC12A6,RHOF,P2RX4,RRAS2,EIF2A,CACNA1D,SPRED1,RPS6,STIMATE,HPSE,GPAT3,AMBRA1,GMDS,TFG,PKIG,TMEM117,CD58,TBC1D7,IFT57,PARP3,VKORC1L1,ARL3,CDC73,NPRL2,SORCS1,GRAMD1C,ARHGAP31,CFAP410,WIPI1,ARFGEF2,ACTL6A,AKAP13,RAB9A,RHOD,TGIF1,RAE1,WDR11,RBM4,CRTC3,SMYD2,UROS,BCCIP,ARHGDIB,FBXO45,EGR2,INO80D,KDM1A,ETV5,USP28,CABIN1,IL1RAP,NDUFA13,PRDX6,MECOM,UBA1,DYNC2H1,UVSSA,ELK1,PELI2,TRRAP,ITFG2,ZMIZ1,KAT2A,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,ETV3,CDK5RAP3,EIF2B2,INO80E,SPG21,PARP16,PRDX2,FLRT2,STXBP4,INTS3,CALM2,INO80C,CYP1A1,RNF138,B9D1,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,RAB12,OMA1,GOLPH3,YJU2,TBC1D24,ITGAE,MOB3A,GFER,RAB39B,ERRFI1,CTNNBIP1,RBM15,UBE4B,GSTM3,USP10,WWOX,GARNL3,FKBP1A,GNAS,RACK1,HUS1,SRXN1,ATP6V1G1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CNIH1,CPNE1,TOMM7,RNF125,RITA1,IGHA2,ATP5IF1,PSENEN,LY96,PTPRN2,RCHY1,PROKR2,FGF10	red	VSMC_M1
GO:0045931	0.08	0.97	7	97	positive regulation of mitotic cell cycle	BP	1	MAD2L1BP,TAL1,PLRG1,HSPA2,CYP1A1,USP22,FGF10	red	VSMC_M1

GO:0009987	0.08	0.94	464	11676	cellular process	BP	1	CS,SMAD4,SGK1,ARG1,DYRK2,MTRF1L,RGS17,ACR,CSNK2B,KLF10,HSPA1L,DYNLT1,DCAF13,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,MEI1,POLR3H,NDRG1,ZFAT,HMGA1,GNG5,TAF11,REEP2,EGR1,TCP11,RHPN1,ZNF76,CTNNA1,NAA35,DNAL4,KCTD20,POLR2F,TRIOBP,TST,EIF3D,TREML2,MTERF2,SRI,UBAP1,RPP25L,MAD2L1BP,DCTN3,RCL1,MUT,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,CLTA,UBE2M,ZNF584,RPS5,COX5B,SLC25A51,ANKRD39,AHR,XPA,CORO2A,INVS,RPL28,KMT5C,CRIPT,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,OSCP1,COQ3,KCNF1,PSMB2,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,NUDT6,FGF2,TAL1,EFR3B,PMPCB,ARHGAP35,ADGRF3,IRF2BP1,SNRPD2,SDK2,STAM,NR2C2,TSC22D1,UBP1,RAB30,FAM171A1,IFT122,TSEN54,ERI3,RECQL5,PCDH17,EIF2B4,WBP2,NRBP1,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,VDAC3,ENGASE,HNRNPL,SPAST,NEB,PSD2,NRG2,PFDN1,COX7B,IL18BP,RNF121,MCRIP1,NDUFA2,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,LTA4H,CDK17,TNKS,MTIF3,SP1,RAB28,CXCL12,TNFRSF19,MTFR1,COPS5,CEBPG,ZNF341,CD8B,IL20RB,KMT5A,PDCD5,CTR9,VTI1B,EDNRA,SMN2,TIMM10,DNAH12,TMSB10,SLC12A6,PTCD2,RPS3A,ELOC,ARFIP1,RHOF,C21orf91,GOT2,P2RX4,RRAS2,PLRG1,EIF2A,C15orf41,EDIL3,CACNA1D,SPRED1,CCNI,RPS6,STIMATE,TLL1,MMP16,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,TFG,CNNM1,PKIG,FARS2,TMEM117,HLCS,ELOVL2,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PSPH,PRDM10,VKORC1L1,ARL3,UNC119B,GCA,FAM118B,YARS,CDC73,CYB561D2,NPRL2,SORCS1,EIF3I,GRAMD1C,PTP4A2,SCN3A,ARH	red	VSMC_M1
GO:0016925	0.08	0.98	4	42	protein sumoylation	BP	1	EGR1,EGR2,ZMIZ1,HMG20A	red	VSMC_M1
GO:0000122	0.09	0.94	33	694	negative regulation of transcription by RNA polymerase II	BP	1	SMAD4,KLF10,ZHX2,EGR1,TAL1,IRF2BP1,NR2C2,HDAC3,KMT5A,CTR9,PKIG,CDC73,IRF2BP2,TGIF1,SMYD2,KDM1A,ETV5,RARA,NR1D1,ETV3,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,DR1,MYPOP,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0035065	0.09	0.97	4	45	regulation of histone acetylation	BP	1	SMAD4,PIH1D1,WBP2,KAT2A	red	VSMC_M1
GO:0031056	0.09	0.96	8	124	regulation of histone modification	BP	1	SMAD4,PIH1D1,WBP2,CTR9,KDM1A,KAT2A,RNF40,WDR5	red	VSMC_M1
GO:0071345	0.09	0.94	29	574	cellular response to cytokine stimulus	BP	1	SMAD4,ARG1,CSNK2B,EGR1,IL1RL1,NPR2,ALAD,WDR35,RPS3,IL18BP,CXCL12,TNFRSF19,IL20RB,CTR9,CD58,IL1RAP,NDUFA13,KAT2A,NR1D1,ETV3,PARP16,STXBP4,IL13RA2,RFFL,RBM15,USP10,TMSB4X,CPNE1,RNF125	red	VSMC_M1
GO:0018394	0.09	0.96	9	143	peptidyl-lysine acetylation	BP	1	SMAD4,PIH1D1,WBP2,ACTL6A,TRRAP,KAT2A,USP22,WDR5,DR1	red	VSMC_M1
GO:1903747	0.09	0.97	4	43	regulation of establishment of protein localization to mitochondrion	BP	1	HSPA1L,PDCD5,TOMM7,ATP5IF1	red	VSMC_M1
GO:0070585	0.09	0.96	8	107	protein localization to mitochondrion	BP	1	HSPA1L,PMPCB,PDCD5,TIMM10,NDUFA13,DNLZ,TOMM7,ATP5IF1	red	VSMC_M1
GO:0055013	0.09	0.97	5	65	cardiac muscle cell development	BP	1	SMAD4,PAK1,NEB,AKAP13,MYO18B	red	VSMC_M1
GO:0045638	0.09	0.97	5	64	negative regulation of myeloid cell differentiation	BP	1	CTR9,CDC73,ITPKB,RARA,RBM15	red	VSMC_M1
GO:0019646	0.09	0.96	7	75	aerobic electron transport chain	BP	1	COX5B,SLC25A51,NDUFA2,NDUFA10,NDUFB7,COX4I1,COX7C	red	VSMC_M1
GO:0042273	0.09	0.97	5	56	ribosomal large subunit biogenesis	BP	1	MALSU1,EBNA1BP2,RPL35A,PES1,RPF1	red	VSMC_M1
GO:0051651	0.09	0.95	10	163	maintenance of location in cell	BP	1	SRI,FKBP1B,FGF2,UVRAG,TMSB10,CALM2,GOLPH3,CIZ1,FKBP1A,TMSB4X	red	VSMC_M1
GO:0003407	0.09	0.97	4	49	neural retina development	BP	1	ZHX2,SDK2,ACTL6A,PROM1	red	VSMC_M1
GO:0050794	0.09	0.92	303	7581	regulation of cellular process	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,KLF10,HSPA1L,DYNLT1,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,NDRG1,ZFAT,HMGA1,GNG5,TAF11,REEP2,EGR1,TCP11,RHPN1,ZNF76,CTNNA1,NAA35,KCTD20,TRIOBP,EIF3D,MTERF2,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,AHR,CORO2A,INVS,KMT5C,CRIPT,EEF1A1,COPS9,MALSU1,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,COQ3,KCNF1,PIH1D1,PARD3,WDR35,FKBP1B,NUDT6,FGF2,TAL1,ARHGAP35,ADGRF3,IRF2BP1,STAM,NR2C2,TSC22D1,UBP1,RAB30,IFT122,RECQL5,PCDH17,EIF2B4,WBP2,NRBP1,PAK1,UVRAG,DGAT2,RPS3,VDAC3,HNRNPL,SPAST,NEB,PSD2,NRG2,PFDN1,IL18BP,MCRIP1,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,CDK17,TNKS,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,ZNF341,CD8B,IL20RB,KMT5A,PDCD5,CTR9,VTI1B,EDNRA,TMSB10,PTCD2,RPS3A,ELOC,ARFIP1,RHOF,P2RX4,RRAS2,PLRG1,EIF2A,EDIL3,CACNA1D,SPRED1,CCNI,RPS6,STIMATE,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,TFG,PKIG,TMEM117,ACOT8,TBC1D7,IFT57,PARP3,TMEFF2,PRDM10,ARL3,CDC73,NPRL2,SORCS1,SCN3A,ARHGAP31,CFAP410,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,RAB9A,RHOD,TGIF1,NIF3L1,PPP1R8,RAE1,ENSA,FAM45A,PPP1R11,KLHL41,WDR11,RBM4,CRTC3,SMYD2,PES1,BCCIP,ARHGDIB,KCNQ2,MAP4,EGR2,KDM1A,ETV5,USP28,MAP2,CABIN1,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,DYNC2H1,ELK1,PELI2,PROM1,TRRAP,ITFG2,ZMIZ1,KAT2A,PFN1,ERC1,PRTG,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,PRRT2,EIF2B2,SPG21,PARP16,PRDX2,MBTD1,FLRT2,STXBP4,GATAD2B,INTS3,SUPT4H1,CALM2,SPARC,PMP22,ARID2B,CYP1A1,ZNF292,RNF	red	VSMC_M1
GO:0019827	0.09	0.96	7	106	stem cell population maintenance	BP	1	KLF10,ZHX2,TAL1,CTR9,CDC73,KAT2A,FGF10	red	VSMC_M1
GO:0009636	0.10	0.95	11	174	response to toxic substance	BP	1	ARG1,AHR,ALAD,OSCP1,WDR35,KDM1A,PRDX6,PRDX2,CYP1A1,GSTM3,SRXN1	red	VSMC_M1
GO:0032496	0.10	0.95	13	225	response to lipopolysaccharide	BP	1	ARG1,ALAD,WDR35,IL18BP,CTR9,CDC73,RARA,NR1D1,PRDX2,SPARC,CYP1A1,LY96,FGF10	red	VSMC_M1

GO:0022607	0.10	0.92	97	2230	cellular component assembly	BP	1	SMAD4,CSNK2B,PFDN6,TAF11,CTNNA1,TRIOBP,EIF3D,MAP4K4,ICK,CLTA,RPS5,FAM161A,ALAD,KCNF1,PIH1D1,PARD3,WDR35,TAL1,ARHGAP35,SNRPD2,SDK2,STAM,FAM171A1,IFT122,PCDH17,PAK1,UVRAG,RPS3,VDAC3,SPAST,NEB,NDUFA2,CSNK1D,HDAC3,KCTD16,TNKS,CXCL12,SMN2,TMSB10,ARFIP1,EIF2A,OGFOD1,AMBRA1,TFG,TBC1D7,IFT57,TMEFF2,ARL3,UNC119B,CDC73,NPRL2,EIF3I,CFAP410,WIPI1,COX19,AKAP13,RHOD,KLHL41,WDR11,CRTC3,NDUFA10,IFT46,BCCIP,MAP4,FBXO45,CEP19,MAP2,CABIN1,IL1RAP,GJC1,NDUFA13,RP2,LSM4,DYNC2H1,KAT2A,PFN1,HSPA2,NDUFB7,VPS37C,DNAL1,PRRT2,FLRT2,PMP22,B9D1,XRCC3,TUBB4A,KANK4,OMA1,GOLPH3,YJU2,CTNNBIP1,DR1,E2F4,NUDT21,FKBP1A,RACK1,TMSB4X	red	VSMC_M1
GO:0009792	0.10	0.93	26	537	embryo development ending in birth or egg hatching	BP	1	SMAD4,INPP5B,RPS7,SF3B6,FGF2,ARHGAP35,IFT122,NDUFA2,CTR9,EDNRA,MMP16,FBXW8,IFT57,PSPH,ACTL6A,MYO18B,EMG1,ZMIZ1,KAT2A,PFN1,RARA,CECR2,MBTD1,B9D1,USP22,HUS1	red	VSMC_M1
GO:0035914	0.10	0.97	4	48	skeletal muscle cell differentiation	BP	1	EGR1,KLHL41,EGR2,MEF2D	red	VSMC_M1
GO:0031400	0.10	0.94	22	426	negative regulation of protein modification process	BP	1	FGFR1OP,COPS9,RPS7,PIH1D1,PARD3,FKBP1B,RPS3,SPRED1,PKIG,PPP1R8,ENSA,PPP1R11,KDM1A,CDK5RAP3,CALM2,HMG20A,ERRFI1,WDR5,PTPA,FKBP1A,RACK1,RPS20	red	VSMC_M1
GO:0032956	0.10	0.94	16	304	regulation of actin cytoskeleton organization	BP	1	SMAD4,TRIOBP,ARHGAP35,PAK1,NEB,CXCL12,TMSB10,ARFIP1,RHOF,TMEFF2,AKAP13,RHOD,ARHGDIB,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0045321	0.10	0.93	29	586	leukocyte activation	BP	1	ARG1,NDRG1,EGR1,TREML2,IL1RL1,AHR,KMT5C,FKBP1B,RPS3,PCID2,CEBPG,CD8B,IL20RB,RPS6,PARP3,IRF2BP2,CRTC3,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,NR1D1,PRDX2,IL13RA2,MYO18A,FKBP1A,IGHA2,FGF10	red	VSMC_M1
GO:0032411	0.10	0.96	6	85	positive regulation of transporter activity	BP	1	SGK1,CACNA2D1,STIMATE,HSPA2,CALM2,TMSB4X	red	VSMC_M1
GO:0072332	0.10	0.96	5	63	intrinsic apoptotic signaling pathway by p53 class mediator	BP	1	DYRK2,RPS7,KDM1A,USP28,WWOX	red	VSMC_M1
GO:0090304	0.10	0.92	166	3916	nucleic acid metabolic process	BP	1	SMAD4,SGK1,KLF10,DCAF13,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,RPP25L,RCL1,SPIN1,ZNF584,AHR,XPA,KMT5C,MEI4,UTP11,APLF,RPS7,PIH1D1,SF3B6,FGF2,TAL1,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,WBP2,UVRAG,EBNA1BP2,RPS3,HNRNPL,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,PTCD2,ELOC,PLRG1,RPS6,PKIG,FARS2,PARP3,PRDM10,YARS,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,RBM4,CRTC3,SMYD2,RPL35A,PES1,BCCIP,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,IL1RAP,EXOSC7,NDUFA13,EMG1,TRMT44,PRDX6,MECOM,LSM4,UVSSA,ELK1,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CECR2,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,INO80E,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,XRCC3,USP22,MIER1,FBXO4,MYO18A,YJU2,CTNNBIP1,RBM15,ZNF276,USP10,CDYL2,WWOX,CIZ1,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,MYPOP,HUS1,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,SF3B5,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0060402	0.10	0.96	7	107	calcium ion transport into cytosol	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0031109	0.10	0.96	7	109	microtubule polymerization or depolymerization	BP	1	PAK1,RPS3,SPAST,CSNK1D,ARL3,MAP2,TUBB4A	red	VSMC_M1
GO:0098727	0.10	0.95	7	108	maintenance of cell number	BP	1	KLF10,ZHX2,TAL1,CTR9,CDC73,KAT2A,FGF10	red	VSMC_M1
GO:0071356	0.10	0.95	10	163	cellular response to tumor necrosis factor	BP	1	WDR35,RPS3,IL18BP,TNFRSF19,CD58,KAT2A,NR1D1,RFFL,TMSB4X,CPNE1	red	VSMC_M1
GO:0021915	0.10	0.95	8	130	neural tube development	BP	1	RPS7,ARHGAP35,IFT122,IFT57,KAT2A,PFN1,RARA,CECR2	red	VSMC_M1
GO:0065007	0.10	0.91	333	8375	biological regulation	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,ACR,CSNK2B,KLF10,HSPA1L,DYNLT1,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,NDRG1,ZFAT,HMGA1,GNG5,TAF11,REEP2,EGR1,TCP11,RHPN1,ZNF76,CTNNA1,NAA35,KCTD20,TRIOBP,EIF3D,MTERF2,SRI,MAD2L1BP,MUT,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,AHR,CORO2A,INVS,KMT5C,CRIPT,EEF1A1,COPS9,MALSU1,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,COQ3,KCNF1,PIH1D1,PARD3,WDR35,FKBP1B,NUDT6,FGF2,TAL1,ARHGAP35,ADGRF3,IRF2BP1,STAM,NR2C2,TSC22D1,UBP1,RAB30,FAM171A1,IFT122,RECQL5,PCDH17,EIF2B4,WBP2,NRBP1,PAK1,UVRAG,DGAT2,RPS3,VDAC3,HNRNPL,SPAST,NEB,PSD2,NRG2,PFDN1,IL18BP,MCRIP1,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,CDK17,TNKS,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,ZNF341,CD8B,IL20RB,KMT5A,PDCD5,CTR9,VTI1B,EDNRA,TMSB10,SLC12A6,PTCD2,RPS3A,ELOC,ARFIP1,RHOF,C21orf91,GOT2,P2RX4,RRAS2,PLRG1,EIF2A,C15orf41,EDIL3,CACNA1D,SPRED1,CCNI,RPS6,STIMATE,MMP16,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,TFG,CNNM1,PKIG,TMEM117,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PRDM10,CUEDC2,ARL3,CDC73,CYB561D2,NPRL2,SORCS1,SCN3A,ARHGAP31,CFAP410,ARFGEF2,COX19,ACTL6A,AKAP13,IRF2BP2,RAB9A,RHOD,TGIF1,NIF3L1,PPP1R8,RAE1,ENSA,FAM45A,PPP1R11,KLHL41,WDR11,RBM4,CRTC3,SMYD2,IFT46,PES1,BCCIP,ARHGDIB,KCNQ2,MAP4,EGR2,KDM1A,ETV5,USP28,MYL4,MAP2,CABIN1,IL1RAP,EXOSC7,GJC1,NDUFA13,PRDX6,USP5,MECOM,RP2,LSM4,TRIM4,DYNC2H1,ELK1,SCNN1A,PELI2,PROM1,TRRAP,RPS24,ITFG2,ZMIZ1,KAT2A,PFN1,ERC1,PRTG,HSPA2,ITP	red	VSMC_M1
GO:0071479	0.11	0.96	5	64	cellular response to ionizing radiation	BP	1	EGR1,KDM1A,ELK1,FBXO4,HUS1	red	VSMC_M1
GO:0097306	0.11	0.96	5	71	cellular response to alcohol	BP	1	CTNNA1,AHR,RECQL5,GRAMD1C,GOLPH3	red	VSMC_M1
GO:0006839	0.11	0.94	13	210	mitochondrial transport	BP	1	HSPA1L,DYNLT1,TST,SLC25A51,PMPCB,PDCD5,TIMM10,NDUFA13,DNLZ,SLC25A1,SLC25A28,TOMM7,ATP5IF1	red	VSMC_M1

GO:0060255	0.11	0.91	184	4468	regulation of macromolecule metabolic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,CSNK2B,KLF10,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,IL1RL1,SPIN1,ZNF584,AHR,KMT5C,EEF1A1,COPS9,MALSU1,FAM161A,INPP5B,ALAD,APLF,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,HNRNPL,PFDN1,CSNK1D,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,IL20RB,KMT5A,PDCD5,CTR9,PTCD2,ELOC,EIF2A,SPRED1,CCNI,SMYD5,HPSE,OGFOD1,FBXW8,PKIG,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PRDM10,CUEDC2,CDC73,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,BCCIP,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,LSM4,TRIM4,ELK1,PELI2,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,HSPA2,ITPKB,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,CALM2,ARID3B,ZNF287,HMG20A,COQ7,IL13RA2,RFFL,USP22,MIER1,FBXO4,MOB3A,ERRFI1,CTNNBIP1,RBM15,ZNF276,WDR5,PTPA,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,FKBP1A,MYPOP,RACK1,HUS1,ELOF1,ZNF614,TIMP3,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,CPNE1,WFDC3,RNF125,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,PSENEN,LY96,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0044257	0.11	0.92	33	685	cellular protein catabolic process	BP	1	ACR,UBAP1,ALAD,RPS7,PSMB2,STAM,RNF121,CSNK1D,ERLIN2,ELOC,FBXW8,PPP1R11,PSMA7,FBXO45,USP28,USP5,UBA1,PSMB6,NR1D1,VPS37C,RNF40,CDK5RAP3,RFFL,USP22,FBXO4,RAB12,OMA1,UBE4B,USP10,RACK1,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0006396	0.11	0.92	48	950	RNA processing	BP	1	DCAF13,RPP25L,RCL1,UTP11,RPS7,PIH1D1,SF3B6,SNRPD2,TSEN54,ERI3,EBNA1BP2,HNRNPL,CTR9,SMN2,PTCD2,PLRG1,RPS6,FARS2,CDC73,PPP1R8,RBM4,RPL35A,PES1,KDM1A,EXOSC7,EMG1,TRMT44,PRDX6,LSM4,FTSJ1,RPS24,RNF40,INTS3,SUPT4H1,YJU2,RBM15,RPF1,SNORA80B,RNU105B,SNORD50B,NUDT21,URM1,SCARNA5,SCARNA7,SCARNA10,NOP10,SF3B5,AHNAK	red	VSMC_M1
GO:0051301	0.11	0.93	26	525	cell division	BP	1	DYNLT1,TRIOBP,DCTN3,CLTA,PARD3,FGF2,TAL1,RECQL5,UVRAG,RPS3,SPAST,TNKS,KMT5A,SMYD5,ARL3,RAE1,ENSA,MAP4,ETV5,ANAPC16,CCDC124,CECR2,ANAPC13,CALM2,EVI5,RACK1	red	VSMC_M1
GO:0030239	0.11	0.96	4	51	myofibril assembly	BP	1	SMAD4,NEB,AKAP13,KLHL41	red	VSMC_M1
GO:0048523	0.11	0.91	151	3647	negative regulation of cellular process	BP	1	SMAD4,ARG1,DYRK2,RGS17,CSNK2B,KLF10,DYNLT1,FGFR1OP,PFDN6,ZHX2,NDRG1,HMGA1,EGR1,CTNNA1,NAA35,TRIOBP,SRI,MAD2L1BP,MAP4K4,NPR2,AHR,INVS,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,NUDT6,FGF2,TAL1,ARHGAP35,IRF2BP1,NR2C2,IFT122,RECQL5,PCDH17,PAK1,DGAT2,RPS3,PFDN1,HDAC3,SOCS2,ERLIN2,PCID2,TNKS,CXCL12,COPS5,IL20RB,KMT5A,PDCD5,CTR9,TMSB10,RPS3A,ARFIP1,SPRED1,RPS6,SMYD5,PKIG,ACOT8,TBC1D7,IFT57,PARP3,TMEFF2,CDC73,NPRL2,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,ARHGDIB,MAP4,KDM1A,ETV5,USP28,MAP2,EXOSC7,NDUFA13,MECOM,ITFG2,KAT2A,PFN1,ERC1,PRTG,HSPA2,ITPKB,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,CDK5RAP3,PRRT2,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,CALM2,SPARC,PMP22,HMG20A,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,TUBB4A,KANK4,MYO18A,OMA1,GOLPH3,YJU2,ERRFI1,CTNNBIP1,RBM15,WDR5,USP10,PTPA,CDYL2,WWOX,DR1,MED31,FKBP1A,MYPOP,RACK1,HUS1,ZNF614,TIMP3,ZNF180,RPS20,TMSB4X,BHLHE41,CPNE1,WFDC3,RNF125,RITA1,ZNF846,ZNF177,ATP5IF1,NAA38,FGF10	red	VSMC_M1
GO:0030705	0.11	0.94	10	173	cytoskeleton-dependent intracellular transport	BP	1	ICK,WDR35,IFT122,SPAST,IFT57,ARL3,IFT46,MAP2,DYNC2H1,MYO5C	red	VSMC_M1
GO:0016482	0.11	0.94	9	153	cytosolic transport	BP	1	VTI1B,ARFIP1,WIPI1,RAB9A,FAM45A,MAP2,ERC1,GOSR1,EVI5	red	VSMC_M1
GO:0034097	0.11	0.92	32	659	response to cytokine	BP	1	SMAD4,ARG1,CSNK2B,EGR1,IL1RL1,NPR2,ALAD,WDR35,RPS3,IL18BP,CXCL12,TNFRSF19,IL20RB,CTR9,CD58,IL1RAP,NDUFA13,KAT2A,RARA,NR1D1,ETV3,PARP16,STXBP4,SPARC,IL13RA2,RFFL,RBM15,USP10,TIMP3,TMSB4X,CPNE1,RNF125	red	VSMC_M1
GO:0007264	0.11	0.93	21	437	small GTPase mediated signal transduction	BP	1	DYNLT1,MAP4K4,FGF2,ARHGAP35,RAB30,PSD2,RHOF,RRAS2,ARL3,ARHGAP31,ARFGEF2,AKAP13,RAB9A,RHOD,ARHGDIB,USP28,ITPKB,RAB12,RAB39B,GARNL3,FGF10	red	VSMC_M1
GO:0042552	0.11	0.95	7	109	myelination	BP	1	NDRG1,PARD3,EIF2B4,EGR2,RARA,EIF2B2,PMP22	red	VSMC_M1
GO:0016579	0.11	0.95	7	108	protein deubiquitination	BP	1	COPS5,USP28,USP5,TRRAP,KAT2A,USP22,USP10	red	VSMC_M1
GO:0045739	0.11	0.96	5	66	positive regulation of DNA repair	BP	1	KMT5C,RPS3,CEBPG,PARP3,FGF10	red	VSMC_M1
GO:0051603	0.11	0.92	31	639	proteolysis involved in cellular protein catabolic process	BP	1	ACR,UBAP1,ALAD,RPS7,PSMB2,STAM,RNF121,CSNK1D,ERLIN2,ELOC,FBXW8,PPP1R11,PSMA7,FBXO45,USP28,USP5,UBA1,PSMB6,NR1D1,VPS37C,RNF40,RFFL,USP22,FBXO4,OMA1,UBE4B,USP10,RACK1,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0060341	0.11	0.92	32	675	regulation of cellular localization	BP	1	HSPA1L,REEP2,CTNNA1,SRI,MAP4K4,CRIPT,PARD3,FKBP1B,PCDH17,PAK1,HDAC3,PDCD5,VTI1B,ARFIP1,P2RX4,PKIG,FAM45A,RBM4,KDM1A,MAP2,NR1D1,CDK5RAP3,STXBP4,CALM2,IL13RA2,FBXO4,GOSR1,KCNAB2,FKBP1A,RACK1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0051648	0.11	0.94	9	154	vesicle localization	BP	1	PCDH17,CSNK1D,TFG,WIPI1,WDR11,CEP19,MAP2,MYO5C,GOSR1	red	VSMC_M1
GO:0007005	0.11	0.92	24	436	mitochondrion organization	BP	1	HSPA1L,DYNLT1,WDR35,PMPCB,NDUFA2,MTFR1,PDCD5,TIMM10,PTCD2,AMBRA1,WIPI1,COX19,NDUFA10,MTFR1L,NDUFA13,KAT2A,NDUFB7,APOOL,TMEM11,OMA1,GOLPH3,DNLZ,TOMM7,ATP5IF1	red	VSMC_M1

GO:0051172	0.11	0.91	77	1770	negative regulation of nitrogen compound metabolic process	BP	1	SMAD4,KLF10,FGFR1OP,PFDN6,ZHX2,HMGA1,EGR1,AHR,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,TAL1,IRF2BP1,NR2C2,RECQL5,RPS3,PFDN1,HDAC3,PCID2,TNKS,KMT5A,CTR9,SPRED1,PKIG,ACOT8,PARP3,CDC73,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,CDK5RAP3,MBTD1,GATAD2B,SUPT4H1,CALM2,HMG20A,RFFL,MIER1,ERRFI1,CTNNBIP1,WDR5,PTPA,CDYL2,DR1,FKBP1A,MYPOP,RACK1,ZNF614,TIMP3,ZNF180,RPS20,BHLHE41,WFDC3,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0007422	0.11	0.96	5	69	peripheral nervous system development	BP	1	NDRG1,PARD3,EGR2,PMP22,GSTM3	red	VSMC_M1
GO:0071310	0.11	0.91	77	1784	cellular response to organic substance	BP	1	SMAD4,ARG1,CSNK2B,KLF10,HSPA1L,EGR1,CTNNA1,SRI,IL1RL1,MAP4K4,NPR2,AHR,EEF1A1,ALAD,PIH1D1,WDR35,FKBP1B,FGF2,RECQL5,WBP2,PAK1,DGAT2,RPS3,IL18BP,CSNK1D,SOCS2,CACNA2D1,SP1,CXCL12,TNFRSF19,COPS5,IL20RB,PDCD5,CTR9,P2RX4,SPRED1,CD58,CDC73,GRAMD1C,TGIF1,RAE1,UROS,EGR2,KDM1A,IL1RAP,NDUFA13,ELK1,ZMIZ1,KAT2A,HSPA2,RARA,NR1D1,ETV3,CDK5RAP3,PARP16,PRDX2,FLRT2,STXBP4,CYP1A1,IL13RA2,RFFL,RAB12,GOLPH3,ERRFI1,RBM15,USP10,WWOX,FKBP1A,GNAS,RACK1,NREP,TMSB4X,CPNE1,RNF125,LY96,PTPRN2,FGF10	red	VSMC_M1
GO:0007272	0.11	0.95	7	110	ensheathment of neurons	BP	1	NDRG1,PARD3,EIF2B4,EGR2,RARA,EIF2B2,PMP22	red	VSMC_M1
GO:0008366	0.11	0.95	7	110	axon ensheathment	BP	1	NDRG1,PARD3,EIF2B4,EGR2,RARA,EIF2B2,PMP22	red	VSMC_M1
GO:0046578	0.12	0.94	9	161	regulation of Ras protein signal transduction	BP	1	DYNLT1,MAP4K4,ARHGAP35,PSD2,ARFGEF2,AKAP13,ARHGDIB,ITPKB,FGF10	red	VSMC_M1
GO:0051056	0.12	0.93	13	259	regulation of small GTPase mediated signal transduction	BP	1	DYNLT1,MAP4K4,ARHGAP35,PSD2,RHOF,ARHGAP31,ARFGEF2,AKAP13,RHOD,ARHGDIB,ITPKB,GARNL3,FGF10	red	VSMC_M1
GO:0055006	0.12	0.96	5	71	cardiac cell development	BP	1	SMAD4,PAK1,NEB,AKAP13,MYO18B	red	VSMC_M1
GO:0019222	0.12	0.90	199	4858	regulation of metabolic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,CSNK2B,KLF10,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,KCTD20,EIF3D,MTERF2,SRI,IL1RL1,SPIN1,ZNF584,AHR,KMT5C,EEF1A1,COPS9,MALSU1,FAM161A,INPP5B,ALAD,APLF,RPS7,COQ3,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,HNRNPL,PFDN1,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,IL20RB,KMT5A,PDCD5,CTR9,PTCD2,ELOC,P2RX4,EIF2A,SPRED1,CCNI,SMYD5,HPSE,OGFOD1,AMBRA1,FBXW8,PKIG,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PRDM10,CUEDC2,CDC73,NPRL2,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,BCCIP,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,LSM4,TRIM4,ELK1,PELI2,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,CALM2,ARID3B,ZNF287,HMG20A,COQ7,IL13RA2,RFFL,USP22,MIER1,FBXO4,OMA1,MOB3A,RAB39B,ERRFI1,CTNNBIP1,RBM15,ZNF276,WDR5,USP10,PTPA,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,FKBP1A,GNAS,MYPOP,RACK1,HUS1,ATP6V1G1,ELOF1,ZNF614,TIMP3,PPP1R14A,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,CPNE1,WFDC3,RNF125,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,IGHA2,ATP5IF1,PSENEN,LY96,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0055002	0.12	0.96	4	52	striated muscle cell development	BP	1	SMAD4,NEB,AKAP13,KLHL41	red	VSMC_M1
GO:0010558	0.12	0.91	51	1150	negative regulation of macromolecule biosynthetic process	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,MALSU1,TAL1,IRF2BP1,NR2C2,RECQL5,RPS3,HDAC3,KMT5A,CTR9,PKIG,ACOT8,PARP3,TMEFF2,CDC73,IRF2BP2,TGIF1,NIF3L1,RBM4,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,RARA,NR1D1,DCP2,ETV3,SAMD1,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,RACK1,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0032970	0.12	0.93	17	337	regulation of actin filament-based process	BP	1	SMAD4,TRIOBP,SRI,ARHGAP35,PAK1,NEB,CXCL12,TMSB10,ARFIP1,RHOF,TMEFF2,AKAP13,RHOD,ARHGDIB,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0048144	0.12	0.95	5	66	fibroblast proliferation	BP	1	CDC73,ZMIZ1,FBXO4,MED31,FGF10	red	VSMC_M1
GO:0048145	0.12	0.95	5	66	regulation of fibroblast proliferation	BP	1	CDC73,ZMIZ1,FBXO4,MED31,FGF10	red	VSMC_M1
GO:0009890	0.12	0.91	54	1222	negative regulation of biosynthetic process	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,MALSU1,WDR35,TAL1,IRF2BP1,NR2C2,RECQL5,RPS3,HDAC3,ERLIN2,KMT5A,CTR9,PKIG,ACOT8,PARP3,TMEFF2,CDC73,IRF2BP2,TGIF1,NIF3L1,RBM4,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,RARA,NR1D1,DCP2,ETV3,SAMD1,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,ERRFI1,CTNNBIP1,CDYL2,DR1,MYPOP,RACK1,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0048511	0.12	0.93	12	223	rhythmic process	BP	1	KLF10,EGR1,AHR,CSNK1D,HDAC3,SP1,RBM4,EGR2,NR1D1,RACK1,BHLHE41,PROKR2	red	VSMC_M1
GO:0000226	0.12	0.92	25	522	microtubule cytoskeleton organization	BP	1	DYNLT1,FGFR1OP,CRIPT,PARD3,PAK1,UVRAG,RPS3,SPAST,CSNK1D,HDAC3,TNKS,PARP3,ARL3,RAE1,BCCIP,MAP4,CEP19,MAP2,KAT2A,DNAL1,XRCC3,TUBB4A,PTPA,E2F4,FGF10	red	VSMC_M1
GO:0043603	0.12	0.91	44	897	cellular amide metabolic process	BP	1	ARG1,MTRF1L,POLDIP3,EIF3D,RPS5,RPL28,EEF1A1,MALSU1,RPS7,RPS11,EIF2B4,DGAT2,RPS3,LTA4H,MTIF3,SP1,COPS5,RPS3A,EIF2A,RPS6,OGFOD1,FARS2,HLCS,ELOVL2,ACOT8,YARS,EIF3I,RBM4,RPL35A,RPL18A,EXOSC7,MRPS14,CHCHD1,FTSJ1,RPS24,RARA,DCP2,EIF2B2,GSTM3,DPH5,SLC25A1,RACK1,RPS20,PSENEN	red	VSMC_M1
GO:0070507	0.12	0.94	8	135	regulation of microtubule cytoskeleton organization	BP	1	PAK1,RPS3,SPAST,PARP3,ARL3,RAE1,MAP2,TUBB4A	red	VSMC_M1

GO:0006366	0.12	0.90	79	1862	transcription by RNA polymerase II	BP	1	SMAD4,KLF10,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,ZNF584,AHR,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,PFN1,RARA,NR1D1,ETV3,MEF2D,CDK5RAP3,ZNF652,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMGA20A,MIER1,CTNNBIP1,RBM15,ZNF276,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:1903533	0.12	0.95	5	69	regulation of protein targeting	BP	1	HSPA1L,PAK1,PDCD5,TOMM7,ATP5IF1	red	VSMC_M1
GO:0048732	0.12	0.92	17	335	gland development	BP	1	SMAD4,ARG1,CSNK2B,WDR35,FGF2,ARHGAP35,SOCS2,CEBPG,PTCD2,GOT2,ELK1,RARA,CDK5RAP3,PRDX2,CYP1A1,GFER,FGF10	red	VSMC_M1
GO:0006259	0.12	0.91	35	741	DNA metabolic process	BP	1	XPA,KMT5C,MEI4,APLF,FGF2,RECQL5,UVRAG,RPS3,TNKS,CEBPG,PARP3,ACTL6A,BCCIP,INO80D,KDM1A,USP28,UVSSA,TRRAP,TOP3B,CECR2,DCP2,INO80E,INTS3,INO80C,CYP1A1,RNF138,XRCC3,FBXO4,MYO18A,USP10,CIZ1,HUS1,NOP10,RCHY1,FGF10	red	VSMC_M1
GO:0031102	0.13	0.96	4	49	neuron projection regeneration	BP	1	CTNNA1,MAP4K4,FKBP1B,NREP	red	VSMC_M1
GO:0007049	0.13	0.90	62	1405	cell cycle	BP	1	DYNLT1,MEI1,TRIOBP,MAD2L1BP,DCTN3,SPIN1,NPR2,CLTA,AHR,MEI4,PARD3,NUDT6,FGF2,TAL1,RECQL5,UVRAG,RPS3,SPAST,CSNK1D,HDAC3,PCID2,CDK17,TNKS,COPS5,KMT5A,PLRG1,CCNI,RPS6,PARP3,ARL3,CDC73,RAE1,ENSA,PES1,BCCIP,MAP4,USP28,ANAPC16,MECOM,CCDC124,KAT2A,HSPA2,RARA,CTDNEP1,CECR2,ANAPC13,CDK5RAP3,STXBP4,INTS3,CALM2,CYP1A1,XRCC3,USP22,FBXO4,TUBB4A,PTPA,EVI5,E2F4,FAM9B,RACK1,HUS1,FGF10	red	VSMC_M1
GO:0007018	0.13	0.92	15	283	microtubule-based movement	BP	1	DYNLT1,DNAL4,ICK,INPP5B,WDR35,IFT122,SPAST,DNAH12,IFT57,ARL3,IFT46,MAP4,MAP2,DYNC2H1,DYNLRB2	red	VSMC_M1
GO:0002237	0.13	0.93	13	236	response to molecule of bacterial origin	BP	1	ARG1,ALAD,WDR35,IL18BP,CTR9,CDC73,RARA,NR1D1,PRDX2,SPARC,CYP1A1,LY96,FGF10	red	VSMC_M1
GO:0007052	0.13	0.94	7	109	mitotic spindle organization	BP	1	SPAST,TNKS,PARP3,RAE1,BCCIP,MAP4,PTPA	red	VSMC_M1
GO:0043535	0.13	0.94	6	87	regulation of blood vessel endothelial cell migration	BP	1	CSNK2B,FGF2,SP1,P2RX4,SPRED1,TMSB4X	red	VSMC_M1
GO:0051171	0.13	0.89	168	4082	regulation of nitrogen compound metabolic process	BP	1	SMAD4,SGK1,CSNK2B,KLF10,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,SPIN1,ZNF584,AHR,KMT5C,EEF1A1,COPS9,MALSU1,FAM161A,INPP5B,ALAD,APLF,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,HNRNPL,PFDN1,CSNK1D,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,PDCD5,CTR9,PTCD2,ELOC,P2RX4,EIF2A,SPRED1,CCNI,OGFOD1,FBXW8,PKIG,ACOT8,TBC1D7,IFT57,PARP3,PRDM10,CDC73,ACTL6A,AKAP13,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,BCCIP,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,ELK1,PELI2,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,HSPA2,ITPKB,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,CALM2,ARID3B,ZNF287,HMGA20A,RFFL,USP22,MIER1,FBXO4,MOB3A,ERRFI1,CTNNBIP1,RBM15,ZNF276,WDR5,PTPA,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,FKBP1A,MYPOP,RACK1,HUS1,ELOF1,ZNF614,TIMP3,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,WFDC3,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,PSENEN,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0021953	0.13	0.94	7	116	central nervous system neuron differentiation	BP	1	TAL1,ARHGAP35,C21orf91,FBXO45,MAP2,DYNC2H1,ZMIZ1	red	VSMC_M1
GO:0038034	0.13	0.96	4	49	signal transduction in absence of ligand	BP	1	CTNNA1,PRDX2,WWOX,FGF10	red	VSMC_M1
GO:0097192	0.13	0.96	4	49	extrinsic apoptotic signaling pathway in absence of ligand	BP	1	CTNNA1,PRDX2,WWOX,FGF10	red	VSMC_M1
GO:2001259	0.13	0.96	4	52	positive regulation of cation channel activity	BP	1	CACNA2D1,STIMATE,CALM2,TMSB4X	red	VSMC_M1
GO:0032271	0.13	0.93	11	199	regulation of protein polymerization	BP	1	TRIOBP,PAK1,RPS3,TMSB10,ARFIP1,ARL3,MAP2,PFN1,TUBB4A,KANK4,TMSB4X	red	VSMC_M1
GO:0046649	0.13	0.91	23	470	lymphocyte activation	BP	1	ARG1,EGR1,TREML2,AHR,KMT5C,FKBP1B,RPS3,PCID2,CEBPG,CD8B,IL20RB,RPS6,PARP3,IRF2BP2,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,FKBP1A,IGHA2,FGF10	red	VSMC_M1
GO:0019751	0.13	0.94	6	88	polyol metabolic process	BP	1	INPP5B,COQ3,FGF2,DGAT2,PTS,ITPKB	red	VSMC_M1
GO:0048736	0.13	0.93	8	140	appendage development	BP	1	SMAD4,IFT122,DYNC2H1,KAT2A,RARA,B9D1,MED31,FGF10	red	VSMC_M1
GO:0060173	0.13	0.93	8	140	limb development	BP	1	SMAD4,IFT122,DYNC2H1,KAT2A,RARA,B9D1,MED31,FGF10	red	VSMC_M1
GO:0034101	0.13	0.94	7	111	erythrocyte homeostasis	BP	1	TAL1,CEBPG,C15orf41,RPS6,RPS24,CDK5RAP3,ATP5IF1	red	VSMC_M1
GO:2000756	0.13	0.95	4	53	regulation of peptidyl-lysine acetylation	BP	1	SMAD4,PIH1D1,WBP2,KAT2A	red	VSMC_M1
GO:0070373	0.13	0.95	4	53	negative regulation of ERK1 and ERK2 cascade	BP	1	SMAD4,SPRED1,ERRFI1,TIMP3	red	VSMC_M1
GO:0051100	0.13	0.93	8	129	negative regulation of binding	BP	1	SRI,TNKS,KDM1A,MAP2,CTNNBIP1,RACK1,TMSB4X,CPNE1	red	VSMC_M1
GO:0010611	0.13	0.95	4	51	regulation of cardiac muscle hypertrophy	BP	1	SMAD4,PAK1,P2RX4,ERRFI1	red	VSMC_M1
GO:0018107	0.13	0.94	6	98	peptidyl-threonine phosphorylation	BP	1	DYRK2,CSNK2B,PARD3,TNKS,SPRED1,CALM2	red	VSMC_M1
GO:0034620	0.13	0.94	6	86	cellular response to unfolded protein	BP	1	HSPA1L,COPS5,HSPA2,CDK5RAP3,PARP16,RACK1	red	VSMC_M1
GO:0032409	0.13	0.92	11	198	regulation of transporter activity	BP	1	SGK1,SRI,FKBP1B,CACNA2D1,CACNA1D,STIMATE,HSPA2,CALM2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1
GO:0032412	0.14	0.93	10	178	regulation of ion transmembrane transporter activity	BP	1	SRI,FKBP1B,CACNA2D1,CACNA1D,STIMATE,HSPA2,CALM2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1

GO:0010605	0.14	0.89	89	2090	negative regulation of macromolecule metabolic process	BP	1	SMAD4,ARG1,KLF10,FGFR1OP,PFDN6,ZHX2,HMGA1,EGR1,IL1RL1,AHR,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,IRF2BP1,NR2C2,RECQL5,RPS3,PFDN1,HDAC3,PCID2,TNKS,IL20RB,KMT5A,CTR9,SPRED1,SMYD5,PKIG,ACOT8,PARP3,TMEFF2,CUEDC2,CDC73,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,LSM4,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,CDK5RAP3,MBTD1,GATAD2B,SUPT4H1,CALM2,HMG20A,IL13RA2,RFFL,MIER1,ERRFI1,CTNNBIP1,WDR5,PTPA,CDYL2,DR1,FKBP1A,MYPOP,RACK1,ZNF614,TIMP3,ZNF180,RPS20,TMSB4X,BHLHE41,CPNE1,WFDC3,RNF125,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:1903507	0.14	0.90	42	945	negative regulation of nucleic acid-templated transcription	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,TAL1,IRF2BP1,NR2C2,RECQL5,HDAC3,KMT5A,CTR9,PKIG,CDC73,IRF2BP2,TGIF1,NIF3L1,SMYD2,KDM1A,ETV5,NDUFA13,MECOM,RARA,NR1D1,ETV3,SAMD1,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0086003	0.14	0.95	4	57	cardiac muscle cell contraction	BP	1	SRI,CACNA2D1,CACNA1D,GJC1	red	VSMC_M1
GO:0098662	0.14	0.90	26	541	inorganic cation transmembrane transport	BP	1	SRI,COX5B,KCNF1,FKBP1B,FGF2,PMPCB,COX7B,CACNA2D1,SLC12A6,P2RX4,CACNA1D,STIMATE,SCN3A,KCNQ2,SCNN1A,CLCN5,HSPA2,CALM2,CACHD1,KCNAB2,COX4I1,FKBP1A,SLC25A28,ATP6V1G1,TMSB4X,AHNAK	red	VSMC_M1
GO:1902679	0.14	0.90	42	946	negative regulation of RNA biosynthetic process	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,TAL1,IRF2BP1,NR2C2,RECQL5,HDAC3,KMT5A,CTR9,PKIG,CDC73,IRF2BP2,TGIF1,NIF3L1,SMYD2,KDM1A,ETV5,NDUFA13,MECOM,RARA,NR1D1,ETV3,SAMD1,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0034622	0.14	0.90	40	830	cellular protein-containing complex assembly	BP	1	SMAD4,CSNK2B,PFDN6,TAF11,TRIOBP,EIF3D,CLTA,RPS5,PIH1D1,TAL1,SNRPD2,PAK1,UVRAG,RPS3,NDUFA2,CSNK1D,SMN2,TMSB10,ARFIP1,ARL3,CDC73,EIF3I,COX19,NDUFA10,MAP2,CABIN1,NDUFA13,LSM4,PFN1,NDUFB7,DNAL1,PRRT2,TUBB4A,KANK4,OMA1,YJU2,DR1,NUDT21,FKBP1A,TMSB4X	red	VSMC_M1
GO:0097553	0.14	0.94	6	95	calcium ion transmembrane import into cytosol	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,CALM2,FKBP1A	red	VSMC_M1
GO:0043543	0.14	0.92	11	202	protein acylation	BP	1	SMAD4,NAA35,FAM161A,PIH1D1,WBP2,ACTL6A,TRRAP,KAT2A,USP22,WDR5,DR1	red	VSMC_M1
GO:0042180	0.14	0.93	9	150	cellular ketone metabolic process	BP	1	EGR1,COQ3,DGAT2,ERLIN2,GOT2,VKORC1L1,NR1D1,COQ7,COQ10A	red	VSMC_M1
GO:0044772	0.14	0.91	18	350	mitotic cell cycle phase transition	BP	1	MAD2L1BP,SPAST,PCID2,CDK17,PLRG1,CCNI,RPS6,CDC73,ENSA,HSPA2,CDK5RAP3,INTS3,CALM2,CYP1A1,XRCC3,E2F4,HUS1,FGF10	red	VSMC_M1
GO:0002694	0.14	0.91	18	352	regulation of leukocyte activation	BP	1	ARG1,IL1RL1,AHR,KMT5C,RPS3,PCID2,IL20RB,PARP3,ZMIZ1,KAT2A,ITPKB,RARA,NR1D1,PRDX2,IL13RA2,MYO18A,IGHA2,FGF10	red	VSMC_M1
GO:0010522	0.14	0.94	5	71	regulation of calcium ion transport into cytosol	BP	1	SRI,FKBP1B,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0014743	0.14	0.95	4	52	regulation of muscle hypertrophy	BP	1	SMAD4,PAK1,P2RX4,ERRFI1	red	VSMC_M1
GO:1902115	0.14	0.93	9	161	regulation of organelle assembly	BP	1	SMAD4,ARHGAP35,STAM,VDAC3,TBC1D7,NPRL2,MAP4,IL1RAP,KAT2A	red	VSMC_M1
GO:0002027	0.14	0.94	5	73	regulation of heart rate	BP	1	SRI,FKBP1B,CACNA2D1,CACNA1D,CALM2	red	VSMC_M1
GO:0006893	0.14	0.95	4	56	Golgi to plasma membrane transport	BP	1	ARL3,ARFGEF2,GOLPH3,RACK1	red	VSMC_M1
GO:0030832	0.14	0.92	9	160	regulation of actin filament length	BP	1	TRIOBP,ARHGAP35,NEB,CXCL12,TMSB10,ARFIP1,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0035051	0.14	0.93	7	119	cardiocyte differentiation	BP	1	SMAD4,PAK1,NEB,AKAP13,MYO18B,KAT2A,RARA	red	VSMC_M1
GO:0009060	0.14	0.92	11	161	aerobic respiration	BP	1	CS,COX5B,SLC25A51,COX7B,NDUFA2,MTFR1,NDUFA10,MTFR1L,NDUFB7,COX4I1,COX7C	red	VSMC_M1
GO:0045787	0.14	0.91	13	243	positive regulation of cell cycle	BP	1	MAD2L1BP,TAL1,SPAST,PCID2,PLRG1,CDC73,HSPA2,RARA,STXBP4,CYP1A1,XRCC3,USP22,FGF10	red	VSMC_M1
GO:0051205	0.14	0.95	4	44	protein insertion into membrane	BP	1	PDCD5,TIMM10,EMC9,NDUFA13	red	VSMC_M1
GO:0050789	0.15	0.87	313	7907	regulation of biological process	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,KLF10,HSPA1L,DYNLT1,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,NDRG1,ZFAT,HMGA1,GNG5,TAF11,REEP2,EGR1,TCP11,RHPN1,ZNF76,CTNNA1,NAA35,KCTD20,TRIOBP,EIF3D,MTERF2,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,AHR,CORO2A,INVS,KMT5C,CRIPT,EEF1A1,COPS9,MALSU1,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,COQ3,KCNF1,PIH1D1,PARD3,WDR35,FKBP1B,NUDT6,FGF2,TAL1,ARHGAP35,ADGRF3,IRF2BP1,STAM,NR2C2,TSC22D1,UBP1,RAB30,FAM171A1,IFT122,RECQL5,PCDH17,EIF2B4,WBP2,NRBP1,PAK1,UVRAG,DGAT2,RPS3,VDAC3,HNRNPL,SPAST,NEB,PSD2,NRG2,PFDN1,IL18BP,MCRIP1,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,CDK17,TNKS,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,ZNF341,CD8B,IL20RB,KMT5A,PDCD5,CTR9,VTI1B,EDNRA,TMSB10,PTCD2,RPS3A,ELOC,ARFIP1,RHOF,C21orf91,P2RX4,RRAS2,PLRG1,EIF2A,EDIL3,CACNA1D,SPRED1,CCNI,RPS6,STIMATE,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,TFG,PKIG,TMEM117,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PRDM10,CUEDC2,ARL3,CDC73,NPRL2,SORCS1,SCN3A,ARHGAP31,CFAP410,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,RAB9A,RHOD,TGIF1,NIF3L1,PPP1R8,RAE1,ENSA,FAM45A,PPP1R11,KLHL41,WDR11,RBM4,CRTC3,SMYD2,PES1,BCCIP,ARHGDIB,KCNQ2,MAP4,EGR2,KDM1A,ETV5,USP28,MYL4,MAP2,CABIN1,IL1RAP,EXOSC7,GJC1,NDUFA13,PRDX6,USP5,MECOM,LSM4,TRIM4,DYNC2H1,ELK1,PELI2,PROM1,TRRAP,ITFG2,ZMIZ1,KAT2A,PFN1,ERC1,PRTG,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,PRRT2,EIF2B2,SPG21,P	red	VSMC_M1
GO:0002262	0.15	0.93	8	134	myeloid cell homeostasis	BP	1	TAL1,CEBPG,C15orf41,RPS6,RPS24,ITPKB,CDK5RAP3,ATP5IF1	red	VSMC_M1
GO:0044770	0.15	0.90	21	426	cell cycle phase transition	BP	1	MAD2L1BP,SPAST,PCID2,CDK17,PLRG1,CCNI,RPS6,CDC73,ENSA,USP28,HSPA2,CDK5RAP3,STXBP4,INTS3,CALM2,CYP1A1,XRCC3,FBXO4,E2F4,HUS1,FGF10	red	VSMC_M1
GO:0007623	0.15	0.92	9	160	circadian rhythm	BP	1	KLF10,EGR1,AHR,CSNK1D,HDAC3,RBM4,NR1D1,BHLHE41,PROKR2	red	VSMC_M1

GO:0022618	0.15	0.92	10	163	ribonucleoprotein complex assembly	BP	1	EIF3D,RPS5,PIH1D1,SNRPD2,SMN2,CDC73,EIF3I,LSM4,YJU2,NUDT21	red	VSMC_M1
GO:0006900	0.15	0.95	4	55	vesicle budding from membrane	BP	1	CSNK1D,TFG,MYO18A,GOLPH3	red	VSMC_M1
GO:0006470	0.15	0.91	12	228	protein dephosphorylation	BP	1	CSNK2B,FKBP1B,PTP4A2,PPP1R8,ENSA,PPP1R11,CTDNEP1,CALM2,PTPA,FKBP1A,ACP1,PTPRN2	red	VSMC_M1
GO:0051054	0.15	0.92	10	176	positive regulation of DNA metabolic process	BP	1	KMT5C,APLF,FGF2,RPS3,TNKS,CEBPG,PARP3,FBXO4,CIZ1,FGF10	red	VSMC_M1
GO:0031124	0.15	0.95	4	56	mRNA 3'-end processing	BP	1	CTR9,CDC73,RNF40,NUDT21	red	VSMC_M1
GO:0071840	0.15	0.87	196	4827	cellular component organization or biogenesis	BP	1	SMAD4,SGK1,MTRF1L,CSNK2B,HSPA1L,DYNLT1,DCAF13,FGFR1OP,PFDN6,MEI1,NDRG1,HMGA1,TAF11,REEP2,CTNNA1,TRIOBP,EIF3D,MAD2L1BP,RCL1,MAP4K4,SPIN1,ICK,CLTA,RPS5,XPA,CRIPT,MALSU1,MEI4,FAM161A,UTP11,ALAD,RPS7,KCNF1,PIH1D1,PARD3,WDR35,FKBP1B,TAL1,PMPCB,ARHGAP35,SNRPD2,SDK2,STAM,RAB30,FAM171A1,IFT122,ERI3,RECQL5,PCDH17,PAK1,UVRAG,EBNA1BP2,RPS3,VDAC3,SPAST,NEB,PFDN1,NDUFA2,CSNK1D,HDAC3,SOCS2,PCID2,KCTD16,TNKS,MTIF3,CXCL12,MTFR1,COPS5,KMT5A,PDCD5,VTI1B,SMN2,TIMM10,TMSB10,SLC12A6,PTCD2,ARFIP1,RHOF,C21orf91,EIF2A,RPS6,TLL1,MMP16,OGFOD1,AMBRA1,FBXW8,TFG,ACOT8,TBC1D7,IFT57,PARP3,TMEFF2,ARL3,UNC119B,GCA,FAM118B,CDC73,NPRL2,EIF3I,GRAMD1C,CFAP410,WIPI1,ARFGEF2,COX19,ACTL6A,AKAP13,RHOD,EMC9,RAE1,KLHL41,WDR11,CRTC3,NDUFA10,IFT46,RPL35A,MTFR1L,PES1,BCCIP,ARHGDIB,MAP4,FBXO45,CEP19,EGR2,KDM1A,MAP2,CABIN1,IL1RAP,EXOSC7,GJC1,NDUFA13,EMG1,MECOM,RP2,LSM4,DYNC2H1,TOP3B,RPS24,ZMIZ1,MYO5C,KAT2A,PFN1,ERC1,HSPA2,CTDNEP1,CECR2,DCP2,NDUFB7,VPS37C,CDK5RAP3,DNAL1,PRRT2,INO80E,MBTD1,FLRT2,APOOL,GATAD2B,SUPT4H1,SPARC,INO80C,PMP22,HMG20A,B9D1,XRCC3,TMEM11,FBXO4,TUBB4A,KANK4,MYO18A,OMA1,GOLPH3,GOSR1,YJU2,TBC1D24,TPRN,RAB39B,DNLZ,CTNNBIP1,WDR5,PTPA,DR1,RPF1,ELMO3,E2F4,NUDT21,FKBP1A,RACK1,HUS1,NREP,KAZALD1,TMSB4X,NOP10,CPNE1,TOMM7,IGHA2,ATP5IF1,FGF10	red	VSMC_M1
GO:0019935	0.15	0.95	4	57	cyclic-nucleotide-mediated signaling	BP	1	TCP11,NPR2,AHR,CRTC3	red	VSMC_M1
GO:0048754	0.15	0.93	7	121	branching morphogenesis of an epithelial tube	BP	1	SMAD4,FGF2,PAK1,EDNRA,CTNNBIP1,RBM15,FGF10	red	VSMC_M1
GO:0044283	0.15	0.90	21	414	small molecule biosynthetic process	BP	1	EGR1,COQ3,FGF2,DGAT2,ERLIN2,LTA4H,GOT2,ELOVL2,ACOT8,PSPH,UROS,PTS,KAT2A,ITPKB,NR1D1,CYP1A1,COQ7,WDR5,SLC25A1,COQ10A,ADI1	red	VSMC_M1
GO:1990542	0.15	0.93	6	84	mitochondrial transmembrane transport	BP	1	TST,SLC25A51,DNLZ,SLC25A1,SLC25A28,TOMM7	red	VSMC_M1
GO:0006807	0.15	0.87	297	7284	nitrogen compound metabolic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,MTRF1L,ACR,CSNK2B,KLF10,DCAF13,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,POLR2F,TRIOBP,TST,EIF3D,MTERF2,SRI,UBAP1,RPP25L,RCL1,MUT,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,ANKRD39,AHR,XPA,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,PSMB2,YAE1,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,FGF2,TAL1,PMPCB,IRF2BP1,SNRPD2,STAM,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,ENGASE,HNRNPL,PFDN1,RNF121,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,PDCD5,CTR9,SMN2,PTCD2,RPS3A,ELOC,GOT2,P2RX4,PLRG1,EIF2A,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,OGFOD1,GMDS,FBXW8,PKIG,FARS2,HLCS,ELOVL2,ACOT8,TBC1D7,IFT57,PARP3,PSPH,PRDM10,VKORC1L1,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ACTL6A,AKAP13,IRF2BP2,TGIF1,WDR5B,NIF3L1,PPP1R8,ENSA,GMPR2,PPP1R11,KLHL41,RBM4,CRTC3,SMYD2,PSMA7,DCAF17,RPL35A,PES1,UROS,BCCIP,RPL18A,FBXO45,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,ANAPC16,EMG1,TRMT44,PRDX6,USP5,MECOM,CHCHD1,LSM4,TRIM4,UBA1,DYNC2H1,UVSSA,ELK1,PELI2,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,PSMB6,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,CECR2,NR1D1,DCP2,VPS37C,ETV3,SAMD1,ANAPC13,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,CALM2,INO80C,ARID3B,CYP1A1,ZNF287,RNF1	red	VSMC_M1
GO:0010033	0.15	0.87	96	2273	response to organic substance	BP	1	SMAD4,ARG1,RGS17,ACR,CSNK2B,KLF10,HSPA1L,EGR1,CTNNA1,SRI,IL1RL1,MAP4K4,NPR2,AHR,EEF1A1,ALAD,PSMB2,PIH1D1,WDR35,FKBP1B,FGF2,RECQL5,EIF2B4,WBP2,PAK1,DGAT2,RPS3,IL18BP,RNF121,CSNK1D,SOCS2,ERLIN2,CACNA2D1,SP1,CXCL12,TNFRSF19,COPS5,IL20RB,PDCD5,CTR9,GOT2,P2RX4,SPRED1,HLCS,CD58,TBC1D7,PSPH,CDC73,GRAMD1C,TGIF1,RAE1,ENSA,UROS,EGR2,KDM1A,IL1RAP,NDUFA13,ELK1,ZMIZ1,KAT2A,HSPA2,RARA,NR1D1,ETV3,RNF40,CDK5RAP3,EIF2B2,PARP16,PRDX2,FLRT2,STXBP4,SPARC,CYP1A1,IL13RA2,XRCC3,RFFL,RAB12,GOLPH3,ERRFI1,RBM15,UBE4B,GSTM3,USP10,WWOX,IER2,FKBP1A,GNAS,RACK1,NREP,TIMP3,TMSB4X,CPNE1,RNF125,LY96,PTPRN2,FGF10	red	VSMC_M1
GO:0031327	0.15	0.88	52	1198	negative regulation of cellular biosynthetic process	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,MALSU1,WDR35,TAL1,IRF2BP1,NR2C2,RECQL5,RPS3,HDAC3,ERLIN2,KMT5A,CTR9,PKIG,ACOT8,PARP3,CDC73,IRF2BP2,TGIF1,NIF3L1,RBM4,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,RARA,NR1D1,DCP2,ETV3,SAMD1,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,RACK1,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:1901655	0.15	0.94	5	77	cellular response to ketone	BP	1	ARG1,AHR,ELK1,GOLPH3,ERRFI1	red	VSMC_M1

GO:0051649	0.15	0.88	72	1679	establishment of localization in cell	BP	1	HSPA1L,DYNLT1,POLDIP3,REEP2,SRI,MAP4K4,ICK,CLTA,PARD3,WDR35,FKBP1B,FGF2,PMPCB,STAM,IFT122,PCDH17,NRBP1,PAK1,SPAST,CSNK1D,HDAC3,PCID2,CACNA2D1,RAB28,PDCD5,VTI1B,TIMM10,ARFIP1,P2RX4,CACNA1D,TFG,PKIG,IFT57,ARL3,WIPI1,AKAP13,RAB9A,ARL4C,RAE1,FAM45A,WDR11,RBM4,IFT46,MAP4,CEP19,EGR2,MAP2,AP1S1,NDUFA13,ARL4D,DYNC2H1,MYO5C,ERC1,NR1D1,VPS37C,COPZ2,TRAPPC1,PRRT2,STXBP4,CALM2,SNUPN,IL13RA2,RAB12,GOSR1,DNLZ,EVI5,FKBP1A,TOMM7,RITA1,ATP5IF1,PTPRN2,FGF10	red	VSMC_M1
GO:0001775	0.15	0.89	32	692	cell activation	BP	1	SMAD4,ARG1,NDRG1,EGR1,TREML2,IL1RL1,AHR,KMT5C,FKBP1B,RPS3,PCID2,CEBPG,CD8B,IL20RB,P2RX4,RPS6,PARP3,IRF2BP2,CRTC3,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,NR1D1,PRDX2,IL13RA2,MYO18A,FKBP1A,GNAS,IGHA2,FGF10	red	VSMC_M1
GO:0031123	0.15	0.93	6	94	RNA 3'-end processing	BP	1	ERI3,CTR9,CDC73,EXOSC7,RNF40,NUDT21	red	VSMC_M1
GO:0018208	0.15	0.94	4	48	peptidyl-proline modification	BP	1	FKBP1B,OGFOD1,PTPA,FKBP1A	red	VSMC_M1
GO:2001022	0.16	0.93	6	95	positive regulation of response to DNA damage stimulus	BP	1	KMT5C,RPS3,CEBPG,SPRED1,PARP3,FGF10	red	VSMC_M1
GO:0042593	0.16	0.91	10	183	glucose homeostasis	BP	1	SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,RPS6,NR1D1,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0043536	0.16	0.94	4	53	positive regulation of blood vessel endothelial cell migration	BP	1	FGF2,SP1,P2RX4,TMSB4X	red	VSMC_M1
GO:0050848	0.16	0.94	4	55	regulation of calcium-mediated signaling	BP	1	DYRK2,P2RX4,STIMATE,CALM2	red	VSMC_M1
GO:0055072	0.16	0.93	5	72	iron ion homeostasis	BP	1	SMAD4,SRI,HMOX2,SLC25A28,ATP6V1G1	red	VSMC_M1
GO:0010212	0.16	0.92	8	137	response to ionizing radiation	BP	1	EGR1,ALAD,KDM1A,USP28,ELK1,INTS3,FBXO4,HUS1	red	VSMC_M1
GO:0042063	0.16	0.91	12	230	gliogenesis	BP	1	NDRG1,PARD3,FGF2,TAL1,EIF2B4,P2RX4,EGR2,ETV5,ZMIZ1,NR1D1,EIF2B2,FGF10	red	VSMC_M1
GO:0051650	0.16	0.92	8	143	establishment of vesicle localization	BP	1	CSNK1D,TFG,WIPI1,WDR11,CEP19,MAP2,MYO5C,GOSR1	red	VSMC_M1
GO:0032507	0.16	0.94	4	55	maintenance of protein location in cell	BP	1	TMSB10,GOLPH3,CIZ1,TMSB4X	red	VSMC_M1
GO:0051641	0.16	0.87	96	2295	cellular localization	BP	1	HSPA1L,DYNLT1,POLDIP3,REEP2,CTNNA1,SRI,MAP4K4,ICK,CLTA,XPA,INVS,CRIPT,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,EFR3B,PMPCB,STAM,IFT122,PCDH17,NRBP1,PAK1,UVRAG,SPAST,CSNK1D,HDAC3,PCID2,CACNA2D1,TNKS,RAB28,PDCD5,VTI1B,TIMM10,TMSB10,ARFIP1,P2RX4,PLRG1,CACNA1D,TFG,PKIG,IFT57,PARP3,ARL3,WIPI1,ARFGEF2,AKAP13,RAB9A,EMC9,ARL4C,RAE1,FAM45A,WDR11,RBM4,IFT46,MAP4,CEP19,EGR2,KDM1A,MAP2,AP1S1,NDUFA13,ARL4D,DYNC2H1,SCG3,MYO5C,KAT2A,ERC1,CTDNEP1,NR1D1,VPS37C,CDK5RAP3,COPZ2,TRAPPC1,PRRT2,STXBP4,CALM2,SNUPN,IL13RA2,FBXO4,RAB12,GOLPH3,GOSR1,KCNAB2,DNLZ,CIZ1,EVI5,FKBP1A,RACK1,TMSB4X,TOMM7,RITA1,ATP5IF1,PTPRN2,FGF10	red	VSMC_M1
GO:2001021	0.16	0.93	5	72	negative regulation of response to DNA damage stimulus	BP	1	RECQL5,RPS3,CXCL12,KDM1A,YJU2	red	VSMC_M1
GO:0023052	0.16	0.86	171	4258	signaling	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,KLF10,DYNLT1,NDRG1,GNG5,EGR1,TCP11,RHPN1,CTNNA1,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,AHR,CORO2A,INVS,INPP5B,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,ADGRF3,STAM,NR2C2,RAB30,IFT122,PCDH17,EIF2B4,WBP2,NRBP1,PAK1,DGAT2,RPS3,PSD2,NRG2,IL18BP,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,TNKS,CXCL12,TNFRSF19,COPS5,CD8B,IL20RB,KMT5A,PDCD5,CTR9,EDNRA,SLC12A6,RHOF,P2RX4,RRAS2,EIF2A,CACNA1D,SPRED1,RPS6,STIMATE,HPSE,GPAT3,GMDS,TFG,PKIG,TMEM117,TBC1D7,IFT57,ARL3,CDC73,NPRL2,SORCS1,SCN3A,ARHGAP31,CFAP410,ARFGEF2,ACTL6A,AKAP13,RAB9A,RHOD,ENSA,WDR11,CRTC3,SMYD2,ARHGDIB,KCNQ2,EGR2,KDM1A,USP28,CABIN1,IL1RAP,GJC1,NDUFA13,MECOM,DYNC2H1,PELI2,ITFG2,ZMIZ1,KAT2A,ERC1,ITPKB,RARA,CTDNEP1,NR1D1,CDK5RAP3,PRRT2,EIF2B2,SPG21,PARP16,PRDX2,FLRT2,STXBP4,INTS3,CALM2,PMP22,RNF138,B9D1,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,RAB12,GOLPH3,YJU2,TBC1D24,ITGAE,MOB3A,GFER,RAB39B,ERRFI1,CTNNBIP1,RBM15,UBE4B,USP10,WWOX,GARNL3,FKBP1A,GNAS,RACK1,HUS1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CNIH1,CPNE1,RNF125,RITA1,IGHA2,ATP5IF1,PSENEN,LY96,PTPRN2,PROKR2,FGF10	red	VSMC_M1
GO:0033500	0.16	0.91	10	184	carbohydrate homeostasis	BP	1	SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,RPS6,NR1D1,STXBP4,RACK1,PTPRN2	red	VSMC_M1
GO:0006282	0.16	0.92	7	118	regulation of DNA repair	BP	1	KMT5C,RECQL5,RPS3,CEBPG,PARP3,KDM1A,FGF10	red	VSMC_M1
GO:0003300	0.16	0.93	5	75	cardiac muscle hypertrophy	BP	1	SMAD4,PAK1,P2RX4,AKAP13,ERRFI1	red	VSMC_M1

GO:0046483	0.16	0.86	182	4376	heterocycle metabolic process	BP	1	SMAD4,SGK1,KLF10,DCAF13,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,RPP25L,RCL1,SPIN1,NPR2,ZNF584,AHR,XPA,KMT5C,MEI4,PGM3,UTP11,ALAD,APLF,RPS7,PIH1D1,SF3B6,FGF2,TAL1,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,WBP2,UVRAG,EBNA1BP2,DGAT2,RPS3,HNRNPL,NAXD,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,PTCD2,ELOC,PLRG1,RPS6,GMDS,PKIG,FARS2,HLCS,ELOVL2,ACOT8,PARP3,PRDM10,YARS,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,GMPR2,RBM4,CRTC3,SMYD2,RPL35A,PES1,UROS,BCCIP,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,EMG1,TRMT44,PRDX6,MECOM,LSM4,UVSSA,ELK1,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CECR2,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,XRCC3,USP22,MIER1,FBXO4,MYO18A,YJU2,HMOX2,CTNNBIP1,RBM15,ZNF276,USP10,CDYL2,WWOX,CIZ1,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,MYPOP,SLC25A1,HUS1,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,SF3B5,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0031503	0.16	0.91	10	186	protein-containing complex localization	BP	1	POLDIP3,ICK,WDR35,IFT122,PCID2,IFT57,ARL3,RAE1,IFT46,DYNC2H1	red	VSMC_M1
GO:0031032	0.16	0.91	9	172	actomyosin structure organization	BP	1	SMAD4,FAM171A1,PAK1,NEB,TMEFF2,AKAP13,KLHL41,PFN1,MYO18A	red	VSMC_M1
GO:0090068	0.16	0.91	10	180	positive regulation of cell cycle process	BP	1	MAD2L1BP,SPAST,PCID2,PLRG1,CDC73,HSPA2,STXBP4,CYP1A1,XRCC3,FGF10	red	VSMC_M1
GO:0007030	0.16	0.92	7	122	Golgi organization	BP	1	RAB30,CSNK1D,VTI1B,FBXW8,DYNC2H1,MYO18A,GOLPH3	red	VSMC_M1
GO:0006457	0.16	0.91	10	166	protein folding	BP	1	HSPA1L,PFDN6,FKBP1B,ENGASE,PFDN1,PDCD5,RP2,HSPA2,DNLZ,FKBP1A	red	VSMC_M1
GO:0045333	0.16	0.90	12	191	cellular respiration	BP	1	CS,COX5B,SLC25A51,COX7B,NDUFA2,MTFR1,NDUFA10,MTFR1L,NDUFB7,COX4I1,COQ10A,COX7C	red	VSMC_M1
GO:1901992	0.16	0.93	5	73	positive regulation of mitotic cell cycle phase transition	BP	1	MAD2L1BP,PLRG1,HSPA2,CYP1A1,FGF10	red	VSMC_M1
GO:0031667	0.16	0.89	18	362	response to nutrient levels	BP	1	ARG1,KLF10,ALAD,FKBP1B,TNKS,EIF2A,HLCS,PSPH,NPRL2,WIPI1,ENSA,ITFG2,KAT2A,RARA,SPARC,CYP1A1,OMA1,COX4I1	red	VSMC_M1
GO:0009991	0.16	0.89	19	385	response to extracellular stimulus	BP	1	ARG1,KLF10,ALAD,FKBP1B,ARHGAP35,TNKS,EIF2A,HLCS,PSPH,NPRL2,WIPI1,ENSA,ITFG2,KAT2A,RARA,SPARC,CYP1A1,OMA1,COX4I1	red	VSMC_M1
GO:0045913	0.17	0.94	4	57	positive regulation of carbohydrate metabolic process	BP	1	DYRK2,DGAT2,KAT2A,WDR5	red	VSMC_M1
GO:0080090	0.17	0.86	171	4206	regulation of primary metabolic process	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,KLF10,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,SPIN1,ZNF584,AHR,KMT5C,EEF1A1,COPS9,MALSU1,FAM161A,INPP5B,ALAD,APLF,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,HNRNPL,PFDN1,CSNK1D,HDAC3,ERLIN2,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,PDCD5,CTR9,PTCD2,ELOC,EIF2A,SPRED1,CCNI,OGFOD1,AMBRA1,FBXW8,PKIG,ACOT8,TBC1D7,IFT57,PARP3,PRDM10,CDC73,ACTL6A,AKAP13,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,BCCIP,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,ELK1,PELI2,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,CALM2,ARID3B,ZNF287,HMG20A,RFFL,USP22,MIER1,FBXO4,MOB3A,ERRFI1,CTNNBIP1,RBM15,ZNF276,WDR5,PTPA,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,FKBP1A,MYPOP,RACK1,HUS1,ELOF1,ZNF614,TIMP3,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,WFDC3,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,PSENEN,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0006725	0.17	0.86	183	4410	cellular aromatic compound metabolic process	BP	1	SMAD4,SGK1,KLF10,DCAF13,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,RPP25L,RCL1,SPIN1,NPR2,ZNF584,AHR,XPA,KMT5C,MEI4,PGM3,UTP11,ALAD,APLF,RPS7,PIH1D1,SF3B6,FGF2,TAL1,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,WBP2,UVRAG,EBNA1BP2,DGAT2,RPS3,HNRNPL,NAXD,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,PTCD2,ELOC,GOT2,PLRG1,RPS6,GMDS,PKIG,FARS2,ELOVL2,ACOT8,PARP3,PRDM10,YARS,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,GMPR2,RBM4,CRTC3,SMYD2,RPL35A,PES1,UROS,BCCIP,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,EMG1,TRMT44,PRDX6,MECOM,LSM4,UVSSA,ELK1,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CECR2,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,XRCC3,USP22,MIER1,FBXO4,MYO18A,YJU2,HMOX2,CTNNBIP1,RBM15,GSTM3,ZNF276,USP10,CDYL2,WWOX,CIZ1,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,MYPOP,SLC25A1,HUS1,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,SF3B5,AHNAK,RCHY1,FGF10	red	VSMC_M1

GO:0008016	0.17	0.91	8	144	regulation of heart contraction	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,MYL4,GJC1,CALM2	red	VSMC_M1
GO:0022898	0.17	0.90	10	186	regulation of transmembrane transporter activity	BP	1	SRI,FKBP1B,CACNA2D1,CACNA1D,STIMATE,HSPA2,CALM2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1
GO:0062013	0.17	0.92	6	96	positive regulation of small molecule metabolic process	BP	1	DYRK2,DGAT2,KAT2A,NR1D1,WDR5,TMSB4X	red	VSMC_M1
GO:0031323	0.17	0.85	178	4391	regulation of cellular metabolic process	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,KLF10,FGFR1OP,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,KCTD20,EIF3D,MTERF2,SRI,SPIN1,ZNF584,AHR,KMT5C,EEF1A1,COPS9,MALSU1,FAM161A,ALAD,APLF,RPS7,COQ3,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,HNRNPL,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,PDCD5,CTR9,PTCD2,ELOC,P2RX4,EIF2A,SPRED1,CCNI,OGFOD1,AMBRA1,FBXW8,PKIG,ACOT8,TBC1D7,IFT57,PARP3,PRDM10,CDC73,NPRL2,ACTL6A,AKAP13,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,BCCIP,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,ELK1,PELI2,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,CALM2,ARID3B,ZNF287,HMG20A,COQ7,RFFL,USP22,MIER1,FBXO4,MOB3A,RAB39B,ERRFI1,CTNNBIP1,RBM15,ZNF276,WDR5,USP10,PTPA,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,FKBP1A,MYPOP,RACK1,HUS1,ATP6V1G1,ELOF1,ZNF614,TIMP3,PPP1R14A,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,WFDC3,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,PSENEN,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0018210	0.17	0.92	6	104	peptidyl-threonine modification	BP	1	DYRK2,CSNK2B,PARD3,TNKS,SPRED1,CALM2	red	VSMC_M1
GO:0030163	0.17	0.87	37	815	protein catabolic process	BP	1	ACR,UBAP1,EEF1A1,ALAD,RPS7,PSMB2,STAM,RNF121,CSNK1D,ERLIN2,ELOC,HPSE,FBXW8,PPP1R11,PSMA7,FBXO45,USP28,NDUFA13,USP5,UBA1,PSMB6,NR1D1,VPS37C,RNF40,CDK5RAP3,RFFL,USP22,FBXO4,RAB12,OMA1,UBE4B,USP10,RACK1,TIMP3,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0000723	0.17	0.92	7	118	telomere maintenance	BP	1	TNKS,PARP3,DCP2,XRCC3,FBXO4,HUS1,NOP10	red	VSMC_M1
GO:2001251	0.17	0.93	5	77	negative regulation of chromosome organization	BP	1	MAD2L1BP,PCID2,TNKS,DCP2,XRCC3	red	VSMC_M1
GO:0099111	0.17	0.91	9	165	microtubule-based transport	BP	1	ICK,WDR35,IFT122,SPAST,IFT57,ARL3,IFT46,MAP2,DYNC2H1	red	VSMC_M1
GO:0030177	0.17	0.91	7	124	positive regulation of Wnt signaling pathway	BP	1	SPIN1,FGF2,CSNK1D,TNKS,CDC73,CTDNEP1,FGF10	red	VSMC_M1
GO:0006816	0.17	0.89	14	282	calcium ion transport	BP	1	SRI,FKBP1B,FGF2,PMPCB,CACNA2D1,CXCL12,P2RX4,CACNA1D,STIMATE,HSPA2,CALM2,CACHD1,FKBP1A,AHNAK	red	VSMC_M1
GO:0034612	0.17	0.90	10	181	response to tumor necrosis factor	BP	1	WDR35,RPS3,IL18BP,TNFRSF19,CD58,KAT2A,NR1D1,RFFL,TMSB4X,CPNE1	red	VSMC_M1
GO:0043010	0.17	0.90	12	242	camera-type eye development	BP	1	ZHX2,FGF2,ARHGAP35,SDK2,IFT122,SPRED1,ACTL6A,PROM1,RARA,CYP1A1,B9D1,FGF10	red	VSMC_M1
GO:0014897	0.17	0.93	5	77	striated muscle hypertrophy	BP	1	SMAD4,PAK1,P2RX4,AKAP13,ERRFI1	red	VSMC_M1
GO:0014706	0.17	0.89	15	307	striated muscle tissue development	BP	1	SMAD4,EGR1,FGF2,PAK1,NEB,PTCD2,AKAP13,MYO18B,KLHL41,EGR2,GJC1,KAT2A,RARA,MEF2D,FKBP1A	red	VSMC_M1
GO:0045892	0.17	0.87	41	943	negative regulation of transcription, DNA-templated	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,TAL1,IRF2BP1,NR2C2,RECQL5,HDAC3,KMT5A,CTR9,PKIG,CDC73,IRF2BP2,TGIF1,SMYD2,KDM1A,ETV5,NDUFA13,MECOM,RARA,NR1D1,ETV3,SAMD1,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0006357	0.17	0.86	74	1784	regulation of transcription by RNA polymerase II	BP	1	SMAD4,KLF10,ZHX2,ZBTB22,ZFAT,HMGA1,EGR1,ZNF76,ZNF584,AHR,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,WBP2,HDAC3,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,PFN1,RARA,NR1D1,ETV3,MEF2D,CDK5RAP3,ZNF652,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,MIER1,CTNNBIP1,RBM15,ZNF276,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ZNF614,ZNF180,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0021954	0.17	0.93	4	61	central nervous system neuron development	BP	1	ARHGAP35,FBXO45,MAP2,ZMIZ1	red	VSMC_M1
GO:0071826	0.17	0.90	10	170	ribonucleoprotein complex subunit organization	BP	1	EIF3D,RPS5,PIH1D1,SNRPD2,SMN2,CDC73,EIF3I,LSM4,YJU2,NUDT21	red	VSMC_M1
GO:0000278	0.17	0.87	33	729	mitotic cell cycle	BP	1	DYNLT1,MAD2L1BP,DCTN3,TAL1,RECQL5,SPAST,PCID2,CDK17,TNKS,KMT5A,PLRG1,CCNI,RPS6,PARP3,ARL3,CDC73,RAE1,ENSA,BCCIP,MAP4,HSPA2,CTDNEP1,CDK5RAP3,INTS3,CALM2,CYP1A1,XRCC3,USP22,TUBB4A,PTPA,E2F4,HUS1,FGF10	red	VSMC_M1
GO:0006397	0.18	0.88	20	407	mRNA processing	BP	1	SF3B6,SNRPD2,TSEN54,HNRNPL,CTR9,SMN2,PTCD2,PLRG1,CDC73,PPP1R8,RBM4,KDM1A,PRDX6,LSM4,RNF40,SUPT4H1,YJU2,RBM15,NUDT21,SF3B5	red	VSMC_M1
GO:0055117	0.18	0.93	4	58	regulation of cardiac muscle contraction	BP	1	SRI,FKBP1B,P2RX4,CALM2	red	VSMC_M1
GO:0001823	0.18	0.92	5	81	mesonephros development	BP	1	SMAD4,FGF2,RARA,CTNNBIP1,FGF10	red	VSMC_M1
GO:0032414	0.18	0.92	5	80	positive regulation of ion transmembrane transporter activity	BP	1	CACNA2D1,STIMATE,HSPA2,CALM2,TMSB4X	red	VSMC_M1
GO:0051960	0.18	0.88	16	344	regulation of nervous system development	BP	1	DYNLT1,CTNNA1,PARD3,PAK1,CXCL12,FBXW8,EGR2,KDM1A,ETV5,MAP2,IL1RAP,PRTG,RARA,NR1D1,FLRT2,BHLHE41	red	VSMC_M1
GO:0051098	0.18	0.88	15	296	regulation of binding	BP	1	SMAD4,CSNK2B,EIF3D,SRI,TNKS,CEBPG,KDM1A,MAP2,RARA,CALM2,CTNNBIP1,FKBP1A,RACK1,TMSB4X,CPNE1	red	VSMC_M1
GO:0032609	0.18	0.93	4	59	interferon-gamma production	BP	1	IL1RL1,CEBPG,IL20RB,RARA	red	VSMC_M1
GO:0032649	0.18	0.93	4	59	regulation of interferon-gamma production	BP	1	IL1RL1,CEBPG,IL20RB,RARA	red	VSMC_M1
GO:0043627	0.18	0.93	4	57	response to estrogen	BP	1	CTNNA1,WBP2,RARA,GSTM3	red	VSMC_M1

GO:0007154	0.18	0.84	172	4300	cell communication	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,KLF10,DYNLT1,NDRG1,GNG5,EGR1,TCP11,RHPN1,CTNNA1,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,AHR,CORO2A,INVS,INPP5B,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,ADGRF3,STAM,NR2C2,RAB30,IFT122,PCDH17,EIF2B4,WBP2,NRBP1,PAK1,DGAT2,RPS3,PSD2,NRG2,IL18BP,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,TNKS,CXCL12,TNFRSF19,COPS5,CD8B,IL20RB,KMT5A,PDCD5,CTR9,EDNRA,SLC12A6,RHOF,P2RX4,RRAS2,EIF2A,CACNA1D,SPRED1,RPS6,STIMATE,HPSE,GPAT3,GMDS,TFG,PKIG,TMEM117,TBC1D7,IFT57,ARL3,CDC73,NPRL2,SORCS1,SCN3A,ARHGAP31,CFAP410,WIPI1,ARFGEF2,ACTL6A,AKAP13,RAB9A,RHOD,ENSA,WDR11,CRTC3,SMYD2,ARHGDIB,KCNQ2,EGR2,KDM1A,USP28,CABIN1,IL1RAP,GJC1,NDUFA13,MECOM,DYNC2H1,PELI2,ITFG2,ZMIZ1,KAT2A,ERC1,ITPKB,RARA,CTDNEP1,NR1D1,CDK5RAP3,PRRT2,EIF2B2,SPG21,PARP16,PRDX2,FLRT2,STXBP4,INTS3,CALM2,PMP22,RNF138,B9D1,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,RAB12,GOLPH3,YJU2,TBC1D24,ITGAE,MOB3A,GFER,RAB39B,ERRFI1,CTNNBIP1,RBM15,UBE4B,USP10,WWOX,GARNL3,FKBP1A,GNAS,RACK1,HUS1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CNIH1,CPNE1,RNF125,RITA1,IGHA2,ATP5IF1,PSENEN,LY96,PTPRN2,PROKR2,FGF10	red	VSMC_M1
GO:0014896	0.18	0.92	5	78	muscle hypertrophy	BP	1	SMAD4,PAK1,P2RX4,AKAP13,ERRFI1	red	VSMC_M1
GO:0044092	0.18	0.86	37	806	negative regulation of molecular function	BP	1	FGFR1OP,SRI,RPS7,PIH1D1,FKBP1B,IL18BP,PCID2,TNKS,CEBPG,SPRED1,PKIG,PARP3,NPRL2,RAB9A,PPP1R8,ENSA,PPP1R11,KDM1A,MAP2,CABIN1,CDK5RAP3,PRDX2,CALM2,RFFL,ERRFI1,CTNNBIP1,PTPA,FKBP1A,RACK1,TIMP3,PPP1R14A,RPS20,TMSB4X,CPNE1,WFDC3,ATP5IF1,PTPRN2	red	VSMC_M1
GO:0045944	0.18	0.86	39	904	positive regulation of transcription by RNA polymerase II	BP	1	SMAD4,KLF10,ZFAT,HMGA1,EGR1,ZNF76,AHR,FGF2,TAL1,NR2C2,UBP1,WBP2,HDAC3,TNKS,SP1,COPS5,CEBPG,PRDM10,CDC73,CRTC3,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,RBM15,WWOX,DR1,E2F4,IER2,FGF10	red	VSMC_M1
GO:2000113	0.18	0.86	49	1144	negative regulation of cellular macromolecule biosynthetic process	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,MALSU1,TAL1,IRF2BP1,NR2C2,RECQL5,RPS3,HDAC3,KMT5A,CTR9,PKIG,ACOT8,PARP3,CDC73,IRF2BP2,TGIF1,RBM4,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,RARA,NR1D1,DCP2,ETV3,SAMD1,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,RACK1,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0001942	0.18	0.93	4	61	hair follicle development	BP	1	SMAD4,TNFRSF19,HPSE,FGF10	red	VSMC_M1
GO:1903047	0.18	0.87	28	608	mitotic cell cycle process	BP	1	DYNLT1,MAD2L1BP,SPAST,PCID2,CDK17,TNKS,KMT5A,PLRG1,CCNI,RPS6,PARP3,ARL3,CDC73,RAE1,ENSA,BCCIP,MAP4,HSPA2,CTDNEP1,CDK5RAP3,INTS3,CALM2,CYP1A1,XRCC3,PTPA,E2F4,HUS1,FGF10	red	VSMC_M1
GO:0010634	0.18	0.90	8	143	positive regulation of epithelial cell migration	BP	1	MAP4K4,FGF2,SP1,P2RX4,PFN1,SPARC,TMSB4X,FGF10	red	VSMC_M1
GO:0006094	0.18	0.93	4	58	gluconeogenesis	BP	1	DGAT2,KAT2A,WDR5,SLC25A1	red	VSMC_M1
GO:1903052	0.19	0.90	7	118	positive regulation of proteolysis involved in cellular protein catabolic process	BP	1	CSNK1D,FBXW8,USP5,RNF40,RACK1,ATP5IF1,RCHY1	red	VSMC_M1
GO:0030218	0.19	0.91	6	102	erythrocyte differentiation	BP	1	TAL1,CEBPG,C15orf41,RPS6,CDK5RAP3,ATP5IF1	red	VSMC_M1
GO:0048598	0.19	0.87	21	469	embryonic morphogenesis	BP	1	SMAD4,TRIOBP,RPS7,FGF2,TAL1,ARHGAP35,IFT122,CTR9,RPS6,MMP16,IFT57,CDC73,DYNC2H1,KAT2A,PFN1,RARA,CECR2,B9D1,TPRN,RACK1,FGF10	red	VSMC_M1
GO:0060401	0.19	0.90	7	126	cytosolic calcium ion transport	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0045185	0.19	0.92	5	80	maintenance of protein location	BP	1	SRI,TMSB10,GOLPH3,CIZ1,TMSB4X	red	VSMC_M1
GO:0110020	0.19	0.92	5	86	regulation of actomyosin structure organization	BP	1	SMAD4,PAK1,TMEFF2,AKAP13,PFN1	red	VSMC_M1
GO:0140694	0.19	0.88	15	305	non-membrane-bounded organelle assembly	BP	1	SMAD4,RPS5,RPS3,NEB,CSNK1D,HDAC3,TNKS,EIF2A,OGFOD1,AKAP13,KLHL41,BCCIP,LSM4,KAT2A,E2F4	red	VSMC_M1
GO:0051279	0.19	0.93	4	58	regulation of release of sequestered calcium ion into cytosol	BP	1	SRI,FKBP1B,CALM2,FKBP1A	red	VSMC_M1
GO:0043434	0.19	0.88	15	308	response to peptide hormone	BP	1	ARG1,EGR1,EIF2B4,PAK1,SOCS2,SP1,CXCL12,GOT2,EGR2,RNF40,EIF2B2,STXBP4,SPARC,RAB12,ERRFI1	red	VSMC_M1
GO:0030030	0.19	0.85	51	1226	cell projection organization	BP	1	SMAD4,SGK1,DYNLT1,FGFR1OP,CTNNA1,TRIOBP,MAP4K4,ICK,FAM161A,PARD3,WDR35,FKBP1B,ARHGAP35,IFT122,PAK1,VDAC3,SPAST,CSNK1D,CXCL12,C21orf91,FBXW8,TBC1D7,IFT57,ARL3,UNC119B,CFAP410,RHOD,WDR11,IFT46,MAP4,FBXO45,CEP19,EGR2,KDM1A,MAP2,RP2,DYNC2H1,KAT2A,PFN1,CECR2,DNAL1,FLRT2,PMP22,B9D1,GOLPH3,TBC1D24,TPRN,WDR5,E2F4,NREP,CPNE1	red	VSMC_M1
GO:0055001	0.19	0.90	8	150	muscle cell development	BP	1	SMAD4,PAK1,NEB,PTCD2,AKAP13,MYO18B,KLHL41,KDM1A	red	VSMC_M1
GO:1904064	0.19	0.91	6	103	positive regulation of cation transmembrane transport	BP	1	SRI,CACNA2D1,STIMATE,HSPA2,CALM2,TMSB4X	red	VSMC_M1
GO:0051209	0.19	0.91	5	82	release of sequestered calcium ion into cytosol	BP	1	SRI,FKBP1B,FGF2,CALM2,FKBP1A	red	VSMC_M1
GO:0035556	0.19	0.84	85	2063	intracellular signal transduction	BP	1	SMAD4,SGK1,DYRK2,DYNLT1,NDRG1,TCP11,MAD2L1BP,MAP4K4,NPR2,ICK,AHR,CORO2A,RPS7,PIH1D1,FKBP1B,FGF2,ARHGAP35,RAB30,NRBP1,PAK1,RPS3,PSD2,NRG2,HDAC3,SOCS2,PCID2,CXCL12,TNFRSF19,COPS5,KMT5A,RHOF,P2RX4,RRAS2,SPRED1,RPS6,STIMATE,HPSE,GPAT3,TFG,TMEM117,TBC1D7,ARL3,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RAB9A,RHOD,CRTC3,SMYD2,ARHGDIB,KDM1A,USP28,NDUFA13,MECOM,PELI2,ITFG2,ERC1,ITPKB,NR1D1,CDK5RAP3,PRDX2,INTS3,CALM2,XRCC3,RFFL,MIER1,FBXO4,RAB12,GOLPH3,YJU2,RAB39B,ERRFI1,USP10,WWOX,GARNL3,FKBP1A,RACK1,HUS1,TIMP3,RPS20,TMSB4X,CPNE1,RNF125,FGF10	red	VSMC_M1

GO:0006303	0.19	0.92	4	59	double-strand break repair via nonhomologous end joining	BP	1	KMT5C,APLF,UVRAG,PARP3	red	VSMC_M1
GO:0043280	0.20	0.90	6	96	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	WDR35,RPS3,PDCD5,IFT57,NDUFA13,RACK1	red	VSMC_M1
GO:0002065	0.20	0.92	4	61	columnar/cuboidal epithelial cell differentiation	BP	1	FGF2,BCCIP,RARA,B9D1	red	VSMC_M1
GO:0002822	0.20	0.90	6	102	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	ARG1,IL1RL1,AHR,KMT5C,IL20RB,PARP3	red	VSMC_M1
GO:0007165	0.20	0.83	157	3919	signal transduction	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,DYNLT1,NDRG1,GNG5,EGR1,TCP11,RHPN1,CTNNA1,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,AHR,CORO2A,INVS,INPP5B,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,ADGRF3,STAM,NR2C2,RAB30,IFT122,EIF2B4,WBP2,NRBP1,PAK1,DGAT2,RPS3,PSD2,NRG2,IL18BP,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,TNKS,CXCL12,TNFRSF19,COPS5,CD8B,IL20RB,KMT5A,PDCD5,CTR9,EDNRA,RHOF,P2RX4,RRAS2,EIF2A,CACNA1D,SPRED1,RPS6,STIMATE,HPSE,GPAT3,GMDS,TFG,PKIG,TMEM117,TBC1D7,IFT57,ARL3,CDC73,NPRL2,SORCS1,ARHGAP31,CFAP410,ARFGEF2,ACTL6A,AKAP13,RAB9A,RHOD,WDR11,CRTC3,SMYD2,ARHGDIB,KDM1A,USP28,CABIN1,IL1RAP,NDUFA13,MECOM,DYNC2H1,PELI2,ITFG2,ZMIZ1,ERC1,ITPKB,RARA,CTDNEP1,NR1D1,CDK5RAP3,EIF2B2,SPG21,PARP16,PRDX2,FLRT2,STXBP4,INTS3,CALM2,RNF138,B9D1,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,RAB12,GOLPH3,YJU2,ITGAE,MOB3A,GFER,RAB39B,ERRFI1,CTNNBIP1,RBM15,UBE4B,USP10,WWOX,GARNL3,FKBP1A,GNAS,RACK1,HUS1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CNIH1,CPNE1,RNF125,RITA1,IGHA2,ATP5IF1,PSENEN,LY96,PROKR2,FGF10	red	VSMC_M1
GO:0051283	0.20	0.91	5	83	negative regulation of sequestering of calcium ion	BP	1	SRI,FKBP1B,FGF2,CALM2,FKBP1A	red	VSMC_M1
GO:0010001	0.20	0.89	9	173	glial cell differentiation	BP	1	NDRG1,PARD3,FGF2,TAL1,EIF2B4,EGR2,NR1D1,EIF2B2,FGF10	red	VSMC_M1
GO:0022404	0.20	0.92	4	63	molting cycle process	BP	1	SMAD4,TNFRSF19,HPSE,FGF10	red	VSMC_M1
GO:0022405	0.20	0.92	4	63	hair cycle process	BP	1	SMAD4,TNFRSF19,HPSE,FGF10	red	VSMC_M1
GO:0033365	0.20	0.85	33	737	protein localization to organelle	BP	1	HSPA1L,CTNNA1,XPA,INVS,CRIPT,PIH1D1,WDR35,PMPCB,STAM,IFT122,CSNK1D,HDAC3,TNKS,PDCD5,TIMM10,PLRG1,PKIG,PARP3,ARL3,EMC9,NDUFA13,DYNC2H1,SCG3,CTDNEP1,VPS37C,CDK5RAP3,SNUPN,FBXO4,GOLPH3,DNLZ,CIZ1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0071897	0.20	0.89	8	150	DNA biosynthetic process	BP	1	FGF2,TNKS,PARP3,DCP2,FBXO4,USP10,NOP10,RCHY1	red	VSMC_M1
GO:0007015	0.20	0.86	17	373	actin filament organization	BP	1	CTNNA1,TRIOBP,ARHGAP35,FAM171A1,PAK1,NEB,CXCL12,TMSB10,ARFIP1,RHOF,TMEFF2,RHOD,MYO5C,PFN1,KANK4,ELMO3,TMSB4X	red	VSMC_M1
GO:0032543	0.20	0.91	5	72	mitochondrial translation	BP	1	MTRF1L,MALSU1,MTIF3,MRPS14,CHCHD1	red	VSMC_M1
GO:0006139	0.20	0.82	176	4274	nucleobase-containing compound metabolic process	BP	1	SMAD4,SGK1,KLF10,DCAF13,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,RPP25L,RCL1,SPIN1,NPR2,ZNF584,AHR,XPA,KMT5C,MEI4,PGM3,UTP11,APLF,RPS7,PIH1D1,SF3B6,FGF2,TAL1,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,WBP2,UVRAG,EBNA1BP2,DGAT2,RPS3,HNRNPL,NAXD,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,PTCD2,ELOC,PLRG1,RPS6,GMDS,PKIG,FARS2,ELOVL2,ACOT8,PARP3,PRDM10,YARS,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,GMPR2,RBM4,CRTC3,SMYD2,RPL35A,PES1,BCCIP,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,IL1RAP,EXOSC7,NDUFA13,EMG1,TRMT44,PRDX6,MECOM,LSM4,UVSSA,ELK1,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CECR2,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,XRCC3,USP22,MIER1,FBXO4,MYO18A,YJU2,CTNNBIP1,RBM15,ZNF276,USP10,CDYL2,WWOX,CIZ1,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,MYPOP,SLC25A1,HUS1,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,SF3B5,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0070646	0.21	0.89	7	125	protein modification by small protein removal	BP	1	COPS5,USP28,USP5,TRRAP,KAT2A,USP22,USP10	red	VSMC_M1
GO:0010927	0.21	0.91	5	87	cellular component assembly involved in morphogenesis	BP	1	SMAD4,NEB,AKAP13,KLHL41,PMP22	red	VSMC_M1
GO:0051282	0.21	0.91	5	84	regulation of sequestering of calcium ion	BP	1	SRI,FKBP1B,FGF2,CALM2,FKBP1A	red	VSMC_M1
GO:0019319	0.21	0.92	4	61	hexose biosynthetic process	BP	1	DGAT2,KAT2A,WDR5,SLC25A1	red	VSMC_M1
GO:0045934	0.21	0.84	47	1115	negative regulation of nucleobase-containing compound metabolic process	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,TAL1,IRF2BP1,NR2C2,RECQL5,RPS3,HDAC3,TNKS,KMT5A,CTR9,PKIG,PARP3,CDC73,IRF2BP2,TGIF1,NIF3L1,SMYD2,KDM1A,ETV5,NDUFA13,MECOM,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0022904	0.21	0.89	7	99	respiratory electron transport chain	BP	1	COX5B,SLC25A51,NDUFA2,NDUFA10,NDUFB7,COX4I1,COX7C	red	VSMC_M1
GO:0022008	0.21	0.83	52	1272	neurogenesis	BP	1	SMAD4,SGK1,DYNLT1,ZHX2,NDRG1,CTNNA1,TRIOBP,MAP4K4,PARD3,FKBP1B,FGF2,TAL1,ARHGAP35,SDK2,EIF2B4,PAK1,SPAST,CSNK1D,SOCS2,CXCL12,C21orf91,P2RX4,FBXW8,ARL3,NIF3L1,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,DYNC2H1,PROM1,ZMIZ1,PRTG,RARA,CECR2,NR1D1,CDK5RAP3,EIF2B2,FLRT2,PMP22,HMG20A,TBC1D24,TPRN,WDR5,IER2,NREP,BHLHE41,CPNE1,RITA1,FGF10	red	VSMC_M1

GO:0031326	0.21	0.82	120	2955	regulation of cellular biosynthetic process	BP	1	SMAD4,SGK1,DYRK2,KLF10,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,SPIN1,ZNF584,AHR,MALSU1,COQ3,PIH1D1,WDR35,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,DGAT2,RPS3,HDAC3,ERLIN2,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,P2RX4,EIF2A,OGFOD1,PKIG,ACOT8,PARP3,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,WDR5,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,RACK1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0032886	0.21	0.87	10	202	regulation of microtubule-based process	BP	1	PAK1,RPS3,SPAST,PARP3,ARL3,RAE1,MAP2,KAT2A,XRCC3,TUBB4A	red	VSMC_M1
GO:0040029	0.21	0.90	5	86	regulation of gene expression, epigenetic	BP	1	WBP2,SMYD5,ZMIZ1,RBM15,ELOF1	red	VSMC_M1
GO:0043086	0.21	0.85	26	555	negative regulation of catalytic activity	BP	1	FGFR1OP,RPS7,PIH1D1,FKBP1B,PCID2,SPRED1,PKIG,PARP3,NPRL2,RAB9A,PPP1R8,ENSA,PPP1R11,CABIN1,CDK5RAP3,RFFL,ERRFI1,PTPA,FKBP1A,RACK1,TIMP3,PPP1R14A,RPS20,WFDC3,ATP5IF1,PTPRN2	red	VSMC_M1
GO:0044249	0.21	0.82	174	4271	cellular biosynthetic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,MTRF1L,KLF10,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,EIF3D,MTERF2,SRI,SPIN1,NPR2,ZNF584,RPS5,AHR,RPL28,EEF1A1,MALSU1,PGM3,ALAD,RPS7,COQ3,RPS11,PIH1D1,WDR35,FGF2,TAL1,EFR3B,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,DGAT2,RPS3,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,RPS3A,ELOC,GOT2,P2RX4,EIF2A,RPS6,GPAT3,OGFOD1,GMDS,PKIG,FARS2,ELOVL2,ACOT8,PARP3,PSPH,PRDM10,YARS,CDC73,EIF3I,WIPI1,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,RPL35A,UROS,RPL18A,EGR2,KDM1A,ETV5,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,MECOM,CHCHD1,ELK1,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,ITPKB,RARA,HDHD5,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,CYP1A1,ZNF287,HMG20A,CHST9,COQ7,USP22,MIER1,FBXO4,GOLPH3,CTNNBIP1,RBM15,ZNF276,WDR5,USP10,DPH5,CDYL2,WWOX,CIZ1,ALG14,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,RACK1,ELOF1,ZNF614,COQ10A,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,TMEM189,ADI1,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,RCHY1,FGF10	red	VSMC_M1
GO:0098660	0.21	0.84	26	574	inorganic ion transmembrane transport	BP	1	SRI,COX5B,KCNF1,FKBP1B,FGF2,PMPCB,COX7B,CACNA2D1,SLC12A6,P2RX4,CACNA1D,STIMATE,SCN3A,KCNQ2,SCNN1A,CLCN5,HSPA2,CALM2,CACHD1,KCNAB2,COX4I1,FKBP1A,SLC25A28,ATP6V1G1,TMSB4X,AHNAK	red	VSMC_M1
GO:0043409	0.21	0.89	7	131	negative regulation of MAPK cascade	BP	1	SMAD4,HDAC3,SPRED1,MECOM,CDK5RAP3,ERRFI1,TIMP3	red	VSMC_M1
GO:0098773	0.21	0.91	4	65	skin epidermis development	BP	1	SMAD4,TNFRSF19,HPSE,FGF10	red	VSMC_M1
GO:0120036	0.21	0.83	49	1193	plasma membrane bounded cell projection organization	BP	1	SMAD4,SGK1,DYNLT1,CTNNA1,TRIOBP,MAP4K4,ICK,FAM161A,PARD3,WDR35,FKBP1B,ARHGAP35,IFT122,PAK1,VDAC3,SPAST,CSNK1D,CXCL12,C21orf91,FBXW8,TBC1D7,IFT57,ARL3,UNC119B,CFAP410,RHOD,WDR11,IFT46,MAP4,FBXO45,CEP19,EGR2,KDM1A,MAP2,RP2,DYNC2H1,PFN1,CECR2,DNAL1,FLRT2,PMP22,B9D1,GOLPH3,TBC1D24,TPRN,WDR5,E2F4,NREP,CPNE1	red	VSMC_M1
GO:0009892	0.21	0.82	93	2254	negative regulation of metabolic process	BP	1	SMAD4,ARG1,KLF10,FGFR1OP,PFDN6,ZHX2,HMGA1,EGR1,IL1RL1,AHR,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,IRF2BP1,NR2C2,RECQL5,DGAT2,RPS3,PFDN1,HDAC3,ERLIN2,PCID2,TNKS,IL20RB,KMT5A,CTR9,SPRED1,SMYD5,PKIG,ACOT8,PARP3,TMEFF2,CUEDC2,CDC73,NPRL2,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,LSM4,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,CDK5RAP3,MBTD1,GATAD2B,SUPT4H1,CALM2,HMG20A,IL13RA2,RFFL,MIER1,ERRFI1,CTNNBIP1,WDR5,PTPA,CDYL2,DR1,FKBP1A,MYPOP,RACK1,ZNF614,TIMP3,ZNF180,RPS20,TMSB4X,BHLHE41,CPNE1,WFDC3,RNF125,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0009889	0.21	0.82	122	3010	regulation of biosynthetic process	BP	1	SMAD4,SGK1,DYRK2,KLF10,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,SPIN1,ZNF584,AHR,MALSU1,COQ3,PIH1D1,WDR35,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,DGAT2,RPS3,HDAC3,ERLIN2,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,P2RX4,EIF2A,OGFOD1,PKIG,ACOT8,PARP3,TMEFF2,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,ERRFI1,CTNNBIP1,RBM15,ZNF276,WDR5,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,RACK1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0000209	0.21	0.87	10	203	protein polyubiquitination	BP	1	ANKRD39,IRF2BP1,TNKS,PELI2,ANAPC13,RNF40,RFFL,FBXO4,UBE4B,RNF125	red	VSMC_M1

GO:0090305	0.21	0.87	11	213	nucleic acid phosphodiester bond hydrolysis	BP	1	RCL1,XPA,MEI4,APLF,ERI3,PPP1R8,REXO2,EXOSC7,CECR2,DCP2,NUDT21	red	VSMC_M1
GO:0007004	0.22	0.91	4	63	telomere maintenance via telomerase	BP	1	TNKS,DCP2,FBXO4,NOP10	red	VSMC_M1
GO:1903311	0.22	0.86	12	247	regulation of mRNA metabolic process	BP	1	HNRNPL,PCID2,CTR9,PTCD2,CDC73,RBM4,EXOSC7,PRDX6,DCP2,RNF40,RBM15,NUDT21	red	VSMC_M1
GO:1903522	0.22	0.87	9	179	regulation of blood circulation	BP	1	SRI,WDR35,FKBP1B,CACNA2D1,P2RX4,CACNA1D,MYL4,GJC1,CALM2	red	VSMC_M1
GO:0050777	0.22	0.88	7	128	negative regulation of immune response	BP	1	ARG1,IL1RL1,AHR,IL20RB,PARP3,IL13RA2,RNF125	red	VSMC_M1
GO:0065009	0.22	0.82	95	2307	regulation of molecular function	BP	1	SMAD4,SGK1,RGS17,ACR,CSNK2B,DYNLT1,FGFR1OP,EGR1,EIF3D,SRI,MUT,MAP4K4,EEF1A1,RPS7,PIH1D1,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,EIF2B4,PAK1,UVRAG,RPS3,PSD2,IL18BP,SOCS2,PCID2,CACNA2D1,TNKS,COPS5,CEBPG,PDCD5,EDNRA,RHOF,CACNA1D,SPRED1,CCNI,STIMATE,MMP16,AMBRA1,PKIG,TBC1D7,IFT57,PARP3,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RAB9A,RHOD,PPP1R8,ENSA,FAM45A,PPP1R11,CRTC3,BCCIP,ARHGDIB,KDM1A,MYL4,MAP2,CABIN1,IL1RAP,NDUFA13,RP2,PFN1,ERC1,HSPA2,RARA,CDK5RAP3,EIF2B2,PARP16,PRDX2,CALM2,RFFL,TBC1D24,ERRFI1,CTNNBIP1,PTPA,GARNL3,EVI5,FKBP1A,GNAS,RACK1,TIMP3,PPP1R14A,RPS20,TMSB4X,CPNE1,WFDC3,ATP5IF1,PSENEN,PTPRN2,AHNAK,FGF10	red	VSMC_M1
GO:0014070	0.22	0.84	31	703	response to organic cyclic compound	BP	1	ARG1,ACR,CSNK2B,EGR1,CTNNA1,AHR,ALAD,PSMB2,FKBP1B,RECQL5,WBP2,PAK1,SOCS2,GOT2,P2RX4,HLCS,PSPH,GRAMD1C,RAE1,KDM1A,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,SPARC,CYP1A1,GOLPH3,ERRFI1,GNAS,FGF10	red	VSMC_M1
GO:0045637	0.22	0.88	8	152	regulation of myeloid cell differentiation	BP	1	KLF10,TAL1,CTR9,CDC73,ITPKB,RARA,CTNNBIP1,RBM15	red	VSMC_M1
GO:0090501	0.22	0.88	7	124	RNA phosphodiester bond hydrolysis	BP	1	RCL1,ERI3,PPP1R8,REXO2,EXOSC7,DCP2,NUDT21	red	VSMC_M1
GO:1901654	0.22	0.88	8	151	response to ketone	BP	1	ARG1,CSNK2B,AHR,WBP2,PSPH,ELK1,GOLPH3,ERRFI1	red	VSMC_M1
GO:0022402	0.22	0.83	41	951	cell cycle process	BP	1	DYNLT1,MEI1,MAD2L1BP,DCTN3,MEI4,RECQL5,UVRAG,RPS3,SPAST,CSNK1D,HDAC3,PCID2,CDK17,TNKS,KMT5A,PLRG1,CCNI,RPS6,PARP3,ARL3,CDC73,RAE1,ENSA,BCCIP,MAP4,USP28,KAT2A,HSPA2,CTDNEP1,CECR2,CDK5RAP3,STXBP4,INTS3,CALM2,CYP1A1,XRCC3,FBXO4,PTPA,E2F4,HUS1,FGF10	red	VSMC_M1
GO:0060537	0.22	0.85	15	323	muscle tissue development	BP	1	SMAD4,EGR1,FGF2,PAK1,NEB,PTCD2,AKAP13,MYO18B,KLHL41,EGR2,GJC1,KAT2A,RARA,MEF2D,FKBP1A	red	VSMC_M1
GO:1903008	0.22	0.89	6	101	organelle disassembly	BP	1	SPAST,MTIF3,AMBRA1,WIPI1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0009411	0.22	0.88	7	127	response to UV	BP	1	XPA,COPS9,KDM1A,USP28,UVSSA,UBE4B,HUS1	red	VSMC_M1
GO:0021782	0.22	0.90	5	86	glial cell development	BP	1	NDRG1,PARD3,EIF2B4,NR1D1,EIF2B2	red	VSMC_M1
GO:0010468	0.22	0.81	138	3428	regulation of gene expression	BP	1	SMAD4,SGK1,ARG1,KLF10,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,IL1RL1,SPIN1,ZNF584,AHR,KMT5C,MALSU1,INPP5B,RPS7,PIH1D1,WDR35,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,RPS3,HNRNPL,CSNK1D,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,IL20RB,KMT5A,PDCD5,CTR9,PTCD2,ELOC,EIF2A,SMYD5,HPSE,OGFOD1,PKIG,CD58,PARP3,PRDM10,CUEDC2,CDC73,ARFGEF2,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R11,RBM4,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,MECOM,LSM4,TRIM4,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,COQ7,IL13RA2,USP22,MIER1,FBXO4,ERRFI1,CTNNBIP1,RBM15,ZNF276,DPH5,CDYL2,WWOX,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,MYPOP,RACK1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,CPNE1,RNF125,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,LY96,AHNAK,FGF10	red	VSMC_M1
GO:0046907	0.22	0.82	54	1261	intracellular transport	BP	1	HSPA1L,POLDIP3,REEP2,ICK,CLTA,PARD3,WDR35,PMPCB,STAM,IFT122,NRBP1,PAK1,SPAST,CSNK1D,HDAC3,PCID2,RAB28,PDCD5,VTI1B,TIMM10,ARFIP1,TFG,PKIG,IFT57,ARL3,WIPI1,AKAP13,RAB9A,ARL4C,RAE1,FAM45A,WDR11,RBM4,IFT46,EGR2,MAP2,AP1S1,NDUFA13,ARL4D,DYNC2H1,MYO5C,ERC1,VPS37C,COPZ2,TRAPPC1,STXBP4,SNUPN,RAB12,GOSR1,DNLZ,EVI5,TOMM7,RITA1,ATP5IF1	red	VSMC_M1
GO:0043009	0.22	0.84	23	522	chordate embryonic development	BP	1	SMAD4,INPP5B,RPS7,SF3B6,ARHGAP35,IFT122,NDUFA2,CTR9,EDNRA,MMP16,FBXW8,IFT57,PSPH,ACTL6A,MYO18B,EMG1,ZMIZ1,KAT2A,PFN1,RARA,CECR2,MBTD1,B9D1	red	VSMC_M1
GO:0006278	0.22	0.91	4	64	RNA-dependent DNA biosynthetic process	BP	1	TNKS,DCP2,FBXO4,NOP10	red	VSMC_M1
GO:0019080	0.22	0.90	5	86	viral gene expression	BP	1	TAF11,EIF3D,UBP1,SP1,PARP16	red	VSMC_M1
GO:0043433	0.22	0.88	7	126	negative regulation of DNA-binding transcription factor activity	BP	1	SRI,CEBPG,KDM1A,CDK5RAP3,PRDX2,CTNNBIP1,TMSB4X	red	VSMC_M1
GO:0002460	0.22	0.87	9	173	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	ARG1,IL1RL1,AHR,KMT5C,IL18BP,IL20RB,PARP3,IL13RA2,IGHA2	red	VSMC_M1
GO:0097305	0.22	0.87	9	174	response to alcohol	BP	1	CTNNA1,AHR,ALAD,RECQL5,GOT2,GRAMD1C,RARA,SPARC,GOLPH3	red	VSMC_M1
GO:0051208	0.22	0.89	5	87	sequestering of calcium ion	BP	1	SRI,FKBP1B,FGF2,CALM2,FKBP1A	red	VSMC_M1
GO:0050790	0.22	0.81	76	1823	regulation of catalytic activity	BP	1	SGK1,RGS17,ACR,CSNK2B,DYNLT1,FGFR1OP,EGR1,MUT,MAP4K4,EEF1A1,RPS7,PIH1D1,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,EIF2B4,PAK1,UVRAG,RPS3,PSD2,SOCS2,PCID2,TNKS,PDCD5,EDNRA,RHOF,CACNA1D,SPRED1,CCNI,MMP16,AMBRA1,PKIG,TBC1D7,IFT57,PARP3,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RAB9A,RHOD,PPP1R8,ENSA,FAM45A,PPP1R11,BCCIP,ARHGDIB,MYL4,CABIN1,NDUFA13,RP2,PFN1,CDK5RAP3,EIF2B2,PARP16,CALM2,RFFL,TBC1D24,ERRFI1,PTPA,GARNL3,EVI5,FKBP1A,GNAS,RACK1,TIMP3,PPP1R14A,RPS20,TMSB4X,WFDC3,ATP5IF1,PSENEN,PTPRN2,FGF10	red	VSMC_M1
GO:0000380	0.22	0.91	4	66	alternative mRNA splicing, via spliceosome	BP	1	HNRNPL,RBM4,KDM1A,RBM15	red	VSMC_M1

GO:0051249	0.22	0.85	14	287	regulation of lymphocyte activation	BP	1	ARG1,AHR,KMT5C,RPS3,PCID2,IL20RB,PARP3,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,IGHA2,FGF10	red	VSMC_M1
GO:0071222	0.23	0.88	7	126	cellular response to lipopolysaccharide	BP	1	ARG1,CTR9,CDC73,RARA,NR1D1,PRDX2,LY96	red	VSMC_M1
GO:0003015	0.23	0.86	9	180	heart process	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,AKAP13,MYL4,GJC1,CALM2	red	VSMC_M1
GO:0051258	0.23	0.85	12	250	protein polymerization	BP	1	TRIOBP,PAK1,RPS3,CSNK1D,TMSB10,ARFIP1,ARL3,MAP2,PFN1,TUBB4A,KANK4,TMSB4X	red	VSMC_M1
GO:2000116	0.23	0.86	9	167	regulation of cysteine-type endopeptidase activity	BP	1	PIH1D1,WDR35,RPS3,PCID2,PDCD5,IFT57,NDUFA13,RFFL,RACK1	red	VSMC_M1
GO:0006310	0.23	0.85	12	245	DNA recombination	BP	1	KMT5C,MEI4,RECQL5,PARP3,ACTL6A,INO80D,KDM1A,INO80E,INO80C,RNF138,XRCC3,HUS1	red	VSMC_M1
GO:0050865	0.23	0.84	18	385	regulation of cell activation	BP	1	ARG1,IL1RL1,AHR,KMT5C,RPS3,PCID2,IL20RB,PARP3,ZMIZ1,KAT2A,ITPKB,RARA,NR1D1,PRDX2,IL13RA2,MYO18A,IGHA2,FGF10	red	VSMC_M1
GO:2001235	0.23	0.88	6	98	positive regulation of apoptotic signaling pathway	BP	1	CTNNA1,RPS7,RPS3,WWOX,RACK1,TIMP3	red	VSMC_M1
GO:0033108	0.23	0.88	6	83	mitochondrial respiratory chain complex assembly	BP	1	NDUFA2,COX19,NDUFA10,NDUFA13,NDUFB7,OMA1	red	VSMC_M1
GO:0032436	0.23	0.89	5	83	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	CSNK1D,FBXW8,USP5,RACK1,RCHY1	red	VSMC_M1
GO:0019221	0.23	0.84	15	306	cytokine-mediated signaling pathway	BP	1	SMAD4,ARG1,CSNK2B,EGR1,IL1RL1,CXCL12,TNFRSF19,IL20RB,CTR9,IL1RAP,IL13RA2,RFFL,RBM15,TMSB4X,CPNE1	red	VSMC_M1
GO:0051246	0.23	0.80	82	1953	regulation of protein metabolic process	BP	1	SMAD4,CSNK2B,FGFR1OP,PFDN6,POLDIP3,EGR1,EIF3D,EEF1A1,COPS9,MALSU1,FAM161A,INPP5B,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,PFDN1,CSNK1D,HDAC3,PCID2,SP1,PDCD5,CTR9,EIF2A,SPRED1,CCNI,OGFOD1,FBXW8,PKIG,ACOT8,TBC1D7,IFT57,AKAP13,PPP1R8,ENSA,PPP1R11,RBM4,BCCIP,KDM1A,EXOSC7,NDUFA13,USP5,PELI2,ZMIZ1,KAT2A,HSPA2,ITPKB,RARA,DCP2,RNF40,CDK5RAP3,EIF2B2,PARP16,CALM2,HMG20A,RFFL,FBXO4,MOB3A,ERRFI1,WDR5,PTPA,DPH5,FKBP1A,RACK1,HUS1,TIMP3,RPS20,WFDC3,ATP5IF1,PSENEN,RCHY1,FGF10	red	VSMC_M1
GO:0044265	0.23	0.82	41	947	cellular macromolecule catabolic process	BP	1	ACR,ZHX2,UBAP1,ALAD,RPS7,PSMB2,STAM,RNF121,CSNK1D,ERLIN2,PCID2,ELOC,HPSE,FBXW8,PPP1R8,PPP1R11,PSMA7,FBXO45,USP28,EXOSC7,USP5,LSM4,UBA1,PSMB6,CECR2,NR1D1,DCP2,VPS37C,RNF40,CDK5RAP3,RFFL,USP22,FBXO4,RAB12,OMA1,UBE4B,USP10,RACK1,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0031399	0.23	0.81	50	1182	regulation of protein modification process	BP	1	SMAD4,CSNK2B,FGFR1OP,EGR1,COPS9,FAM161A,RPS7,PIH1D1,PARD3,FKBP1B,FGF2,TAL1,WBP2,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,CTR9,SPRED1,CCNI,PKIG,TBC1D7,AKAP13,PPP1R8,ENSA,PPP1R11,BCCIP,KDM1A,PELI2,ZMIZ1,KAT2A,HSPA2,ITPKB,RNF40,CDK5RAP3,PARP16,CALM2,HMG20A,FBXO4,MOB3A,ERRFI1,WDR5,PTPA,FKBP1A,RACK1,HUS1,RPS20,RCHY1,FGF10	red	VSMC_M1
GO:0120254	0.23	0.89	5	86	olefinic compound metabolic process	BP	1	EGR1,DGAT2,ELOVL2,ACOT8,CYP1A1	red	VSMC_M1
GO:0006403	0.23	0.86	9	171	RNA localization	BP	1	POLDIP3,TST,PIH1D1,PCID2,TNKS,RAE1,DCP2,SNUPN,NOP10	red	VSMC_M1
GO:0043534	0.23	0.88	6	108	blood vessel endothelial cell migration	BP	1	CSNK2B,FGF2,SP1,P2RX4,SPRED1,TMSB4X	red	VSMC_M1
GO:0071478	0.23	0.87	8	150	cellular response to radiation	BP	1	EGR1,XPA,COPS9,KDM1A,USP28,ELK1,FBXO4,HUS1	red	VSMC_M1
GO:1902107	0.23	0.88	6	110	positive regulation of leukocyte differentiation	BP	1	KLF10,PCID2,ZMIZ1,ITPKB,RARA,CTNNBIP1	red	VSMC_M1
GO:1903708	0.23	0.88	6	110	positive regulation of hemopoiesis	BP	1	KLF10,PCID2,ZMIZ1,ITPKB,RARA,CTNNBIP1	red	VSMC_M1
GO:1901800	0.23	0.88	6	104	positive regulation of proteasomal protein catabolic process	BP	1	CSNK1D,FBXW8,USP5,RNF40,RACK1,RCHY1	red	VSMC_M1
GO:0070252	0.24	0.90	4	70	actin-mediated cell contraction	BP	1	SRI,CACNA2D1,CACNA1D,GJC1	red	VSMC_M1
GO:0032200	0.24	0.87	7	130	telomere organization	BP	1	TNKS,PARP3,DCP2,XRCC3,FBXO4,HUS1,NOP10	red	VSMC_M1
GO:0015980	0.24	0.84	14	259	energy derivation by oxidation of organic compounds	BP	1	CS,DYRK2,COX5B,SLC25A51,COX7B,NDUFA2,MTFR1,NDUFA10,MTFR1L,NR1D1,NDUFB7,COX4I1,COQ10A,COX7C	red	VSMC_M1
GO:0051129	0.24	0.82	25	569	negative regulation of cellular component organization	BP	1	SMAD4,PFDN6,TRIOBP,MAD2L1BP,MAP4K4,PFDN1,PCID2,TNKS,TMSB10,TBC1D7,TMEFF2,MAP4,MAP2,KAT2A,PFN1,HSPA2,DCP2,PRRT2,PMP22,XRCC3,TUBB4A,KANK4,OMA1,CTNNBIP1,TMSB4X	red	VSMC_M1
GO:0008630	0.24	0.89	5	84	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	DYRK2,RPS3,CXCL12,KDM1A,USP28	red	VSMC_M1
GO:0043632	0.24	0.82	25	561	modification-dependent macromolecule catabolic process	BP	1	UBAP1,RPS7,STAM,RNF121,CSNK1D,ERLIN2,ELOC,FBXW8,PPP1R11,PSMA7,FBXO45,USP28,EXOSC7,USP5,UBA1,VPS37C,RNF40,RFFL,USP22,FBXO4,UBE4B,USP10,RACK1,RNF125,RCHY1	red	VSMC_M1
GO:0006119	0.24	0.86	8	119	oxidative phosphorylation	BP	1	COX5B,SLC25A51,COX7B,NDUFA2,NDUFA10,NDUFB7,COX4I1,COX7C	red	VSMC_M1
GO:0031324	0.24	0.80	78	1896	negative regulation of cellular metabolic process	BP	1	SMAD4,KLF10,FGFR1OP,ZHX2,HMGA1,EGR1,AHR,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,TAL1,IRF2BP1,NR2C2,RECQL5,DGAT2,RPS3,HDAC3,ERLIN2,PCID2,TNKS,KMT5A,CTR9,SPRED1,PKIG,ACOT8,PARP3,CDC73,NPRL2,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,SMYD2,KDM1A,ETV5,EXOSC7,NDUFA13,MECOM,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,CDK5RAP3,MBTD1,GATAD2B,SUPT4H1,CALM2,HMG20A,RFFL,MIER1,ERRFI1,CTNNBIP1,WDR5,PTPA,CDYL2,DR1,FKBP1A,MYPOP,RACK1,ZNF614,TIMP3,ZNF180,RPS20,BHLHE41,WFDC3,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0042752	0.24	0.88	5	89	regulation of circadian rhythm	BP	1	KLF10,CSNK1D,HDAC3,RBM4,NR1D1	red	VSMC_M1

GO:0016070	0.24	0.79	143	3480	RNA metabolic process	BP	1	SMAD4,SGK1,KLF10,DCAF13,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,RPP25L,RCL1,SPIN1,ZNF584,AHR,UTP11,RPS7,PIH1D1,SF3B6,FGF2,TAL1,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,WBP2,EBNA1BP2,RPS3,HNRNPL,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,PTCD2,ELOC,PLRG1,RPS6,PKIG,FARS2,PRDM10,YARS,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,RBM4,CRTC3,SMYD2,RPL35A,PES1,EGR2,KDM1A,ETV5,REXO2,IL1RAP,EXOSC7,NDUFA13,EMG1,TRMT44,PRDX6,MECOM,LSM4,ELK1,TRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,YJU2,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,MYPOP,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,SF3B5,AHNAK,FGF10	red	VSMC_M1
GO:0034645	0.24	0.79	143	3533	cellular macromolecule biosynthetic process	BP	1	SMAD4,SGK1,DYRK2,MTRF1L,KLF10,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,EIF3D,MTERF2,SRI,SPIN1,ZNF584,RPS5,AHR,RPL28,EEF1A1,MALSU1,PGM3,RPS7,RPS11,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,RPS3A,ELOC,EIF2A,RPS6,OGFOD1,PKIG,FARS2,ACOT8,PARP3,PRDM10,YARS,CDC73,EIF3I,WIPI1,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,RPL35A,RPL18A,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,MRPS14,MECOM,CHCHD1,ELK1,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,CHST9,USP22,MIER1,FBXO4,GOLPH3,CTNNBIP1,RBM15,ZNF276,USP10,DPH5,CDYL2,WWOX,CIZ1,ALG14,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,RACK1,ELOF1,ZNF614,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,RCHY1,FGF10	red	VSMC_M1
GO:0008064	0.24	0.86	8	159	regulation of actin polymerization or depolymerization	BP	1	TRIOBP,ARHGAP35,CXCL12,TMSB10,ARFIP1,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0051253	0.24	0.81	43	1032	negative regulation of RNA metabolic process	BP	1	SMAD4,KLF10,ZHX2,HMGA1,EGR1,AHR,TAL1,IRF2BP1,NR2C2,RECQL5,HDAC3,KMT5A,CTR9,PKIG,CDC73,IRF2BP2,TGIF1,NIF3L1,SMYD2,KDM1A,ETV5,NDUFA13,MECOM,RARA,NR1D1,ETV3,SAMD1,RNF40,MBTD1,GATAD2B,SUPT4H1,HMG20A,MIER1,CTNNBIP1,CDYL2,DR1,MYPOP,ZNF614,ZNF180,BHLHE41,RITA1,ZNF846,ZNF177	red	VSMC_M1
GO:0030879	0.24	0.87	6	114	mammary gland development	BP	1	ARG1,FGF2,ARHGAP35,SOCS2,GOT2,FGF10	red	VSMC_M1
GO:0046364	0.24	0.89	4	65	monosaccharide biosynthetic process	BP	1	DGAT2,KAT2A,WDR5,SLC25A1	red	VSMC_M1
GO:0006888	0.25	0.87	6	106	endoplasmic reticulum to Golgi vesicle-mediated transport	BP	1	NRBP1,SPAST,CSNK1D,TFG,TRAPPC1,GOSR1	red	VSMC_M1
GO:0046660	0.25	0.88	5	88	female sex differentiation	BP	1	SMAD4,CTNNA1,EIF2B4,EIF2B2,FGF10	red	VSMC_M1
GO:0055076	0.25	0.87	6	107	transition metal ion homeostasis	BP	1	SMAD4,SRI,COX19,HMOX2,SLC25A28,ATP6V1G1	red	VSMC_M1
GO:0035967	0.25	0.87	6	103	cellular response to topologically incorrect protein	BP	1	HSPA1L,COPS5,HSPA2,CDK5RAP3,PARP16,RACK1	red	VSMC_M1
GO:0009790	0.25	0.81	35	841	embryo development	BP	1	SMAD4,TRIOBP,INPP5B,RPS7,SF3B6,FGF2,TAL1,ARHGAP35,NR2C2,IFT122,NDUFA2,CTR9,EDNRA,RPS6,MMP16,FBXW8,IFT57,PSPH,CDC73,ACTL6A,MYO18B,EMG1,DYNC2H1,ZMIZ1,KAT2A,PFN1,RARA,CECR2,MBTD1,B9D1,USP22,TPRN,RACK1,HUS1,FGF10	red	VSMC_M1
GO:0001936	0.25	0.87	6	111	regulation of endothelial cell proliferation	BP	1	ARG1,FGF2,SP1,CXCL12,SPARC,ATP5IF1	red	VSMC_M1
GO:1903321	0.25	0.88	5	82	negative regulation of protein modification by small protein conjugation or removal	BP	1	COPS9,RPS7,RPS3,HMG20A,RPS20	red	VSMC_M1
GO:0007010	0.25	0.80	48	1177	cytoskeleton organization	BP	1	SMAD4,DYNLT1,FGFR1OP,CTNNA1,TRIOBP,CRIPT,PARD3,ARHGAP35,FAM171A1,PAK1,UVRAG,RPS3,SPAST,NEB,CSNK1D,HDAC3,TNKS,CXCL12,TMSB10,ARFIP1,RHOF,PARP3,TMEFF2,ARL3,CFAP410,AKAP13,RHOD,RAE1,KLHL41,BCCIP,ARHGDIB,MAP4,CEP19,MAP2,MYO5C,KAT2A,PFN1,CECR2,DNAL1,XRCC3,TUBB4A,KANK4,MYO18A,PTPA,ELMO3,E2F4,TMSB4X,FGF10	red	VSMC_M1
GO:0000075	0.25	0.86	8	155	cell cycle checkpoint signaling	BP	1	MAD2L1BP,PCID2,USP28,CDK5RAP3,INTS3,XRCC3,FBXO4,HUS1	red	VSMC_M1

GO:1901564	0.25	0.78	195	4789	organonitrogen compound metabolic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,MTRF1L,ACR,CSNK2B,DCAF13,FGFR1OP,PFDN6,POLDIP3,EGR1,NAA35,TRIOBP,TST,EIF3D,UBAP1,MUT,MAP4K4,NPR2,ICK,UBE2M,RPS5,ANKRD39,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,PGM3,FAM161A,INPP5B,ALAD,RPS7,PSMB2,YAE1,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,FGF2,TAL1,PMPCB,IRF2BP1,STAM,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,ENGASE,PFDN1,RNF121,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,KMT5A,PDCD5,CTR9,RPS3A,ELOC,GOT2,EIF2A,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,OGFOD1,FBXW8,PKIG,FARS2,HLCS,ELOVL2,ACOT8,TBC1D7,IFT57,PARP3,PSPH,VKORC1L1,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ACTL6A,AKAP13,WDR5B,PPP1R8,ENSA,GMPR2,PPP1R11,KLHL41,RBM4,SMYD2,PSMA7,DCAF17,RPL35A,UROS,BCCIP,RPL18A,FBXO45,EGR2,KDM1A,USP28,PTS,EXOSC7,NDUFA13,MRPS14,ANAPC16,USP5,MECOM,CHCHD1,TRIM4,UBA1,DYNC2H1,UVSSA,PELI2,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PSMB6,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,VPS37C,ANAPC13,RNF40,CDK5RAP3,EIF2B2,PARP16,CALM2,CYP1A1,RNF138,HMG20A,CHST9,RFFL,USP22,MIER1,FBXO4,RAB12,OMA1,GOLPH3,HMOX2,MOB3A,ERRFI1,UBE4B,GSTM3,WDR5,USP10,PTPA,DPH5,ALG14,DR1,MED31,URM1,FKBP1A,SLC25A1,RACK1,HUS1,TIMP3,RPS20,ACP1,TMSB4X,ADI1,CPNE1,WFDC3,RNF125,ATP5IF1,PSENEN,PTPRN2,RCHY1,FGF10	red	VSMC_M1
GO:0071774	0.25	0.88	5	91	response to fibroblast growth factor	BP	1	FGF2,ELK1,FLRT2,IER2,FGF10	red	VSMC_M1
GO:0006464	0.25	0.78	115	2859	cellular protein modification process	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,DCAF13,FGFR1OP,EGR1,NAA35,TRIOBP,MAP4K4,NPR2,ICK,UBE2M,ANKRD39,KMT5C,COPS9,PGM3,FAM161A,RPS7,PIH1D1,PARD3,ADCK2,FKBP1B,FGF2,TAL1,IRF2BP1,WBP2,PAK1,UVRAG,RPS3,ENGASE,RNF121,CSNK1D,HDAC3,SOCS2,CDK17,TNKS,COPS5,KMT5A,CTR9,EIF2A,SPRED1,CCNI,SMYD5,OGFOD1,FBXW8,PKIG,HLCS,TBC1D7,PARP3,VKORC1L1,CDC73,NPRL2,PTP4A2,WIPI1,ACTL6A,AKAP13,WDR5B,PPP1R8,ENSA,PPP1R11,KLHL41,SMYD2,DCAF17,BCCIP,FBXO45,EGR2,KDM1A,USP28,ANAPC16,USP5,MECOM,TRIM4,UBA1,UVSSA,PELI2,TRRAP,ZMIZ1,KAT2A,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,ANAPC13,RNF40,CDK5RAP3,PARP16,CALM2,RNF138,HMG20A,RFFL,USP22,MIER1,FBXO4,MOB3A,ERRFI1,UBE4B,WDR5,USP10,PTPA,DPH5,ALG14,DR1,MED31,URM1,FKBP1A,RACK1,HUS1,RPS20,ACP1,RNF125,PTPRN2,RCHY1,FGF10	red	VSMC_M1
GO:0036211	0.25	0.78	115	2859	protein modification process	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,DCAF13,FGFR1OP,EGR1,NAA35,TRIOBP,MAP4K4,NPR2,ICK,UBE2M,ANKRD39,KMT5C,COPS9,PGM3,FAM161A,RPS7,PIH1D1,PARD3,ADCK2,FKBP1B,FGF2,TAL1,IRF2BP1,WBP2,PAK1,UVRAG,RPS3,ENGASE,RNF121,CSNK1D,HDAC3,SOCS2,CDK17,TNKS,COPS5,KMT5A,CTR9,EIF2A,SPRED1,CCNI,SMYD5,OGFOD1,FBXW8,PKIG,HLCS,TBC1D7,PARP3,VKORC1L1,CDC73,NPRL2,PTP4A2,WIPI1,ACTL6A,AKAP13,WDR5B,PPP1R8,ENSA,PPP1R11,KLHL41,SMYD2,DCAF17,BCCIP,FBXO45,EGR2,KDM1A,USP28,ANAPC16,USP5,MECOM,TRIM4,UBA1,UVSSA,PELI2,TRRAP,ZMIZ1,KAT2A,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,ANAPC13,RNF40,CDK5RAP3,PARP16,CALM2,RNF138,HMG20A,RFFL,USP22,MIER1,FBXO4,MOB3A,ERRFI1,UBE4B,WDR5,USP10,PTPA,DPH5,ALG14,DR1,MED31,URM1,FKBP1A,RACK1,HUS1,RPS20,ACP1,RNF125,PTPRN2,RCHY1,FGF10	red	VSMC_M1
GO:0006942	0.25	0.89	4	68	regulation of striated muscle contraction	BP	1	SRI,FKBP1B,P2RX4,CALM2	red	VSMC_M1
GO:0042773	0.25	0.87	6	83	ATP synthesis coupled electron transport	BP	1	COX5B,NDUFA2,NDUFA10,NDUFB7,COX4I1,COX7C	red	VSMC_M1
GO:0042775	0.25	0.87	6	83	mitochondrial ATP synthesis coupled electron transport	BP	1	COX5B,NDUFA2,NDUFA10,NDUFB7,COX4I1,COX7C	red	VSMC_M1
GO:0006511	0.25	0.81	24	542	ubiquitin-dependent protein catabolic process	BP	1	UBAP1,RPS7,STAM,RNF121,CSNK1D,ERLIN2,ELOC,FBXW8,PPP1R11,PSMA7,FBXO45,USP28,USP5,UBA1,VPS37C,RNF40,RFFL,USP22,FBXO4,UBE4B,USP10,RACK1,RNF125,RCHY1	red	VSMC_M1
GO:2001056	0.25	0.87	6	105	positive regulation of cysteine-type endopeptidase activity	BP	1	WDR35,RPS3,PDCD5,IFT57,NDUFA13,RACK1	red	VSMC_M1
GO:0007338	0.25	0.88	5	86	single fertilization	BP	1	SMAD4,ACR,HSPA1L,C11orf74,CECR2	red	VSMC_M1
GO:0009059	0.25	0.78	144	3569	macromolecule biosynthetic process	BP	1	SMAD4,SGK1,DYRK2,MTRF1L,KLF10,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,EIF3D,MTERF2,SRI,SPIN1,ZNF584,RPS5,AHR,RPL28,EEF1A1,MALSU1,PGM3,RPS7,RPS11,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,RPS3A,ELOC,EIF2A,RPS6,OGFOD1,PKIG,FARS2,ACOT8,PARP3,TMEFF2,PRDM10,YARS,CDC73,EIF3I,WIPI1,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,RPL35A,RPL18A,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,MRPS14,MECOM,CHCHD1,ELK1,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,CHST9,USP22,MIER1,FBXO4,GOLPH3,CTNNBIP1,RBM15,ZNF276,USP10,DPH5,CDYL2,WWOX,CIZ1,ALG14,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,RACK1,ELOF1,ZNF614,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,RCHY1,FGF10	red	VSMC_M1
GO:0002819	0.25	0.87	6	111	regulation of adaptive immune response	BP	1	ARG1,IL1RL1,AHR,KMT5C,IL20RB,PARP3	red	VSMC_M1
GO:0001570	0.25	0.89	4	71	vasculogenesis	BP	1	SPRED1,MYO18B,GJC1,ZMIZ1	red	VSMC_M1

GO:0090263	0.25	0.87	5	92	positive regulation of canonical Wnt signaling pathway	BP	1	FGF2,CSNK1D,TNKS,CTDNEP1,FGF10	red	VSMC_M1
GO:0043270	0.26	0.85	9	182	positive regulation of ion transport	BP	1	SRI,CACNA2D1,CXCL12,P2RX4,CACNA1D,STIMATE,HSPA2,CALM2,TMSB4X	red	VSMC_M1
GO:0140053	0.26	0.86	6	101	mitochondrial gene expression	BP	1	MTRF1L,MTERF2,MALSU1,MTIF3,MRPS14,CHCHD1	red	VSMC_M1
GO:0031099	0.26	0.85	8	150	regeneration	BP	1	CSNK2B,CTNNA1,MAP4K4,WDR35,FKBP1B,CXCL12,NREP,FGF10	red	VSMC_M1
GO:0030048	0.26	0.87	5	97	actin filament-based movement	BP	1	SRI,CACNA2D1,CACNA1D,GJC1,MYO5C	red	VSMC_M1
GO:0042440	0.26	0.88	4	65	pigment metabolic process	BP	1	ALAD,UROS,HMOX2,ATP5IF1	red	VSMC_M1
GO:0001824	0.26	0.87	5	86	blastocyst development	BP	1	SF3B6,NDUFA2,CTR9,ACTL6A,EMG1	red	VSMC_M1
GO:0010556	0.26	0.78	114	2846	regulation of macromolecule biosynthetic process	BP	1	SMAD4,SGK1,DYRK2,KLF10,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,SPIN1,ZNF584,AHR,MALSU1,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,EIF2A,OGFOD1,PKIG,ACOT8,PARP3,TMEFF2,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,RACK1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0010950	0.26	0.85	7	127	positive regulation of endopeptidase activity	BP	1	WDR35,RPS3,PDCD5,IFT57,NDUFA13,RACK1,PSENEN	red	VSMC_M1
GO:0034767	0.26	0.86	6	114	positive regulation of ion transmembrane transport	BP	1	SRI,CACNA2D1,STIMATE,HSPA2,CALM2,TMSB4X	red	VSMC_M1
GO:0031647	0.26	0.83	12	249	regulation of protein stability	BP	1	RPS7,HDAC3,CDC73,IFT46,USP28,KAT2A,PFN1,NR1D1,STXBP4,FBXO4,DNLZ,TOMM7	red	VSMC_M1
GO:2000112	0.26	0.77	113	2822	regulation of cellular macromolecule biosynthetic process	BP	1	SMAD4,SGK1,DYRK2,KLF10,POLDIP3,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,MTERF2,SRI,SPIN1,ZNF584,AHR,MALSU1,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,EIF2A,OGFOD1,PKIG,ACOT8,PARP3,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,DPH5,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,RACK1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:1901652	0.26	0.82	17	375	response to peptide	BP	1	ARG1,KLF10,EGR1,EIF2B4,PAK1,SOCS2,CACNA2D1,SP1,CXCL12,GOT2,EGR2,RNF40,EIF2B2,STXBP4,SPARC,RAB12,ERRFI1	red	VSMC_M1
GO:0002706	0.26	0.87	5	92	regulation of lymphocyte mediated immunity	BP	1	ARG1,AHR,KMT5C,IL20RB,PARP3	red	VSMC_M1
GO:0009058	0.26	0.77	177	4393	biosynthetic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,MTRF1L,KLF10,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,EIF3D,MTERF2,SRI,SPIN1,NPR2,ZNF584,RPS5,AHR,RPL28,EEF1A1,MALSU1,PGM3,ALAD,RPS7,COQ3,RPS11,PIH1D1,GPT2,WDR35,FGF2,TAL1,EFR3B,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,DGAT2,RPS3,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,RPS3A,ELOC,GOT2,P2RX4,EIF2A,RPS6,GPAT3,OGFOD1,GMDS,PKIG,FARS2,ELOVL2,ACOT8,PARP3,TMEFF2,PSPH,PRDM10,YARS,CDC73,EIF3I,WIPI1,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,RPL35A,UROS,RPL18A,EGR2,KDM1A,ETV5,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,MECOM,CHCHD1,ELK1,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,ITPKB,RARA,HDHD5,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,CYP1A1,ZNF287,HMG20A,CHST9,COQ7,USP22,MIER1,FBXO4,GOLPH3,ERRFI1,CTNNBIP1,RBM15,ZNF276,WDR5,USP10,DPH5,CDYL2,WWOX,CIZ1,ALG14,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,RACK1,ELOF1,ZNF614,COQ10A,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,TMEM189,ADI1,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,RCHY1,FGF10	red	VSMC_M1
GO:0009966	0.26	0.78	90	2237	regulation of signal transduction	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,DYNLT1,EGR1,TCP11,CTNNA1,MAD2L1BP,MAP4K4,SPIN1,NPR2,INVS,RPS7,PIH1D1,FGF2,ARHGAP35,IFT122,WBP2,PAK1,RPS3,PSD2,IL18BP,CSNK1D,HDAC3,SOCS2,PCID2,KCTD16,TNKS,CXCL12,TNFRSF19,COPS5,KMT5A,RHOF,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,GPAT3,TFG,TBC1D7,CDC73,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RHOD,WDR11,CRTC3,SMYD2,ARHGDIB,KDM1A,NDUFA13,MECOM,DYNC2H1,PELI2,ITFG2,ZMIZ1,ITPKB,CTDNEP1,NR1D1,CDK5RAP3,PRDX2,CALM2,XRCC3,RFFL,MIER1,FBXO4,GOLPH3,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,GARNL3,FKBP1A,RACK1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CPNE1,RNF125,RITA1,LY96,FGF10	red	VSMC_M1

GO:0008283	0.26	0.78	60	1442	cell population proliferation	BP	1	SMAD4,SGK1,ARG1,CSNK2B,KLF10,FGFR1OP,NDRG1,HMGA1,EGR1,CTNNA1,NAA35,AHR,COPS9,FKBP1B,NUDT6,FGF2,TAL1,PAK1,RPS3,SP1,CXCL12,IL20RB,PDCD5,EDNRA,RPS6,MMP16,HPSE,OGFOD1,FBXW8,IFT57,CDC73,PPP1R8,KLHL41,SMYD2,PES1,KDM1A,ETV5,USP28,MECOM,ZMIZ1,KAT2A,ITPKB,RARA,NR1D1,ETV3,MEF2D,CDK5RAP3,PRDX2,STXBP4,SPARC,PMP22,CYP1A1,FBXO4,ERRFI1,CTNNBIP1,E2F4,MED31,YPEL5,ATP5IF1,FGF10	red	VSMC_M1
GO:0002449	0.26	0.84	8	159	lymphocyte mediated immunity	BP	1	ARG1,AHR,KMT5C,CEBPG,IL20RB,PARP3,IL13RA2,IGHA2	red	VSMC_M1
GO:0072359	0.27	0.79	37	902	circulatory system development	BP	1	SMAD4,EGR1,SRI,AHR,FGF2,TAL1,UBP1,IFT122,PAK1,NEB,SP1,EDNRA,SLC12A6,PTCD2,SPRED1,HPSE,FBXW8,IFT57,AKAP13,MYO18B,WDR11,SMYD2,GJC1,DYNC2H1,ZMIZ1,KAT2A,RARA,MEF2D,FLRT2,SPARC,B9D1,ERRFI1,RBM15,FKBP1A,BORCS8,ATP5IF1,FGF10	red	VSMC_M1
GO:0022900	0.27	0.84	9	149	electron transport chain	BP	1	COX5B,SLC25A51,COX7B,NDUFA2,NDUFA10,NDUFA13,NDUFB7,COX4I1,COX7C	red	VSMC_M1
GO:0042116	0.27	0.88	4	69	macrophage activation	BP	1	IL1RL1,CRTC3,NR1D1,MYO18A	red	VSMC_M1
GO:0009755	0.27	0.85	7	142	hormone-mediated signaling pathway	BP	1	CSNK2B,WBP2,PAK1,KDM1A,ZMIZ1,RARA,NR1D1	red	VSMC_M1
GO:0071219	0.27	0.84	7	133	cellular response to molecule of bacterial origin	BP	1	ARG1,CTR9,CDC73,RARA,NR1D1,PRDX2,LY96	red	VSMC_M1
GO:0010646	0.27	0.76	100	2513	regulation of cell communication	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,DYNLT1,EGR1,TCP11,CTNNA1,SRI,MAD2L1BP,MAP4K4,SPIN1,NPR2,INVS,RPS7,PIH1D1,FKBP1B,FGF2,ARHGAP35,IFT122,PCDH17,WBP2,PAK1,RPS3,PSD2,IL18BP,CSNK1D,HDAC3,SOCS2,PCID2,KCTD16,TNKS,CXCL12,TNFRSF19,COPS5,KMT5A,RHOF,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,GPAT3,TFG,TBC1D7,CDC73,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RHOD,ENSA,WDR11,CRTC3,SMYD2,ARHGDIB,EGR2,KDM1A,NDUFA13,MECOM,DYNC2H1,PELI2,ITFG2,ZMIZ1,KAT2A,ERC1,ITPKB,RARA,CTDNEP1,NR1D1,CDK5RAP3,PRRT2,PRDX2,STXBP4,CALM2,XRCC3,RFFL,MIER1,FBXO4,GOLPH3,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,GARNL3,FKBP1A,RACK1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CPNE1,RNF125,RITA1,LY96,FGF10	red	VSMC_M1
GO:0010632	0.27	0.83	10	208	regulation of epithelial cell migration	BP	1	CSNK2B,MAP4K4,FGF2,SP1,P2RX4,SPRED1,PFN1,SPARC,TMSB4X,FGF10	red	VSMC_M1
GO:0048519	0.27	0.76	157	3961	negative regulation of biological process	BP	1	SMAD4,ARG1,DYRK2,RGS17,CSNK2B,KLF10,DYNLT1,FGFR1OP,PFDN6,ZHX2,NDRG1,HMGA1,EGR1,CTNNA1,NAA35,TRIOBP,SRI,MAD2L1BP,IL1RL1,MAP4K4,NPR2,AHR,INVS,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,NUDT6,FGF2,TAL1,ARHGAP35,IRF2BP1,NR2C2,UBP1,IFT122,RECQL5,PCDH17,PAK1,DGAT2,RPS3,PFDN1,HDAC3,SOCS2,ERLIN2,PCID2,TNKS,CXCL12,COPS5,IL20RB,KMT5A,PDCD5,CTR9,TMSB10,RPS3A,ARFIP1,P2RX4,SPRED1,RPS6,SMYD5,PKIG,ACOT8,TBC1D7,IFT57,PARP3,TMEFF2,CUEDC2,CDC73,NPRL2,IRF2BP2,TGIF1,NIF3L1,PPP1R8,ENSA,PPP1R11,RBM4,CRTC3,SMYD2,ARHGDIB,MAP4,KDM1A,ETV5,USP28,MAP2,EXOSC7,NDUFA13,MECOM,LSM4,ITFG2,KAT2A,PFN1,ERC1,PRTG,HSPA2,ITPKB,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,CDK5RAP3,PRRT2,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,CALM2,SPARC,PMP22,HMG20A,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,TUBB4A,KANK4,MYO18A,OMA1,GOLPH3,YJU2,ERRFI1,CTNNBIP1,RBM15,WDR5,USP10,PTPA,CDYL2,WWOX,DR1,MED31,FKBP1A,MYPOP,RACK1,HUS1,ZNF614,TIMP3,ZNF180,RPS20,TMSB4X,BHLHE41,CPNE1,WFDC3,RNF125,RITA1,ZNF846,ZNF177,ATP5IF1,PTPRN2,NAA38,FGF10	red	VSMC_M1
GO:1903706	0.27	0.82	12	258	regulation of hemopoiesis	BP	1	KLF10,TAL1,PCID2,CTR9,CDC73,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,CTNNBIP1,RBM15	red	VSMC_M1
GO:0019941	0.28	0.79	24	550	modification-dependent protein catabolic process	BP	1	UBAP1,RPS7,STAM,RNF121,CSNK1D,ERLIN2,ELOC,FBXW8,PPP1R11,PSMA7,FBXO45,USP28,USP5,UBA1,VPS37C,RNF40,RFFL,USP22,FBXO4,UBE4B,USP10,RACK1,RNF125,RCHY1	red	VSMC_M1
GO:0051302	0.28	0.84	7	138	regulation of cell division	BP	1	FGF2,TAL1,UVRAG,SPAST,SMYD5,CALM2,RACK1	red	VSMC_M1
GO:0043281	0.28	0.83	8	153	regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	1	PIH1D1,WDR35,RPS3,PDCD5,IFT57,NDUFA13,RFFL,RACK1	red	VSMC_M1
GO:0045619	0.28	0.85	6	117	regulation of lymphocyte differentiation	BP	1	PCID2,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0051053	0.28	0.86	5	94	negative regulation of DNA metabolic process	BP	1	RECQL5,RPS3,TNKS,PARP3,DCP2	red	VSMC_M1
GO:0003012	0.28	0.81	15	332	muscle system process	BP	1	SMAD4,SRI,FKBP1B,PAK1,CACNA2D1,EDNRA,P2RX4,CACNA1D,AKAP13,SSPN,KLHL41,MYL4,GJC1,CALM2,ERRFI1	red	VSMC_M1
GO:0001701	0.28	0.81	14	314	in utero embryonic development	BP	1	SMAD4,INPP5B,SF3B6,NDUFA2,CTR9,EDNRA,FBXW8,PSPH,ACTL6A,MYO18B,EMG1,ZMIZ1,KAT2A,B9D1	red	VSMC_M1
GO:0060348	0.28	0.83	8	172	bone development	BP	1	NPR2,TAL1,MMP16,AKAP13,KAT2A,RARA,MEF2D,GNAS	red	VSMC_M1
GO:0018130	0.28	0.75	116	2900	heterocycle biosynthetic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,SPIN1,NPR2,ZNF584,AHR,PGM3,ALAD,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,NAXD,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,ELOC,GMDS,PKIG,ELOVL2,PARP3,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,UROS,EGR2,KDM1A,ETV5,PTS,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,USP10,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,RCHY1,FGF10	red	VSMC_M1

GO:0019438	0.28	0.75	116	2902	aromatic compound biosynthetic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,SPIN1,NPR2,ZNF584,AHR,PGM3,ALAD,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,NAXD,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,ELOC,GMDS,PKIG,ELOVL2,PARP3,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,UROS,EGR2,KDM1A,ETV5,PTS,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,USP10,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,RCHY1,FGF10	red	VSMC_M1
GO:0042303	0.28	0.87	4	75	molting cycle	BP	1	SMAD4,TNFRSF19,HPSE,FGF10	red	VSMC_M1
GO:0042633	0.28	0.87	4	75	hair cycle	BP	1	SMAD4,TNFRSF19,HPSE,FGF10	red	VSMC_M1
GO:0061024	0.28	0.78	26	599	membrane organization	BP	1	DYNLT1,NDRG1,REEP2,CRIPT,UVRAG,SPAST,CSNK1D,PDCD5,VTI1B,TIMM10,TFG,TMEFF2,GCA,GRAMD1C,EMC9,NDUFA13,CTDNEP1,PRRT2,APOOL,TMEM11,MYO18A,OMA1,GOLPH3,GOSR1,IGHA2,ATP5IF1	red	VSMC_M1
GO:0072080	0.29	0.87	4	75	nephron tubule development	BP	1	SMAD4,FGF2,PROM1,CTNNBIP1	red	VSMC_M1
GO:0023051	0.29	0.75	100	2524	regulation of signaling	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,DYNLT1,EGR1,TCP11,CTNNA1,SRI,MAD2L1BP,MAP4K4,SPIN1,NPR2,INVS,RPS7,PIH1D1,FKBP1B,FGF2,ARHGAP35,IFT122,PCDH17,WBP2,PAK1,RPS3,PSD2,IL18BP,CSNK1D,HDAC3,SOCS2,PCID2,KCTD16,TNKS,CXCL12,TNFRSF19,COPS5,KMT5A,RHOF,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,GPAT3,TFG,TBC1D7,CDC73,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RHOD,ENSA,WDR11,CRTC3,SMYD2,ARHGDIB,EGR2,KDM1A,NDUFA13,MECOM,DYNC2H1,PELI2,ITFG2,ZMIZ1,KAT2A,ERC1,ITPKB,RARA,CTDNEP1,NR1D1,CDK5RAP3,PRRT2,PRDX2,STXBP4,CALM2,XRCC3,RFFL,MIER1,FBXO4,GOLPH3,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,GARNL3,FKBP1A,RACK1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CPNE1,RNF125,RITA1,LY96,FGF10	red	VSMC_M1
GO:0043412	0.29	0.75	121	3029	macromolecule modification	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,DCAF13,FGFR1OP,EGR1,NAA35,TRIOBP,MAP4K4,NPR2,ICK,UBE2M,ANKRD39,KMT5C,COPS9,PGM3,FAM161A,RPS7,PIH1D1,PARD3,ADCK2,FKBP1B,FGF2,TAL1,IRF2BP1,WBP2,PAK1,UVRAG,RPS3,ENGASE,RNF121,CSNK1D,HDAC3,SOCS2,CDK17,TNKS,COPS5,KMT5A,CTR9,EIF2A,SPRED1,CCNI,SMYD5,OGFOD1,FBXW8,PKIG,HLCS,TBC1D7,PARP3,VKORC1L1,CDC73,NPRL2,PTP4A2,WIPI1,ACTL6A,AKAP13,WDR5B,PPP1R8,ENSA,PPP1R11,KLHL41,SMYD2,DCAF17,BCCIP,FBXO45,EGR2,KDM1A,USP28,ANAPC16,EMG1,TRMT44,USP5,MECOM,TRIM4,UBA1,UVSSA,PELI2,TRRAP,FTSJ1,ZMIZ1,KAT2A,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,ANAPC13,RNF40,CDK5RAP3,PARP16,CALM2,CYP1A1,RNF138,HMG20A,RFFL,USP22,MIER1,FBXO4,MOB3A,ERRFI1,RBM15,UBE4B,WDR5,USP10,PTPA,DPH5,ALG14,DR1,MED31,URM1,FKBP1A,RACK1,HUS1,RPS20,ACP1,NOP10,RNF125,PTPRN2,RCHY1,FGF10	red	VSMC_M1
GO:0006355	0.29	0.75	96	2411	regulation of transcription, DNA-templated	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,MTERF2,SRI,SPIN1,ZNF584,AHR,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0050954	0.29	0.84	6	120	sensory perception of mechanical stimulus	BP	1	TRIOBP,CXCL12,TIMM10,P2RX4,CACNA1D,TPRN	red	VSMC_M1
GO:0010257	0.29	0.87	4	53	NADH dehydrogenase complex assembly	BP	1	NDUFA2,NDUFA10,NDUFA13,NDUFB7	red	VSMC_M1
GO:0032981	0.29	0.87	4	53	mitochondrial respiratory chain complex I assembly	BP	1	NDUFA2,NDUFA10,NDUFA13,NDUFB7	red	VSMC_M1
GO:2001252	0.29	0.86	4	72	positive regulation of chromosome organization	BP	1	MAD2L1BP,TAL1,TNKS,FBXO4	red	VSMC_M1
GO:0045621	0.29	0.86	4	72	positive regulation of lymphocyte differentiation	BP	1	PCID2,ZMIZ1,ITPKB,RARA	red	VSMC_M1
GO:1903506	0.29	0.75	96	2412	regulation of nucleic acid-templated transcription	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,MTERF2,SRI,SPIN1,ZNF584,AHR,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0042110	0.29	0.80	14	310	T cell activation	BP	1	ARG1,EGR1,TREML2,FKBP1B,RPS3,CD8B,IL20RB,RPS6,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,FKBP1A	red	VSMC_M1
GO:0030901	0.29	0.86	4	69	midbrain development	BP	1	FGF2,CSNK1D,KAT2A,CALM2	red	VSMC_M1
GO:1903364	0.29	0.83	7	137	positive regulation of cellular protein catabolic process	BP	1	CSNK1D,FBXW8,USP5,RNF40,RACK1,ATP5IF1,RCHY1	red	VSMC_M1
GO:0010948	0.29	0.81	11	237	negative regulation of cell cycle process	BP	1	MAD2L1BP,PCID2,TNKS,CDC73,USP28,KAT2A,CDK5RAP3,INTS3,XRCC3,FBXO4,HUS1	red	VSMC_M1

GO:0061138	0.29	0.83	7	147	morphogenesis of a branching epithelium	BP	1	SMAD4,FGF2,PAK1,EDNRA,CTNNBIP1,RBM15,FGF10	red	VSMC_M1
GO:0010565	0.29	0.85	5	95	regulation of cellular ketone metabolic process	BP	1	EGR1,COQ3,DGAT2,ERLIN2,NR1D1	red	VSMC_M1
GO:0051153	0.29	0.86	4	72	regulation of striated muscle cell differentiation	BP	1	SMAD4,PAK1,KAT2A,BHLHE41	red	VSMC_M1
GO:0032268	0.29	0.75	75	1819	regulation of cellular protein metabolic process	BP	1	SMAD4,CSNK2B,FGFR1OP,POLDIP3,EGR1,EIF3D,COPS9,MALSU1,FAM161A,ALAD,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,EIF2B4,WBP2,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,PCID2,PDCD5,CTR9,EIF2A,SPRED1,CCNI,OGFOD1,FBXW8,PKIG,TBC1D7,IFT57,AKAP13,PPP1R8,ENSA,PPP1R11,RBM4,BCCIP,KDM1A,EXOSC7,NDUFA13,USP5,PELI2,ZMIZ1,KAT2A,HSPA2,ITPKB,RARA,DCP2,RNF40,CDK5RAP3,EIF2B2,PARP16,CALM2,HMG20A,RFFL,FBXO4,MOB3A,ERRFI1,WDR5,PTPA,DPH5,FKBP1A,RACK1,HUS1,TIMP3,RPS20,WFDC3,ATP5IF1,PSENEN,RCHY1,FGF10	red	VSMC_M1
GO:0008037	0.29	0.85	5	97	cell recognition	BP	1	ACR,HSPA1L,ARHGAP35,MYO18A,IGHA2	red	VSMC_M1
GO:0050864	0.30	0.85	5	93	regulation of B cell activation	BP	1	AHR,KMT5C,PCID2,PARP3,IGHA2	red	VSMC_M1
GO:2001141	0.30	0.74	96	2416	regulation of RNA biosynthetic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,MTERF2,SRI,SPIN1,ZNF584,AHR,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:1901360	0.30	0.74	185	4575	organic cyclic compound metabolic process	BP	1	SMAD4,SGK1,KLF10,DCAF13,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,RPP25L,RCL1,SPIN1,NPR2,ZNF584,AHR,XPA,KMT5C,MEI4,PGM3,UTP11,ALAD,APLF,RPS7,PIH1D1,SF3B6,FGF2,TAL1,IRF2BP1,SNRPD2,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,WBP2,UVRAG,EBNA1BP2,DGAT2,RPS3,HNRNPL,NAXD,HDAC3,ERLIN2,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,PTCD2,ELOC,GOT2,PLRG1,RPS6,GMDS,PKIG,FARS2,HLCS,ELOVL2,ACOT8,PARP3,PRDM10,YARS,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,PPP1R8,GMPR2,RBM4,CRTC3,SMYD2,RPL35A,PES1,UROS,BCCIP,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,EMG1,TRMT44,PRDX6,MECOM,LSM4,UVSSA,ELK1,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,RARA,CECR2,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,INO80C,ARID3B,CYP1A1,ZNF287,RNF138,HMG20A,XRCC3,USP22,MIER1,FBXO4,MYO18A,YJU2,HMOX2,CTNNBIP1,RBM15,GSTM3,ZNF276,USP10,CDYL2,WWOX,CIZ1,DR1,RPF1,E2F4,SNORA80B,RNU105B,SNORD50B,IER2,NUDT21,MED31,ZBTB43,URM1,MYPOP,SLC25A1,HUS1,SCARNA5,SCARNA7,SCARNA10,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,SF3B5,AHNAK,RCHY1,FGF10	red	VSMC_M1
GO:0009057	0.30	0.76	46	1102	macromolecule catabolic process	BP	1	ACR,ZHX2,UBAP1,EEF1A1,ALAD,RPS7,PSMB2,FGF2,STAM,UVRAG,RNF121,CSNK1D,ERLIN2,PCID2,ELOC,HPSE,FBXW8,PPP1R8,PPP1R11,PSMA7,FBXO45,USP28,EXOSC7,NDUFA13,USP5,LSM4,UBA1,PSMB6,CECR2,NR1D1,DCP2,VPS37C,RNF40,CDK5RAP3,RFFL,USP22,FBXO4,RAB12,OMA1,UBE4B,USP10,RACK1,TIMP3,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0008285	0.30	0.77	24	548	negative regulation of cell population proliferation	BP	1	SMAD4,ARG1,CSNK2B,KLF10,NDRG1,HMGA1,CTNNA1,NUDT6,FGF2,PAK1,IL20RB,PDCD5,IFT57,CDC73,SMYD2,RARA,ETV3,SPARC,PMP22,FBXO4,CTNNBIP1,MED31,ATP5IF1,FGF10	red	VSMC_M1
GO:0030029	0.30	0.77	27	662	actin filament-based process	BP	1	SMAD4,CTNNA1,TRIOBP,SRI,ARHGAP35,FAM171A1,PAK1,NEB,CACNA2D1,CXCL12,TMSB10,ARFIP1,RHOF,CACNA1D,TMEFF2,AKAP13,RHOD,KLHL41,ARHGDIB,GJC1,MYO5C,PFN1,KANK4,MYO18A,ELMO3,TMSB4X,FGF10	red	VSMC_M1
GO:0051248	0.30	0.76	35	813	negative regulation of protein metabolic process	BP	1	FGFR1OP,PFDN6,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,FKBP1B,RPS3,PFDN1,PCID2,SPRED1,PKIG,ACOT8,PPP1R8,ENSA,PPP1R11,RBM4,KDM1A,EXOSC7,RARA,DCP2,CDK5RAP3,CALM2,HMG20A,RFFL,ERRFI1,WDR5,PTPA,FKBP1A,RACK1,TIMP3,RPS20,WFDC3	red	VSMC_M1
GO:0043502	0.30	0.86	4	71	regulation of muscle adaptation	BP	1	SMAD4,PAK1,P2RX4,ERRFI1	red	VSMC_M1
GO:2000278	0.30	0.84	5	95	regulation of DNA biosynthetic process	BP	1	FGF2,TNKS,PARP3,DCP2,FBXO4	red	VSMC_M1
GO:1901700	0.30	0.75	51	1234	response to oxygen-containing compound	BP	1	ARG1,CSNK2B,KLF10,EGR1,CTNNA1,SRI,MAP4K4,AHR,ALAD,PIH1D1,WDR35,FKBP1B,RECQL5,EIF2B4,WBP2,PAK1,DGAT2,RPS3,IL18BP,SOCS2,CACNA2D1,SP1,CXCL12,CTR9,GOT2,P2RX4,HLCS,PSPH,CDC73,GRAMD1C,ENSA,EGR2,KDM1A,NDUFA13,ELK1,RARA,NR1D1,RNF40,EIF2B2,PRDX2,STXBP4,SPARC,CYP1A1,RAB12,GOLPH3,ERRFI1,GNAS,RACK1,LY96,PTPRN2,FGF10	red	VSMC_M1
GO:0061326	0.30	0.86	4	77	renal tubule development	BP	1	SMAD4,FGF2,PROM1,CTNNBIP1	red	VSMC_M1

GO:0007399	0.30	0.74	73	1867	nervous system development	BP	1	SMAD4,SGK1,DYNLT1,ZHX2,NDRG1,CTNNA1,TRIOBP,MAP4K4,UTP11,RPS7,PARD3,FKBP1B,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,IFT122,PCDH17,EIF2B4,PAK1,SPAST,NRG2,COX7B,CSNK1D,SOCS2,CXCL12,EDNRA,SMN2,C21orf91,P2RX4,AMBRA1,FBXW8,IFT57,ARL3,UNC119B,ACTL6A,NIF3L1,KCNQ2,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,PTS,IL1RAP,DYNC2H1,PROM1,ZMIZ1,KAT2A,PFN1,PRTG,RARA,CECR2,NR1D1,MEF2D,CDK5RAP3,EIF2B2,FLRT2,CALM2,PMP22,HMG20A,TBC1D24,TPRN,GSTM3,WDR5,IER2,NREP,BHLHE41,CPNE1,RITA1,FGF10	red	VSMC_M1
GO:0060993	0.30	0.86	4	77	kidney morphogenesis	BP	1	SMAD4,FGF2,CTNNBIP1,FGF10	red	VSMC_M1
GO:1902105	0.30	0.81	9	193	regulation of leukocyte differentiation	BP	1	KLF10,TAL1,PCID2,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,CTNNBIP1	red	VSMC_M1
GO:0043254	0.30	0.78	16	361	regulation of protein-containing complex assembly	BP	1	TRIOBP,PIH1D1,TAL1,PAK1,RPS3,TMSB10,ARFIP1,ARL3,MAP2,PFN1,PRRT2,TUBB4A,KANK4,CTNNBIP1,RACK1,TMSB4X	red	VSMC_M1
GO:0010833	0.30	0.86	4	73	telomere maintenance via telomere lengthening	BP	1	TNKS,DCP2,FBXO4,NOP10	red	VSMC_M1
GO:0010959	0.30	0.80	12	263	regulation of metal ion transport	BP	1	SRI,FKBP1B,CACNA2D1,CXCL12,P2RX4,CACNA1D,STIMATE,HSPA2,CALM2,KCNAB2,FKBP1A,AHNAK	red	VSMC_M1
GO:0008585	0.30	0.86	4	72	female gonad development	BP	1	SMAD4,CTNNA1,EIF2B4,EIF2B2	red	VSMC_M1
GO:0051252	0.30	0.74	105	2654	regulation of RNA metabolic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,MTERF2,SRI,SPIN1,ZNF584,AHR,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HNRNPL,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,PTCD2,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,AHNAK,FGF10	red	VSMC_M1
GO:1901576	0.30	0.73	173	4324	organic substance biosynthetic process	BP	1	SMAD4,SGK1,ARG1,DYRK2,MTRF1L,KLF10,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,EIF3D,MTERF2,SRI,SPIN1,NPR2,ZNF584,RPS5,AHR,RPL28,EEF1A1,MALSU1,PGM3,ALAD,RPS7,COQ3,RPS11,PIH1D1,FGF2,TAL1,EFR3B,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,EIF2B4,WBP2,DGAT2,RPS3,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,RPS3A,ELOC,GOT2,EIF2A,RPS6,GPAT3,OGFOD1,GMDS,PKIG,FARS2,ELOVL2,ACOT8,PARP3,TMEFF2,PSPH,PRDM10,YARS,CDC73,EIF3I,WIPI1,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,RPL35A,UROS,RPL18A,EGR2,KDM1A,ETV5,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,MECOM,CHCHD1,ELK1,TRRAP,FTSJ1,RPS24,ZMIZ1,KAT2A,PFN1,ERC1,ITPKB,RARA,HDHD5,CTDNEP1,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,EIF2B2,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,CYP1A1,ZNF287,HMG20A,CHST9,COQ7,USP22,MIER1,FBXO4,GOLPH3,CTNNBIP1,RBM15,ZNF276,WDR5,USP10,DPH5,CDYL2,WWOX,CIZ1,ALG14,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,RACK1,ELOF1,ZNF614,COQ10A,ZNF180,RPS20,TMSB4X,BHLHE41,ZFP2,TMEM189,ADI1,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,RCHY1,FGF10	red	VSMC_M1
GO:0000422	0.30	0.85	4	71	autophagy of mitochondrion	BP	1	AMBRA1,WIPI1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0061726	0.30	0.85	4	71	mitochondrion disassembly	BP	1	AMBRA1,WIPI1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0030099	0.30	0.79	13	293	myeloid cell differentiation	BP	1	KLF10,TAL1,CEBPG,CTR9,C15orf41,RPS6,CDC73,ITPKB,RARA,CDK5RAP3,CTNNBIP1,RBM15,ATP5IF1	red	VSMC_M1
GO:0051640	0.31	0.77	19	447	organelle localization	BP	1	DYNLT1,PARD3,PCDH17,UVRAG,SPAST,CSNK1D,VTI1B,TFG,WIPI1,WDR11,MAP4,CEP19,MAP2,MYO5C,KAT2A,IL13RA2,RAB12,GOSR1,FGF10	red	VSMC_M1
GO:0051336	0.31	0.76	32	754	regulation of hydrolase activity	BP	1	CSNK2B,DYNLT1,MUT,MAP4K4,PIH1D1,WDR35,FKBP1B,FGF2,RPS3,PCID2,PDCD5,EDNRA,TBC1D7,IFT57,PPP1R11,MYL4,NDUFA13,PFN1,CDK5RAP3,CALM2,RFFL,PTPA,GARNL3,EVI5,FKBP1A,RACK1,TIMP3,WFDC3,ATP5IF1,PSENEN,PTPRN2,FGF10	red	VSMC_M1
GO:0019218	0.31	0.85	4	73	regulation of steroid metabolic process	BP	1	EGR1,DGAT2,ERLIN2,NR1D1	red	VSMC_M1
GO:0030968	0.31	0.85	4	69	endoplasmic reticulum unfolded protein response	BP	1	COPS5,CDK5RAP3,PARP16,RACK1	red	VSMC_M1
GO:0140352	0.31	0.76	26	618	export from cell	BP	1	SMAD4,SRI,MAP4K4,OSCP1,FKBP1B,STAM,PAK1,CXCL12,COPS5,VTI1B,ARFIP1,P2RX4,ARFGEF2,RAB9A,ENSA,ARL4D,NR1D1,PRRT2,STXBP4,CALM2,IL13RA2,RAB12,MYO18A,GOLPH3,PTPRN2,FGF10	red	VSMC_M1
GO:0008015	0.31	0.78	16	369	blood circulation	BP	1	SGK1,SRI,NPR2,WDR35,FKBP1B,ARHGAP35,CACNA2D1,CXCL12,EDNRA,P2RX4,CACNA1D,MYL4,GJC1,CALM2,CTNNBIP1,E2F4	red	VSMC_M1
GO:1901991	0.31	0.82	7	142	negative regulation of mitotic cell cycle phase transition	BP	1	MAD2L1BP,PCID2,CDC73,CDK5RAP3,INTS3,XRCC3,HUS1	red	VSMC_M1
GO:2000060	0.31	0.84	5	95	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	CSNK1D,FBXW8,USP5,RACK1,RCHY1	red	VSMC_M1
GO:0031401	0.31	0.75	31	747	positive regulation of protein modification process	BP	1	SMAD4,CSNK2B,EGR1,FAM161A,PIH1D1,FGF2,TAL1,WBP2,PAK1,RPS3,CSNK1D,HDAC3,CTR9,TBC1D7,AKAP13,KDM1A,PELI2,KAT2A,HSPA2,RNF40,CDK5RAP3,PARP16,CALM2,FBXO4,MOB3A,WDR5,PTPA,FKBP1A,RACK1,RCHY1,FGF10	red	VSMC_M1
GO:0045580	0.31	0.83	5	98	regulation of T cell differentiation	BP	1	ZMIZ1,KAT2A,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0032535	0.31	0.78	14	325	regulation of cellular component size	BP	1	TRIOBP,ARHGAP35,PAK1,NEB,CXCL12,TMSB10,SLC12A6,ARFIP1,KDM1A,MAP2,PFN1,KANK4,E2F4,TMSB4X	red	VSMC_M1
GO:1901987	0.31	0.78	14	311	regulation of cell cycle phase transition	BP	1	MAD2L1BP,PCID2,PLRG1,CDC73,USP28,HSPA2,CDK5RAP3,STXBP4,INTS3,CYP1A1,XRCC3,FBXO4,HUS1,FGF10	red	VSMC_M1
GO:0001654	0.31	0.79	12	280	eye development	BP	1	ZHX2,FGF2,ARHGAP35,SDK2,IFT122,SPRED1,ACTL6A,PROM1,RARA,CYP1A1,B9D1,FGF10	red	VSMC_M1

GO:0007093	0.31	0.82	6	117	mitotic cell cycle checkpoint signaling	BP	1	MAD2L1BP,PCID2,CDK5RAP3,INTS3,XRCC3,HUS1	red	VSMC_M1
GO:0050768	0.31	0.83	5	102	negative regulation of neurogenesis	BP	1	DYNLT1,CTNNA1,MAP2,PRTG,NR1D1	red	VSMC_M1
GO:0010648	0.31	0.74	43	1047	negative regulation of cell communication	BP	1	SMAD4,ARG1,DYRK2,RGS17,EGR1,CTNNA1,MAD2L1BP,MAP4K4,INVS,PIH1D1,FKBP1B,FGF2,ARHGAP35,IFT122,PCDH17,HDAC3,SOCS2,CXCL12,SPRED1,TBC1D7,NPRL2,CRTC3,KDM1A,NDUFA13,MECOM,ITFG2,NR1D1,CDK5RAP3,PRDX2,RFFL,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,FKBP1A,RACK1,TIMP3,TMSB4X,CPNE1,RNF125,RITA1,FGF10	red	VSMC_M1
GO:0030182	0.31	0.74	42	1067	neuron differentiation	BP	1	SMAD4,SGK1,DYNLT1,ZHX2,CTNNA1,TRIOBP,MAP4K4,PARD3,FKBP1B,TAL1,ARHGAP35,SDK2,PAK1,SPAST,CSNK1D,SOCS2,CXCL12,C21orf91,FBXW8,ARL3,NIF3L1,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,DYNC2H1,PROM1,ZMIZ1,RARA,CECR2,CDK5RAP3,FLRT2,PMP22,HMG20A,TBC1D24,TPRN,WDR5,IER2,NREP,CPNE1	red	VSMC_M1
GO:0016311	0.31	0.78	15	342	dephosphorylation	BP	1	CSNK2B,INPP5B,FKBP1B,PSPH,PTP4A2,PPP1R8,ENSA,PPP1R11,CTDNEP1,CDK5RAP3,CALM2,PTPA,FKBP1A,ACP1,PTPRN2	red	VSMC_M1
GO:0060047	0.31	0.80	8	172	heart contraction	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,MYL4,GJC1,CALM2	red	VSMC_M1
GO:0051345	0.32	0.77	19	440	positive regulation of hydrolase activity	BP	1	MUT,MAP4K4,WDR35,FGF2,RPS3,PDCD5,EDNRA,TBC1D7,IFT57,MYL4,NDUFA13,PFN1,CALM2,PTPA,GARNL3,EVI5,RACK1,PSENEN,FGF10	red	VSMC_M1
GO:0023057	0.32	0.74	43	1048	negative regulation of signaling	BP	1	SMAD4,ARG1,DYRK2,RGS17,EGR1,CTNNA1,MAD2L1BP,MAP4K4,INVS,PIH1D1,FKBP1B,FGF2,ARHGAP35,IFT122,PCDH17,HDAC3,SOCS2,CXCL12,SPRED1,TBC1D7,NPRL2,CRTC3,KDM1A,NDUFA13,MECOM,ITFG2,NR1D1,CDK5RAP3,PRDX2,RFFL,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,FKBP1A,RACK1,TIMP3,TMSB4X,CPNE1,RNF125,RITA1,FGF10	red	VSMC_M1
GO:1904062	0.32	0.79	11	241	regulation of cation transmembrane transport	BP	1	SRI,FKBP1B,CACNA2D1,CACNA1D,STIMATE,HSPA2,CALM2,KCNAB2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1
GO:0009306	0.32	0.78	12	266	protein secretion	BP	1	SRI,MAP4K4,FKBP1B,ARFIP1,ENSA,ARL4D,NR1D1,STXBP4,RAB12,MYO18A,GOLPH3,PTPRN2	red	VSMC_M1
GO:0035592	0.32	0.78	12	266	establishment of protein localization to extracellular region	BP	1	SRI,MAP4K4,FKBP1B,ARFIP1,ENSA,ARL4D,NR1D1,STXBP4,RAB12,MYO18A,GOLPH3,PTPRN2	red	VSMC_M1
GO:0002695	0.32	0.82	6	118	negative regulation of leukocyte activation	BP	1	ARG1,IL20RB,PARP3,NR1D1,PRDX2,IL13RA2	red	VSMC_M1
GO:0001657	0.32	0.84	4	78	ureteric bud development	BP	1	SMAD4,FGF2,RARA,CTNNBIP1	red	VSMC_M1
GO:0009968	0.32	0.74	40	973	negative regulation of signal transduction	BP	1	SMAD4,ARG1,DYRK2,RGS17,EGR1,CTNNA1,MAD2L1BP,INVS,PIH1D1,FGF2,ARHGAP35,IFT122,HDAC3,SOCS2,CXCL12,SPRED1,TBC1D7,NPRL2,CRTC3,KDM1A,NDUFA13,MECOM,ITFG2,NR1D1,CDK5RAP3,PRDX2,RFFL,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,FKBP1A,RACK1,TIMP3,TMSB4X,CPNE1,RNF125,RITA1,FGF10	red	VSMC_M1
GO:0001935	0.32	0.82	6	123	endothelial cell proliferation	BP	1	ARG1,FGF2,SP1,CXCL12,SPARC,ATP5IF1	red	VSMC_M1
GO:0150063	0.32	0.78	12	282	visual system development	BP	1	ZHX2,FGF2,ARHGAP35,SDK2,IFT122,SPRED1,ACTL6A,PROM1,RARA,CYP1A1,B9D1,FGF10	red	VSMC_M1
GO:0048729	0.32	0.76	20	490	tissue morphogenesis	BP	1	SMAD4,CSNK2B,RPS7,FGF2,TAL1,ARHGAP35,IFT122,PAK1,EDNRA,PTCD2,IFT57,TMEFF2,KAT2A,PFN1,RARA,CECR2,CTNNBIP1,RBM15,FKBP1A,FGF10	red	VSMC_M1
GO:2000779	0.32	0.84	4	76	regulation of double-strand break repair	BP	1	KMT5C,RECQL5,PARP3,KDM1A	red	VSMC_M1
GO:0071396	0.32	0.76	18	422	cellular response to lipid	BP	1	ARG1,AHR,WDR35,WBP2,PAK1,DGAT2,CTR9,CDC73,GRAMD1C,KDM1A,NDUFA13,ELK1,ZMIZ1,RARA,NR1D1,PRDX2,ERRFI1,LY96	red	VSMC_M1
GO:0034765	0.32	0.77	14	323	regulation of ion transmembrane transport	BP	1	SRI,KCNF1,FKBP1B,CACNA2D1,CACNA1D,STIMATE,SCN3A,KCNQ2,HSPA2,CALM2,KCNAB2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1
GO:0060284	0.32	0.76	16	384	regulation of cell development	BP	1	SMAD4,DYNLT1,TCP11,CTNNA1,TRIOBP,NPR2,PAK1,CXCL12,FBXW8,EGR2,KDM1A,ETV5,MAP2,PRTG,NR1D1,BHLHE41	red	VSMC_M1
GO:0097190	0.33	0.75	21	471	apoptotic signaling pathway	BP	1	DYRK2,CTNNA1,RPS7,PIH1D1,WDR35,RPS3,CXCL12,PDCD5,P2RX4,TMEM117,KDM1A,USP28,NDUFA13,PRDX2,RFFL,UBE4B,WWOX,RACK1,TIMP3,ATP5IF1,FGF10	red	VSMC_M1
GO:1901990	0.33	0.78	11	237	regulation of mitotic cell cycle phase transition	BP	1	MAD2L1BP,PCID2,PLRG1,CDC73,HSPA2,CDK5RAP3,INTS3,CYP1A1,XRCC3,HUS1,FGF10	red	VSMC_M1
GO:0072163	0.33	0.84	4	79	mesonephric epithelium development	BP	1	SMAD4,FGF2,RARA,CTNNBIP1	red	VSMC_M1
GO:0072164	0.33	0.84	4	79	mesonephric tubule development	BP	1	SMAD4,FGF2,RARA,CTNNBIP1	red	VSMC_M1
GO:0000377	0.33	0.78	12	255	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1	SF3B6,SNRPD2,HNRNPL,SMN2,PLRG1,RBM4,KDM1A,PRDX6,LSM4,YJU2,RBM15,SF3B5	red	VSMC_M1
GO:0000398	0.33	0.78	12	255	mRNA splicing, via spliceosome	BP	1	SF3B6,SNRPD2,HNRNPL,SMN2,PLRG1,RBM4,KDM1A,PRDX6,LSM4,YJU2,RBM15,SF3B5	red	VSMC_M1
GO:0046545	0.33	0.84	4	75	development of primary female sexual characteristics	BP	1	SMAD4,CTNNA1,EIF2B4,EIF2B2	red	VSMC_M1
GO:0090150	0.33	0.78	10	210	establishment of protein localization to membrane	BP	1	REEP2,PARD3,PAK1,PDCD5,TIMM10,EMC9,NDUFA13,VPS37C,GOLPH3,RACK1	red	VSMC_M1
GO:0043122	0.33	0.79	9	197	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	TNFRSF19,TFG,AKAP13,PELI2,NR1D1,MIER1,USP10,FKBP1A,CPNE1	red	VSMC_M1
GO:0002250	0.33	0.78	11	244	adaptive immune response	BP	1	ARG1,IL1RL1,AHR,KMT5C,IL18BP,CD8B,IL20RB,PARP3,IL13RA2,RNF125,IGHA2	red	VSMC_M1
GO:0051348	0.33	0.78	10	219	negative regulation of transferase activity	BP	1	FGFR1OP,RPS7,SPRED1,PKIG,PARP3,NPRL2,CDK5RAP3,ERRFI1,RACK1,RPS20	red	VSMC_M1
GO:0018193	0.33	0.73	41	997	peptidyl-amino acid modification	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,FGFR1OP,EGR1,NAA35,KMT5C,PIH1D1,PARD3,FKBP1B,WBP2,PAK1,CSNK1D,TNKS,KMT5A,CTR9,SPRED1,SMYD5,OGFOD1,VKORC1L1,ACTL6A,WDR5B,SMYD2,EGR2,KDM1A,MECOM,TRAP,ZMIZ1,KAT2A,CALM2,HMG20A,USP22,ERRFI1,WDR5,PTPA,DPH5,DR1,FKBP1A,RACK1,FGF10	red	VSMC_M1
GO:0002009	0.33	0.76	17	412	morphogenesis of an epithelium	BP	1	SMAD4,CSNK2B,RPS7,FGF2,ARHGAP35,IFT122,PAK1,EDNRA,IFT57,TMEFF2,KAT2A,PFN1,RARA,CECR2,CTNNBIP1,RBM15,FGF10	red	VSMC_M1
GO:0010721	0.33	0.81	6	130	negative regulation of cell development	BP	1	DYNLT1,CTNNA1,NPR2,MAP2,PRTG,NR1D1	red	VSMC_M1

GO:0016043	0.33	0.70	182	4652	cellular component organization	BP	1	SMAD4,SGK1,MTRF1L,CSNK2B,HSPA1L,DYNLT1,FGFR1OP,PFDN6,MEI1,NDRG1,HMGA1,TAF11,REEP2,CTNNA1,TRIOBP,EIF3D,MAD2L1BP,MAP4K4,SPIN1,ICK,CLTA,RPS5,XPA,CRIPT,MEI4,FAM161A,ALAD,KCNF1,PIH1D1,PARD3,WDR35,FKBP1B,TAL1,PMPCB,ARHGAP35,SNRPD2,SDK2,STAM,RAB30,FAM171A1,IFT122,RECQL5,PCDH17,PAK1,UVRAG,RPS3,VDAC3,SPAST,NEB,PFDN1,NDUFA2,CSNK1D,HDAC3,SOCS2,PCID2,KCTD16,TNKS,MTIF3,CXCL12,MTFR1,KMT5A,PDCD5,VTI1B,SMN2,TIMM10,TMSB10,SLC12A6,PTCD2,ARFIP1,RHOF,C21orf91,EIF2A,TLL1,MMP16,OGFOD1,AMBRA1,FBXW8,TFG,ACOT8,TBC1D7,IFT57,PARP3,TMEFF2,ARL3,UNC119B,GCA,FAM118B,CDC73,NPRL2,EIF3I,GRAMD1C,CFAP410,WIPI1,ARFGEF2,COX19,ACTL6A,AKAP13,RHOD,EMC9,RAE1,KLHL41,WDR11,CRTC3,NDUFA10,IFT46,MTFR1L,BCCIP,ARHGDIB,MAP4,FBXO45,CEP19,EGR2,KDM1A,MAP2,CABIN1,IL1RAP,GJC1,NDUFA13,EMG1,MECOM,RP2,LSM4,DYNC2H1,TOP3B,ZMIZ1,MYO5C,KAT2A,PFN1,ERC1,HSPA2,CTDNEP1,CECR2,DCP2,NDUFB7,VPS37C,CDK5RAP3,DNAL1,PRRT2,INO80E,MBTD1,FLRT2,APOOL,GATAD2B,SUPT4H1,SPARC,INO80C,PMP22,HMG20A,B9D1,XRCC3,TMEM11,FBXO4,TUBB4A,KANK4,MYO18A,OMA1,GOLPH3,GOSR1,YJU2,TBC1D24,TPRN,RAB39B,DNLZ,CTNNBIP1,WDR5,PTPA,DR1,ELMO3,E2F4,NUDT21,FKBP1A,RACK1,HUS1,NREP,KAZALD1,TMSB4X,NOP10,CPNE1,TOMM7,IGHA2,ATP5IF1,FGF10	red	VSMC_M1
GO:0009719	0.33	0.72	48	1202	response to endogenous stimulus	BP	1	SMAD4,ARG1,ACR,CSNK2B,KLF10,EGR1,CTNNA1,AHR,EEF1A1,ALAD,FGF2,RECQL5,EIF2B4,WBP2,PAK1,CSNK1D,SOCS2,CACNA2D1,SP1,CXCL12,PDCD5,GOT2,P2RX4,SPRED1,UROS,EGR2,KDM1A,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,RNF40,EIF2B2,FLRT2,STXBP4,SPARC,RAB12,GOLPH3,ERRFI1,GSTM3,WWOX,IER2,FKBP1A,GNAS,NREP,TIMP3,FGF10	red	VSMC_M1
GO:0046394	0.33	0.78	10	213	carboxylic acid biosynthetic process	BP	1	ERLIN2,LTA4H,GOT2,ELOVL2,ACOT8,PSPH,UROS,NR1D1,CYP1A1,ADI1	red	VSMC_M1
GO:0032940	0.33	0.74	24	574	secretion by cell	BP	1	SMAD4,SRI,MAP4K4,FKBP1B,STAM,PAK1,CXCL12,COPS5,VTI1B,ARFIP1,P2RX4,ARFGEF2,RAB9A,ENSA,ARL4D,NR1D1,PRRT2,STXBP4,IL13RA2,RAB12,MYO18A,GOLPH3,PTPRN2,FGF10	red	VSMC_M1
GO:0016071	0.33	0.74	25	586	mRNA metabolic process	BP	1	ZHX2,SF3B6,SNRPD2,TSEN54,HNRNPL,PCID2,CEBPG,CTR9,SMN2,PTCD2,PLRG1,CDC73,PPP1R8,RBM4,KDM1A,EXOSC7,PRDX6,LSM4,DCP2,RNF40,SUPT4H1,YJU2,RBM15,NUDT21,SF3B5	red	VSMC_M1
GO:0001938	0.34	0.83	4	78	positive regulation of endothelial cell proliferation	BP	1	ARG1,FGF2,SP1,CXCL12	red	VSMC_M1
GO:0046328	0.34	0.81	5	104	regulation of JNK cascade	BP	1	MAP4K4,HDAC3,TNFRSF19,COPS5,MECOM	red	VSMC_M1
GO:0050767	0.34	0.77	12	285	regulation of neurogenesis	BP	1	DYNLT1,CTNNA1,PAK1,CXCL12,FBXW8,EGR2,KDM1A,ETV5,MAP2,PRTG,NR1D1,BHLHE41	red	VSMC_M1
GO:0048880	0.34	0.76	12	286	sensory system development	BP	1	ZHX2,FGF2,ARHGAP35,SDK2,IFT122,SPRED1,ACTL6A,PROM1,RARA,CYP1A1,B9D1,FGF10	red	VSMC_M1
GO:1901362	0.34	0.70	119	3012	organic cyclic compound biosynthetic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,SPIN1,NPR2,ZNF584,AHR,PGM3,ALAD,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,NAXD,HDAC3,ERLIN2,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,ELOC,GMDS,PKIG,ELOVL2,ACOT8,PARP3,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,UROS,EGR2,KDM1A,ETV5,PTS,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,CYP1A1,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,USP10,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,ATP5IF1,RCHY1,FGF10	red	VSMC_M1
GO:0070727	0.34	0.71	59	1462	cellular macromolecule localization	BP	1	HSPA1L,REEP2,CTNNA1,CLTA,XPA,INVS,CRIPT,PIH1D1,PARD3,WDR35,EFR3B,PMPCB,STAM,IFT122,PAK1,CSNK1D,HDAC3,PCID2,TNKS,RAB28,PDCD5,VTI1B,TIMM10,TMSB10,ARFIP1,PLRG1,PKIG,PARP3,ARL3,WIPI1,EMC9,ARL4C,WDR11,EGR2,KDM1A,MAP2,AP1S1,NDUFA13,ARL4D,DYNC2H1,SCG3,CTDNEP1,VPS37C,CDK5RAP3,COPZ2,STXBP4,SNUPN,FBXO4,RAB12,GOLPH3,KCNAB2,DNLZ,CIZ1,EVI5,RACK1,TMSB4X,TOMM7,ATP5IF1,FGF10	red	VSMC_M1
GO:0051961	0.34	0.81	5	106	negative regulation of nervous system development	BP	1	DYNLT1,CTNNA1,MAP2,PRTG,NR1D1	red	VSMC_M1
GO:0022411	0.34	0.75	16	375	cellular component disassembly	BP	1	MTRF1L,HMGA1,TRIOBP,MAP4K4,UVRAG,SPAST,MTIF3,OGFOD1,AMBRA1,WIPI1,HSPA2,CTDNEP1,CECR2,CDK5RAP3,TOMM7,ATP5IF1	red	VSMC_M1
GO:0007249	0.34	0.77	10	222	I-kappaB kinase/NF-kappaB signaling	BP	1	TNFRSF19,TFG,AKAP13,PELI2,ERC1,NR1D1,MIER1,USP10,FKBP1A,CPNE1	red	VSMC_M1
GO:0071692	0.34	0.76	12	271	protein localization to extracellular region	BP	1	SRI,MAP4K4,FKBP1B,ARFIP1,ENSA,ARL4D,NR1D1,STXBP4,RAB12,MYO18A,GOLPH3,PTPRN2	red	VSMC_M1
GO:0035821	0.34	0.83	4	75	modulation of process of other organism	BP	1	ARG1,TAF11,SP1,RAB9A	red	VSMC_M1
GO:0051225	0.34	0.81	5	101	spindle assembly	BP	1	RPS3,CSNK1D,HDAC3,TNKS,BCCIP	red	VSMC_M1

GO:0044237	0.34	0.69	316	7918	cellular metabolic process	BP	1	CS,SMAD4,SGK1,ARG1,DYRK2,MTRF1L,ACR,CSNK2B,KLF10,DCAF13,FGFR1OP,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,KCTD20,POLR2F,TRIOBP,TST,EIF3D,MTERF2,SRI,UBAP1,RPP25L,RCL1,MUT,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,COX5B,SLC25A51,ANKRD39,AHR,XPA,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,COQ3,PSMB2,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,FGF2,TAL1,EFR3B,PMPCB,IRF2BP1,SNRPD2,STAM,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,ENGASE,HNRNPL,COX7B,RNF121,NDUFA2,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,MTFR1,COPS5,CEBPG,ZNF341,KMT5A,PDCD5,CTR9,VTI1B,SMN2,PTCD2,RPS3A,ELOC,GOT2,P2RX4,PLRG1,EIF2A,SPRED1,CCNI,RPS6,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,PKIG,FARS2,HLCS,ELOVL2,ACOT8,TBC1D7,IFT57,PARP3,PSPH,PRDM10,VKORC1L1,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,TGIF1,WDR5B,NIF3L1,PPP1R8,ENSA,GMPR2,PPP1R11,KLHL41,RBM4,CRTC3,SMYD2,PSMA7,NDUFA10,DCAF17,RPL35A,MTFR1L,PES1,UROS,BCCIP,RPL18A,FBXO45,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,ANAPC16,EMG1,TRMT44,PRDX6,USP5,MECOM,CHCHD1,LSM4,TRIM4,UBA1,UVSSA,ELK1,PELI2,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,PSMB6,ERC1,HSPA2,ITPKB,RARA,HDHD5,CTDNEP1,CECR2,NR1D1,DCP2,NDUFB7,VPS37C,ETV3,SAMD1,ANAPC13,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,INO80	red	VSMC_M1
GO:2001236	0.34	0.80	6	121	regulation of extrinsic apoptotic signaling pathway	BP	1	CTNNA1,PRDX2,RFFL,WWOX,TIMP3,FGF10	red	VSMC_M1
GO:0051052	0.34	0.76	13	297	regulation of DNA metabolic process	BP	1	KMT5C,APLF,FGF2,RECQL5,RPS3,TNKS,CEBPG,PARP3,KDM1A,DCP2,FBXO4,CIZ1,FGF10	red	VSMC_M1
GO:0030073	0.34	0.79	7	149	insulin secretion	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4,PTPRN2	red	VSMC_M1
GO:0034654	0.34	0.70	112	2841	nucleobase-containing compound biosynthetic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,SPIN1,NPR2,ZNF584,AHR,PGM3,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,NAXD,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,ELOC,GMDS,PKIG,ELOVL2,PARP3,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PARP16,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,USP10,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,SLC25A1,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,NOP10,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,RCHY1,FGF10	red	VSMC_M1
GO:0016053	0.34	0.77	10	215	organic acid biosynthetic process	BP	1	ERLIN2,LTA4H,GOT2,ELOVL2,ACOT8,PSPH,UROS,NR1D1,CYP1A1,ADI1	red	VSMC_M1
GO:0001510	0.34	0.83	4	73	RNA methylation	BP	1	EMG1,TRMT44,FTSJ1,RBM15	red	VSMC_M1
GO:0043255	0.35	0.82	4	78	regulation of carbohydrate biosynthetic process	BP	1	DYRK2,DGAT2,KAT2A,WDR5	red	VSMC_M1
GO:0051235	0.35	0.76	11	248	maintenance of location	BP	1	SRI,FKBP1B,FGF2,UVRAG,DGAT2,TMSB10,CALM2,GOLPH3,CIZ1,FKBP1A,TMSB4X	red	VSMC_M1
GO:0006399	0.35	0.78	8	162	tRNA metabolic process	BP	1	RPP25L,TSEN54,FARS2,YARS,EXOSC7,TRMT44,FTSJ1,URM1	red	VSMC_M1
GO:0050708	0.35	0.77	9	200	regulation of protein secretion	BP	1	SRI,MAP4K4,FKBP1B,ARFIP1,ENSA,NR1D1,STXBP4,MYO18A,GOLPH3	red	VSMC_M1
GO:0000375	0.35	0.76	12	259	RNA splicing, via transesterification reactions	BP	1	SF3B6,SNRPD2,HNRNPL,SMN2,PLRG1,RBM4,KDM1A,PRDX6,LSM4,YJU2,RBM15,SF3B5	red	VSMC_M1
GO:0065003	0.35	0.71	51	1210	protein-containing complex assembly	BP	1	SMAD4,CSNK2B,PFDN6,TAF11,TRIOBP,EIF3D,CLTA,RPS5,ALAD,KCNF1,PIH1D1,PARD3,TAL1,SNRPD2,PAK1,UVRAG,RPS3,SPAST,NDUFA2,CSNK1D,KCTD16,CXCL12,SMN2,TMSB10,ARFIP1,TFG,ARL3,CDC73,EIF3I,COX19,CRTC3,NDUFA10,MAP2,CABIN1,IL1RAP,NDUFA13,LSM4,PFN1,NDUFB7,DNAL1,PRRT2,TUBB4A,KANK4,OMA1,YJU2,CTNNBIP1,DR1,NUDT21,FKBP1A,RACK1,TMSB4X	red	VSMC_M1
GO:0001763	0.35	0.79	7	157	morphogenesis of a branching structure	BP	1	SMAD4,FGF2,PAK1,EDNRA,CTNNBIP1,RBM15,FGF10	red	VSMC_M1
GO:0032269	0.35	0.72	32	760	negative regulation of cellular protein metabolic process	BP	1	FGFR1OP,COPS9,MALSU1,ALAD,RPS7,PIH1D1,PARD3,FKBP1B,RPS3,PCID2,SPRED1,PKIG,PPP1R8,ENSA,PPP1R11,RBM4,KDM1A,EXOSC7,RARA,DCP2,CDK5RAP3,CALM2,HMG20A,RFFL,ERRFI1,WDR5,PTPA,FKBP1A,RACK1,TIMP3,RPS20,WFDC3	red	VSMC_M1
GO:0000086	0.35	0.79	6	124	G2/M transition of mitotic cell cycle	BP	1	ENSA,HSPA2,CDK5RAP3,INTS3,CALM2,HUS1	red	VSMC_M1
GO:0033209	0.35	0.82	4	75	tumor necrosis factor-mediated signaling pathway	BP	1	TNFRSF19,RFFL,TMSB4X,CPNE1	red	VSMC_M1
GO:0098655	0.35	0.72	26	623	cation transmembrane transport	BP	1	SRI,COX5B,KCNF1,FKBP1B,FGF2,PMPCB,COX7B,CACNA2D1,SLC12A6,P2RX4,CACNA1D,STIMATE,SCN3A,KCNQ2,SCNN1A,CLCN5,HSPA2,CALM2,CACHD1,KCNAB2,COX4I1,FKBP1A,SLC25A28,ATP6V1G1,TMSB4X,AHNAK	red	VSMC_M1
GO:1901701	0.35	0.71	36	887	cellular response to oxygen-containing compound	BP	1	ARG1,KLF10,EGR1,CTNNA1,SRI,MAP4K4,AHR,PIH1D1,WDR35,FKBP1B,RECQL5,PAK1,DGAT2,RPS3,IL18BP,SOCS2,CACNA2D1,SP1,CTR9,P2RX4,CDC73,GRAMD1C,KDM1A,NDUFA13,ELK1,RARA,NR1D1,PRDX2,STXBP4,RAB12,GOLPH3,ERRFI1,GNAS,RACK1,LY96,PTPRN2	red	VSMC_M1
GO:0001818	0.35	0.77	9	195	negative regulation of cytokine production	BP	1	ARG1,IL1RL1,IL20RB,CUEDC2,PPP1R11,RARA,ERRFI1,TMSB4X,RNF125	red	VSMC_M1
GO:0009617	0.35	0.74	16	362	response to bacterium	BP	1	ARG1,ALAD,WDR35,IL18BP,CTR9,CDC73,PPP1R11,RARA,NR1D1,PRDX2,SPARC,CYP1A1,WFDC3,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0030111	0.35	0.75	12	277	regulation of Wnt signaling pathway	BP	1	EGR1,SPIN1,INVS,FGF2,CSNK1D,TNKS,CDC73,CTDNEP1,CTNNBIP1,WWOX,RACK1,FGF10	red	VSMC_M1

GO:0050896	0.35	0.68	229	5876	response to stimulus	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,ACR,CSNK2B,KLF10,HSPA1L,DYNLT1,POLR3H,NDRG1,HMGA1,GNG5,EGR1,TCP11,RHPN1,CTNNA1,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,AHR,XPA,CORO2A,INVS,KMT5C,EEF1A1,COPS9,FAM161A,INPP5B,ALAD,APLF,RPS7,OSCP1,PSMB2,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,ADGRF3,STAM,NR2C2,RAB30,IFT122,RECQL5,EIF2B4,WBP2,NRBP1,PAK1,UVRAG,DGAT2,RPS3,PSD2,NRG2,IL18BP,RNF121,CSNK1D,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,TNKS,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,CD8B,IL20RB,KMT5A,PDCD5,CTR9,EDNRA,SLC12A6,RHOF,GOT2,P2RX4,RRAS2,EIF2A,CACNA1D,SPRED1,RPS6,STIMATE,HPSE,GPAT3,AMBRA1,GMDS,TFG,PKIG,TMEM117,HLCS,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PSPH,VKORC1L1,CUEDC2,ARL3,CDC73,NPRL2,SORCS1,GRAMD1C,ARHGAP31,CFAP410,WIPI1,ARFGEF2,ACTL6A,AKAP13,RAB9A,RHOD,TGIF1,RAE1,ENSA,PPP1R11,WDR11,RBM4,CRTC3,SMYD2,UROS,BCCIP,RPL18A,ARHGDIB,FBXO45,EGR2,INO80D,KDM1A,ETV5,USP28,AP1S1,CABIN1,IL1RAP,NDUFA13,PRDX6,MECOM,TRIM4,UBA1,DYNC2H1,UVSSA,ELK1,SCNN1A,PELI2,TRRAP,ITFG2,ZMIZ1,KAT2A,ERC1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,ETV3,RNF40,CDK5RAP3,EIF2B2,INO80E,SPG21,PARP16,PRDX2,FLRT2,STXBP4,INTS3,CALM2,SPARC,INO80C,CYP1A1,RNF138,B9D1,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,RAB12,OMA1,GOLPH3,YJU2,HMOX2,TBC1D24,ITGAE,MOB3A,GFER,RAB39B,ERRFI1,CTNNBIP1,RBM15,UBE4B,GSTM3,COX4I1,USP10,WWOX,GARNL3,IER2,FKBP1A,GNAS,RACK1,HUS1,SRXN1,ATP6V1G1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CNIH1,CPNE1,WFDC3,TOMM	red	VSMC_M1
GO:0098754	0.35	0.80	5	90	detoxification	BP	1	OSCP1,PRDX6,PRDX2,GSTM3,SRXN1	red	VSMC_M1
GO:0002832	0.35	0.82	4	77	negative regulation of response to biotic stimulus	BP	1	ARG1,AHR,PRDX2,RNF125	red	VSMC_M1
GO:0006351	0.35	0.69	99	2521	transcription, DNA-templated	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,SPIN1,ZNF584,AHR,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0032091	0.35	0.82	4	76	negative regulation of protein binding	BP	1	KDM1A,MAP2,CTNNBIP1,RACK1	red	VSMC_M1
GO:0050678	0.35	0.75	12	275	regulation of epithelial cell proliferation	BP	1	ARG1,FGF2,SP1,CXCL12,IFT57,CDC73,NR1D1,STXBP4,SPARC,ERRFI1,ATP5IF1,FGF10	red	VSMC_M1
GO:0050796	0.35	0.79	6	127	regulation of insulin secretion	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4	red	VSMC_M1
GO:0097659	0.35	0.69	99	2522	nucleic acid-templated transcription	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,SPIN1,ZNF584,AHR,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0006605	0.35	0.75	12	262	protein targeting	BP	1	HSPA1L,PARD3,PMPCB,PAK1,PDCD5,TIMM10,NDUFA13,VPS37C,STXBP4,DNLZ,TOMM7,ATP5IF1	red	VSMC_M1
GO:0007369	0.36	0.79	6	138	gastrulation	BP	1	SMAD4,TAL1,CTR9,RPS6,CDC73,RACK1	red	VSMC_M1
GO:0042692	0.36	0.75	13	303	muscle cell differentiation	BP	1	SMAD4,PAK1,NEB,PTCD2,AKAP13,MYO18B,KLHL41,RBM4,KDM1A,KAT2A,RARA,BHLHE41,FGF10	red	VSMC_M1
GO:1901988	0.36	0.76	9	201	negative regulation of cell cycle phase transition	BP	1	MAD2L1BP,PCID2,CDC73,USP28,CDK5RAP3,INTS3,XRCC3,FBXO4,HUS1	red	VSMC_M1
GO:0010952	0.36	0.78	7	142	positive regulation of peptidase activity	BP	1	WDR35,RPS3,PDCD5,IFT57,NDUFA13,RACK1,PSENEN	red	VSMC_M1
GO:0045935	0.36	0.69	59	1489	positive regulation of nucleobase-containing compound metabolic process	BP	1	SMAD4,KLF10,ZFAT,HMGA1,TAF11,EGR1,ZNF76,SPIN1,AHR,KMT5C,APLF,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,RPS3,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PARP3,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,EXOSC7,PRDX6,MECOM,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,DCP2,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,FBXO4,RBM15,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,ELOF1,TMSB4X,FGF10	red	VSMC_M1
GO:0051726	0.36	0.71	34	827	regulation of cell cycle	BP	1	MAD2L1BP,NPR2,NUDT6,FGF2,TAL1,UVRAG,SPAST,PCID2,CDK17,TNKS,COPS5,PLRG1,CCNI,PARP3,CDC73,RAE1,PES1,BCCIP,USP28,MECOM,KAT2A,HSPA2,RARA,CDK5RAP3,STXBP4,INTS3,CALM2,CYP1A1,XRCC3,USP22,FBXO4,RACK1,HUS1,FGF10	red	VSMC_M1
GO:0034644	0.36	0.81	4	77	cellular response to UV	BP	1	XPA,COPS9,KDM1A,USP28	red	VSMC_M1
GO:0033993	0.36	0.71	27	657	response to lipid	BP	1	ARG1,ACR,CSNK2B,AHR,ALAD,WDR35,WBP2,PAK1,DGAT2,IL18BP,SOCS2,CTR9,PSPH,CDC73,GRAMD1C,KDM1A,NDUFA13,ELK1,ZMIZ1,RARA,NR1D1,PRDX2,SPARC,CYP1A1,ERRFI1,LY96,FGF10	red	VSMC_M1
GO:0110053	0.36	0.75	10	237	regulation of actin filament organization	BP	1	TRIOBP,ARHGAP35,PAK1,CXCL12,TMSB10,ARFIP1,TMEFF2,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0120162	0.36	0.81	4	78	positive regulation of cold-induced thermogenesis	BP	1	HDAC3,KDM1A,OMA1,GNAS	red	VSMC_M1
GO:0016197	0.36	0.76	9	209	endosomal transport	BP	1	STAM,VTI1B,ARFIP1,RAB9A,ARL4C,FAM45A,ERC1,GOSR1,EVI5	red	VSMC_M1
GO:1903050	0.36	0.76	9	192	regulation of proteolysis involved in cellular protein catabolic process	BP	1	ALAD,RPS7,CSNK1D,FBXW8,USP5,RNF40,RACK1,ATP5IF1,RCHY1	red	VSMC_M1
GO:0008033	0.37	0.78	6	117	tRNA processing	BP	1	RPP25L,TSEN54,FARS2,TRMT44,FTSJ1,URM1	red	VSMC_M1

GO:0051656	0.37	0.73	14	334	establishment of organelle localization	BP	1	DYNLT1,PARD3,SPAST,CSNK1D,TFG,WIPI1,WDR11,MAP4,CEP19,MAP2,MYO5C,IL13RA2,GOSR1,FGF10	red	VSMC_M1
GO:0008152	0.37	0.67	337	8467	metabolic process	BP	1	CS,SMAD4,SGK1,ARG1,DYRK2,MTRF1L,ACR,CSNK2B,KLF10,DCAF13,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,KCTD20,POLR2F,TRIOBP,TST,EIF3D,MTERF2,SRI,UBAP1,RPP25L,RCL1,MUT,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,COX5B,SLC25A51,ANKRD39,ALDH1B1,AHR,XPA,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,COQ3,PSMB2,YAE1,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,FGF2,TAL1,EFR3B,PMPCB,IRF2BP1,SNRPD2,STAM,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,ENGASE,HNRNPL,SPAST,PFDN1,COX7B,RNF121,NDUFA2,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,MTFR1,COPS5,CEBPG,ZNF341,IL20RB,KMT5A,PDCD5,CTR9,VTI1B,SMN2,PTCD2,RPS3A,ELOC,GOT2,P2RX4,PLRG1,EIF2A,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,PKIG,FARS2,HLCS,ELOVL2,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PSPH,PRDM10,VKORC1L1,CUEDC2,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,TGIF1,WDR5B,NIF3L1,PPP1R8,RAE1,ENSA,GMPR2,PPP1R11,KLHL41,RBM4,CRTC3,SMYD2,PSMA7,NDUFA10,DCAF17,RPL35A,MTFR1L,PES1,UROS,BCCIP,RPL18A,FBXO45,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,ANAPC16,EMG1,TRMT44,PRDX6,USP5,MECOM,CHCHD1,LSM4,TRIM4,UBA1,DYNC2H1,UVSSA,ELK1,PELI2,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,PSMB6,ERC1,HSPA2,ITPKB,RARA,HDHD5,CTDNEP1,CECR2,NR1	red	VSMC_M1
GO:0006936	0.37	0.74	11	256	muscle contraction	BP	1	SRI,FKBP1B,CACNA2D1,EDNRA,P2RX4,CACNA1D,SSPN,KLHL41,MYL4,GJC1,CALM2	red	VSMC_M1
GO:0008154	0.37	0.76	8	183	actin polymerization or depolymerization	BP	1	TRIOBP,ARHGAP35,CXCL12,TMSB10,ARFIP1,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0030098	0.37	0.74	11	259	lymphocyte differentiation	BP	1	EGR1,PCID2,CEBPG,RPS6,IRF2BP2,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0034613	0.37	0.68	58	1451	cellular protein localization	BP	1	HSPA1L,REEP2,CTNNA1,CLTA,XPA,INVS,CRIPT,PIH1D1,PARD3,WDR35,EFR3B,PMPCB,STAM,IFT122,PAK1,CSNK1D,HDAC3,TNKS,RAB28,PDCD5,VTI1B,TIMM10,TMSB10,ARFIP1,PLRG1,PKIG,PARP3,ARL3,WIPI1,EMC9,ARL4C,WDR11,EGR2,KDM1A,MAP2,AP1S1,NDUFA13,ARL4D,DYNC2H1,SCG3,CTDNEP1,VPS37C,CDK5RAP3,COPZ2,STXBP4,SNUPN,FBXO4,RAB12,GOLPH3,KCNAB2,DNLZ,CIZ1,EVI5,RACK1,TMSB4X,TOMM7,ATP5IF1,FGF10	red	VSMC_M1
GO:0002697	0.37	0.75	9	206	regulation of immune effector process	BP	1	ARG1,AHR,KMT5C,IL20RB,PARP3,CUEDC2,RARA,IL13RA2,MYO18A	red	VSMC_M1
GO:0032774	0.37	0.67	99	2534	RNA biosynthetic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,POLR2F,MTERF2,SRI,SPIN1,ZNF584,AHR,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,SMN2,ELOC,PKIG,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,ETV3,SAMD1,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,DR1,E2F4,IER2,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,FGF10	red	VSMC_M1
GO:0002700	0.37	0.79	5	106	regulation of production of molecular mediator of immune response	BP	1	ARG1,KMT5C,PARP3,CUEDC2,IL13RA2	red	VSMC_M1
GO:2001237	0.37	0.80	4	79	negative regulation of extrinsic apoptotic signaling pathway	BP	1	CTNNA1,PRDX2,RFFL,FGF10	red	VSMC_M1
GO:1901565	0.37	0.68	44	1069	organonitrogen compound catabolic process	BP	1	ARG1,ACR,TST,UBAP1,EEF1A1,ALAD,RPS7,PSMB2,GPT2,FGF2,STAM,RNF121,CSNK1D,ERLIN2,LTA4H,ELOC,GOT2,HPSE,FBXW8,PPP1R11,PSMA7,FBXO45,USP28,NDUFA13,USP5,UBA1,PSMB6,NR1D1,VPS37C,RNF40,CDK5RAP3,RFFL,USP22,FBXO4,RAB12,OMA1,HMOX2,UBE4B,USP10,RACK1,TIMP3,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0016050	0.38	0.74	11	255	vesicle organization	BP	1	STAM,UVRAG,CSNK1D,VTI1B,TFG,ARFGEF2,VPS37C,PRRT2,MYO18A,GOLPH3,GOSR1	red	VSMC_M1
GO:0045786	0.38	0.73	13	306	negative regulation of cell cycle	BP	1	MAD2L1BP,NPR2,NUDT6,PCID2,TNKS,CDC73,USP28,KAT2A,CDK5RAP3,INTS3,XRCC3,FBXO4,HUS1	red	VSMC_M1
GO:0048856	0.38	0.66	161	4193	anatomical structure development	BP	1	SMAD4,SGK1,ARG1,CSNK2B,KLF10,DYNLT1,EGFL8,ZHX2,NDRG1,ZFAT,EGR1,TCP11,CTNNA1,TRIOBP,TST,SRI,MUT,MAP4K4,NPR2,AHR,KMT5C,MEI4,PGM3,UTP11,INPP5B,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,SF3B6,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,UBP1,FAM171A1,IFT122,PCDH17,EIF2B4,PAK1,DGAT2,SPAST,NEB,NRG2,COX7B,MCRIP1,NDUFA2,CSNK1D,SOCS2,PCID2,SP1,CXCL12,TNFRSF19,CEBPG,CTR9,EDNRA,SMN2,SLC12A6,PTCD2,RHOF,C21orf91,GOT2,P2RX4,C15orf41,SPRED1,RPS6,TLL1,MMP16,HPSE,AMBRA1,FBXW8,IFT57,PARP3,TMEFF2,PSPH,ARL3,UNC119B,CDC73,CFAP410,ACTL6A,AKAP13,IRF2BP2,MYO18B,RHOD,NIF3L1,KLHL41,WDR11,RBM4,SMYD2,BCCIP,ARHGDIB,KCNQ2,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,PTS,IL1RAP,GJC1,EMG1,MECOM,RP2,DYNC2H1,ELK1,PROM1,ITFG2,ZMIZ1,KAT2A,PFN1,ERC1,PRTG,HSPA2,ITPKB,RARA,CTDNEP1,CECR2,NR1D1,MEF2D,CDK5RAP3,EIF2B2,PRDX2,MBTD1,FLRT2,CALM2,SPARC,PMP22,CYP1A1,HMG20A,COQ7,B9D1,USP22,OMA1,TBC1D24,GFER,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,WDR5,WWOX,E2F4,IER2,NUDT21,MED31,FKBP1A,GNAS,FAM9B,BORCS8,RACK1,HUS1,NREP,BHLHE41,CPNE1,RITA1,ATP5IF1,FGF10	red	VSMC_M1

GO:0042098	0.38	0.77	6	127	T cell proliferation	BP	1	ARG1,FKBP1B,RPS3,IL20RB,RPS6,PRDX2	red	VSMC_M1
GO:0070887	0.38	0.67	88	2230	cellular response to chemical stimulus	BP	1	SMAD4,ARG1,CSNK2B,KLF10,HSPA1L,NDRG1,EGR1,CTNNA1,SRI,IL1RL1,MAP4K4,NPR2,AHR,EEF1A1,ALAD,PIH1D1,WDR35,FKBP1B,FGF2,RECQL5,WBP2,PAK1,DGAT2,RPS3,IL18BP,CSNK1D,SOCS2,CACNA2D1,TNKS,SP1,CXCL12,TNFRSF19,COPS5,IL20RB,PDCD5,CTR9,SLC12A6,P2RX4,SPRED1,CD58,VKORC1L1,CDC73,GRAMD1C,TGIF1,RAE1,UROS,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,PRDX6,ELK1,ZMIZ1,KAT2A,HSPA2,ITPKB,RARA,NR1D1,ETV3,CDK5RAP3,PARP16,PRDX2,FLRT2,STXBP4,CYP1A1,IL13RA2,RFFL,RAB12,GOLPH3,TBC1D24,ERRFI1,RBM15,GSTM3,USP10,WWOX,FKBP1A,GNAS,RACK1,SRXN1,ATP6V1G1,NREP,TMSB4X,CPNE1,RNF125,LY96,PTPRN2,FGF10	red	VSMC_M1
GO:0060541	0.38	0.76	7	163	respiratory system development	BP	1	ARG1,FGF2,ELK1,RARA,SPARC,ERRFI1,FGF10	red	VSMC_M1
GO:0048872	0.38	0.74	10	229	homeostasis of number of cells	BP	1	TAL1,CEBPG,IL20RB,C15orf41,RPS6,RPS24,ITPKB,CDK5RAP3,PRDX2,ATP5IF1	red	VSMC_M1
GO:0048699	0.38	0.68	45	1177	generation of neurons	BP	1	SMAD4,SGK1,DYNLT1,ZHX2,CTNNA1,TRIOBP,MAP4K4,PARD3,FKBP1B,TAL1,ARHGAP35,SDK2,PAK1,SPAST,CSNK1D,SOCS2,CXCL12,C21orf91,FBXW8,ARL3,NIF3L1,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,DYNC2H1,PROM1,ZMIZ1,PRTG,RARA,CECR2,NR1D1,CDK5RAP3,FLRT2,PMP22,HMG20A,TBC1D24,TPRN,WDR5,IER2,NREP,BHLHE41,CPNE1	red	VSMC_M1
GO:0051346	0.38	0.73	11	242	negative regulation of hydrolase activity	BP	1	PIH1D1,FKBP1B,PCID2,PPP1R11,RFFL,PTPA,FKBP1A,TIMP3,WFDC3,ATP5IF1,PTPRN2	red	VSMC_M1
GO:0007281	0.38	0.75	8	177	germ cell development	BP	1	TCP11,NPR2,MEI4,RPS6,ETV5,HSPA2,RARA,FAM9B	red	VSMC_M1
GO:0006637	0.38	0.80	4	78	acyl-CoA metabolic process	BP	1	DGAT2,ELOVL2,ACOT8,SLC25A1	red	VSMC_M1
GO:0035383	0.38	0.80	4	78	thioester metabolic process	BP	1	DGAT2,ELOVL2,ACOT8,SLC25A1	red	VSMC_M1
GO:0032880	0.38	0.69	28	693	regulation of protein localization	BP	1	HSPA1L,CTNNA1,SRI,MAP4K4,CRIPT,FKBP1B,PAK1,HDAC3,PDCD5,VTI1B,ARFIP1,PKIG,RAB9A,ENSA,KDM1A,MAP2,NR1D1,CDK5RAP3,STXBP4,B9D1,FBXO4,MYO18A,GOLPH3,KCNAB2,FKBP1A,RACK1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0010243	0.38	0.69	32	793	response to organonitrogen compound	BP	1	ARG1,RGS17,KLF10,EGR1,CTNNA1,AHR,ALAD,PSMB2,RECQL5,EIF2B4,PAK1,RNF121,SOCS2,ERLIN2,CACNA2D1,SP1,CXCL12,GOT2,P2RX4,HLCS,UROS,EGR2,KDM1A,RNF40,EIF2B2,STXBP4,SPARC,RAB12,GOLPH3,ERRFI1,UBE4B,GNAS	red	VSMC_M1
GO:1903362	0.38	0.74	10	222	regulation of cellular protein catabolic process	BP	1	ALAD,RPS7,CSNK1D,FBXW8,USP5,RNF40,CDK5RAP3,RACK1,ATP5IF1,RCHY1	red	VSMC_M1
GO:1903313	0.38	0.78	5	105	positive regulation of mRNA metabolic process	BP	1	CDC73,EXOSC7,PRDX6,DCP2,NUDT21	red	VSMC_M1
GO:0044843	0.38	0.75	8	180	cell cycle G1/S phase transition	BP	1	CDK17,PLRG1,RPS6,CDC73,STXBP4,CYP1A1,E2F4,FGF10	red	VSMC_M1
GO:0000018	0.38	0.79	4	83	regulation of DNA recombination	BP	1	KMT5C,RECQL5,PARP3,KDM1A	red	VSMC_M1
GO:0010563	0.38	0.71	15	356	negative regulation of phosphorus metabolic process	BP	1	FGFR1OP,PARD3,FKBP1B,SPRED1,PKIG,NPRL2,PPP1R8,ENSA,PPP1R11,CDK5RAP3,CALM2,ERRFI1,PTPA,FKBP1A,RACK1	red	VSMC_M1
GO:0045936	0.38	0.71	15	356	negative regulation of phosphate metabolic process	BP	1	FGFR1OP,PARD3,FKBP1B,SPRED1,PKIG,NPRL2,PPP1R8,ENSA,PPP1R11,CDK5RAP3,CALM2,ERRFI1,PTPA,FKBP1A,RACK1	red	VSMC_M1
GO:0051046	0.38	0.71	18	434	regulation of secretion	BP	1	SMAD4,SGK1,SRI,MAP4K4,FKBP1B,STAM,CXCL12,ARFIP1,P2RX4,RAB9A,ENSA,NR1D1,STXBP4,IL13RA2,RAB12,MYO18A,GOLPH3,FGF10	red	VSMC_M1
GO:1902600	0.39	0.76	6	115	proton transmembrane transport	BP	1	COX5B,COX7B,CLCN5,COX4I1,ATP6V1G1,TMSB4X	red	VSMC_M1
GO:0007275	0.39	0.65	146	3815	multicellular organism development	BP	1	SMAD4,SGK1,ARG1,CSNK2B,KLF10,DYNLT1,ZHX2,NDRG1,ZFAT,EGR1,TCP11,CTNNA1,TRIOBP,SRI,MUT,MAP4K4,NPR2,AHR,KMT5C,PGM3,UTP11,INPP5B,RPS7,PARD3,WDR35,FKBP1B,SF3B6,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,UBP1,IFT122,PCDH17,EIF2B4,PAK1,DGAT2,SPAST,NEB,NRG2,COX7B,MCRIP1,NDUFA2,CSNK1D,SOCS2,PCID2,SP1,CXCL12,TNFRSF19,CEBPG,CTR9,EDNRA,SMN2,SLC12A6,PTCD2,C21orf91,GOT2,P2RX4,C15orf41,SPRED1,RPS6,TLL1,MMP16,HPSE,AMBRA1,FBXW8,IFT57,PARP3,TMEFF2,PSPH,ARL3,UNC119B,CDC73,ACTL6A,AKAP13,IRF2BP2,MYO18B,NIF3L1,KLHL41,WDR11,SMYD2,ARHGDIB,KCNQ2,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,PTS,IL1RAP,GJC1,EMG1,MECOM,DYNC2H1,ELK1,PROM1,ITFG2,ZMIZ1,KAT2A,PFN1,ERC1,PRTG,ITPKB,RARA,CECR2,NR1D1,MEF2D,CDK5RAP3,EIF2B2,PRDX2,MBTD1,FLRT2,CALM2,SPARC,PMP22,CYP1A1,HMG20A,COQ7,B9D1,USP22,TBC1D24,GFER,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,WDR5,WWOX,E2F4,IER2,NUDT21,MED31,FKBP1A,GNAS,BORCS8,RACK1,HUS1,NREP,BHLHE41,CPNE1,RITA1,ATP5IF1,FGF10	red	VSMC_M1
GO:0048585	0.39	0.67	49	1229	negative regulation of response to stimulus	BP	1	SMAD4,ARG1,DYRK2,RGS17,EGR1,CTNNA1,MAD2L1BP,IL1RL1,MAP4K4,AHR,INVS,PIH1D1,FKBP1B,FGF2,ARHGAP35,IFT122,RECQL5,RPS3,HDAC3,SOCS2,CXCL12,IL20RB,SPRED1,TBC1D7,PARP3,NPRL2,CRTC3,KDM1A,NDUFA13,MECOM,ITFG2,NR1D1,CDK5RAP3,PRDX2,IL13RA2,RFFL,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,FKBP1A,RACK1,TIMP3,TMSB4X,CPNE1,RNF125,RITA1,FGF10	red	VSMC_M1
GO:0010389	0.39	0.79	4	82	regulation of G2/M transition of mitotic cell cycle	BP	1	HSPA2,CDK5RAP3,INTS3,HUS1	red	VSMC_M1
GO:0046651	0.39	0.74	8	177	lymphocyte proliferation	BP	1	ARG1,AHR,FKBP1B,RPS3,IL20RB,RPS6,PRDX2,FGF10	red	VSMC_M1
GO:0010595	0.39	0.77	5	105	positive regulation of endothelial cell migration	BP	1	FGF2,SP1,P2RX4,SPARC,TMSB4X	red	VSMC_M1
GO:0043401	0.39	0.77	5	111	steroid hormone mediated signaling pathway	BP	1	WBP2,PAK1,KDM1A,ZMIZ1,NR1D1	red	VSMC_M1
GO:0071407	0.39	0.70	18	448	cellular response to organic cyclic compound	BP	1	ARG1,EGR1,CTNNA1,AHR,RECQL5,WBP2,PAK1,P2RX4,GRAMD1C,RAE1,KDM1A,ELK1,ZMIZ1,NR1D1,CYP1A1,GOLPH3,ERRFI1,GNAS	red	VSMC_M1
GO:0016051	0.39	0.75	7	155	carbohydrate biosynthetic process	BP	1	DYRK2,DGAT2,KAT2A,NR1D1,CHST9,WDR5,SLC25A1	red	VSMC_M1
GO:0045862	0.39	0.71	13	297	positive regulation of proteolysis	BP	1	WDR35,RPS3,CSNK1D,PDCD5,FBXW8,IFT57,NDUFA13,USP5,RNF40,RACK1,ATP5IF1,PSENEN,RCHY1	red	VSMC_M1
GO:0006986	0.39	0.76	6	124	response to unfolded protein	BP	1	HSPA1L,COPS5,HSPA2,CDK5RAP3,PARP16,RACK1	red	VSMC_M1
GO:0002252	0.39	0.71	15	360	immune effector process	BP	1	ARG1,AHR,KMT5C,PAK1,CEBPG,IL20RB,RPS6,PARP3,CUEDC2,ITFG2,RARA,PRDX2,IL13RA2,MYO18A,IGHA2	red	VSMC_M1

GO:0051168	0.39	0.76	6	131	nuclear export	BP	1	POLDIP3,PCID2,AKAP13,RAE1,EGR2,RITA1	red	VSMC_M1
GO:0045834	0.39	0.77	5	109	positive regulation of lipid metabolic process	BP	1	FGF2,DGAT2,AMBRA1,CTDNEP1,NR1D1	red	VSMC_M1
GO:0002703	0.40	0.76	6	136	regulation of leukocyte mediated immunity	BP	1	ARG1,AHR,KMT5C,IL20RB,PARP3,IL13RA2	red	VSMC_M1
GO:0072009	0.40	0.78	4	89	nephron epithelium development	BP	1	SMAD4,FGF2,PROM1,CTNNBIP1	red	VSMC_M1
GO:0032943	0.40	0.74	8	179	mononuclear cell proliferation	BP	1	ARG1,AHR,FKBP1B,RPS3,IL20RB,RPS6,PRDX2,FGF10	red	VSMC_M1
GO:0045595	0.40	0.66	45	1153	regulation of cell differentiation	BP	1	SMAD4,KLF10,DYNLT1,ZHX2,TCP11,CTNNA1,TRIOBP,NPR2,FGF2,TAL1,PAK1,MCRIP1,CSNK1D,SOCS2,PCID2,CXCL12,CTR9,SPRED1,SMYD5,FBXW8,CDC73,KLHL41,RBM4,EGR2,KDM1A,ETV5,MAP2,PROM1,ZMIZ1,KAT2A,PRTG,ITPKB,RARA,NR1D1,CDK5RAP3,PRDX2,HMG20A,ERRFI1,CTNNBIP1,RBM15,NUDT21,NREP,BHLHE41,CPNE1,FGF10	red	VSMC_M1
GO:0002761	0.40	0.78	4	86	regulation of myeloid leukocyte differentiation	BP	1	KLF10,TAL1,RARA,CTNNBIP1	red	VSMC_M1
GO:0006352	0.40	0.77	5	105	DNA-templated transcription, initiation	BP	1	POLR3H,TAF11,PIH1D1,CTNNBIP1,DR1	red	VSMC_M1
GO:1901605	0.40	0.74	7	146	alpha-amino acid metabolic process	BP	1	ARG1,TST,MUT,GPT2,GOT2,PSPH,ADI1	red	VSMC_M1
GO:0010564	0.40	0.68	21	515	regulation of cell cycle process	BP	1	MAD2L1BP,UVRAG,SPAST,PCID2,TNKS,PLRG1,PARP3,CDC73,RAE1,USP28,KAT2A,HSPA2,CDK5RAP3,STXBP4,INTS3,CALM2,CYP1A1,XRCC3,FBXO4,HUS1,FGF10	red	VSMC_M1
GO:0070301	0.40	0.78	4	79	cellular response to hydrogen peroxide	BP	1	ARG1,RPS3,IL18BP,RACK1	red	VSMC_M1
GO:0048024	0.40	0.78	4	85	regulation of mRNA splicing, via spliceosome	BP	1	HNRNPL,RBM4,PRDX6,RBM15	red	VSMC_M1
GO:2001233	0.40	0.70	13	292	regulation of apoptotic signaling pathway	BP	1	CTNNA1,RPS7,PIH1D1,RPS3,CXCL12,KDM1A,NDUFA13,PRDX2,RFFL,WWOX,RACK1,TIMP3,FGF10	red	VSMC_M1
GO:0072073	0.40	0.76	5	115	kidney epithelium development	BP	1	SMAD4,FGF2,PROM1,RARA,CTNNBIP1	red	VSMC_M1
GO:0046903	0.40	0.67	27	673	secretion	BP	1	SMAD4,SGK1,SRI,MAP4K4,FKBP1B,STAM,PAK1,SOCS2,CXCL12,COPS5,VTI1B,ARFIP1,GOT2,P2RX4,ARFGEF2,RAB9A,ENSA,ARL4D,NR1D1,PRRT2,STXBP4,IL13RA2,RAB12,MYO18A,GOLPH3,PTPRN2,FGF10	red	VSMC_M1
GO:0044839	0.40	0.75	6	132	cell cycle G2/M phase transition	BP	1	ENSA,HSPA2,CDK5RAP3,INTS3,CALM2,HUS1	red	VSMC_M1
GO:0010594	0.40	0.74	7	157	regulation of endothelial cell migration	BP	1	CSNK2B,FGF2,SP1,P2RX4,SPRED1,SPARC,TMSB4X	red	VSMC_M1
GO:0017148	0.41	0.74	7	158	negative regulation of translation	BP	1	MALSU1,RPS3,RBM4,EXOSC7,RARA,DCP2,RACK1	red	VSMC_M1
GO:0071383	0.41	0.74	7	163	cellular response to steroid hormone stimulus	BP	1	ARG1,WBP2,PAK1,KDM1A,ZMIZ1,NR1D1,ERRFI1	red	VSMC_M1
GO:0009725	0.41	0.67	26	652	response to hormone	BP	1	ARG1,ACR,CSNK2B,EGR1,CTNNA1,ALAD,EIF2B4,WBP2,PAK1,SOCS2,SP1,CXCL12,GOT2,EGR2,KDM1A,ZMIZ1,RARA,NR1D1,RNF40,EIF2B2,STXBP4,SPARC,RAB12,ERRFI1,GSTM3,TIMP3	red	VSMC_M1
GO:0071216	0.41	0.73	7	157	cellular response to biotic stimulus	BP	1	ARG1,CTR9,CDC73,RARA,NR1D1,PRDX2,LY96	red	VSMC_M1
GO:0007219	0.41	0.74	6	138	Notch signaling pathway	BP	1	GMDS,ZMIZ1,RBM15,RITA1,PSENEN,FGF10	red	VSMC_M1
GO:0051223	0.41	0.68	17	412	regulation of protein transport	BP	1	HSPA1L,SRI,MAP4K4,FKBP1B,PAK1,HDAC3,PDCD5,ARFIP1,PKIG,ENSA,NR1D1,STXBP4,MYO18A,GOLPH3,RACK1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0030324	0.41	0.74	6	141	lung development	BP	1	ARG1,FGF2,ELK1,SPARC,ERRFI1,FGF10	red	VSMC_M1
GO:0034762	0.41	0.68	16	396	regulation of transmembrane transport	BP	1	SRI,KCNF1,FKBP1B,CACNA2D1,EDNRA,CACNA1D,STIMATE,SCN3A,KCNQ2,HSPA2,STXBP4,CALM2,KCNAB2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1
GO:0051897	0.41	0.77	4	88	positive regulation of protein kinase B signaling	BP	1	FGF2,P2RX4,HPSE,CPNE1	red	VSMC_M1
GO:0019219	0.42	0.63	110	2852	regulation of nucleobase-containing compound metabolic process	BP	1	SMAD4,SGK1,KLF10,ZHX2,ZBTB22,ZFAT,HMGA1,TAF11,EGR1,ZNF76,MTERF2,SRI,SPIN1,ZNF584,AHR,KMT5C,APLF,PIH1D1,FGF2,TAL1,IRF2BP1,NR2C2,TSC22D1,UBP1,RECQL5,WBP2,RPS3,HNRNPL,HDAC3,PCID2,CDK17,TNKS,SP1,COPS5,CEBPG,ZNF341,KMT5A,CTR9,PTCD2,ELOC,PKIG,PARP3,PRDM10,CDC73,ACTL6A,IRF2BP2,TGIF1,NIF3L1,RBM4,CRTC3,SMYD2,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,MECOM,ELK1,TRRAP,ZMIZ1,KAT2A,PFN1,ERC1,RARA,NR1D1,DCP2,ETV3,SAMD1,RNF40,MEF2D,CDK5RAP3,ZNF652,PRDX2,MBTD1,GATAD2B,SUPT4H1,ARID3B,ZNF287,HMG20A,USP22,MIER1,FBXO4,CTNNBIP1,RBM15,ZNF276,CDYL2,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,MED31,ZBTB43,MYPOP,ELOF1,ZNF614,ZNF180,TMSB4X,BHLHE41,ZFP2,RITA1,ZNF790,ZNF846,ZNF177,ZNF32,AHNAK,FGF10	red	VSMC_M1
GO:0001822	0.42	0.71	10	248	kidney development	BP	1	SMAD4,EGR1,FGF2,PTCD2,ARL3,DYNC2H1,PROM1,RARA,CTNNBIP1,FGF10	red	VSMC_M1
GO:0006950	0.42	0.63	107	2715	response to stress	BP	1	SMAD4,ARG1,DYRK2,KLF10,HSPA1L,POLR3H,NDRG1,HMGA1,EGR1,CTNNA1,IL1RL1,MAP4K4,XPA,KMT5C,ALAD,APLF,FKBP1B,FGF2,ARHGAP35,RECQL5,EIF2B4,PAK1,UVRAG,RPS3,IL18BP,RNF121,HDAC3,ERLIN2,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,IL20RB,KMT5A,EDNRA,SLC12A6,P2RX4,EIF2A,SPRED1,HPSE,AMBRA1,TMEM117,CD58,PARP3,TMEFF2,VKORC1L1,CUEDC2,NPRL2,CFAP410,WIPI1,ACTL6A,PPP1R11,RBM4,SMYD2,BCCIP,FBXO45,INO80D,KDM1A,ETV5,USP28,IL1RAP,PRDX6,MECOM,TRIM4,UBA1,UVSSA,TRRAP,ITFG2,HSPA2,NR1D1,CDK5RAP3,EIF2B2,INO80E,PARP16,PRDX2,STXBP4,INTS3,SPARC,INO80C,CYP1A1,RNF138,XRCC3,FBXO4,OMA1,YJU2,HMOX2,TBC1D24,ERRFI1,CTNNBIP1,UBE4B,GSTM3,USP10,GNAS,RACK1,HUS1,SRXN1,NREP,TMSB4X,WFDC3,TOMM7,RNF125,IGHA2,ATP5IF1,LY96,RCHY1,FGF10	red	VSMC_M1
GO:0030522	0.42	0.71	9	217	intracellular receptor signaling pathway	BP	1	AHR,NR2C2,WBP2,PAK1,KDM1A,ZMIZ1,RARA,NR1D1,RNF125	red	VSMC_M1
GO:0045165	0.42	0.73	7	172	cell fate commitment	BP	1	SMAD4,FGF2,TAL1,CTR9,CDC73,RARA,FGF10	red	VSMC_M1
GO:0019932	0.42	0.71	9	218	second-messenger-mediated signaling	BP	1	DYRK2,TCP11,NPR2,AHR,FKBP1B,P2RX4,STIMATE,CRTC3,CALM2	red	VSMC_M1
GO:0072006	0.42	0.75	5	118	nephron development	BP	1	SMAD4,EGR1,FGF2,PROM1,CTNNBIP1	red	VSMC_M1
GO:0000082	0.42	0.73	7	160	G1/S transition of mitotic cell cycle	BP	1	CDK17,PLRG1,RPS6,CDC73,CYP1A1,E2F4,FGF10	red	VSMC_M1
GO:0046916	0.42	0.77	4	86	cellular transition metal ion homeostasis	BP	1	SMAD4,SRI,COX19,ATP6V1G1	red	VSMC_M1
GO:0044057	0.42	0.68	16	398	regulation of system process	BP	1	SMAD4,SGK1,SRI,PARD3,WDR35,FKBP1B,PAK1,CACNA2D1,P2RX4,CACNA1D,EGR2,MYL4,GJC1,CALM2,ERRFI1,FGF10	red	VSMC_M1
GO:0016055	0.42	0.68	15	373	Wnt signaling pathway	BP	1	CSNK2B,EGR1,SPIN1,INVS,FGF2,CSNK1D,TNKS,CTR9,CDC73,CTDNEP1,RNF138,CTNNBIP1,WWOX,RACK1,FGF10	red	VSMC_M1
GO:0051304	0.42	0.77	4	85	chromosome separation	BP	1	MAD2L1BP,RECQL5,PCID2,XRCC3	red	VSMC_M1
GO:0006520	0.42	0.70	10	224	cellular amino acid metabolic process	BP	1	ARG1,TST,MUT,GPT2,GOT2,FARS2,PSPH,YARS,PTS,ADI1	red	VSMC_M1
GO:0048592	0.42	0.75	5	118	eye morphogenesis	BP	1	ZHX2,FGF2,SDK2,IFT122,PROM1	red	VSMC_M1

GO:0071560	0.42	0.71	8	199	cellular response to transforming growth factor beta stimulus	BP	1	SMAD4,ARG1,PDCD5,SPRED1,ZMIZ1,WWOX,FKBP1A,NREP	red	VSMC_M1
GO:0198738	0.42	0.68	15	374	cell-cell signaling by wnt	BP	1	CSNK2B,EGR1,SPIN1,INVS,FGF2,CSNK1D,TNKS,CTR9,CDC73,CTDNEP1,RNF138,CTNNBIP1,WWOX,RACK1,FGF10	red	VSMC_M1
GO:0009408	0.42	0.76	4	84	response to heat	BP	1	EIF2B4,CXCL12,HSPA2,EIF2B2	red	VSMC_M1
GO:0019220	0.42	0.64	42	1074	regulation of phosphate metabolic process	BP	1	SMAD4,CSNK2B,FGFR1OP,EGR1,KCTD20,EEF1A1,PIH1D1,PARD3,FKBP1B,FGF2,TAL1,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,SOCS2,SPRED1,CCNI,AMBRA1,PKIG,NPRL2,AKAP13,PPP1R8,ENSA,PPP1R11,BCCIP,PELI2,HSPA2,ITPKB,CDK5RAP3,PARP16,CALM2,MOB3A,ERRFI1,PTPA,FKBP1A,RACK1,HUS1,PPP1R14A,TMSB4X,FGF10	red	VSMC_M1
GO:0051174	0.42	0.64	42	1074	regulation of phosphorus metabolic process	BP	1	SMAD4,CSNK2B,FGFR1OP,EGR1,KCTD20,EEF1A1,PIH1D1,PARD3,FKBP1B,FGF2,TAL1,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,SOCS2,SPRED1,CCNI,AMBRA1,PKIG,NPRL2,AKAP13,PPP1R8,ENSA,PPP1R11,BCCIP,PELI2,HSPA2,ITPKB,CDK5RAP3,PARP16,CALM2,MOB3A,ERRFI1,PTPA,FKBP1A,RACK1,HUS1,PPP1R14A,TMSB4X,FGF10	red	VSMC_M1
GO:0090596	0.43	0.71	8	198	sensory organ morphogenesis	BP	1	ZHX2,TRIOBP,FGF2,SDK2,IFT122,PROM1,TPRN,FGF10	red	VSMC_M1
GO:0052548	0.43	0.69	12	270	regulation of endopeptidase activity	BP	1	PIH1D1,WDR35,RPS3,PCID2,PDCD5,IFT57,NDUFA13,RFFL,RACK1,TIMP3,WFDC3,PSENEN	red	VSMC_M1
GO:0035239	0.43	0.65	27	699	tube morphogenesis	BP	1	SMAD4,CSNK2B,RPS7,FGF2,TAL1,ARHGAP35,UBP1,IFT122,PAK1,SP1,EDNRA,SLC12A6,SPRED1,HPSE,IFT57,MYO18B,GJC1,ZMIZ1,KAT2A,PFN1,RARA,CECR2,SPARC,CTNNBIP1,RBM15,ATP5IF1,FGF10	red	VSMC_M1
GO:0008104	0.43	0.62	79	2028	protein localization	BP	1	HSPA1L,DYNLT1,REEP2,CTNNA1,SRI,UBAP1,MAP4K4,CLTA,XPA,INVS,CRIPT,PIH1D1,PARD3,WDR35,FKBP1B,EFR3B,PMPCB,STAM,IFT122,WBP2,PAK1,CSNK1D,HDAC3,PCID2,TNKS,RAB28,PDCD5,VTI1B,TIMM10,TMSB10,ARFIP1,PLRG1,PKIG,PARP3,ARL3,UNC119B,WIPI1,ARFGEF2,RAB9A,EMC9,ARL4C,ENSA,FAM45A,WDR11,EGR2,KDM1A,MAP2,AP1S1,NDUFA13,ARL4D,RP2,DYNC2H1,SCG3,ERC1,CTDNEP1,NR1D1,VPS37C,CDK5RAP3,COPZ2,STXBP4,SNUPN,B9D1,FBXO4,RAB12,MYO18A,GOLPH3,GOSR1,KCNAB2,RAB39B,DNLZ,CIZ1,EVI5,FKBP1A,RACK1,TMSB4X,TOMM7,ATP5IF1,PTPRN2,FGF10	red	VSMC_M1
GO:0010256	0.43	0.67	17	422	endomembrane system organization	BP	1	NDRG1,REEP2,STAM,RAB30,SPAST,CSNK1D,VTI1B,FBXW8,TMEFF2,ARFGEF2,EMC9,DYNC2H1,CTDNEP1,VPS37C,PRRT2,MYO18A,GOLPH3	red	VSMC_M1
GO:0016064	0.43	0.76	4	85	immunoglobulin mediated immune response	BP	1	KMT5C,PARP3,IL13RA2,IGHA2	red	VSMC_M1
GO:1902749	0.43	0.76	4	87	regulation of cell cycle G2/M phase transition	BP	1	HSPA2,CDK5RAP3,INTS3,HUS1	red	VSMC_M1
GO:1903131	0.43	0.68	12	297	mononuclear cell differentiation	BP	1	EGR1,PCID2,CEBPG,RPS6,IRF2BP2,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,CTNNBIP1	red	VSMC_M1
GO:0045893	0.43	0.63	48	1244	positive regulation of transcription, DNA-templated	BP	1	SMAD4,KLF10,ZFAT,HMGA1,TAF11,EGR1,ZNF76,SPIN1,AHR,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,RBM15,WWOX,DR1,E2F4,IER2,ELOF1,FGF10	red	VSMC_M1
GO:1903508	0.43	0.63	48	1244	positive regulation of nucleic acid-templated transcription	BP	1	SMAD4,KLF10,ZFAT,HMGA1,TAF11,EGR1,ZNF76,SPIN1,AHR,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,RBM15,WWOX,DR1,E2F4,IER2,ELOF1,FGF10	red	VSMC_M1
GO:0030036	0.43	0.65	23	600	actin cytoskeleton organization	BP	1	SMAD4,CTNNA1,TRIOBP,ARHGAP35,FAM171A1,PAK1,NEB,CXCL12,TMSB10,ARFIP1,RHOF,TMEFF2,AKAP13,RHOD,KLHL41,ARHGDIB,MYO5C,PFN1,KANK4,MYO18A,ELMO3,TMSB4X,FGF10	red	VSMC_M1
GO:0030900	0.43	0.69	11	282	forebrain development	BP	1	FGF2,ARHGAP35,CXCL12,C21orf91,FBXO45,KDM1A,DYNC2H1,ZMIZ1,KAT2A,RARA,FGF10	red	VSMC_M1
GO:0051606	0.43	0.72	6	135	detection of stimulus	BP	1	PAK1,RPS3,CXCL12,CFAP410,CALM2,LY96	red	VSMC_M1
GO:0046683	0.43	0.75	4	94	response to organophosphorus	BP	1	AHR,P2RX4,KDM1A,SPARC	red	VSMC_M1
GO:0061640	0.43	0.75	4	87	cytoskeleton-dependent cytokinesis	BP	1	DCTN3,SPAST,ARL3,CECR2	red	VSMC_M1
GO:0030038	0.43	0.75	4	95	contractile actin filament bundle assembly	BP	1	FAM171A1,PAK1,TMEFF2,PFN1	red	VSMC_M1
GO:0043149	0.43	0.75	4	95	stress fiber assembly	BP	1	FAM171A1,PAK1,TMEFF2,PFN1	red	VSMC_M1
GO:0032386	0.44	0.68	12	290	regulation of intracellular transport	BP	1	HSPA1L,REEP2,PAK1,HDAC3,PDCD5,ARFIP1,PKIG,FAM45A,RBM4,MAP2,TOMM7,ATP5IF1	red	VSMC_M1
GO:0043406	0.44	0.75	4	93	positive regulation of MAP kinase activity	BP	1	FGF2,PAK1,RPS3,AKAP13	red	VSMC_M1
GO:1902680	0.44	0.62	48	1246	positive regulation of RNA biosynthetic process	BP	1	SMAD4,KLF10,ZFAT,HMGA1,TAF11,EGR1,ZNF76,SPIN1,AHR,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,RBM15,WWOX,DR1,E2F4,IER2,ELOF1,FGF10	red	VSMC_M1
GO:0051146	0.44	0.69	9	220	striated muscle cell differentiation	BP	1	SMAD4,PAK1,NEB,AKAP13,MYO18B,KLHL41,KAT2A,RARA,BHLHE41	red	VSMC_M1
GO:1900180	0.44	0.73	5	116	regulation of protein localization to nucleus	BP	1	CTNNA1,HDAC3,PKIG,CDK5RAP3,FBXO4	red	VSMC_M1
GO:0034504	0.44	0.69	10	244	protein localization to nucleus	BP	1	CTNNA1,XPA,HDAC3,PLRG1,PKIG,CTDNEP1,CDK5RAP3,SNUPN,FBXO4,CIZ1	red	VSMC_M1
GO:0007600	0.44	0.67	13	320	sensory perception	BP	1	REEP2,TRIOBP,FAM161A,CXCL12,TIMM10,P2RX4,CACNA1D,GJC1,RP2,SCNN1A,TPRN,GNAS,TIMP3	red	VSMC_M1
GO:0051251	0.44	0.70	8	186	positive regulation of lymphocyte activation	BP	1	KMT5C,RPS3,PCID2,ZMIZ1,ITPKB,RARA,IGHA2,FGF10	red	VSMC_M1
GO:0030323	0.44	0.72	6	145	respiratory tube development	BP	1	ARG1,FGF2,ELK1,SPARC,ERRFI1,FGF10	red	VSMC_M1
GO:0007423	0.44	0.66	16	415	sensory organ development	BP	1	ZHX2,TRIOBP,FGF2,ARHGAP35,SDK2,IFT122,SPRED1,ACTL6A,PROM1,RARA,CECR2,SPARC,CYP1A1,B9D1,TPRN,FGF10	red	VSMC_M1
GO:0050657	0.44	0.72	6	135	nucleic acid transport	BP	1	POLDIP3,TST,PCID2,TNKS,RAE1,SNUPN	red	VSMC_M1
GO:0050658	0.44	0.72	6	135	RNA transport	BP	1	POLDIP3,TST,PCID2,TNKS,RAE1,SNUPN	red	VSMC_M1
GO:0060429	0.44	0.63	31	810	epithelium development	BP	1	SMAD4,CSNK2B,TRIOBP,TST,RPS7,PIH1D1,FGF2,ARHGAP35,IFT122,PAK1,TNFRSF19,EDNRA,SPRED1,HPSE,IFT57,TMEFF2,BCCIP,PROM1,KAT2A,PFN1,RARA,CECR2,CYP1A1,B9D1,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,E2F4,FGF10	red	VSMC_M1

GO:0050866	0.44	0.72	6	136	negative regulation of cell activation	BP	1	ARG1,IL20RB,PARP3,NR1D1,PRDX2,IL13RA2	red	VSMC_M1
GO:0090276	0.44	0.72	6	140	regulation of peptide hormone secretion	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4	red	VSMC_M1
GO:0050921	0.44	0.73	5	109	positive regulation of chemotaxis	BP	1	FGF2,CXCL12,P2RX4,TMSB4X,FGF10	red	VSMC_M1
GO:0002683	0.44	0.67	12	290	negative regulation of immune system process	BP	1	ARG1,IL1RL1,AHR,CXCL12,IL20RB,PARP3,CUEDC2,RARA,NR1D1,PRDX2,IL13RA2,RNF125	red	VSMC_M1
GO:0000910	0.45	0.71	6	141	cytokinesis	BP	1	DCTN3,UVRAG,SPAST,ARL3,CECR2,CALM2	red	VSMC_M1
GO:1903038	0.45	0.74	4	87	negative regulation of leukocyte cell-cell adhesion	BP	1	ARG1,CXCL12,IL20RB,PRDX2	red	VSMC_M1
GO:0045471	0.45	0.74	4	87	response to ethanol	BP	1	ALAD,GOT2,RARA,SPARC	red	VSMC_M1
GO:1903530	0.45	0.65	16	399	regulation of secretion by cell	BP	1	SMAD4,SRI,MAP4K4,FKBP1B,STAM,CXCL12,ARFIP1,P2RX4,RAB9A,ENSA,NR1D1,STXBP4,IL13RA2,RAB12,MYO18A,GOLPH3	red	VSMC_M1
GO:0019725	0.45	0.63	25	638	cellular homeostasis	BP	1	SMAD4,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,FGF2,DGAT2,CACNA2D1,CXCL12,EDNRA,SLC12A6,P2RX4,COX19,PRDX6,NR1D1,PRDX2,STXBP4,CALM2,FBXO4,E2F4,FKBP1A,RACK1,ATP6V1G1,PTPRN2	red	VSMC_M1
GO:0019724	0.45	0.74	4	87	B cell mediated immunity	BP	1	KMT5C,PARP3,IL13RA2,IGHA2	red	VSMC_M1
GO:0044238	0.45	0.59	301	7641	primary metabolic process	BP	1	CS,SMAD4,SGK1,ARG1,DYRK2,MTRF1L,ACR,CSNK2B,KLF10,DCAF13,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,POLR2F,TRIOBP,TST,EIF3D,MTERF2,SRI,UBAP1,RPP25L,RCL1,MUT,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,ANKRD39,ALDH1B1,AHR,XPA,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,COQ3,PSMB2,YAE1,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,FGF2,TAL1,EFR3B,PMPCB,IRF2BP1,SNRPD2,STAM,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,ENGASE,HNRNPL,PFDN1,RNF121,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,KMT5A,PDCD5,CTR9,SMN2,PTCD2,RPS3A,ELOC,GOT2,PLRG1,EIF2A,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,PKIG,FARS2,HLCS,ELOVL2,ACOT8,TBC1D7,IFT57,PARP3,PSPH,PRDM10,VKORC1L1,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ACTL6A,AKAP13,IRF2BP2,TGIF1,WDR5B,NIF3L1,PPP1R8,ENSA,GMPR2,PPP1R11,KLHL41,RBM4,CRTC3,SMYD2,PSMA7,DCAF17,RPL35A,PES1,BCCIP,RPL18A,FBXO45,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,ANAPC16,EMG1,TRMT44,PRDX6,USP5,MECOM,CHCHD1,LSM4,TRIM4,UBA1,DYNC2H1,UVSSA,ELK1,PELI2,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,PSMB6,ERC1,HSPA2,ITPKB,RARA,HDHD5,CTDNEP1,CECR2,NR1D1,DCP2,VPS37C,ETV3,SAMD1,ANAPC13,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,INO80E,PARP16,PRDX2,MBTD1,GATAD2B,INTS3,SUPT4H1,CAL	red	VSMC_M1
GO:0032273	0.45	0.72	5	116	positive regulation of protein polymerization	BP	1	PAK1,RPS3,ARFIP1,ARL3,PFN1	red	VSMC_M1
GO:0050851	0.45	0.72	5	117	antigen receptor-mediated signaling pathway	BP	1	EIF2B4,RPS3,EIF2B2,SPG21,IGHA2	red	VSMC_M1
GO:0001659	0.45	0.71	6	141	temperature homeostasis	BP	1	EGR1,HDAC3,KDM1A,NR1D1,OMA1,GNAS	red	VSMC_M1
GO:1902806	0.45	0.72	5	115	regulation of cell cycle G1/S phase transition	BP	1	PLRG1,CDC73,STXBP4,CYP1A1,FGF10	red	VSMC_M1
GO:0009967	0.45	0.61	44	1127	positive regulation of signal transduction	BP	1	SMAD4,CSNK2B,DYNLT1,CTNNA1,MAP4K4,SPIN1,NPR2,RPS7,PIH1D1,FGF2,WBP2,PAK1,RPS3,CSNK1D,HDAC3,PCID2,TNKS,TNFRSF19,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,TFG,CDC73,AKAP13,DYNC2H1,PELI2,ZMIZ1,ITPKB,CTDNEP1,CDK5RAP3,PRDX2,XRCC3,MIER1,GOLPH3,WWOX,FKBP1A,RACK1,TIMP3,RPS20,CPNE1,LY96,FGF10	red	VSMC_M1
GO:0043500	0.45	0.74	4	88	muscle adaptation	BP	1	SMAD4,PAK1,P2RX4,ERRFI1	red	VSMC_M1
GO:0031328	0.45	0.60	58	1503	positive regulation of cellular biosynthetic process	BP	1	SMAD4,DYRK2,KLF10,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,SPIN1,AHR,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,DGAT2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,P2RX4,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,RARA,CTDNEP1,NR1D1,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,FBXO4,RBM15,WDR5,WWOX,CIZ1,DR1,E2F4,IER2,ELOF1,TMSB4X,FGF10	red	VSMC_M1
GO:0071417	0.45	0.64	18	466	cellular response to organonitrogen compound	BP	1	ARG1,KLF10,EGR1,CTNNA1,AHR,RECQL5,PAK1,SOCS2,CACNA2D1,SP1,P2RX4,UROS,KDM1A,STXBP4,RAB12,GOLPH3,ERRFI1,GNAS	red	VSMC_M1
GO:0072001	0.45	0.67	10	256	renal system development	BP	1	SMAD4,EGR1,FGF2,PTCD2,ARL3,DYNC2H1,PROM1,RARA,CTNNBIP1,FGF10	red	VSMC_M1
GO:0071559	0.45	0.69	8	205	response to transforming growth factor beta	BP	1	SMAD4,ARG1,PDCD5,SPRED1,ZMIZ1,WWOX,FKBP1A,NREP	red	VSMC_M1
GO:0045184	0.45	0.60	55	1395	establishment of protein localization	BP	1	HSPA1L,DYNLT1,REEP2,SRI,UBAP1,MAP4K4,CLTA,CRIPT,PIH1D1,PARD3,FKBP1B,PMPCB,STAM,WBP2,PAK1,HDAC3,PCID2,TNKS,RAB28,PDCD5,VTI1B,TIMM10,ARFIP1,PKIG,ARL3,UNC119B,ARFGEF2,RAB9A,EMC9,ARL4C,ENSA,FAM45A,WDR11,EGR2,AP1S1,NDUFA13,ARL4D,RP2,ERC1,NR1D1,VPS37C,COPZ2,STXBP4,SNUPN,RAB12,MYO18A,GOLPH3,GOSR1,RAB39B,DNLZ,EVI5,RACK1,TOMM7,ATP5IF1,PTPRN2	red	VSMC_M1
GO:1990748	0.45	0.74	4	79	cellular detoxification	BP	1	PRDX6,PRDX2,GSTM3,SRXN1	red	VSMC_M1
GO:0042113	0.45	0.69	8	193	B cell activation	BP	1	AHR,KMT5C,PCID2,CEBPG,PARP3,IRF2BP2,ITFG2,IGHA2	red	VSMC_M1
GO:0030072	0.46	0.69	7	168	peptide hormone secretion	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4,PTPRN2	red	VSMC_M1
GO:0051236	0.46	0.70	6	138	establishment of RNA localization	BP	1	POLDIP3,TST,PCID2,TNKS,RAE1,SNUPN	red	VSMC_M1
GO:0007204	0.46	0.68	8	194	positive regulation of cytosolic calcium ion concentration	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,EDNRA,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0051147	0.46	0.72	5	115	regulation of muscle cell differentiation	BP	1	SMAD4,PAK1,RBM4,KAT2A,BHLHE41	red	VSMC_M1
GO:0002520	0.46	0.62	27	694	immune system development	BP	1	KLF10,ZFAT,EGR1,KMT5C,PGM3,TAL1,PCID2,CEBPG,CTR9,C15orf41,RPS6,PARP3,CDC73,IRF2BP2,MECOM,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,CDK5RAP3,PRDX2,CTNNBIP1,RBM15,NUDT21,ATP5IF1,FGF10	red	VSMC_M1
GO:1902533	0.46	0.62	29	731	positive regulation of intracellular signal transduction	BP	1	DYNLT1,MAP4K4,NPR2,RPS7,PIH1D1,FGF2,PAK1,RPS3,HDAC3,PCID2,TNFRSF19,P2RX4,SPRED1,STIMATE,HPSE,TFG,AKAP13,PELI2,ITPKB,CDK5RAP3,PRDX2,XRCC3,MIER1,GOLPH3,FKBP1A,RACK1,RPS20,CPNE1,FGF10	red	VSMC_M1
GO:0033044	0.46	0.69	7	168	regulation of chromosome organization	BP	1	MAD2L1BP,TAL1,PCID2,TNKS,DCP2,XRCC3,FBXO4	red	VSMC_M1

GO:0071902	0.46	0.69	7	170	positive regulation of protein serine/threonine kinase activity	BP	1	PIH1D1,FGF2,PAK1,RPS3,AKAP13,PARP16,CALM2	red	VSMC_M1
GO:0051254	0.46	0.60	52	1357	positive regulation of RNA metabolic process	BP	1	SMAD4,KLF10,ZFAT,HMGA1,TAF11,EGR1,ZNF76,SPIN1,AHR,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,EXOSC7,PRDX6,MECOM,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,DCP2,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,RBM15,WWOX,DR1,E2F4,IER2,NUDT21,ELOF1,FGF10	red	VSMC_M1
GO:0009566	0.46	0.72	5	113	fertilization	BP	1	SMAD4,ACR,HSPA1L,C11orf74,CECR2	red	VSMC_M1
GO:0003013	0.46	0.64	17	437	circulatory system process	BP	1	SGK1,SRI,NPR2,WDR35,FKBP1B,ARHGAP35,CACNA2D1,CXCL12,EDNRA,P2RX4,CACNA1D,AKAP13,MYL4,GJC1,CALM2,CTNNBIP1,E2F4	red	VSMC_M1
GO:1903532	0.46	0.68	8	196	positive regulation of secretion by cell	BP	1	SMAD4,SRI,STAM,CXCL12,P2RX4,RAB9A,MYO18A,GOLPH3	red	VSMC_M1
GO:1901698	0.46	0.61	33	845	response to nitrogen compound	BP	1	ARG1,RGS17,KLF10,EGR1,CTNNA1,AHR,ALAD,PSMB2,RECQL5,EIF2B4,PAK1,RNF121,SOCS2,ERLIN2,CACNA2D1,SP1,CXCL12,GOT2,P2RX4,HLCS,UROS,EGR2,KDM1A,RNF40,EIF2B2,STXBP4,SPARC,RAB12,GOLPH3,ERRFI1,UBE4B,GSTM3,GNAS	red	VSMC_M1
GO:0002791	0.46	0.70	6	142	regulation of peptide secretion	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4	red	VSMC_M1
GO:0008380	0.46	0.64	15	356	RNA splicing	BP	1	SF3B6,SNRPD2,TSEN54,HNRNPL,SMN2,PLRG1,PPP1R8,RBM4,KDM1A,PRDX6,LSM4,YJU2,RBM15,SF3B5,AHNAK	red	VSMC_M1
GO:0006906	0.46	0.73	4	90	vesicle fusion	BP	1	UVRAG,VTI1B,PRRT2,GOSR1	red	VSMC_M1
GO:0030833	0.46	0.70	6	145	regulation of actin filament polymerization	BP	1	TRIOBP,TMSB10,ARFIP1,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0048584	0.46	0.59	58	1488	positive regulation of response to stimulus	BP	1	SMAD4,ARG1,CSNK2B,DYNLT1,HMGA1,CTNNA1,IL1RL1,MAP4K4,SPIN1,NPR2,KMT5C,RPS7,PIH1D1,FKBP1B,FGF2,EIF2B4,WBP2,PAK1,RPS3,CSNK1D,HDAC3,PCID2,TNKS,CXCL12,TNFRSF19,CEBPG,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,TFG,PARP3,CDC73,AKAP13,DYNC2H1,PELI2,ZMIZ1,ITPKB,RARA,CTDNEP1,CDK5RAP3,EIF2B2,SPG21,PRDX2,XRCC3,MIER1,GOLPH3,WWOX,FKBP1A,RACK1,TIMP3,RPS20,TMSB4X,CPNE1,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0007416	0.46	0.71	5	132	synapse assembly	BP	1	SDK2,PCDH17,FBXO45,IL1RAP,FLRT2	red	VSMC_M1
GO:0006417	0.46	0.64	14	341	regulation of translation	BP	1	POLDIP3,EIF3D,MALSU1,EIF2B4,RPS3,EIF2A,OGFOD1,RBM4,EXOSC7,RARA,DCP2,EIF2B2,DPH5,RACK1	red	VSMC_M1
GO:0030097	0.47	0.62	24	618	hemopoiesis	BP	1	KLF10,ZFAT,EGR1,PGM3,TAL1,PCID2,CEBPG,CTR9,C15orf41,RPS6,CDC73,IRF2BP2,MECOM,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,CDK5RAP3,PRDX2,CTNNBIP1,RBM15,NUDT21,ATP5IF1	red	VSMC_M1
GO:0051604	0.47	0.66	10	230	protein maturation	BP	1	NAA35,INPP5B,YAE1,FKBP1B,PMPCB,MMP16,DYNC2H1,OMA1,FKBP1A,PSENEN	red	VSMC_M1
GO:0048646	0.47	0.61	33	877	anatomical structure formation involved in morphogenesis	BP	1	SMAD4,RPS7,SF3B6,FGF2,TAL1,ARHGAP35,SDK2,UBP1,IFT122,NEB,SP1,CTR9,EDNRA,SLC12A6,SPRED1,HPSE,IFT57,CDC73,ACTL6A,AKAP13,KLHL41,EGR2,PROM1,KAT2A,PFN1,RARA,CECR2,SPARC,PMP22,RBM15,FKBP1A,ATP5IF1,FGF10	red	VSMC_M1
GO:0048593	0.47	0.73	4	96	camera-type eye morphogenesis	BP	1	ZHX2,SDK2,IFT122,PROM1	red	VSMC_M1
GO:2001234	0.47	0.67	8	187	negative regulation of apoptotic signaling pathway	BP	1	CTNNA1,PIH1D1,CXCL12,KDM1A,NDUFA13,PRDX2,RFFL,FGF10	red	VSMC_M1
GO:0045596	0.47	0.63	19	489	negative regulation of cell differentiation	BP	1	SMAD4,DYNLT1,ZHX2,CTNNA1,NPR2,PAK1,CTR9,SPRED1,CDC73,MAP2,PRTG,ITPKB,RARA,NR1D1,PRDX2,HMG20A,RBM15,BHLHE41,FGF10	red	VSMC_M1
GO:0002696	0.47	0.66	9	218	positive regulation of leukocyte activation	BP	1	IL1RL1,KMT5C,RPS3,PCID2,ZMIZ1,ITPKB,RARA,IGHA2,FGF10	red	VSMC_M1
GO:0071900	0.47	0.65	12	300	regulation of protein serine/threonine kinase activity	BP	1	PIH1D1,FGF2,PAK1,UVRAG,RPS3,CCNI,PKIG,AKAP13,BCCIP,CDK5RAP3,PARP16,CALM2	red	VSMC_M1
GO:0015031	0.47	0.59	51	1301	protein transport	BP	1	HSPA1L,DYNLT1,REEP2,SRI,UBAP1,MAP4K4,CLTA,PARD3,FKBP1B,PMPCB,STAM,PAK1,HDAC3,PCID2,TNKS,RAB28,PDCD5,VTI1B,TIMM10,ARFIP1,PKIG,ARL3,UNC119B,ARFGEF2,RAB9A,ARL4C,ENSA,FAM45A,WDR11,EGR2,AP1S1,NDUFA13,ARL4D,RP2,ERC1,NR1D1,VPS37C,COPZ2,STXBP4,SNUPN,RAB12,MYO18A,GOLPH3,GOSR1,RAB39B,DNLZ,EVI5,RACK1,TOMM7,ATP5IF1,PTPRN2	red	VSMC_M1
GO:0030518	0.47	0.72	4	96	intracellular steroid hormone receptor signaling pathway	BP	1	WBP2,PAK1,KDM1A,ZMIZ1	red	VSMC_M1
GO:0090087	0.47	0.69	6	144	regulation of peptide transport	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4	red	VSMC_M1
GO:0003231	0.48	0.72	4	101	cardiac ventricle development	BP	1	SMAD4,PTCD2,RBM15,FKBP1A	red	VSMC_M1
GO:1901566	0.48	0.58	54	1317	organonitrogen compound biosynthetic process	BP	1	ARG1,MTRF1L,POLDIP3,EIF3D,NPR2,RPS5,RPL28,EEF1A1,MALSU1,PGM3,ALAD,RPS7,RPS11,EIF2B4,RPS3,NAXD,MTIF3,COPS5,RPS3A,GOT2,EIF2A,RPS6,OGFOD1,FARS2,ELOVL2,ACOT8,PSPH,YARS,EIF3I,WIPI1,RBM4,RPL35A,UROS,RPL18A,PTS,EXOSC7,MRPS14,CHCHD1,FTSJ1,RPS24,RARA,DCP2,EIF2B2,PARP16,CHST9,GOLPH3,DPH5,ALG14,SLC25A1,RACK1,RPS20,TMSB4X,ADI1,ATP5IF1	red	VSMC_M1
GO:0090066	0.48	0.62	16	418	regulation of anatomical structure size	BP	1	TRIOBP,WDR35,ARHGAP35,PAK1,NEB,CXCL12,EDNRA,TMSB10,SLC12A6,ARFIP1,KDM1A,MAP2,PFN1,KANK4,E2F4,TMSB4X	red	VSMC_M1
GO:0051099	0.48	0.68	6	141	positive regulation of binding	BP	1	EIF3D,CEBPG,KDM1A,RARA,CALM2,FKBP1A	red	VSMC_M1
GO:0048534	0.48	0.60	25	649	hematopoietic or lymphoid organ development	BP	1	KLF10,ZFAT,EGR1,PGM3,TAL1,PCID2,CEBPG,CTR9,C15orf41,RPS6,CDC73,IRF2BP2,MECOM,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,CDK5RAP3,PRDX2,CTNNBIP1,RBM15,NUDT21,ATP5IF1,FGF10	red	VSMC_M1
GO:0051090	0.48	0.63	13	328	regulation of DNA-binding transcription factor activity	BP	1	SGK1,SRI,RPS3,COPS5,CEBPG,CRTC3,KDM1A,IL1RAP,ERC1,CDK5RAP3,PRDX2,CTNNBIP1,TMSB4X	red	VSMC_M1
GO:0006302	0.48	0.65	9	225	double-strand break repair	BP	1	KMT5C,APLF,RECQL5,UVRAG,PARP3,KDM1A,RNF138,XRCC3,HUS1	red	VSMC_M1
GO:0030183	0.48	0.71	4	96	B cell differentiation	BP	1	PCID2,CEBPG,IRF2BP2,ITFG2	red	VSMC_M1
GO:0002790	0.49	0.67	7	172	peptide secretion	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4,PTPRN2	red	VSMC_M1

GO:0031325	0.49	0.56	95	2483	positive regulation of cellular metabolic process	BP	1	SMAD4,DYRK2,CSNK2B,KLF10,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,KCTD20,EIF3D,SPIN1,AHR,KMT5C,FAM161A,APLF,PIH1D1,WDR35,FGF2,TAL1,NR2C2,UBP1,WBP2,PAK1,UVRAG,DGAT2,RPS3,CSNK1D,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PDCD5,CTR9,P2RX4,AMBRA1,FBXW8,TBC1D7,IFT57,PARP3,PRDM10,CDC73,NPRL2,ACTL6A,AKAP13,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,ELK1,PELI2,ZMIZ1,KAT2A,HSPA2,RARA,CTDNEP1,NR1D1,DCP2,RNF40,MEF2D,CDK5RAP3,PARP16,SUPT4H1,CALM2,ARID3B,USP22,FBXO4,MOB3A,RBM15,WDR5,PTPA,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,FKBP1A,RACK1,ELOF1,TMSB4X,ATP5IF1,PSENEN,RCHY1,FGF10	red	VSMC_M1
GO:0071466	0.49	0.71	4	92	cellular response to xenobiotic stimulus	BP	1	AHR,RECQL5,CYP1A1,GSTM3	red	VSMC_M1
GO:2001242	0.49	0.68	6	135	regulation of intrinsic apoptotic signaling pathway	BP	1	RPS7,RPS3,CXCL12,KDM1A,NDUFA13,RACK1	red	VSMC_M1
GO:0002429	0.49	0.68	6	148	immune response-activating cell surface receptor signaling pathway	BP	1	EIF2B4,PAK1,RPS3,EIF2B2,SPG21,IGHA2	red	VSMC_M1
GO:0002757	0.49	0.68	6	148	immune response-activating signal transduction	BP	1	EIF2B4,PAK1,RPS3,EIF2B2,SPG21,IGHA2	red	VSMC_M1
GO:0035295	0.49	0.59	32	849	tube development	BP	1	SMAD4,ARG1,CSNK2B,RPS7,FGF2,TAL1,ARHGAP35,UBP1,IFT122,PAK1,SP1,EDNRA,SLC12A6,SPRED1,HPSE,IFT57,MYO18B,GJC1,ELK1,PROM1,ZMIZ1,KAT2A,PFN1,RARA,CECR2,SPARC,CYP1A1,ERRFI1,CTNNBIP1,RBM15,ATP5IF1,FGF10	red	VSMC_M1
GO:0071805	0.49	0.69	5	131	potassium ion transmembrane transport	BP	1	KCNF1,SLC12A6,CACNA1D,KCNQ2,KCNAB2	red	VSMC_M1
GO:0031334	0.49	0.65	8	199	positive regulation of protein-containing complex assembly	BP	1	PIH1D1,TAL1,PAK1,RPS3,ARFIP1,ARL3,PFN1,RACK1	red	VSMC_M1
GO:0097193	0.49	0.63	10	242	intrinsic apoptotic signaling pathway	BP	1	DYRK2,RPS7,RPS3,CXCL12,TMEM117,KDM1A,USP28,NDUFA13,WWOX,RACK1	red	VSMC_M1
GO:0044087	0.49	0.58	30	801	regulation of cellular component biogenesis	BP	1	SMAD4,TRIOBP,MAP4K4,MALSU1,PIH1D1,TAL1,ARHGAP35,STAM,PAK1,RPS3,VDAC3,TMSB10,ARFIP1,TBC1D7,TMEFF2,ARL3,NPRL2,MAP4,MAP2,IL1RAP,KAT2A,PFN1,HSPA2,PRRT2,FLRT2,TUBB4A,KANK4,CTNNBIP1,RACK1,TMSB4X	red	VSMC_M1
GO:0090174	0.49	0.70	4	94	organelle membrane fusion	BP	1	UVRAG,VTI1B,PRRT2,GOSR1	red	VSMC_M1
GO:0030217	0.50	0.66	7	179	T cell differentiation	BP	1	EGR1,RPS6,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0048284	0.50	0.68	5	120	organelle fusion	BP	1	UVRAG,VTI1B,PRRT2,OMA1,GOSR1	red	VSMC_M1
GO:0055065	0.50	0.60	17	438	metal ion homeostasis	BP	1	SMAD4,SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,SLC12A6,P2RX4,CNNM1,COX19,SCNN1A,CALM2,HMOX2,FKBP1A,SLC25A28,ATP6V1G1	red	VSMC_M1
GO:0016192	0.50	0.57	45	1192	vesicle-mediated transport	BP	1	HSPA1L,CLTA,STAM,PCDH17,NRBP1,PAK1,UVRAG,SPAST,CSNK1D,COPS5,VTI1B,ARFIP1,TFG,ARL3,SORCS1,WIPI1,ARFGEF2,RAB9A,ARL4C,FAM45A,WDR11,CEP19,AP1S1,ARL4D,RP2,ERC1,CLCN5,HSPA2,RARA,CECR2,COPZ2,TRAPPC1,PRRT2,IL13RA2,RAB12,MYO18A,GOLPH3,GOSR1,RAB39B,EVI5,ELMO3,RACK1,CNIH1,CPNE1,IGHA2	red	VSMC_M1
GO:2000058	0.50	0.67	6	143	regulation of ubiquitin-dependent protein catabolic process	BP	1	RPS7,CSNK1D,FBXW8,USP5,RACK1,RCHY1	red	VSMC_M1
GO:0000724	0.50	0.68	5	124	double-strand break repair via homologous recombination	BP	1	RECQL5,KDM1A,RNF138,XRCC3,HUS1	red	VSMC_M1
GO:0003206	0.50	0.70	4	101	cardiac chamber morphogenesis	BP	1	SMAD4,PTCD2,RBM15,FKBP1A	red	VSMC_M1
GO:0046883	0.50	0.65	7	174	regulation of hormone secretion	BP	1	SMAD4,SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4	red	VSMC_M1
GO:0061564	0.50	0.61	14	380	axon development	BP	1	SMAD4,DYNLT1,CTNNA1,PARD3,FKBP1B,ARHGAP35,PAK1,SPAST,CXCL12,FBXO45,EGR2,MAP2,FLRT2,NREP	red	VSMC_M1
GO:0010906	0.50	0.70	4	96	regulation of glucose metabolic process	BP	1	DYRK2,DGAT2,KAT2A,WDR5	red	VSMC_M1
GO:0032868	0.50	0.64	8	206	response to insulin	BP	1	EGR1,PAK1,SP1,GOT2,EGR2,STXBP4,RAB12,ERRFI1	red	VSMC_M1
GO:0001819	0.50	0.62	12	304	positive regulation of cytokine production	BP	1	EGR1,IL1RL1,RPS3,CEBPG,IL20RB,HPSE,CD58,ARFGEF2,IL1RAP,KAT2A,RARA,LY96	red	VSMC_M1
GO:0008361	0.50	0.66	6	157	regulation of cell size	BP	1	PAK1,CXCL12,SLC12A6,KDM1A,MAP2,E2F4	red	VSMC_M1
GO:0006508	0.50	0.56	51	1295	proteolysis	BP	1	ACR,UBAP1,INPP5B,ALAD,RPS7,PSMB2,PIH1D1,WDR35,PMPCB,STAM,RPS3,RNF121,CSNK1D,ERLIN2,PCID2,LTA4H,COPS5,PDCD5,ELOC,TLL1,MMP16,FBXW8,IFT57,PPP1R11,PSMA7,FBXO45,USP28,NDUFA13,USP5,UBA1,DYNC2H1,TRRAP,KAT2A,PSMB6,NR1D1,VPS37C,RNF40,RFFL,USP22,FBXO4,OMA1,UBE4B,USP10,RACK1,TIMP3,CPNE1,WFDC3,RNF125,ATP5IF1,PSENEN,RCHY1	red	VSMC_M1
GO:0061136	0.50	0.65	7	166	regulation of proteasomal protein catabolic process	BP	1	ALAD,CSNK1D,FBXW8,USP5,RNF40,RACK1,RCHY1	red	VSMC_M1
GO:0071482	0.50	0.69	4	94	cellular response to light stimulus	BP	1	XPA,COPS9,KDM1A,USP28	red	VSMC_M1
GO:0098876	0.50	0.67	5	129	vesicle-mediated transport to the plasma membrane	BP	1	ARL3,ARFGEF2,ARL4C,GOLPH3,RACK1	red	VSMC_M1
GO:0017015	0.51	0.69	4	102	regulation of transforming growth factor beta receptor signaling pathway	BP	1	SMAD4,SPRED1,FKBP1A,NREP	red	VSMC_M1
GO:0070201	0.51	0.59	17	436	regulation of establishment of protein localization	BP	1	HSPA1L,SRI,MAP4K4,FKBP1B,PAK1,HDAC3,PDCD5,ARFIP1,PKIG,ENSA,NR1D1,STXBP4,MYO18A,GOLPH3,RACK1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0097237	0.51	0.69	4	85	cellular response to toxic substance	BP	1	PRDX6,PRDX2,GSTM3,SRXN1	red	VSMC_M1
GO:0001817	0.51	0.59	19	492	regulation of cytokine production	BP	1	SMAD4,ARG1,EGR1,IL1RL1,RPS3,CEBPG,IL20RB,HPSE,CD58,CUEDC2,ARFGEF2,PPP1R11,IL1RAP,KAT2A,RARA,ERRFI1,TMSB4X,RNF125,LY96	red	VSMC_M1
GO:0043244	0.51	0.69	4	107	regulation of protein-containing complex disassembly	BP	1	TRIOBP,UVRAG,SPAST,OGFOD1	red	VSMC_M1
GO:0043269	0.51	0.59	17	444	regulation of ion transport	BP	1	ARG1,SRI,KCNF1,FKBP1B,CACNA2D1,CXCL12,P2RX4,CACNA1D,STIMATE,SCN3A,KCNQ2,HSPA2,CALM2,KCNAB2,FKBP1A,TMSB4X,AHNAK	red	VSMC_M1
GO:0050867	0.51	0.63	9	226	positive regulation of cell activation	BP	1	IL1RL1,KMT5C,RPS3,PCID2,ZMIZ1,ITPKB,RARA,IGHA2,FGF10	red	VSMC_M1
GO:0002285	0.51	0.67	5	127	lymphocyte activation involved in immune response	BP	1	KMT5C,RPS6,PARP3,ITFG2,RARA	red	VSMC_M1
GO:0009314	0.51	0.60	14	359	response to radiation	BP	1	EGR1,XPA,COPS9,ALAD,CXCL12,RBM4,KDM1A,USP28,UVSSA,ELK1,INTS3,FBXO4,UBE4B,HUS1	red	VSMC_M1
GO:0043484	0.51	0.67	5	126	regulation of RNA splicing	BP	1	HNRNPL,RBM4,PRDX6,RBM15,AHNAK	red	VSMC_M1
GO:0000725	0.51	0.67	5	126	recombinational repair	BP	1	RECQL5,KDM1A,RNF138,XRCC3,HUS1	red	VSMC_M1

GO:0043933	0.51	0.55	54	1370	protein-containing complex subunit organization	BP	1	SMAD4,MTRF1L,CSNK2B,PFDN6,HMGA1,TAF11,TRIOBP,EIF3D,CLTA,RPS5,ALAD,KCNF1,PIH1D1,PARD3,TAL1,SNRPD2,PAK1,UVRAG,RPS3,SPAST,NDUFA2,CSNK1D,KCTD16,CXCL12,SMN2,TMSB10,ARFIP1,OGFOD1,TFG,ARL3,CDC73,EIF3I,COX19,CRTC3,NDUFA10,MAP2,CABIN1,IL1RAP,NDUFA13,LSM4,PFN1,NDUFB7,DNAL1,PRRT2,TUBB4A,KANK4,OMA1,YJU2,CTNNBIP1,DR1,NUDT21,FKBP1A,RACK1,TMSB4X	red	VSMC_M1
GO:0106106	0.51	0.67	5	123	cold-induced thermogenesis	BP	1	HDAC3,KDM1A,NR1D1,OMA1,GNAS	red	VSMC_M1
GO:0120161	0.51	0.67	5	123	regulation of cold-induced thermogenesis	BP	1	HDAC3,KDM1A,NR1D1,OMA1,GNAS	red	VSMC_M1
GO:0051962	0.51	0.63	8	216	positive regulation of nervous system development	BP	1	PAK1,CXCL12,FBXW8,EGR2,KDM1A,ETV5,IL1RAP,FLRT2	red	VSMC_M1
GO:0006790	0.51	0.61	11	270	sulfur compound metabolic process	BP	1	TST,MUT,DGAT2,SP1,HLCS,ELOVL2,ACOT8,CHST9,GSTM3,SLC25A1,ADI1	red	VSMC_M1
GO:0030001	0.52	0.57	22	587	metal ion transport	BP	1	SGK1,SRI,KCNF1,FKBP1B,FGF2,PMPCB,CACNA2D1,CXCL12,SLC12A6,P2RX4,CACNA1D,STIMATE,SCN3A,KCNQ2,SCNN1A,HSPA2,CALM2,CACHD1,KCNAB2,FKBP1A,SLC25A28,AHNAK	red	VSMC_M1
GO:0042221	0.52	0.53	112	2921	response to chemical	BP	1	SMAD4,ARG1,RGS17,ACR,CSNK2B,KLF10,HSPA1L,NDRG1,EGR1,CTNNA1,SRI,IL1RL1,MAP4K4,NPR2,AHR,EEF1A1,ALAD,OSCP1,PSMB2,PIH1D1,WDR35,FKBP1B,FGF2,ARHGAP35,RECQL5,EIF2B4,WBP2,PAK1,DGAT2,RPS3,IL18BP,RNF121,CSNK1D,SOCS2,ERLIN2,CACNA2D1,TNKS,SP1,CXCL12,TNFRSF19,COPS5,IL20RB,PDCD5,CTR9,SLC12A6,GOT2,P2RX4,SPRED1,HLCS,CD58,TBC1D7,PSPH,VKORC1L1,CDC73,GRAMD1C,TGIF1,RAE1,ENSA,RBM4,UROS,RPL18A,EGR2,KDM1A,ETV5,IL1RAP,NDUFA13,PRDX6,ELK1,ZMIZ1,KAT2A,HSPA2,ITPKB,RARA,NR1D1,ETV3,RNF40,CDK5RAP3,EIF2B2,PARP16,PRDX2,FLRT2,STXBP4,CALM2,SPARC,CYP1A1,IL13RA2,XRCC3,RFFL,RAB12,GOLPH3,TBC1D24,ERRFI1,RBM15,UBE4B,GSTM3,COX4I1,USP10,WWOX,IER2,FKBP1A,GNAS,RACK1,SRXN1,ATP6V1G1,NREP,TIMP3,TMSB4X,CPNE1,RNF125,LY96,PTPRN2,FGF10	red	VSMC_M1
GO:0034764	0.52	0.65	6	155	positive regulation of transmembrane transport	BP	1	SRI,CACNA2D1,STIMATE,HSPA2,CALM2,TMSB4X	red	VSMC_M1
GO:0051896	0.52	0.66	5	125	regulation of protein kinase B signaling	BP	1	FGF2,P2RX4,HPSE,RACK1,CPNE1	red	VSMC_M1
GO:2000045	0.52	0.68	4	97	regulation of G1/S transition of mitotic cell cycle	BP	1	PLRG1,CDC73,CYP1A1,FGF10	red	VSMC_M1
GO:0008150	0.52	0.55	475	12183	biological_process	BP	1	CS,SMAD4,SGK1,ARG1,DYRK2,MTRF1L,RGS17,ACR,CSNK2B,KLF10,HSPA1L,DYNLT1,DCAF13,EGFL8,FGFR1OP,KIAA0930,PFDN6,POLDIP3,ZHX2,ZBTB22,MEI1,POLR3H,NDRG1,ZFAT,HMGA1,GNG5,TAF11,REEP2,EGR1,TCP11,RHPN1,ZNF76,CTNNA1,NAA35,DNAL4,KCTD20,POLR2F,TRIOBP,TST,EIF3D,TREML2,MTERF2,SRI,UBAP1,RPP25L,MAD2L1BP,DCTN3,RCL1,MUT,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,CLTA,UBE2M,ZNF584,RPS5,COX5B,SLC25A51,ANKRD39,ALDH1B1,AHR,XPA,CORO2A,INVS,RPL28,KMT5C,CRIPT,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,OSCP1,COQ3,KCNF1,PSMB2,YAE1,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,NUDT6,FGF2,TAL1,EFR3B,PMPCB,ARHGAP35,ADGRF3,IRF2BP1,SNRPD2,SDK2,STAM,NR2C2,TSC22D1,UBP1,RAB30,FAM171A1,IFT122,TSEN54,ERI3,RECQL5,PCDH17,EIF2B4,WBP2,NRBP1,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,VDAC3,ENGASE,HNRNPL,SPAST,NEB,PSD2,NRG2,PFDN1,COX7B,IL18BP,RNF121,MCRIP1,NDUFA2,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,KCTD16,CACNA2D1,LTA4H,CDK17,TNKS,MTIF3,C11orf74,SP1,RAB28,CXCL12,TNFRSF19,MTFR1,COPS5,CEBPG,ZNF341,CD8B,IL20RB,KMT5A,PDCD5,CTR9,VTI1B,EDNRA,SMN2,TIMM10,DNAH12,TMSB10,SLC12A6,PTCD2,RPS3A,ELOC,ARFIP1,RHOF,C21orf91,GOT2,P2RX4,RRAS2,PLRG1,EIF2A,C15orf41,EDIL3,CACNA1D,SPRED1,CCNI,RPS6,STIMATE,TLL1,MMP16,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,TFG,CNNM1,PKIG,FARS2,TMEM117,HLCS,ELOVL2,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PSPH,PRDM10,VKORC1L1,CUEDC2,ARL3,UNC119B,GCA,FAM118B,YARS,CDC73,CYB561	red	VSMC_M1
GO:0009891	0.52	0.54	58	1533	positive regulation of biosynthetic process	BP	1	SMAD4,DYRK2,KLF10,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,SPIN1,AHR,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,DGAT2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,P2RX4,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,RARA,CTDNEP1,NR1D1,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,FBXO4,RBM15,WDR5,WWOX,CIZ1,DR1,E2F4,IER2,ELOF1,TMSB4X,FGF10	red	VSMC_M1
GO:0045732	0.52	0.62	8	203	positive regulation of protein catabolic process	BP	1	CSNK1D,FBXW8,NDUFA13,USP5,RNF40,RACK1,ATP5IF1,RCHY1	red	VSMC_M1
GO:1903844	0.52	0.68	4	104	regulation of cellular response to transforming growth factor beta stimulus	BP	1	SMAD4,SPRED1,FKBP1A,NREP	red	VSMC_M1
GO:0009451	0.52	0.64	6	141	RNA modification	BP	1	EMG1,TRMT44,FTSJ1,RBM15,URM1,NOP10	red	VSMC_M1
GO:0043123	0.52	0.64	6	153	positive regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	TNFRSF19,TFG,AKAP13,PELI2,MIER1,FKBP1A	red	VSMC_M1
GO:0048545	0.52	0.60	10	258	response to steroid hormone	BP	1	ARG1,ACR,ALAD,WBP2,PAK1,KDM1A,ZMIZ1,NR1D1,SPARC,ERRFI1	red	VSMC_M1
GO:0010498	0.52	0.58	17	434	proteasomal protein catabolic process	BP	1	ALAD,PSMB2,RNF121,CSNK1D,ERLIN2,FBXW8,PSMA7,FBXO45,USP5,PSMB6,NR1D1,RNF40,RFFL,FBXO4,UBE4B,RACK1,RCHY1	red	VSMC_M1
GO:0046879	0.53	0.62	8	206	hormone secretion	BP	1	SMAD4,SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4,PTPRN2	red	VSMC_M1
GO:0046034	0.53	0.60	10	219	ATP metabolic process	BP	1	COX5B,SLC25A51,COX7B,NDUFA2,NDUFA10,NDUFB7,COX4I1,TMSB4X,ATP5IF1,COX7C	red	VSMC_M1
GO:0032270	0.53	0.54	41	1066	positive regulation of cellular protein metabolic process	BP	1	SMAD4,CSNK2B,POLDIP3,EGR1,EIF3D,FAM161A,PIH1D1,WDR35,FGF2,TAL1,WBP2,PAK1,RPS3,CSNK1D,HDAC3,PDCD5,CTR9,FBXW8,TBC1D7,IFT57,AKAP13,KDM1A,NDUFA13,USP5,PELI2,KAT2A,HSPA2,RNF40,CDK5RAP3,PARP16,CALM2,FBXO4,MOB3A,WDR5,PTPA,FKBP1A,RACK1,ATP5IF1,PSENEN,RCHY1,FGF10	red	VSMC_M1
GO:0070661	0.53	0.62	8	201	leukocyte proliferation	BP	1	ARG1,AHR,FKBP1B,RPS3,IL20RB,RPS6,PRDX2,FGF10	red	VSMC_M1
GO:0007605	0.53	0.67	4	102	sensory perception of sound	BP	1	TRIOBP,TIMM10,CACNA1D,TPRN	red	VSMC_M1

GO:0061025	0.53	0.65	5	125	membrane fusion	BP	1	UVRAG,VTI1B,GCA,PRRT2,GOSR1	red	VSMC_M1
GO:0050679	0.53	0.64	6	154	positive regulation of epithelial cell proliferation	BP	1	ARG1,FGF2,SP1,CXCL12,STXBP4,FGF10	red	VSMC_M1
GO:0070848	0.53	0.56	21	570	response to growth factor	BP	1	SMAD4,ARG1,EGR1,EEF1A1,FGF2,CSNK1D,PDCD5,SPRED1,TBC1D7,TGIF1,ELK1,ZMIZ1,KAT2A,FLRT2,ERRFI1,WWOX,IER2,FKBP1A,RACK1,NREP,FGF10	red	VSMC_M1
GO:0032434	0.53	0.65	5	121	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	CSNK1D,FBXW8,USP5,RACK1,RCHY1	red	VSMC_M1
GO:0060041	0.53	0.67	4	108	retina development in camera-type eye	BP	1	ZHX2,SDK2,ACTL6A,PROM1	red	VSMC_M1
GO:0097191	0.53	0.62	7	173	extrinsic apoptotic signaling pathway	BP	1	CTNNA1,NDUFA13,PRDX2,RFFL,WWOX,TIMP3,FGF10	red	VSMC_M1
GO:0090257	0.53	0.62	7	179	regulation of muscle system process	BP	1	SMAD4,SRI,FKBP1B,PAK1,P2RX4,CALM2,ERRFI1	red	VSMC_M1
GO:0051250	0.53	0.67	4	99	negative regulation of lymphocyte activation	BP	1	ARG1,IL20RB,PARP3,PRDX2	red	VSMC_M1
GO:0010631	0.53	0.60	10	261	epithelial cell migration	BP	1	CSNK2B,MAP4K4,FGF2,SP1,P2RX4,SPRED1,PFN1,SPARC,TMSB4X,FGF10	red	VSMC_M1
GO:0035966	0.53	0.63	6	143	response to topologically incorrect protein	BP	1	HSPA1L,COPS5,HSPA2,CDK5RAP3,PARP16,RACK1	red	VSMC_M1
GO:0042542	0.53	0.65	5	118	response to hydrogen peroxide	BP	1	ARG1,FKBP1B,RPS3,IL18BP,RACK1	red	VSMC_M1
GO:0030855	0.54	0.57	16	430	epithelial cell differentiation	BP	1	SMAD4,TRIOBP,TST,PIH1D1,FGF2,SPRED1,BCCIP,PROM1,RARA,CYP1A1,B9D1,TPRN,ERRFI1,GSTM3,E2F4,FGF10	red	VSMC_M1
GO:0006913	0.54	0.59	10	257	nucleocytoplasmic transport	BP	1	POLDIP3,HDAC3,PCID2,PKIG,AKAP13,RAE1,RBM4,EGR2,SNUPN,RITA1	red	VSMC_M1
GO:0051169	0.54	0.59	10	257	nuclear transport	BP	1	POLDIP3,HDAC3,PCID2,PKIG,AKAP13,RAE1,RBM4,EGR2,SNUPN,RITA1	red	VSMC_M1
GO:0090132	0.54	0.59	10	262	epithelium migration	BP	1	CSNK2B,MAP4K4,FGF2,SP1,P2RX4,SPRED1,PFN1,SPARC,TMSB4X,FGF10	red	VSMC_M1
GO:0000956	0.54	0.66	4	102	nuclear-transcribed mRNA catabolic process	BP	1	PCID2,EXOSC7,LSM4,DCP2	red	VSMC_M1
GO:0050673	0.54	0.58	12	316	epithelial cell proliferation	BP	1	ARG1,FGF2,SP1,CXCL12,IFT57,CDC73,NR1D1,STXBP4,SPARC,ERRFI1,ATP5IF1,FGF10	red	VSMC_M1
GO:0002682	0.54	0.53	35	915	regulation of immune system process	BP	1	ARG1,KLF10,IL1RL1,AHR,KMT5C,TAL1,EIF2B4,PAK1,RPS3,PCID2,CXCL12,CD8B,IL20RB,CTR9,P2RX4,PARP3,CUEDC2,CDC73,ZMIZ1,KAT2A,ITPKB,RARA,NR1D1,EIF2B2,SPG21,PRDX2,IL13RA2,MYO18A,CTNNBIP1,RBM15,FKBP1A,RNF125,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0044272	0.54	0.64	5	127	sulfur compound biosynthetic process	BP	1	SP1,ELOVL2,CHST9,SLC25A1,ADI1	red	VSMC_M1
GO:0062197	0.54	0.58	11	282	cellular response to chemical stress	BP	1	ARG1,RPS3,IL18BP,SLC12A6,VKORC1L1,ETV5,PRDX2,TBC1D24,ERRFI1,RACK1,SRXN1	red	VSMC_M1
GO:0046890	0.54	0.64	5	127	regulation of lipid biosynthetic process	BP	1	EGR1,DGAT2,ERLIN2,CTDNEP1,NR1D1	red	VSMC_M1
GO:0051260	0.54	0.64	5	128	protein homooligomerization	BP	1	ALAD,KCNF1,SPAST,KCTD16,CRTC3	red	VSMC_M1
GO:0034220	0.54	0.53	29	765	ion transmembrane transport	BP	1	SRI,COX5B,KCNF1,FKBP1B,FGF2,PMPCB,VDAC3,COX7B,CACNA2D1,SLC12A6,P2RX4,CACNA1D,STIMATE,SCN3A,KCNQ2,GJC1,SCNN1A,CLCN5,HSPA2,CALM2,CACHD1,KCNAB2,COX4I1,FKBP1A,SLC25A1,SLC25A28,ATP6V1G1,TMSB4X,AHNAK	red	VSMC_M1
GO:0002768	0.55	0.62	6	158	immune response-regulating cell surface receptor signaling pathway	BP	1	EIF2B4,PAK1,RPS3,EIF2B2,SPG21,IGHA2	red	VSMC_M1
GO:0006813	0.55	0.63	5	140	potassium ion transport	BP	1	KCNF1,SLC12A6,CACNA1D,KCNQ2,KCNAB2	red	VSMC_M1
GO:0001816	0.55	0.55	19	504	cytokine production	BP	1	SMAD4,ARG1,EGR1,IL1RL1,RPS3,CEBPG,IL20RB,HPSE,CD58,CUEDC2,ARFGEF2,PPP1R11,IL1RAP,KAT2A,RARA,ERRFI1,TMSB4X,RNF125,LY96	red	VSMC_M1
GO:0051173	0.55	0.50	88	2331	positive regulation of nitrogen compound metabolic process	BP	1	SMAD4,CSNK2B,KLF10,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,SPIN1,AHR,KMT5C,FAM161A,APLF,PIH1D1,WDR35,FGF2,TAL1,NR2C2,UBP1,WBP2,PAK1,RPS3,CSNK1D,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PDCD5,CTR9,P2RX4,FBXW8,TBC1D7,IFT57,PARP3,PRDM10,CDC73,ACTL6A,AKAP13,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,ELK1,PELI2,ZMIZ1,KAT2A,HSPA2,RARA,NR1D1,DCP2,RNF40,MEF2D,CDK5RAP3,PARP16,SUPT4H1,CALM2,ARID3B,USP22,FBXO4,MOB3A,RBM15,WDR5,PTPA,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,FKBP1A,RACK1,ELOF1,TMSB4X,ATP5IF1,PSENEN,RCHY1,FGF10	red	VSMC_M1
GO:0006694	0.55	0.63	5	126	steroid biosynthetic process	BP	1	EGR1,ERLIN2,ACOT8,NR1D1,CYP1A1	red	VSMC_M1
GO:0008360	0.55	0.63	5	134	regulation of cell shape	BP	1	ARHGAP35,FAM171A1,RHOF,CFAP410,RHOD	red	VSMC_M1
GO:0050863	0.55	0.60	8	206	regulation of T cell activation	BP	1	ARG1,RPS3,IL20RB,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0008219	0.55	0.51	61	1587	cell death	BP	1	SMAD4,SGK1,ARG1,DYRK2,DYNLT1,EGR1,CTNNA1,NAA35,MAP4K4,UBE2M,AHR,UTP11,RPS7,PIH1D1,WDR35,FGF2,PAK1,RPS3,HDAC3,SOCS2,PCID2,CXCL12,TNFRSF19,COPS5,PDCD5,RPS3A,P2RX4,RRAS2,RPS6,TMEM117,IFT57,YARS,CDC73,KDM1A,USP28,NDUFA13,MECOM,ELK1,ERC1,ITPKB,RARA,CECR2,MEF2D,CDK5RAP3,PARP16,PRDX2,PMP22,RFFL,MYO18A,OMA1,GOLPH3,TBC1D24,UBE4B,PTPA,WWOX,ELMO3,RACK1,TIMP3,ATP5IF1,NAA38,FGF10	red	VSMC_M1
GO:0051480	0.55	0.60	8	212	regulation of cytosolic calcium ion concentration	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,EDNRA,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0006006	0.55	0.62	6	155	glucose metabolic process	BP	1	DYRK2,DGAT2,KAT2A,OMA1,WDR5,SLC25A1	red	VSMC_M1
GO:0051047	0.55	0.60	8	211	positive regulation of secretion	BP	1	SMAD4,SRI,STAM,CXCL12,P2RX4,RAB9A,MYO18A,GOLPH3	red	VSMC_M1
GO:0007254	0.55	0.63	5	134	JNK cascade	BP	1	MAP4K4,HDAC3,TNFRSF19,COPS5,MECOM	red	VSMC_M1

GO:0048731	0.55	0.49	132	3556	system development	BP	1	SMAD4,SGK1,ARG1,CSNK2B,KLF10,DYNLT1,ZHX2,NDRG1,ZFAT,EGR1,CTNNA1,TRIOBP,SRI,MAP4K4,NPR2,AHR,KMT5C,PGM3,UTP11,RPS7,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,UBP1,IFT122,PCDH17,EIF2B4,PAK1,DGAT2,SPAST,NEB,NRG2,COX7B,MCRIP1,CSNK1D,SOCS2,PCID2,SP1,CXCL12,TNFRSF19,CEBPG,CTR9,EDNRA,SMN2,SLC12A6,PTCD2,C21orf91,GOT2,P2RX4,C15orf41,SPRED1,RPS6,TLL1,MMP16,HPSE,AMBRA1,FBXW8,IFT57,PARP3,TMEFF2,ARL3,UNC119B,CDC73,ACTL6A,AKAP13,IRF2BP2,MYO18B,NIF3L1,KLHL41,WDR11,SMYD2,KCNQ2,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,PTS,IL1RAP,GJC1,MECOM,DYNC2H1,ELK1,PROM1,ITFG2,ZMIZ1,KAT2A,PFN1,PRTG,ITPKB,RARA,CECR2,NR1D1,MEF2D,CDK5RAP3,EIF2B2,PRDX2,MBTD1,FLRT2,CALM2,SPARC,PMP22,CYP1A1,HMG20A,B9D1,TBC1D24,GFER,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,WDR5,WWOX,E2F4,IER2,NUDT21,FKBP1A,GNAS,BORCS8,NREP,BHLHE41,CPNE1,RITA1,ATP5IF1,FGF10	red	VSMC_M1
GO:0052547	0.55	0.57	12	294	regulation of peptidase activity	BP	1	PIH1D1,WDR35,RPS3,PCID2,PDCD5,IFT57,NDUFA13,RFFL,RACK1,TIMP3,WFDC3,PSENEN	red	VSMC_M1
GO:1903037	0.55	0.59	8	206	regulation of leukocyte cell-cell adhesion	BP	1	ARG1,RPS3,CXCL12,IL20RB,ZMIZ1,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0010821	0.55	0.63	5	124	regulation of mitochondrion organization	BP	1	WDR35,PDCD5,OMA1,GOLPH3,ATP5IF1	red	VSMC_M1
GO:0072594	0.55	0.56	14	355	establishment of protein localization to organelle	BP	1	HSPA1L,PIH1D1,PMPCB,STAM,HDAC3,PDCD5,TIMM10,PKIG,NDUFA13,VPS37C,SNUPN,DNLZ,TOMM7,ATP5IF1	red	VSMC_M1
GO:0003007	0.55	0.60	7	197	heart morphogenesis	BP	1	SMAD4,PTCD2,IFT57,ZMIZ1,FLRT2,RBM15,FKBP1A	red	VSMC_M1
GO:0080135	0.55	0.54	21	553	regulation of cellular response to stress	BP	1	HMGA1,MAP4K4,KMT5C,FKBP1B,RECQL5,RPS3,HDAC3,CXCL12,TNFRSF19,COPS5,CEBPG,KMT5A,SPRED1,PARP3,SMYD2,KDM1A,MECOM,FBXO4,YJU2,RACK1,FGF10	red	VSMC_M1
GO:0030041	0.55	0.61	6	160	actin filament polymerization	BP	1	TRIOBP,TMSB10,ARFIP1,PFN1,KANK4,TMSB4X	red	VSMC_M1
GO:0014074	0.55	0.65	4	109	response to purine-containing compound	BP	1	AHR,P2RX4,KDM1A,SPARC	red	VSMC_M1
GO:0009914	0.56	0.59	8	212	hormone transport	BP	1	SMAD4,SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4,PTPRN2	red	VSMC_M1
GO:0051222	0.56	0.58	9	241	positive regulation of protein transport	BP	1	HSPA1L,SRI,PAK1,HDAC3,PDCD5,MYO18A,GOLPH3,RACK1,TOMM7	red	VSMC_M1
GO:0007159	0.56	0.58	9	234	leukocyte cell-cell adhesion	BP	1	ARG1,RPS3,CXCL12,IL20RB,ZMIZ1,ITPKB,RARA,PRDX2,GOLPH3	red	VSMC_M1
GO:0051017	0.56	0.62	5	139	actin filament bundle assembly	BP	1	FAM171A1,PAK1,TMEFF2,RHOD,PFN1	red	VSMC_M1
GO:0048839	0.56	0.62	5	139	inner ear development	BP	1	TRIOBP,CECR2,SPARC,TPRN,FGF10	red	VSMC_M1
GO:0007292	0.56	0.64	4	101	female gamete generation	BP	1	NPR2,MEI4,RPS6,ZMIZ1	red	VSMC_M1
GO:0030856	0.56	0.64	4	106	regulation of epithelial cell differentiation	BP	1	FGF2,SPRED1,PROM1,ERRFI1	red	VSMC_M1
GO:0010638	0.56	0.54	16	428	positive regulation of organelle organization	BP	1	MAD2L1BP,WDR35,TAL1,ARHGAP35,PAK1,UVRAG,RPS3,SPAST,TNKS,PDCD5,ARFIP1,ARL3,PFN1,PRRT2,FBXO4,ATP5IF1	red	VSMC_M1
GO:0001764	0.56	0.64	4	113	neuron migration	BP	1	CXCL12,FBXO45,ZMIZ1,FLRT2	red	VSMC_M1
GO:0090130	0.56	0.57	10	266	tissue migration	BP	1	CSNK2B,MAP4K4,FGF2,SP1,P2RX4,SPRED1,PFN1,SPARC,TMSB4X,FGF10	red	VSMC_M1
GO:0035264	0.56	0.64	4	108	multicellular organism growth	BP	1	SOCS2,WDR11,KAT2A,RARA	red	VSMC_M1
GO:0071214	0.56	0.57	10	267	cellular response to abiotic stimulus	BP	1	EGR1,XPA,COPS9,SLC12A6,KDM1A,USP28,ELK1,FBXO4,ERRFI1,HUS1	red	VSMC_M1
GO:0104004	0.56	0.57	10	267	cellular response to environmental stimulus	BP	1	EGR1,XPA,COPS9,SLC12A6,KDM1A,USP28,ELK1,FBXO4,ERRFI1,HUS1	red	VSMC_M1
GO:0034249	0.57	0.59	7	183	negative regulation of cellular amide metabolic process	BP	1	MALSU1,RPS3,RBM4,EXOSC7,RARA,DCP2,RACK1	red	VSMC_M1
GO:0006909	0.57	0.60	6	163	phagocytosis	BP	1	PAK1,RARA,MYO18A,ELMO3,RACK1,IGHA2	red	VSMC_M1
GO:0051239	0.57	0.49	72	1937	regulation of multicellular organismal process	BP	1	SMAD4,SGK1,ARG1,CSNK2B,KLF10,DYNLT1,EGR1,TCP11,CTNNA1,SRI,IL1RL1,MAP4K4,KMT5C,PARD3,WDR35,FKBP1B,FGF2,TAL1,NR2C2,PAK1,RPS3,HDAC3,SOCS2,PCID2,CACNA2D1,SP1,CXCL12,CEBPG,IL20RB,CTR9,P2RX4,CACNA1D,SPRED1,HPSE,FBXW8,CD58,PARP3,CUEDC2,CDC73,ARFGEF2,PPP1R11,ARHGDIB,EGR2,KDM1A,ETV5,MYL4,MAP2,IL1RAP,GJC1,PROM1,ZMIZ1,KAT2A,PFN1,PRTG,ITPKB,RARA,NR1D1,PRDX2,FLRT2,CALM2,SPARC,OMA1,ERRFI1,CTNNBIP1,RBM15,GNAS,RACK1,TMSB4X,BHLHE41,RNF125,LY96,FGF10	red	VSMC_M1
GO:0009416	0.57	0.57	9	239	response to light stimulus	BP	1	XPA,COPS9,RBM4,KDM1A,USP28,UVSSA,ELK1,UBE4B,HUS1	red	VSMC_M1
GO:0009893	0.57	0.48	106	2815	positive regulation of metabolic process	BP	1	SMAD4,DYRK2,CSNK2B,KLF10,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,KCTD20,EIF3D,IL1RL1,SPIN1,AHR,KMT5C,FAM161A,APLF,RPS7,PIH1D1,WDR35,FGF2,TAL1,NR2C2,UBP1,WBP2,PAK1,UVRAG,DGAT2,RPS3,CSNK1D,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,IL20RB,PDCD5,CTR9,P2RX4,HPSE,AMBRA1,FBXW8,CD58,TBC1D7,IFT57,PARP3,PRDM10,CDC73,NPRL2,ARFGEF2,ACTL6A,AKAP13,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,ELK1,PELI2,ZMIZ1,KAT2A,HSPA2,RARA,CTDNEP1,NR1D1,DCP2,RNF40,MEF2D,CDK5RAP3,PARP16,SUPT4H1,CALM2,ARID3B,USP22,FBXO4,OMA1,MOB3A,RBM15,WDR5,PTPA,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,FKBP1A,GNAS,RACK1,ELOF1,TMSB4X,IGHA2,ATP5IF1,PSENEN,LY96,RCHY1,FGF10	red	VSMC_M1
GO:0035265	0.57	0.61	5	134	organ growth	BP	1	FGF2,PAK1,AKAP13,RARA,FGF10	red	VSMC_M1
GO:0061572	0.57	0.61	5	141	actin filament bundle organization	BP	1	FAM171A1,PAK1,TMEFF2,RHOD,PFN1	red	VSMC_M1
GO:0045930	0.57	0.58	7	186	negative regulation of mitotic cell cycle	BP	1	MAD2L1BP,PCID2,CDC73,CDK5RAP3,INTS3,XRCC3,HUS1	red	VSMC_M1
GO:0002274	0.57	0.60	6	156	myeloid leukocyte activation	BP	1	NDRG1,IL1RL1,CRTC3,NR1D1,IL13RA2,MYO18A	red	VSMC_M1
GO:0015833	0.57	0.58	7	186	peptide transport	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4,PTPRN2	red	VSMC_M1
GO:0006979	0.57	0.54	14	357	response to oxidative stress	BP	1	ARG1,ALAD,FKBP1B,RPS3,IL18BP,SP1,VKORC1L1,ETV5,PRDX6,PRDX2,HMOX2,TBC1D24,RACK1,SRXN1	red	VSMC_M1
GO:0034614	0.57	0.61	5	124	cellular response to reactive oxygen species	BP	1	ARG1,RPS3,IL18BP,PRDX2,RACK1	red	VSMC_M1
GO:0000077	0.57	0.63	4	105	DNA damage checkpoint signaling	BP	1	USP28,CDK5RAP3,FBXO4,HUS1	red	VSMC_M1
GO:1990845	0.57	0.61	5	132	adaptive thermogenesis	BP	1	HDAC3,KDM1A,NR1D1,OMA1,GNAS	red	VSMC_M1

GO:2000026	0.57	0.50	37	1014	regulation of multicellular organismal development	BP	1	SMAD4,KLF10,DYNLT1,CTNNA1,PARD3,FGF2,TAL1,NR2C2,PAK1,PCID2,SP1,CXCL12,CTR9,SPRED1,HPSE,FBXW8,CDC73,EGR2,KDM1A,ETV5,MAP2,IL1RAP,PROM1,ZMIZ1,KAT2A,PRTG,ITPKB,RARA,NR1D1,PRDX2,FLRT2,SPARC,ERRFI1,CTNNBIP1,RBM15,RACK1,BHLHE41	red	VSMC_M1
GO:0015931	0.57	0.58	7	181	nucleobase-containing compound transport	BP	1	POLDIP3,TST,SLC25A51,PCID2,TNKS,RAE1,SNUPN	red	VSMC_M1
GO:0034599	0.58	0.56	9	234	cellular response to oxidative stress	BP	1	ARG1,RPS3,IL18BP,VKORC1L1,ETV5,PRDX2,TBC1D24,RACK1,SRXN1	red	VSMC_M1
GO:0051384	0.58	0.62	4	104	response to glucocorticoid	BP	1	ARG1,ALAD,SPARC,ERRFI1	red	VSMC_M1
GO:0002521	0.58	0.53	14	383	leukocyte differentiation	BP	1	KLF10,EGR1,TAL1,PCID2,CEBPG,RPS6,IRF2BP2,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,CTNNBIP1	red	VSMC_M1
GO:0006886	0.58	0.50	28	739	intracellular protein transport	BP	1	HSPA1L,REEP2,CLTA,PARD3,PMPCB,STAM,PAK1,HDAC3,RAB28,PDCD5,VTI1B,TIMM10,ARFIP1,PKIG,ARL4C,WDR11,EGR2,AP1S1,NDUFA13,ARL4D,VPS37C,COPZ2,STXBP4,SNUPN,DNLZ,EVI5,TOMM7,ATP5IF1	red	VSMC_M1
GO:0048659	0.58	0.60	5	128	smooth muscle cell proliferation	BP	1	NAA35,FGF2,PAK1,MEF2D,CTNNBIP1	red	VSMC_M1
GO:0033865	0.58	0.62	4	102	nucleoside bisphosphate metabolic process	BP	1	DGAT2,ELOVL2,ACOT8,SLC25A1	red	VSMC_M1
GO:0033875	0.58	0.62	4	102	ribonucleoside bisphosphate metabolic process	BP	1	DGAT2,ELOVL2,ACOT8,SLC25A1	red	VSMC_M1
GO:0034032	0.58	0.62	4	102	purine nucleoside bisphosphate metabolic process	BP	1	DGAT2,ELOVL2,ACOT8,SLC25A1	red	VSMC_M1
GO:0010557	0.58	0.48	53	1433	positive regulation of macromolecule biosynthetic process	BP	1	SMAD4,DYRK2,KLF10,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,SPIN1,AHR,PIH1D1,FGF2,TAL1,NR2C2,UBP1,WBP2,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,PRDM10,CDC73,ACTL6A,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,MECOM,ELK1,ZMIZ1,KAT2A,RARA,NR1D1,MEF2D,CDK5RAP3,SUPT4H1,ARID3B,USP22,FBXO4,RBM15,WWOX,CIZ1,DR1,E2F4,IER2,ELOF1,FGF10	red	VSMC_M1
GO:0071704	0.58	0.45	315	8083	organic substance metabolic process	BP	1	CS,SMAD4,SGK1,ARG1,DYRK2,MTRF1L,ACR,CSNK2B,KLF10,DCAF13,FGFR1OP,PFDN6,POLDIP3,ZHX2,ZBTB22,POLR3H,ZFAT,HMGA1,TAF11,EGR1,ZNF76,NAA35,POLR2F,TRIOBP,TST,EIF3D,MTERF2,SRI,UBAP1,RPP25L,RCL1,MUT,IL1RL1,MAP4K4,SPIN1,NPR2,ICK,UBE2M,ZNF584,RPS5,ANKRD39,ALDH1B1,AHR,XPA,RPL28,KMT5C,EEF1A1,COPS9,MALSU1,MEI4,PGM3,FAM161A,UTP11,INPP5B,ALAD,APLF,RPS7,COQ3,PSMB2,YAE1,RPS11,PIH1D1,GPT2,PARD3,WDR35,ADCK2,FKBP1B,SF3B6,FGF2,TAL1,EFR3B,PMPCB,IRF2BP1,SNRPD2,STAM,NR2C2,TSC22D1,UBP1,TSEN54,ERI3,RECQL5,EIF2B4,WBP2,PAK1,UVRAG,EBNA1BP2,DGAT2,RPS3,ENGASE,HNRNPL,PFDN1,RNF121,CSNK1D,NAXD,HDAC3,SOCS2,ERLIN2,PCID2,LTA4H,CDK17,TNKS,MTIF3,SP1,COPS5,CEBPG,ZNF341,IL20RB,KMT5A,PDCD5,CTR9,SMN2,PTCD2,RPS3A,ELOC,GOT2,PLRG1,EIF2A,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,GPAT3,OGFOD1,AMBRA1,GMDS,FBXW8,PKIG,FARS2,HLCS,ELOVL2,ACOT8,CD58,TBC1D7,IFT57,PARP3,TMEFF2,PSPH,PRDM10,VKORC1L1,CUEDC2,YARS,CDC73,NPRL2,EIF3I,PTP4A2,WIPI1,ARFGEF2,ACTL6A,AKAP13,IRF2BP2,TGIF1,WDR5B,NIF3L1,PPP1R8,RAE1,ENSA,GMPR2,PPP1R11,KLHL41,RBM4,CRTC3,SMYD2,PSMA7,DCAF17,RPL35A,PES1,UROS,BCCIP,RPL18A,FBXO45,EGR2,INO80D,KDM1A,ETV5,REXO2,USP28,PTS,IL1RAP,EXOSC7,NDUFA13,MRPS14,ANAPC16,EMG1,TRMT44,PRDX6,USP5,MECOM,CHCHD1,LSM4,TRIM4,UBA1,DYNC2H1,UVSSA,ELK1,PELI2,TRRAP,FTSJ1,TOP3B,RPS24,ZMIZ1,KAT2A,PFN1,PSMB6,ERC1,HSPA2,ITPKB,RARA,HDHD5,CTDNEP1,CECR2,NR1D1,DCP2,VPS37C,ETV3,SAMD1,ANAPC13,RNF40,MEF2D,CDK5RAP3,ZNF652,EIF2B2,INO	red	VSMC_M1
GO:0001655	0.58	0.55	10	283	urogenital system development	BP	1	SMAD4,EGR1,FGF2,PTCD2,ARL3,DYNC2H1,PROM1,RARA,CTNNBIP1,FGF10	red	VSMC_M1
GO:0042176	0.58	0.53	13	342	regulation of protein catabolic process	BP	1	EEF1A1,ALAD,RPS7,CSNK1D,FBXW8,NDUFA13,USP5,RNF40,CDK5RAP3,RACK1,TIMP3,ATP5IF1,RCHY1	red	VSMC_M1
GO:0033673	0.58	0.57	7	191	negative regulation of kinase activity	BP	1	FGFR1OP,SPRED1,PKIG,NPRL2,CDK5RAP3,ERRFI1,RACK1	red	VSMC_M1
GO:0042177	0.58	0.62	4	101	negative regulation of protein catabolic process	BP	1	ALAD,RPS7,CDK5RAP3,TIMP3	red	VSMC_M1
GO:0042592	0.58	0.48	48	1295	homeostatic process	BP	1	SMAD4,DYNLT1,EGR1,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,FGF2,TAL1,DGAT2,HDAC3,CACNA2D1,CXCL12,CEBPG,IL20RB,EDNRA,SLC12A6,P2RX4,C15orf41,RPS6,CNNM1,CYB561D2,COX19,CRTC3,KDM1A,PRDX6,SCNN1A,PROM1,RPS24,ITPKB,NR1D1,CDK5RAP3,PRDX2,STXBP4,CALM2,FBXO4,OMA1,HMOX2,E2F4,FKBP1A,GNAS,RACK1,SLC25A28,ATP6V1G1,IGHA2,ATP5IF1,PTPRN2	red	VSMC_M1
GO:0045017	0.59	0.56	8	214	glycerolipid biosynthetic process	BP	1	FGF2,EFR3B,DGAT2,SOCS2,GPAT3,ITPKB,HDHD5,CTDNEP1	red	VSMC_M1
GO:0048583	0.59	0.46	106	2834	regulation of response to stimulus	BP	1	SMAD4,SGK1,ARG1,DYRK2,RGS17,CSNK2B,DYNLT1,HMGA1,EGR1,TCP11,CTNNA1,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,AHR,INVS,KMT5C,RPS7,PIH1D1,FKBP1B,FGF2,ARHGAP35,IFT122,RECQL5,EIF2B4,WBP2,PAK1,RPS3,PSD2,IL18BP,CSNK1D,HDAC3,SOCS2,PCID2,KCTD16,TNKS,CXCL12,TNFRSF19,COPS5,CEBPG,CD8B,IL20RB,KMT5A,RHOF,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,GPAT3,TFG,TBC1D7,PARP3,CDC73,NPRL2,ARHGAP31,ARFGEF2,AKAP13,RHOD,WDR11,CRTC3,SMYD2,ARHGDIB,KDM1A,NDUFA13,MECOM,DYNC2H1,PELI2,ITFG2,ZMIZ1,ITPKB,RARA,CTDNEP1,NR1D1,CDK5RAP3,EIF2B2,SPG21,PRDX2,CALM2,IL13RA2,XRCC3,RFFL,MIER1,FBXO4,GOLPH3,YJU2,ERRFI1,CTNNBIP1,USP10,WWOX,GARNL3,FKBP1A,RACK1,NREP,KAZALD1,TIMP3,RPS20,TMSB4X,CPNE1,RNF125,RITA1,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0034248	0.59	0.52	15	395	regulation of cellular amide metabolic process	BP	1	POLDIP3,EIF3D,MALSU1,EIF2B4,RPS3,SP1,EIF2A,OGFOD1,RBM4,EXOSC7,RARA,DCP2,EIF2B2,DPH5,RACK1	red	VSMC_M1
GO:0051338	0.59	0.49	26	706	regulation of transferase activity	BP	1	FGFR1OP,EGR1,EEF1A1,RPS7,PIH1D1,FGF2,TAL1,PAK1,UVRAG,RPS3,SOCS2,TNKS,SPRED1,CCNI,AMBRA1,PKIG,PARP3,NPRL2,AKAP13,BCCIP,CDK5RAP3,PARP16,CALM2,ERRFI1,RACK1,RPS20	red	VSMC_M1
GO:0001666	0.59	0.55	9	244	response to hypoxia	BP	1	SMAD4,NDRG1,EGR1,ALAD,PAK1,CXCL12,EDNRA,CYP1A1,HMOX2	red	VSMC_M1

GO:0030162	0.59	0.50	21	538	regulation of proteolysis	BP	1	INPP5B,ALAD,RPS7,PIH1D1,WDR35,RPS3,CSNK1D,PCID2,PDCD5,FBXW8,IFT57,NDUFA13,USP5,RNF40,RFFL,RACK1,TIMP3,WFDC3,ATP5IF1,PSENEN,RCHY1	red	VSMC_M1
GO:0046488	0.59	0.59	5	138	phosphatidylinositol metabolic process	BP	1	INPP5B,FGF2,EFR3B,SOCS2,ITPKB	red	VSMC_M1
GO:1905114	0.59	0.51	16	448	cell surface receptor signaling pathway involved in cell-cell signaling	BP	1	CSNK2B,EGR1,SPIN1,INVS,FGF2,CSNK1D,TNKS,CTR9,P2RX4,CDC73,CTDNEP1,RNF138,CTNNBIP1,WWOX,RACK1,FGF10	red	VSMC_M1
GO:0044706	0.59	0.57	6	159	multi-multicellular organism process	BP	1	ARG1,ACR,GOT2,ARHGDIB,RARA,CYP1A1	red	VSMC_M1
GO:0062012	0.59	0.54	9	243	regulation of small molecule metabolic process	BP	1	DYRK2,EGR1,COQ3,DGAT2,ERLIN2,KAT2A,NR1D1,WDR5,TMSB4X	red	VSMC_M1
GO:0090316	0.59	0.58	5	136	positive regulation of intracellular protein transport	BP	1	HSPA1L,PAK1,HDAC3,PDCD5,TOMM7	red	VSMC_M1
GO:0033036	0.60	0.45	88	2356	macromolecule localization	BP	1	HSPA1L,DYNLT1,POLDIP3,REEP2,CTNNA1,TST,SRI,UBAP1,MAP4K4,CLTA,XPA,INVS,CRIPT,PIH1D1,PARD3,WDR35,FKBP1B,EFR3B,PMPCB,STAM,IFT122,WBP2,PAK1,DGAT2,CSNK1D,HDAC3,PCID2,TNKS,RAB28,PDCD5,VTI1B,TIMM10,TMSB10,ARFIP1,GOT2,P2RX4,PLRG1,PKIG,PARP3,ARL3,UNC119B,GRAMD1C,WIPI1,ARFGEF2,RAB9A,EMC9,ARL4C,RAE1,ENSA,FAM45A,WDR11,EGR2,KDM1A,MAP2,AP1S1,NDUFA13,ARL4D,RP2,DYNC2H1,SCG3,ERC1,CTDNEP1,NR1D1,DCP2,VPS37C,CDK5RAP3,COPZ2,STXBP4,SNUPN,B9D1,FBXO4,RAB12,MYO18A,GOLPH3,GOSR1,KCNAB2,RAB39B,DNLZ,CIZ1,EVI5,FKBP1A,RACK1,TMSB4X,NOP10,TOMM7,ATP5IF1,PTPRN2,FGF10	red	VSMC_M1
GO:0030902	0.60	0.60	4	116	hindbrain development	BP	1	FGF2,PAK1,EGR2,KAT2A	red	VSMC_M1
GO:0006091	0.60	0.50	16	392	generation of precursor metabolites and energy	BP	1	CS,DYRK2,COX5B,SLC25A51,COX7B,NDUFA2,MTFR1,NDUFA10,MTFR1L,NDUFA13,NR1D1,NDUFB7,COX4I1,COQ10A,ATP5IF1,COX7C	red	VSMC_M1
GO:0050680	0.60	0.60	4	108	negative regulation of epithelial cell proliferation	BP	1	IFT57,CDC73,SPARC,ATP5IF1	red	VSMC_M1
GO:0048609	0.60	0.49	21	563	multicellular organismal reproductive process	BP	1	SMAD4,ARG1,ACR,EGR1,TCP11,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,C11orf74,CCNI,RPS6,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,CYP1A1,FAM9B	red	VSMC_M1
GO:0006997	0.60	0.60	4	112	nucleus organization	BP	1	SPAST,FAM118B,EMG1,CTDNEP1	red	VSMC_M1
GO:0003002	0.60	0.53	9	251	regionalization	BP	1	SMAD4,FGF2,IFT57,EGR2,DYNC2H1,KAT2A,CTNNBIP1,BHLHE41,FGF10	red	VSMC_M1
GO:0001667	0.60	0.51	13	360	ameboidal-type cell migration	BP	1	CSNK2B,MAP4K4,FGF2,PAK1,SP1,P2RX4,SPRED1,ARHGDIB,PFN1,SPARC,RFFL,TMSB4X,FGF10	red	VSMC_M1
GO:0035107	0.61	0.59	4	115	appendage morphogenesis	BP	1	SMAD4,DYNC2H1,B9D1,FGF10	red	VSMC_M1
GO:0035108	0.61	0.59	4	115	limb morphogenesis	BP	1	SMAD4,DYNC2H1,B9D1,FGF10	red	VSMC_M1
GO:0043624	0.61	0.59	4	119	cellular protein complex disassembly	BP	1	MTRF1L,TRIOBP,SPAST,OGFOD1	red	VSMC_M1
GO:0043549	0.61	0.48	22	612	regulation of kinase activity	BP	1	FGFR1OP,EGR1,EEF1A1,PIH1D1,FGF2,TAL1,PAK1,UVRAG,RPS3,SOCS2,SPRED1,CCNI,AMBRA1,PKIG,NPRL2,AKAP13,BCCIP,CDK5RAP3,PARP16,CALM2,ERRFI1,RACK1	red	VSMC_M1
GO:0045597	0.61	0.48	23	639	positive regulation of cell differentiation	BP	1	SMAD4,KLF10,TRIOBP,FGF2,TAL1,PAK1,CSNK1D,SOCS2,PCID2,CXCL12,FBXW8,RBM4,EGR2,KDM1A,ETV5,PROM1,ZMIZ1,KAT2A,ITPKB,RARA,CTNNBIP1,NUDT21,CPNE1	red	VSMC_M1
GO:0010817	0.61	0.51	12	331	regulation of hormone levels	BP	1	SMAD4,EGR1,SRI,MAP4K4,FKBP1B,DGAT2,ENSA,NR1D1,STXBP4,CYP1A1,CHST9,PTPRN2	red	VSMC_M1
GO:0050808	0.61	0.51	11	329	synapse organization	BP	1	NDRG1,CRIPT,SDK2,PCDH17,FBXO45,IL1RAP,PFN1,ERC1,FLRT2,SPARC,RAB39B	red	VSMC_M1
GO:0002764	0.61	0.52	10	278	immune response-regulating signaling pathway	BP	1	EIF2B4,PAK1,RPS3,IL20RB,NR1D1,EIF2B2,SPG21,RNF125,IGHA2,LY96	red	VSMC_M1
GO:0048863	0.61	0.55	6	171	stem cell differentiation	BP	1	SMAD4,FGF2,TAL1,EDNRA,SMYD5,NUDT21	red	VSMC_M1
GO:0032640	0.61	0.59	4	111	tumor necrosis factor production	BP	1	ARFGEF2,RARA,ERRFI1,LY96	red	VSMC_M1
GO:0032680	0.61	0.59	4	111	regulation of tumor necrosis factor production	BP	1	ARFGEF2,RARA,ERRFI1,LY96	red	VSMC_M1
GO:1901699	0.61	0.48	18	508	cellular response to nitrogen compound	BP	1	ARG1,KLF10,EGR1,CTNNA1,AHR,RECQL5,PAK1,SOCS2,CACNA2D1,SP1,P2RX4,UROS,KDM1A,STXBP4,RAB12,GOLPH3,ERRFI1,GNAS	red	VSMC_M1
GO:0002443	0.61	0.53	8	221	leukocyte mediated immunity	BP	1	ARG1,AHR,KMT5C,CEBPG,IL20RB,PARP3,IL13RA2,IGHA2	red	VSMC_M1
GO:0031570	0.61	0.59	4	111	DNA integrity checkpoint signaling	BP	1	USP28,CDK5RAP3,FBXO4,HUS1	red	VSMC_M1
GO:0002376	0.61	0.44	62	1656	immune system process	BP	1	ARG1,KLF10,POLR3H,NDRG1,ZFAT,EGR1,TREML2,IL1RL1,AHR,KMT5C,PGM3,FKBP1B,TAL1,EIF2B4,PAK1,RPS3,IL18BP,PCID2,CXCL12,CEBPG,CD8B,IL20RB,CTR9,P2RX4,C15orf41,RPS6,CD58,PARP3,CUEDC2,CDC73,IRF2BP2,PPP1R11,CRTC3,IL1RAP,MECOM,TRIM4,RPS24,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,NR1D1,CDK5RAP3,EIF2B2,SPG21,PRDX2,STXBP4,IL13RA2,MYO18A,GOLPH3,CTNNBIP1,RBM15,NUDT21,FKBP1A,CNIH1,WFDC3,RNF125,IGHA2,ATP5IF1,LY96,FGF10	red	VSMC_M1
GO:0048167	0.61	0.56	5	143	regulation of synaptic plasticity	BP	1	EGR2,KAT2A,ERC1,RARA,PRRT2	red	VSMC_M1
GO:0007266	0.61	0.58	4	116	Rho protein signal transduction	BP	1	ARHGAP35,AKAP13,RHOD,ARHGDIB	red	VSMC_M1
GO:0008544	0.61	0.54	7	201	epidermis development	BP	1	SMAD4,TRIOBP,TNFRSF19,HPSE,TPRN,ERRFI1,FGF10	red	VSMC_M1
GO:0051050	0.62	0.47	24	660	positive regulation of transport	BP	1	SMAD4,SGK1,HSPA1L,SRI,STAM,PAK1,HDAC3,CACNA2D1,CXCL12,PDCD5,P2RX4,CACNA1D,STIMATE,RAB9A,MAP2,HSPA2,PRRT2,CALM2,MYO18A,GOLPH3,RACK1,TMSB4X,TOMM7,ATP5IF1	red	VSMC_M1
GO:0051321	0.62	0.54	7	192	meiotic cell cycle	BP	1	MEI1,SPIN1,NPR2,MEI4,HSPA2,FAM9B,HUS1	red	VSMC_M1
GO:0042325	0.62	0.45	35	967	regulation of phosphorylation	BP	1	SMAD4,CSNK2B,FGFR1OP,EGR1,KCTD20,EEF1A1,PIH1D1,PARD3,FGF2,TAL1,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,SOCS2,SPRED1,CCNI,AMBRA1,PKIG,NPRL2,AKAP13,BCCIP,PELI2,HSPA2,ITPKB,CDK5RAP3,PARP16,CALM2,MOB3A,ERRFI1,RACK1,HUS1,PPP1R14A,FGF10	red	VSMC_M1
GO:0022412	0.62	0.52	9	247	cellular process involved in reproduction in multicellular organism	BP	1	TCP11,NPR2,MEI4,RPS6,ETV5,ZMIZ1,HSPA2,RARA,FAM9B	red	VSMC_M1
GO:0002440	0.62	0.56	5	138	production of molecular mediator of immune response	BP	1	ARG1,KMT5C,PARP3,CUEDC2,IL13RA2	red	VSMC_M1
GO:0046165	0.62	0.58	4	108	alcohol biosynthetic process	BP	1	FGF2,ERLIN2,PTS,ITPKB	red	VSMC_M1
GO:0071248	0.62	0.56	5	141	cellular response to metal ion	BP	1	ALAD,P2RX4,ITPKB,CYP1A1,CPNE1	red	VSMC_M1
GO:0051028	0.62	0.58	4	109	mRNA transport	BP	1	POLDIP3,PCID2,TNKS,RAE1	red	VSMC_M1
GO:0002684	0.62	0.47	20	542	positive regulation of immune system process	BP	1	ARG1,KLF10,IL1RL1,KMT5C,EIF2B4,PAK1,RPS3,PCID2,CXCL12,P2RX4,ZMIZ1,ITPKB,RARA,EIF2B2,SPG21,IL13RA2,MYO18A,CTNNBIP1,IGHA2,FGF10	red	VSMC_M1
GO:0043405	0.62	0.55	5	146	regulation of MAP kinase activity	BP	1	FGF2,PAK1,RPS3,AKAP13,CDK5RAP3	red	VSMC_M1

GO:0043542	0.62	0.53	7	195	endothelial cell migration	BP	1	CSNK2B,FGF2,SP1,P2RX4,SPRED1,SPARC,TMSB4X	red	VSMC_M1
GO:0060548	0.62	0.45	28	754	negative regulation of cell death	BP	1	SMAD4,DYNLT1,CTNNA1,NAA35,MAP4K4,PIH1D1,FGF2,HDAC3,SOCS2,PCID2,CXCL12,COPS5,RPS3A,RPS6,CDC73,KDM1A,NDUFA13,MECOM,ERC1,ITPKB,PARP16,PRDX2,RFFL,MYO18A,GOLPH3,RACK1,NAA38,FGF10	red	VSMC_M1
GO:0051241	0.63	0.45	27	743	negative regulation of multicellular organismal process	BP	1	SMAD4,ARG1,CSNK2B,DYNLT1,CTNNA1,SRI,IL1RL1,FKBP1B,FGF2,PAK1,SOCS2,IL20RB,P2RX4,SPRED1,PARP3,CUEDC2,PPP1R11,ARHGDIB,MAP2,PRTG,RARA,NR1D1,PRDX2,SPARC,ERRFI1,TMSB4X,RNF125	red	VSMC_M1
GO:0032504	0.63	0.46	21	571	multicellular organism reproduction	BP	1	SMAD4,ARG1,ACR,EGR1,TCP11,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,C11orf74,CCNI,RPS6,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,CYP1A1,FAM9B	red	VSMC_M1
GO:0050670	0.63	0.55	5	137	regulation of lymphocyte proliferation	BP	1	ARG1,AHR,RPS3,IL20RB,FGF10	red	VSMC_M1
GO:0051592	0.63	0.57	4	114	response to calcium ion	BP	1	ITPKB,CALM2,SPARC,CPNE1	red	VSMC_M1
GO:0044093	0.63	0.43	42	1151	positive regulation of molecular function	BP	1	SGK1,EGR1,EIF3D,MUT,MAP4K4,PIH1D1,WDR35,FGF2,TAL1,PAK1,RPS3,CACNA2D1,TNKS,COPS5,CEBPG,PDCD5,EDNRA,CACNA1D,STIMATE,AMBRA1,TBC1D7,IFT57,AKAP13,CRTC3,KDM1A,MYL4,IL1RAP,NDUFA13,PFN1,ERC1,HSPA2,RARA,PARP16,CALM2,PTPA,GARNL3,EVI5,FKBP1A,RACK1,TMSB4X,PSENEN,FGF10	red	VSMC_M1
GO:0032502	0.63	0.41	170	4589	developmental process	BP	1	SMAD4,SGK1,ARG1,CSNK2B,KLF10,DYNLT1,EGFL8,ZHX2,NDRG1,ZFAT,HMGA1,EGR1,TCP11,CTNNA1,TRIOBP,TST,SRI,MUT,MAP4K4,NPR2,AHR,KMT5C,MEI4,PGM3,UTP11,INPP5B,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,SF3B6,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,UBP1,FAM171A1,IFT122,PCDH17,EIF2B4,PAK1,DGAT2,SPAST,NEB,NRG2,COX7B,MCRIP1,NDUFA2,CSNK1D,SOCS2,PCID2,C11orf74,SP1,CXCL12,TNFRSF19,CEBPG,CTR9,EDNRA,SMN2,SLC12A6,PTCD2,RPS3A,RHOF,C21orf91,GOT2,P2RX4,RRAS2,C15orf41,SPRED1,CCNI,RPS6,TLL1,MMP16,SMYD5,HPSE,AMBRA1,FBXW8,IFT57,PARP3,TMEFF2,PSPH,ARL3,UNC119B,CDC73,CFAP410,ACTL6A,AKAP13,IRF2BP2,MYO18B,RHOD,NIF3L1,KLHL41,WDR11,RBM4,SMYD2,BCCIP,ARHGDIB,KCNQ2,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,PTS,IL1RAP,GJC1,EMG1,MECOM,RP2,DYNC2H1,ELK1,PROM1,ITFG2,ZMIZ1,KAT2A,PFN1,ERC1,PRTG,HSPA2,ITPKB,RARA,CTDNEP1,CECR2,NR1D1,ETV3,MEF2D,CDK5RAP3,EIF2B2,PRDX2,MBTD1,FLRT2,CALM2,SPARC,PMP22,CYP1A1,HMG20A,COQ7,B9D1,USP22,FBXO4,OMA1,TBC1D24,GFER,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,WDR5,WWOX,E2F4,IER2,NUDT21,MED31,FKBP1A,GNAS,FAM9B,BORCS8,RACK1,HUS1,NREP,KAZALD1,BHLHE41,CPNE1,RITA1,ATP5IF1,FGF10	red	VSMC_M1
GO:0030178	0.63	0.55	5	142	negative regulation of Wnt signaling pathway	BP	1	EGR1,INVS,CTNNBIP1,WWOX,RACK1	red	VSMC_M1
GO:0055082	0.63	0.46	20	564	cellular chemical homeostasis	BP	1	SMAD4,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,FGF2,DGAT2,CACNA2D1,CXCL12,EDNRA,P2RX4,COX19,NR1D1,STXBP4,CALM2,FKBP1A,RACK1,ATP6V1G1,PTPRN2	red	VSMC_M1
GO:0048522	0.63	0.41	157	4212	positive regulation of cellular process	BP	1	SMAD4,ARG1,DYRK2,CSNK2B,KLF10,HSPA1L,DYNLT1,FGFR1OP,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,CTNNA1,KCTD20,TRIOBP,EIF3D,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,UBE2M,AHR,KMT5C,COPS9,FAM161A,UTP11,APLF,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,STAM,NR2C2,UBP1,WBP2,PAK1,UVRAG,DGAT2,RPS3,SPAST,CSNK1D,HDAC3,SOCS2,PCID2,CACNA2D1,TNKS,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,ZNF341,PDCD5,CTR9,ARFIP1,P2RX4,RRAS2,PLRG1,EIF2A,EDIL3,SPRED1,RPS6,STIMATE,HPSE,AMBRA1,FBXW8,TFG,TBC1D7,IFT57,PARP3,PRDM10,ARL3,CDC73,NPRL2,ACTL6A,AKAP13,RAB9A,RHOD,NIF3L1,RBM4,CRTC3,EGR2,KDM1A,ETV5,MAP2,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,DYNC2H1,ELK1,PELI2,PROM1,ZMIZ1,KAT2A,PFN1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,RNF40,MEF2D,CDK5RAP3,PRRT2,PARP16,PRDX2,FLRT2,STXBP4,SUPT4H1,CALM2,SPARC,ARID3B,CYP1A1,XRCC3,USP22,MIER1,FBXO4,MYO18A,OMA1,GOLPH3,MOB3A,CTNNBIP1,RBM15,WDR5,PTPA,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,FKBP1A,RACK1,ELOF1,TIMP3,RPS20,TMSB4X,CPNE1,TOMM7,IGHA2,ATP5IF1,PSENEN,LY96,RCHY1,FGF10	red	VSMC_M1
GO:0000070	0.63	0.55	5	143	mitotic sister chromatid segregation	BP	1	MAD2L1BP,PCID2,TNKS,KMT5A,XRCC3	red	VSMC_M1
GO:0009611	0.63	0.47	15	422	response to wounding	BP	1	ARG1,CTNNA1,FKBP1B,FGF2,ARHGAP35,PAK1,P2RX4,HPSE,TMEFF2,PRDX2,SPARC,CYP1A1,GNAS,NREP,FGF10	red	VSMC_M1
GO:0032944	0.63	0.54	5	138	regulation of mononuclear cell proliferation	BP	1	ARG1,AHR,RPS3,IL20RB,FGF10	red	VSMC_M1
GO:0033157	0.63	0.52	7	196	regulation of intracellular protein transport	BP	1	HSPA1L,PAK1,HDAC3,PDCD5,PKIG,TOMM7,ATP5IF1	red	VSMC_M1
GO:0032388	0.64	0.53	6	173	positive regulation of intracellular transport	BP	1	HSPA1L,PAK1,HDAC3,PDCD5,MAP2,TOMM7	red	VSMC_M1
GO:0006469	0.64	0.53	6	172	negative regulation of protein kinase activity	BP	1	FGFR1OP,SPRED1,PKIG,CDK5RAP3,ERRFI1,RACK1	red	VSMC_M1
GO:1904951	0.64	0.50	9	257	positive regulation of establishment of protein localization	BP	1	HSPA1L,SRI,PAK1,HDAC3,PDCD5,MYO18A,GOLPH3,RACK1,TOMM7	red	VSMC_M1
GO:0071706	0.64	0.56	4	115	tumor necrosis factor superfamily cytokine production	BP	1	ARFGEF2,RARA,ERRFI1,LY96	red	VSMC_M1
GO:1903555	0.64	0.56	4	115	regulation of tumor necrosis factor superfamily cytokine production	BP	1	ARFGEF2,RARA,ERRFI1,LY96	red	VSMC_M1
GO:0002699	0.64	0.54	5	142	positive regulation of immune effector process	BP	1	ARG1,KMT5C,RARA,IL13RA2,MYO18A	red	VSMC_M1
GO:0007346	0.64	0.47	13	360	regulation of mitotic cell cycle	BP	1	MAD2L1BP,TAL1,PCID2,PLRG1,CDC73,HSPA2,CDK5RAP3,INTS3,CYP1A1,XRCC3,USP22,HUS1,FGF10	red	VSMC_M1
GO:0070482	0.64	0.49	10	280	response to oxygen levels	BP	1	SMAD4,NDRG1,EGR1,ALAD,PAK1,CXCL12,EDNRA,CYP1A1,HMOX2,ATP6V1G1	red	VSMC_M1
GO:0006661	0.64	0.56	4	115	phosphatidylinositol biosynthetic process	BP	1	FGF2,EFR3B,SOCS2,ITPKB	red	VSMC_M1

GO:0006812	0.64	0.44	29	796	cation transport	BP	1	SGK1,ARG1,SRI,COX5B,KCNF1,FKBP1B,FGF2,PMPCB,COX7B,CACNA2D1,CXCL12,SLC12A6,P2RX4,CACNA1D,STIMATE,SCN3A,KCNQ2,SCNN1A,CLCN5,HSPA2,CALM2,CACHD1,KCNAB2,COX4I1,FKBP1A,SLC25A28,ATP6V1G1,TMSB4X,AHNAK	red	VSMC_M1
GO:0048469	0.64	0.56	4	116	cell maturation	BP	1	TCP11,NPR2,TAL1,KDM1A	red	VSMC_M1
GO:0010038	0.64	0.49	10	279	response to metal ion	BP	1	ARG1,NDRG1,ALAD,P2RX4,UROS,ITPKB,CALM2,SPARC,CYP1A1,CPNE1	red	VSMC_M1
GO:0051093	0.64	0.44	24	676	negative regulation of developmental process	BP	1	SMAD4,DYNLT1,ZHX2,CTNNA1,MAP4K4,NPR2,PAK1,SOCS2,CTR9,SPRED1,PARP3,CDC73,MAP2,PRTG,ITPKB,RARA,NR1D1,PRDX2,SPARC,HMG20A,OMA1,RBM15,BHLHE41,FGF10	red	VSMC_M1
GO:0051247	0.64	0.42	42	1140	positive regulation of protein metabolic process	BP	1	SMAD4,CSNK2B,POLDIP3,EGR1,EIF3D,FAM161A,PIH1D1,WDR35,FGF2,TAL1,WBP2,PAK1,RPS3,CSNK1D,HDAC3,SP1,PDCD5,CTR9,FBXW8,TBC1D7,IFT57,AKAP13,KDM1A,NDUFA13,USP5,PELI2,KAT2A,HSPA2,RNF40,CDK5RAP3,PARP16,CALM2,FBXO4,MOB3A,WDR5,PTPA,FKBP1A,RACK1,ATP5IF1,PSENEN,RCHY1,FGF10	red	VSMC_M1
GO:0010675	0.64	0.55	4	114	regulation of cellular carbohydrate metabolic process	BP	1	DYRK2,DGAT2,KAT2A,WDR5	red	VSMC_M1
GO:0048518	0.64	0.39	169	4533	positive regulation of biological process	BP	1	SMAD4,SGK1,ARG1,DYRK2,CSNK2B,KLF10,HSPA1L,DYNLT1,FGFR1OP,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,CTNNA1,KCTD20,TRIOBP,EIF3D,SRI,MAD2L1BP,IL1RL1,MAP4K4,SPIN1,NPR2,UBE2M,AHR,KMT5C,COPS9,FAM161A,UTP11,APLF,RPS7,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,STAM,NR2C2,UBP1,EIF2B4,WBP2,PAK1,UVRAG,DGAT2,RPS3,SPAST,CSNK1D,HDAC3,SOCS2,PCID2,CACNA2D1,TNKS,SP1,CXCL12,TNFRSF19,COPS5,CEBPG,ZNF341,IL20RB,PDCD5,CTR9,ARFIP1,C21orf91,P2RX4,RRAS2,PLRG1,EIF2A,EDIL3,CACNA1D,SPRED1,RPS6,STIMATE,HPSE,AMBRA1,FBXW8,TFG,CD58,TBC1D7,IFT57,PARP3,PRDM10,ARL3,CDC73,NPRL2,ARFGEF2,ACTL6A,AKAP13,RAB9A,RHOD,NIF3L1,RBM4,CRTC3,EGR2,KDM1A,ETV5,MAP2,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,DYNC2H1,ELK1,PELI2,PROM1,ZMIZ1,KAT2A,PFN1,HSPA2,ITPKB,RARA,CTDNEP1,NR1D1,DCP2,RNF40,MEF2D,CDK5RAP3,PRRT2,EIF2B2,SPG21,PARP16,PRDX2,FLRT2,STXBP4,SUPT4H1,CALM2,SPARC,ARID3B,CYP1A1,IL13RA2,XRCC3,USP22,MIER1,FBXO4,MYO18A,OMA1,GOLPH3,MOB3A,CTNNBIP1,RBM15,WDR5,PTPA,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,FKBP1A,GNAS,RACK1,ELOF1,TIMP3,RPS20,TMSB4X,NOP10,CPNE1,TOMM7,IGHA2,ATP5IF1,PSENEN,LY96,RCHY1,FGF10	red	VSMC_M1
GO:0019722	0.64	0.53	5	147	calcium-mediated signaling	BP	1	DYRK2,FKBP1B,P2RX4,STIMATE,CALM2	red	VSMC_M1
GO:0050769	0.64	0.52	6	181	positive regulation of neurogenesis	BP	1	PAK1,CXCL12,FBXW8,EGR2,KDM1A,ETV5	red	VSMC_M1
GO:0061061	0.64	0.45	18	504	muscle structure development	BP	1	SMAD4,EGR1,SRI,PAK1,NEB,PTCD2,AKAP13,MYO18B,KLHL41,RBM4,EGR2,KDM1A,KAT2A,RARA,MEF2D,FKBP1A,BHLHE41,FGF10	red	VSMC_M1
GO:0031175	0.65	0.43	27	784	neuron projection development	BP	1	SMAD4,SGK1,DYNLT1,CTNNA1,TRIOBP,MAP4K4,PARD3,FKBP1B,ARHGAP35,PAK1,SPAST,CXCL12,C21orf91,FBXW8,MAP4,FBXO45,EGR2,KDM1A,MAP2,CECR2,FLRT2,PMP22,TBC1D24,TPRN,WDR5,NREP,CPNE1	red	VSMC_M1
GO:0007276	0.65	0.45	17	469	gamete generation	BP	1	SMAD4,TCP11,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,C11orf74,CCNI,RPS6,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,FAM9B	red	VSMC_M1
GO:1903827	0.65	0.45	16	454	regulation of cellular protein localization	BP	1	HSPA1L,CTNNA1,CRIPT,PAK1,HDAC3,PDCD5,VTI1B,PKIG,KDM1A,MAP2,CDK5RAP3,FBXO4,KCNAB2,RACK1,TOMM7,ATP5IF1	red	VSMC_M1
GO:1902905	0.65	0.51	6	179	positive regulation of supramolecular fiber organization	BP	1	PAK1,RPS3,SPAST,ARFIP1,ARL3,PFN1	red	VSMC_M1
GO:1905475	0.65	0.53	5	147	regulation of protein localization to membrane	BP	1	CRIPT,PAK1,PDCD5,VTI1B,RACK1	red	VSMC_M1
GO:0051259	0.65	0.51	6	174	protein complex oligomerization	BP	1	ALAD,KCNF1,SPAST,KCTD16,CRTC3,NUDT21	red	VSMC_M1
GO:0006810	0.65	0.39	123	3300	transport	BP	1	SMAD4,SGK1,ARG1,HSPA1L,DYNLT1,POLDIP3,REEP2,TST,SRI,UBAP1,MAP4K4,ICK,CLTA,COX5B,SLC25A51,OSCP1,KCNF1,PARD3,WDR35,FKBP1B,FGF2,PMPCB,STAM,IFT122,PCDH17,NRBP1,PAK1,UVRAG,VDAC3,SPAST,COX7B,CSNK1D,HDAC3,SOCS2,PCID2,CACNA2D1,TNKS,RAB28,CXCL12,COPS5,PDCD5,VTI1B,EDNRA,TIMM10,SLC12A6,ARFIP1,GOT2,P2RX4,CACNA1D,STIMATE,TFG,CNNM1,PKIG,IFT57,ARL3,UNC119B,CYB561D2,SORCS1,GRAMD1C,SCN3A,WIPI1,ARFGEF2,AKAP13,RAB9A,ARL4C,RAE1,ENSA,FAM45A,WDR11,RBM4,IFT46,KCNQ2,CEP19,EGR2,MAP2,AP1S1,GJC1,NDUFA13,ARL4D,RP2,DYNC2H1,SCNN1A,MYO5C,ERC1,CLCN5,HSPA2,RARA,CECR2,NR1D1,VPS37C,COPZ2,TRAPPC1,PRRT2,STXBP4,CALM2,SNUPN,IL13RA2,CACHD1,RAB12,MYO18A,GOLPH3,GOSR1,KCNAB2,RAB39B,DNLZ,COX4I1,EVI5,ELMO3,FKBP1A,SLC25A1,RACK1,SLC25A28,ATP6V1G1,TMSB4X,CNIH1,CPNE1,TOMM7,RITA1,IGHA2,ATP5IF1,PTPRN2,AHNAK,FGF10	red	VSMC_M1
GO:0034976	0.65	0.49	8	222	response to endoplasmic reticulum stress	BP	1	RNF121,ERLIN2,COPS5,TMEM117,CDK5RAP3,PARP16,UBE4B,RACK1	red	VSMC_M1

GO:0051234	0.65	0.39	128	3429	establishment of localization	BP	1	SMAD4,SGK1,ARG1,HSPA1L,DYNLT1,POLDIP3,REEP2,TST,SRI,UBAP1,MAP4K4,ICK,CLTA,COX5B,SLC25A51,CRIPT,OSCP1,KCNF1,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,PMPCB,STAM,IFT122,PCDH17,WBP2,NRBP1,PAK1,UVRAG,VDAC3,SPAST,COX7B,CSNK1D,HDAC3,SOCS2,PCID2,CACNA2D1,TNKS,RAB28,CXCL12,COPS5,PDCD5,VTI1B,EDNRA,TIMM10,SLC12A6,ARFIP1,GOT2,P2RX4,CACNA1D,STIMATE,TFG,CNNM1,PKIG,IFT57,ARL3,UNC119B,CYB561D2,SORCS1,GRAMD1C,SCN3A,WIPI1,ARFGEF2,AKAP13,RAB9A,EMC9,ARL4C,RAE1,ENSA,FAM45A,WDR11,RBM4,IFT46,KCNQ2,MAP4,CEP19,EGR2,MAP2,AP1S1,GJC1,NDUFA13,ARL4D,RP2,DYNC2H1,SCNN1A,MYO5C,ERC1,CLCN5,HSPA2,RARA,CECR2,NR1D1,VPS37C,COPZ2,TRAPPC1,PRRT2,STXBP4,CALM2,SNUPN,IL13RA2,CACHD1,RAB12,MYO18A,GOLPH3,GOSR1,KCNAB2,RAB39B,DNLZ,COX4I1,EVI5,ELMO3,FKBP1A,SLC25A1,RACK1,SLC25A28,ATP6V1G1,TMSB4X,CNIH1,CPNE1,TOMM7,RITA1,IGHA2,ATP5IF1,PTPRN2,AHNAK,FGF10	red	VSMC_M1
GO:0051091	0.65	0.49	7	204	positive regulation of DNA-binding transcription factor activity	BP	1	RPS3,COPS5,CEBPG,CRTC3,KDM1A,IL1RAP,ERC1	red	VSMC_M1
GO:0007517	0.66	0.48	9	259	muscle organ development	BP	1	SMAD4,EGR1,SRI,NEB,PTCD2,KLHL41,EGR2,MEF2D,FKBP1A	red	VSMC_M1
GO:0055085	0.66	0.41	38	1047	transmembrane transport	BP	1	TST,SRI,COX5B,SLC25A51,OSCP1,KCNF1,FKBP1B,FGF2,PMPCB,VDAC3,COX7B,CACNA2D1,EDNRA,SLC12A6,P2RX4,CACNA1D,STIMATE,CNNM1,CYB561D2,SCN3A,KCNQ2,GJC1,SCNN1A,CLCN5,HSPA2,STXBP4,CALM2,CACHD1,KCNAB2,DNLZ,COX4I1,FKBP1A,SLC25A1,SLC25A28,ATP6V1G1,TMSB4X,TOMM7,AHNAK	red	VSMC_M1
GO:0032501	0.66	0.38	185	5003	multicellular organismal process	BP	1	SMAD4,SGK1,ARG1,ACR,CSNK2B,KLF10,DYNLT1,ZHX2,NDRG1,ZFAT,REEP2,EGR1,TCP11,CTNNA1,TRIOBP,SRI,MUT,IL1RL1,MAP4K4,SPIN1,NPR2,COX5B,AHR,KMT5C,MEI4,PGM3,FAM161A,UTP11,INPP5B,RPS7,PARD3,WDR35,FKBP1B,SF3B6,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,UBP1,IFT122,PCDH17,EIF2B4,PAK1,DGAT2,RPS3,SPAST,NEB,NRG2,COX7B,MCRIP1,NDUFA2,CSNK1D,HDAC3,SOCS2,PCID2,CACNA2D1,C11orf74,SP1,CXCL12,TNFRSF19,CEBPG,IL20RB,CTR9,EDNRA,SMN2,TIMM10,SLC12A6,PTCD2,C21orf91,GOT2,P2RX4,RRAS2,C15orf41,CACNA1D,SPRED1,CCNI,RPS6,TLL1,MMP16,HPSE,AMBRA1,FBXW8,CD58,IFT57,PARP3,TMEFF2,PSPH,CUEDC2,ARL3,UNC119B,CDC73,SCN3A,ARFGEF2,ACTL6A,AKAP13,SSPN,IRF2BP2,MYO18B,NIF3L1,PPP1R11,KLHL41,WDR11,RBM4,CRTC3,SMYD2,ARHGDIB,KCNQ2,MAP4,FBXO45,EGR2,KDM1A,ETV5,MYL4,MAP2,PTS,IL1RAP,GJC1,EMG1,MECOM,RP2,DYNC2H1,ELK1,SCNN1A,PROM1,ITFG2,ZMIZ1,KAT2A,PFN1,ERC1,PRTG,CLCN5,HSPA2,ITPKB,RARA,CTDNEP1,CECR2,NR1D1,MEF2D,CDK5RAP3,PRRT2,EIF2B2,PRDX2,MBTD1,FLRT2,CALM2,SPARC,PMP22,CYP1A1,HMG20A,COQ7,B9D1,USP22,OMA1,TBC1D24,GFER,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,WDR5,WWOX,E2F4,IER2,NUDT21,MED31,FKBP1A,GNAS,FAM9B,BORCS8,RACK1,HUS1,NREP,KAZALD1,TIMP3,TMSB4X,BHLHE41,CPNE1,RNF125,RITA1,IGHA2,ATP5IF1,LY96,FGF10	red	VSMC_M1
GO:0031345	0.66	0.52	5	150	negative regulation of cell projection organization	BP	1	MAP4K4,TBC1D7,MAP4,MAP2,PMP22	red	VSMC_M1
GO:0007179	0.66	0.52	5	156	transforming growth factor beta receptor signaling pathway	BP	1	SMAD4,SPRED1,ZMIZ1,FKBP1A,NREP	red	VSMC_M1
GO:0036293	0.66	0.47	9	258	response to decreased oxygen levels	BP	1	SMAD4,NDRG1,EGR1,ALAD,PAK1,CXCL12,EDNRA,CYP1A1,HMOX2	red	VSMC_M1
GO:0001944	0.66	0.43	21	607	vasculature development	BP	1	EGR1,AHR,FGF2,TAL1,UBP1,SP1,EDNRA,SLC12A6,SPRED1,HPSE,FBXW8,MYO18B,GJC1,DYNC2H1,ZMIZ1,SPARC,B9D1,ERRFI1,RBM15,ATP5IF1,FGF10	red	VSMC_M1
GO:0072330	0.66	0.51	5	144	monocarboxylic acid biosynthetic process	BP	1	ERLIN2,ELOVL2,ACOT8,NR1D1,CYP1A1	red	VSMC_M1
GO:0021537	0.66	0.50	6	184	telencephalon development	BP	1	CXCL12,FBXO45,KDM1A,ZMIZ1,KAT2A,RARA	red	VSMC_M1
GO:0032872	0.66	0.51	5	148	regulation of stress-activated MAPK cascade	BP	1	MAP4K4,HDAC3,TNFRSF19,COPS5,MECOM	red	VSMC_M1
GO:0043491	0.66	0.51	5	147	protein kinase B signaling	BP	1	FGF2,P2RX4,HPSE,RACK1,CPNE1	red	VSMC_M1
GO:0010604	0.66	0.38	95	2586	positive regulation of macromolecule metabolic process	BP	1	SMAD4,DYRK2,CSNK2B,KLF10,POLDIP3,ZFAT,HMGA1,TAF11,EGR1,ZNF76,EIF3D,IL1RL1,SPIN1,AHR,KMT5C,FAM161A,APLF,RPS7,PIH1D1,WDR35,FGF2,TAL1,NR2C2,UBP1,WBP2,PAK1,RPS3,CSNK1D,HDAC3,PCID2,TNKS,SP1,COPS5,CEBPG,ZNF341,IL20RB,PDCD5,CTR9,HPSE,FBXW8,CD58,TBC1D7,IFT57,PARP3,PRDM10,CDC73,ARFGEF2,ACTL6A,AKAP13,NIF3L1,CRTC3,EGR2,KDM1A,ETV5,IL1RAP,EXOSC7,NDUFA13,PRDX6,USP5,MECOM,ELK1,PELI2,ZMIZ1,KAT2A,HSPA2,RARA,NR1D1,DCP2,RNF40,MEF2D,CDK5RAP3,PARP16,SUPT4H1,CALM2,ARID3B,USP22,FBXO4,MOB3A,RBM15,WDR5,PTPA,WWOX,CIZ1,DR1,E2F4,IER2,NUDT21,FKBP1A,RACK1,ELOF1,ATP5IF1,PSENEN,LY96,RCHY1,FGF10	red	VSMC_M1
GO:0045859	0.67	0.43	18	513	regulation of protein kinase activity	BP	1	FGFR1OP,EGR1,PIH1D1,FGF2,TAL1,PAK1,UVRAG,RPS3,SPRED1,CCNI,PKIG,AKAP13,BCCIP,CDK5RAP3,PARP16,CALM2,ERRFI1,RACK1	red	VSMC_M1
GO:0007601	0.67	0.53	4	123	visual perception	BP	1	FAM161A,GJC1,RP2,TIMP3	red	VSMC_M1
GO:0006887	0.67	0.46	9	266	exocytosis	BP	1	STAM,PAK1,COPS5,VTI1B,ARFGEF2,RAB9A,PRRT2,IL13RA2,RAB12	red	VSMC_M1
GO:0050801	0.67	0.42	19	542	ion homeostasis	BP	1	SMAD4,SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,SLC12A6,P2RX4,CNNM1,CYB561D2,COX19,SCNN1A,CALM2,HMOX2,FKBP1A,RACK1,SLC25A28,ATP6V1G1	red	VSMC_M1
GO:0006066	0.67	0.46	9	258	alcohol metabolic process	BP	1	ALDH1B1,INPP5B,COQ3,FGF2,DGAT2,ERLIN2,PTS,ITPKB,CYP1A1	red	VSMC_M1
GO:0017038	0.67	0.49	6	174	protein import	BP	1	HDAC3,PDCD5,PKIG,SNUPN,DNLZ,TOMM7	red	VSMC_M1
GO:0010951	0.67	0.50	5	137	negative regulation of endopeptidase activity	BP	1	PIH1D1,PCID2,RFFL,TIMP3,WFDC3	red	VSMC_M1
GO:0050776	0.67	0.42	19	538	regulation of immune response	BP	1	ARG1,IL1RL1,AHR,KMT5C,EIF2B4,PAK1,RPS3,CD8B,IL20RB,PARP3,RARA,NR1D1,EIF2B2,SPG21,IL13RA2,FKBP1A,RNF125,IGHA2,LY96	red	VSMC_M1
GO:0007059	0.67	0.45	10	288	chromosome segregation	BP	1	MAD2L1BP,MEI4,RECQL5,UVRAG,RPS3,PCID2,TNKS,KMT5A,TOP3B,XRCC3	red	VSMC_M1

GO:0009653	0.67	0.38	72	2050	anatomical structure morphogenesis	BP	1	SMAD4,SGK1,ARG1,CSNK2B,DYNLT1,ZHX2,CTNNA1,TRIOBP,MAP4K4,RPS7,PARD3,SF3B6,FGF2,TAL1,ARHGAP35,SDK2,UBP1,FAM171A1,IFT122,PAK1,SPAST,NEB,SP1,CXCL12,CTR9,EDNRA,SLC12A6,PTCD2,RHOF,SPRED1,RPS6,MMP16,HPSE,FBXW8,IFT57,TMEFF2,CDC73,CFAP410,ACTL6A,AKAP13,MYO18B,RHOD,KLHL41,FBXO45,EGR2,MAP2,GJC1,RP2,DYNC2H1,PROM1,ZMIZ1,KAT2A,PFN1,RARA,CECR2,MEF2D,FLRT2,SPARC,PMP22,B9D1,OMA1,TPRN,ERRFI1,CTNNBIP1,RBM15,WWOX,E2F4,FKBP1A,RACK1,CPNE1,ATP5IF1,FGF10	red	VSMC_M1
GO:0031023	0.67	0.52	4	127	microtubule organizing center organization	BP	1	UVRAG,KAT2A,XRCC3,E2F4	red	VSMC_M1
GO:0031960	0.67	0.52	4	117	response to corticosteroid	BP	1	ARG1,ALAD,SPARC,ERRFI1	red	VSMC_M1
GO:0010647	0.67	0.39	45	1251	positive regulation of cell communication	BP	1	SMAD4,CSNK2B,DYNLT1,CTNNA1,SRI,MAP4K4,SPIN1,NPR2,RPS7,PIH1D1,FGF2,WBP2,PAK1,RPS3,CSNK1D,HDAC3,PCID2,TNKS,TNFRSF19,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,TFG,CDC73,AKAP13,DYNC2H1,PELI2,ZMIZ1,ITPKB,CTDNEP1,CDK5RAP3,PRDX2,XRCC3,MIER1,GOLPH3,WWOX,FKBP1A,RACK1,TIMP3,RPS20,CPNE1,LY96,FGF10	red	VSMC_M1
GO:0001503	0.67	0.44	11	328	ossification	BP	1	KLF10,NPR2,FGF2,RRAS2,MMP16,EGR2,MEF2D,SPARC,CTNNBIP1,WWOX,KAZALD1	red	VSMC_M1
GO:0070302	0.67	0.50	5	151	regulation of stress-activated protein kinase signaling cascade	BP	1	MAP4K4,HDAC3,TNFRSF19,COPS5,MECOM	red	VSMC_M1
GO:0016485	0.68	0.48	6	170	protein processing	BP	1	INPP5B,PMPCB,MMP16,DYNC2H1,OMA1,PSENEN	red	VSMC_M1
GO:0034329	0.68	0.44	10	318	cell junction assembly	BP	1	CTNNA1,MAP4K4,PARD3,SDK2,PCDH17,RHOD,FBXO45,IL1RAP,GJC1,FLRT2	red	VSMC_M1
GO:0030154	0.68	0.36	107	2966	cell differentiation	BP	1	SMAD4,SGK1,KLF10,DYNLT1,ZHX2,NDRG1,ZFAT,EGR1,TCP11,CTNNA1,TRIOBP,TST,MAP4K4,NPR2,MEI4,RPS7,PIH1D1,PARD3,FKBP1B,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,EIF2B4,PAK1,SPAST,NEB,MCRIP1,CSNK1D,SOCS2,PCID2,CXCL12,CEBPG,CTR9,EDNRA,PTCD2,RPS3A,C21orf91,P2RX4,RRAS2,C15orf41,SPRED1,RPS6,TLL1,SMYD5,AMBRA1,FBXW8,TMEFF2,ARL3,CDC73,AKAP13,IRF2BP2,MYO18B,NIF3L1,KLHL41,RBM4,BCCIP,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,GJC1,MECOM,DYNC2H1,ELK1,PROM1,ITFG2,ZMIZ1,KAT2A,PRTG,HSPA2,ITPKB,RARA,CECR2,NR1D1,ETV3,MEF2D,CDK5RAP3,EIF2B2,PRDX2,FLRT2,PMP22,CYP1A1,HMG20A,B9D1,TBC1D24,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,WDR5,WWOX,E2F4,IER2,NUDT21,FAM9B,NREP,KAZALD1,BHLHE41,CPNE1,RITA1,ATP5IF1,FGF10	red	VSMC_M1
GO:0002366	0.68	0.48	6	181	leukocyte activation involved in immune response	BP	1	KMT5C,RPS6,PARP3,ITFG2,RARA,IL13RA2	red	VSMC_M1
GO:0060828	0.68	0.46	7	210	regulation of canonical Wnt signaling pathway	BP	1	EGR1,INVS,FGF2,CSNK1D,TNKS,CTDNEP1,FGF10	red	VSMC_M1
GO:0023061	0.68	0.44	11	325	signal release	BP	1	SMAD4,SRI,MAP4K4,FKBP1B,CXCL12,P2RX4,ENSA,NR1D1,PRRT2,STXBP4,PTPRN2	red	VSMC_M1
GO:0010941	0.68	0.38	45	1223	regulation of cell death	BP	1	SMAD4,SGK1,ARG1,DYNLT1,EGR1,CTNNA1,NAA35,MAP4K4,UBE2M,UTP11,RPS7,PIH1D1,WDR35,FGF2,RPS3,HDAC3,SOCS2,PCID2,CXCL12,COPS5,PDCD5,RPS3A,RRAS2,RPS6,IFT57,CDC73,KDM1A,NDUFA13,MECOM,ELK1,ERC1,ITPKB,RARA,PARP16,PRDX2,RFFL,MYO18A,OMA1,GOLPH3,PTPA,WWOX,RACK1,TIMP3,NAA38,FGF10	red	VSMC_M1
GO:0071705	0.68	0.37	59	1609	nitrogen compound transport	BP	1	ARG1,HSPA1L,DYNLT1,POLDIP3,REEP2,TST,SRI,UBAP1,MAP4K4,CLTA,SLC25A51,PARD3,FKBP1B,PMPCB,STAM,PAK1,VDAC3,HDAC3,PCID2,TNKS,RAB28,CXCL12,PDCD5,VTI1B,TIMM10,SLC12A6,ARFIP1,PKIG,ARL3,UNC119B,ARFGEF2,RAB9A,ARL4C,RAE1,ENSA,FAM45A,WDR11,EGR2,AP1S1,NDUFA13,ARL4D,RP2,ERC1,NR1D1,VPS37C,COPZ2,STXBP4,SNUPN,RAB12,MYO18A,GOLPH3,GOSR1,RAB39B,DNLZ,EVI5,RACK1,TOMM7,ATP5IF1,PTPRN2	red	VSMC_M1
GO:0007519	0.68	0.51	4	122	skeletal muscle tissue development	BP	1	EGR1,KLHL41,EGR2,MEF2D	red	VSMC_M1
GO:0050953	0.68	0.51	4	126	sensory perception of light stimulus	BP	1	FAM161A,GJC1,RP2,TIMP3	red	VSMC_M1
GO:0006937	0.68	0.51	4	121	regulation of muscle contraction	BP	1	SRI,FKBP1B,P2RX4,CALM2	red	VSMC_M1
GO:0023056	0.68	0.37	45	1258	positive regulation of signaling	BP	1	SMAD4,CSNK2B,DYNLT1,CTNNA1,SRI,MAP4K4,SPIN1,NPR2,RPS7,PIH1D1,FGF2,WBP2,PAK1,RPS3,CSNK1D,HDAC3,PCID2,TNKS,TNFRSF19,P2RX4,EIF2A,SPRED1,STIMATE,HPSE,TFG,CDC73,AKAP13,DYNC2H1,PELI2,ZMIZ1,ITPKB,CTDNEP1,CDK5RAP3,PRDX2,XRCC3,MIER1,GOLPH3,WWOX,FKBP1A,RACK1,TIMP3,RPS20,CPNE1,LY96,FGF10	red	VSMC_M1
GO:0032103	0.69	0.43	10	286	positive regulation of response to external stimulus	BP	1	ARG1,IL1RL1,FKBP1B,FGF2,PAK1,CXCL12,P2RX4,TMSB4X,LY96,FGF10	red	VSMC_M1
GO:0050770	0.69	0.50	4	132	regulation of axonogenesis	BP	1	ARHGAP35,PAK1,CXCL12,MAP2	red	VSMC_M1
GO:0030308	0.69	0.48	5	153	negative regulation of cell growth	BP	1	SMAD4,PAK1,MAP2,NDUFA13,RACK1	red	VSMC_M1
GO:0021543	0.69	0.50	4	127	pallium development	BP	1	FBXO45,KDM1A,ZMIZ1,RARA	red	VSMC_M1
GO:1901653	0.69	0.44	9	270	cellular response to peptide	BP	1	ARG1,KLF10,PAK1,SOCS2,CACNA2D1,SP1,STXBP4,RAB12,ERRFI1	red	VSMC_M1
GO:0016236	0.69	0.44	9	265	macroautophagy	BP	1	STAM,UVRAG,VTI1B,AMBRA1,NPRL2,WIPI1,VPS37C,ATP6V1G1,TOMM7	red	VSMC_M1
GO:0051240	0.69	0.37	37	1050	positive regulation of multicellular organismal process	BP	1	SMAD4,KLF10,EGR1,IL1RL1,KMT5C,PARD3,WDR35,FGF2,NR2C2,PAK1,RPS3,HDAC3,PCID2,SP1,CXCL12,CEBPG,IL20RB,HPSE,FBXW8,CD58,ARFGEF2,EGR2,KDM1A,ETV5,IL1RAP,ZMIZ1,KAT2A,ITPKB,RARA,PRDX2,FLRT2,OMA1,CTNNBIP1,GNAS,RACK1,LY96,FGF10	red	VSMC_M1
GO:0055080	0.69	0.40	17	494	cation homeostasis	BP	1	SMAD4,SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,SLC12A6,P2RX4,CNNM1,COX19,SCNN1A,CALM2,HMOX2,FKBP1A,SLC25A28,ATP6V1G1	red	VSMC_M1
GO:1901617	0.69	0.46	6	178	organic hydroxy compound biosynthetic process	BP	1	FGF2,ERLIN2,ACOT8,PTS,ITPKB,NR1D1	red	VSMC_M1
GO:0042391	0.69	0.43	10	302	regulation of membrane potential	BP	1	SRI,FKBP1B,CACNA2D1,P2RX4,CACNA1D,SCN3A,GJC1,KCNAB2,RACK1,ATP5IF1	red	VSMC_M1
GO:0071495	0.70	0.37	35	1018	cellular response to endogenous stimulus	BP	1	SMAD4,ARG1,CSNK2B,KLF10,EGR1,CTNNA1,AHR,EEF1A1,FGF2,RECQL5,WBP2,PAK1,CSNK1D,SOCS2,CACNA2D1,SP1,PDCD5,P2RX4,SPRED1,UROS,KDM1A,ZMIZ1,KAT2A,RARA,NR1D1,FLRT2,STXBP4,RAB12,GOLPH3,ERRFI1,WWOX,FKBP1A,GNAS,NREP,FGF10	red	VSMC_M1

GO:0007267	0.70	0.36	40	1146	cell-cell signaling	BP	1	SMAD4,CSNK2B,KLF10,EGR1,SRI,MAP4K4,SPIN1,INVS,FKBP1B,FGF2,PCDH17,CSNK1D,CACNA2D1,TNKS,CXCL12,CTR9,SLC12A6,P2RX4,CACNA1D,CDC73,ENSA,KCNQ2,EGR2,IL1RAP,GJC1,KAT2A,ERC1,RARA,CTDNEP1,NR1D1,PRRT2,STXBP4,PMP22,RNF138,TBC1D24,CTNNBIP1,WWOX,RACK1,PTPRN2,FGF10	red	VSMC_M1
GO:0019953	0.70	0.39	20	565	sexual reproduction	BP	1	SMAD4,ACR,HSPA1L,TCP11,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,C11orf74,CCNI,RPS6,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,CECR2,FAM9B	red	VSMC_M1
GO:0042886	0.70	0.44	7	210	amide transport	BP	1	SRI,MAP4K4,FKBP1B,ENSA,NR1D1,STXBP4,PTPRN2	red	VSMC_M1
GO:0048468	0.70	0.35	55	1587	cell development	BP	1	SMAD4,SGK1,DYNLT1,NDRG1,TCP11,CTNNA1,TRIOBP,MAP4K4,NPR2,MEI4,PARD3,FKBP1B,FGF2,TAL1,ARHGAP35,EIF2B4,PAK1,SPAST,NEB,CXCL12,EDNRA,PTCD2,C21orf91,RPS6,FBXW8,TMEFF2,ARL3,AKAP13,MYO18B,KLHL41,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,GJC1,ZMIZ1,PRTG,HSPA2,RARA,CECR2,NR1D1,EIF2B2,FLRT2,PMP22,TBC1D24,TPRN,GSTM3,WDR5,E2F4,FAM9B,NREP,BHLHE41,CPNE1	red	VSMC_M1
GO:0043583	0.70	0.47	5	162	ear development	BP	1	TRIOBP,CECR2,SPARC,TPRN,FGF10	red	VSMC_M1
GO:0012501	0.70	0.35	54	1474	programmed cell death	BP	1	SGK1,ARG1,DYRK2,EGR1,CTNNA1,NAA35,MAP4K4,UBE2M,AHR,UTP11,RPS7,PIH1D1,WDR35,FGF2,PAK1,RPS3,HDAC3,SOCS2,PCID2,CXCL12,TNFRSF19,COPS5,PDCD5,RPS3A,P2RX4,RPS6,TMEM117,IFT57,YARS,CDC73,KDM1A,USP28,NDUFA13,MECOM,ERC1,ITPKB,RARA,CECR2,MEF2D,CDK5RAP3,PRDX2,RFFL,MYO18A,OMA1,GOLPH3,UBE4B,PTPA,WWOX,ELMO3,RACK1,TIMP3,ATP5IF1,NAA38,FGF10	red	VSMC_M1
GO:0002263	0.70	0.45	6	185	cell activation involved in immune response	BP	1	KMT5C,RPS6,PARP3,ITFG2,RARA,IL13RA2	red	VSMC_M1
GO:0007188	0.70	0.48	4	129	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	BP	1	EDNRA,CACNA1D,AKAP13,GNAS	red	VSMC_M1
GO:0008217	0.71	0.48	4	122	regulation of blood pressure	BP	1	SGK1,NPR2,EDNRA,P2RX4	red	VSMC_M1
GO:0032984	0.71	0.45	6	195	protein-containing complex disassembly	BP	1	MTRF1L,HMGA1,TRIOBP,UVRAG,SPAST,OGFOD1	red	VSMC_M1
GO:0051094	0.71	0.36	34	982	positive regulation of developmental process	BP	1	SMAD4,KLF10,HMGA1,TRIOBP,KMT5C,FKBP1B,FGF2,TAL1,NR2C2,PAK1,CSNK1D,SOCS2,PCID2,SP1,CXCL12,C21orf91,HPSE,FBXW8,RBM4,EGR2,KDM1A,ETV5,IL1RAP,PROM1,ZMIZ1,KAT2A,ITPKB,RARA,FLRT2,CTNNBIP1,NUDT21,RACK1,CPNE1,FGF10	red	VSMC_M1
GO:0032869	0.71	0.46	5	161	cellular response to insulin stimulus	BP	1	PAK1,SP1,STXBP4,RAB12,ERRFI1	red	VSMC_M1
GO:0120032	0.71	0.46	5	158	regulation of plasma membrane bounded cell projection assembly	BP	1	ARHGAP35,VDAC3,TBC1D7,MAP4,PFN1	red	VSMC_M1
GO:0090092	0.71	0.44	6	193	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SMAD4,CSNK2B,SPRED1,FKBP1A,NREP,FGF10	red	VSMC_M1
GO:0071375	0.71	0.43	7	219	cellular response to peptide hormone stimulus	BP	1	ARG1,PAK1,SOCS2,SP1,STXBP4,RAB12,ERRFI1	red	VSMC_M1
GO:0003205	0.71	0.48	4	135	cardiac chamber development	BP	1	SMAD4,PTCD2,RBM15,FKBP1A	red	VSMC_M1
GO:0072593	0.71	0.44	6	176	reactive oxygen species metabolic process	BP	1	NDUFA13,PRDX6,PRDX2,CYP1A1,COQ7,ATP5IF1	red	VSMC_M1
GO:0010608	0.71	0.38	17	480	posttranscriptional regulation of gene expression	BP	1	POLDIP3,EIF3D,MALSU1,EIF2B4,RPS3,PCID2,EIF2A,OGFOD1,RBM4,EXOSC7,RARA,DCP2,EIF2B2,FBXO4,DPH5,NUDT21,RACK1	red	VSMC_M1
GO:0046661	0.71	0.48	4	128	male sex differentiation	BP	1	SMAD4,CTNNA1,RARA,FGF10	red	VSMC_M1
GO:0071363	0.71	0.38	18	545	cellular response to growth factor stimulus	BP	1	SMAD4,ARG1,EGR1,EEF1A1,FGF2,CSNK1D,PDCD5,SPRED1,TGIF1,ZMIZ1,KAT2A,FLRT2,ERRFI1,WWOX,FKBP1A,RACK1,NREP,FGF10	red	VSMC_M1
GO:0060491	0.71	0.45	5	159	regulation of cell projection assembly	BP	1	ARHGAP35,VDAC3,TBC1D7,MAP4,PFN1	red	VSMC_M1
GO:0098771	0.71	0.38	17	502	inorganic ion homeostasis	BP	1	SMAD4,SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,SLC12A6,P2RX4,CNNM1,COX19,SCNN1A,CALM2,HMOX2,FKBP1A,SLC25A28,ATP6V1G1	red	VSMC_M1
GO:0010466	0.72	0.45	5	145	negative regulation of peptidase activity	BP	1	PIH1D1,PCID2,RFFL,TIMP3,WFDC3	red	VSMC_M1
GO:1903034	0.72	0.47	4	123	regulation of response to wounding	BP	1	FKBP1B,FGF2,HPSE,PRDX2	red	VSMC_M1
GO:0009888	0.72	0.33	48	1389	tissue development	BP	1	SMAD4,CSNK2B,KLF10,EGR1,TRIOBP,TST,RPS7,PIH1D1,FGF2,TAL1,ARHGAP35,IFT122,PAK1,DGAT2,NEB,MCRIP1,TNFRSF19,CTR9,EDNRA,PTCD2,SPRED1,HPSE,IFT57,TMEFF2,CDC73,AKAP13,MYO18B,KLHL41,BCCIP,EGR2,GJC1,PROM1,KAT2A,PFN1,RARA,CTDNEP1,CECR2,MEF2D,CYP1A1,B9D1,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,E2F4,FKBP1A,FGF10	red	VSMC_M1
GO:0051704	0.72	0.35	25	709	multi-organism process	BP	1	SMAD4,ARG1,ACR,HSPA1L,DYNLT1,TCP11,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,C11orf74,GOT2,CCNI,RPS6,ARHGDIB,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,CECR2,CYP1A1,FAM9B	red	VSMC_M1
GO:0050793	0.72	0.33	65	1852	regulation of developmental process	BP	1	SMAD4,KLF10,DYNLT1,ZHX2,HMGA1,TCP11,CTNNA1,TRIOBP,MAP4K4,NPR2,KMT5C,PARD3,FKBP1B,FGF2,TAL1,ARHGAP35,NR2C2,FAM171A1,PAK1,MCRIP1,CSNK1D,SOCS2,PCID2,SP1,CXCL12,CTR9,RHOF,C21orf91,SPRED1,SMYD5,HPSE,FBXW8,PARP3,CDC73,CFAP410,RHOD,KLHL41,RBM4,EGR2,KDM1A,ETV5,MAP2,IL1RAP,PROM1,ZMIZ1,KAT2A,PRTG,ITPKB,RARA,NR1D1,CDK5RAP3,PRDX2,FLRT2,SPARC,HMG20A,OMA1,ERFI1,CTNNBIP1,RBM15,NUDT21,RACK1,NREP,BHLHE41,CPNE1,FGF10	red	VSMC_M1
GO:0022604	0.72	0.40	8	261	regulation of cell morphogenesis	BP	1	TRIOBP,ARHGAP35,FAM171A1,RHOF,FBXW8,CFAP410,RHOD,SPARC	red	VSMC_M1
GO:0051049	0.72	0.33	45	1276	regulation of transport	BP	1	SMAD4,SGK1,ARG1,HSPA1L,REEP2,SRI,MAP4K4,KCNF1,FKBP1B,STAM,PAK1,HDAC3,CACNA2D1,CXCL12,PDCD5,EDNRA,ARFIP1,P2RX4,CACNA1D,STIMATE,PKIG,SCN3A,RAB9A,ENSA,FAM45A,RBM4,KCNQ2,MAP2,HSPA2,NR1D1,PRRT2,STXBP4,CALM2,IL13RA2,RAB12,MYO18A,GOLPH3,KCNAB2,FKBP1A,RACK1,TMSB4X,TOMM7,ATP5IF1,AHNAK,FGF10	red	VSMC_M1
GO:0010035	0.72	0.37	15	435	response to inorganic substance	BP	1	ARG1,NDRG1,ALAD,FKBP1B,RPS3,IL18BP,P2RX4,UROS,ITPKB,PRDX2,CALM2,SPARC,CYP1A1,RACK1,CPNE1	red	VSMC_M1

GO:0042127	0.73	0.33	44	1230	regulation of cell population proliferation	BP	1	SMAD4,SGK1,ARG1,CSNK2B,KLF10,FGFR1OP,NDRG1,HMGA1,EGR1,CTNNA1,AHR,COPS9,NUDT6,FGF2,TAL1,PAK1,RPS3,SP1,CXCL12,IL20RB,PDCD5,RPS6,HPSE,IFT57,CDC73,KLHL41,SMYD2,KDM1A,ETV5,ZMIZ1,RARA,NR1D1,ETV3,MEF2D,STXBP4,SPARC,PMP22,FBXO4,ERRFI1,CTNNBIP1,E2F4,MED31,ATP5IF1,FGF10	red	VSMC_M1
GO:0070663	0.73	0.44	5	153	regulation of leukocyte proliferation	BP	1	ARG1,AHR,RPS3,IL20RB,FGF10	red	VSMC_M1
GO:0043408	0.73	0.36	17	502	regulation of MAPK cascade	BP	1	SMAD4,MAP4K4,FGF2,PAK1,RPS3,HDAC3,TNFRSF19,COPS5,SPRED1,AKAP13,MECOM,PELI2,CDK5RAP3,PRDX2,ERRFI1,TIMP3,FGF10	red	VSMC_M1
GO:0046474	0.73	0.42	6	185	glycerophospholipid biosynthetic process	BP	1	FGF2,EFR3B,SOCS2,GPAT3,ITPKB,HDHD5	red	VSMC_M1
GO:0048666	0.73	0.34	29	877	neuron development	BP	1	SMAD4,SGK1,DYNLT1,CTNNA1,TRIOBP,MAP4K4,PARD3,FKBP1B,ARHGAP35,PAK1,SPAST,CXCL12,C21orf91,FBXW8,ARL3,MAP4,FBXO45,EGR2,KDM1A,MAP2,ZMIZ1,CECR2,FLRT2,PMP22,TBC1D24,TPRN,WDR5,NREP,CPNE1	red	VSMC_M1
GO:0019318	0.73	0.42	6	185	hexose metabolic process	BP	1	DYRK2,DGAT2,KAT2A,OMA1,WDR5,SLC25A1	red	VSMC_M1
GO:0006915	0.73	0.32	52	1436	apoptotic process	BP	1	SGK1,DYRK2,EGR1,CTNNA1,NAA35,MAP4K4,UBE2M,AHR,UTP11,RPS7,PIH1D1,WDR35,PAK1,RPS3,HDAC3,SOCS2,PCID2,CXCL12,TNFRSF19,COPS5,PDCD5,RPS3A,P2RX4,RPS6,TMEM117,IFT57,YARS,CDC73,KDM1A,USP28,NDUFA13,MECOM,ERC1,ITPKB,RARA,CECR2,MEF2D,CDK5RAP3,PRDX2,RFFL,MYO18A,OMA1,GOLPH3,UBE4B,PTPA,WWOX,ELMO3,RACK1,TIMP3,ATP5IF1,NAA38,FGF10	red	VSMC_M1
GO:0051495	0.73	0.42	6	194	positive regulation of cytoskeleton organization	BP	1	PAK1,RPS3,SPAST,ARFIP1,ARL3,PFN1	red	VSMC_M1
GO:0042594	0.73	0.43	5	158	response to starvation	BP	1	KLF10,EIF2A,NPRL2,WIPI1,ITFG2	red	VSMC_M1
GO:0050821	0.73	0.43	5	154	protein stabilization	BP	1	RPS7,IFT46,PFN1,STXBP4,DNLZ	red	VSMC_M1
GO:0051128	0.73	0.31	66	1877	regulation of cellular component organization	BP	1	SMAD4,SGK1,DYNLT1,FGFR1OP,PFDN6,TRIOBP,MAD2L1BP,MAP4K4,CRIPT,PIH1D1,WDR35,FKBP1B,TAL1,ARHGAP35,STAM,PAK1,UVRAG,RPS3,VDAC3,SPAST,NEB,PFDN1,SOCS2,PCID2,TNKS,CXCL12,PDCD5,TMSB10,ARFIP1,RHOF,OGFOD1,FBXW8,TBC1D7,PARP3,TMEFF2,ARL3,CDC73,NPRL2,AKAP13,RHOD,RAE1,ARHGDIB,MAP4,KDM1A,MAP2,IL1RAP,NDUFA13,KAT2A,PFN1,HSPA2,DCP2,PRRT2,FLRT2,SPARC,PMP22,XRCC3,FBXO4,TUBB4A,KANK4,OMA1,GOLPH3,CTNNBIP1,RACK1,KAZALD1,TMSB4X,ATP5IF1	red	VSMC_M1
GO:0043547	0.73	0.41	6	202	positive regulation of GTPase activity	BP	1	MUT,MAP4K4,TBC1D7,GARNL3,EVI5,RACK1	red	VSMC_M1
GO:0009267	0.73	0.45	4	130	cellular response to starvation	BP	1	KLF10,NPRL2,WIPI1,ITFG2	red	VSMC_M1
GO:0048660	0.73	0.45	4	124	regulation of smooth muscle cell proliferation	BP	1	FGF2,PAK1,MEF2D,CTNNBIP1	red	VSMC_M1
GO:0001568	0.73	0.35	19	576	blood vessel development	BP	1	EGR1,AHR,FGF2,TAL1,UBP1,SP1,EDNRA,SLC12A6,SPRED1,HPSE,FBXW8,MYO18B,GJC1,DYNC2H1,ZMIZ1,SPARC,RBM15,ATP5IF1,FGF10	red	VSMC_M1
GO:0001932	0.74	0.33	29	845	regulation of protein phosphorylation	BP	1	SMAD4,CSNK2B,FGFR1OP,EGR1,PIH1D1,PARD3,FGF2,TAL1,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,SPRED1,CCNI,PKIG,AKAP13,BCCIP,PELI2,HSPA2,ITPKB,CDK5RAP3,PARP16,CALM2,MOB3A,ERRFI1,RACK1,HUS1,FGF10	red	VSMC_M1
GO:0000302	0.74	0.41	6	177	response to reactive oxygen species	BP	1	ARG1,FKBP1B,RPS3,IL18BP,PRDX2,RACK1	red	VSMC_M1
GO:0044703	0.74	0.34	24	688	multi-organism reproductive process	BP	1	SMAD4,ARG1,ACR,HSPA1L,TCP11,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,C11orf74,GOT2,CCNI,RPS6,ARHGDIB,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,CECR2,CYP1A1,FAM9B	red	VSMC_M1
GO:0048869	0.74	0.30	108	3033	cellular developmental process	BP	1	SMAD4,SGK1,KLF10,DYNLT1,ZHX2,NDRG1,ZFAT,HMGA1,EGR1,TCP11,CTNNA1,TRIOBP,TST,MAP4K4,NPR2,MEI4,RPS7,PIH1D1,PARD3,FKBP1B,FGF2,TAL1,ARHGAP35,SDK2,NR2C2,EIF2B4,PAK1,SPAST,NEB,MCRIP1,CSNK1D,SOCS2,PCID2,CXCL12,CEBPG,CTR9,EDNRA,PTCD2,RPS3A,C21orf91,P2RX4,RRAS2,C15orf41,SPRED1,RPS6,TLL1,SMYD5,AMBRA1,FBXW8,TMEFF2,ARL3,CDC73,AKAP13,IRF2BP2,MYO18B,NIF3L1,KLHL41,RBM4,BCCIP,MAP4,FBXO45,EGR2,KDM1A,ETV5,MAP2,GJC1,MECOM,DYNC2H1,ELK1,PROM1,ITFG2,ZMIZ1,KAT2A,PRTG,HSPA2,ITPKB,RARA,CECR2,NR1D1,ETV3,MEF2D,CDK5RAP3,EIF2B2,PRDX2,FLRT2,PMP22,CYP1A1,HMG20A,B9D1,TBC1D24,TPRN,ERRFI1,CTNNBIP1,RBM15,GSTM3,WDR5,WWOX,E2F4,IER2,NUDT21,FAM9B,NREP,KAZALD1,BHLHE41,CPNE1,RITA1,ATP5IF1,FGF10	red	VSMC_M1
GO:0001558	0.74	0.37	11	339	regulation of cell growth	BP	1	SMAD4,SGK1,FGFR1OP,PAK1,SOCS2,CXCL12,CDC73,MAP2,NDUFA13,RACK1,KAZALD1	red	VSMC_M1
GO:0016049	0.74	0.36	13	399	cell growth	BP	1	SMAD4,SGK1,FGFR1OP,PAK1,SOCS2,CXCL12,CDC73,AKAP13,MAP2,NDUFA13,RACK1,KAZALD1,CPNE1	red	VSMC_M1
GO:0022408	0.74	0.44	4	130	negative regulation of cell-cell adhesion	BP	1	ARG1,CXCL12,IL20RB,PRDX2	red	VSMC_M1
GO:0002253	0.74	0.40	6	191	activation of immune response	BP	1	EIF2B4,PAK1,RPS3,EIF2B2,SPG21,IGHA2	red	VSMC_M1
GO:0001934	0.74	0.34	18	543	positive regulation of protein phosphorylation	BP	1	SMAD4,CSNK2B,EGR1,PIH1D1,FGF2,TAL1,PAK1,RPS3,CSNK1D,HDAC3,AKAP13,PELI2,HSPA2,PARP16,CALM2,MOB3A,RACK1,FGF10	red	VSMC_M1
GO:0060538	0.74	0.43	4	132	skeletal muscle organ development	BP	1	EGR1,KLHL41,EGR2,MEF2D	red	VSMC_M1
GO:0010720	0.74	0.39	7	231	positive regulation of cell development	BP	1	TRIOBP,PAK1,CXCL12,FBXW8,EGR2,KDM1A,ETV5	red	VSMC_M1
GO:0002064	0.74	0.41	5	173	epithelial cell development	BP	1	TRIOBP,RARA,TPRN,GSTM3,E2F4	red	VSMC_M1
GO:0043067	0.75	0.31	40	1119	regulation of programmed cell death	BP	1	SGK1,ARG1,EGR1,CTNNA1,NAA35,MAP4K4,UBE2M,UTP11,RPS7,PIH1D1,WDR35,FGF2,RPS3,HDAC3,SOCS2,PCID2,CXCL12,COPS5,PDCD5,RPS3A,RPS6,IFT57,CDC73,KDM1A,NDUFA13,MECOM,ERC1,ITPKB,RARA,PRDX2,RFFL,MYO18A,OMA1,GOLPH3,PTPA,WWOX,RACK1,TIMP3,NAA38,FGF10	red	VSMC_M1
GO:0006874	0.75	0.37	9	283	cellular calcium ion homeostasis	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0043588	0.75	0.41	5	171	skin development	BP	1	SMAD4,TNFRSF19,HPSE,ERRFI1,FGF10	red	VSMC_M1
GO:0019216	0.75	0.38	8	251	regulation of lipid metabolic process	BP	1	EGR1,FGF2,DGAT2,ERLIN2,AMBRA1,CRTC3,CTDNEP1,NR1D1	red	VSMC_M1
GO:0045926	0.75	0.39	6	195	negative regulation of growth	BP	1	SMAD4,PAK1,SOCS2,MAP2,NDUFA13,RACK1	red	VSMC_M1
GO:0071241	0.75	0.41	5	165	cellular response to inorganic substance	BP	1	ALAD,P2RX4,ITPKB,CYP1A1,CPNE1	red	VSMC_M1
GO:0007568	0.75	0.37	8	252	aging	BP	1	ARG1,HMGA1,CTNNA1,FGF2,ZMIZ1,CYP1A1,COQ7,FBXO4	red	VSMC_M1
GO:0008406	0.75	0.40	5	166	gonad development	BP	1	SMAD4,CTNNA1,EIF2B4,RARA,EIF2B2	red	VSMC_M1

GO:0042327	0.76	0.32	20	612	positive regulation of phosphorylation	BP	1	SMAD4,CSNK2B,EGR1,KCTD20,PIH1D1,FGF2,TAL1,PAK1,RPS3,CSNK1D,HDAC3,AMBRA1,AKAP13,PELI2,HSPA2,PARP16,CALM2,MOB3A,RACK1,FGF10	red	VSMC_M1
GO:0043393	0.76	0.40	5	162	regulation of protein binding	BP	1	KDM1A,MAP2,CTNNBIP1,FKBP1A,RACK1	red	VSMC_M1
GO:0010562	0.76	0.32	22	669	positive regulation of phosphorus metabolic process	BP	1	SMAD4,CSNK2B,EGR1,KCTD20,PIH1D1,FGF2,TAL1,PAK1,RPS3,CSNK1D,HDAC3,AMBRA1,AKAP13,PELI2,HSPA2,PARP16,CALM2,MOB3A,PTPA,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0045937	0.76	0.32	22	669	positive regulation of phosphate metabolic process	BP	1	SMAD4,CSNK2B,EGR1,KCTD20,PIH1D1,FGF2,TAL1,PAK1,RPS3,CSNK1D,HDAC3,AMBRA1,AKAP13,PELI2,HSPA2,PARP16,CALM2,MOB3A,PTPA,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0010976	0.76	0.42	4	140	positive regulation of neuron projection development	BP	1	DYNLT1,FKBP1B,ARHGAP35,KDM1A	red	VSMC_M1
GO:0050870	0.76	0.42	4	130	positive regulation of T cell activation	BP	1	RPS3,ZMIZ1,ITPKB,RARA	red	VSMC_M1
GO:0042445	0.76	0.42	4	133	hormone metabolic process	BP	1	EGR1,DGAT2,CYP1A1,CHST9	red	VSMC_M1
GO:0061448	0.76	0.38	6	203	connective tissue development	BP	1	EGR1,FGF2,DGAT2,KAT2A,RARA,MEF2D	red	VSMC_M1
GO:0000819	0.76	0.39	5	168	sister chromatid segregation	BP	1	MAD2L1BP,PCID2,TNKS,KMT5A,XRCC3	red	VSMC_M1
GO:0001501	0.76	0.33	13	413	skeletal system development	BP	1	NPR2,FGF2,TAL1,TLL1,MMP16,AKAP13,KAT2A,RARA,MEF2D,MBTD1,WDR5,WWOX,GNAS	red	VSMC_M1
GO:0007034	0.76	0.41	4	137	vacuolar transport	BP	1	STAM,VTI1B,VPS37C,RAB12	red	VSMC_M1
GO:1990138	0.76	0.41	4	147	neuron projection extension	BP	1	PAK1,CXCL12,MAP2,CPNE1	red	VSMC_M1
GO:0048871	0.76	0.33	12	378	multicellular organismal homeostasis	BP	1	EGR1,HDAC3,IL20RB,P2RX4,CRTC3,KDM1A,SCNN1A,PROM1,NR1D1,OMA1,GNAS,IGHA2	red	VSMC_M1
GO:0032989	0.77	0.31	19	609	cellular component morphogenesis	BP	1	SMAD4,SGK1,DYNLT1,MAP4K4,PARD3,ARHGAP35,PAK1,SPAST,NEB,CXCL12,FBXW8,AKAP13,KLHL41,FBXO45,EGR2,MAP2,FLRT2,PMP22,CPNE1	red	VSMC_M1
GO:0010942	0.77	0.32	16	470	positive regulation of cell death	BP	1	ARG1,EGR1,CTNNA1,UBE2M,UTP11,RPS7,WDR35,RPS3,PDCD5,RPS6,ELK1,OMA1,PTPA,WWOX,RACK1,TIMP3	red	VSMC_M1
GO:0048878	0.77	0.29	28	832	chemical homeostasis	BP	1	SMAD4,DYNLT1,SRI,MAP4K4,PIH1D1,WDR35,FKBP1B,FGF2,DGAT2,CACNA2D1,CXCL12,EDNRA,SLC12A6,P2RX4,RPS6,CNNM1,CYB561D2,COX19,SCNN1A,NR1D1,STXBP4,CALM2,HMOX2,FKBP1A,RACK1,SLC25A28,ATP6V1G1,PTPRN2	red	VSMC_M1
GO:0045137	0.77	0.38	5	170	development of primary sexual characteristics	BP	1	SMAD4,CTNNA1,EIF2B4,RARA,EIF2B2	red	VSMC_M1
GO:0071824	0.77	0.38	5	163	protein-DNA complex subunit organization	BP	1	HMGA1,TAF11,PIH1D1,CABIN1,DR1	red	VSMC_M1
GO:0007178	0.77	0.34	8	272	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SMAD4,CSNK2B,EGR1,SPRED1,ZMIZ1,FKBP1A,NREP,FGF10	red	VSMC_M1
GO:0065004	0.77	0.40	4	132	protein-DNA complex assembly	BP	1	TAF11,PIH1D1,CABIN1,DR1	red	VSMC_M1
GO:0055074	0.77	0.34	9	291	calcium ion homeostasis	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0007411	0.77	0.37	5	181	axon guidance	BP	1	SMAD4,ARHGAP35,CXCL12,EGR2,FLRT2	red	VSMC_M1
GO:0006109	0.78	0.39	4	139	regulation of carbohydrate metabolic process	BP	1	DYRK2,DGAT2,KAT2A,WDR5	red	VSMC_M1
GO:0007409	0.78	0.33	10	341	axonogenesis	BP	1	SMAD4,PARD3,ARHGAP35,PAK1,SPAST,CXCL12,FBXO45,EGR2,MAP2,FLRT2	red	VSMC_M1
GO:0031346	0.78	0.33	9	302	positive regulation of cell projection organization	BP	1	DYNLT1,FKBP1B,ARHGAP35,PAK1,CXCL12,FBXW8,KDM1A,KAT2A,PFN1	red	VSMC_M1
GO:0048285	0.78	0.31	13	401	organelle fission	BP	1	MEI1,MAD2L1BP,MEI4,SPAST,PCID2,TNKS,MTFR1,KMT5A,ACOT8,MTFR1L,BCCIP,HSPA2,XRCC3	red	VSMC_M1
GO:0072507	0.78	0.33	10	323	divalent inorganic cation homeostasis	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,P2RX4,CNNM1,CALM2,FKBP1A	red	VSMC_M1
GO:0006875	0.78	0.32	12	381	cellular metal ion homeostasis	BP	1	SMAD4,SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,P2RX4,COX19,CALM2,FKBP1A,ATP6V1G1	red	VSMC_M1
GO:0097485	0.78	0.37	5	182	neuron projection guidance	BP	1	SMAD4,ARHGAP35,CXCL12,EGR2,FLRT2	red	VSMC_M1
GO:0045861	0.78	0.35	7	213	negative regulation of proteolysis	BP	1	ALAD,RPS7,PIH1D1,PCID2,RFFL,TIMP3,WFDC3	red	VSMC_M1
GO:0044262	0.78	0.35	7	229	cellular carbohydrate metabolic process	BP	1	DYRK2,INPP5B,COQ3,DGAT2,KAT2A,NR1D1,WDR5	red	VSMC_M1
GO:0046486	0.78	0.32	10	317	glycerolipid metabolic process	BP	1	INPP5B,FGF2,EFR3B,DGAT2,SOCS2,GPAT3,PRDX6,ITPKB,HDHD5,CTDNEP1	red	VSMC_M1
GO:0006650	0.78	0.34	8	257	glycerophospholipid metabolic process	BP	1	INPP5B,FGF2,EFR3B,SOCS2,GPAT3,PRDX6,ITPKB,HDHD5	red	VSMC_M1
GO:0050920	0.78	0.37	5	167	regulation of chemotaxis	BP	1	FGF2,CXCL12,P2RX4,TMSB4X,FGF10	red	VSMC_M1
GO:0000902	0.78	0.28	25	799	cell morphogenesis	BP	1	SMAD4,SGK1,DYNLT1,TRIOBP,MAP4K4,PARD3,TAL1,ARHGAP35,FAM171A1,PAK1,SPAST,CXCL12,RHOF,FBXW8,TMEFF2,CFAP410,RHOD,FBXO45,EGR2,MAP2,RP2,FLRT2,SPARC,TPRN,CPNE1	red	VSMC_M1
GO:0051272	0.78	0.30	15	466	positive regulation of cellular component movement	BP	1	FGFR1OP,MAP4K4,FGF2,PAK1,SP1,CXCL12,P2RX4,RRAS2,RHOD,MAP2,PFN1,SPARC,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0043069	0.79	0.28	23	681	negative regulation of programmed cell death	BP	1	CTNNA1,NAA35,MAP4K4,PIH1D1,HDAC3,SOCS2,PCID2,CXCL12,COPS5,RPS3A,RPS6,CDC73,KDM1A,NDUFA13,MECOM,ERC1,ITPKB,PRDX2,RFFL,MYO18A,GOLPH3,NAA38,FGF10	red	VSMC_M1
GO:0006468	0.79	0.26	41	1223	protein phosphorylation	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,FGFR1OP,EGR1,MAP4K4,NPR2,ICK,PIH1D1,PARD3,ADCK2,FGF2,TAL1,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,CDK17,TNKS,EIF2A,SPRED1,CCNI,PKIG,NPRL2,AKAP13,BCCIP,PELI2,ERC1,HSPA2,ITPKB,RARA,CDK5RAP3,PARP16,CALM2,MOB3A,ERFI1,RACK1,HUS1,FGF10	red	VSMC_M1
GO:0043068	0.79	0.30	14	422	positive regulation of programmed cell death	BP	1	ARG1,CTNNA1,UBE2M,UTP11,RPS7,WDR35,RPS3,PDCD5,RPS6,OMA1,PTPA,WWOX,RACK1,TIMP3	red	VSMC_M1
GO:0072657	0.79	0.29	15	466	protein localization to membrane	BP	1	REEP2,CRIPT,PARD3,EFR3B,PAK1,PDCD5,VTI1B,TIMM10,ARL3,EMC9,NDUFA13,VPS37C,RAB12,GOLPH3,RACK1	red	VSMC_M1
GO:0031668	0.79	0.34	6	205	cellular response to extracellular stimulus	BP	1	KLF10,ARHGAP35,TNKS,NPRL2,WIPI1,ITFG2	red	VSMC_M1
GO:1901575	0.79	0.25	58	1628	organic substance catabolic process	BP	1	ARG1,ACR,ZHX2,TST,UBAP1,ALDH1B1,EEF1A1,INPP5B,ALAD,RPS7,PSMB2,GPT2,FGF2,STAM,UVRAG,RNF121,CSNK1D,ERLIN2,PCID2,LTA4H,ELOC,GOT2,HPSE,FBXW8,ACOT8,PPP1R8,PPP1R11,CRTC3,PSMA7,FBXO45,USP28,EXOSC7,NDUFA13,PRDX6,USP5,LSM4,UBA1,PSMB6,CECR2,NR1D1,DCP2,VPS37C,RNF40,CDK5RAP3,CYP1A1,RFFL,USP22,FBXO4,RAB12,OMA1,HMOX2,UBE4B,USP10,RACK1,TIMP3,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:2000146	0.79	0.33	7	234	negative regulation of cell motility	BP	1	CSNK2B,CTNNA1,FGF2,CXCL12,SPRED1,TMEFF2,ARHGDIB	red	VSMC_M1

GO:0006928	0.79	0.25	53	1565	movement of cell or subcellular component	BP	1	SMAD4,SGK1,CSNK2B,DYNLT1,FGFR1OP,CTNNA1,DNAL4,SRI,MAP4K4,ICK,INPP5B,WDR35,FGF2,ARHGAP35,IFT122,PAK1,SPAST,CACNA2D1,SP1,CXCL12,DNAH12,TMSB10,RHOF,P2RX4,RRAS2,CACNA1D,SPRED1,IFT57,TMEFF2,ARL3,RHOD,IFT46,ARHGDIB,MAP4,FBXO45,EGR2,MAP2,GJC1,DYNC2H1,ZMIZ1,MYO5C,PFN1,FLRT2,SPARC,RFFL,MYO18A,GOLPH3,DYNLRB2,ELMO3,IER2,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0007548	0.79	0.34	6	206	sex differentiation	BP	1	SMAD4,CTNNA1,EIF2B4,RARA,EIF2B2,FGF10	red	VSMC_M1
GO:0009887	0.79	0.27	25	784	animal organ morphogenesis	BP	1	SMAD4,ARG1,ZHX2,CTNNA1,TRIOBP,FGF2,SDK2,IFT122,PTCD2,MMP16,IFT57,TMEFF2,PROM1,ZMIZ1,RARA,MEF2D,FLRT2,TPRN,ERRFI1,CTNNBIP1,RBM15,WWOX,E2F4,FKBP1A,FGF10	red	VSMC_M1
GO:0048812	0.80	0.28	15	503	neuron projection morphogenesis	BP	1	SMAD4,SGK1,DYNLT1,MAP4K4,PARD3,ARHGAP35,PAK1,SPAST,CXCL12,FBXW8,FBXO45,EGR2,MAP2,FLRT2,CPNE1	red	VSMC_M1
GO:0009266	0.80	0.36	4	137	response to temperature stimulus	BP	1	EIF2B4,CXCL12,HSPA2,EIF2B2	red	VSMC_M1
GO:0043087	0.80	0.31	8	285	regulation of GTPase activity	BP	1	DYNLT1,MUT,MAP4K4,TBC1D7,GARNL3,EVI5,RACK1,PTPRN2	red	VSMC_M1
GO:0034330	0.80	0.28	16	541	cell junction organization	BP	1	NDRG1,CTNNA1,MAP4K4,CRIPT,PARD3,SDK2,PCDH17,RHOD,FBXO45,IL1RAP,GJC1,PFN1,ERC1,FLRT2,SPARC,RAB39B	red	VSMC_M1
GO:0030335	0.80	0.29	14	443	positive regulation of cell migration	BP	1	FGFR1OP,MAP4K4,FGF2,PAK1,SP1,CXCL12,P2RX4,RRAS2,RHOD,PFN1,SPARC,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0005996	0.80	0.33	6	199	monosaccharide metabolic process	BP	1	DYRK2,DGAT2,KAT2A,OMA1,WDR5,SLC25A1	red	VSMC_M1
GO:0007565	0.80	0.36	4	139	female pregnancy	BP	1	ARG1,GOT2,ARHGDIB,RARA	red	VSMC_M1
GO:1903829	0.80	0.32	7	241	positive regulation of cellular protein localization	BP	1	HSPA1L,PAK1,HDAC3,PDCD5,CDK5RAP3,RACK1,TOMM7	red	VSMC_M1
GO:0043085	0.80	0.25	29	875	positive regulation of catalytic activity	BP	1	EGR1,MUT,MAP4K4,PIH1D1,WDR35,FGF2,TAL1,PAK1,RPS3,TNKS,PDCD5,EDNRA,CACNA1D,AMBRA1,TBC1D7,IFT57,AKAP13,MYL4,NDUFA13,PFN1,PARP16,CALM2,PTPA,GARNL3,EVI5,RACK1,TMSB4X,PSENEN,FGF10	red	VSMC_M1
GO:0048513	0.80	0.23	88	2529	animal organ development	BP	1	SMAD4,ARG1,CSNK2B,KLF10,ZHX2,ZFAT,EGR1,CTNNA1,TRIOBP,SRI,NPR2,PGM3,WDR35,FGF2,TAL1,ARHGAP35,SDK2,IFT122,EIF2B4,PAK1,DGAT2,NEB,NRG2,MCRIP1,CSNK1D,SOCS2,PCID2,CXCL12,TNFRSF19,CEBPG,CTR9,EDNRA,PTCD2,C21orf91,GOT2,C15orf41,SPRED1,RPS6,MMP16,HPSE,FBXW8,IFT57,TMEFF2,ARL3,CDC73,ACTL6A,AKAP13,IRF2BP2,MYO18B,KLHL41,WDR11,SMYD2,FBXO45,EGR2,KDM1A,GJC1,MECOM,DYNC2H1,ELK1,PROM1,ITFG2,ZMIZ1,KAT2A,ITPKB,RARA,CECR2,MEF2D,CDK5RAP3,EIF2B2,PRDX2,FLRT2,CALM2,SPARC,CYP1A1,B9D1,GFER,TPRN,ERRFI1,CTNNBIP1,RBM15,WWOX,E2F4,NUDT21,FKBP1A,GNAS,BORCS8,ATP5IF1,FGF10	red	VSMC_M1
GO:0043066	0.81	0.26	22	662	negative regulation of apoptotic process	BP	1	CTNNA1,NAA35,MAP4K4,PIH1D1,HDAC3,SOCS2,PCID2,CXCL12,COPS5,RPS3A,RPS6,CDC73,KDM1A,NDUFA13,ERC1,ITPKB,PRDX2,RFFL,MYO18A,GOLPH3,NAA38,FGF10	red	VSMC_M1
GO:0044248	0.81	0.23	62	1755	cellular catabolic process	BP	1	ARG1,ACR,ZHX2,TST,UBAP1,EEF1A1,ALAD,RPS7,PSMB2,GPT2,STAM,UVRAG,RNF121,CSNK1D,ERLIN2,PCID2,LTA4H,VTI1B,ELOC,GOT2,HPSE,AMBRA1,FBXW8,ACOT8,NPRL2,WIPI1,PPP1R8,PPP1R11,PSMA7,FBXO45,USP28,EXOSC7,PRDX6,USP5,LSM4,UBA1,PSMB6,CECR2,NR1D1,DCP2,VPS37C,RNF40,CDK5RAP3,PRDX2,CYP1A1,RFFL,USP22,FBXO4,RAB12,OMA1,HMOX2,RAB39B,UBE4B,GSTM3,USP10,RACK1,ATP6V1G1,TIMP3,TOMM7,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0048667	0.81	0.28	13	446	cell morphogenesis involved in neuron differentiation	BP	1	SMAD4,TRIOBP,PARD3,ARHGAP35,PAK1,SPAST,CXCL12,FBXW8,FBXO45,EGR2,MAP2,FLRT2,TPRN	red	VSMC_M1
GO:0033002	0.81	0.33	5	174	muscle cell proliferation	BP	1	NAA35,FGF2,PAK1,MEF2D,CTNNBIP1	red	VSMC_M1
GO:1903039	0.81	0.35	4	143	positive regulation of leukocyte cell-cell adhesion	BP	1	RPS3,ZMIZ1,ITPKB,RARA	red	VSMC_M1
GO:0009152	0.81	0.34	4	137	purine ribonucleotide biosynthetic process	BP	1	NPR2,ELOVL2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0009952	0.81	0.34	4	150	anterior/posterior pattern specification	BP	1	SMAD4,KAT2A,CTNNBIP1,BHLHE41	red	VSMC_M1
GO:0017157	0.82	0.34	4	147	regulation of exocytosis	BP	1	STAM,RAB9A,IL13RA2,RAB12	red	VSMC_M1
GO:0045860	0.82	0.28	9	305	positive regulation of protein kinase activity	BP	1	EGR1,PIH1D1,FGF2,TAL1,PAK1,RPS3,AKAP13,PARP16,CALM2	red	VSMC_M1
GO:0051271	0.82	0.30	7	241	negative regulation of cellular component movement	BP	1	CSNK2B,CTNNA1,FGF2,CXCL12,SPRED1,TMEFF2,ARHGDIB	red	VSMC_M1
GO:0051216	0.82	0.34	4	154	cartilage development	BP	1	FGF2,KAT2A,RARA,MEF2D	red	VSMC_M1
GO:0045785	0.82	0.28	9	306	positive regulation of cell adhesion	BP	1	TRIOBP,MAP4K4,RPS3,CXCL12,EDIL3,RHOD,ZMIZ1,ITPKB,RARA	red	VSMC_M1
GO:0051668	0.82	0.25	17	537	localization within membrane	BP	1	REEP2,CRIPT,PARD3,EFR3B,PAK1,PDCD5,VTI1B,TIMM10,ARL3,ARFGEF2,EMC9,ARL4C,NDUFA13,VPS37C,RAB12,GOLPH3,RACK1	red	VSMC_M1
GO:0006914	0.82	0.26	14	450	autophagy	BP	1	EEF1A1,STAM,UVRAG,VTI1B,AMBRA1,NPRL2,WIPI1,VPS37C,RAB12,RAB39B,USP10,ATP6V1G1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0061919	0.82	0.26	14	450	process utilizing autophagic mechanism	BP	1	EEF1A1,STAM,UVRAG,VTI1B,AMBRA1,NPRL2,WIPI1,VPS37C,RAB12,RAB39B,USP10,ATP6V1G1,TOMM7,ATP5IF1	red	VSMC_M1
GO:0044419	0.82	0.23	32	948	biological process involved in interspecies interaction between organisms	BP	1	ARG1,DYNLT1,POLR3H,HMGA1,TAF11,ALAD,WDR35,PAK1,UVRAG,IL18BP,SP1,CXCL12,CEBPG,CTR9,CD58,CDC73,RAB9A,PPP1R11,AP1S1,IL1RAP,TRIM4,RARA,NR1D1,PRDX2,STXBP4,SPARC,CYP1A1,WFDC3,RNF125,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0072503	0.82	0.28	9	306	cellular divalent inorganic cation homeostasis	BP	1	SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,P2RX4,CALM2,FKBP1A	red	VSMC_M1
GO:0009165	0.82	0.30	6	198	nucleotide biosynthetic process	BP	1	NPR2,NAXD,ELOVL2,PARP16,SLC25A1,TMSB4X	red	VSMC_M1
GO:0031669	0.82	0.31	5	182	cellular response to nutrient levels	BP	1	KLF10,TNKS,NPRL2,WIPI1,ITFG2	red	VSMC_M1
GO:0007162	0.82	0.30	6	215	negative regulation of cell adhesion	BP	1	ARG1,MAP4K4,CXCL12,IL20RB,ARHGDIB,PRDX2	red	VSMC_M1
GO:0010629	0.82	0.23	25	766	negative regulation of gene expression	BP	1	ARG1,ZHX2,IL1RL1,MALSU1,WDR35,FGF2,RPS3,PCID2,IL20RB,SMYD5,PARP3,CUEDC2,TGIF1,PPP1R11,RBM4,EXOSC7,LSM4,RARA,DCP2,IL13RA2,ERRFI1,RACK1,TMSB4X,CPNE1,RNF125	red	VSMC_M1
GO:0001933	0.83	0.28	8	276	negative regulation of protein phosphorylation	BP	1	FGFR1OP,PARD3,SPRED1,PKIG,CDK5RAP3,CALM2,ERRFI1,RACK1	red	VSMC_M1
GO:1901293	0.83	0.29	6	199	nucleoside phosphate biosynthetic process	BP	1	NPR2,NAXD,ELOVL2,PARP16,SLC25A1,TMSB4X	red	VSMC_M1

GO:0007166	0.83	0.21	66	1935	cell surface receptor signaling pathway	BP	1	SMAD4,ARG1,DYRK2,CSNK2B,EGR1,CTNNA1,IL1RL1,SPIN1,NPR2,INVS,FGF2,TAL1,ADGRF3,IFT122,EIF2B4,PAK1,RPS3,CSNK1D,SOCS2,TNKS,CXCL12,TNFRSF19,CD8B,IL20RB,CTR9,P2RX4,SPRED1,GMDS,IFT57,ARL3,CDC73,CFAP410,WDR11,CABIN1,IL1RAP,NDUFA13,DYNC2H1,PELI2,ZMIZ1,ITPKB,CTDNEP1,EIF2B2,SPG21,PRDX2,FLRT2,STXBP4,RNF138,B9D1,IL13RA2,RFFL,ITGAE,ERRFI1,CTNNBIP1,RBM15,WWOX,FKBP1A,RACK1,NREP,TIMP3,TMSB4X,CPNE1,RITA1,IGHA2,PSENEN,LY96,FGF10	red	VSMC_M1
GO:0120039	0.83	0.25	15	517	plasma membrane bounded cell projection morphogenesis	BP	1	SMAD4,SGK1,DYNLT1,MAP4K4,PARD3,ARHGAP35,PAK1,SPAST,CXCL12,FBXW8,FBXO45,EGR2,MAP2,FLRT2,CPNE1	red	VSMC_M1
GO:0070372	0.83	0.29	6	211	regulation of ERK1 and ERK2 cascade	BP	1	SMAD4,FGF2,SPRED1,ERRFI1,TIMP3,FGF10	red	VSMC_M1
GO:2000147	0.83	0.25	14	455	positive regulation of cell motility	BP	1	FGFR1OP,MAP4K4,FGF2,PAK1,SP1,CXCL12,P2RX4,RRAS2,RHOD,PFN1,SPARC,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0140014	0.83	0.28	7	244	mitotic nuclear division	BP	1	MAD2L1BP,SPAST,PCID2,TNKS,KMT5A,BCCIP,XRCC3	red	VSMC_M1
GO:0099537	0.83	0.25	14	477	trans-synaptic signaling	BP	1	PCDH17,SLC12A6,P2RX4,KCNQ2,EGR2,IL1RAP,GJC1,KAT2A,ERC1,RARA,PRRT2,PMP22,TBC1D24,PTPRN2	red	VSMC_M1
GO:0048589	0.83	0.24	15	501	developmental growth	BP	1	SMAD4,FGF2,PAK1,SOCS2,CXCL12,CTR9,AKAP13,WDR11,MAP2,ZMIZ1,KAT2A,RARA,GNAS,CPNE1,FGF10	red	VSMC_M1
GO:0043065	0.83	0.25	13	410	positive regulation of apoptotic process	BP	1	CTNNA1,UBE2M,UTP11,RPS7,WDR35,RPS3,PDCD5,RPS6,OMA1,PTPA,WWOX,RACK1,TIMP3	red	VSMC_M1
GO:0007186	0.83	0.25	14	458	G protein-coupled receptor signaling pathway	BP	1	RGS17,DYNLT1,GNG5,PARD3,ADGRF3,KCTD16,CXCL12,EDNRA,CACNA1D,SORCS1,AKAP13,CALM2,GNAS,PROKR2	red	VSMC_M1
GO:0060070	0.83	0.28	7	250	canonical Wnt signaling pathway	BP	1	EGR1,INVS,FGF2,CSNK1D,TNKS,CTDNEP1,FGF10	red	VSMC_M1
GO:0002573	0.83	0.31	4	154	myeloid leukocyte differentiation	BP	1	KLF10,TAL1,RARA,CTNNBIP1	red	VSMC_M1
GO:0048858	0.83	0.24	15	520	cell projection morphogenesis	BP	1	SMAD4,SGK1,DYNLT1,MAP4K4,PARD3,ARHGAP35,PAK1,SPAST,CXCL12,FBXW8,FBXO45,EGR2,MAP2,FLRT2,CPNE1	red	VSMC_M1
GO:0006814	0.83	0.31	4	161	sodium ion transport	BP	1	SGK1,P2RX4,SCN3A,SCNN1A	red	VSMC_M1
GO:0007283	0.83	0.25	11	357	spermatogenesis	BP	1	SMAD4,TCP11,MEI4,PGM3,INPP5B,NR2C2,C11orf74,CCNI,ETV5,HSPA2,FAM9B	red	VSMC_M1
GO:0044089	0.83	0.24	13	441	positive regulation of cellular component biogenesis	BP	1	MAP4K4,PIH1D1,TAL1,ARHGAP35,STAM,PAK1,RPS3,ARFIP1,ARL3,IL1RAP,PFN1,FLRT2,RACK1	red	VSMC_M1
GO:0031348	0.83	0.31	4	149	negative regulation of defense response	BP	1	ARG1,IL20RB,NR1D1,RNF125	red	VSMC_M1
GO:0050778	0.84	0.26	9	306	positive regulation of immune response	BP	1	ARG1,KMT5C,EIF2B4,PAK1,RPS3,RARA,EIF2B2,SPG21,IGHA2	red	VSMC_M1
GO:0042326	0.84	0.25	9	311	negative regulation of phosphorylation	BP	1	FGFR1OP,PARD3,SPRED1,PKIG,NPRL2,CDK5RAP3,CALM2,ERRFI1,RACK1	red	VSMC_M1
GO:0031331	0.84	0.24	11	366	positive regulation of cellular catabolic process	BP	1	UVRAG,CSNK1D,FBXW8,NPRL2,EXOSC7,USP5,DCP2,RNF40,RACK1,ATP5IF1,RCHY1	red	VSMC_M1
GO:0032879	0.84	0.19	71	2074	regulation of localization	BP	1	SMAD4,SGK1,ARG1,CSNK2B,HSPA1L,FGFR1OP,REEP2,CTNNA1,SRI,MAP4K4,CRIPT,KCNF1,PARD3,FKBP1B,FGF2,STAM,PCDH17,PAK1,HDAC3,CACNA2D1,SP1,CXCL12,PDCD5,VTI1B,EDNRA,TMSB10,ARFIP1,P2RX4,RRAS2,CACNA1D,SPRED1,STIMATE,PKIG,TMEFF2,SCN3A,RAB9A,RHOD,ENSA,FAM45A,RBM4,ARHGDIB,KCNQ2,KDM1A,MAP2,PFN1,HSPA2,NR1D1,DCP2,CDK5RAP3,PRRT2,FLRT2,STXBP4,CALM2,SPARC,B9D1,IL13RA2,RFFL,FBXO4,RAB12,MYO18A,GOLPH3,GOSR1,KCNAB2,FKBP1A,RACK1,TMSB4X,NOP10,TOMM7,ATP5IF1,AHNAK,FGF10	red	VSMC_M1
GO:0000165	0.84	0.22	18	579	MAPK cascade	BP	1	SMAD4,MAP4K4,FGF2,PAK1,RPS3,HDAC3,TNFRSF19,COPS5,SPRED1,AKAP13,MECOM,PELI2,ITPKB,CDK5RAP3,PRDX2,ERRFI1,TIMP3,FGF10	red	VSMC_M1
GO:0050807	0.84	0.30	4	165	regulation of synapse organization	BP	1	CRIPT,IL1RAP,FLRT2,SPARC	red	VSMC_M1
GO:0060560	0.84	0.28	5	200	developmental growth involved in morphogenesis	BP	1	PAK1,CXCL12,MAP2,CPNE1,FGF10	red	VSMC_M1
GO:0048588	0.84	0.28	5	195	developmental cell growth	BP	1	PAK1,CXCL12,AKAP13,MAP2,CPNE1	red	VSMC_M1
GO:0040017	0.84	0.23	14	462	positive regulation of locomotion	BP	1	FGFR1OP,MAP4K4,FGF2,PAK1,SP1,CXCL12,P2RX4,RRAS2,RHOD,PFN1,SPARC,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0043161	0.84	0.24	11	368	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	RNF121,CSNK1D,ERLIN2,FBXW8,FBXO45,USP5,RFFL,FBXO4,UBE4B,RACK1,RCHY1	red	VSMC_M1
GO:0065008	0.84	0.19	96	2770	regulation of biological quality	BP	1	SMAD4,SGK1,DYNLT1,EGR1,TRIOBP,SRI,MAP4K4,NPR2,RPS5,CRIPT,RPS7,PIH1D1,WDR35,FKBP1B,FGF2,TAL1,ARHGAP35,FAM171A1,PAK1,DGAT2,NEB,HDAC3,SOCS2,PCID2,CACNA2D1,CXCL12,CEBPG,IL20RB,EDNRA,TMSB10,SLC12A6,ARFIP1,RHOF,GOT2,P2RX4,C15orf41,CACNA1D,RPS6,HPSE,CNNM1,CDC73,CYB561D2,SCN3A,CFAP410,COX19,RHOD,ENSA,CRTC3,IFT46,EGR2,KDM1A,USP28,MYL4,MAP2,IL1RAP,EXOSC7,GJC1,PRDX6,SCNN1A,PROM1,RPS24,KAT2A,PFN1,ERC1,ITPKB,RARA,NR1D1,DCP2,CDK5RAP3,PRRT2,PRDX2,FLRT2,STXBP4,CALM2,SPARC,CYP1A1,CHST9,FBXO4,KANK4,OMA1,HMOX2,KCNAB2,DNLZ,CTNNBIP1,E2F4,FKBP1A,GNAS,RACK1,SLC25A28,ATP6V1G1,TMSB4X,TOMM7,IGHA2,ATP5IF1,PTPRN2,FGF10	red	VSMC_M1
GO:0042981	0.84	0.20	37	1092	regulation of apoptotic process	BP	1	SGK1,EGR1,CTNNA1,NAA35,MAP4K4,UBE2M,UTP11,RPS7,PIH1D1,WDR35,RPS3,HDAC3,SOCS2,PCID2,CXCL12,COPS5,PDCD5,RPS3A,RPS6,IFT57,CDC73,KDM1A,NDUFA13,ERC1,ITPKB,RARA,PRDX2,RFFL,MYO18A,OMA1,GOLPH3,PTPA,WWOX,RACK1,TIMP3,NAA38,FGF10	red	VSMC_M1
GO:0080134	0.84	0.20	32	970	regulation of response to stress	BP	1	ARG1,HMGA1,IL1RL1,MAP4K4,KMT5C,FKBP1B,FGF2,RECQL5,PAK1,RPS3,HDAC3,CXCL12,TNFRSF19,COPS5,CEBPG,IL20RB,KMT5A,SPRED1,HPSE,PARP3,SMYD2,KDM1A,MECOM,NR1D1,PRDX2,FBXO4,YJU2,ERRFI1,RACK1,TMSB4X,RNF125,FGF10	red	VSMC_M1
GO:0051403	0.85	0.28	5	190	stress-activated MAPK cascade	BP	1	MAP4K4,HDAC3,TNFRSF19,COPS5,MECOM	red	VSMC_M1
GO:0090287	0.85	0.27	6	230	regulation of cellular response to growth factor stimulus	BP	1	SMAD4,FGF2,SPRED1,FKBP1A,NREP,FGF10	red	VSMC_M1

GO:0043207	0.85	0.21	27	820	response to external biotic stimulus	BP	1	ARG1,POLR3H,HMGA1,ALAD,WDR35,PAK1,IL18BP,CXCL12,CEBPG,CTR9,CD58,CDC73,PPP1R11,AP1S1,IL1RAP,TRIM4,RARA,NR1D1,PRDX2,STXBP4,SPARC,CYP1A1,WFDC3,RNF125,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0051707	0.85	0.21	27	820	response to other organism	BP	1	ARG1,POLR3H,HMGA1,ALAD,WDR35,PAK1,IL18BP,CXCL12,CEBPG,CTR9,CD58,CDC73,PPP1R11,AP1S1,IL1RAP,TRIM4,RARA,NR1D1,PRDX2,STXBP4,SPARC,CYP1A1,WFDC3,RNF125,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0001649	0.85	0.27	5	190	osteoblast differentiation	BP	1	FGF2,RRAS2,MEF2D,CTNNBIP1,WWOX	red	VSMC_M1
GO:0048514	0.85	0.21	15	508	blood vessel morphogenesis	BP	1	FGF2,TAL1,UBP1,SP1,EDNRA,SLC12A6,SPRED1,HPSE,MYO18B,GJC1,ZMIZ1,SPARC,RBM15,ATP5IF1,FGF10	red	VSMC_M1
GO:0008202	0.85	0.25	6	217	steroid metabolic process	BP	1	EGR1,DGAT2,ERLIN2,ACOT8,NR1D1,CYP1A1	red	VSMC_M1
GO:1903046	0.86	0.28	4	153	meiotic cell cycle process	BP	1	MEI1,MEI4,HSPA2,HUS1	red	VSMC_M1
GO:0030336	0.86	0.25	6	223	negative regulation of cell migration	BP	1	CSNK2B,FGF2,CXCL12,SPRED1,TMEFF2,ARHGDIB	red	VSMC_M1
GO:0009607	0.86	0.19	28	856	response to biotic stimulus	BP	1	ARG1,POLR3H,HMGA1,AHR,ALAD,WDR35,PAK1,IL18BP,CXCL12,CEBPG,CTR9,CD58,CDC73,PPP1R11,AP1S1,IL1RAP,TRIM4,RARA,NR1D1,PRDX2,STXBP4,SPARC,CYP1A1,WFDC3,RNF125,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0051179	0.86	0.17	164	4586	localization	BP	1	SMAD4,SGK1,ARG1,CSNK2B,HSPA1L,DYNLT1,FGFR1OP,POLDIP3,REEP2,CTNNA1,TST,SRI,UBAP1,MAP4K4,ICK,CLTA,COX5B,SLC25A51,XPA,INVS,CRIPT,INPP5B,OSCP1,KCNF1,PIH1D1,PARD3,WDR35,FKBP1B,FGF2,EFR3B,PMPCB,ARHGAP35,STAM,IFT122,PCDH17,WBP2,NRBP1,PAK1,UVRAG,DGAT2,VDAC3,SPAST,COX7B,CSNK1D,HDAC3,SOCS2,PCID2,CACNA2D1,TNKS,SP1,RAB28,CXCL12,COPS5,PDCD5,VTI1B,EDNRA,TIMM10,TMSB10,SLC12A6,ARFIP1,RHOF,GOT2,P2RX4,RRAS2,PLRG1,CACNA1D,SPRED1,STIMATE,TFG,CNNM1,PKIG,IFT57,PARP3,TMEFF2,ARL3,UNC119B,CYB561D2,SORCS1,GRAMD1C,SCN3A,WIPI1,ARFGEF2,AKAP13,RAB9A,RHOD,EMC9,ARL4C,RAE1,ENSA,FAM45A,WDR11,RBM4,IFT46,ARHGDIB,KCNQ2,MAP4,FBXO45,CEP19,EGR2,KDM1A,MAP2,AP1S1,GJC1,NDUFA13,ARL4D,RP2,DYNC2H1,SCNN1A,SCG3,ZMIZ1,MYO5C,KAT2A,PFN1,ERC1,CLCN5,HSPA2,RARA,CTDNEP1,CECR2,NR1D1,DCP2,VPS37C,CDK5RAP3,COPZ2,TRAPPC1,PRRT2,FLRT2,STXBP4,CALM2,SPARC,SNUPN,B9D1,IL13RA2,RFFL,FBXO4,CACHD1,RAB12,MYO18A,GOLPH3,GOSR1,KCNAB2,RAB39B,DNLZ,COX4I1,CIZ1,EVI5,ELMO3,IER2,FKBP1A,SLC25A1,RACK1,SLC25A28,ATP6V1G1,TMSB4X,CNIH1,NOP10,CPNE1,TOMM7,RITA1,IGHA2,ATP5IF1,PTPRN2,AHNAK,FGF10	red	VSMC_M1
GO:0032870	0.86	0.21	13	450	cellular response to hormone stimulus	BP	1	ARG1,CSNK2B,WBP2,PAK1,SOCS2,SP1,KDM1A,ZMIZ1,RARA,NR1D1,STXBP4,RAB12,ERRFI1	red	VSMC_M1
GO:0050803	0.86	0.28	4	170	regulation of synapse structure or activity	BP	1	CRIPT,IL1RAP,FLRT2,SPARC	red	VSMC_M1
GO:0048762	0.86	0.26	5	198	mesenchymal cell differentiation	BP	1	SMAD4,MCRIP1,EDNRA,SPRED1,FGF10	red	VSMC_M1
GO:0009260	0.86	0.27	4	149	ribonucleotide biosynthetic process	BP	1	NPR2,ELOVL2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0051130	0.86	0.19	27	870	positive regulation of cellular component organization	BP	1	DYNLT1,MAD2L1BP,MAP4K4,PIH1D1,WDR35,FKBP1B,TAL1,ARHGAP35,PAK1,UVRAG,RPS3,SPAST,TNKS,CXCL12,PDCD5,ARFIP1,FBXW8,ARL3,KDM1A,IL1RAP,KAT2A,PFN1,PRRT2,FLRT2,FBXO4,RACK1,ATP5IF1	red	VSMC_M1
GO:0006164	0.86	0.27	4	149	purine nucleotide biosynthetic process	BP	1	NPR2,ELOVL2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0071695	0.86	0.27	4	163	anatomical structure maturation	BP	1	TCP11,NPR2,TAL1,KDM1A	red	VSMC_M1
GO:0051051	0.86	0.22	9	314	negative regulation of transport	BP	1	SRI,MAP4K4,FKBP1B,ARFIP1,PKIG,PRRT2,CALM2,IL13RA2,RACK1	red	VSMC_M1
GO:0002831	0.86	0.24	6	224	regulation of response to biotic stimulus	BP	1	ARG1,AHR,PAK1,PRDX2,RNF125,LY96	red	VSMC_M1
GO:0048232	0.87	0.21	11	371	male gamete generation	BP	1	SMAD4,TCP11,MEI4,PGM3,INPP5B,NR2C2,C11orf74,CCNI,ETV5,HSPA2,FAM9B	red	VSMC_M1
GO:0008654	0.87	0.24	6	222	phospholipid biosynthetic process	BP	1	FGF2,EFR3B,SOCS2,GPAT3,ITPKB,HDHD5	red	VSMC_M1
GO:0031098	0.87	0.25	5	197	stress-activated protein kinase signaling cascade	BP	1	MAP4K4,HDAC3,TNFRSF19,COPS5,MECOM	red	VSMC_M1
GO:0099536	0.87	0.20	14	494	synaptic signaling	BP	1	PCDH17,SLC12A6,P2RX4,KCNQ2,EGR2,IL1RAP,GJC1,KAT2A,ERC1,RARA,PRRT2,PMP22,TBC1D24,PTPRN2	red	VSMC_M1
GO:0040013	0.87	0.23	7	261	negative regulation of locomotion	BP	1	CSNK2B,CTNNA1,FGF2,CXCL12,SPRED1,TMEFF2,ARHGDIB	red	VSMC_M1
GO:0032990	0.87	0.19	15	536	cell part morphogenesis	BP	1	SMAD4,SGK1,DYNLT1,MAP4K4,PARD3,ARHGAP35,PAK1,SPAST,CXCL12,FBXW8,FBXO45,EGR2,MAP2,FLRT2,CPNE1	red	VSMC_M1
GO:1901615	0.87	0.20	11	382	organic hydroxy compound metabolic process	BP	1	ALDH1B1,INPP5B,COQ3,FGF2,DGAT2,ERLIN2,ACOT8,PTS,ITPKB,NR1D1,CYP1A1	red	VSMC_M1
GO:0022407	0.87	0.22	8	293	regulation of cell-cell adhesion	BP	1	ARG1,RPS3,CXCL12,IL20RB,ZMIZ1,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0007389	0.87	0.21	9	329	pattern specification process	BP	1	SMAD4,FGF2,IFT57,EGR2,DYNC2H1,KAT2A,CTNNBIP1,BHLHE41,FGF10	red	VSMC_M1
GO:0006955	0.87	0.17	33	1012	immune response	BP	1	ARG1,POLR3H,IL1RL1,AHR,KMT5C,EIF2B4,PAK1,RPS3,IL18BP,CXCL12,CEBPG,CD8B,IL20RB,RPS6,CD58,PARP3,CUEDC2,PPP1R11,IL1RAP,TRIM4,ITFG2,RARA,NR1D1,EIF2B2,SPG21,STXBP4,IL13RA2,FKBP1A,CNIH1,WFDC3,RNF125,IGHA2,LY96	red	VSMC_M1
GO:0042060	0.87	0.21	9	329	wound healing	BP	1	FGF2,ARHGAP35,PAK1,HPSE,TMEFF2,PRDX2,SPARC,GNAS,FGF10	red	VSMC_M1
GO:0071103	0.87	0.24	5	200	DNA conformation change	BP	1	HMGA1,RECQL5,KMT5A,CABIN1,TOP3B	red	VSMC_M1
GO:0070371	0.87	0.23	6	227	ERK1 and ERK2 cascade	BP	1	SMAD4,FGF2,SPRED1,ERRFI1,TIMP3,FGF10	red	VSMC_M1
GO:0007417	0.87	0.17	24	795	central nervous system development	BP	1	FGF2,TAL1,ARHGAP35,EIF2B4,PAK1,COX7B,CSNK1D,CXCL12,C21orf91,ACTL6A,FBXO45,EGR2,KDM1A,MAP2,PTS,DYNC2H1,ZMIZ1,KAT2A,RARA,NR1D1,CDK5RAP3,EIF2B2,CALM2,FGF10	red	VSMC_M1
GO:0006402	0.88	0.23	5	201	mRNA catabolic process	BP	1	ZHX2,PCID2,EXOSC7,LSM4,DCP2	red	VSMC_M1
GO:0006811	0.88	0.17	33	1026	ion transport	BP	1	SGK1,ARG1,SRI,COX5B,KCNF1,FKBP1B,FGF2,PMPCB,VDAC3,COX7B,CACNA2D1,CXCL12,SLC12A6,P2RX4,CACNA1D,STIMATE,CNNM1,SCN3A,KCNQ2,GJC1,SCNN1A,CLCN5,HSPA2,CALM2,CACHD1,KCNAB2,COX4I1,FKBP1A,SLC25A1,SLC25A28,ATP6V1G1,TMSB4X,AHNAK	red	VSMC_M1
GO:0098813	0.88	0.22	6	230	nuclear chromosome segregation	BP	1	MAD2L1BP,MEI4,PCID2,TNKS,KMT5A,XRCC3	red	VSMC_M1

GO:0007268	0.88	0.19	13	471	chemical synaptic transmission	BP	1	PCDH17,SLC12A6,P2RX4,KCNQ2,EGR2,GJC1,KAT2A,ERC1,RARA,PRRT2,PMP22,TBC1D24,PTPRN2	red	VSMC_M1
GO:0098916	0.88	0.19	13	471	anterograde trans-synaptic signaling	BP	1	PCDH17,SLC12A6,P2RX4,KCNQ2,EGR2,GJC1,KAT2A,ERC1,RARA,PRRT2,PMP22,TBC1D24,PTPRN2	red	VSMC_M1
GO:0048608	0.88	0.20	9	330	reproductive structure development	BP	1	SMAD4,CTNNA1,EIF2B4,RPS6,FBXW8,RARA,EIF2B2,RBM15,FGF10	red	VSMC_M1
GO:0016054	0.88	0.23	5	186	organic acid catabolic process	BP	1	ARG1,TST,GPT2,GOT2,ACOT8	red	VSMC_M1
GO:0021700	0.88	0.22	5	204	developmental maturation	BP	1	TCP11,NPR2,TAL1,KDM1A,PFN1	red	VSMC_M1
GO:0001525	0.88	0.18	12	428	angiogenesis	BP	1	FGF2,TAL1,UBP1,SP1,EDNRA,SLC12A6,SPRED1,HPSE,SPARC,RBM15,ATP5IF1,FGF10	red	VSMC_M1
GO:0010975	0.88	0.19	10	376	regulation of neuron projection development	BP	1	DYNLT1,MAP4K4,FKBP1B,ARHGAP35,PAK1,CXCL12,FBXW8,KDM1A,MAP2,PMP22	red	VSMC_M1
GO:0050877	0.88	0.17	20	678	nervous system process	BP	1	SGK1,REEP2,TRIOBP,FAM161A,PARD3,FKBP1B,CXCL12,TIMM10,P2RX4,CACNA1D,SCN3A,EGR2,GJC1,RP2,SCNN1A,KAT2A,PRRT2,TPRN,GNAS,TIMP3	red	VSMC_M1
GO:0046390	0.88	0.23	4	156	ribose phosphate biosynthetic process	BP	1	NPR2,ELOVL2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0061458	0.88	0.19	9	333	reproductive system development	BP	1	SMAD4,CTNNA1,EIF2B4,RPS6,FBXW8,RARA,EIF2B2,RBM15,FGF10	red	VSMC_M1
GO:0000280	0.88	0.19	10	355	nuclear division	BP	1	MEI1,MAD2L1BP,MEI4,SPAST,PCID2,TNKS,KMT5A,BCCIP,HSPA2,XRCC3	red	VSMC_M1
GO:0019752	0.89	0.16	21	659	carboxylic acid metabolic process	BP	1	CS,ARG1,TST,MUT,GPT2,DGAT2,ERLIN2,LTA4H,GOT2,FARS2,HLCS,ELOVL2,ACOT8,PSPH,YARS,UROS,PTS,NR1D1,CYP1A1,TMEM189,ADI1	red	VSMC_M1
GO:0009628	0.89	0.16	28	891	response to abiotic stimulus	BP	1	SMAD4,NDRG1,EGR1,XPA,COPS9,ALAD,EIF2B4,PAK1,CXCL12,EDNRA,SLC12A6,PSPH,RBM4,KDM1A,USP28,UVSSA,ELK1,HSPA2,EIF2B2,INTS3,SPARC,CYP1A1,FBXO4,HMOX2,ERRFI1,UBE4B,HUS1,ATP6V1G1	red	VSMC_M1
GO:0003008	0.89	0.15	39	1240	system process	BP	1	SMAD4,SGK1,REEP2,TRIOBP,SRI,NPR2,FAM161A,PARD3,WDR35,FKBP1B,ARHGAP35,PAK1,CACNA2D1,CXCL12,EDNRA,TIMM10,P2RX4,CACNA1D,SCN3A,AKAP13,SSPN,KLHL41,EGR2,MYL4,GJC1,RP2,SCNN1A,KAT2A,CLCN5,PRRT2,CALM2,TPRN,ERRFI1,CTNNBIP1,E2F4,GNAS,TIMP3,IGHA2,FGF10	red	VSMC_M1
GO:0060322	0.89	0.17	18	624	head development	BP	1	FGF2,ARHGAP35,PAK1,CSNK1D,CXCL12,EDNRA,C21orf91,WDR11,FBXO45,EGR2,KDM1A,DYNC2H1,ZMIZ1,KAT2A,RARA,CDK5RAP3,CALM2,FGF10	red	VSMC_M1
GO:0006401	0.89	0.21	6	237	RNA catabolic process	BP	1	ZHX2,PCID2,PPP1R8,EXOSC7,LSM4,DCP2	red	VSMC_M1
GO:0022414	0.89	0.15	33	1029	reproductive process	BP	1	SMAD4,ARG1,ACR,HSPA1L,MEI1,EGR1,TCP11,CTNNA1,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,EIF2B4,C11orf74,GOT2,CCNI,RPS6,FBXW8,ARHGDIB,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,CECR2,EIF2B2,CYP1A1,RBM15,FAM9B,HUS1,FGF10	red	VSMC_M1
GO:0033674	0.89	0.18	10	373	positive regulation of kinase activity	BP	1	EGR1,PIH1D1,FGF2,TAL1,PAK1,RPS3,AMBRA1,AKAP13,PARP16,CALM2	red	VSMC_M1
GO:0009896	0.89	0.18	12	420	positive regulation of catabolic process	BP	1	UVRAG,CSNK1D,FBXW8,NPRL2,EXOSC7,NDUFA13,USP5,DCP2,RNF40,RACK1,ATP5IF1,RCHY1	red	VSMC_M1
GO:0048568	0.89	0.19	9	341	embryonic organ development	BP	1	TRIOBP,TAL1,IFT122,MMP16,FBXW8,IFT57,RARA,TPRN,FGF10	red	VSMC_M1
GO:0072522	0.89	0.23	4	157	purine-containing compound biosynthetic process	BP	1	NPR2,ELOVL2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0030334	0.89	0.16	22	735	regulation of cell migration	BP	1	SGK1,CSNK2B,FGFR1OP,MAP4K4,FGF2,PAK1,SP1,CXCL12,TMSB10,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,PFN1,FLRT2,SPARC,RFFL,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0000003	0.89	0.15	33	1031	reproduction	BP	1	SMAD4,ARG1,ACR,HSPA1L,MEI1,EGR1,TCP11,CTNNA1,SPIN1,NPR2,MEI4,PGM3,INPP5B,NR2C2,EIF2B4,C11orf74,GOT2,CCNI,RPS6,FBXW8,ARHGDIB,ETV5,ZMIZ1,HSPA2,RARA,CTDNEP1,CECR2,EIF2B2,CYP1A1,RBM15,FAM9B,HUS1,FGF10	red	VSMC_M1
GO:0016310	0.89	0.14	46	1440	phosphorylation	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,FGFR1OP,EGR1,KCTD20,MAP4K4,NPR2,ICK,EEF1A1,PIH1D1,PARD3,ADCK2,FGF2,TAL1,PAK1,UVRAG,RPS3,CSNK1D,HDAC3,SOCS2,CDK17,TNKS,EIF2A,SPRED1,CCNI,AMBRA1,PKIG,NPRL2,AKAP13,BCCIP,PELI2,ERC1,HSPA2,ITPKB,RARA,CDK5RAP3,PARP16,CALM2,MOB3A,ERRFI1,RACK1,HUS1,PPP1R14A,FGF10	red	VSMC_M1
GO:0031344	0.89	0.16	15	538	regulation of cell projection organization	BP	1	DYNLT1,MAP4K4,FKBP1B,ARHGAP35,PAK1,VDAC3,CXCL12,FBXW8,TBC1D7,MAP4,KDM1A,MAP2,KAT2A,PFN1,PMP22	red	VSMC_M1
GO:0044282	0.89	0.18	8	284	small molecule catabolic process	BP	1	ARG1,TST,ALDH1B1,INPP5B,GPT2,GOT2,ACOT8,CYP1A1	red	VSMC_M1
GO:0030003	0.90	0.16	12	434	cellular cation homeostasis	BP	1	SMAD4,SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,P2RX4,COX19,CALM2,FKBP1A,ATP6V1G1	red	VSMC_M1
GO:0051270	0.90	0.14	25	830	regulation of cellular component movement	BP	1	SGK1,CSNK2B,FGFR1OP,CTNNA1,SRI,MAP4K4,FGF2,PAK1,SP1,CXCL12,TMSB10,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,MAP2,PFN1,FLRT2,SPARC,RFFL,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0044403	0.90	0.20	5	206	biological process involved in symbiotic interaction	BP	1	ARG1,DYNLT1,TAF11,UVRAG,SP1	red	VSMC_M1
GO:0040007	0.90	0.14	22	742	growth	BP	1	SMAD4,SGK1,FGFR1OP,FGF2,PAK1,SOCS2,CXCL12,CTR9,CDC73,ACTL6A,AKAP13,WDR11,MAP2,NDUFA13,ZMIZ1,KAT2A,RARA,GNAS,RACK1,KAZALD1,CPNE1,FGF10	red	VSMC_M1
GO:0018105	0.90	0.19	6	249	peptidyl-serine phosphorylation	BP	1	SGK1,DYRK2,PAK1,CSNK1D,TNKS,RACK1	red	VSMC_M1
GO:2000145	0.90	0.14	23	772	regulation of cell motility	BP	1	SGK1,CSNK2B,FGFR1OP,CTNNA1,MAP4K4,FGF2,PAK1,SP1,CXCL12,TMSB10,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,PFN1,FLRT2,SPARC,RFFL,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0044281	0.90	0.13	44	1301	small molecule metabolic process	BP	1	CS,ARG1,DYRK2,EGR1,TST,MUT,NPR2,ALDH1B1,PGM3,INPP5B,COQ3,GPT2,FGF2,DGAT2,NAXD,ERLIN2,LTA4H,GOT2,GMDS,FARS2,HLCS,ELOVL2,ACOT8,PSPH,VKORC1L1,YARS,GMPR2,UROS,KDM1A,REXO2,PTS,KAT2A,ITPKB,NR1D1,PARP16,CYP1A1,COQ7,OMA1,WDR5,SLC25A1,COQ10A,TMSB4X,TMEM189,ADI1	red	VSMC_M1

GO:0009056	0.90	0.12	68	2000	catabolic process	BP	1	ARG1,ACR,ZHX2,TST,UBAP1,ALDH1B1,EEF1A1,INPP5B,ALAD,RPS7,PSMB2,GPT2,FGF2,STAM,UVRAG,RNF121,CSNK1D,ERLIN2,PCID2,LTA4H,VTI1B,ELOC,GOT2,MMP16,HPSE,AMBRA1,FBXW8,ACOT8,NPRL2,WIPI1,PPP1R8,PPP1R11,CRTC3,PSMA7,FBXO45,USP28,EXOSC7,NDUFA13,PRDX6,USP5,LSM4,UBA1,PSMB6,CECR2,NR1D1,DCP2,VPS37C,RNF40,CDK5RAP3,PRDX2,CYP1A1,RFFL,USP22,FBXO4,RAB12,OMA1,HMOX2,RAB39B,UBE4B,GSTM3,USP10,RACK1,ATP6V1G1,TIMP3,TOMM7,RNF125,ATP5IF1,RCHY1	red	VSMC_M1
GO:0050878	0.90	0.17	7	273	regulation of body fluid levels	BP	1	SOCS2,GOT2,HPSE,SCNN1A,PRDX2,GNAS,FGF10	red	VSMC_M1
GO:0071702	0.90	0.12	63	1891	organic substance transport	BP	1	ARG1,HSPA1L,DYNLT1,POLDIP3,REEP2,TST,SRI,UBAP1,MAP4K4,CLTA,SLC25A51,PARD3,FKBP1B,PMPCB,STAM,PAK1,VDAC3,HDAC3,PCID2,TNKS,RAB28,CXCL12,PDCD5,VTI1B,EDNRA,TIMM10,ARFIP1,GOT2,P2RX4,PKIG,ARL3,UNC119B,GRAMD1C,ARFGEF2,RAB9A,ARL4C,RAE1,ENSA,FAM45A,WDR11,EGR2,AP1S1,NDUFA13,ARL4D,RP2,ERC1,NR1D1,VPS37C,COPZ2,STXBP4,SNUPN,RAB12,MYO18A,GOLPH3,GOSR1,RAB39B,DNLZ,EVI5,SLC25A1,RACK1,TOMM7,ATP5IF1,PTPRN2	red	VSMC_M1
GO:0000904	0.90	0.15	15	562	cell morphogenesis involved in differentiation	BP	1	SMAD4,TRIOBP,PARD3,TAL1,ARHGAP35,PAK1,SPAST,CXCL12,FBXW8,TMEFF2,FBXO45,EGR2,MAP2,FLRT2,TPRN	red	VSMC_M1
GO:0030258	0.91	0.20	4	171	lipid modification	BP	1	INPP5B,DGAT2,ACOT8,CYP1A1	red	VSMC_M1
GO:0022409	0.91	0.20	4	176	positive regulation of cell-cell adhesion	BP	1	RPS3,ZMIZ1,ITPKB,RARA	red	VSMC_M1
GO:0055086	0.91	0.14	13	439	nucleobase-containing small molecule metabolic process	BP	1	NPR2,PGM3,DGAT2,NAXD,GMDS,ELOVL2,ACOT8,GMPR2,KDM1A,REXO2,PARP16,SLC25A1,TMSB4X	red	VSMC_M1
GO:0005975	0.91	0.14	13	458	carbohydrate metabolic process	BP	1	CS,DYRK2,ALDH1B1,PGM3,INPP5B,COQ3,DGAT2,KAT2A,NR1D1,CHST9,OMA1,WDR5,SLC25A1	red	VSMC_M1
GO:0006873	0.91	0.14	12	444	cellular ion homeostasis	BP	1	SMAD4,SRI,FKBP1B,FGF2,CACNA2D1,CXCL12,EDNRA,P2RX4,COX19,CALM2,FKBP1A,ATP6V1G1	red	VSMC_M1
GO:0043436	0.91	0.13	21	677	oxoacid metabolic process	BP	1	CS,ARG1,TST,MUT,GPT2,DGAT2,ERLIN2,LTA4H,GOT2,FARS2,HLCS,ELOVL2,ACOT8,PSPH,YARS,UROS,PTS,NR1D1,CYP1A1,TMEM189,ADI1	red	VSMC_M1
GO:0048705	0.92	0.18	4	186	skeletal system morphogenesis	BP	1	MMP16,RARA,MEF2D,WWOX	red	VSMC_M1
GO:0120035	0.92	0.13	14	524	regulation of plasma membrane bounded cell projection organization	BP	1	DYNLT1,MAP4K4,FKBP1B,ARHGAP35,PAK1,VDAC3,CXCL12,FBXW8,TBC1D7,MAP4,KDM1A,MAP2,PFN1,PMP22	red	VSMC_M1
GO:0048562	0.92	0.16	5	225	embryonic organ morphogenesis	BP	1	TRIOBP,MMP16,IFT57,TPRN,FGF10	red	VSMC_M1
GO:0006793	0.92	0.10	72	2169	phosphorus metabolic process	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,FGFR1OP,EGR1,KCTD20,MAP4K4,NPR2,ICK,EEF1A1,PGM3,INPP5B,PIH1D1,PARD3,ADCK2,FKBP1B,FGF2,TAL1,EFR3B,PAK1,UVRAG,DGAT2,RPS3,CSNK1D,NAXD,HDAC3,SOCS2,CDK17,TNKS,EIF2A,SPRED1,CCNI,GPAT3,AMBRA1,GMDS,PKIG,ELOVL2,ACOT8,PSPH,NPRL2,PTP4A2,AKAP13,PPP1R8,ENSA,GMPR2,PPP1R11,BCCIP,REXO2,PRDX6,PELI2,ERC1,HSPA2,ITPKB,RARA,HDHD5,CTDNEP1,CDK5RAP3,PARP16,CALM2,MOB3A,ERRFI1,PTPA,FKBP1A,SLC25A1,RACK1,HUS1,PPP1R14A,ACP1,TMSB4X,PTPRN2,FGF10	red	VSMC_M1
GO:0010628	0.92	0.11	24	803	positive regulation of gene expression	BP	1	POLDIP3,EGR1,EIF3D,IL1RL1,KMT5C,RPS7,FGF2,WBP2,RPS3,SP1,CEBPG,IL20RB,PDCD5,HPSE,CD58,ARFGEF2,IL1RAP,PRDX6,ZMIZ1,KAT2A,RARA,ELOF1,LY96,FGF10	red	VSMC_M1
GO:0007420	0.92	0.12	16	587	brain development	BP	1	FGF2,ARHGAP35,PAK1,CSNK1D,CXCL12,C21orf91,FBXO45,EGR2,KDM1A,DYNC2H1,ZMIZ1,KAT2A,RARA,CDK5RAP3,CALM2,FGF10	red	VSMC_M1
GO:0098609	0.92	0.12	16	592	cell-cell adhesion	BP	1	ARG1,CTNNA1,SDK2,PCDH17,RPS3,CXCL12,IL20RB,CD58,LPP,IL1RAP,ZMIZ1,ITPKB,RARA,PRDX2,GOLPH3,GNAS	red	VSMC_M1
GO:0003006	0.92	0.12	20	685	developmental process involved in reproduction	BP	1	SMAD4,TCP11,CTNNA1,NPR2,MEI4,PGM3,INPP5B,NR2C2,EIF2B4,C11orf74,CCNI,RPS6,FBXW8,ETV5,HSPA2,RARA,EIF2B2,RBM15,FAM9B,FGF10	red	VSMC_M1
GO:0006082	0.92	0.11	21	689	organic acid metabolic process	BP	1	CS,ARG1,TST,MUT,GPT2,DGAT2,ERLIN2,LTA4H,GOT2,FARS2,HLCS,ELOVL2,ACOT8,PSPH,YARS,UROS,PTS,NR1D1,CYP1A1,TMEM189,ADI1	red	VSMC_M1
GO:0006644	0.93	0.13	8	314	phospholipid metabolic process	BP	1	INPP5B,FGF2,EFR3B,SOCS2,GPAT3,PRDX6,ITPKB,HDHD5	red	VSMC_M1
GO:0006796	0.93	0.09	71	2150	phosphate-containing compound metabolic process	BP	1	SMAD4,SGK1,DYRK2,CSNK2B,FGFR1OP,EGR1,KCTD20,MAP4K4,NPR2,ICK,EEF1A1,PGM3,INPP5B,PIH1D1,PARD3,ADCK2,FKBP1B,FGF2,TAL1,EFR3B,PAK1,UVRAG,DGAT2,RPS3,CSNK1D,NAXD,HDAC3,SOCS2,CDK17,TNKS,EIF2A,SPRED1,CCNI,GPAT3,AMBRA1,PKIG,ELOVL2,ACOT8,PSPH,NPRL2,PTP4A2,AKAP13,PPP1R8,ENSA,GMPR2,PPP1R11,BCCIP,REXO2,PRDX6,PELI2,ERC1,HSPA2,ITPKB,RARA,HDHD5,CTDNEP1,CDK5RAP3,PARP16,CALM2,MOB3A,ERRFI1,PTPA,FKBP1A,SLC25A1,RACK1,HUS1,PPP1R14A,ACP1,TMSB4X,PTPRN2,FGF10	red	VSMC_M1
GO:0040012	0.93	0.11	23	796	regulation of locomotion	BP	1	SGK1,CSNK2B,FGFR1OP,CTNNA1,MAP4K4,FGF2,PAK1,SP1,CXCL12,TMSB10,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,PFN1,FLRT2,SPARC,RFFL,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0001894	0.93	0.16	4	189	tissue homeostasis	BP	1	IL20RB,P2RX4,PROM1,IGHA2	red	VSMC_M1
GO:0031329	0.93	0.11	20	689	regulation of cellular catabolic process	BP	1	EEF1A1,ALAD,RPS7,UVRAG,CSNK1D,PCID2,FBXW8,NPRL2,EXOSC7,USP5,DCP2,RNF40,CDK5RAP3,RAB39B,USP10,RACK1,ATP6V1G1,TIMP3,ATP5IF1,RCHY1	red	VSMC_M1
GO:0016032	0.93	0.13	8	325	viral process	BP	1	DYNLT1,TAF11,EIF3D,UBP1,UVRAG,SP1,VPS37C,PARP16	red	VSMC_M1
GO:0018209	0.93	0.13	6	267	peptidyl-serine modification	BP	1	SGK1,DYRK2,PAK1,CSNK1D,TNKS,RACK1	red	VSMC_M1
GO:0060485	0.94	0.13	5	235	mesenchyme development	BP	1	SMAD4,MCRIP1,EDNRA,SPRED1,FGF10	red	VSMC_M1
GO:0009100	0.94	0.12	7	299	glycoprotein metabolic process	BP	1	PGM3,ENGASE,HPSE,ACOT8,CHST9,GOLPH3,ALG14	red	VSMC_M1
GO:0009615	0.94	0.13	6	253	response to virus	BP	1	POLR3H,HMGA1,CXCL12,AP1S1,CYP1A1,RNF125	red	VSMC_M1
GO:0003018	0.94	0.14	4	200	vascular process in circulatory system	BP	1	WDR35,ARHGAP35,EDNRA,CTNNBIP1	red	VSMC_M1
GO:0050730	0.94	0.14	4	193	regulation of peptidyl-tyrosine phosphorylation	BP	1	FGFR1OP,ERRFI1,RACK1,FGF10	red	VSMC_M1
GO:0016358	0.94	0.14	4	204	dendrite development	BP	1	DYNLT1,C21orf91,FBXW8,MAP2	red	VSMC_M1
GO:0010506	0.94	0.12	6	268	regulation of autophagy	BP	1	EEF1A1,UVRAG,NPRL2,RAB39B,USP10,ATP6V1G1	red	VSMC_M1
GO:0071496	0.94	0.12	6	267	cellular response to external stimulus	BP	1	KLF10,ARHGAP35,TNKS,NPRL2,WIPI1,ITFG2	red	VSMC_M1

GO:0009150	0.94	0.11	7	286	purine ribonucleotide metabolic process	BP	1	NPR2,DGAT2,ELOVL2,ACOT8,GMPR2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0046395	0.94	0.13	4	182	carboxylic acid catabolic process	BP	1	ARG1,GPT2,GOT2,ACOT8	red	VSMC_M1
GO:0008610	0.94	0.09	15	544	lipid biosynthetic process	BP	1	EGR1,FGF2,EFR3B,DGAT2,SOCS2,ERLIN2,GPAT3,ELOVL2,ACOT8,ITPKB,HDHD5,CTDNEP1,NR1D1,CYP1A1,TMEM189	red	VSMC_M1
GO:0045927	0.94	0.13	4	199	positive regulation of growth	BP	1	FGFR1OP,FGF2,PAK1,CXCL12	red	VSMC_M1
GO:0046700	0.94	0.10	9	357	heterocycle catabolic process	BP	1	ZHX2,PCID2,PPP1R8,EXOSC7,LSM4,CECR2,DCP2,CYP1A1,HMOX2	red	VSMC_M1
GO:0072521	0.95	0.10	8	319	purine-containing compound metabolic process	BP	1	NPR2,DGAT2,ELOVL2,ACOT8,GMPR2,KDM1A,SLC25A1,TMSB4X	red	VSMC_M1
GO:0072659	0.95	0.12	5	239	protein localization to plasma membrane	BP	1	EFR3B,VTI1B,RAB12,GOLPH3,RACK1	red	VSMC_M1
GO:0051347	0.95	0.09	11	441	positive regulation of transferase activity	BP	1	EGR1,PIH1D1,FGF2,TAL1,PAK1,RPS3,TNKS,AMBRA1,AKAP13,PARP16,CALM2	red	VSMC_M1
GO:0032102	0.95	0.11	6	266	negative regulation of response to external stimulus	BP	1	ARG1,FGF2,IL20RB,NR1D1,PRDX2,RNF125	red	VSMC_M1
GO:0009117	0.95	0.09	10	381	nucleotide metabolic process	BP	1	NPR2,DGAT2,NAXD,ELOVL2,ACOT8,GMPR2,REXO2,PARP16,SLC25A1,TMSB4X	red	VSMC_M1
GO:0008284	0.95	0.08	19	681	positive regulation of cell population proliferation	BP	1	SMAD4,ARG1,FGFR1OP,EGR1,COPS9,FGF2,PAK1,RPS3,SP1,CXCL12,RPS6,HPSE,KDM1A,ETV5,ZMIZ1,RARA,MEF2D,STXBP4,FGF10	red	VSMC_M1
GO:0090407	0.95	0.09	12	452	organophosphate biosynthetic process	BP	1	NPR2,FGF2,EFR3B,NAXD,SOCS2,GPAT3,ELOVL2,ITPKB,HDHD5,PARP16,SLC25A1,TMSB4X	red	VSMC_M1
GO:0044270	0.95	0.09	9	361	cellular nitrogen compound catabolic process	BP	1	ZHX2,TST,PCID2,PPP1R8,EXOSC7,LSM4,CECR2,DCP2,HMOX2	red	VSMC_M1
GO:0031589	0.95	0.10	6	294	cell-substrate adhesion	BP	1	TRIOBP,MAP4K4,EDIL3,HPSE,TMEFF2,RHOD	red	VSMC_M1
GO:1990778	0.95	0.10	6	279	protein localization to cell periphery	BP	1	EFR3B,VTI1B,ARL3,RAB12,GOLPH3,RACK1	red	VSMC_M1
GO:0006753	0.95	0.08	10	387	nucleoside phosphate metabolic process	BP	1	NPR2,DGAT2,NAXD,ELOVL2,ACOT8,GMPR2,REXO2,PARP16,SLC25A1,TMSB4X	red	VSMC_M1
GO:0015849	0.95	0.11	4	203	organic acid transport	BP	1	ARG1,GOT2,P2RX4,SLC25A1	red	VSMC_M1
GO:0009101	0.96	0.09	5	245	glycoprotein biosynthetic process	BP	1	PGM3,ACOT8,CHST9,GOLPH3,ALG14	red	VSMC_M1
GO:0040008	0.96	0.07	13	518	regulation of growth	BP	1	SMAD4,SGK1,FGFR1OP,FGF2,PAK1,SOCS2,CXCL12,CDC73,ACTL6A,MAP2,NDUFA13,RACK1,KAZALD1	red	VSMC_M1
GO:0031330	0.96	0.10	4	207	negative regulation of cellular catabolic process	BP	1	ALAD,RPS7,CDK5RAP3,TIMP3	red	VSMC_M1
GO:0009259	0.96	0.08	7	302	ribonucleotide metabolic process	BP	1	NPR2,DGAT2,ELOVL2,ACOT8,GMPR2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0006163	0.96	0.08	7	302	purine nucleotide metabolic process	BP	1	NPR2,DGAT2,ELOVL2,ACOT8,GMPR2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0006631	0.96	0.08	6	271	fatty acid metabolic process	BP	1	DGAT2,ERLIN2,ELOVL2,ACOT8,CYP1A1,TMEM189	red	VSMC_M1
GO:0019439	0.96	0.07	9	375	aromatic compound catabolic process	BP	1	ZHX2,PCID2,PPP1R8,EXOSC7,LSM4,CECR2,DCP2,CYP1A1,HMOX2	red	VSMC_M1
GO:0048638	0.96	0.08	5	257	regulation of developmental growth	BP	1	FGF2,PAK1,SOCS2,CXCL12,MAP2	red	VSMC_M1
GO:0060326	0.96	0.09	4	206	cell chemotaxis	BP	1	FGF2,CXCL12,P2RX4,TMSB4X	red	VSMC_M1
GO:0009410	0.96	0.07	7	314	response to xenobiotic stimulus	BP	1	ARG1,AHR,ALAD,RECQL5,TGIF1,CYP1A1,GSTM3	red	VSMC_M1
GO:0060249	0.96	0.09	4	218	anatomical structure homeostasis	BP	1	IL20RB,P2RX4,PROM1,IGHA2	red	VSMC_M1
GO:1901214	0.96	0.08	5	251	regulation of neuron death	BP	1	EGR1,UBE2M,RRAS2,ELK1,RACK1	red	VSMC_M1
GO:0007610	0.97	0.07	9	406	behavior	BP	1	SGK1,EGR1,TAL1,PCDH17,CXCL12,P2RX4,EGR2,KAT2A,NR1D1	red	VSMC_M1
GO:0043410	0.97	0.07	8	356	positive regulation of MAPK cascade	BP	1	FGF2,PAK1,RPS3,TNFRSF19,AKAP13,PELI2,PRDX2,FGF10	red	VSMC_M1
GO:0030155	0.97	0.06	13	541	regulation of cell adhesion	BP	1	ARG1,TRIOBP,MAP4K4,RPS3,CXCL12,IL20RB,EDIL3,RHOD,ARHGDIB,ZMIZ1,ITPKB,RARA,PRDX2	red	VSMC_M1
GO:0070997	0.97	0.07	6	288	neuron death	BP	1	EGR1,UBE2M,RRAS2,ELK1,TBC1D24,RACK1	red	VSMC_M1
GO:0045087	0.97	0.06	11	459	innate immune response	BP	1	ARG1,POLR3H,PAK1,CEBPG,CD58,IL1RAP,TRIM4,STXBP4,WFDC3,IGHA2,LY96	red	VSMC_M1
GO:0019693	0.97	0.06	7	312	ribose phosphate metabolic process	BP	1	NPR2,DGAT2,ELOVL2,ACOT8,GMPR2,SLC25A1,TMSB4X	red	VSMC_M1
GO:0009894	0.97	0.05	22	806	regulation of catabolic process	BP	1	EEF1A1,ALAD,RPS7,UVRAG,CSNK1D,PCID2,FBXW8,NPRL2,CRTC3,EXOSC7,NDUFA13,USP5,DCP2,RNF40,CDK5RAP3,RAB39B,USP10,RACK1,ATP6V1G1,TIMP3,ATP5IF1,RCHY1	red	VSMC_M1
GO:0009895	0.97	0.07	5	254	negative regulation of catabolic process	BP	1	ALAD,RPS7,CRTC3,CDK5RAP3,TIMP3	red	VSMC_M1
GO:0060627	0.97	0.06	9	403	regulation of vesicle-mediated transport	BP	1	STAM,ARFIP1,RAB9A,FAM45A,PRRT2,IL13RA2,RAB12,MYO18A,RACK1	red	VSMC_M1
GO:0050804	0.98	0.05	6	317	modulation of chemical synaptic transmission	BP	1	PCDH17,EGR2,KAT2A,ERC1,RARA,PRRT2	red	VSMC_M1
GO:1901361	0.98	0.05	9	395	organic cyclic compound catabolic process	BP	1	ZHX2,PCID2,PPP1R8,EXOSC7,LSM4,CECR2,DCP2,CYP1A1,HMOX2	red	VSMC_M1
GO:0045765	0.98	0.06	4	229	regulation of angiogenesis	BP	1	FGF2,SP1,SPRED1,SPARC	red	VSMC_M1
GO:0099177	0.98	0.05	6	318	regulation of trans-synaptic signaling	BP	1	PCDH17,EGR2,KAT2A,ERC1,RARA,PRRT2	red	VSMC_M1
GO:1901342	0.98	0.06	4	232	regulation of vasculature development	BP	1	FGF2,SP1,SPRED1,SPARC	red	VSMC_M1
GO:0034655	0.98	0.05	7	335	nucleobase-containing compound catabolic process	BP	1	ZHX2,PCID2,PPP1R8,EXOSC7,LSM4,CECR2,DCP2	red	VSMC_M1
GO:0007155	0.98	0.03	27	1044	cell adhesion	BP	1	ARG1,CTNNA1,TRIOBP,MAP4K4,PARD3,SDK2,PCDH17,RPS3,CXCL12,IL20RB,EDIL3,HPSE,CD58,TMEFF2,SSPN,RHOD,ARHGDIB,LPP,IL1RAP,ZMIZ1,ITPKB,RARA,PRDX2,FLRT2,GOLPH3,ITGAE,GNAS	red	VSMC_M1
GO:0022610	0.98	0.03	27	1050	biological adhesion	BP	1	ARG1,CTNNA1,TRIOBP,MAP4K4,PARD3,SDK2,PCDH17,RPS3,CXCL12,IL20RB,EDIL3,HPSE,CD58,TMEFF2,SSPN,RHOD,ARHGDIB,LPP,IL1RAP,ZMIZ1,ITPKB,RARA,PRDX2,FLRT2,GOLPH3,ITGAE,GNAS	red	VSMC_M1
GO:0030198	0.98	0.05	4	250	extracellular matrix organization	BP	1	TLL1,MMP16,FLRT2,KAZALD1	red	VSMC_M1
GO:0006935	0.98	0.04	9	426	chemotaxis	BP	1	SMAD4,FGF2,ARHGAP35,CXCL12,P2RX4,EGR2,FLRT2,TMSB4X,FGF10	red	VSMC_M1
GO:0043062	0.98	0.05	4	251	extracellular structure organization	BP	1	TLL1,MMP16,FLRT2,KAZALD1	red	VSMC_M1
GO:0045229	0.98	0.05	4	251	external encapsulating structure organization	BP	1	TLL1,MMP16,FLRT2,KAZALD1	red	VSMC_M1
GO:0042330	0.98	0.04	9	427	taxis	BP	1	SMAD4,FGF2,ARHGAP35,CXCL12,P2RX4,EGR2,FLRT2,TMSB4X,FGF10	red	VSMC_M1
GO:0018108	0.98	0.04	5	287	peptidyl-tyrosine phosphorylation	BP	1	DYRK2,FGFR1OP,ERRFI1,RACK1,FGF10	red	VSMC_M1
GO:0006820	0.98	0.04	6	319	anion transport	BP	1	ARG1,VDAC3,SLC12A6,P2RX4,CLCN5,SLC25A1	red	VSMC_M1
GO:0018212	0.98	0.04	5	290	peptidyl-tyrosine modification	BP	1	DYRK2,FGFR1OP,ERRFI1,RACK1,FGF10	red	VSMC_M1
GO:0050727	0.99	0.04	4	239	regulation of inflammatory response	BP	1	IL1RL1,IL20RB,NR1D1,TMSB4X	red	VSMC_M1
GO:0019637	0.99	0.02	19	743	organophosphate metabolic process	BP	1	NPR2,PGM3,INPP5B,FGF2,EFR3B,DGAT2,NAXD,SOCS2,GPAT3,ELOVL2,ACOT8,GMPR2,REXO2,PRDX6,ITPKB,HDHD5,PARP16,SLC25A1,TMSB4X	red	VSMC_M1

GO:0009605	0.99	0.02	52	1770	response to external stimulus	BP	1	SMAD4,ARG1,KLF10,POLR3H,HMGA1,IL1RL1,XPA,ALAD,WDR35,FKBP1B,FGF2,ARHGAP35,PAK1,IL18BP,TNKS,CXCL12,CEBPG,IL20RB,CTR9,P2RX4,EIF2A,HPSE,HLCS,CD58,PSPH,CDC73,NPRL2,WIPI1,ENSA,PPP1R11,RBM4,EGR2,AP1S1,IL1RAP,TRIM4,ITFG2,KAT2A,RARA,NR1D1,PRDX2,FLRT2,STXBP4,SPARC,CYP1A1,OMA1,COX4I1,TMSB4X,WFDC3,RNF125,IGHA2,LY96,FGF10	red	VSMC_M1
GO:0016477	0.99	0.02	29	1120	cell migration	BP	1	SGK1,CSNK2B,FGFR1OP,CTNNA1,MAP4K4,FGF2,ARHGAP35,PAK1,SP1,CXCL12,TMSB10,RHOF,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,FBXO45,ZMIZ1,PFN1,FLRT2,SPARC,RFFL,MYO18A,GOLPH3,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0098542	0.99	0.02	13	574	defense response to other organism	BP	1	ARG1,POLR3H,PAK1,CEBPG,CD58,PPP1R11,IL1RAP,TRIM4,STXBP4,WFDC3,RNF125,IGHA2,LY96	red	VSMC_M1
GO:0007167	0.99	0.02	17	752	enzyme linked receptor protein signaling pathway	BP	1	SMAD4,CSNK2B,EGR1,NPR2,FGF2,TAL1,PAK1,SOCS2,CD8B,SPRED1,ZMIZ1,FLRT2,STXBP4,ERRFI1,FKBP1A,NREP,FGF10	red	VSMC_M1
GO:0032101	0.99	0.02	15	646	regulation of response to external stimulus	BP	1	ARG1,IL1RL1,FKBP1B,FGF2,PAK1,CXCL12,IL20RB,P2RX4,HPSE,NR1D1,PRDX2,TMSB4X,RNF125,LY96,FGF10	red	VSMC_M1
GO:0032787	0.99	0.02	8	404	monocarboxylic acid metabolic process	BP	1	DGAT2,ERLIN2,HLCS,ELOVL2,ACOT8,NR1D1,CYP1A1,TMEM189	red	VSMC_M1
GO:0022603	0.99	0.02	17	761	regulation of anatomical structure morphogenesis	BP	1	TRIOBP,FGF2,ARHGAP35,FAM171A1,PAK1,SP1,CXCL12,RHOF,SPRED1,FBXW8,CFAP410,RHOD,MAP2,SPARC,OMA1,RACK1,FGF10	red	VSMC_M1
GO:0048870	0.99	0.01	32	1234	cell motility	BP	1	SGK1,CSNK2B,FGFR1OP,CTNNA1,MAP4K4,INPP5B,FGF2,ARHGAP35,PAK1,SP1,CXCL12,TMSB10,RHOF,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,FBXO45,ZMIZ1,PFN1,FLRT2,SPARC,RFFL,MYO18A,GOLPH3,ELMO3,IER2,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0051674	0.99	0.01	32	1234	localization of cell	BP	1	SGK1,CSNK2B,FGFR1OP,CTNNA1,MAP4K4,INPP5B,FGF2,ARHGAP35,PAK1,SP1,CXCL12,TMSB10,RHOF,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,FBXO45,ZMIZ1,PFN1,FLRT2,SPARC,RFFL,MYO18A,GOLPH3,ELMO3,IER2,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:1901137	0.99	0.01	10	494	carbohydrate derivative biosynthetic process	BP	1	NPR2,PGM3,GMDS,ELOVL2,ACOT8,CHST9,GOLPH3,ALG14,SLC25A1,TMSB4X	red	VSMC_M1
GO:0007169	1.00	0.01	9	499	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	FGF2,TAL1,PAK1,SOCS2,CD8B,FLRT2,STXBP4,ERRFI1,FGF10	red	VSMC_M1
GO:0031347	1.00	0.01	7	397	regulation of defense response	BP	1	ARG1,IL1RL1,PAK1,IL20RB,NR1D1,TMSB4X,RNF125	red	VSMC_M1
GO:0040011	1.00	0.01	34	1349	locomotion	BP	1	SMAD4,SGK1,CSNK2B,FGFR1OP,CTNNA1,MAP4K4,INPP5B,FGF2,ARHGAP35,PAK1,SP1,CXCL12,TMSB10,RHOF,P2RX4,RRAS2,SPRED1,TMEFF2,RHOD,ARHGDIB,FBXO45,EGR2,ZMIZ1,PFN1,FLRT2,SPARC,RFFL,MYO18A,GOLPH3,ELMO3,IER2,RACK1,TMSB4X,FGF10	red	VSMC_M1
GO:0006629	1.00	0.01	24	982	lipid metabolic process	BP	1	EGR1,INPP5B,FGF2,EFR3B,DGAT2,SOCS2,ERLIN2,LTA4H,GPAT3,AMBRA1,ELOVL2,ACOT8,CRTC3,PRDX6,ITPKB,HDHD5,CTDNEP1,NR1D1,CYP1A1,OMA1,ALG14,TMEM189,CPNE1,PTPRN2	red	VSMC_M1
GO:0006954	1.00	0.01	9	497	inflammatory response	BP	1	IL1RL1,IL20RB,CUEDC2,IL1RAP,NR1D1,PRDX2,CTNNBIP1,TMSB4X,LY96	red	VSMC_M1
GO:0010876	1.00	0.01	4	311	lipid localization	BP	1	DGAT2,GOT2,P2RX4,GRAMD1C	red	VSMC_M1
GO:0044255	1.00	0.004	16	743	cellular lipid metabolic process	BP	1	INPP5B,FGF2,EFR3B,DGAT2,SOCS2,ERLIN2,GPAT3,ELOVL2,ACOT8,PRDX6,ITPKB,HDHD5,CTDNEP1,CYP1A1,ALG14,TMEM189	red	VSMC_M1
GO:0006952	1.00	0.002	21	949	defense response	BP	1	ARG1,POLR3H,IL1RL1,PAK1,CXCL12,CEBPG,IL20RB,CD58,CUEDC2,PPP1R11,IL1RAP,TRIM4,NR1D1,PRDX2,STXBP4,CTNNBIP1,TMSB4X,WFDC3,RNF125,IGHA2,LY96	red	VSMC_M1
GO:1901135	1.00	0.001	16	791	carbohydrate derivative metabolic process	BP	1	NPR2,PGM3,FGF2,DGAT2,ENGASE,HPSE,GPAT3,GMDS,ELOVL2,ACOT8,GMPR2,CHST9,GOLPH3,ALG14,SLC25A1,TMSB4X	red	VSMC_M1
GO:0006897	1.00	0.001	5	444	endocytosis	BP	1	CLTA,AP1S1,CLCN5,MYO18A,IGHA2	red	VSMC_M1